Software Manual

Biomek 4000

Laboratory Automation Workstation

B08852AA
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Beckman Coulter, Inc.
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BECKMAN COULTER

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Revision History

Initial Issue, 10/2012
Software Version 4.0

This document applies to the latest software listed and higher versions. When a subsequent software version affects the information in this document, a new issue will be released to the Beckman Coulter website. For labeling updates, go to www.beckmancoulter.com and download the latest version of the manual or system help for your instrument.

Safety Notice

Overview

Read all product manuals and consult with Beckman Coulter-trained personnel before attempting to operate the instrument. Do not attempt to perform any procedure before carefully reading all instructions. Always follow product labeling and manufacturer's recommendations. If in doubt as to how to proceed in any situation, contact your Beckman Coulter Representative.

Beckman Coulter, Inc. urges its customers and employees to comply with all national health and safety standards such as the use of barrier protection. This may include, but is not limited to, protective eyewear, gloves, and suitable laboratory attire when operating or maintaining this or any other automated laboratory instrumentation.

⚠ WARNING

If the equipment is used in a manner not specified by Beckman Coulter, Inc., the protection provided by the equipment may be impaired.

Alerts for Warning, Caution, Important, and Note

All Warnings and Cautions in this document include an exclamation point, framed within a triangle.

The exclamation point symbol is an international symbol which serves as a reminder that all safety instructions should be read and understood before installation, use, maintenance, and servicing are attempted.

⚠ WARNING

WARNING indicates a potentially hazardous situation which, if not avoided, could result in death or serious injury.

⚠ CAUTION

CAUTION indicates a potentially hazardous situation, which, if not avoided, may result in minor or moderate injury. It may also be used to alert against unsafe practices.

IMPORTANT IMPORTANT is used for comments that add value to the step or procedure being performed. Following the advice in the Important adds benefit to the performance of a piece of equipment or to a process.

NOTE NOTE is used to call attention to notable information that should be followed during installation, use, or servicing of this equipment.

Instrument Safety Precautions

⚠ WARNING

Risk of operator injury if:

- **All doors, covers and panels are not closed and secured in place prior to and during instrument operation.**
- **The integrity of safety interlocks and sensors is compromised.**
- **You contact moving parts.**
- **You mishandle broken parts.**
- **Doors, covers and panels are not opened, closed, removed and/or replaced with care.**
- **Improper tools are used for troubleshooting.**

To avoid injury:

- **Keep doors, covers and panels closed and secured in place while the instrument is in use.**
- **Take full advantage of the safety features of the instrument. Do not defeat safety interlocks and sensors.**
- **Acknowledge and act upon instrument alarms and error messages.**
- **Keep away from moving parts.**
- **Report any broken parts to your Beckman Coulter Representative.**
- **Use the proper tools when troubleshooting.**

⚠ CAUTION

System integrity could be compromised and operational failures could occur if:

- **This equipment is used in a manner other than specified. Operate the instrument as instructed in the Product Manuals.**
- **You introduce software that is not authorized by Beckman Coulter into your computer. Only operate your system's computer with software authorized by Beckman Coulter.**
- **You install software that is not an original copyrighted version. Only use software that is an original copyrighted version to prevent virus contamination.**

⚠ CAUTION

If you purchased this product from anyone other than Beckman Coulter or an authorized Beckman Coulter distributor, and, if it is not presently under a Beckman Coulter Service Maintenance Agreement, Beckman Coulter cannot guarantee that the product is fitted with the most current mandatory engineering revisions or that you will receive the most current information bulletins concerning the product. If you purchased this product from a third party and would like further information concerning this topic, contact your Beckman Coulter Representative.

Electrical Safety

To prevent electrically related injuries and property damage, properly inspect all electrical equipment prior to use and immediately report any electrical deficiencies. Contact a Beckman Coulter Representative for any servicing of equipment requiring the removal of covers or panels.

High Voltage



This symbol indicates the potential of an electrical shock hazard existing from a high-voltage source and that all safety instructions should be read and understood before proceeding with the installation, maintenance, and servicing of all modules.

Do not remove system covers. To avoid electrical shock, use supplied power cords only and connect to properly grounded (three-holed) outlets.

Laser Light



This symbol indicates that a potential hazard to personal safety exists from a laser source. When this symbol is displayed in this manual, pay special attention to the specific safety information associated with the symbol.

Laser Specifications

- **Laser Type:** Class II Laser Diode
- **Maximum Output:** 11 mW
- **Wavelength:** 670 nm

Disposal of Electronic Equipment

It is important to understand and follow all laws regarding the safe and proper disposal of electrical instrumentation.



The symbol of a crossed-out wheeled bin on the product is required in accordance with the Waste Electrical and Electronic Equipment (WEEE) Directive of the European Union. The presence of this marking on the product indicates:

- That the device was put on the European Market after August 13, 2005 and
- That the device is not to be disposed via the municipal waste collection system of any member state of the European Union.

For products under the requirement of WEEE directive, please contact your dealer or local Beckman Coulter office for the proper decontamination information and take back program which will facilitate the proper collection, treatment, recovery, recycling, and safe disposal of device.

Chemical and Biological Safety



If a hazardous substance such as blood is spilled onto the instrument, ALPs, or accessories, clean up the spill by using a 10% bleach solution, or use your laboratory decontamination solution. Then follow your laboratory procedure for disposal of hazardous materials. If the instrument, ALPs, or accessories need to be decontaminated, contact your Beckman Coulter Representative.

⚠ WARNING

Risk of chemical injury from bleach. To avoid contact with the bleach, use barrier protection, including protective eyewear, gloves, and suitable laboratory attire. Refer to the Safety Data Sheet for details about chemical exposure before using the chemical.

⚠ WARNING

Before running with chemistry or any biological samples, new labware types will require testing to determine if labware offsets are necessary to move to or from the Peltier ALP, or to access the labware during pipetting operations while on the Peltier ALP. If you do not do the required testing, the labware could crash and the contents could spill if the offset is incorrect.

Normal operation of the instrument may involve the use of materials that are toxic, flammable, or otherwise biologically harmful. When using such materials, observe the following precautions:

- **Handle infectious samples according to good laboratory procedures and methods to prevent the spread of disease.**
- **Observe all cautionary information printed on the original solutions' containers prior to their use.**
- **Dispose of all waste solutions according to your facility's waste disposal procedures.**
- **Operate the instrument in accordance with the instructions outlined in this manual and take all the necessary precautions when using pathological, toxic, or radioactive materials.**
- **Splashing of liquids may occur; therefore, take appropriate safety precautions, such as using safety glasses and wearing protective clothing, when working with potentially hazardous liquids.**
- **Use an appropriately-contained environment when using hazardous materials.**
- **Observe the appropriate cautionary procedures as defined by your safety officer when using flammable solvents in or near a powered-up instrument.**
- **Observe the appropriate cautionary procedures as defined by your safety officer when using toxic, pathological, or radioactive materials.**

NOTE Observe all warnings and cautions listed for any external devices attached or used during operation of the instrument. Refer to applicable external device user's manuals for operating procedures of that device.

NOTE For Safety Data Sheets (SDS/MSDS) information, go to the Beckman Coulter website at **www.beckmancoulter.com**.

Moving Parts

⚠ WARNING

Risk of personal injury. To avoid injury due to moving parts, observe the following:

- **Never attempt to exchange labware, reagents, or tools while the instrument is operating.**
- **Never attempt to physically restrict any of the moving components of the instrument.**
- **Keep the instrument work area clear to prevent obstruction of the movement.**

Cleaning

Observe the cleaning procedures outlined in this user's manual for the instrument. Prior to cleaning equipment that has been exposed to hazardous material:

- Contact the appropriate Chemical and Biological Safety personnel.
- Review the Chemical and Biological Safety information in the user's manual.

Maintenance

Perform only the maintenance described in this manual. Maintenance other than that specified in this manual should be performed only by service engineers.

IMPORTANT It is your responsibility to decontaminate components of the instrument before requesting service by a Beckman Coulter Representative or returning parts to Beckman Coulter for repair. Beckman Coulter will NOT accept any items which have not been decontaminated where it is appropriate to do so. If any parts are returned, they must be enclosed in a sealed plastic bag stating that the contents are safe to handle and are not contaminated.

RoHS Notice

These labels and materials declaration table (the Table of Hazardous Substance's Name and Concentration) are to meet People's Republic of China Electronic Industry Standard SJ/T11364-2006 "Marking for Control of Pollution Caused by Electronic Information Products" requirements.

China RoHS Caution Label

This logo indicates that this electronic information product contains certain toxic or hazardous substances or elements, and can be used safely during its environmental protection use period. The number in the middle of the logo indicates the environmental protection use period for the product. The outer circle indicates that the product can be recycled. The logo also signifies that the product should be recycled immediately after its environmental protection use period has expired. The date on the label indicates the date of manufacture.



China RoHS Environmental Label

This logo indicates that the product does not contain any toxic or hazardous substances or elements. The "e" stands for electrical, electronic and environmental electronic information products. This logo indicates that this electronic information product does not contain any toxic or hazardous substances or elements, and is green and environmental. The outer circle indicates that the product can be recycled. The logo also signifies that the product can be recycled after being discarded, and should not be casually discarded.



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Introduction

About Biomek Software, Version 4.0

Biomek Software is used to control the Beckman Coulter Biomek 4000 Laboratory Automation Workstation. Biomek Software consists of a method editor and other tools and editors for configuring the system to perform desired operations.

Configuring the instrument is necessary to achieve the desired results from automated methods. The software must have information on the deck layout, labware and tips utilized in the method, liquid types to pipette, and how to perform pipetting operations.

Biomek Software comes with a default set of parameters suitable for many applications; many opportunities are presented for customization to achieve a wide variety of desired results.

Information about the liquid-handling system is stored in two separate files. The instrument file includes information specific to an instrument, including additional components installed, deck layout, and framing information. A project file stores information about labware, tip, and liquid types, and pipetting techniques and templates.

Effectively using Biomek Software includes using the method editor for method building and the various tools and editors to appropriately configure the instrument and project files for the desired task or application.

Instrument Files

An instrument file contains all pertinent information relating to the physical hardware. This includes:

- instrument type and configuration.
- devices installed on the instrument deck.
- external devices integrated with the instrument.
- deck layout and framing information.
- tools.

The instrument configuration must accurately represent the instrument hardware to prevent collisions between the instrument and any on-deck components. All instrument configuration is done using **Hardware Setup**, **Device Editor**, and the **Deck Editor**.

Hardware Setup is used to configure the tools, certain devices, and accessories available to the instrument. The Device Editor is used to configure devices, such as the Static Peltier and the Shaking Peltier ALPs. The **Deck Editor** is used to configure the precise location of all labware positions on the deck and associate any devices or accessories to those positions. The pod must then be precisely aligned to each deck position by framing the deck.

Refer to CHAPTER 3, *Using Instrument Files and Settings*, for more information on instrument files.

Project Files

A project file stores custom information about liquid types, labware and tip types, and pipetting techniques and templates that are used to configure the actions of the instrument in a database. Project files store a history of all changes, additions, and deletions from the project file.

Project items are configured using the following editors:

- **Labware Type Editor**
- **Tip Type Editor**
- **Liquid Type Editor**
- **Technique Editor**
- **Pipetting Template Editor**
- **Well Patterns Editor**

Project items may be checked in, which creates a revision of the project item. Checked in revisions can always be recovered and reused, ensuring that checked in or validated methods are reproducible even if project items are subsequently modified or deleted. Refer to CHAPTER 6, *Understanding and Using Project Files*, for more information on project files.

Methods

Methods contain the precise information for performing a specific sequence of actions to complete a task, and utilize information from the project and instrument files to configure and customize those actions.

The method editor is used to create methods that control the liquid-handling system. Methods comprise a series of steps that together perform various operations, such as liquid transfers or labware moves using the gripper. Additional operations, such as microplate shaking, can be performed in a method through active ALPs or integrated devices that are controlled through the instrument via serial communications. Refer to CHAPTER 12, *Creating and Using Methods*, for more information on building and working with methods.

NOTE ALPs (Automated Labware Positioners) are removable and interchangeable platform structures installed on the deck to allow automated assays to be performed.

About This Manual

The information in this manual on Biomek Software, version 4.0, refers to the Biomek 4000 instrument only. This manual should be used in conjunction with the other Biomek 4000 manuals including the following:

- *Biomek 4000 Hardware Manual*
- *Biomek 4000 ALPs and Accessories Manual*
- *Biomek 4000 Preinstallation Manual*
- *Biomek 4000 Customer Start-Up Guide*
- *Biomek 4000 Software Tutorial*
- *Biomek 4000 Migration Guide For Biomek 3000 Methods*
- *Shaking Peltier ALP Instruction Manual For Biomek 4000 Instruments*
- *Static Peltier ALP Instruction Manual For Biomek 4000 Instruments*

A glossary containing terms and definitions relating to the Biomek 4000 instrument, ALPs, and Biomek Software is located in the *Glossary*.

CHAPTER 1

Using Accounts and Permissions

Overview

Beckman Coulter Accounts & Permissions is an integrated set of features built into Beckman Coulter software that assists users in complying with electronic signature requirements (such as 21 CFR Part 11) for closed systems. With Biomek Software, support is extended only for the instrument; devices integrated with the instrument are not supported unless specified in separate documentation.

Accounts & Permissions provides support only for closed systems; networked systems are not supported. In a location where several Beckman Coulter systems are present, Accounts & Permissions must be installed and enabled separately for each system where compliance is desired. Users require a separate account for each system they need to access.

For each Beckman Coulter system, a single administrator sets up the level of support provided by Accounts & Permissions, creates, manages, and sets permissions for user accounts, and configures system parameters relating to Accounts & Permissions.

This chapter covers:

- *Installing and Setting the Level of Support for Accounts and Permissions*
- *Administering User Accounts and Permissions*
- *Restoring the Administrator Password*
- *Viewing the Audit Log*
- *Using Biomek Software With Accounts & Permissions Enabled*

Installing and Setting the Level of Support for Accounts and Permissions

Some Accounts & Permissions functionality is built into Biomek Software; however, additional options that allow Accounts & Permissions to be enabled and configured are installed separately. This section covers:

- *Installing Accounts and Permissions*
- *Setting the Level of Support for Accounts and Permissions*

Installing Accounts and Permissions

Beckman Coulter Accounts & Permissions support may be installed before or after Biomek Software is installed on the system.

NOTE Site processes should be in place to ensure that access to the Accounts & Permissions installation CD is controlled.

To install support for Accounts & Permissions:

1. Close all open applications on the computer.
2. Place the Beckman Coulter Accounts & Permissions Installer CD in the drive, and browse to the contents of the CD.
3. Double click **Beckman Coulter Accounts & Permissions.exe**. **Beckman Coulter Accounts & Permissions Setup** appears.

   NOTE If Accounts & Permissions is already installed, options to repair, modify, and remove the application appear.
4. Follow the steps in the setup wizard.
5. Restart the computer.
6. After the computer is restarted, set the level of Accounts & Permissions support desired (refer to *Setting the Level of Support for Accounts and Permissions*).

Setting the Level of Support for Accounts and Permissions

The administrator may change the level of support for Accounts & Permissions at any time.

NOTE The site must have processes in place to govern all system administration activities, as specified in the 21 CFR Part 11 regulation.

To set the level of support for Accounts & Permissions:

1. Log off and close Biomek Software and any other Beckman Coulter software applications using Accounts & Permissions, if necessary.

2 Place the Beckman Coulter Accounts & Permissions Installer CD in the drive, and browse to the contents of the CD.

3 Double click **Beckman Coulter Accounts & Permissions - Support Options.exe.**

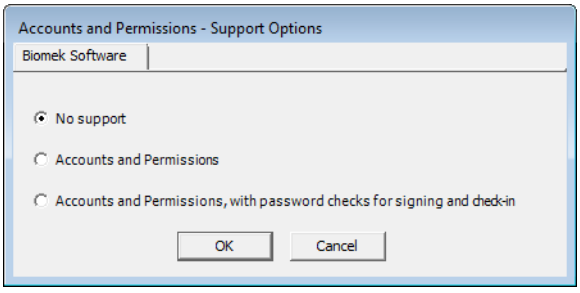
4 In **Administrator Login**, enter the default Administrator password, which is "**password.**"

IMPORTANT Passwords are case-sensitive.

5 When prompted, enter a new password into the required fields and choose **OK**. **Support Options** appears (Figure 1.1). A series of tabs displays all installed software applications compatible with Beckman Coulter Accounts & Permissions.

NOTE If the **Administration Password** is lost, forgotten, or not known, follow the steps in *Restoring the Administrator Password*.

Figure 1.1 Support Options



6 Choose the **Biomek Software** tab, if multiple Beckman Coulter software applications supporting Accounts & Permissions are installed on the system.

7 Select the level of support. When several Beckman Coulter software applications are installed on the same system, the level of support selected must be the same for each application.

- **No support** — User accounts are not required to access Biomek Software. Users have access to all software operations and functionality.

  NOTE System activity, such as creating, editing, or running methods, is still logged in the audit trail and can be viewed in the **Audit Log** (refer to *Viewing the Audit Log*).

- **Accounts and Permissions** — Enables the use of user accounts and permissions for Biomek Software. Users must log in to use the software and may access only features and operations for which they have permission. Operations such as checking in, validating, or signing methods do not require password confirmation.

  NOTE Accounts and Permissions without password checks may not provide adequate support for 21 CFR Part 11 compliance. Each site must evaluate the level of support required for a given system.

- **Accounts and Permissions, with password checks for signing and saving** — Enables the use of user accounts and permissions with electronic signatures for Biomek Software. Users must log in to use the software and may access only features and operations for which they have permission. Support for 21 CFR Part 11 is provided by requiring password checks for operations such as saving, validating, and signing methods.

  NOTE Compliance with 21 CFR Part 11 requires implementing site processes beyond the control of the software.

8 Choose **OK** to activate the level of support chosen and close **Support Options**.

OR

Choose **Cancel** to close **Support Options** without changing the level of support.

Administering User Accounts and Permissions

System administration tasks for Beckman Coulter Accounts & Permissions are performed in Account Management, a separate application from Biomek Software. The system administrator sets up and configures user accounts, passwords, roles, and permissions, and configures system settings such as automatic password expiration and system logout time.

A single system administrator password is used on a system. System administration tasks may be performed only on the computer where Account Management is installed; access to Account Management over a network is not supported.

NOTE The administrator is not automatically given a user account on the system. If the administrator requires an account, one must be created in Account Management.

NOTE The 21 CFR Part 11 regulation contains additional requirements for account management beyond the control of the software.

This section covers opening Account Management and provides an overview of permissions available for Biomek Software users (refer to *Biomek Software Permissions*). Refer to the Account Management online help for detailed information about administering user accounts, roles, and permissions.

To open Account Management:

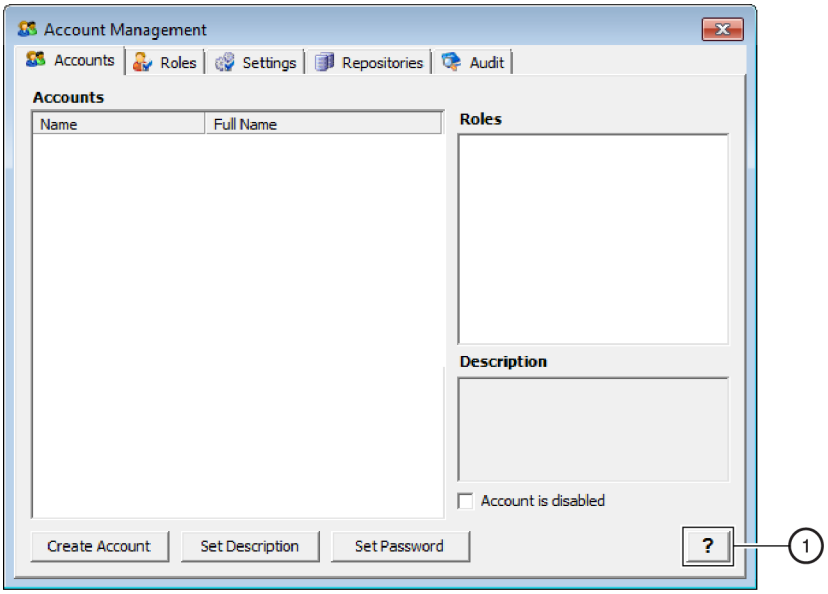
1 Log off and close Biomek Software and any other Beckman Coulter software applications using Accounts & Permissions.

2 In the Windows **Start** menu, select **All Programs**, and then select **Administrative Tools**.

3 In **Administrative Tools**, double click **Account Management**.

4 In the **Administrator Login** dialog box, enter the administrator password and choose **OK**. **Account Management** displays (Figure 1.2).

Figure 1.2 Account Management



1. **Choose ? or press F1 to access online help**.

5 Create and configure accounts as necessary. Instructions for configuring accounts are located in the Account Management online help (Figure 1.2). Specifically, topics include the following:

- Configuring User Accounts
- Configuring Roles
- Configuring System Settings and Project Access
- Working With Repositories
- Viewing and Exporting the Audit Log of System Activity

Biomek Software Permissions

The administrator assigns permissions for each role in Account Management. Table 1.1 describes the permissions available for Biomek Software user roles. Multiple permissions can be assigned to each role, and multiple roles can be assigned to each user account. Refer to the Account Management online help (Figure 1.2) for detailed information on creating roles, editing roles, assigning roles to accounts, and assigning permissions.

Table 1.1 Biomek Software Permissions

Permission	Description
Change the Biomek instrument setup	Allows the user to configure instrument settings in **Hardware Setup** (CHAPTER 4, *Configuring Hardware Setup*), the **Deck Editor** (CHAPTER 5, *Preparing and Managing the Deck*), the **Device Editor** (CHAPTER 21, *Using the Devices Step Palette*), and the **Import/Export Utility** (CHAPTER 3, *Sharing Instrument Settings Using the Import/Export Utility*).
Change the Biomek Software preferences	Allows the user to modify **Preferences** and **Log Configurations** (CHAPTER 28, *Changing Window Appearance* and CHAPTER 25, *Generating and Using Log Data*).
Control the Biomek instrument via manual control	Allows the user to control instrument actions outside a method using **Manual Control** (CHAPTER 26, *Using Manual Control*).
Create, modify, and run Biomek methods	Allows the user to open and run methods that have not been validated, develop new methods and edit existing methods CHAPTER 12, *Creating and Using Methods*.
Create, modify, or delete projects	Allows the user to create and edit project files CHAPTER 6, *Understanding and Using Project Files*.
Run validated Biomek methods	Allows the user to open and run validated methods. A validated method is a revision of a method that cannot be modified or associated with a different instrument.
Validate Biomek methods	Allows the user to validate a revision of a method. Once validated, that revision of the method cannot be modified or associated with a different instrument.

Restoring the Administrator Password

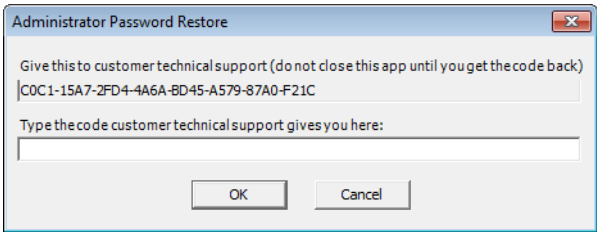
Only one administrator account exists on a system with Accounts & Permissions installed. If the administrator password is lost or forgotten, Beckman Coulter Customer Technical Support must be contacted to restore access to the Account Management application.

To restore the administrator password:

1 Place the Beckman Coulter Accounts & Permissions Installer CD in the drive, and browse to the contents of the CD.

2 Double click **Beckman Coulter Accounts & Permissions Admin Password Restore.exe**. **Password Restore** appears (Figure 1.3).

Figure 1.3 Password Restore



3 Contact Beckman Coulter Customer Technical Support and provide the code displayed in the upper field of **Password Restore**.

NOTE Leave **Password Restore** open until Beckman Coulter Customer Technical Support supplies a new code. The new code is based on the code displayed in the upper field, which changes each time **Password Restore** is opened.

4 In the lower field of **Password Restore**, enter the new code provided by Beckman Coulter Customer Technical Support.

5 Choose **OK** to close **Password Restore** and accept the new code.

OR

Choose **Cancel** to close **Password Restore** without accepting the new code.

6 Follow any additional instructions provided by Beckman Coulter Customer Technical Support.

Viewing the Audit Log

Audit Log displays the audit trail for all user activity in software applications that support Beckman Coulter Accounts & Permissions. System activity is logged, even when Accounts & Permissions is set to **No Support** (refer to CHAPTER 1, *Setting the Level of Support for Accounts and Permissions*).

NOTE Administrator activity other than changing the level of support for Accounts & Permissions is not available in the **Audit Log**. However, all administrator activity is logged and may be viewed in Account Management.

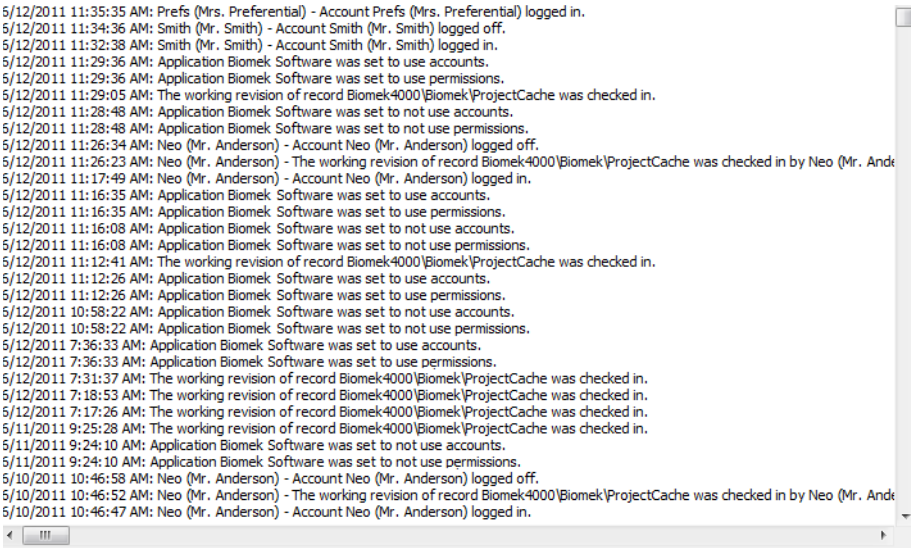
To view the **Audit Log**:

1 In the Windows **Start** menu, choose **Control Panel. Control Panel** appears.

2 In **Control Panel**, select **System and Security**, and then select **Administrative Tools. Administrative Tools** appears.

3 In **Administrative Tools**, double click **Audit Log.** The **Audit Log** appears (Figure 1.4).

Figure 1.4 Accounts & Permissions Audit Log



4 Choose **Export** to export the entire audit log to a text file, if desired. The exported file may be opened, read, and printed in any application that supports text files.

NOTE When the **Audit Log** is open while Biomek Software is running, system activity is logged, but not refreshed automatically in the **Audit Log**. Choose **Refresh** to view system activity logged since the **Audit Log** was opened or the last time displayed data was refreshed.

Using Biomek Software With Accounts & Permissions Enabled

When Beckman Coulter Accounts & Permissions is enabled, all users must log on to use Biomek Software. Only one user may be logged on at a time. Users are permitted to perform only the operations for which the administrator has assigned them permission.

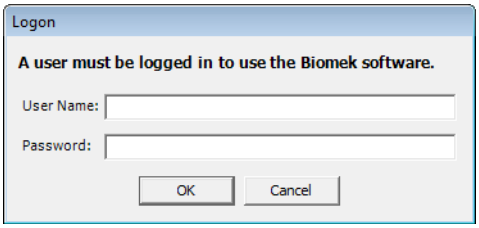
NOTE This section covers logging on and off Biomek Software. Refer to CHAPTER 12, *Creating and Using Methods* for information about saving, validating, and signing methods when Accounts & Permissions is enabled. Refer to CHAPTER 6, *Deleting, Restoring and Renaming Project Files* for information about checking in projects.

Logging Onto Biomek Software

To log onto Biomek Software:

1 With accounts enabled, double click on the Biomek Software icon. Logon displays (Figure 1.5).

Figure 1.5 Logon



2 Enter the account **User Name** and **Password.**

NOTE The first time a user logs on using a new account, or after having the password changed by the administrator, Biomek Software automatically prompts for the password to be changed.

The new password must be different from the original and may include alphanumeric characters and spaces and be up to 250 characters in length. Accounts & Permissions passwords are case insensitive.

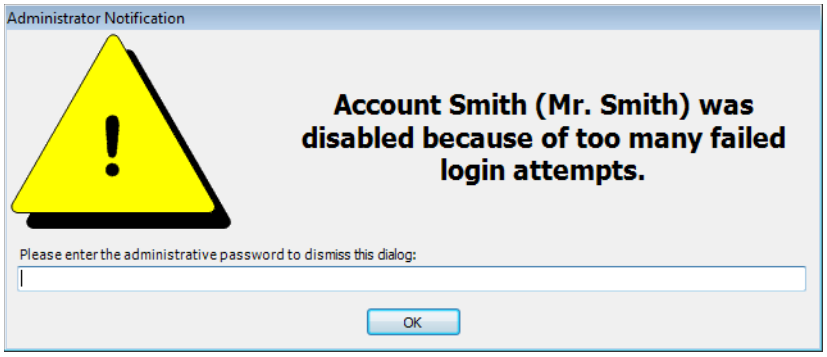
3 Choose **OK** to log onto Biomek Software. The name of the user logged on appears to the left of the log off button (Figure 1.7).

Handling Disabled Accounts

User accounts may be disabled by the administrator, or automatically after a number of logon attempts for the account fail. Allowing accounts to be automatically disabled after a number of failed logon attempts is optional, and configured by the administrator.

When an account is automatically disabled, **Administrator Notification** appears (Figure 1.6). The administrator password must be entered before Biomek Software can be accessed by users.

Figure 1.6 Administrator Notification

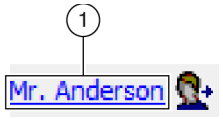


Viewing the Logged On User's Permissions

To view the permissions of the user currently logged onto Biomek Software:

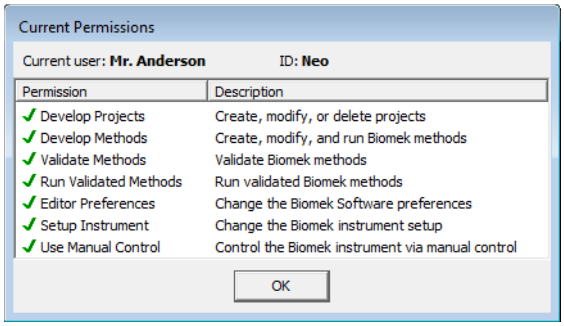
1 On the toolbar, choose the user name (Figure 1.7). **Current Permissions** appears (Figure 1.8).

Figure 1.7 User Logged On



1. **The User Name appears when Accounts & Permissions is enabled and user is logged on.**

Figure 1.8 Current Permissions



2 Choose **OK** to close **Current Permissions**.

Logging Off Biomek Software

To log off Biomek Software:

1 On the toolbar, choose the log off button (Figure 1.9) next to the user name. The user is logged off the system.

NOTE Closing Biomek Software will not automatically log a user off. The current user will remain logged on until the software is reopened and the account is logged off, or until the login times out automatically.

Figure 1.9 Log Off Button—User Logged On



1. Log off button

2 **Logon** appears, allowing another user to log on. If you wish to exit from the software, select **Cancel**, and select **OK** in the **Confirm** dialog to confirm your decision to exit.

CHAPTER 2

Using Password Protection

Overview

Password Protection is a feature of Biomek Software that allows folders or methods to be locked or unlocked with a password. This feature can work with or without Accounts & Permissions. It is accessed and controlled only through **Open Method** or **Save Method**.

The sections in this chapter include:

- *Protecting Folders*
- *Protecting Methods*

Protecting Folders

An entire folder with methods may be locked to prevent it from being opened or modified.

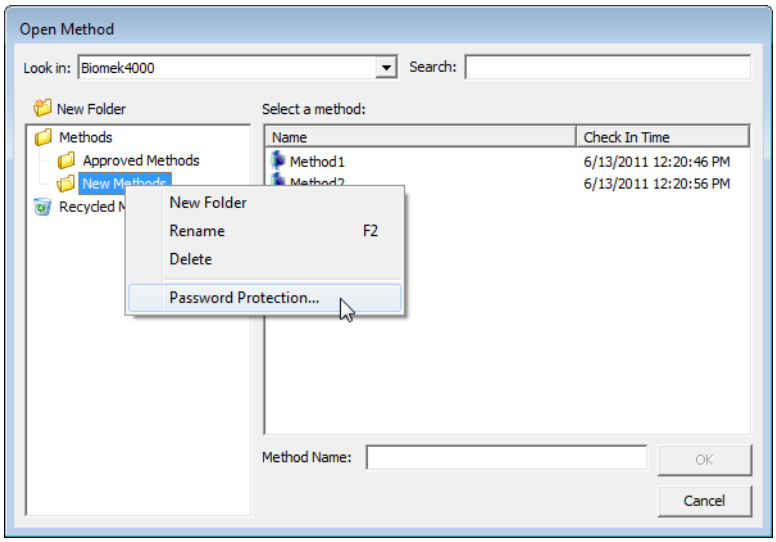
Locking a Folder

To lock a folder:

1. Choose **File > Open. Open Method** appears.

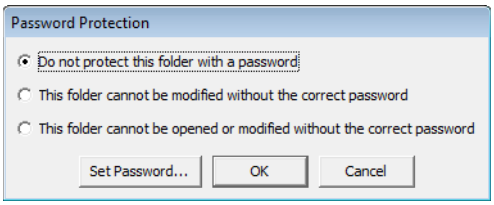
2. Right click on the desired folder and choose **Password Protection** (Figure 2.1). **Password Protection** appears (Figure 2.2)

Figure 2.1 Open Method with Password Protection Chosen to Lock a Folder



NOTE If Accounts & Permissions is enabled, **Open Method** includes **Last Checked In By**.

Figure 2.2 Password Protection for Folders



3 Choose one of the following options:

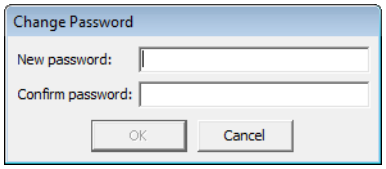
- **Do not protect this folder with a password** — To allow the default of no protection of the folder to remain.
- **This folder cannot be modified without the correct password** — To require the correct password be entered to modify the folder. **Change Password** appears (Figure 2.3).

  NOTE When this option is chosen, the correct password must be entered to add, delete, change, or to import methods to the folder (Figure 2.4).

- **This folder cannot be opened or modified without the correct password** — To require the correct password be entered to open or modify the folder. **Change Password** appears (Figure 2.3).

  NOTE When this option is chosen, the folder may not be opened and Figure 2.5 appears when an attempt to open is made without the correct password. The password must be entered to open the folder and export methods. Once the method has been exported, it is no longer protected.

Figure 2.3 Change Password



4 In **New password**, enter a password.

5 In **Confirm password**, confirm the password.

6 Choose **OK**. **Change Password** closes and **Password Protection** appears (Figure 2.2).

7 Choose **OK** to close **Password Protection** with the new password and the chosen option.

OR

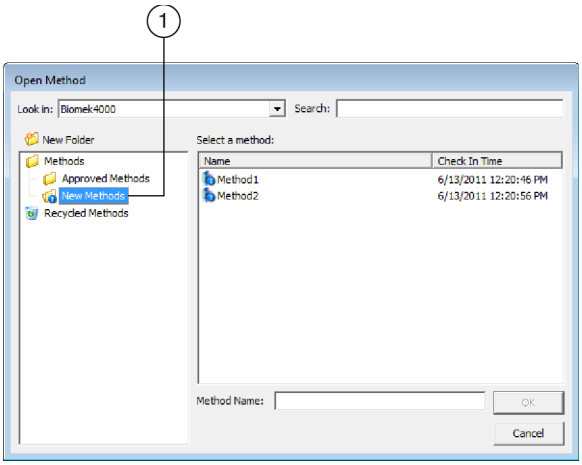
Choose **Cancel** to close **Password Protection** without the new password and chosen option.

OR

Choose **Set Password** to set a new password.

NOTE The folder is locked once the software is closed and then opened.

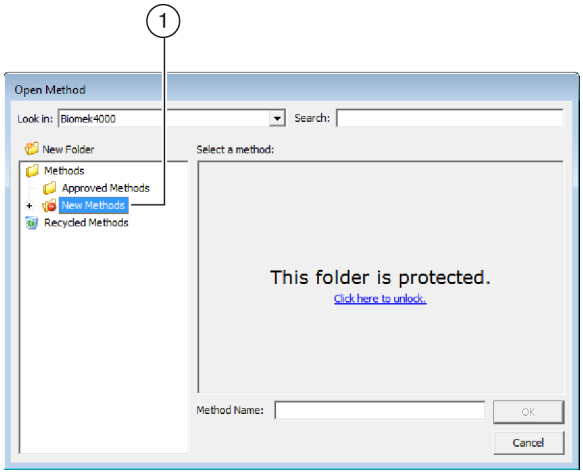
Figure 2.4 Folder is Protected and May Not Be Modified



1. **Folder may not be modified.**

NOTE If Accounts & Permissions is enabled, **Open Method** includes **Last Checked In By**.

Figure 2.5 Folder is Protected and May Not be Opened or Modified



1. **Folder may not be opened or modified.**

Unlocking a Folder

When a folder is protected from being opened or modified, it may be unlocked by entering the correct password in **Password Required**.

To open or modify a locked folder:

1 From **Open Method**, double click the desired folder. **Password Required** appears (Figure 2.6 or Figure 2.7) depending on whether the folder has been protected from being opened or modified.

Figure 2.6 Password Required to Open Folder

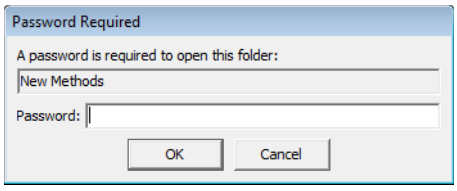
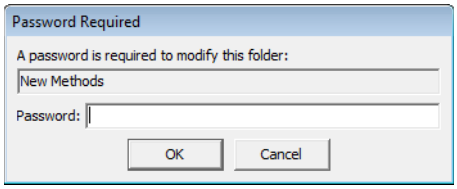


Figure 2.7 Password Required to Modify Folder



2 In **Password**, enter the correct password.

3 Choose **OK**. The folder is unlocked.

NOTE When a folder is password protected and has been unlocked with the correct password, it is identified with a green check mark (Figure 2.8).

Protecting Methods

A method may be locked to prevent it from being opened or modified.

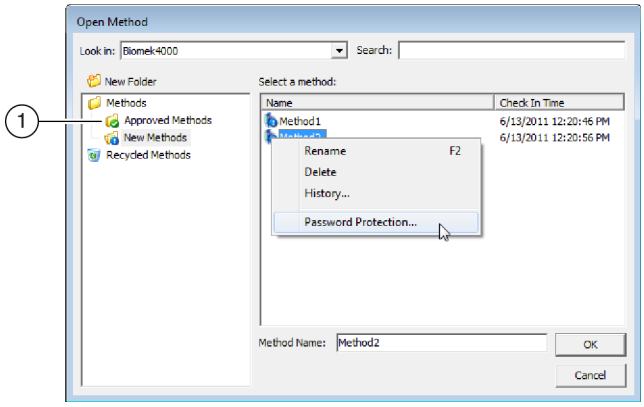
Locking a Method

To lock a method:

1 Choose **File > Open**. **Open Method** appears.

2 Right click on the desired method and choose **Password Protection** (Figure 2.8). **Password Protection** displays (Figure 2.9).

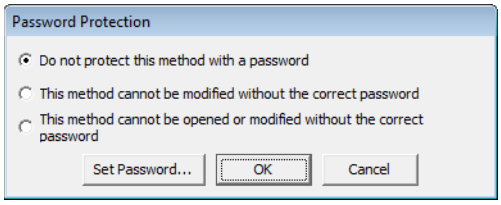
Figure 2.8 Open Method with Password Protection Chosen to Lock a Method



1. **Green check mark:** Indicates the folder has been unlocked with the correct password.

NOTE If Accounts & Permissions is enabled, **Open Method** includes **Last Checked In By**.

Figure 2.9 Password Protection for Methods



3 Choose one of the following options:

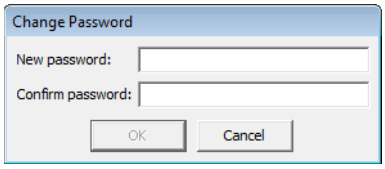
- **Do not protect this method with a password** — To allow the default of no protection of the method to remain.
- **This method cannot be modified without the correct password** — To require the correct password be entered to modify the method. **Change Password** appears (Figure 2.10).

  NOTE When this option is chosen, the correct password must be entered to modify the method (Figure 2.11).

- **This method cannot be opened or modified without the correct password** — To require the correct password be entered to open or modify the method. **Change Password** appears (Figure 2.10).

  NOTE When this option is chosen, the method may not be modified (Figure 2.11) and (Figure 2.13) appears when an attempt to open is made without the correct password.

Figure 2.10 Change Password



4 In **New password**, enter a password.

5 In **Confirm password**, confirm the password.

6 Choose **OK**. **Change Password** closes and **Password Protection** appears. (Figure 2.9).

7 Choose **OK** to close **Password Protection** with the new password and the chosen option.

OR

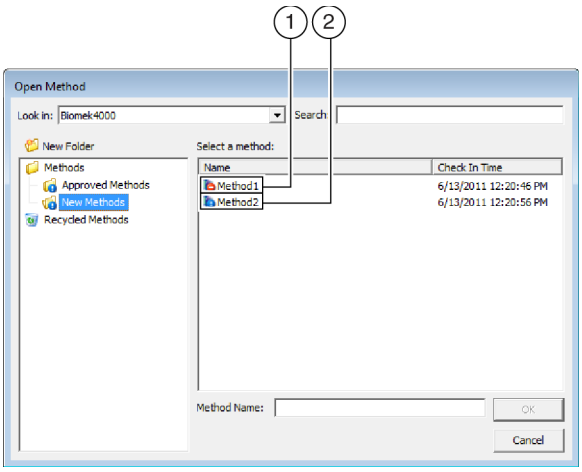
Choose **Cancel** to close **Password Protection** without the new password and chosen option.

OR

Choose **Set Password** to set a new password.

NOTE The method is locked once the software is closed and then opened.

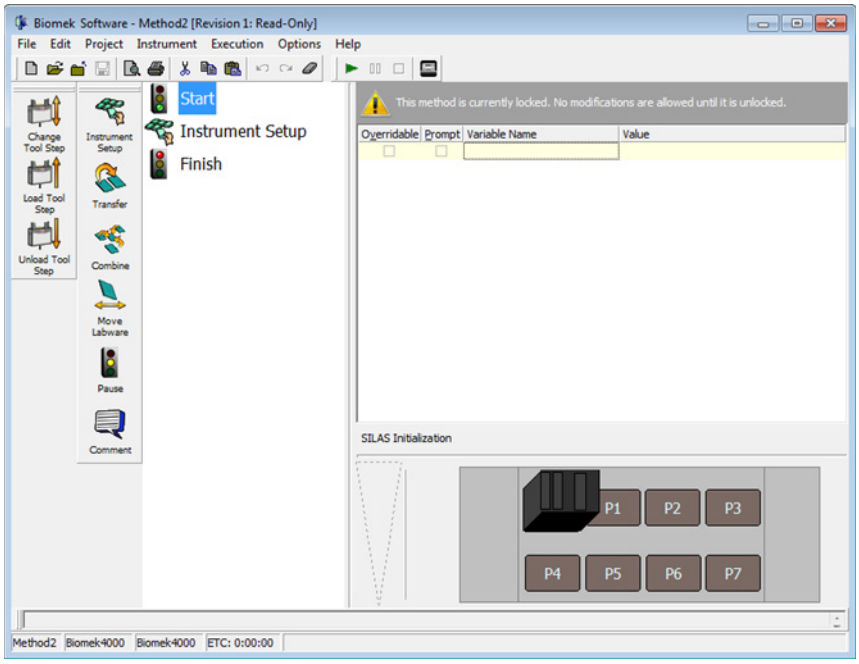
Figure 2.11 Open Method with Methods Locked



1. **Method cannot be opened without the correct password.**
2. **Method cannot be modified without the correct password.**

NOTE If Accounts & Permissions is enabled, **Open Method** includes **Last Checked In By**.

Figure 2.12 Locked Read-Only Method



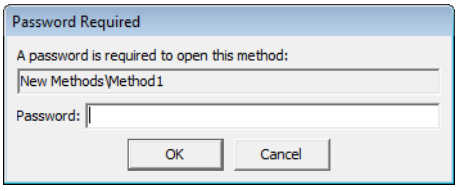
Unlocking a Method

When a method is protected from being opened or modified, it may be unlocked by entering the correct password in **Password Required.**

To open or modify a locked method:

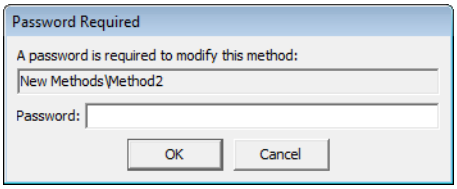
1 From **Open Method**, double click the desired locked method. **Password Required** appears (Figure 2.13 or Figure 2.14).

Figure 2.13 Password Required to Open Method



NOTE The method will not open if **Cancel** is selected.

Figure 2.14 Password Required to Modify Method



NOTE If a password is required for modifying the method, selecting **Cancel** still opens the method, but you will be unable to make modifications. The method will appear similar to Figure 2.12.

2 In **Password**, enter the correct password.

3 Choose **OK**. The method is unlocked.

CHAPTER 3

Using Instrument Files and Settings

Overview

An instrument file stores information about the hardware configuration and deck layout of the instrument. Instrument files can represent different Biomek instruments, or different hardware configurations for the same instrument.

The instrument configuration must accurately represent the hardware to prevent collisions between the pod and any on-deck components. All instrument configuration is done using **Hardware Setup** (refer to CHAPTER 4, *Configuring Hardware Setup*)and the **Deck Editor** (refer to CHAPTER 5, *Preparing and Managing the Deck*).

The **Instrument** menu contains options to open and save instrument files, as well as provide access to the editors to configure the instrument file.

The sections in this chapter include:

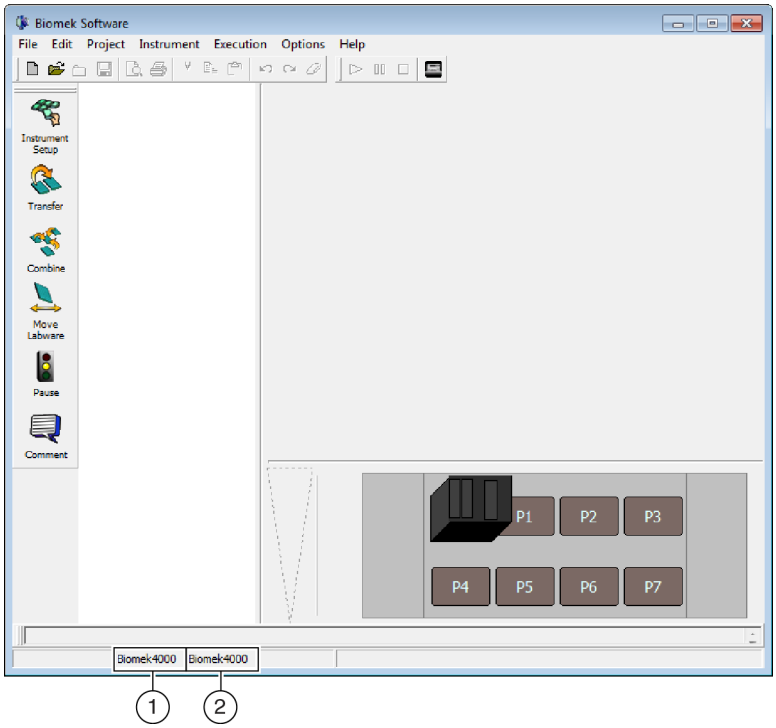
- *Saving and Opening Instrument Files* — Save the current configuration of an instrument or open an existing instrument file.
- *Restoring Instrument Settings from Backup Files* — If settings are deleted or lost, workspace settings or an entire workspace can be restored from one of the automatic daily, weekly, or monthly backup files created by Biomek Software.
- *Sharing Instrument Settings Using the Import/Export Utility* — Settings may be shared with another host computer or sent to Beckman Coulter Technical Support for analysis using the **Import/Export Utility**. This utility allows instrument settings (decks, framing tools, pod settings) to be imported and exported as import files (.imp).

Instrument Display in a Method Editor

The active instrument file and project file are displayed in the status bar of the method editor (Figure 3.1.) Any instrument file can be used with any project file and method. Validated methods, however, are validated for a specific instrument and are no longer validated when used with a different instrument file, even if the instrument file is equivalent to the one on which the method is validated (refer to CHAPTER 12, *Validating a Method*).

NOTE A validated method for a specific instrument is not the same as validating a method before a run to internally test the method for errors before it is actually run. To validate a method to test for errors before it is run, check **Validate the current method before running it** in **Preferences** (refer to CHAPTER 28, *Changing Window Appearance*).

Figure 3.1 Biomek Method Editor



1. **Active project file**
2. **Active instrument file**

Contents of an Instrument File

An instrument file contains all:

- Hardware configurations — Information about the instrument and integrated ALPs or devices as configured in **Hardware Setup**.
- Pod settings — Axis limit values and other settings for the pod(s).
- Deck layouts and framing information — Layout of ALPs and devices on the instrument deck as configured in the **Deck Editor**.

Saving and Opening Instrument Files

Instrument files are saved as *.bif files that may be opened on any system in Biomek Software.

Instrument files can represent different Biomek instruments, or different hardware configurations for the same instrument. These instrument files can be used to:

- Quickly change the instrument configuration between two or more commonly used configurations for an instrument.
- Change instruments when developing methods in simulation mode for multiple instruments on one computer.
- Share the instrument configuration with other users or Beckman Coulter Technical Support to ensure a method is being run using an equivalent instrument.

Saving an Instrument File

An instrument file may be saved at any time. The instrument file is automatically saved when another instrument file is opened or Biomek Software is closed; however, to save the current instrument file without closing it, use **Save Instrument**.

To save changes made to an instrument file:

1 From the **Instrument** menu, choose **Save Instrument**. The active instrument file is saved.

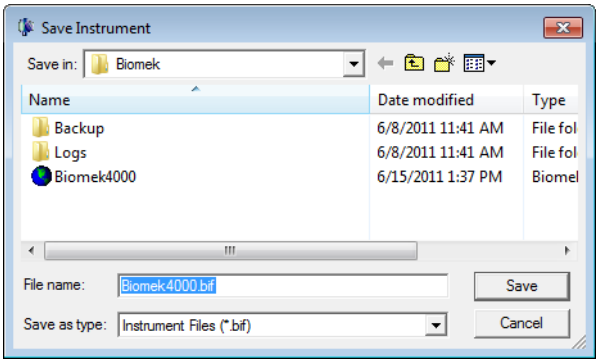
Creating a New Instrument File

A new instrument file is created by saving the current active instrument file with a new file name. The new instrument file has the same settings as the active instrument when it was saved; however, any changes made to the active instrument file are saved as the new instrument and not with the original instrument file.

To create a new instrument file:

1 From the **Instrument** menu, choose **Save Instrument As. Save Instrument** appears (Figure 3.2).

Figure 3.2 Save Instrument



2 In **Save Instrument**, browse to the desired drive and directory in which to save the instrument file.

3 In **File Name**, enter the desired file name for the instrument file.

4 Choose **Save**. The instrument file is saved in the selected drive and directory with the specified file name and opened as the active instrument file.

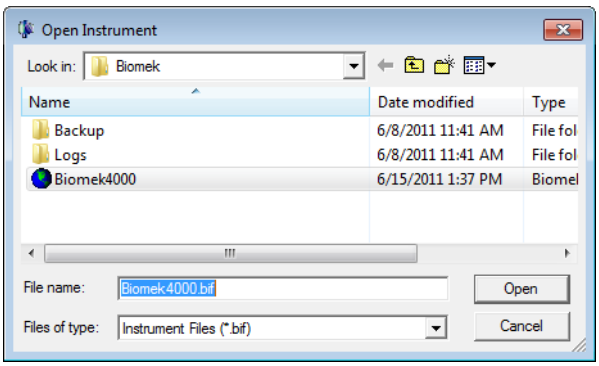
Opening an Existing Instrument File

Any existing instrument file may be opened at any time to develop methods using a specific instrument configuration.

To open an existing instrument file:

1 From the **Instrument** menu, choose **Open**. **Open Instrument** appears.

Figure 3.3 Open Instrument



2 In **Open Instrument**, browse to and select the desired instrument file (*.bif) to open.

NOTE To open one of the daily, weekly, or monthly backup files, enter ***.*backup** in **File name** and press **Enter**. All the backup files are displayed in **Open Instrument**.

3 Choose **Open** to open the selected instrument file. The selected instrument file is opened.

NOTE When an instrument file is imported, the deck framing is reset to **Unframed** and the deck must be framed again.

Restoring Instrument Settings from Backup Files

Backup files are created daily, weekly, and monthly by Biomek Software whenever an instrument file is saved, typically when **File** > **Save Instrument** is selected or when Biomek Software is closed.

NOTE By default, backup files for instruments are saved in the **C:\Documents and Settings\All Users\Shared Documents\Biomek** directory with the following naming convention:

- **<Instrument File Name>.bif.DailyBackup**
- **<Instrument File Name>.bif.WeeklyBackup**
- **<Instrument File Name>.bif.MonthlyBackup**

To restore an instrument file from a backup file when settings are deleted or lost:

1 Close the Biomek Software main editor.

2 Open Windows Explorer and locate the instrument file (*.bif) in the shared application data directory. Typically, the path to this directory is: **C:\Documents and Settings\All Users\Shared Documents\Biomek\.**

3 If the instrument file needs to be replaced rather than recovered, rename the latest instrument file to **<Instrument File Name>.old.**

NOTE Rename the original only if it is available.

OR

If the instrument file needs to be recovered, rename the backup file to the instrument file name, such as **<Instrument File Name>.bif.DailyBackup** to **<Instrument File Name>.bif.**

4 Open the Biomek Software main editor. The instrument file has been restored.

Sharing Instrument Settings Using the Import/Export Utility

Specific segments of a current instrument file, called instrument file settings, can be restored using the **Import/Export Utility** (Figure 3.4). Exporting settings allows settings to be shared with another system, while importing settings allows settings developed on another system to be used. Settings are imported from and exported to import files (.imp).

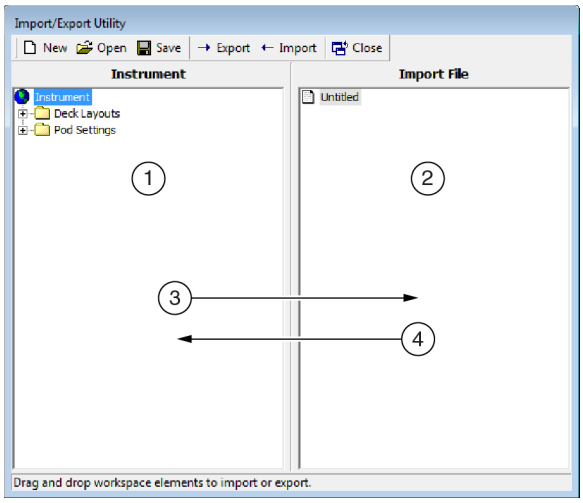
To share a method between two computers, any instrument settings different from the default installed with the software must be exported from the original computer and imported to the new computer using the **Import/Export Utility**.

Figure 3.4 shows how the **Import/Export Utility** works. The **Instrument** side of the utility displays the list of settings in the current instrument file. The **Import File** side of the utility displays the list of settings in the currently opened import file.

To restore settings of a current instrument file, settings from **Instrument** are dragged (exported) to the **Import File**. From **Import File**, these import settings can be dragged (imported) to the current **Instrument**.

NOTE Settings may also be imported or exported by choosing **Import** or **Export** on the toolbar.

Figure 3.4 Import/Export Utility



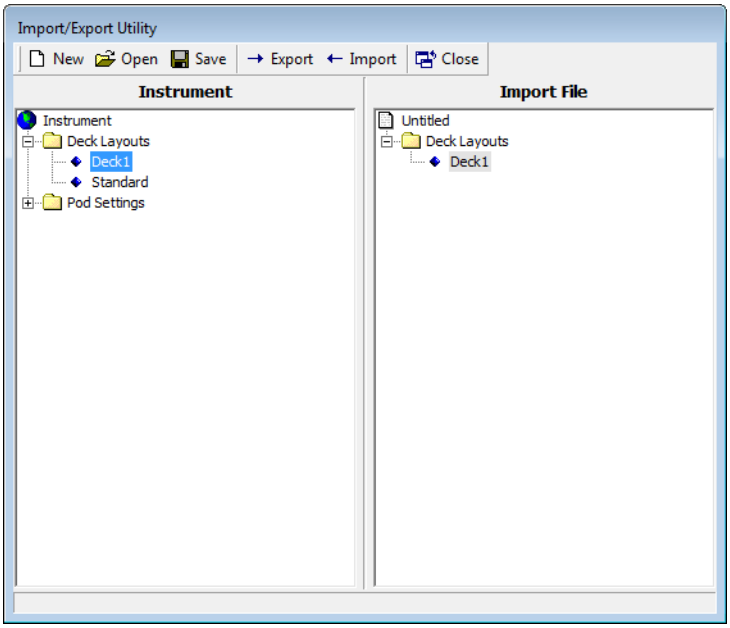
1. **Instrument:** Displays list of settings in the current workspace.
2. **Import File:** Displays list of settings in the current import file.
3. **Export settings from current instrument to the import file.**
4. **Import settings from the import file to the current instrument**.

Exporting Settings to an Import File

To export settings to an import file:

1 From the **Instrument** menu, choose **Import/Export Utility**. **Import/Export Utility** appears (Figure 3.5).

Figure 3.5 Exporting Deck Layout Deck1 to an Import File



2 Drag and drop the desired settings from **Instrument** to **Import File**.

OR

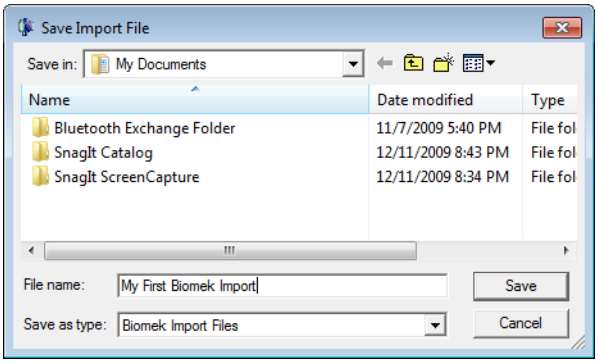
Highlight the desired settings from **Instrument** and choose **Export**. The folder containing the desired setting and the setting itself appear in the **Import File** (Figure 3.5).

NOTE Dragging a folder copies all of the settings in that folder.

3 Continue to export settings using step 2 until all desired settings are exported.

4 Choose **Save** to save the Biomek Import File. **Save As** (Figure 3.6) appears.

Figure 3.6 Save Import File



5 Browse to the desired file location to save the import file.

6 In **File name**, enter a name for the import file.

7 Choose **Save**. The import file is created and **Save As** closes.

NOTE Note that the name of the new import file is now displayed on the top of the **Import File** window.

8 Choose **Close**. **Import/Export Utility** closes.

NOTE When exporting a deck with a fixed (stationary) labware type, such as a Liquid Waste Station, the fixed labware must be present in the destination project or exported to the import file.

Importing Settings from an Import File

To import settings from an import file:

1 From the **Instrument** menu, choose **Import/Export Utility**. **Import/Export Utility** appears (Figure 3.5).

2 Choose **Open** and open the .imp file.

3 Open the desired folder by clicking the + containing the desired settings from the import file.

NOTE If a setting with the same name is used in the import file and in the current instrument, it will be overwritten.

4 Drag and drop the setting from **Import File** to **Instrument** to overwrite the setting in the current workspace with the one from the import file.

OR

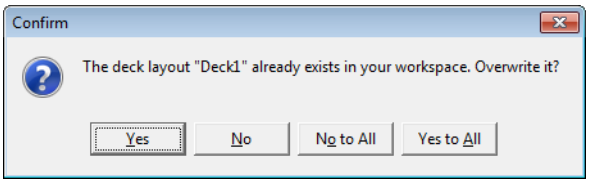
Rename the setting in the **Import** side, then drag and drop the setting from **Import File** to **Instrument** to not overwrite the setting.

NOTE Rename a setting by highlighting the setting, single-clicking, pausing until the name becomes editable, typing a new name, and pressing the (Enter) key.

NOTE Dragging an entire folder copies all of the settings in that folder.

NOTE If a setting being imported exists in the instrument file and, therefore, can be overwritten, a **Confirm** similar to Figure 3.7 displays. Answer **Yes** to overwrite the setting in the instrument file. Answer **No** to cancel the import of that setting. **Yes to All** and **No to All** allow multiple imported settings to overwrite the contents of the instrument file or be cancelled at the same time.

Figure 3.7 Confirmation to Overwrite an Imported Setting



5 Continue to import settings using step 4 until all desired settings are imported.

6 Choose **Close** to exit the **Import/Export Utility**.

7 Select **Instrument** > **Save Instrument** to save any changes made to the workspace.

NOTE When Biomek Software is updated, a backup of the instrument file is made to save previous settings. The backup instrument file is located in **C:\Documents and Settings\All Users\Shared Documents\Biomek\Backup**.

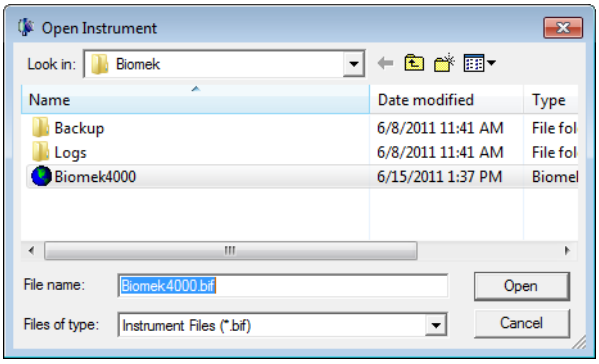
Restoring Instrument Settings from Backup Files

To restore instrument file settings from a backup file, such as when settings are deleted or incorrectly changed:

1 Make a note of the current instrument file, which in found in the lower left of the user interface (see Figure 3.1 for location). This file name will be used throughout this procedure.

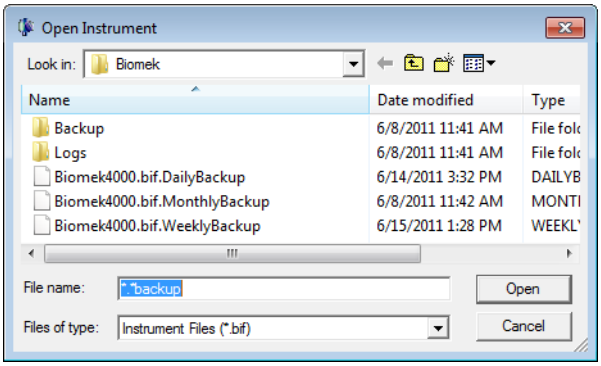
2 From **Instrument**, choose **Open** to open the backup file for the instrument file. **Open Instrument** appears (Figure 3.8).

Figure 3.8 Open Instrument File



3 In **File name**, enter ***.*backup** and press Enter to show all daily, weekly, and monthly backup files in **Open Instrument** (Figure 3.9).

Figure 3.9 Open Instrument Showing Backup Files



4 Select the desired backup file.

5 Choose **Open.** The selected backup file is opened as the current instrument.

6 Use the **Import/Export Utility** to create an import file with the desired settings from the backup instrument file (refer to *Exporting Settings to an Import File*).

7 From the **Instrument** menu, choose **Open Instrument.**

8 Select the original instrument file, named as noted in Step 1.

9 Choose **Open**.

10 Use the **Import/Export Utility** to import settings from the import file created in step 5 (refer to *Importing Settings from an Import File*).

NOTE When Biomek Software is updated, a backup of the instrument file is made to save previous settings. The backup instrument file is located in **C:\Documents and Settings\All Users\Shared Documents\Biomek\Backup\.**

CHAPTER 4

Configuring Hardware Setup

Overview

Hardware Setup is used to configure Biomek Software with the instrument information, including which tools and devices are available for use. The Biomek Simulator, which shows a 3-D animation of the instrument performing methods, is also configured in **Hardware Setup**.

After a Beckman Coulter Representative has physically installed a device, the device is detected on the instrument and must be properly installed and configured in **Hardware Setup**. While the Beckman Coulter Representative normally installs and configures new devices, it may be necessary to install, configure, and remove other devices using **Hardware Setup**.

For specific information on configuring your Biomek instrument in **Hardware Setup**, refer to the *Biomek 4000 Hardware Manual*.

Refer to the *Biomek 4000 ALPs and Accessories Manual* for information on configuring specific ALPs and devices.

The sections in this chapter include:

- *Accessing Hardware Setup*
- *Understanding the Options in Hardware Setup*
- *Configuring the Biomek 4000 Simulator*

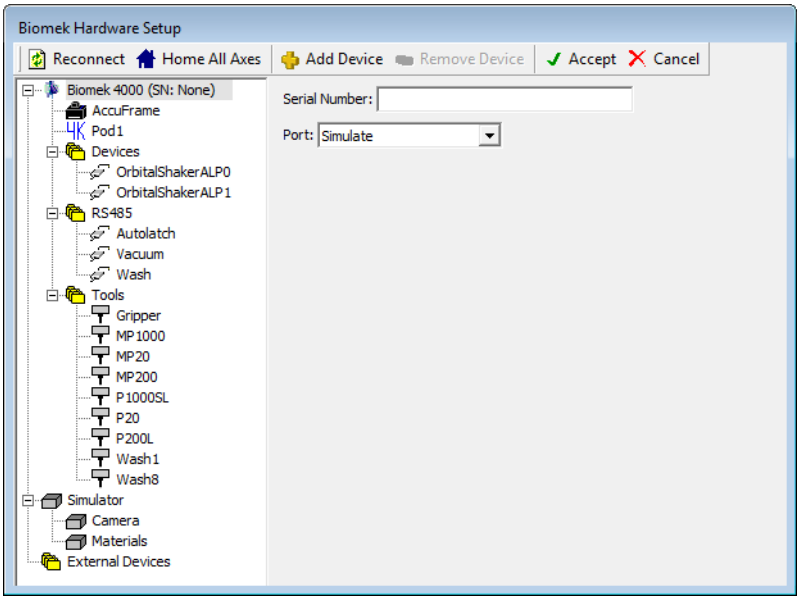
Accessing Hardware Setup

Hardware Setup is accessed from within Biomek Software.

To access **Hardware Setup**:

1 From the **Instrument** menu, choose **Hardware Setup**. A **Connecting** notification window quickly appears while the software searching for installed devices. After locating the installed devices, **Hardware Setup** appears (Figure 4.1).

Figure 4.1 Hardware Setup for a Biomek 4000 Instrument



NOTE The devices displayed in **Hardware Setup** are dependent on instrument configuration.

Understanding the Options in Hardware Setup

An understanding of the options on the toolbar in **Hardware Setup** is necessary to properly install, configure, and remove devices.

Table 4.1 lists and describes the toolbar options in **Hardware Setup**.

Table 4.1 Hardware Setup Options

Option	Description
Reconnect	Allows **Hardware Setup** to reexamine the devices present. Choose this option to determine what devices are present rather than closing and reopening **Hardware Setup**.
Home All Axes	Gives the instrument a point of reference from which to make subsequent moves. For the Biomek 4000 instrument, the home position is left, back. **NOTE** The pod must be homed each time the instrument is powered on. After confirming that the actions have been addressed properly, in the **Warning** that appears, choose **OK**.
Add Device	Installs a device.
Remove Device	Removes a device.
Accept	Saves all changes to the instrument and closes **Hardware Setup**. Choose this option after the device has been installed and configured.
Cancel	Closes **Hardware Setup** without saving the modifications to the instrument.

Configuring the Biomek 4000 Simulator

When a method is run in **Simulate** mode, the Biomek Simulator appears, showing an animated 3-D model of the instrument performing the method. Simulator settings can be configured in **Hardware Setup**.

NOTE Modifying simulator settings is optional. The default settings are appropriate for most computers.

Configuring the simulator includes:

- *Configuring Simulator Settings*
- *Configuring Camera Controls*
- *Configuring Materials*

Configuring Simulator Settings

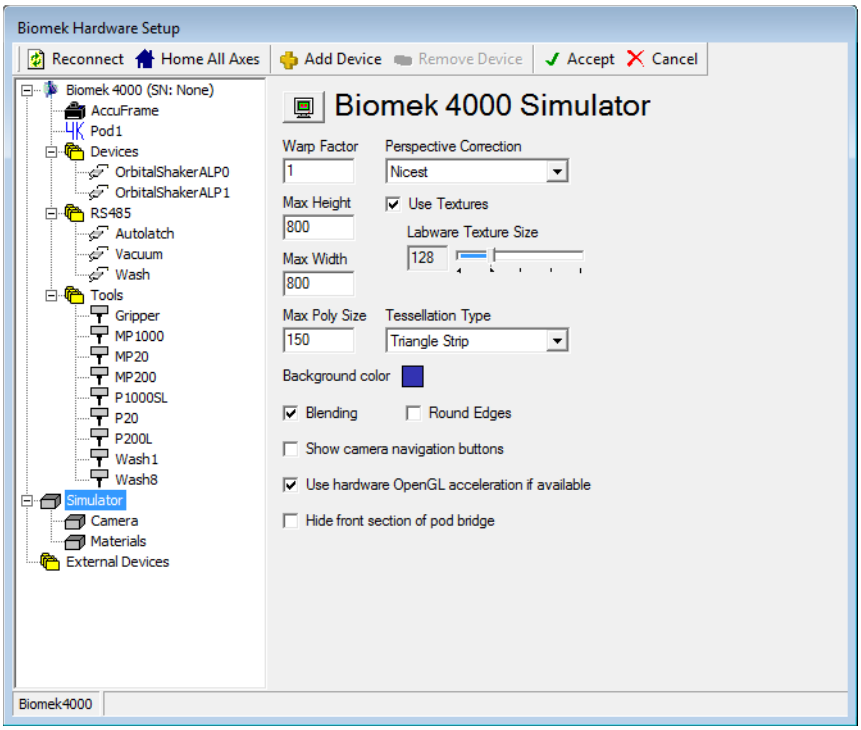
Simulator configures view settings, including animation speed, simulator display size, and image quality. Many of the view settings increase or decrease the image quality of the 3-D model shown in simulations. In general, increasing image quality, such as enabling blending, requires a faster computer to run the animated simulation smoothly. Conversely, decreasing image quality requires less computing power, and will run simulations more smoothly on slower computers.

The default settings in **Simulator** provide a good balance between image quality and smooth animation playback on most computers. Change the settings only if higher image quality or smoother playback is desired.

To configure simulator settings:

1 From the left pane of **Hardware Setup**, choose **Simulator**. The Biomek Simulator settings appear (Figure 4.2).

Figure 4.2 Hardware Setup—Configuring the Simulator Settings



2 In **Warp Factor**, change the playback speed for simulated methods. **Warp Factor 1** runs simulated methods in real time.

3 Enter the **Max Height** in pixels for the simulator display.

4 Enter the **Max Width** in pixels for the simulator display.

5 In **Max Poly Size**, enter the maximum size of the polygons that make up the model of the instrument shown in the simulator. Decreasing the polygon size creates a more detailed simulator view, but requires more computing power. Increasing the polygon size creates a less detailed simulator view, but requires less computing power.

6 Choose the method of **Perspective Correction**:

- **Nicest** — Performs more accurate perspective correction; better for faster computers.
- **Fastest** — Performs less accurate correction; better for slower computers.
- **Don't Care** — Biomek Software automatically chooses the most appropriate correction method.

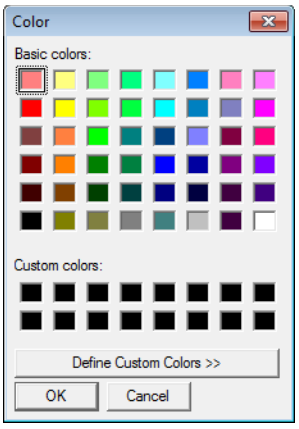
7 Choose **Use Textures** to include textures, such as microplate wells, on the instrument and labware surfaces displayed in the simulator.

8 If **Use Textures** is chosen, choose a **Labware Texture Size**, if desired. Dragging the slider to the right increases texture detail; dragging to the left reduces texture detail.

9 Change **Tesselation Type** to **Triangle Fan** or **Quad Strip** if a slight enhancement in image quality is desired. The default setting, **Triangle Strip**, is adequate for most computers.

10 Choose the colored box to the right of **Background Color** to change the background color in the simulator display. **Color** appears (Figure 4.3).

Figure 4.3 Selecting a Background Color



11 Select a new color, or define a custom color for the simulator background.

12 Choose **OK** to set the new background color.

OR

Choose **Cancel** to retain the original background color.

13 Select **Blending** to render semi-transparent objects, such as tips, correctly.

NOTE When **Blending** is disabled, semi-transparent objects appear opaque; for example, liquid is not visible inside tips. Leaving **Blending** disabled is recommended for slower computers.

14 Select **Round Edges** to smooth out and round the edges of the instrument in the simulator display.

15 Select **Show camera navigation buttons** to display camera navigation controls by default during simulated method runs and in **Simulator Preview**.

NOTE The camera is the position from where the 3-D model is being viewed. The camera navigation controls are used to move or rotate the camera, which changes the viewing angle of the model in the simulator.

NOTE Camera navigation controls may also be toggled on and off during simulated method runs by pressing the tilde (~) key to enable the simulator controls (refer to CHAPTER 12, *Using the Simulator Controls*).

16 Select **Use hardware OpenGL acceleration if available** to provide smoother rendering of the model and animation on supported computers.

17 Select **Hide front section of pod bridge** to hide the front section of the bridge of the instrument to provide an unobstructed view of the pod performing the steps in the method.

18 Choose  (**Preview**) to access **Simulator Preview** at any time during simulator configuration (refer to *Viewing the Simulator Preview*).

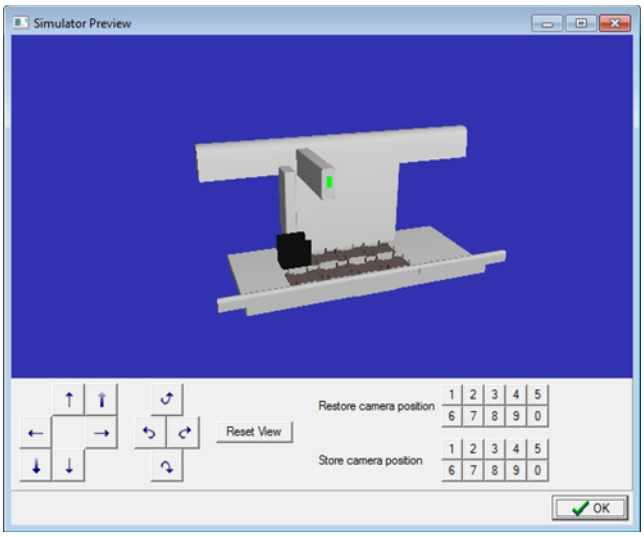
Viewing the Simulator Preview

Simulator Preview shows the 3-D model of the instrument, including current configuration changes, as it appears in animated simulations. **Simulator Preview** is accessible from **Simulator, Camera**, or **Materials** at any time.

To view the **Simulator Preview**:

1 Choose  to view changes made to the settings, if desired. **Simulator Preview** appears (Figure 4.4).

Figure 4.4 Simulator Preview with Camera Navigation Buttons Enabled



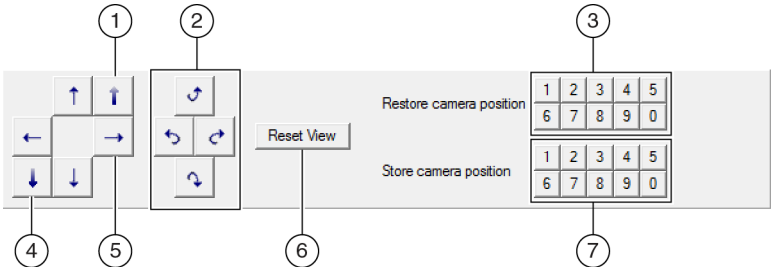
2 Change the view by clicking the cursor in the simulator display and using the keyboard control keys defined in **Camera** (refer to *Configuring Camera Controls*).

OR

Use the camera navigation buttons to change, save, and reset the view (Figure 4.5). The camera navigation buttons are displayed only when enabled in **Simulator** (refer to *Configuring Simulator Settings*).

NOTE The camera is the position from where the 3-D model is being viewed. The camera navigation buttons move or rotate the camera, which changes the angle at which the model is being viewed in the simulator.

Figure 4.5 Camera Navigation Buttons



1. **Move In:** Moves the instrument closer.
2. **Rotate camera position:** Rotates the camera position in the indicated direction.
3. **Restore camera position:** Choose a position to show the view stored in that position.
4. **Move Out:** Moves the instrument further away.
5. **Move camera position:** Moves the camera position in the indicated direction.
6. **Reset View:** Restores the default view.
7. **Store camera position:** Choose a position to save the current view. Up to ten positions may be saved.

3 Choose **OK** to close **Simulator Preview** and return to the simulator configuration in **Hardware Setup**.

Configuring Camera Controls

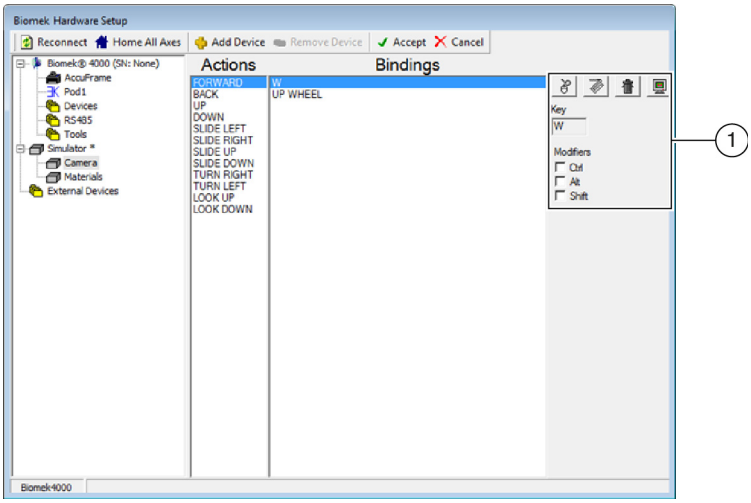
The camera is the position from where the 3-D model of the instrument is being viewed. To change the view of the model, the camera can be moved using the keyboard, mouse, or optional camera navigation buttons. In **Camera**, movements are called **Actions**. Keyboard and mouse controls are called **Bindings**. Keyboard and mouse controls can be created, edited, or deleted in **Camera.**

NOTE Camera navigation buttons are enabled and disabled in **Simulator** (refer to *Configuring Simulator Settings*).

To add or modify a camera control:

1 From the left pane of **Hardware Setup**, expand the **Simulator** tree by clicking the +, if necessary, and choose **Camera.** Camera appears (Figure 4.6).

Figure 4.6 Hardware Setup—Configuring Camera Controls



1. **Settings to configure binding.**

2 In the **Actions** pane, select the camera control to modify. The current keyboard and mouse control settings appear in **Bindings**.

3 In **Bindings**, select the binding to delete or modify.

4 Choose  (**Delete Bind**) to delete the selected binding.

OR

Modify the binding. Modifications include:

- *Creating or Editing a Mouse Binding*
- *Recording or Editing a Key Binding*

Creating or Editing a Mouse Binding

Mouse bindings control camera actions using mouse controls. They may be configured to use a single mouse control, a combination of mouse controls, or a combination of mouse controls and modifier keys on the keyboard.

NOTE The mouse buttons, wheel, and directional movement are all considered mouse controls.

To create or edit a mouse binding:

1 To create a new mouse binding, choose  (**Add Mouse Bind**).

OR

To edit an existing mouse binding, select the desired binding.

2 In **Mouse Command**, choose the desired command.

3 In **Modifiers**, select any desired keyboard modifiers and/or mouse commands.

NOTE The (Ctrl) , (Alt) , and (Shift) keys are keyboard modifiers. Mouse command modifiers are **Right**, **Left**, and **Middle**, which represent mouse buttons and **Double**, which represents double clicking.

4 If creating a new mouse binding, choose  (**Add Mouse Bind**) to add the new binding to the selected **Action**.

5 To test the mouse binding, choose  to access **Simulator Preview** at any time during simulator configuration (refer to *Viewing the Simulator Preview*).

Recording or Editing a Key Binding

Key bindings control camera actions with keys on the keyboard. They may be configured to require a single key, such as "**T**", or a combination of a key and modifier.

To record or edit a key binding:

1 To create a new key binding, choose  (**Record Key Bind**).

OR

To edit an existing key binding, select the desired binding.

2 If creating a new binding, press the desired key.

3 In **Modifiers**, select a modifier key, if desired.

4 To test the key binding, choose  to access **Simulator Preview** at any time during simulator configuration (refer to *Viewing the Simulator Preview*).

Configuring Materials

Each component of the 3-D instrument model is made of a material which has visual properties, such as color and reflectivity, specified. Properties can be edited in **Materials**. However, configuring the properties of materials is not necessary or recommended.

Materials can also be created and deleted by choosing  (**Create Materials**) or  (**Delete Materials**) buttons in **Materials.** Materials *should never* be deleted, because the deleted material will no longer be visible in the simulator. Likewise, materials created by users will not appear in the simulator either.

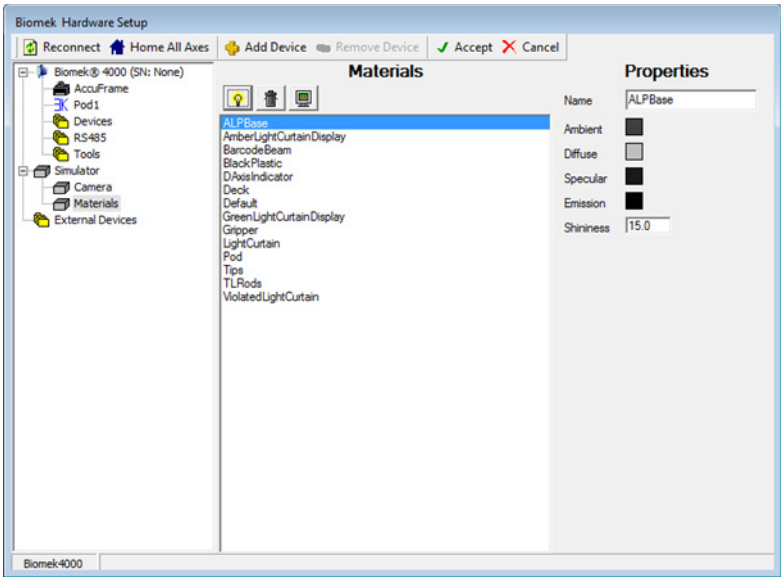
NOTE Always preview changes in **Simulator Preview** before saving the new configuration. Refer to *Viewing the Simulator Preview*, for more information.

To configure **Materials:**

---

1 From the left pane of **Hardware Setup**, expand the **Simulator** tree, if necessary, and choose **Materials**. **Materials** appears (Figure 4.7).

Figure 4.7 Hardware Setup—Configuring Camera Controls



NOTE In **Materials**, select the material to edit. The properties of the material appear. Table 4.2 provides descriptions of each material

---

2 In **Properties**, *do not* change the **Name.** Changing the name of a material causes it to no longer be visible in the simulator.

---

3 Choose the colored box to the right of a color parameter to change the color of the material. **Color** appears.

NOTE **Ambient** and **Diffuse** define the color of the material when light is present. **Specular** defines the color of specular highlights (glare). **Emission** defines the color of the material in the absence of light.

---

4 In **Color**, select a new color, or define a custom color for the color parameter.

5 Enter a new value for **Shininess**, if desired.

NOTE **Shininess** defines the reflectivity of the material on a scale of 0 – 100, with 100 being the most reflective.

6 To view changes made to materials, choose **Preview**. to access **Simulator Preview** at any time during simulator configuration (refer to *Viewing the Simulator Preview*).

Table 4.2 Materials

Material	Description
ALPBase	Base or stand of an ALP.
AmberLightCurtainDisplay	Color of the front panel indicator light during a method run.
BarcodeBeam	Laser beam emitted by a barcode reader.
BlackPlastic	Biomek 4000 tool bodies.
DAxisIndicator	Color band that encircles the pod to show upward and downward movement.
Deck	Instrument deck.
Default	Default color of a material when deleted from the simulator.
GreenLightCurtainDisplay	The color of the front panel indicator light when the instrument is not running a method.
Gripper	Gripper.
LightCurtain	*Not used for Biomek 4000 instruments.*
Pod	Instrument pod.
Tips	Tips.
TLRods	Locking rods.
ViolatedLightCurtain	**Emission** is the only property used on Biomek 4000 instruments. This property is used for the color of indicator light when the **STOP** button has been pressed.

CHAPTER 5

Preparing and Managing the Deck

Overview

The **Deck Editor** is used to define and change the deck configurations stored in the current instrument file. A deck is a software representation of the Biomek 4000 deck (Figure 5.1) and can be stored and used for multiple methods; however, the software deck must always match the physical deck of the instrument used in the method.

A deck is created and modified in the **Deck Editor,** configured for the method in the **Instrument Setup** step, and used extensively by the software. A deck also stores framing information and device associations for each position on the deck.

The **Deck Editor** can be used to:

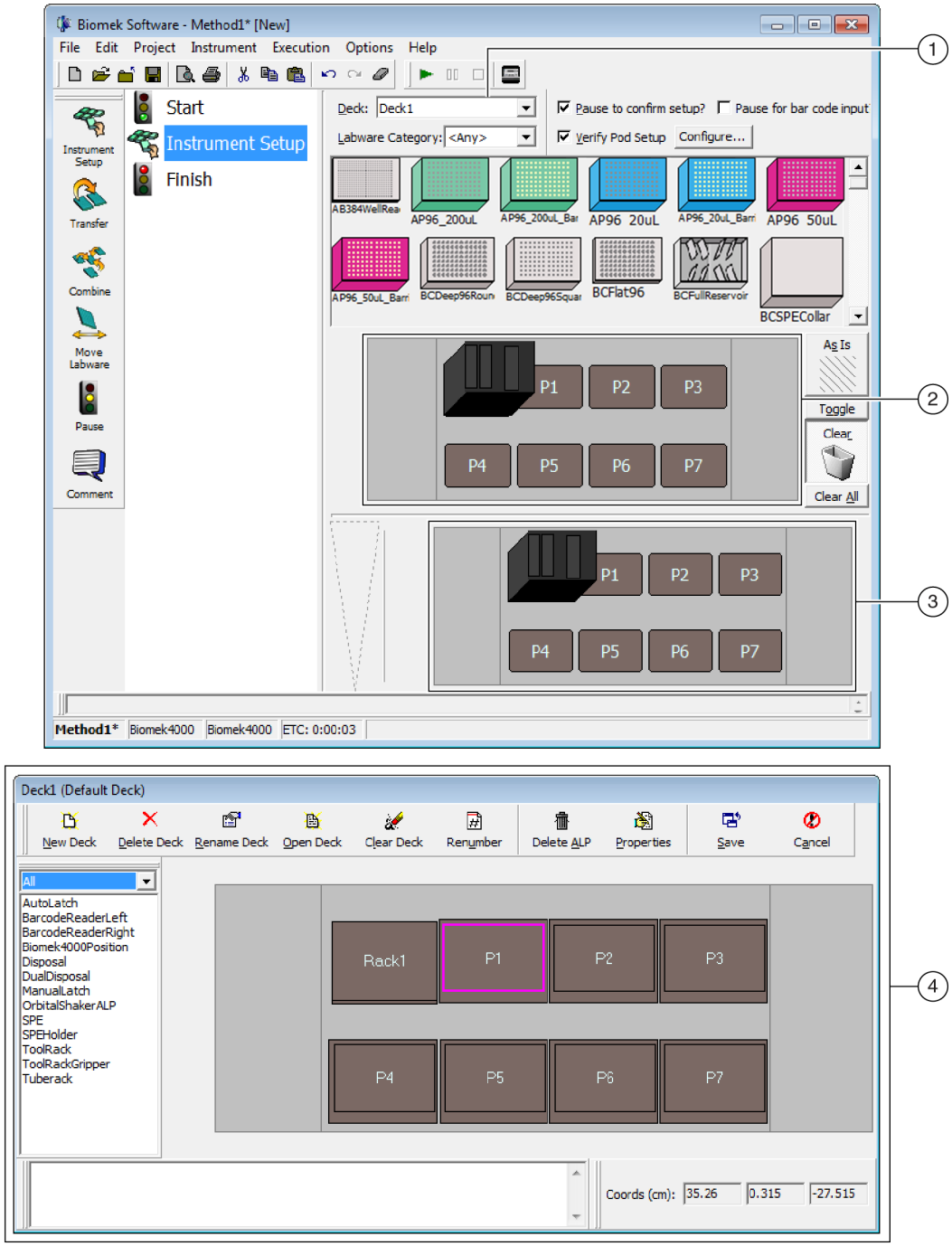
- Create new decks.
- Delete unused decks.
- Define the types and locations of ALPs, labware positioners, and devices positioned on a Biomek instrument deck.
- Control device associations.
- Frame (teach) the physical positions of ALPs, labware positioners, and devices.
- Aid in mapping decks from methods imported from other Biomek instruments.

The sections in this chapter include:

- *Understanding the Deck Editor*
- *Opening, Selecting, Creating, Deleting, or Renaming a Deck*
- *Modifying a Deck*
- *Deck Mapping*

The **Deck Editor** displays decks to be used during the method-building process. A deck is set as the default deck in the **Deck Editor**. The default deck appears when the Deck Editor is opened and is selected automatically when the **Instrument Setup** step is inserted into a method. The **Instrument Setup** step allows selection of any previously defined deck (Figure 5.1).

Figure 5.1 Deck Relationship in Biomek Software



1. **Deck Selection**: Allows a deck to be selected during the method-building process. The deck set as the default deck in the **Deck Editor** is selected automatically.
2. **Deck**: Area used to configure the selected deck during **Instrument Setup**.
3. **Deck Display**: Illustrates the configuration of the current deck.
4. **Deck Editor**: Access from **Instrument** menu. Shows for Biomek 4000 deck, and allows for deck modification.

Framing the Deck

Framing the deck allows Biomek Software to remember each deck position, and the **Deck Editor** is used to set the properties of each ALP and position. Several properties, such as **Position Span** and **Labware Offset**, are pre-programmed into Biomek Software; however, other properties, such as **Position**, must be set by teaching.

The position offsets are taught using the framing tools with the instrument. However, different framing tools are used according to the instrument configuration (AccuFrame options) and the deck position. Refer to the *Biomek 4000 Hardware Manual* for information on framing the Biomek 4000 Laboratory Automation Workstation.

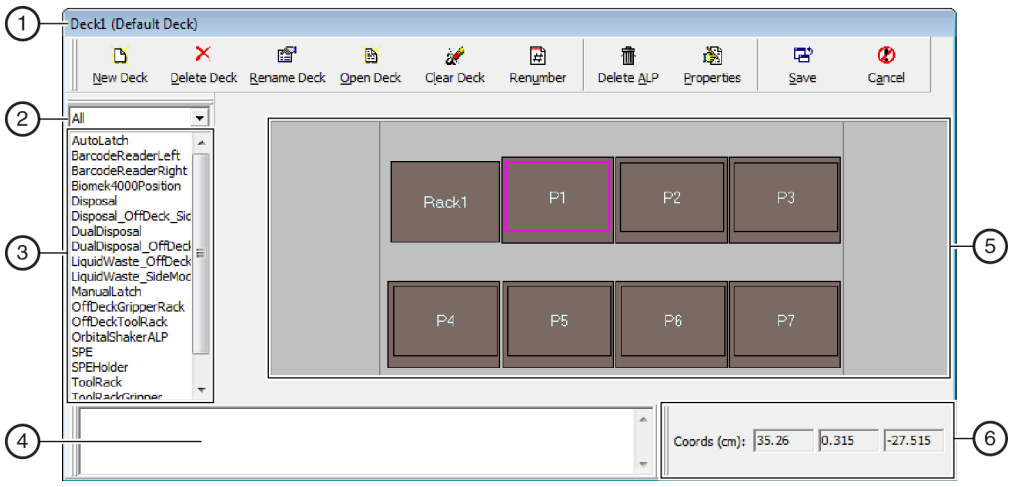
Understanding the Deck Editor

The **Deck Editor** creates and modifies decks based on the physical deck of the instrument.

To access the **Deck Editor**:

1 Select **Instrument > Deck Editor.** The **Deck Editor** displays (Figure 5.2).

Figure 5.2 Deck Editor Showing Deck1



1. **Current Deck Name**: Name of currently opened deck. The deck set as the default in the **Deck Editor** is identified as (**Default Deck**).
2. **Used to filter specific types of ALPs, such as All, Basic, Devices, Tool Slot, Trash, and Tubes.**
3. **ALP Type List**: Lists available ALPs and devices for placement on deck.
4. **Deck Notation Area**: Provides an area for making notes during deck configuration.
5. **Deck View**: View of currently open deck.
6. **Coordinates of Position on Deck**: Shows coordinates of selected position. Display can be docked as desired.

The **Deck Editor** has several options located on the toolbar that are used to modify decks; these options are described in Table 5.1.

Table 5.1 Deck Editor

Options	Description
New Deck	Creates a new deck based upon the current deck.
Delete Deck	Permanently removes the current deck.
Rename Deck	Changes the current deck name.
Open Deck	Opens an existing deck and sets it as the current deck.
Clear Deck	Removes all ALPs and devices from the deck.
Renumber	Renames all of the deck items based on position starting in the upper left corner.
Delete ALP	Removes an ALP or device from the deck.
Properties	Opens the properties for the selected deck position or ALP.
Save	Saves the deck and closes the **Deck Editor**.
Cancel	Cancels the changes made to the opened deck and closes the **Deck Editor**.

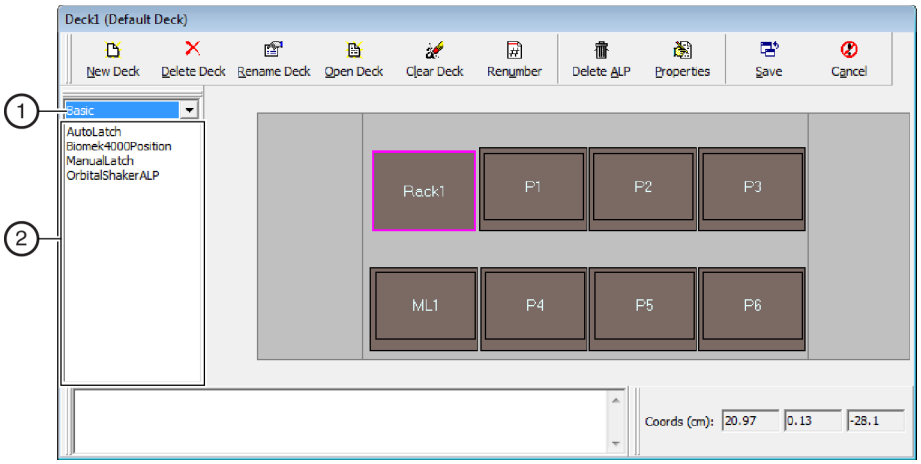
Viewing the ALP Types List

The ALP Types List (Figure 5.3) shows all standard ALPs, labware positioners, and devices available to place on the deck. Use the filter to list only specific types of ALPs.

⚠ CAUTION

Make sure the correct ALP is chosen when configuring the deck setup in the Biomek Software "Deck Editor." ALPs vary in height, and failure to choose the correct ALP in the "Deck Editor" can result in collisions, causing equipment damage and/or hazardous waste spills.

Figure 5.3 Deck Editor



1. **Filter**
2. **ALP Types List**

NOTE Refer to *Adding ALPs and Deck Positions* for more information on adding the ALPs to a deck. Refer to the *Biomek 4000 ALPs and Accessories Manual* for more information about specific ALPs.

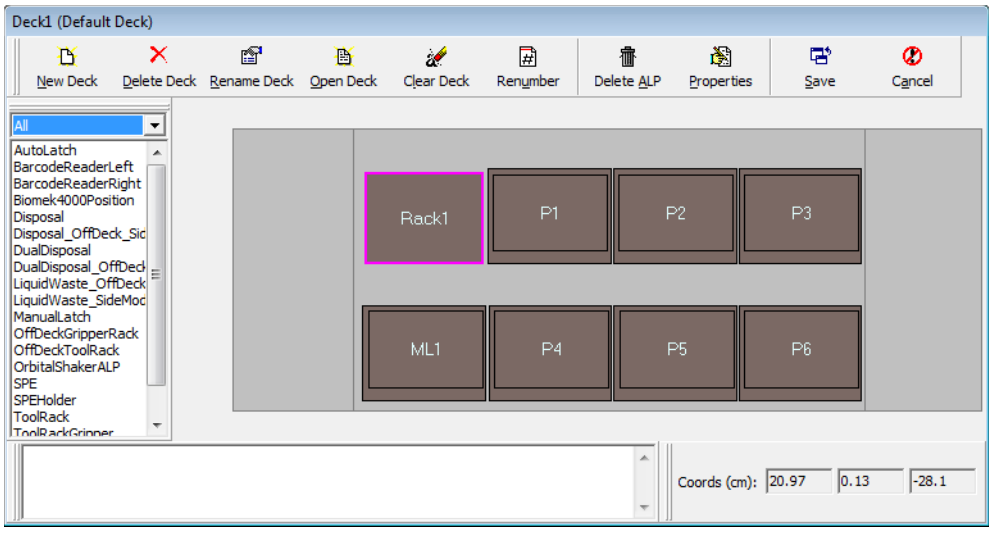
Biomek 4000 Deck Types

Each initial deck (Figure 5.4) contains 1 tool rack position (**ToolRack**) and 7 deck positions (areas where tool racks and devices may be placed).

- **Deck1** — Initially has 1 tool rack position and 7 deck positions; can be modified to include other tool racks and devices (Figure 5.4).
- **Standard** — Has 1 tool rack position and 7 deck positions; cannot be modified; can be copied to create new decks

NOTE Do not use the **Standard** deck in a method; it cannot be modified and is used only to create new decks by using the **New Deck** option.

Figure 5.4 Deck Editor



Opening, Selecting, Creating, Deleting, or Renaming a Deck

The **Deck Editor** is used to open, select, create, delete, or rename a deck in Biomek Software.

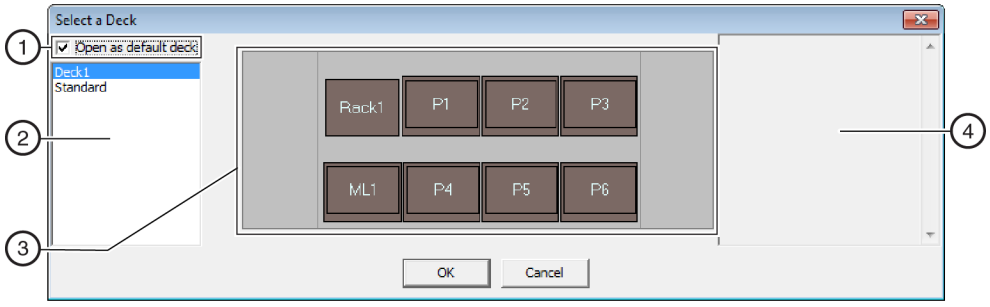
Opening and Selecting a Deck

A deck is selected in **Deck Editor** as the default deck. Each time an **Instrument Setup** step is inserted into a method, the default deck appears.

To select a deck:

1 In the **Deck Editor,** choose Open Deck. **Select a Deck** appears (Figure 5.5).

Figure 5.5 Previews Deck Selected



1. **Check mark opens the deck as the default.**
2. **Deck List**: Lists available decks.
3. **Deck Preview**
4. **Notes made in the Deck Notation Area appear here.**

2 Select the desired deck from the deck list.

3 Choose **OK**. The deck appears as the current deck.

4 Choose **Save** to save the deck and exit **Deck Editor**.

Creating a New Deck

When a new deck is created, it is initially a copy of the currently open deck. A new deck may be created for many reasons, including:

- To maintain the previous deck configuration when switching between different deck layouts.
- When similar deck configurations exist, but with differences between one or two positions.
- When devices replace deck positions.

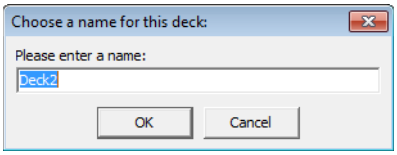
To create a new deck:

1 In the **Deck Editor**, open the deck to copy as a basis for the new deck (refer to *Opening and Selecting a Deck*).

2 Select 

. **Choose a name for this deck:** displays (Figure 5.6).

Figure 5.6 Enter a New Name for the Deck



3 Enter a name for the new deck.

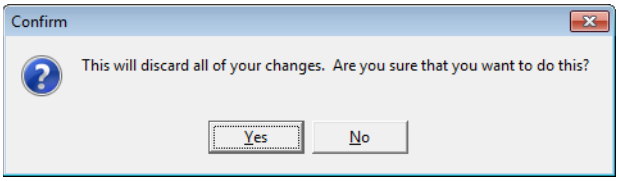
4 Choose **OK** to save the deck name and return to the **Deck Editor.** A copy of the selected deck appears, using the new name, and is ready for modification.

5 If desired, make modifications to the new deck.

6 Choose **Save** to save the new deck and exit **Deck Editor.**

NOTE Choose **Cancel** to cancel the modifications made to the deck. A **Confirm** message appears to confirm cancellation of the changes (Figure 5.7).

Figure 5.7 Confirmation to Cancel



Deleting a Deck

If a deck is no longer needed, it may be deleted.

NOTE Once a deck is deleted in the **Deck Editor,** it cannot be retrieved via the **Deck Editor**. It can be retrieved, however, using the **Import/Export Utility** (refer to CHAPTER 3, *Using Instrument Files and Settings*).

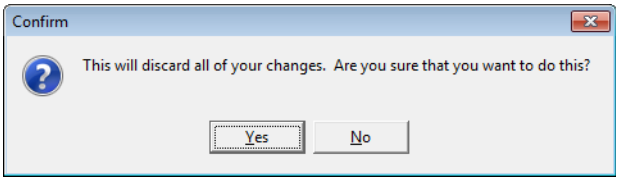
To delete a deck:

1 Open the deck to delete (refer to *Opening and Selecting a Deck*).

2 Select 

. A **Confirm** message appears (Figure 5.8).

Figure 5.8 Delete Deck Confirmation



3 Choose **Yes** to delete the deck. The deck is deleted.

4 Choose **Save** to exit the **Deck Editor**.

NOTE Choose **Cancel** to cancel the deletion of the deck.

Renaming a Deck

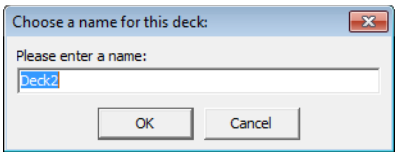
Rename a deck to easily identify it.

To rename a deck:

1 Open the deck to rename (refer to *Opening and Selecting a Deck*).

2 Choose Rename Deck. **Choose a name for this deck:** appears (Figure 5.9).

Figure 5.9 Change Deck Name



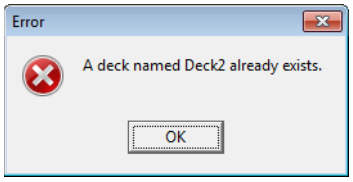
3 Enter the desired deck name.

NOTE Names for deck positions must be alphanumeric with no spaces; the only non-alphanumeric character allowed is "_" (underscore). The first character must be a letter.

4 Choose **OK** to save the deck under the new name.

NOTE An **Error** similar to Figure 5.10 appears if the new name already exists. Choose another name.

Figure 5.10 Error in Renaming



5 Choose **Save** to exit the **Deck Editor.**

NOTE Choose **Cancel** to cancel the renaming of the deck.

Modifying a Deck

Labware positioners and devices on a Biomek 4000 instrument are referred to as ALPs in **Deck Editor.** Modifying a deck includes:

- Opening the deck to modify or create a new deck (refer to *Creating a New Deck*).
- Deleting ALPs and deck positions from the open deck as necessary.
- Adding ALPs and deck positions as necessary.
- Setting ALP and deck position properties.

Deleting ALPs and Deck Positions from a Deck

When a deck is copied or a new deck is created, it is necessary to remove ALPs no longer needed. Remove these ALPs so that other ALPs can be added.

To remove ALPs:

1 Click on the ALP to delete in the Deck View.

NOTE Notice that the ALP is highlighted with a pink border, and deck positions are highlighted with a yellow border. If a single position within a multiposition ALP is selected, it is highlighted pink.

2 Select **Delete ALP** from the toolbar.

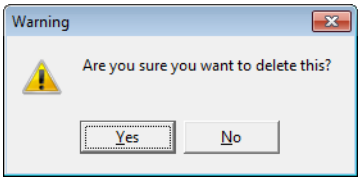
OR

Press (Delete) on the keyboard.

OR

Right click on the deck position and select **Delete** from the menu that appears. A **Warning** prompt appears (Figure 5.11).

Figure 5.11 Confirmation to Delete ALP



3 Choose **Yes** to delete the ALP. The modified deck appears in the Deck View.

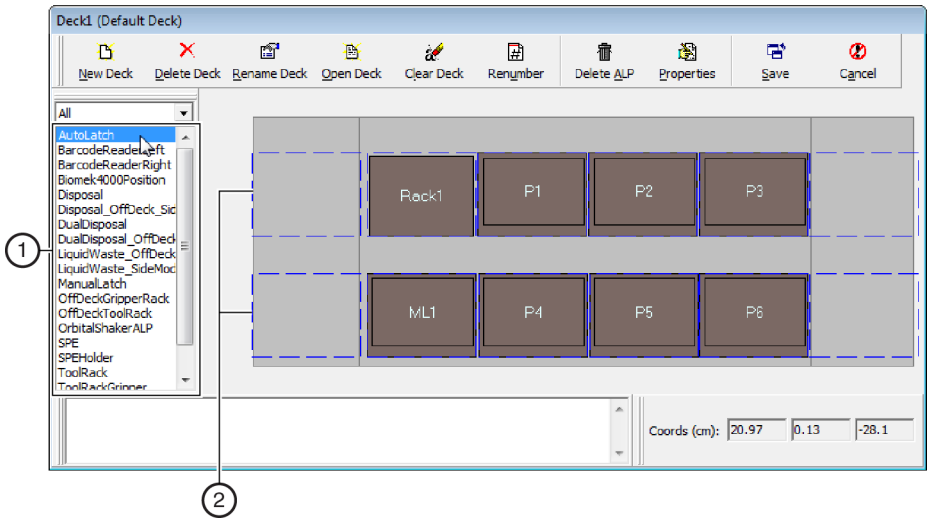
Adding ALPs and Deck Positions

New ALPs can be added to the deck in the appropriate locations. Deck positions are part of ALPs and are named automatically when added to a deck.

To add ALPs to the deck:

1 Click and hold the mouse button on the desired ALP in the ALP Types List (Figure 5.12). Notice that the locations capable of supporting the ALP are indicated by dashed boxes.

Figure 5.12 Possible Autolatch Deck Positions



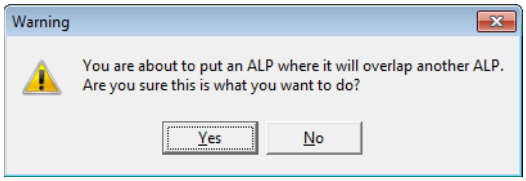
1. **ALP Types List**
2. **Dashed lines indicate where the selected ALP can be placed on the deck.**

2 **Drag and drop the ALP** from the ALP Types list to the desired location. The ALP appears and deck positions are named automatically.

NOTE The positions may be renamed (refer to *Setting ALP Properties and Deck Positions*).

NOTE If the desired ALP is about to be placed where another ALP is currently placed on the deck, the following warning appears (Figure 5.13). Delete the currently-placed ALP before placing the desired ALP on the deck (refer to *Deleting ALPs and Deck Positions from a Deck*).

Figure 5.13 Warning Appears Because an ALP is About to be Placed Where it Will Overlap Another ALP



Setting ALP Properties and Deck Positions

After a new ALP is placed on the deck, set the properties of the ALP and related deck positions (Table 5.2).

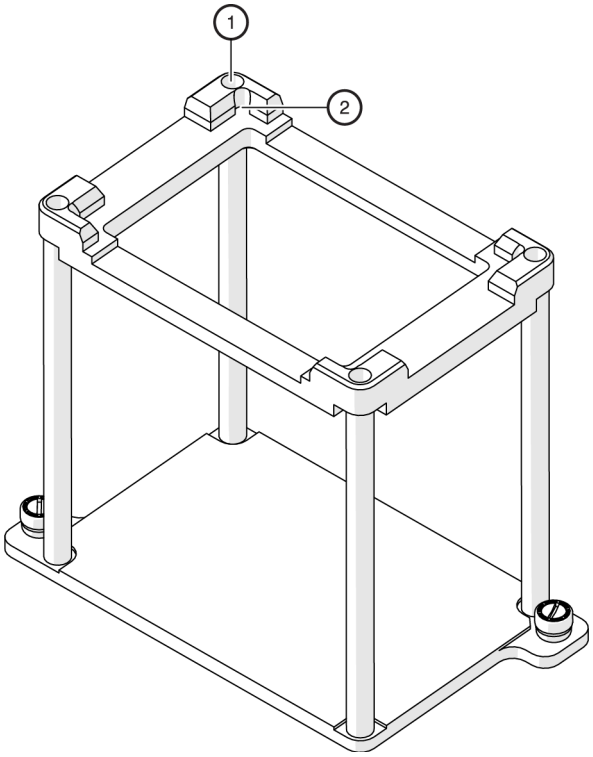
The following properties may be configured for ALPs or deck positions:

Table 5.2 ALP and Position Properties

Property	Description	Applies To...
Name	The name of the deck position as shown in the **Instrument Setup** step. ALPs have related names that do not appear in the **Instrument Setup**.	Position and ALP
Pod1 Coordinates	The coordinate location of the back left corner of the position on the instrument platform (Figure 5.14).	Position and ALP
Device	Instrument associated with a deck position (refer to *Setting ALP Properties*). Displayed only when **More** > is selected.	Position
Device Index	Location of labware in the device associated with a deck position (refer to *Setting ALP Properties*). Displayed only when **More** > is selected.	Position
Labware Offset	The coordinate difference from the Position to the back left corner of the labware (Figure 5.14). Refer to *Setting ALP Properties*. Displayed only when **More** > is selected.	Position
Position Span	Area of the platform the ALP or position covers. (The span for an ALP may be different from the span of a position.) Displayed only when **More** > is selected.	Position and ALP
Min Safe Height	Reserved height above position needed to avoid collisions. Displayed only when **More** > is selected.	Position
Per-Labware Offsets	Coordinate difference between the set Labware Offset to where specific types of labware sit on the deck position (Figure 5.14). Useful for tip loading and when using the SPE Manifold (refer to *Setting ALP Properties*). Displayed only when **More** > is selected.	Position

NOTE Not all properties listed in Table 5.2 may be present. Properties vary according to the instrument and configuration.

Figure 5.14 Position and Labware Offset Locations on the One-By-One ALP



1. **Position**
2. **Labware Position**

Setting ALP Properties

To set properties of the ALP:

---

1 From the Deck View, select the ALP to modify.

NOTE The ALP is selected when the outer edges of the ALP are highlighted pink, and the associated deck positions are highlighted in yellow within the Deck View. Deck positions with green highlights are associated with devices.

---

2 Choose **Properties.**

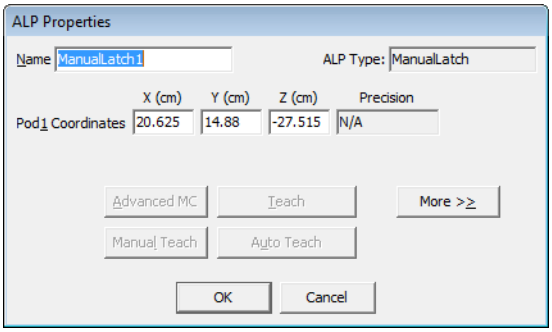
OR

Right click on the ALP in the **Deck Editor** or any of its positions and select **ALP Properties.**

OR

Double click on the ALP on the deck layout. **ALP Properties** appears (Figure 5.15).

Figure 5.15 Biomek 4000 ALP Properties



NOTE Not all properties listed on Figure 5.15 may be present. Properties vary according to the configuration.

3 Change the **Name** of the ALP, if desired.

4 Choose **OK** to save the ALP properties. **Current Deck** appears.

5 Choose **Save** to close the **Deck Editor**.

Setting Deck Position Properties

Deck position properties are similar to ALP properties; however, deck positions include **Labware Offsets** that place the labware in the appropriate place for pipetting operations. Because some deck positions are associated with devices, the **Device** property must be set for these deck positions.

⚠ WARNING

Risk of contamination. Improper Biomek Software configuration of "Hardware Setup," the "Device Action" step, or AutoLatch "Position Properties" in the Deck Editor can cause tip boxes or tips to collide with labware containing biologically or chemically hazardous material, resulting in spills on the Biomek 4000 deck. Always test the system configuration and associated device operations with water before using biological or chemical agents.

To set deck position properties:

1 Select the position to modify.

NOTE The deck position is highlighted with a pink line inside the ALP.

2 Select Properties.

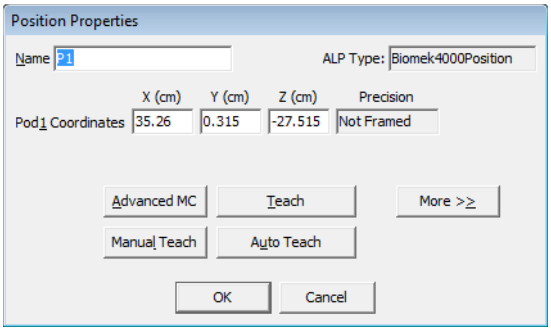
OR

Double click on the deck position.

OR

Right click on the desired position and select **Properties** from the menu that appears. **Position Properties** appears (Figure 5.16).

Figure 5.16 Biomek 4000 Position Properties



NOTE Not all properties listed on Figure 5.16 may be present. Properties vary according to the configuration.

3 Rename the deck position, if desired.

NOTE Names for deck positions must be alphanumeric with no spaces; the only non-alphanumeric character allowed is "_" (underscore). The first character must be a letter.

4 Enter the **X**, **Y**, and **Z Coordinates** of the appropriate pod by framing the ALP. Refer to the *Biomek 4000 Hardware Manual*.

5 Select **More >>**, if necessary.

6 Choose the **Device** name to associate with the position, if required.

NOTE For devices controlled through SILAS, the SILAS module for the device must be installed prior to associating the device with a deck position.

7 If appropriate, select the **Device Index**.

NOTE The **Device Index** works with software modules operating instruments that have more than one position.

8 If appropriate, choose the desired **Sensor Device** to associate the Waste/Sensor with the position.

9 Choose **Per-labware Offsets** to customize the offsets for specific types of labware (refer to *Changing Per-Labware Offsets*).

10 Set the **Min Safe Height**.

NOTE The **Labware Offsets** and **Position Span** are predefined in the software. Do not modify these properties.

11 Choose **OK** to save the deck position properties. **Current Deck** appears.

12 Choose **Save** to close the **Deck Editor**.

Changing Per-Labware Offsets

Modify the per-labware offsets when specialized needs arise. The X, Y, and Z coordinates for the deck position may be modified based upon the labware type. For example, the Z offsets can be changed for a plasmid filter when performing a filtration-based DNA plasmid purification.

To modify the per-labware offsets:

1 Select **Instrument** > **Deck Editor**.

2 Open the desired deck (refer to *Opening and Selecting a Deck*).

3 Select the position to modify.

4 Select **Properties**.

OR

Double click on the deck position.

OR

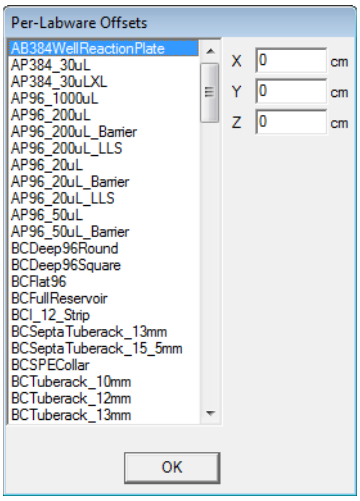
Right click on the desired position and select **Properties**. **Position Properties** appears (Figure 5.16).

5 Choose **More >>**, if necessary.

6 Choose **Per-labware Offsets**.

7 In **Per-Labware Offsets**, select the labware to modify (Figure 5.17).

Figure 5.17 Per-Labware Offsets



NOTE **Per-Labware Offsets** includes labware that is specific to the project file.

8 Enter the desired **X**, **Y**, and **Z** offsets.

NOTE While the offset values may be calculated using calipers, a more precise measurement should be obtained from the manufacturer's drawings.

9 Choose **OK** to save the offset values. **Position Properties** appears (Figure 5.16).

10 Choose **OK**.

11 Choose **Save** to close **Deck Editor**.

Deck Mapping

Deck mapping is the process of mapping an **Instrument Setup** configuration from one Biomek deck layout to another. Deck mapping is necessary when a method is imported from another system with a different deck, or when the deck selection within the **Instrument Setup** step of method is changed. The **Instrument Setup** step allows a user to specify on which deck the proceeding method is written. (See CHAPTER 15, *Instrument Setup Step* for details in configuring an **Instrument Setup** step.)

If a deck of the same name is not available when migrating a method from another system, Biomek Software prompts you to **Map Onto** an existing deck on that system.

NOTE Labware mapped from one deck to another is directly tied to the labware position name. If position names are different, additional steps will need to be taken to ensure successful deck mapping. In most cases, tools will need to be reconfigured on the new deck.

Depending on the setup configurations of the two Biomek systems, when importing a method from another Biomek system onto the Biomek 4000 system, you will need to proceed with the option below that applies to the current circumstances.

NOTE The sections below require methods to be exported from Biomek Software, version 3.3, and imported into Biomek Software, version 4.0. Instructions for importing and exporting methods can be found in CHAPTER 12, *Importing and Exporting Methods*.

- *Identical Deck Names, Identical Configurations*
- *Identical Deck Names, Different Configurations*
  - *Same Position Names, Different Layout*
  - *Different Position Names*
- *Different Deck Name, Identical Configurations*
- *Different Deck Name, Different Configuration*

Identical Deck Names, Identical Configurations

To import Biomek methods containing the same deck name with the same configuration as the Biomek 4000 deck:

1 Export the method from the original Biomek system.

2 Import the method into Biomek Software, version 4.0. No further action is required.

Identical Deck Names, Different Configurations

If the original Biomek method contains the same deck name as the Biomek 4000 method, but the decks are configured differently from each other, determine which of the following scenarios applies to the method, and complete the instructions provided:

- *Same Position Names, Different Layout*
- *Different Position Names*

Same Position Names, Different Layout

For decks that have the same position names, but the layouts of those positions are different, do the following:

1 Open the method on the original Biomek instrument.

2 View the **Instrument Setup** step, noting the details of the following:

- Name of the deck used in **Instrument Setup** step
- Deck layout
- Labware used
- Labware properties
- Deck positions of the labware

3 Export the method from the original Biomek system.

4 Open Biomek Software on the Biomek 4000 instrument.

5 Examine the current deck layout, taking note of the location of the deck positions.

6 Import the method onto Biomek Software, version 4.0.

NOTE All labware maps to the new deck, but the deck layout is different than the previous deck. For example, Figure 5.18 shows the deck in a Biomek 3000 method, and Figure 5.19 shows the same deck after being imported into Biomek Software, version 4.0. Figure 5.20 and Figure 5.21 show the decks in the **Deck Editor**.

Figure 5.18 Biomek 3000 Deck—Instrument Setup

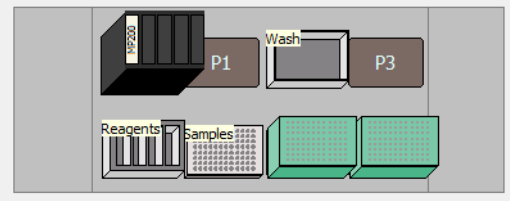


Figure 5.19 Biomek 4000 Deck—Instrument Setup

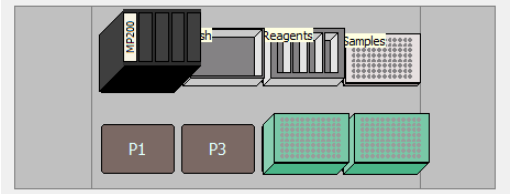


Figure 5.20 Biomek 3000 Deck—Deck Editor

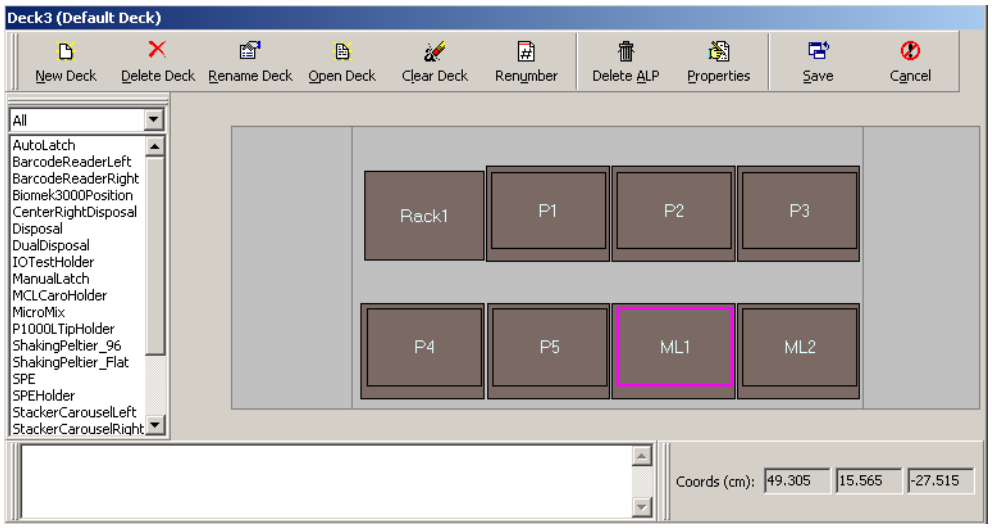
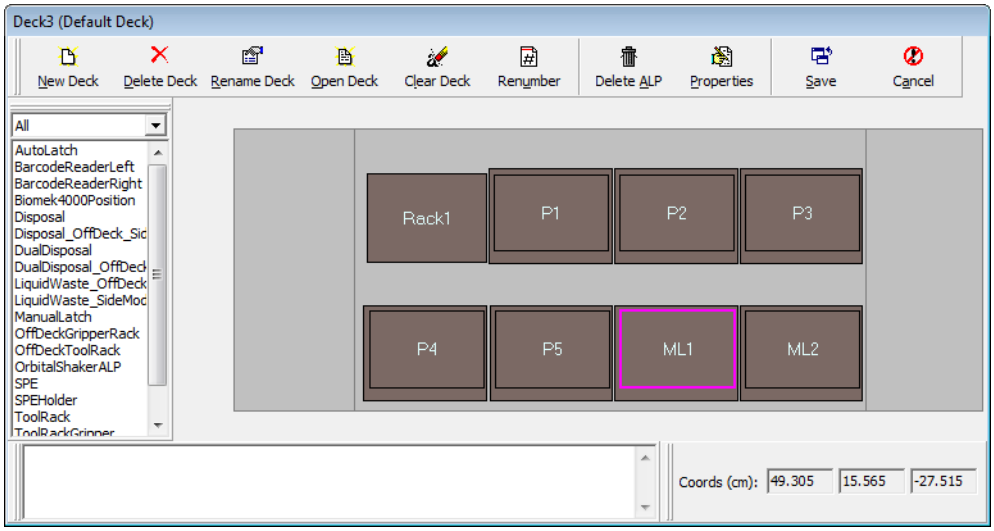


Figure 5.21 Biomek 4000 Deck—Deck Editor



7 Proceed with one of the following. If you wish to:

- **Keep labware in the new configuration**, no further method rework is required.
- **Reconfigure the labware on the deck to reduce flyover and to optimize labware placement for efficiency**, some method steps might need to be reconfigured to be compatible with the new deck setup (see *Deck Mapping and Method Repair* for details).

8 Confirm that all original labware has mapped onto the new deck.

9 Select the **Finish** step in the method to check for any validation errors.

10 If necessary, correct any validation errors. See CHAPTER 24, *Validation Errors* for additional information.

IMPORTANT Always run modified method in simulation mode or with water before live execution.

Different Position Names

If the decks from both Biomek systems have identical names, but contain different position names, reconfigure the setup by doing the following:

1 Open the method on the original Biomek system.

2 View the **Instrument Setup** step, noting the details of the following:

- Name of the deck used in **Instrument Setup** step
- Deck layout
- Labware used
- Labware properties
- Deck positions of the labware

3 Correct the data mismatch using one of the three options below:

***Option 1*—Reconstruct the deck using the Biomek 4000 system:**

a. Export the method from the original Biomek system.

b. Import the method onto Biomek Software, version 4.0.

NOTE This might cause labware to be lost. For example, Figure 5.22 shows the deck in the Biomek 3000 method, and Figure 5.23 shows the same deck after being imported into Biomek Software, version 4.0. Figure 5.24 and Figure 5.25 show the decks in the **Deck Editor**.

Figure 5.22 Biomek 3000 Deck—Instrument Setup

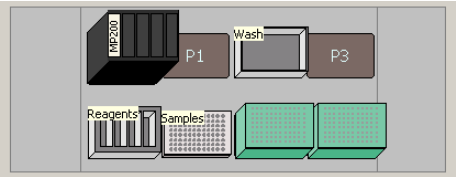


Figure 5.23 Biomek 4000 Deck—Instrument Setup

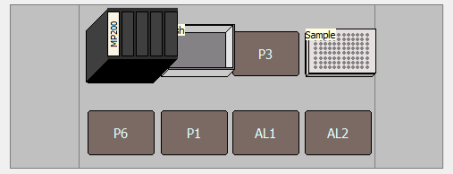


Figure 5.24 Biomek 3000 Deck—Deck Editor

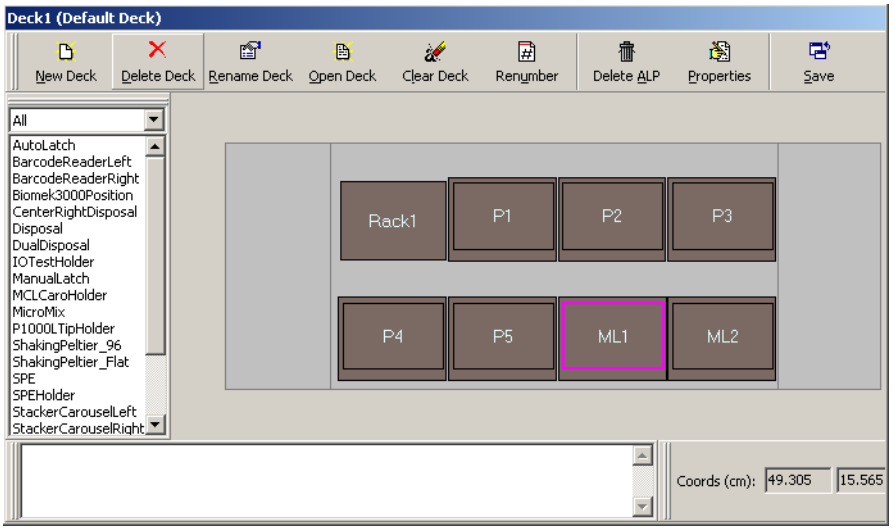
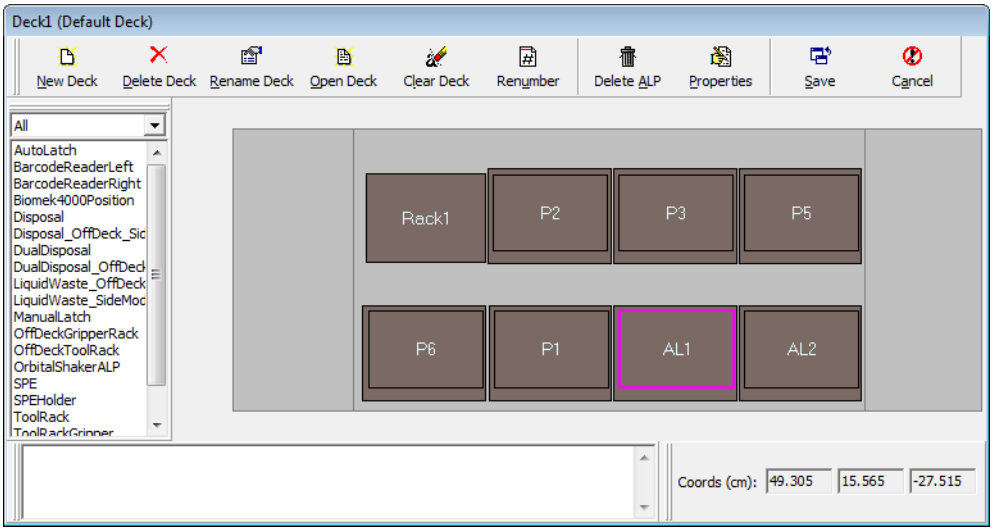


Figure 5.25 Biomek 4000 Deck—Deck Editor



c. Reconfigure the deck to match the original Biomek method, adding lost labware and making other adjustments in the **Instrument Setup** step of the new method.

***Option 2*—Change the names of the deck positions in Biomek Software, version 4.0, to match those used in the original Biomek method.**

a. Export the method from the original Biomek system.

b. Rename deck positions on the Biomek 4000 system to match those of the original system.

IMPORTANT This option is only viable on systems that do not already have other methods using the current deck.

c. Import the method to the Biomek 4000 system.

Option 3—**Change the deck in the original Biomek method to allow for easy importing into the Biomek 4000 system:**

a. Rearrange labware in the original Biomek method **Instrument Setup** step to use only the positions existing on the Biomek 4000 deck.

b. Export the method from the original Biomek system.

c. Import the method to the Biomek 4000 system.

4 Confirm that all original labware has been placed onto the new deck.

5 Select the **Finish** step check for validation errors. Some method steps may need to be reconfigured to be compatible with the new deck setup. See *Deck Mapping and Method Repair* for details.

IMPORTANT Always run modified method in simulation or with water before live execution.

Different Deck Name, Identical Configurations

If the original Biomek method contains a different deck name from the Biomek 4000 method, but the decks are configured exactly the same, as shown in Figure 5.26 (Deck1) and Figure 5.27 (Deck4), follow the procedure below.

Figure 5.26 Biomek 3000 Deck

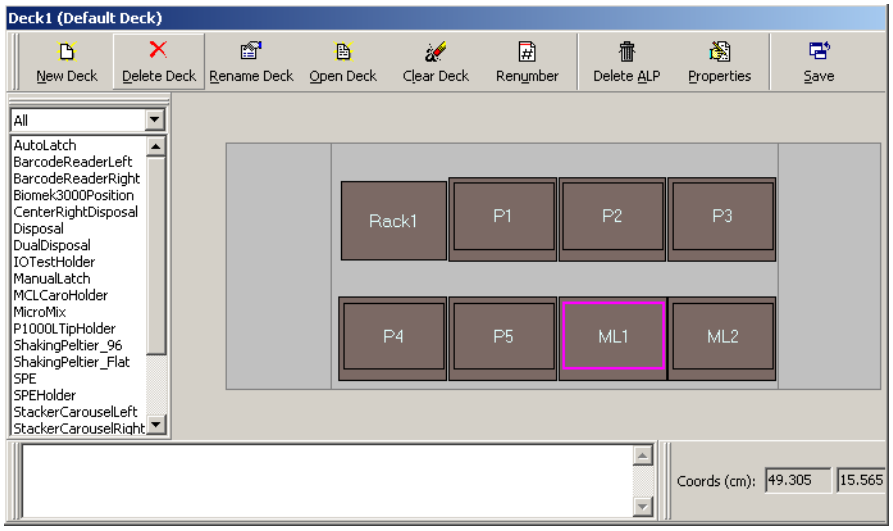
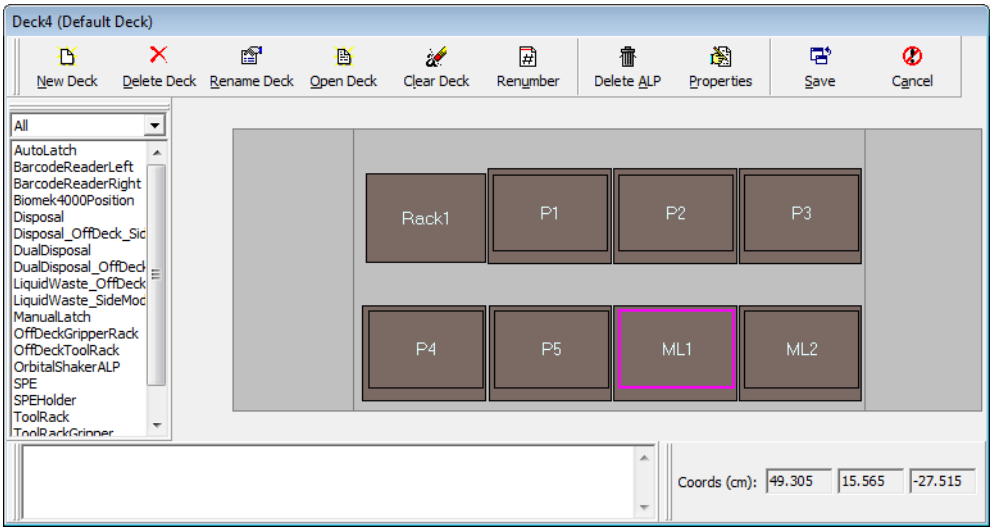


Figure 5.27 Biomek 4000 Deck



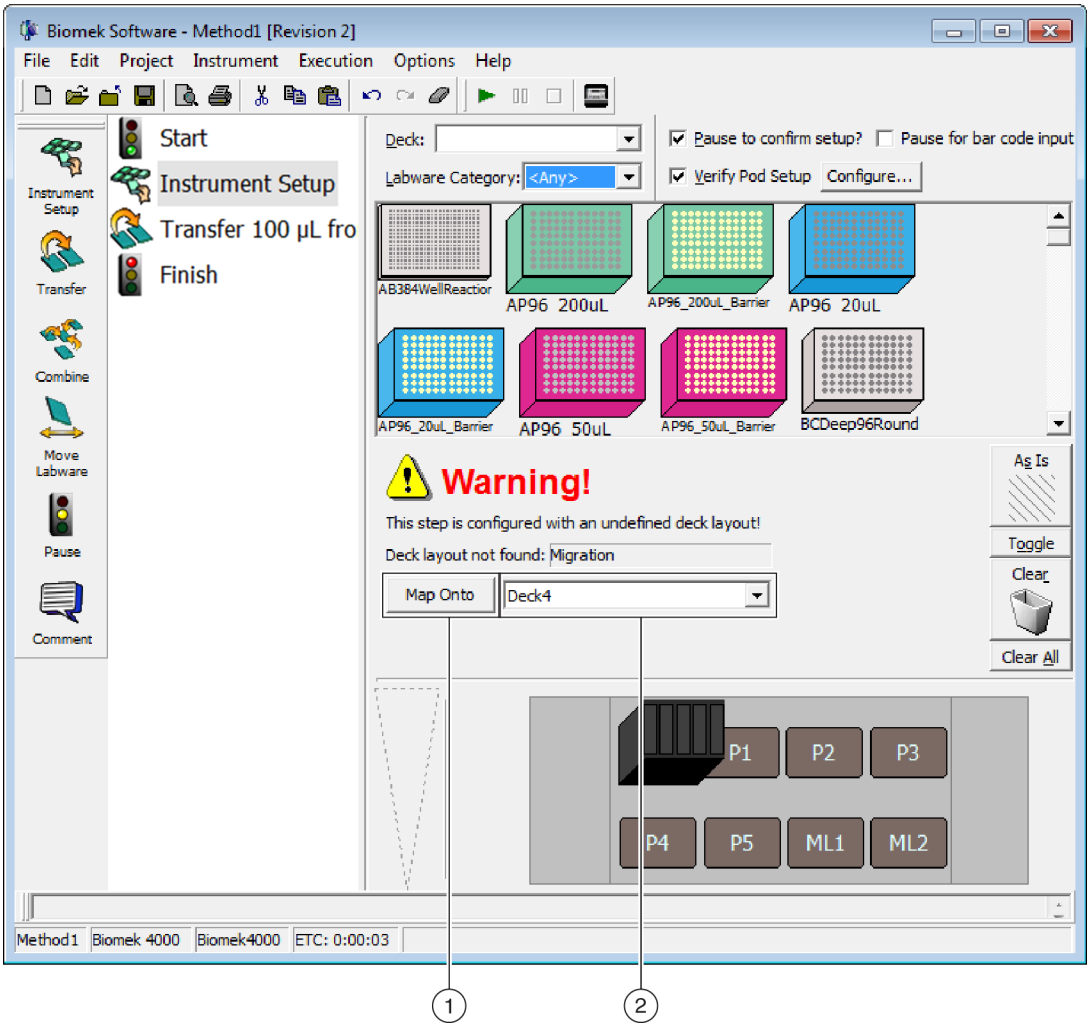
1 Export the method from the original Biomek system.

2 Import the method into the Biomek 4000 system.

The **Instrument Setup** step(s) produces the following warning: **This step is configured with an undefined deck layout!**

3 Choose the appropriate deck in the drop-down, and then select **Map Onto** (see Figure 5.28).

Figure 5.28 Undefined Deck in Instrument Setup Step



1. **Map Onto**: Select after choosing the appropriate deck to use in the method.
2. **Deck** drop-down: Choose the appropriate deck to use for the method from the drop-down.

4 Confirm that all original labware (Figure 5.29) is located on the new deck (Figure 5.30).

Figure 5.29 Original Labware on Deck1 in Biomek Software (Version 3.3)

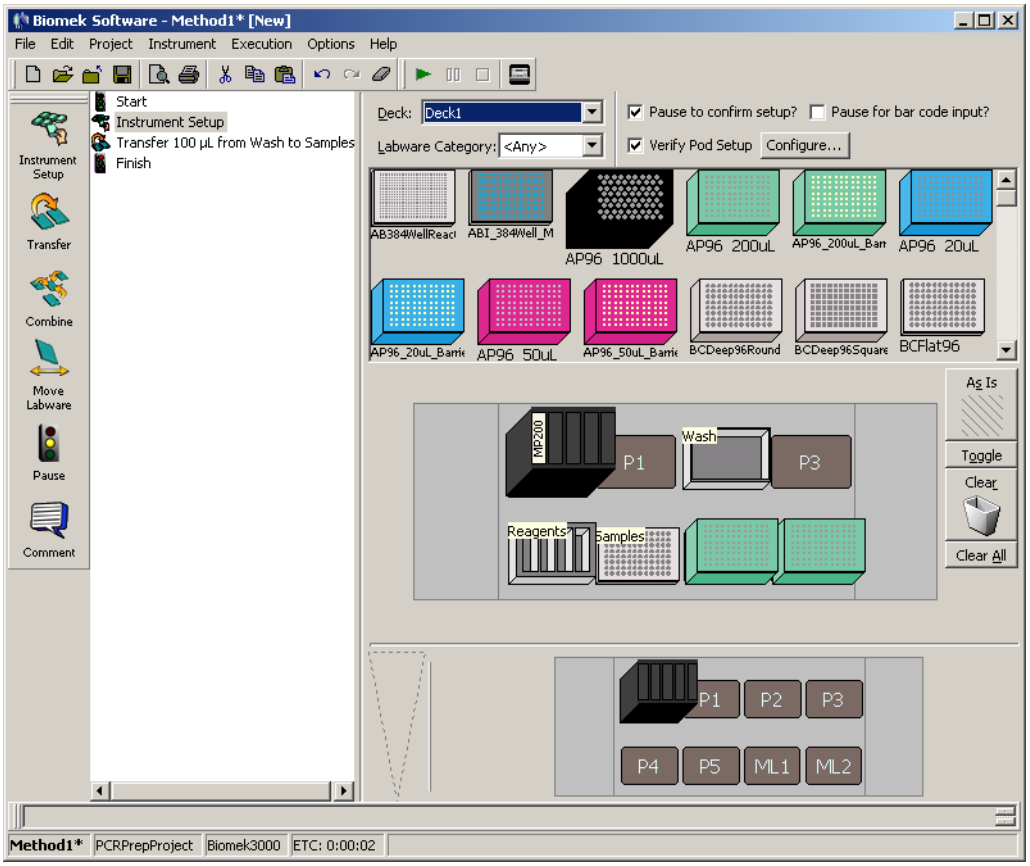
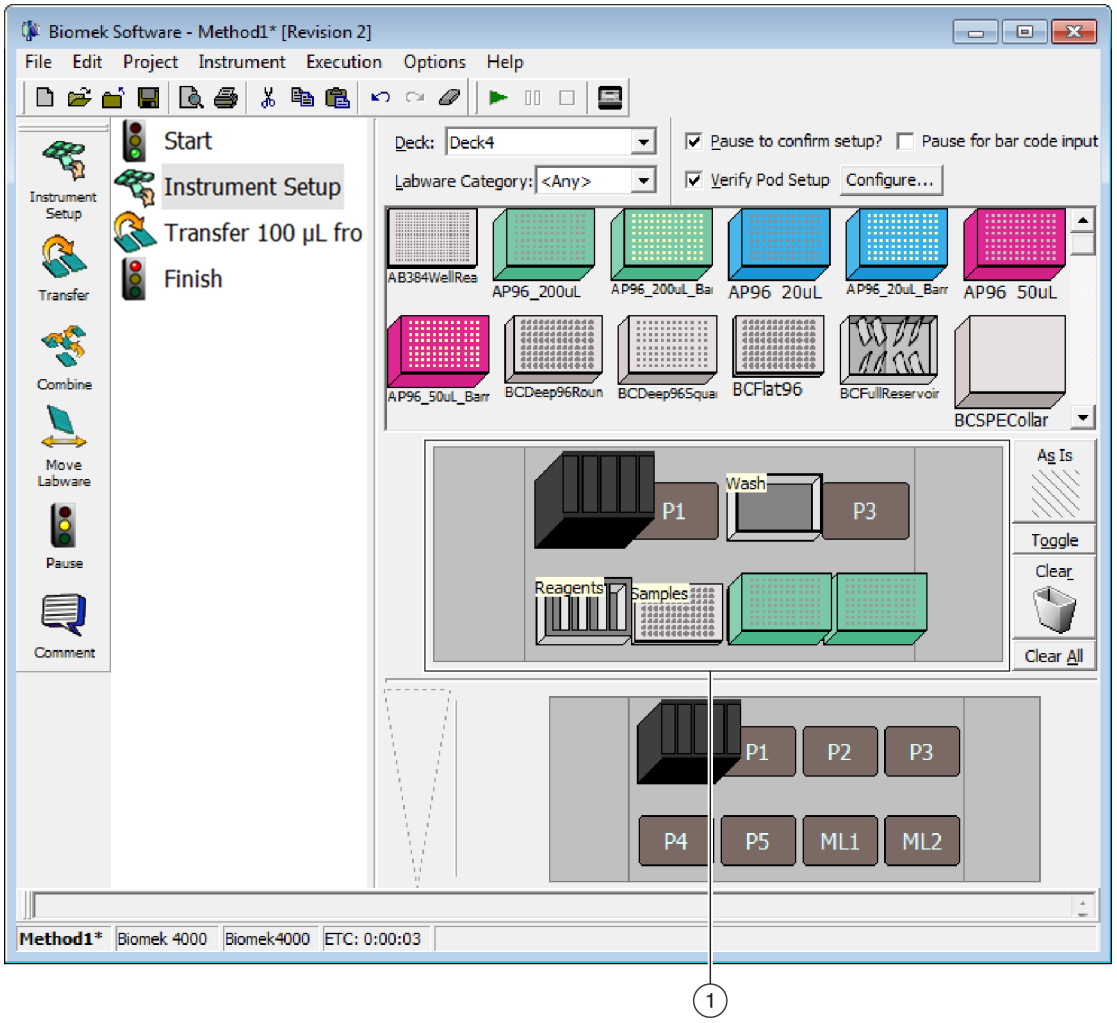


Figure 5.30 New Deck Defined in the Biomek Software (Version 4.0) Instrument Setup Step



1. Verify that the all labware from the Biomek 3000 method is present on the Biomek 4000 deck.

Different Deck Name, Different Configuration

If the original Biomek method contains a different deck name from the Biomek 4000 method, and the decks are configured differently, do the following:

---

1 Open the method on the original Biomek system and view the **Instrument Setup** step, noting the details of the following:

- Name of the deck used in **Instrument Setup** step
- Deck layout
- Labware used
- Labware properties
- Deck positions of the labware

---

2 Open Biomek Software on the Biomek 4000 instrument, taking note of the available deck and all deck positions available for use.

---

3 Correct the data mismatch using one of the three options below:

***Option 1*—Reconstruct the deck using the Biomek 4000 system:**

a. Export the method from the original Biomek system.

b. Import the method to the Biomek 4000 system.

c. The **Instrument Setup** step(s) produces the following warning: **This step is configured with an undefined deck layout!**

d. Choose the appropriate deck from the drop-down, and then select **Map Onto** (Figure 5.28).

NOTE This might cause labware to be lost.

e. Add lost labware and configure in the **Instrument Setup** step of the method on the new system to match the original system.

***Option 2*—Change the names of the deck positions in Biomek Software, version 4.0, to match those used in the original Biomek method.**

a. Export the method from the original Biomek system.

b. Rename deck positions on the Biomek 4000 system to match those of the original system.

c. Import the method to the new system.

d. The **Instrument Setup** step(s) produces the warning: **This step is configured with an undefined deck layout!**

e. Choose the appropriate deck from the drop-down, and then select **Map Onto** (Figure 5.28).

IMPORTANT This option is only viable on systems that do not already have other methods using the current deck.

***Option 3*—Change the deck in the original Biomek method to allow for ease of importing into the Biomek 4000 system:**

a. Rearrange labware on the original Biomek **Instrument Setup** step to use only those positions that are existing on the Biomek 4000 deck.

b. Export the method from the original Biomek system.

c. Import the method into the Biomek 4000 system.

d. The **Instrument Setup** step(s) produce the warning: **This step is configured with an undefined deck layout!**

e. Choose the appropriate deck from the drop-down, and then select **Map Onto** (Figure 5.28).

4 Confirm that all original labware has been placed onto the new deck.

5 Select the **Finish** step to check for validation errors. If errors occur, correct them (see CHAPTER 24, *Validation Errors* for details).

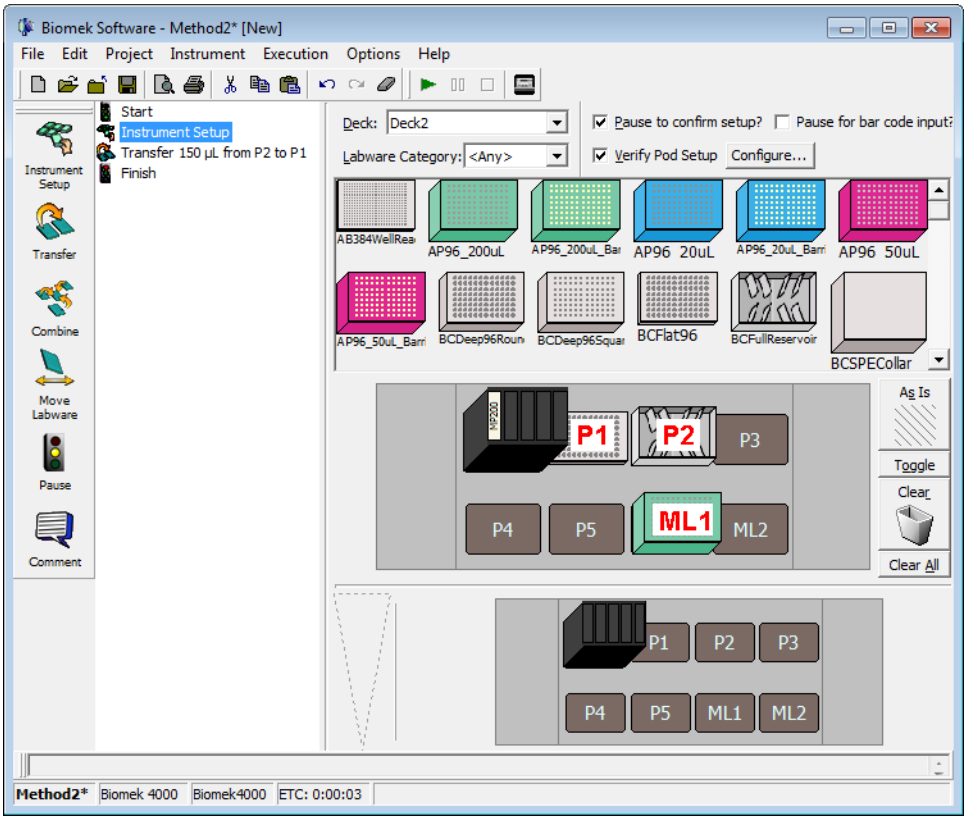
IMPORTANT Always run modified method in simulation or with water before live execution

Deck Mapping and Method Repair

If your Biomek 4000 deck layout has changed significantly from the layout of your original Biomek deck, steps within imported methods could contain validation errors, requiring reconfiguration to work properly. Likewise, labware within the **Instrument Setup** step might need to be rearranged for optimal placement.

TIP When building methods, it is helpful to name labware by right-clicking on the labware (in the **Instrument Setup** step), selecting **Properties**, and entering the name in the **Name** field). This allows for method steps (**Transfer** step, **Move Labware** step, tip loading) to use the labware name instead of position names. When mapping to various deck configurations, this requires less method rework, as labware names will not change when mapping a deck.

Figure 5.31 Biomek 3000 Method Imported Into Biomek Software, Version 4.0



To successfully map the deck, labware from the imported method (Figure 5.31) is relocated to new positions on the deck (Figure 5.33). The steps within method remain as configured on the original deck (transfer from **P2** to **P1**) causing a validation error (Figure 5.32). Each step within the method using these labware items will require reconfiguration to prevent validation errors.

Figure 5.32 Validation Error

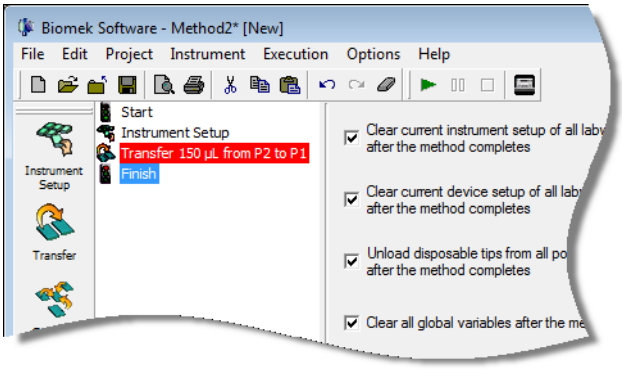
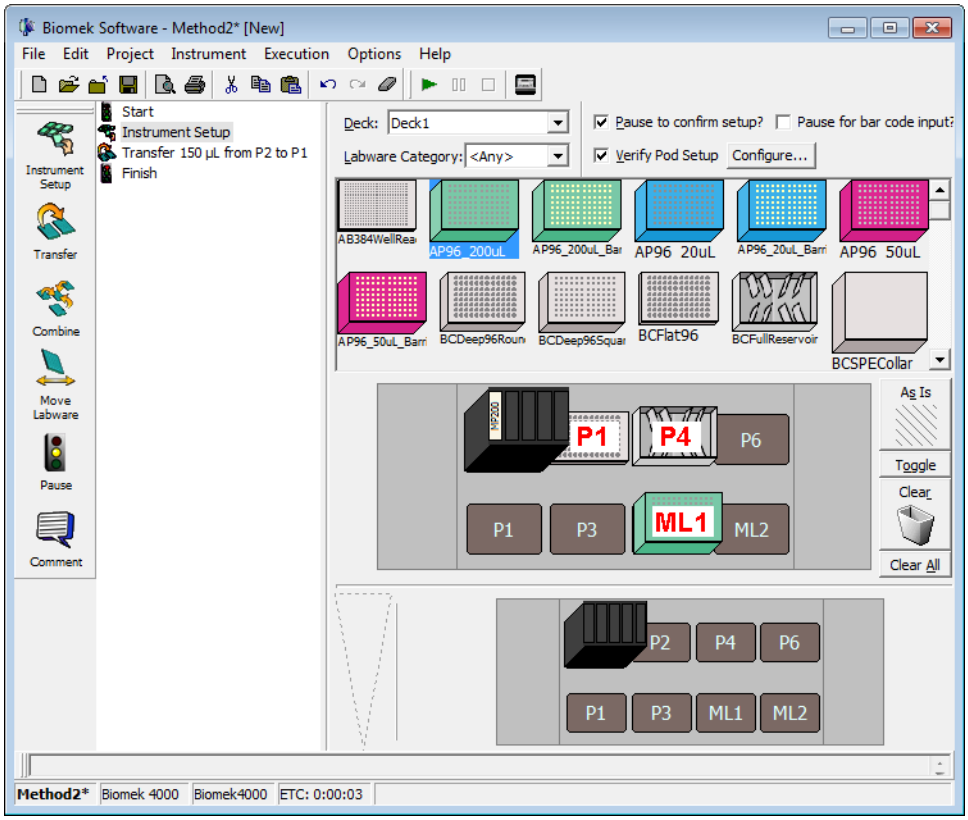


Figure 5.33 Mapped Method



Using Named Labware

When the method in Figure 5.34 is mapped, the **Transfer** step uses labware names instead of positions within the method, and, therefore, does not require further attention. Figure 5.35 shows the method mapped to a different deck; validation errors are not present.

Figure 5.34 Biomek 3000 Method Imported Into Biomek Software, Version 4.0

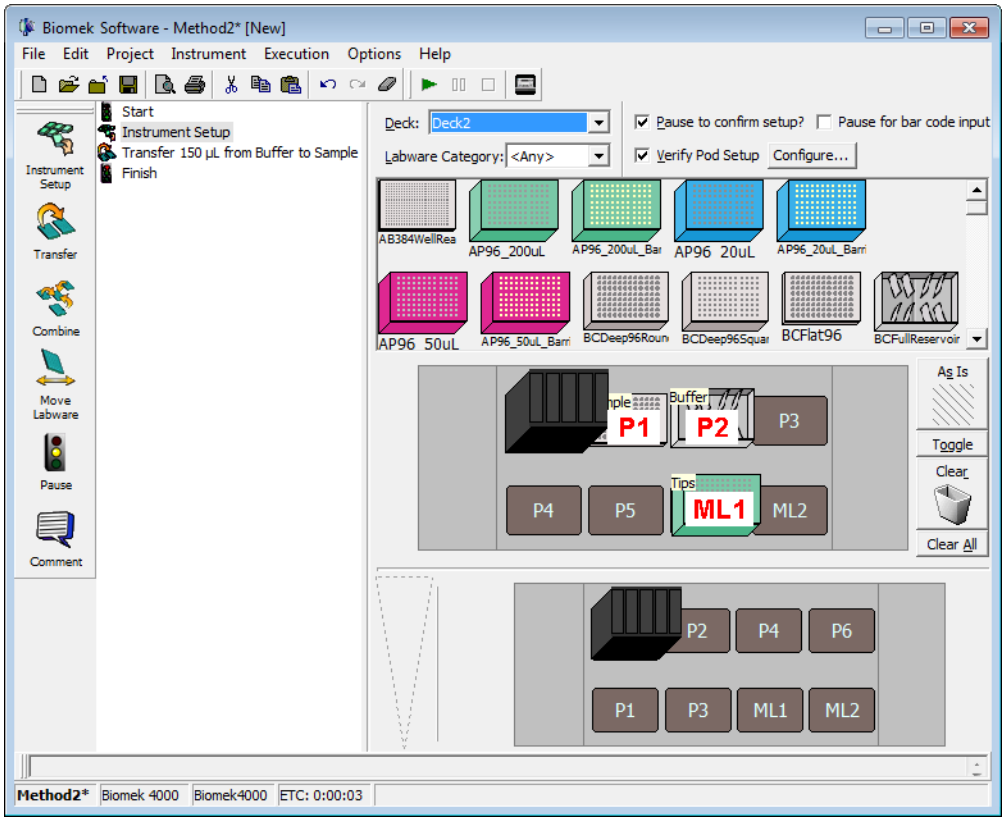
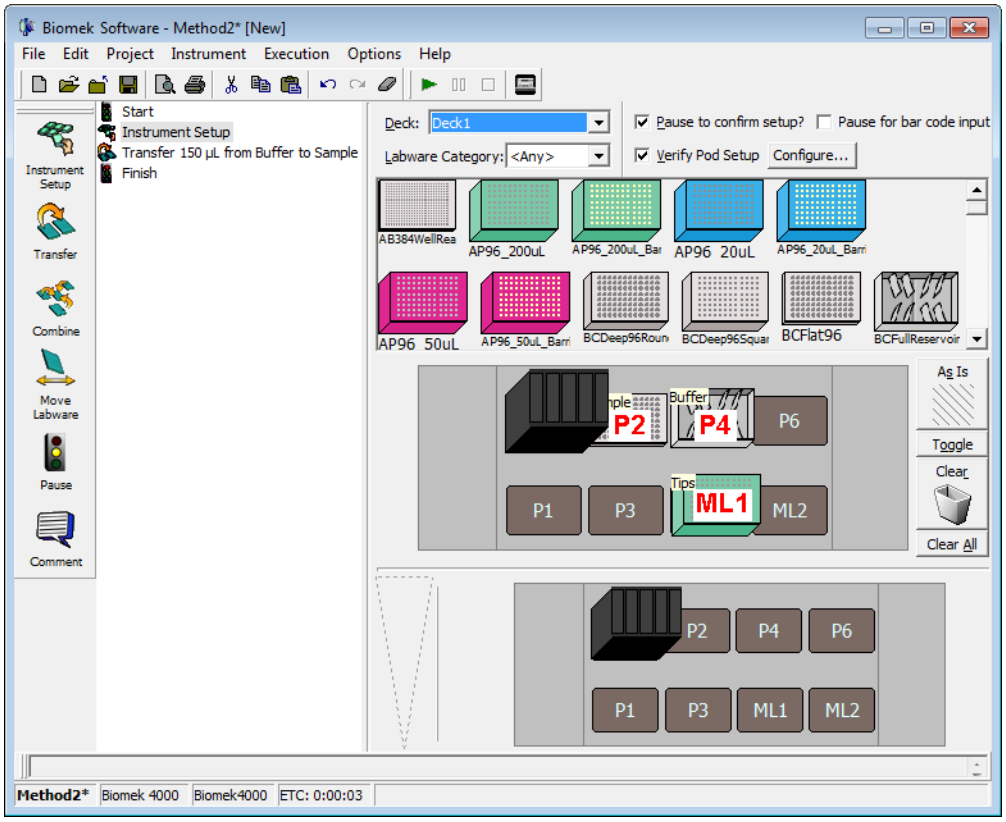


Figure 5.35 Mapped Method



CHAPTER 6

Understanding and Using Project Files

Overview

A project file stores information about liquid types; labware and tip types; well patterns; and pipetting templates and techniques as revisions that are used by a method file to configure the actions of the instrument. Project files store a history of all changes, additions, and deletions of items from the project file.

When a project file is checked in, all items become revisions that are permanently saved. If an item is deleted, that item is no longer available in method building; however, the revision remains in the project file and is used for older validated methods that utilize that revision. If an item is modified, the new definition is stored as a separate revision. Older revisions remain as part of the project file and are used by older validated methods that utilize that record. However, only the newest revision, or working revision, is available in method building. In this way, a validated method can always be run with the exact same revisions of project items, even if those project items have since been modified or deleted (refer to CHAPTER 12, *Validating a Method*).

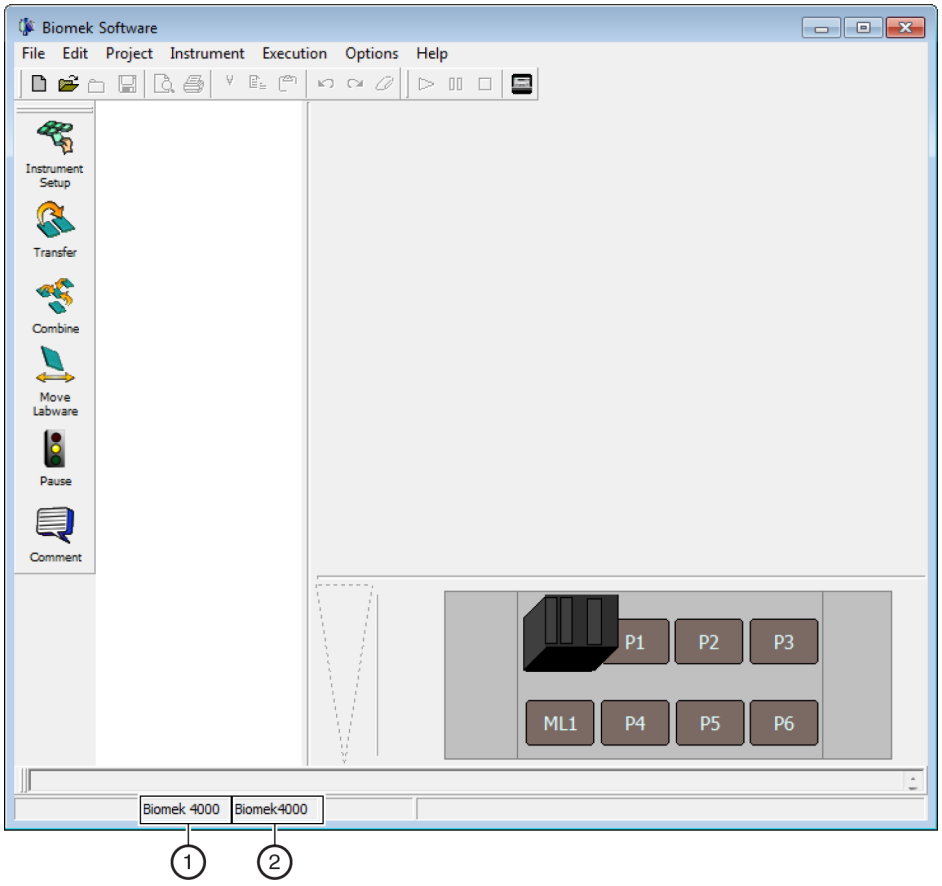
Methods are associated with projects and contain all of the items required to perform the method. Saving a method automatically checks in the method, creating a record of the revision that preserves the method configuration at the time it was saved (refer to CHAPTER 12, *Saving a Method*).

NOTE If Beckman Coulter Accounts & Permissions is used with Biomek Software, project files also maintain a history of who makes changes to any revisions in the project file.

The active project file and instrument file are displayed in the status bar of the method editor (Figure 6.1). Any project file can be used with any instrument file. Validated methods, however, are validated for a specific instrument and are no longer validated when used with a different instrument file, even if the instrument file is equivalent to the one on which the method is validated.

NOTE Validating a method for a specific instrument is not the same as validating a method before a run to internally test the method for errors before it is run. To validate a method to test for errors before it is run, check **Validate the current method before running it** in **Preferences** (refer to CHAPTER 28, *Changing Window Appearance*).

Figure 6.1 Biomek Method Editor



1. **Active project file**
2. **Active instrument file**

The **Project** menu contains options to access, create, save, view contents of, import, and export projects, as well as provide access to the editors to create, modify, and delete project items.

The sections in this chapter include:

- *Creating a New Project File*
- *Opening a Project File*
- *Deleting, Restoring and Renaming Project Files*
- *Creating a Copy of a Project File*
- *Modifying Project Items*
- *Viewing Project Contents*
- *Reverting Projects*
- *Changing Access to Projects*
- *Importing and Exporting Project Files*

Contents of a Project File

A project file contains all:

- **Labware Classes** — Definitions for microplates, reservoirs, tip boxes, and other labware used in a method, as specified in the **Labware Type Editor** (refer to CHAPTER 7, *Defining Labware Types*).
- **Labware Patterns** — Definitions of patterns of wells to aspirate or dispense from, as specified in the **Well Pattern Editor** (refer to CHAPTER 11, *Creating Well Patterns*).
- **Liquid Types** — Definitions for reagents used in a method, as specified in the **Liquid Type Editor** (refer to CHAPTER 8, *Understanding and Creating Liquid Types*).
- **Pipetting Templates** — Templates of how pipetting operations are performed, as specified in the **Pipetting Template Editor** (refer to CHAPTER 10, *Using the Pipetting Template Editor*).
- **Techniques** — Configuration of properties and parameters for all pipetting operations, as specified in the **Technique Browser** and **Technique Editor** (refer to CHAPTER 9, *Understanding and Creating Techniques*).
- **Tip Classes** — Definitions for tips used in a method, as specified in the **Tip Type Editor** (refer to CHAPTER 7, *Defining Tips*).

In addition, methods are associated with a project file. To open a method, the project file that was used to create the method must be the active project.

NOTE If a method is open when a project file is closed to open a new project, a prompt appears to check in, save, or discard the current method.

Creating a New Project File

Any number of project files may exist on any system. This allows separate project files to be created for different applications or different users. Project files customize the instrument performance to the needs of users. For example, users could create their own project files. In this way, users can guarantee that the definitions used are not changed without their knowledge, and keep labware and liquid type catalogs limited to only the ones they use.

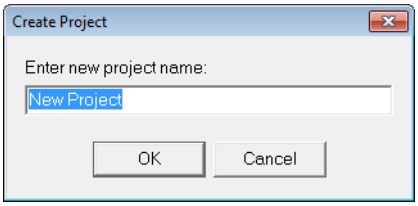
Create Project is used to create a new, blank project file. A new project file has no existing revisions for labware types, liquid types, tip types, pipetting templates or techniques, or well patterns.

NOTE A default project file is automatically created during installation of Biomek Software. The contents of the default project file depend on the options selected during the software installation.

To create a new blank project file:

1 From the **Project** menu, choose **New Project**. **Create Project** appears (Figure 6.2).

Figure 6.2 Create New Project



2 Enter a name for the new project file.

NOTE The project file name must be different from all other project files.

3 Choose **OK** to create a new project with the specified name. **Create Project** closes and the new project becomes the active project file.

OR

Choose **Cancel** to close **Create Project** without creating a new project file.

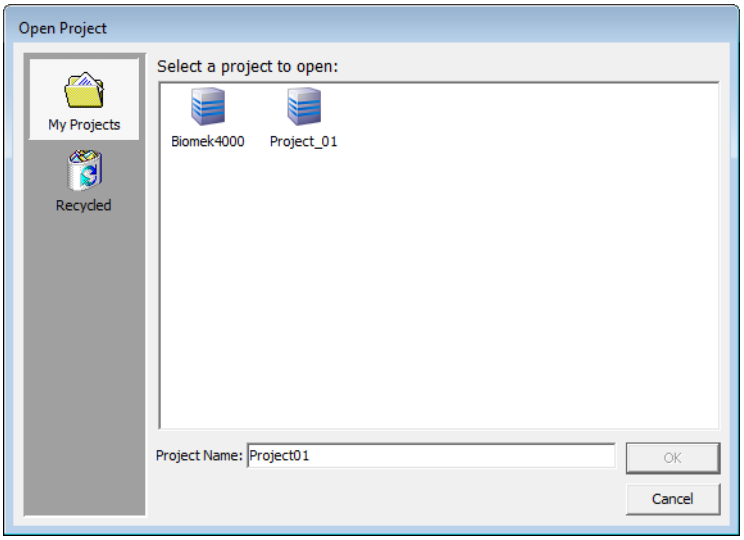
Opening a Project File

A project file can be opened at any time. Opening a project file closes the current active project and any methods that may be open, and opens the selected project.

To open a project file:

1 From the **Project** menu, choose **Open Project**. **Open Project** appears (Figure 6.3).

Figure 6.3 Opening a Project File



2 Select the desired project file to open.

3 Choose **OK** to open the selected (highlighted) project file. **Open Project** closes and the selected project file becomes the active project.

OR

Choose **Cancel** to close **Open Project** without opening a new project file. The current project remains active.

Deleting, Restoring and Renaming Project Files

Projects may be deleted, but are never permanently removed from the system, and may be restored at any time. A saved project may also be renamed.

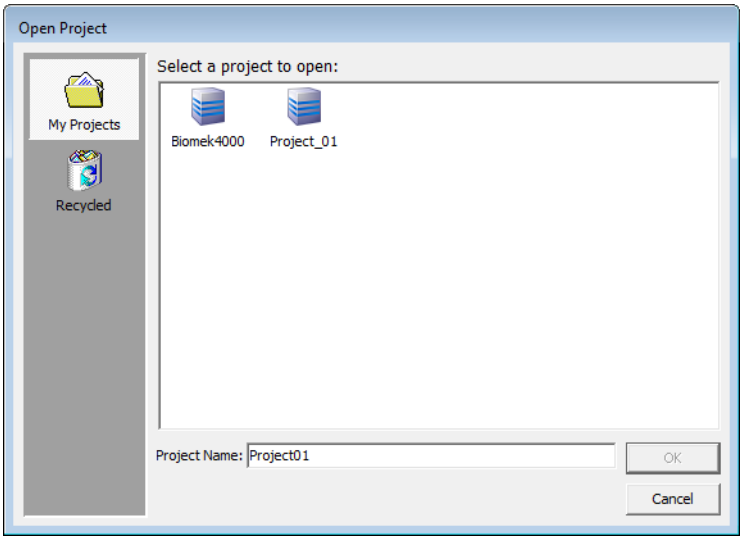
NOTE When multiple instances of Biomek Software are running simultaneously, such as when controlling multiple Biomek instruments, project files are locked. Locked project files may be opened, but not deleted, renamed, or saved.

Deleting Projects

To delete a project:

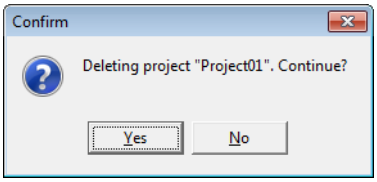
1 From the **Project** menu, choose **Open Project**. **Open Project** appears (Figure 6.4).

Figure 6.4 Open Project



2 Right click the desired project to delete and choose **Delete**. A confirmation appears (Figure 6.5).

Figure 6.5 Confirm Deletion of Selected Project



3 Choose **Yes** to confirm deletion of the selected project. The project is removed from **My Projects** and placed in **Recycled**.

OR

Choose **No** to keep the selected project.

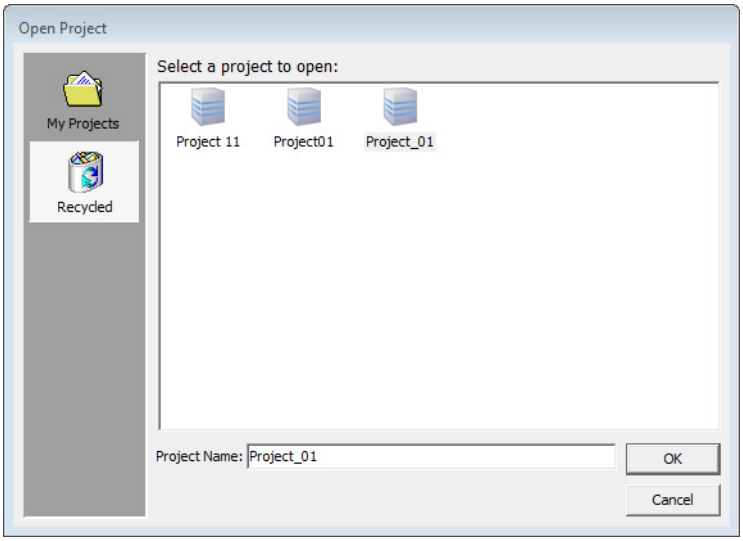
Restoring Projects

To restore a deleted project:

1 From the **Project** menu, choose **Open Project**. **Open Project** appears (Figure 6.4).

2 In the left panel of **Open Method**, choose **Recycled** to view all the projects that have previously been deleted.

Figure 6.6 Recycled Projects



3 Right click the desired project to restore and choose **Restore**. The project is moved from **Recycled** to **My Projects.**

NOTE A project may be opened directly from the **Recycled** folder by selecting the project and choosing **OK**. A confirmation appears stating that the project will be restored prior to opening the project. Choose **OK** to restore and open the project.

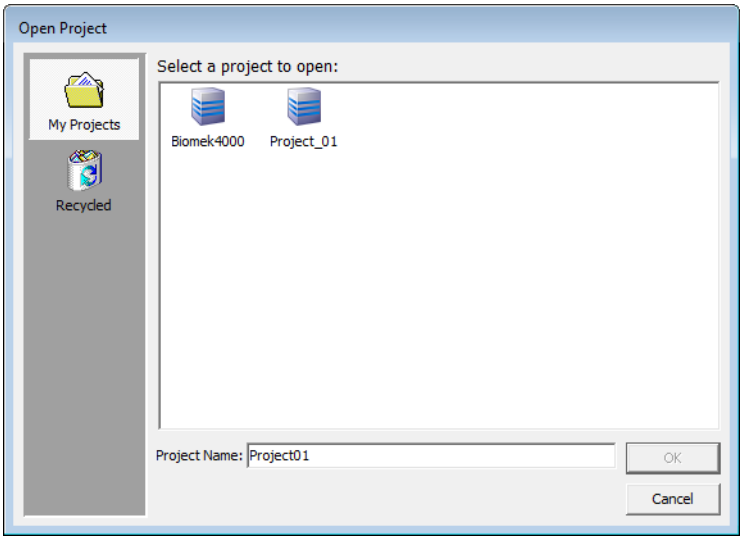
Renaming Projects

NOTE To save a copy of a project file with a new name, use the **Save Project As** command (refer to *Creating a Copy of a Project File*).

To rename a saved project:

1 From the **Project** menu, choose **Open Project**. **Open Project** appears (Figure 6.7).

Figure 6.7 Open Project



2 Right click the desired project to rename and choose **Rename**. The project file name is highlighted.

3 Enter a new name, and press the Enter key.

4 Choose **OK** to close **Open Project**, save the project file with the new name, and open the renamed project file.

OR

Choose **Cancel** to close **Open Project** and save the project with the new name only.

Creating a Copy of a Project File

A project file can be copied to create a new project file based on the original using the **Save Project As** command. A new project created using **Save Project As** maintains all the records from the original project in a new project file.

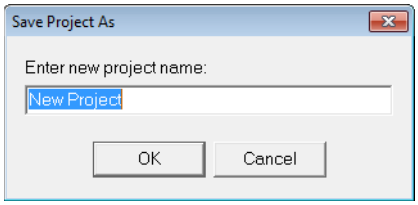
NOTE Using **Save Project As** copies only the working revision of each project item and does not include prior revisions of project items or any method files in the project. Methods must be imported separately using the import and export options in the **File** menu. Refer to CHAPTER 12, *Importing and Exporting Methods*, CHAPTER 12, *Exporting a Method*, and CHAPTER 12, *Exporting All Methods Associated With a Project File*, for more information.

To create a copy of a project file:

1 If the project file to copy is not the active file, open the desired project file (refer to *Opening a Project File*).

2 From the **Project** menu, choose **Save Project As**. **Save Project As** appears (Figure 6.8).

Figure 6.8 Saving Project As—To Create a Copy



3 Enter a name for the new copied project file.

NOTE The project file name must be different from all other project files.

4 Choose **OK** to create a new copied project with the specified name. **Save Project As** closes and the new copied project becomes the active project file.

OR

Choose **Cancel** to close **Save Project As** without creating a new project file.

Modifying Project Items

Modifications to any item in a project file are edited and saved in the Biomek Software editor, such as the **Labware Type Editor** for labware types, and the time is automatically recorded in **Project Contents**. The modification of the item is part of the project file; however, previous modifications can never be lost and if a project item is later modified or deleted, any revision of the project item may be restored.

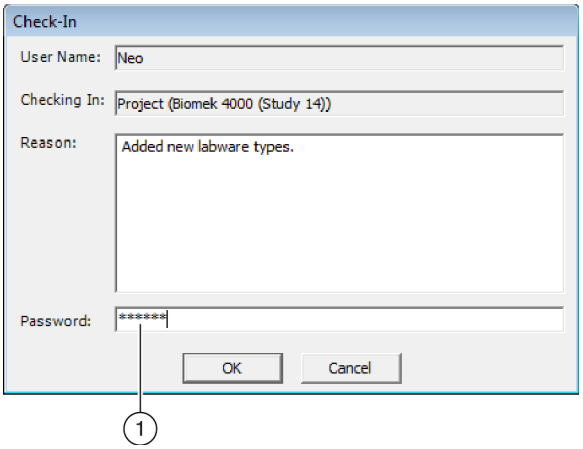
NOTE If Beckman Coulter Accounts & Permissions is enabled, methods may be validated. A validated method is a revision of a method that is saved, approved with an electronic signature, and protected from further modification (refer to CHAPTER 12, *Validating a Method*). Before a method can be validated, all items used in the method must be checked in as revisions in the project file.

To modify a project item:

1. In Biomek Software, use the correct editor, such as the **Labware Type Editor** if modifying a labware type, to modify the project item. The time of the modification is automatically recorded and may be viewed in **Project Contents**.

2. If Accounts & Permissions is enabled, **Check-In** appears (Figure 6.9). Enter a **Reason** for checking in the project.

Figure 6.9 Check-In (Accounts & Permissions Enabled)



1. **Password**: Only displays when Accounts & Permissions is configured to require password checks (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

3. If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password**.

4 Choose **OK** to check in all selected project items as revisions in the project file and close **Check In**.

OR

Choose **Cancel** to close **Check-In** without checking in the project.

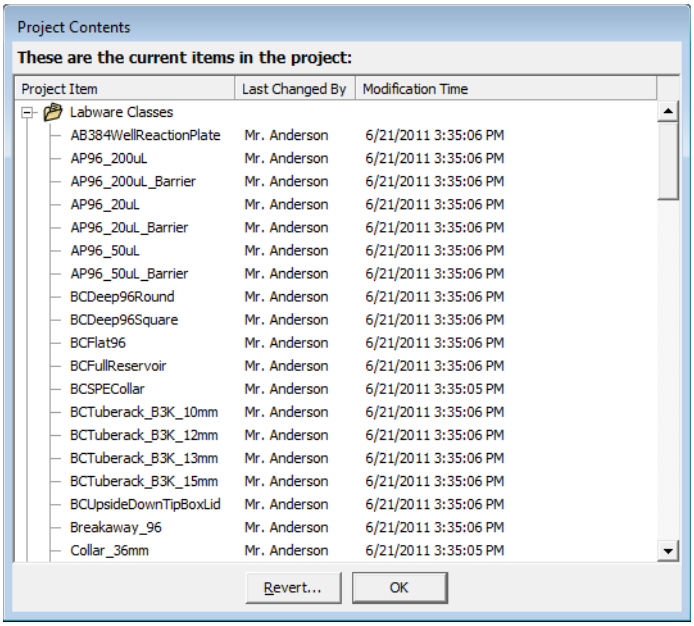
Viewing Project Contents

The contents of a project file and status of each project item can be viewed at any time.

To view the contents of a project file:

1 From the **Project** menu, choose **Project Contents**. **Project Contents** displays a list of all project items, the status of the project item, and time of the modification (Figure 6.10).

Figure 6.10 Viewing Project Contents (Accounts & Permissions Enabled)

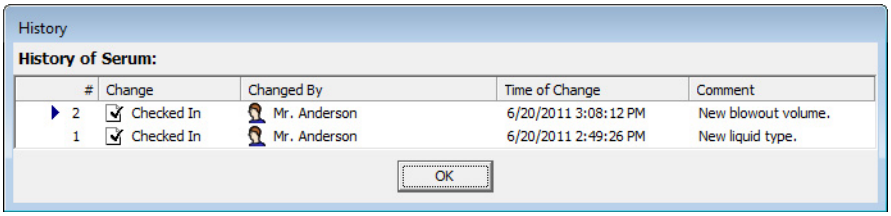


NOTE When Accounts & Permissions is not enabled, **Last Changed By** and the name of the user who modified the project item do not appear.

2 Right click on any project item and choose **History** from the menu to view the history for that record (Figure 6.11). **History** displays the history of changes, who made the changes, the time changes were made, and any comments that may have been entered.

NOTE **Changed By** and **Comment** are blank unless Beckman Coulter Accounts & Permissions is enabled.

Figure 6.11 History of a Project Record



3 When finished viewing the history for the record, choose **OK** to close **History**.

4 Repeat steps 2 and 3 to view the history for additional records, if desired.

5 Choose **OK** to close **Project Contents**.

Restoring Deleted Project Items

A deleted project item may be restored at any time and made available again for method building. Restoring a project item makes available the last revision of the project item that was checked in before it was deleted.

To restore a deleted project item:

1 From the **Project** menu, choose **Project Contents**. **Project Contents** displays a list of all project items and their status.

2 Right click in **Project Contents** and select **Show Deleted Items.** All project items that have been deleted are listed in **Project Contents** with a red X.

3 Right click on the desired deleted item to restore and select **Restore** from the menu. The project item no longer is listed with a red X and the project item may now be used in method building.

Reverting Projects

A project file can be reverted back to a previous revision state, if desired.

NOTE A revision is created each time a project is checked in.

Options for reverting project files are:

- *Reverting Project Contents to a Certain Date and Time*
- *Reverting Individual Project Items to a Specific Revision*

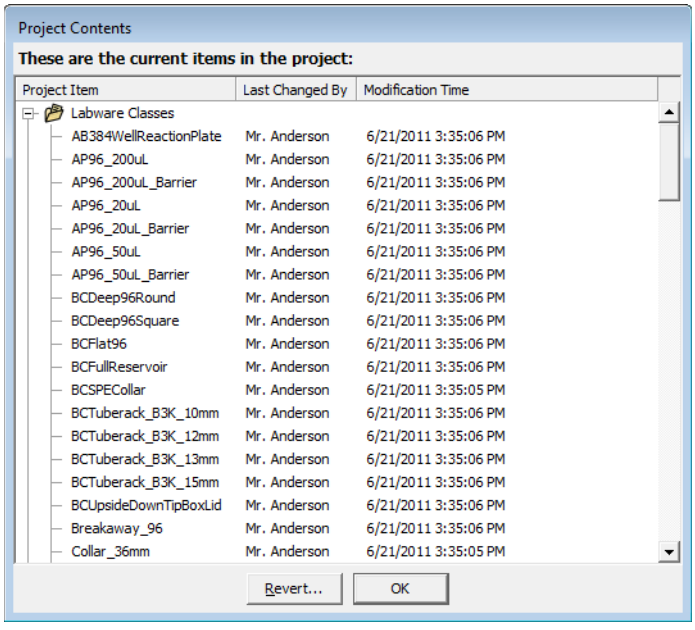
Reverting Project Contents to a Certain Date and Time

All items in a project file may be reverted to the working revision at a previous date and time. When reverting project contents to a date and time, the latest revision prior to the specified date and time is restored as the active working revision. Revisions saved after the specified date and time remain in the project file, but are not active.

To revert project contents to a specific date and time:

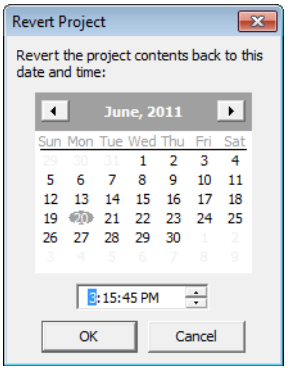
1 From the **Project** menu, choose **Project Contents**. **Project Contents** displays a list of all project items and their status (Figure 6.12).

Figure 6.12 Viewing Project Contents



2 Choose **Revert. Revert Project** appears (Figure 6.13).

Figure 6.13 Reverting a Project File to a Specific Date and Time



3 On the calendar, browse to and select the desired date.

4 Beneath the calendar, enter the desired time.

5 Choose **OK**. **Revert Project** closes and the project contents are reverted to the latest revision checked in prior to the specified date and time.

OR

Choose **Cancel** to close **Revert Project** without reverting the project contents.

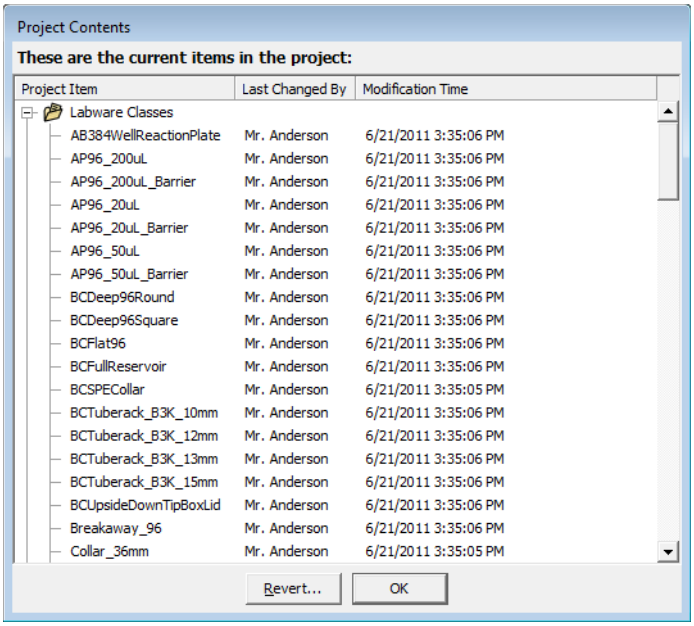
Reverting Individual Project Items to a Specific Revision

An individual project item may also be reverted back to a specific revision, if desired.

To restore an individual project item to a specific revision:

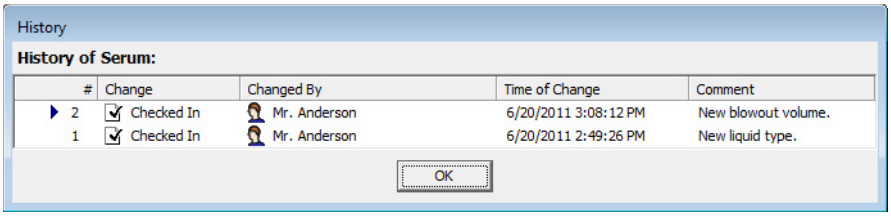
1 From the **Project** menu, choose **Project Contents**. **Project Contents** displays a list of all project items and their status (Figure 6.14).

Figure 6.14 Viewing Project Contents



2 Right click the desired project item to revert. **History** appears and displays a list of all the revisions of the project item that have been checked in. A blue arrow points to the active working revision for the project item (Figure 6.15).

Figure 6.15 History of a Project Item



3 Double click on the desired revision number of the project item to revert.

OR

Right click the desired revision number and choose **Revert Changes** from the menu. The blue arrow moves to the revision to use as the working revision.

4 Choose **OK**. **History** closes and the selected revision is set as the working revision for the project item.

Changing Access to Projects

When Accounts & Permissions is enabled, access to projects may be changed. Project access is changed from **Open Project**.

To change access to a project:

1 From the **Project** menu, choose **Open Project**. **Open Project** displays.

2 Right click the desired project to change access and choose **Change Access** (Figure 6.16). **Project Access** displays (Figure 6.17).

NOTE By default, a new project is owned by the account that created it and **Change Access** is enabled only to the owner of the project.

Figure 6.16 Changing Project Access from Open Project

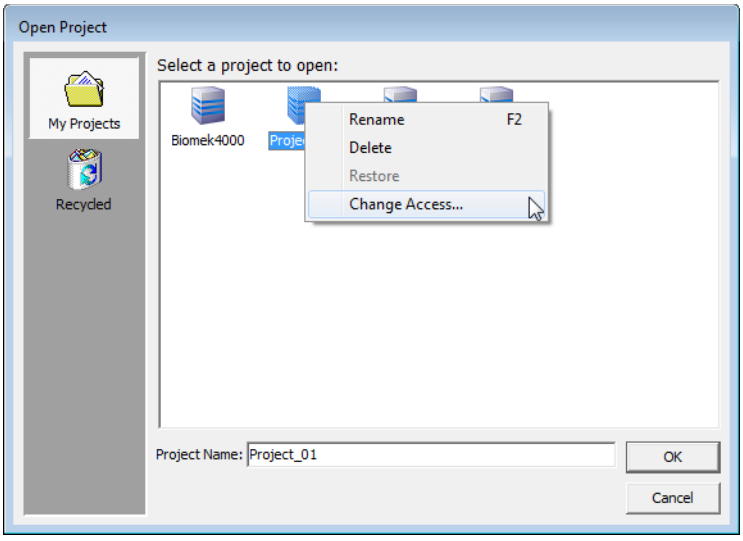
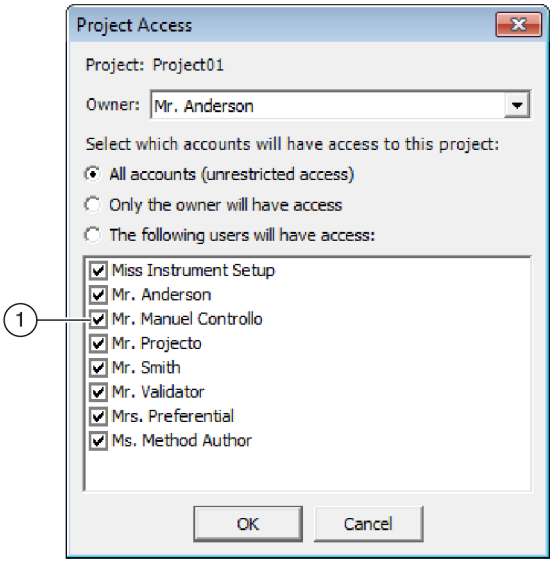


Figure 6.17 Selecting Project Access



1. **With a check mark, select users to have project access.**

3 In **Owner**, choose the account desired to be the owner.

OR

If no owner is desired, in **Owner** choose **Administrator**.

4 Select which user accounts may access the project:

- **All accounts (unrestricted access)** — All user accounts configured in the system may access the project.
- **Only the owner will have access** — Only the account selected in the previous step may access the project. This option is available only when a user account is selected as the project owner.
- **The following users will have access** — Only users selected in **Project Access** may access the project (Figure 6.17).

5 If **The following users will have access** is chosen, select each account desired to have access to the project.

6 Choose **OK** to save the new access configuration and close **Project Access**.

OR

Choose **Cancel** to close **Project Access** without saving changes to the access configuration.

Importing and Exporting Project Files

Project files and individual records can be freely shared among projects or transferred from one computer to another using **Import Project** and **Export Project**.

NOTE When Beckman Coulter Accounts & Permissions is enabled, users with the **Run Validated Methods** or **Develop Methods** permission may export methods, but only those with the **Develop Methods** permission may import methods into a project (refer to CHAPTER 1, *Using Accounts and Permissions*).

NOTE Methods may also be imported and exported. Refer to CHAPTER 12, *Importing and Exporting Methods*, for more information.

This section covers:

- *Exporting a Project File to a Biomek Import File*
- *Importing a Project File From a Biomek Import File*

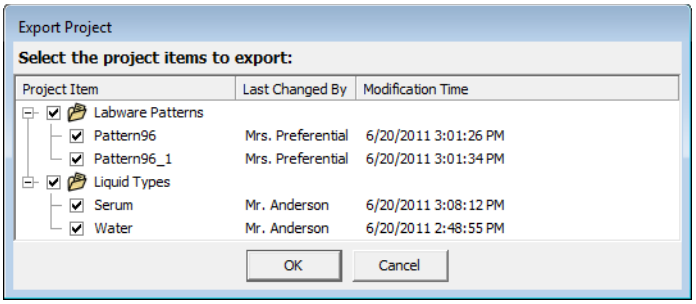
Exporting a Project File to a Biomek Import File

A project file or individual records from a project file can be exported to a Biomek import file, which may be imported into a different project file. Exporting a project file always exports the working revisions from the current active project file. The specific items to export from the project file are then selected from all available project items.

To export a project file:

1 From the **Project** menu, choose **Export Project**. **Export Project** appears, displaying a list of all records in the project file (Figure 6.18).

Figure 6.18 Selecting Project Contents to Export



2 Select all project items to include in the Biomek import file by selecting the check box to the left of each project item. By default, all project items are selected.

NOTE Project items are listed in a tree structure that lists items by type. Branches may be expanded or collapsed using the + and - buttons to the left of the project item name.

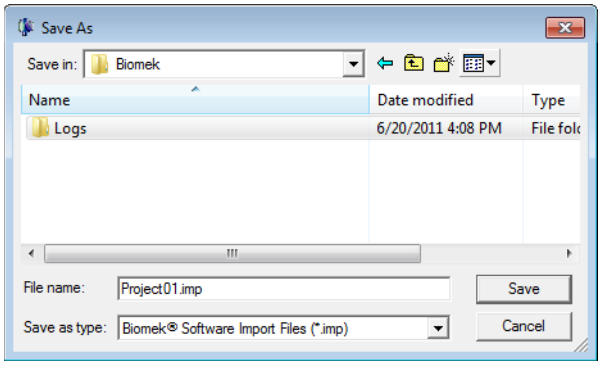
To select or deselect all project items of a specific type, select the check box to the left of folder representing the desired type of project item. Alternately, right click on a type of project item and choose **Select All** from the menu to select all project items of that type, or choose **Select None** to deselect all project items of that type. Right click on whitespace and choose **Select All** or **Select None** to select or deselect all project items for all types.

3 Choose **OK** to include all selected project items in the Biomek import file and close **Export Project**. **Save As** appears (Figure 6.19).

OR

Choose **Cancel** to close **Export Project** without exporting the project to a Biomek import file.

Figure 6.19 Save Import File



4 In **Save As**, browse to and select the location to save the Biomek import file.

5 In **File Name**, enter a name for the import file.

6 Choose **Save** to create the new import file.

Importing a Project File From a Biomek Import File

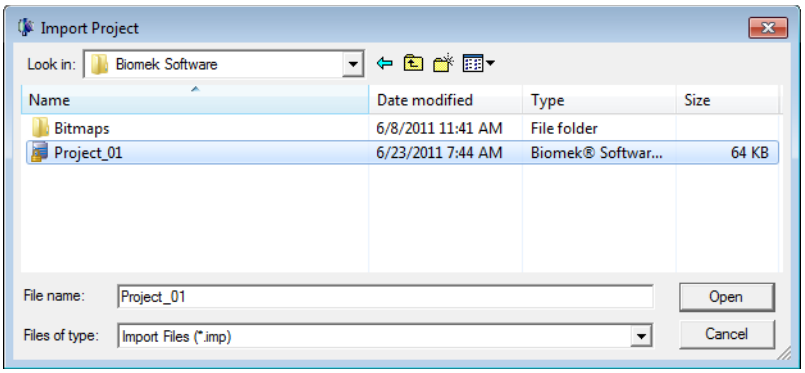
A Biomek import file previously exported from a project file can be imported into the current active project file. The records to import are selected from all available records in the import file. Biomek Software compares the selected project items in the import file to the current project and only imports those items that are different.

To import a project file from a Biomek import file:

1 If necessary, open the project file in which to import the Biomek import file.

2 From the **Project** menu, choose **Import Project**. **Import Project** appears (Figure 6.20).

Figure 6.20 Open Import File

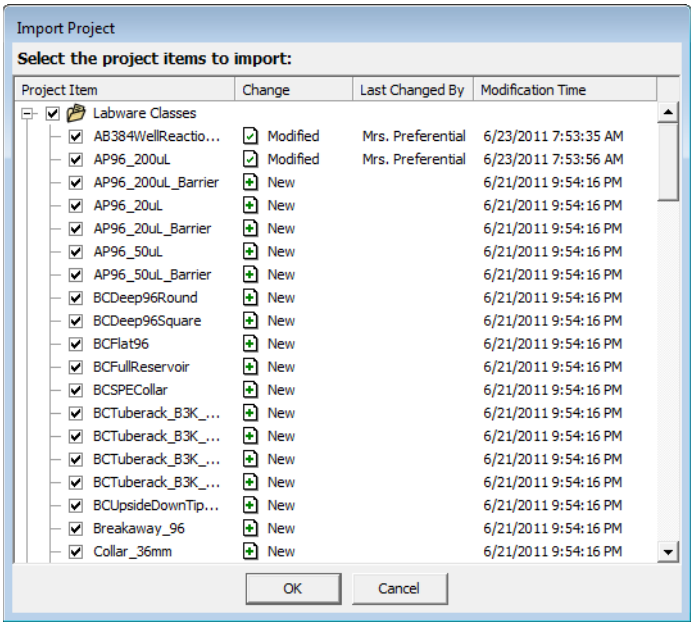


3 In **Import Project**, browse to and select the Biomek import file to import.

4 Choose **Open**. **Import Project** appears, displaying a list of all project items in the project file to import (Figure 6.21).

NOTE Biomek Software compares the project items in the import file to the current project. If all items from the import file match the current project, Figure 6.21 does not appear.

Figure 6.21 Selecting Project Items to Import



5 Select all project items from the Biomek import file to import by selecting the check box to the left of each project item. By default, all project items are selected.

NOTE Project items are listed in a tree structure that lists items by type. Branches may be expanded or collapsed using the + and - buttons to the left of the project item name.

Right click on a type of project item and choose **Select All** from the menu to select all project items of that type, or choose **Select None** to deselect all project items of that type.

6 Choose **OK** to import all selected project items from the Biomek import file into the project file and close **Import Project**.

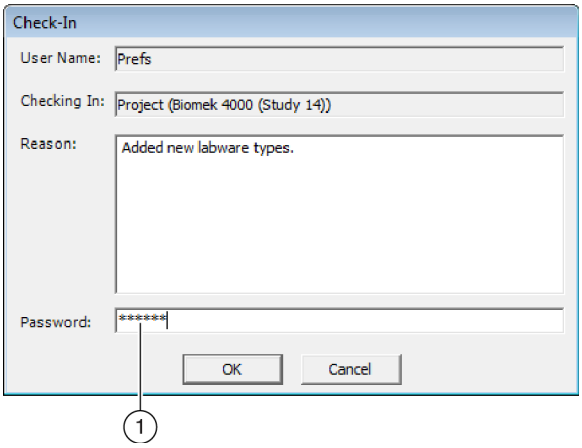
NOTE If Beckman Coulter Accounts & Permissions is not in use, the import is complete.

OR

Choose **Cancel** to close **Import Project** without including any project items in the Biomek import file.

7 If Accounts & Permissions is enabled, **Check-In** appears (Figure 6.22). Enter a **Reason** for checking in the project.

Figure 6.22 Check-In (Accounts * Permissions)



1. **Password**: Only displays when Accounts & Permissions is configured to require password checks (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

8 If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password**.

9 Choose **OK** to close **Check-In**. The project items from the import file are imported to the project file.

CHAPTER 7

Creating and Modifying Tip and Labware Types

Overview

Biomek Software must know the properties of the tips and labware used with the instrument to correctly perform liquid handling and gripper movement operations. A set of predefined tip and labware types commonly used in automated laboratories is pre-loaded with the software.

However, there may be instances when a tip or labware type used in the laboratory is not predefined in Biomek Software, or specifications of a predefined tip or labware type change. When this occurs, tip modifications are made in the **Tip Type Editor** and labware type modifications are made in the **Labware Type Editor**.

NOTE Tips must be associated with a labware type in order to be used in a method.

All labware types have a graphic associated with them in Biomek Software. Any new labware type created in the **Labware Type Editor** will have a corresponding graphic generated, based upon the labware type properties. The graphic then appears in the Labware Category Graphical Display of the **Instrument Setup** step for use in methods (Figure 7.1).

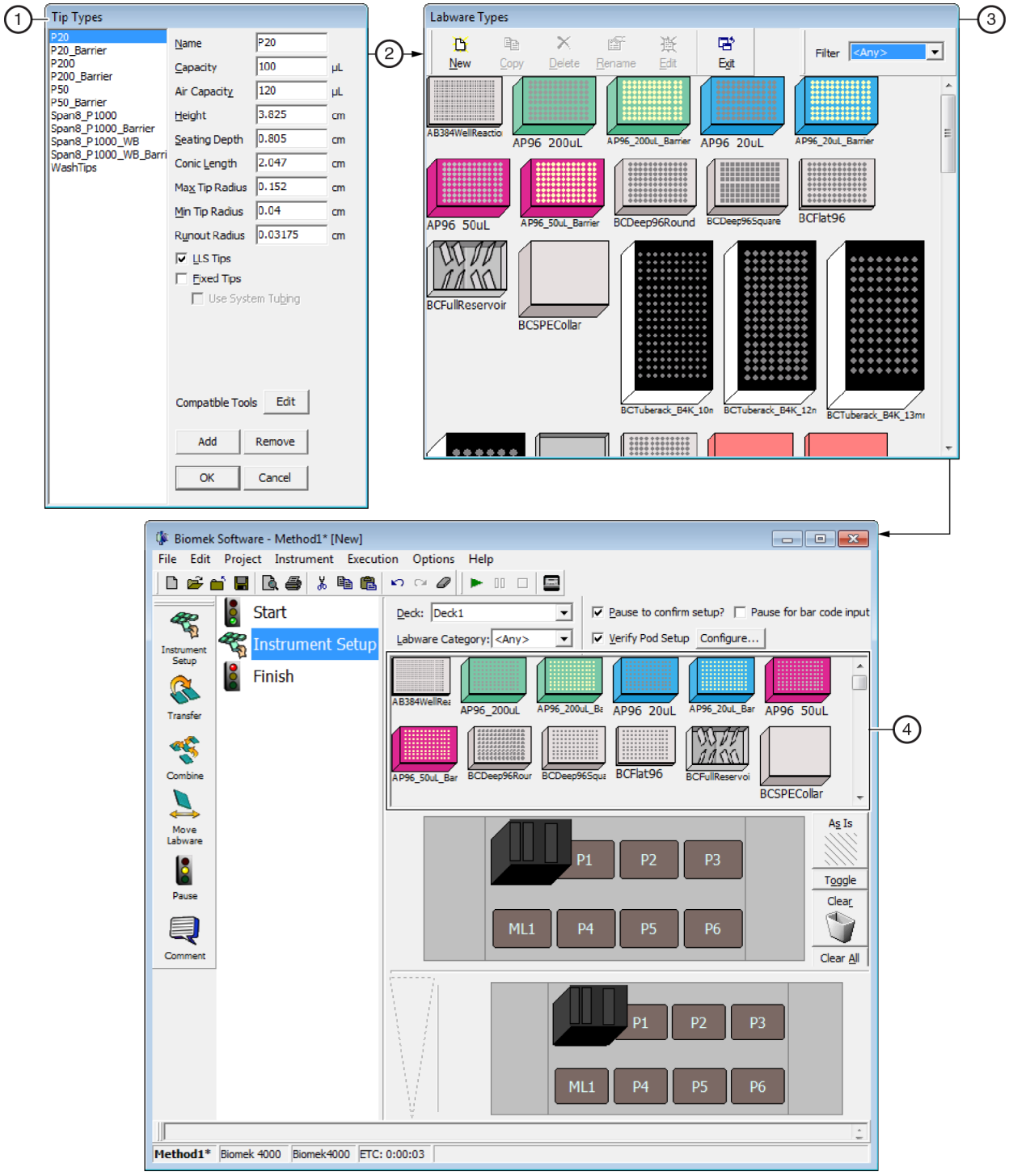
Tip and labware types, along with information about liquid types, well patterns, and pipetting templates and techniques, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to CHAPTER 6, *Understanding and Using Project Files*, for more information on project files.

NOTE When Beckman Coulter Accounts & Permissions is enabled, only users with the **Develop Projects** permission assigned may open, edit, create, and delete tip and labware types (refer to CHAPTER 1, *Using Accounts and Permissions*).

The sections in this chapter include:

- *Defining Tips*
- *Defining Labware Types*

Figure 7.1 Relationship for Labware and Tips in Biomek Software



1. **Tip Type Editor:** Provides means to accommodate new tip.
2. **Tips must be associated with a tip box in the Labware Type Editor.**
3. **Labware Type Editor:** Provides means to create and customize labware types, including tip boxes.
4. **Graphical Display in Instrument Setup Step**: Displays labware and tips to be selected and placed on the deck during method building.

Defining Tips

Most Beckman Coulter tip types may be used on Biomek 4000 instruments, except LLS, 348-well, 72-count P1000, certain Span-8, and WashTips, which are only used internally with Biomek Software on the wash tool.

NOTE The Biomek 4000 pod is capable of accessing all types of labware supported by the Biomek 4000 instrument; however, some tools cannot access specific types of labware. For example, multi-channel pipette tools cannot access test tubes.

NOTE Refer to the *Biomek 4000 Hardware Manual* on tips and tip properties.

In order to use tips that are not predefined, use the **Tip Type Editor** to:

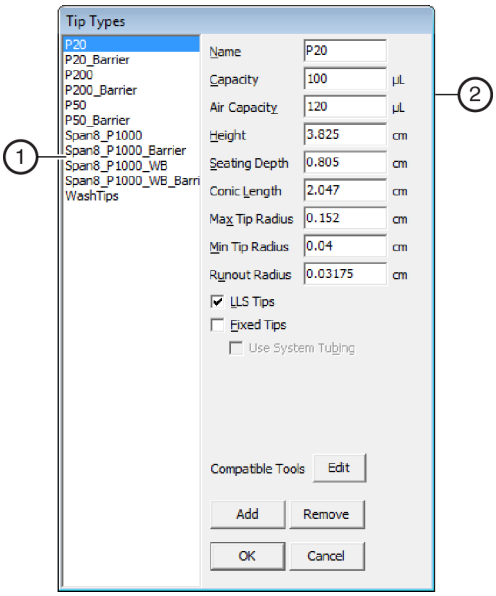
- Add new tips.
- Change tip properties, such as capacity and size.
- Remove tips.

Accessing the Tip Type Editor

To access the **Tip Type Editor**:

1 Choose **Project > Tip Type Editor**. **Tip Types** display (Figure 7.2).

Figure 7.2 Tip Types



1. **Tip List:** Displays Lists currently defined tip types.
2. **Labware Type Tip Properties:** Displays properties of currently selected tips.

Adding New Tips

Add tips that are not previously defined to ensure that liquid transfers are performed accurately.

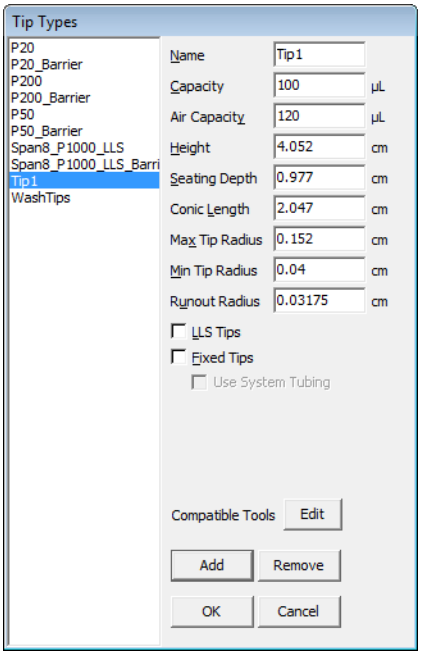
To add tips:

1 In the **Tip Type Editor**, highlight the tip type that most closely resembles the new tip type.

NOTE Adding tips copies the selected tip type, including its properties.

2 Choose **Add**. The tip type appears in the Tip List as “Tip” followed by a number. For example, the first tips created are named “Tip1”.

Figure 7.3 Adding a New Tip Type



⚠ CAUTION

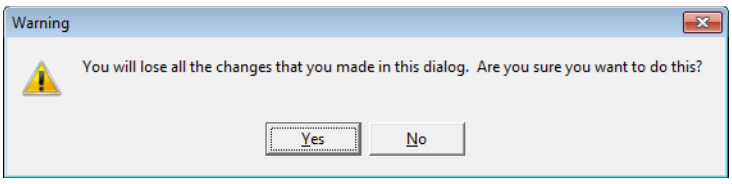
After new tips are added, the correct properties must be defined in the Biomek Software "Tip Type Editor" according to the manufacturer's specifications. Inaccurate specifications may lead to collisions, resulting in equipment damage.

3 Modify the tip properties according to the manufacturer's specifications (refer to *Changing Tip Properties*).

4 Choose **OK**.

NOTE Choose **Cancel** to cancel the addition of the tip type. A **Warning** appears to confirm the cancellation of changes (Figure 7.4).

Figure 7.4 Warning to Confirm Cancellation of Changes



Changing Tip Properties

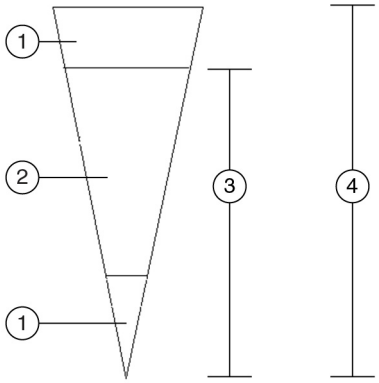
Change tip properties in the **Tip Type Editor** when defining new tips or changing the existing tip properties.

Tip properties include the following (Table 7.1):

Table 7.1 Tip Properties

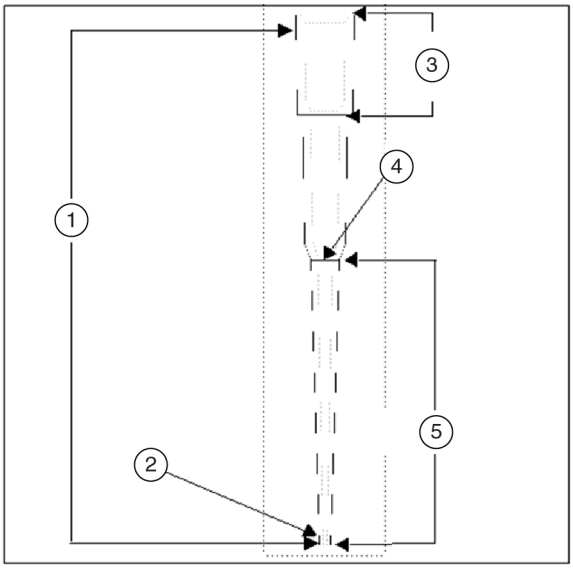
Property	Description
Name	Names the tips for easy identification. **NOTE** Tip names must begin with a letter, and only letters, numbers, and underscores (_) can be used.
Capacity	The maximum liquid volume the tip holds.
Air Capacity	The total amount of leading air gap, plus liquid that can be aspirated. Trailing air gaps are counted against liquid capacity since they displace liquid further into the tips (Figure 7.5).
Height	The total height of the tip (Figure 7.6).
Seating Depth	The depth at which the tip seats properly on the mandrels (Figure 7.6).
Conic Length	The lowest triangular section of a tip (Figure 7.6)
Max Tip Radius	Radius of the tip at the top of the conic length (Figure 7.6).
Min Tip Radius	Radius of the tip at its narrowest point (Figure 7.6).
Runout Radius	Defined area around a tip to account for manufacturing tolerances and tip bending.
LLS Tips	Indicates the tips are capable of Liquid Level Sensing.
Fixed Tips	Indicates the tips are not disposable.
Use System Tubing	Indicates the sample aspiration is allowed to enter the system tubing. Used for WashTips.
X-Span	*Applies to Wash tools only.* Distance from the left-most side of the left tube to the right-most side of the right tube, along the X-axis. **IMPORTANT** Do **NOT** change this value.
Y-Span	*Applies to Wash tools only.* Distance from the back side of the larger tube to the front side of the larger tube, along the Y-axis. **IMPORTANT** Do **NOT** change this value.
Compatible Tools	Allows you to view the default tools used with each tip type. You can make edits to the default compatible tools and priority levels of tool auto-selection.

Figure 7.5 Tip Capacity and Air Capacity



1. **Air**
2. **Liquid**
3. **This amount cannot exceed liquid capacity.**
4. **This amount cannot exceed air capacity.**

Figure 7.6 Tip Dimensions



1. **Height**
2. **Minimum Radius**
3. **Seating Depth**
4. **Maximum Radius**
5. **Conic Length**

To change tip properties:

1 In the **Tip Type Editor**, select the desired tips from the Tip List (Figure 7.2). The current properties of the tips display in Tip Properties.

2 Change the desired properties (Table 7.1) according to the manufacturer's specifications.

3 Choose **OK**.

NOTE Choose **Cancel** to cancel the changes made to the properties. A **Warning** appears to confirm the cancellation of changes (Figure 7.4).

Removing Tips

Remove obsolete tips from the Tip List.

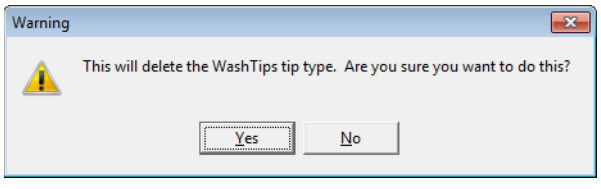
NOTE The **Tip Type Editor** does not allow tips to be deleted that are used by any labware class or that are on the pod. To delete a tip type, delete the labware type in the **Labware Type Editor** first (refer to *Editing Labware Type Properties*)

To remove tips:

1 In the **Tip Type Editor**, select the desired tips from the Tip List.

2 Choose **Remove**. A **Warning** appears (Figure 7.7)

Figure 7.7 Remove Tips Warning



3 Choose **Yes** to confirm the removal. The tips are removed from the Tip List.

4 Choose **OK**.

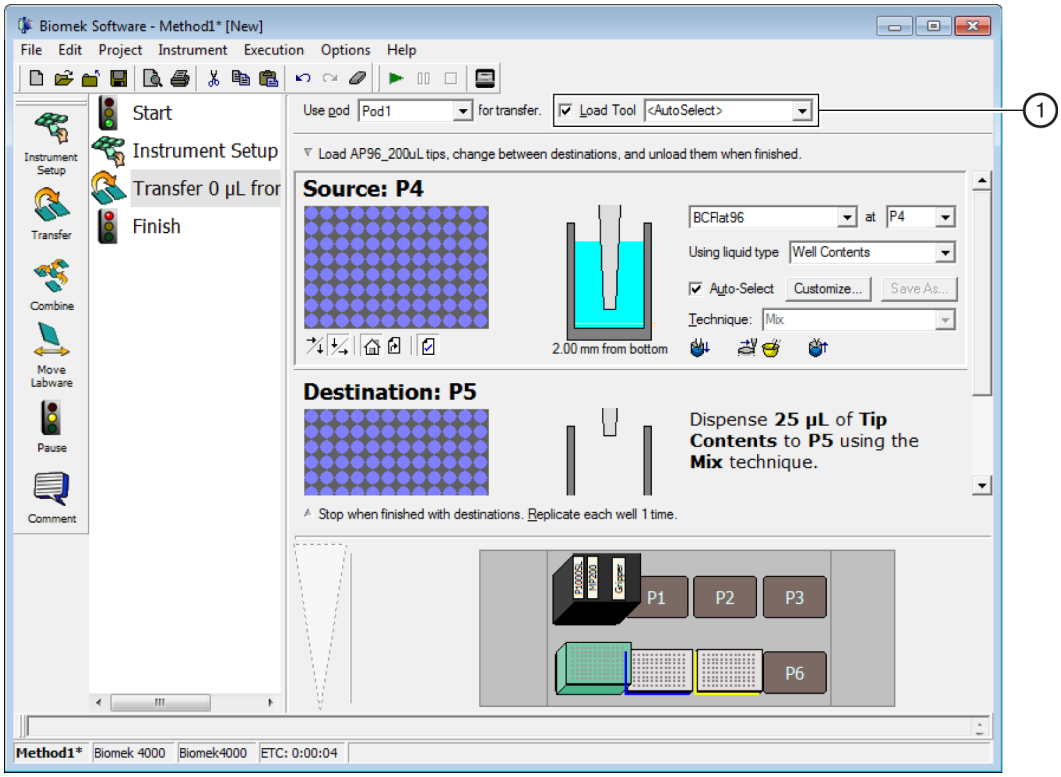
NOTE Choose **Cancel** to cancel the removal of the tip type. A **Warning** appears to confirm the cancellation of changes (Figure 7.4).

Editing Compatible Tools

Biomek Software contains default list of tools that can be used with each tip type. The list of tools associated with each tip can be changed using the **Compatible Tools Editor**.

The automatic tool-selection feature available in pipetting steps (see Figure 7.8) depends on the accuracy of configurations designated in the **Compatible Tools Editor**. The software selects the best tool for pipetting operations based on the list of compatible tools, as well as the priority given to each compatible tool associated with the selected tip type.

Figure 7.8 <AutoSelect> Option Selected for Pipetting Operations



1. When **<AutoSelect>** is chosen in the **Load Tool** drop-down, the software selects the tool based on loaded tip type, tool priority, and availability.

To update tool compatibility:

---

1 From the **Tip Type Editor**, select the tip for which you wish to update compatible tools, and then select **Edit**. The **Compatible Tools Editor** appears.

---

2 Deselect **Use default tool list.** All tools currently deemed as compatible with the tip are listed under **Compatible Tools.** All other tools added to your instrument, but not currently associated with the tip type, are listed under **Available Tools.**

3 Make the desired changes to **Compatible Tools**:

- Select a tool from the **Available Tools** list, and then selecting **Add** to move it to the **Compatible Tools** list.

  AND/OR

- Select a tool from the **Compatible Tools** list and selecting **Remove** to disable the tool for use with a tip type.

4 Continue adding and removing tools until the lists are updated to your needs.

5 Review the list of **Compatible Tools**. **Compatible Tool** priority is taken into account when you use the **<AutoSelect>** option for loading tools in pipetting operations. The highest priority tool should be located at the top of the list, and the remaining tools are in descending order of priority.

6 If necessary, make changes to priority by selecting a tool and then selecting **Move Up** or **Move Down**. Continue making changes until you are satisfied with the order.

7 Select **OK** to accept the changes.

NOTE You can restore the default at any time by selecting the **Use default tool list** check box and then selecting **OK**.

Defining Labware Types

Labware types are divided into categories, such as titerplates, reservoirs, tube racks, lids, and tip boxes. In Biomek Software, each labware category contains specific predefined labware, such as BCDeep96Square, BCUpsideDownTip, BoxLid, and BCTuberack_10mm.

Use the **Labware Type Editor** for:

- *Adding a New Labware Type*
- *Copying a Labware Type*
- *Deleting a Labware Type*
- *Renaming a Labware Type*
- *Editing Labware Type Properties*

⚠ CAUTION

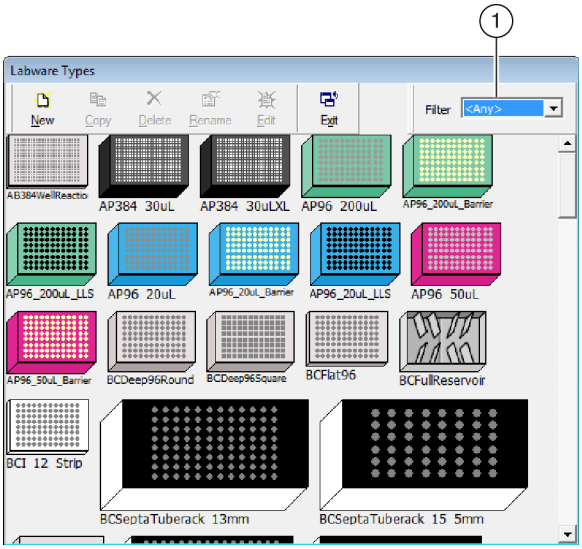
Incorrect labware definitions in the Biomek Software "Labware Type Editor" can cause system crashes or hazardous waste spills. Verify definitions are correct prior to executing a method run.

Accessing the Labware Type Editor

To access the **Labware Type Editor**:

1 Choose **Project > Labware Type Editor. Labware Types** appears (Figure 7.9).

Figure 7.9 Labware Types



1. **Filter**: Used to display specific categories of labware, such as **Any** (which displays all categories), **TiterPlate, Reservoir**, **Tuberack**, **Lid**, **Reservation**, or **TipBox**.

NOTE The labware that is displayed in the **Labware Type Editor** is dependent on the current project file.

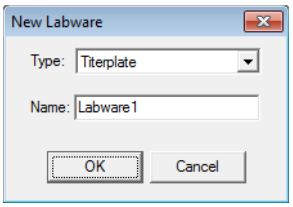
Adding a New Labware Type

Add a new labware type when the desired type is not predefined in Biomek Software. When a new labware type is added, default properties are inserted into the appropriate fields. The default properties may need to be changed to meet the manufacturer's specifications of the new labware type.

To add a new labware type:

1 From **Labware Types**, select **New** from the toolbar at the top. **New Labware** appears (Figure 7.10).

Figure 7.10 New Labware



2 Choose the labware type from the pull-down list.

3 Enter a name for the labware or use the default name.

NOTE The new labware is assigned the default name of **Labware** plus a number representing the order in which the labware was created. For example, the first labware created is given the default name **Labware1** and the second is given the default name **Labware2**.

4 Choose **OK**. The new labware appears graphically in **Labware Types.** (Figure 7.9).

NOTE Use **Filter** or scroll down **Labware Types** to locate the new labware type (Figure 7.9).

Copying a Labware Type

Copying a labware type creates an exact copy of it, including current properties. The properties of the copied labware type can be modified to create a new labware type.

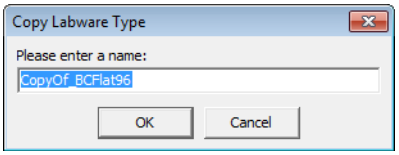
To copy a labware type:

1 From **Labware Types**, highlight the graphic representing the labware and select **Copy** from the toolbar at the top.

OR

Right click the graphic for the labware type and choose **Copy**. **Copy Labware Type** appears (Figure 7.11).

Figure 7.11 Copy Labware Type



2 Enter a name for the labware or use the default name.

NOTE Labware names must begin with a letter, and can contain only letters, numbers, and underscores (_) or an error message appears. The default name assigned to a labware type consists of the name of the labware type preceded by **CopyOf_**. For example, a copy of BCFlat96 is **CopyOf_BCFlat96**

3 Choose **OK**. The copied labware appears graphically in **Labware Types**. (Figure 7.9).

Deleting a Labware Type

Delete any labware type from **Labware Types** that is no longer used.

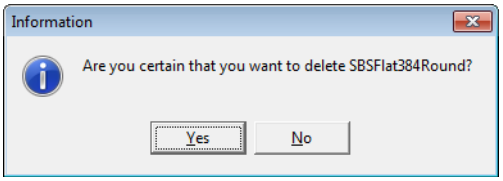
To delete a labware type:

1 From **Labware Types**, highlight the graphic representing the labware and select **Delete** from the toolbar at the top.

OR

Right click the graphic for the labware type and choose **Delete**. **Information** appears (Figure 7.12).

Figure 7.12 Information



2 Choose **Yes** to confirm the removal. The labware is deleted from **Labware Types** (Figure 7.9).

Renaming a Labware Type

Renaming a labware type provides the opportunity to assign a descriptive name to a labware type for easy identification.

NOTE If labware types are renamed, any methods with labware under the old name will generate an error when the method is validated. The name must be changed to reflect the new name in the **Instrument Setup** step and any step that refers to the old name, such as in the **Transfer** step.

NOTE The labware type names appear on the **Instrument Setup** configuration. Refer to CHAPTER 15, *Instrument Setup Step*, for more information about **Instrument Setup**.

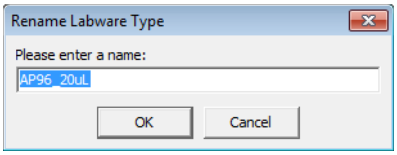
To rename a labware type:

1 From **Labware Types**, highlight the graphic representing the labware and select **Rename** from the toolbar at the top.

OR

Right click the graphic for the labware type and choose **Rename. Rename Labware Type** appears (Figure 7.13).

Figure 7.13 Rename Labware Type



2 Enter a new name.

NOTE Labware type names must begin with a letter, and only letters, numbers, and underscores (_) can be used.

3 Choose **OK** to save the new labware name. The new labware name appears in **Labware Types** (Figure 7.9).

Using Secure Stacking

Use **Secure Stacking** when it is necessary to securely stack more than two plates. The notations made in **Secure Stacking** are used by the software to allow the creation of stacks for a Solid Phase Extraction (SPE) assembly or tall stacks. It is necessary to use **Secure Stacking** with **Stackable Items** to ensure that specific labware can be stacked on top of other specific labware.

Like **Stackable Items, Secure Stacking** allows check marks to be entered when it is necessary to stack a specific type of labware on another specific type of labware for certain methods. The information entered in **Secure Stacking** will be used by the software when moving labware, for example, in the **Move Labware** step.

To effectively use **Secure Stacking**, an understanding of the stacking rules is necessary. the stacking rules apply to stacks on all Biomek instrument decks.

Editing Labware Type Properties

The applicable properties for a labware type are arranged in the **Labware Type Editor** according to the following categories (Table 7.2).

Table 7.2 Labware Type Properties

Category	Properties
Basic Information	Span, height, and description of the labware; optional bitmap graphic; and an option to edit the color of the labware (refer to *Changing Labware Colors*).
Magbead	*Not supported on the Biomek 4000 system.*
Miscellaneous	Name of the default lid, sensitivity, and clamp force, and option to hide the labware so it is not visible in the editor, and/or the option to choose a self-refilling reservoir. **NOTE** Sensitivity and clamp force are not used on the Biomek 4000 system.
Movement Information	Gripper offset, gripper squeeze, gripper unsqueeze, speed limit, and an option to use the gripper sensor when available.
Orbital Shaker	Allows the maximum speed to be set for labware used on the Orbital Shaker ALP (refer to the *Biomek 4000 ALPs and Accessories Manual*).
Ordering Information	Manufacturer and part number.
Sections	An option to configure sections used in a reservoir (refer to *Configuring a Reservoir with Sections*).
Stacking	Stack offsets and options to edit the stack offsets (refer to *Specifying Stackable Items*), to edit on which labware types or ALP types the labware can be securely stacked on top (refer to *Using Secure Stacking*), and the option to define the labware as self-stacking or not.
Reservation Information	"Caption" field that identifies the label that appears on the reservation and a "Reserve For" field that identifies the reason the space is reserved.

Table 7.2 Labware Type Properties

Category	Properties
Wells_1	Well offset, count, spacing, maximum volume, format, column 2 offset, default volume, known default volume, and an option to configure well dimensions (refer to *Configuring Well Properties*). **Well Offset**, **Well Spacing**, and **Column 2 Offset** are defined as the following: • **Well Offset** — **X**—Distance from the edge of the labware to the center of the well in the back left corner of the labware, along the X-axis. — **Y**—Distance from the edge of the labware to the center of the well in the back left corner of the labware, along the Y-axis. • **Well Spacing** — **X**—Distance from the center of one well to the center of the well next to it. In a standard 96-well microplate, this measurement is 0.9 cm. — **Y**—The number of wells along the Y-axis of the labware (e.g., 8 for a 96-well plate). • **Column 2 Offset**—Distance along the Y-axis from the edge of the labware to the center of the well in the second column, toward the back of the unit.
Tips	Tip offset, count, spacing, tip load Z offset, tip unload Z offset, and tip type. **Tip Offset**, **Tip Load Z Offset**, and **Tip Unload Z Offset** are defined as the following: • **Tip Offset** — **X**—Distance from the edge of the labware to the center of the well in the back left corner of the labware, along the X-axis. — **Y**—Distance from the edge of the labware to the center of the well in the back left corner of the labware, along the Y-axis. • **Tip Load Z Offset**—Distance below the tip box to load along the Z-axis. A negative number. • **Tip Unload Z Offset**—Distance from the tip box to unload along the Z-axis.

To edit labware properties:

1 From **Labware Types**, highlight the graphic representing the labware and choose **Edit** from the toolbar.

OR

Right click the graphic and choose **Edit.**

OR

Double click the graphic.

2 Choose the appropriate labware category and make the desired changes to the labware properties that appear.

NOTE All distances are in centimeters unless otherwise specified.

3 Choose **Save**.

NOTE Three sections of hints are offered at the bottom of the edit option. The first section displays a graphic of the labware, the second section explains the selected field, and the third section explains any errors resulting from editing the labware properties. Place the cursor over the desired labware properties field and click to access these hints.

Changing Labware Colors

Make labware stand out in the **Instrument Setup** step by changing the colors of the labware as desired. For example, each titerplate could be a different color. Changing labware colors also helps to make labware distinguishable in the Biomek Software main editor.

NOTE The color fuchsia (RGB 255, 0, 255) is the system transparency color and causes odd visual behavior.

To change labware colors:

1 From **Labware Types**, highlight the graphic representing the labware and choose **Edit** from the toolbar at the top.

OR

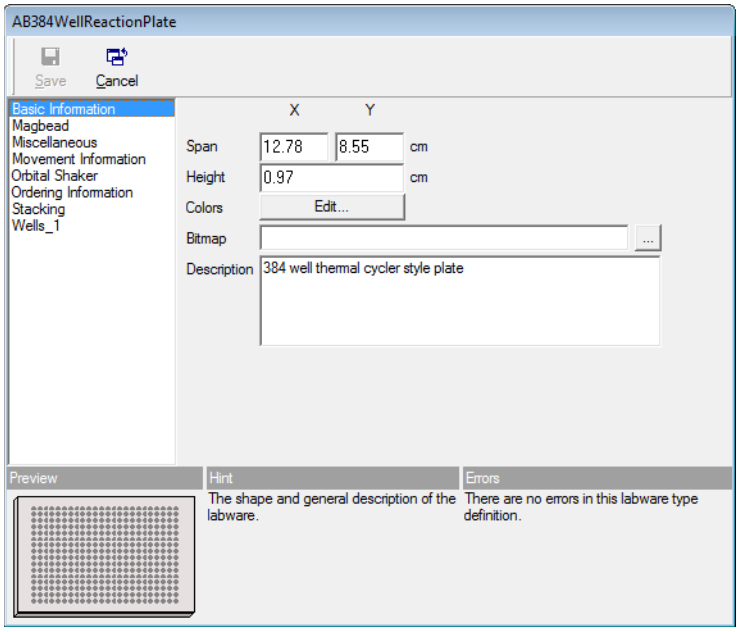
Right click the graphic and choose **Edit**.

OR

Double click the graphic.

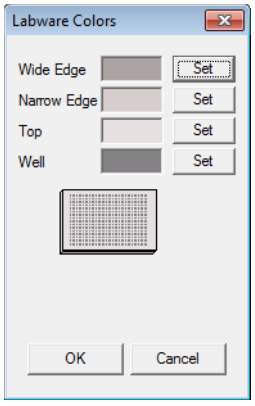
2 Choose **Basic Information** (Figure 7.14)

Figure 7.14 Basic Information Chosen



3 Choose **Edit** next to **Colors. Labware Colors** appears (Figure 7.15)

Figure 7.15 Labware Colors

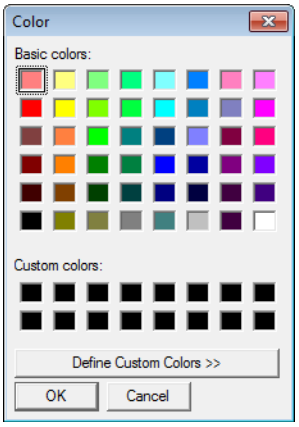


4 Choose **Set** to configure the color for the following sections of the labware:

- **Wide Edge**
- **Narrow Edge**
- **Top**
- **Well**

Color appears (Figure 7.16).

Figure 7.16 Color



5 Select the desired color or define a custom color for the labware section.

6 Choose **OK**.

NOTE Choose **Cancel** to cancel the color selections.

7 Repeat the process for each section of the labware, if desired.

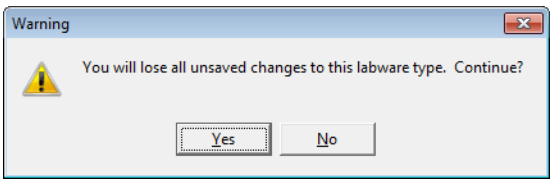
8 Choose **OK** in **Labware Colors** when complete.

NOTE Choose **Cancel** to cancel the color selections.

9 Choose **Save**. **Labware Types** appears (Figure 7.9).

NOTE Choose **Cancel** to cancel the changes made to the labware type. A **Warning** appears to confirm the cancellation of unsaved changes to the labware (Figure 7.17).

Figure 7.17 Warning to Confirm Cancellation of Changes



10 Choose **Exit**.

Configuring a Reservoir with Sections

Some methods require the use of a reservoir with sections. Use **Sections** to configure a reservoir with sections. This allows the pod to accurately aspirate, dispense, and transfer liquid using a reservoir with sections.

To configure a reservoir with sections:

1 Open **Labware Types** (refer to *Accessing the Labware Type Editor*).

2 Copy an existing reservoir (refer to *Copying a Labware Type*) or create a new one (refer to *Adding a New Labware Type*). The new labware appears in **Labware Types.**

3 Highlight the graphic representing the new reservoir and choose **Edit** at the top of **Labware Types.**

OR

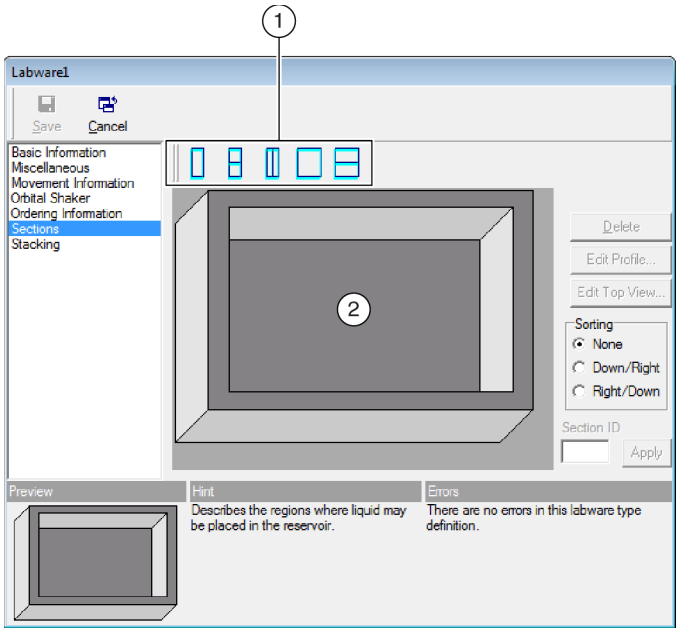
Right click the graphic and choose **Edit.**

OR

Double click the graphic.

4 Choose **Sections** (Figure 7.18).

Figure 7.18 Sections Chosen

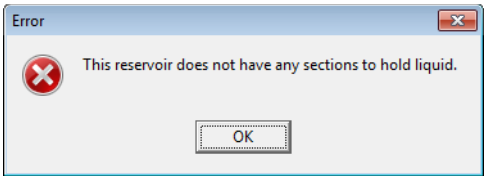


1. **Section Shapes**
2. **Drag the desired section shapes to this area after step 6 below.**

5 Click in the reservoir. A green rectangle appears.

6 Choose **Delete**. **Error** appears as a reminder that sections are deleted and new sections must be added (Figure 7.19).

Figure 7.19 Error Reminder that Sections Are Deleted



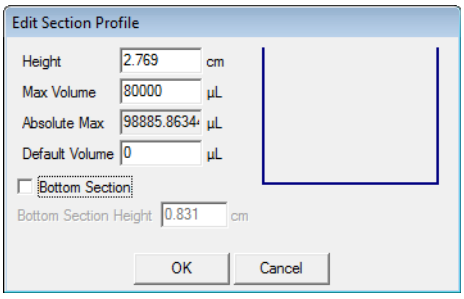
7 Choose **OK**.

8 Drag the shape of the section(s) to the reservoir.

9 Click the area around a specific section. A green rectangle appears.

10 Choose **Edit Profile**. **Edit Section Profile** appears (Figure 7.20).

Figure 7.20 Edit Section Profile



11 If necessary, change the values in **Height, Max Volume**, and **Default Volume** according to the manufacturer's specifications.

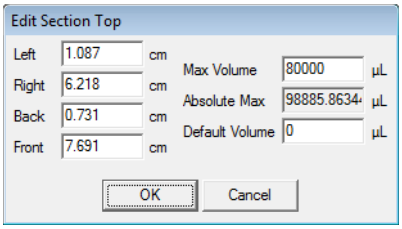
12 Check **Bottom Section** if the section includes a triangular bottom.

NOTE If **Bottom Section** is checked, enter the value in **Bottom Section Height**.

13 Choose **OK**.

14 Choose **Edit Top View. Edit Section Top** appears (Figure 7.21).

Figure 7.21 Edit Section Top



15 If necessary, change the values in **Left, Right, Back, Front, Max Volume**, and **Default Volume** according to the manufacturer's specifications.

16 Choose **OK**.

17 Repeat steps 8 through 16 for each section in the reservoir.

18 Select reservoir section sorting direction in **Sorting.**

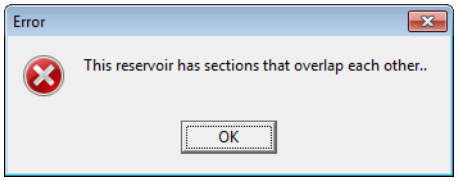
- Choose **Down/Right** or **Right/Down** to automatically sort (number) the reservoir sections accordingly. To verify Section IDs, click on a specific section. The Section ID appears in the **Section ID** field.
- Choose **None** to deselect automatic sorting options. Through **None**, you can manually assign valid Section IDs in any order by selecting the reservoir section you wish to change, entering the edited value into the **Section ID** field, and choosing **Apply.** Repeat this process for each reservoir section you wish to change.

  NOTE Valid IDs are based on the number of sections in the reservoir. The software ensures that no numbers are repeated or skipped; therefore, if you assign a number to a reservoir using a number that had already been used, the section that had previously used that number will be renumbered with the available Section ID. Invalid Section ID values display in red font.

19 When all sections have been configured, choose **Save** (Figure 7.18). A graphic representing the reservoir with the sections appears in **Labware Types**.

NOTE An **Error** (Figure 7.22) appears if the sections are not configured properly. Choose **OK** and reconfigure the sections.

Figure 7.22 Error for an Improperly Configured Reservoir



NOTE Choose **Cancel** to cancel the changes made to the labware type. A **Warning** appears to confirm the cancellation of unsaved changes to the labware (Figure 7.17).

Biomek Stacking Rules

When stacking or unstacking labware, Biomek Software works from the bottom up. If there is a stack of four microplates on deck, the top three are moved by the gripper, then the top two, and finally the top piece of labware.

The maximum height of stacks of microplates allowed on the instrument decks is 6.0 cm (2.36 in.).

NOTE A stack of four standard 96-well plates is approximately 5.2 cm (2.05 in.) tall.

A plate (or stack of plates) can be removed from the source position if one of the following conditions is true:

- The stack at the source position has fewer than three plates.
- The entire stack is being moved.
- The selected plate to be moved is the plate, or stack of plates, immediately above the bottom plate.
- All of the plates below the selected plate to be moved securely stack to each other.
- The selected plate to be moved securely stacks to the source position.
- The plate immediately below the selected plate to be moved securely stacks to the source position.

A plate (or stack of plates) can be moved to a destination position if one of the following conditions is true:

- The destination position has fewer than two plates (one or none).
- All of the plates that are currently stacked at the destination position securely stack to each other.
- The top plate of the destination stack securely stacks to the destination position.
- The selected plate to be moved securely stacks to the destination position.

Specifying Stackable Items

Many common microplates are stackable up to six centimeters in height; however, items such as reservoirs, tube racks, and tip boxes are not.

Specifying stackable items is necessary to allow the software to effectively move labware stacks during liquid-handling operations. For items that are stackable, use **Stackable Items** to specify the distance from one piece of labware to the labware above it (stack offset). A stack offset is the

distance between stacked labware, measured from the bottom, back-left corner on the labware to the bottom back-left corner on the labware above it. The distance is measured using X, Y, and Z coordinates.

NOTE If it is desired to place more than two pieces of labware in a stack, they must either stack securely to each other (refer to *Using Secure Stacking*) or be built in a top-down manner.

Stackable Items allows you to specify which labware types can be stacked on the labware being edited.

The information entered in **Stackable Items** is used by the software when moving labware, for example, in the **Move Labware** step.

To specify stacking offset:

1 From **Labware Types**, highlight the graphic representing the labware and choose **Edit** from the toolbar at the top.

OR

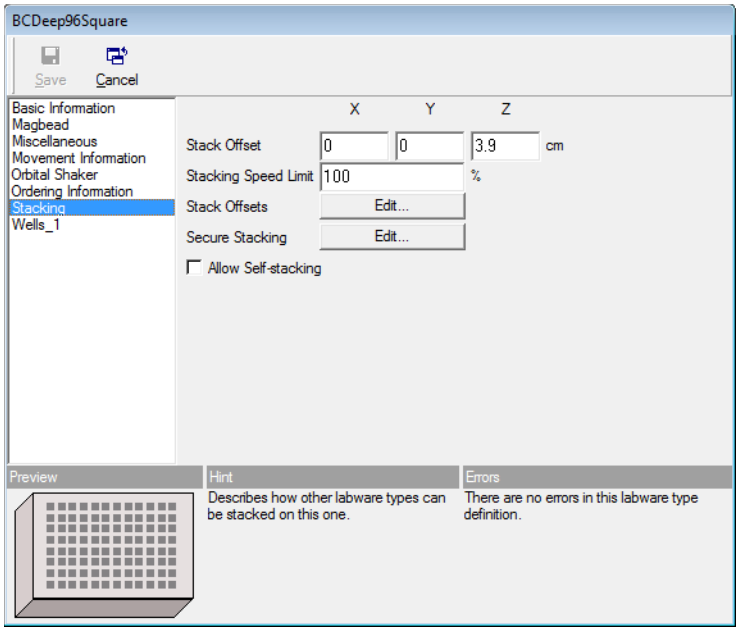
Right click the graphic and choose **Edit**.

OR

Double click the graphic.

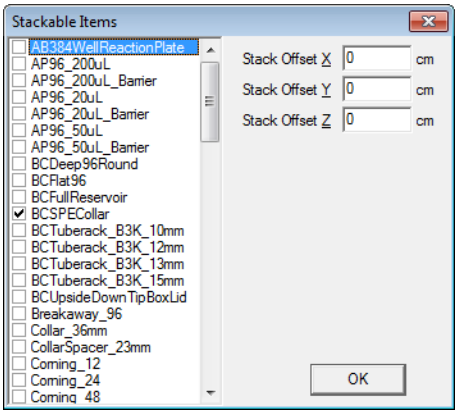
2 Choose **Stacking** (Figure 7.23)

Figure 7.23 Stacking Chosen



3 Choose **Edit** next to **Stack Offsets**. **Stackable Item**s appears (Figure 7.24).

Figure 7.24 Stackable Items



4 Choose the desired labware types that can be stacked on top of the labware type being edited.

NOTE If an item does not have a check mark next to it, that type of labware cannot be stacked on the labware type being edited (selected in **Labware Types**); however, if **Allow Self-stacking** is checked in **Stacking**, it is not necessary to check stackable labware in **Stackable Items**.

5 If applicable, type the desired value for **Stack Offset X, Stack Offset Y**, and **Stack Offset Z.**

NOTE While the offset values may be calculated using calipers, a more precise measurement should be obtained from the manufacturer's specifications.

6 Choose **OK** to save the stackable items settings.

7 Choose **Save. Labware Types** appears.

NOTE Choose **Cancel** to cancel the changes made to the labware type. A **Warning** appears to confirm the cancellation of unsaved changes to the labware (Figure 7.17).

8 Choose **Exit.**

Using Secure Stacking

Use **Secure Stacking** when it is necessary to securely stack more than two plates. The notations made in **Secure Stacking** are used by the software to allow the creation of stacks for a Solid Phase Extraction (SPE) assembly or tall stacks. It is necessary to use **Secure Stacking** with **Stackable Items** to ensure that specific labware can be stacked on top of other specific labware.

Like **Stackable Items**, **Secure Stacking** allows check marks to be entered when it is necessary to stack a specific type of labware on another specific type of labware for certain methods. The information

entered in **Secure Stacking** will be used by the software when moving labware, for example, in the **Move Labware** step.

To effectively use **Secure Stacking**, an understanding of the stacking rules is necessary. the stacking rules apply to stacks on all Biomek instrument decks.

Configuring Secure Stacking

To use **Secure Stacking**:

1 From **Labware Type Editor**, highlight the graphic representing the labware and choose **Edit**.

OR

Right click the graphic and choose **Edit.**

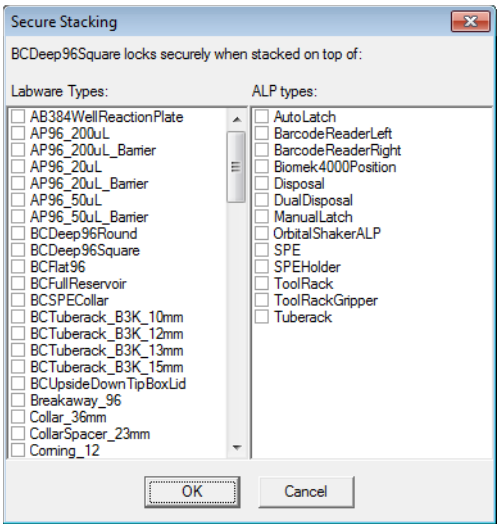
OR

Double click on the graphic.

2 Choose **Stacking** (Figure 7.23).

3 Choose **Edit** next to **Secure Stacking**. **Secure Stacking** appears (Figure 7.25).

Figure 7.25 Secure Stacking



4 Check the labware types and/or ALP types to which the labware being edited locks securely.

5 Choose **OK** to save the settings.

6 Choose **Save**. **Labware Types** appears.

NOTE Choose **Cancel** to cancel the changes made to the labware type. A **Warning** appears to confirm the cancellation of unsaved changes to the labware (Figure 7.17).

7 Choose **Exit**.

Configuring Well Properties

Well properties must be configured when new labware is added to the software.

⚠ CAUTION

The correct well properties must be defined in the Biomek Software "Labware Type Editor" according to the manufacturer's specifications. Inaccurate specifications may lead to inaccurate pipetting, especially when using Liquid Level Sensing.

To configure well properties:

1 From **Labware Types**, highlight the graphic representing the labware and choose **Edit**.

OR

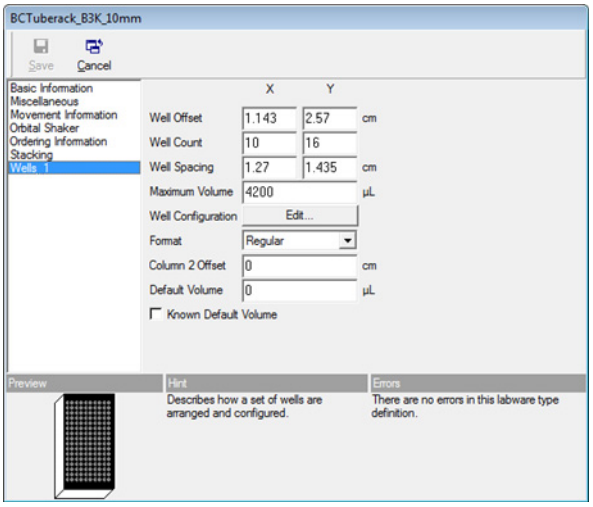
Right click the graphic and choose **Edit**.

OR

Double click the graphic.

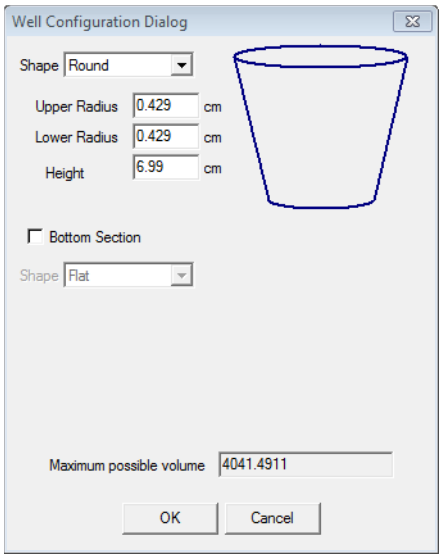
2 Choose **Wells_1** (Figure 7.26).

Figure 7.26 Wells_1 Chosen



3 Choose **Edit** next to **Well Configuration**. **Well Configuration Dialog** appears (Figure 7.27).

Figure 7.27 Well Configuration Dialog

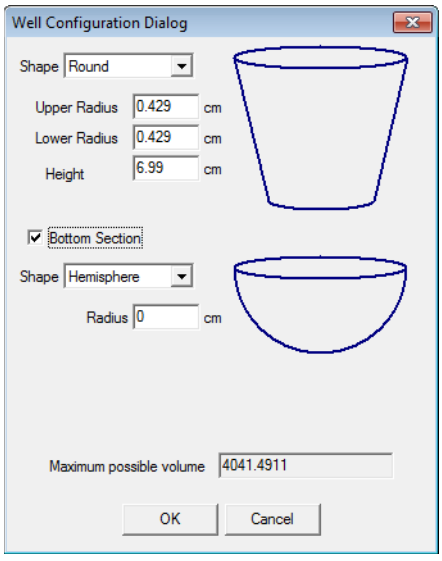


4 Choose the **Shape** from the drop down menu.

5 Configure the specifications according to the manufacturer's specifications.

NOTE Placing the cursor in the specification fields identifies the measurement area on the graphic shape. Placing a check in the **Bottom Section** field identifies the measurement area on the graphic shape that represents the bottom section of the well (Figure 7.28).

Figure 7.28 Well Configuration Dialog with Bottom Section Checked



6 Choose **OK** in **Well Configuration Dialog** when complete.

7 Choose **Save**. **Labware Types** appears.

NOTE Choose **Cancel** to cancel the changes made to the labware type. A **Warning** appears to confirm the cancellation of unsaved changes to the labware (Figure 7.17).

8 Choose **Exit**.

CHAPTER 8

Understanding and Creating Liquid Types

Overview

The **Liquid Type Editor** (Figure 8.1) is used to create new liquid types or to modify existing liquid types for methods. Each time a new liquid type is created, it becomes available for all new and existing methods created in a Biomek 4000 project file. Any liquid type may be set as the default liquid type. In a method, the default liquid type is used when a piece of labware is not configured with a specific liquid.

NOTE When Beckman Coulter Accounts & Permissions is enabled, only users with **Develop Projects** permission may open, edit, create, and delete liquid types (refer to CHAPTER 1, *Using Accounts and Permissions*)

The following is configured in the **Liquid Type Editor**:

- **Aspirate** — Configures the delay, speed, and trailing air gap applicable to the liquid.

  NOTE A trailing air gap draws air into the tips after aspirate to help prevent drips during a method run.

- **Blowout** — Configures the amount of air used in the blowout, and the delay after the air has been dispensed.
- **Prewet** — Configures the amount of additional liquid to aspirate, and the amount of time to pause before dispensing.
- **Wash** — **Wash** is *not* applicable for liquid types on Biomek 4000 instruments.
- **Dispense** — Configures the delay and speed of the dispense operation during a method run.

  NOTE **Cutoff Velocity** is *not* applicable to Biomek 4000 instruments.

- **Tip Touch** — Configures the position and amount of time to pause while the tip is in contact with the side of the well and the speed at which the pod should move during the operation.
- **Wash Tool Liquid Settings** — Allows wash operation parameters to be configured for the currently selected liquid, including the following:
  - **Purge** — Sets the volume of liquid to purge when switching liquids or loading a wash tool, the desired purge speed, and the delay, unless overridden in the **Purge** step itself.
  - **Backup** — To prevent dripping, this operation sets default values for the volume of air to aspirate, aspiration speed, and the amount of time to delay after the operation is completed for the **Aspirate Backup** step.
  - **Vacuum** — Sets the default value for the delay in the **Vacuum** step.

— **Blowout** — Sets **Blowout Backup** step default values for speed and delay to dispense the air gap created during Backup operations. Volume is not needed, as it was set in the Backup section.

— **Dispense** — Sets default value for speed and delay for the **Dispense** step.

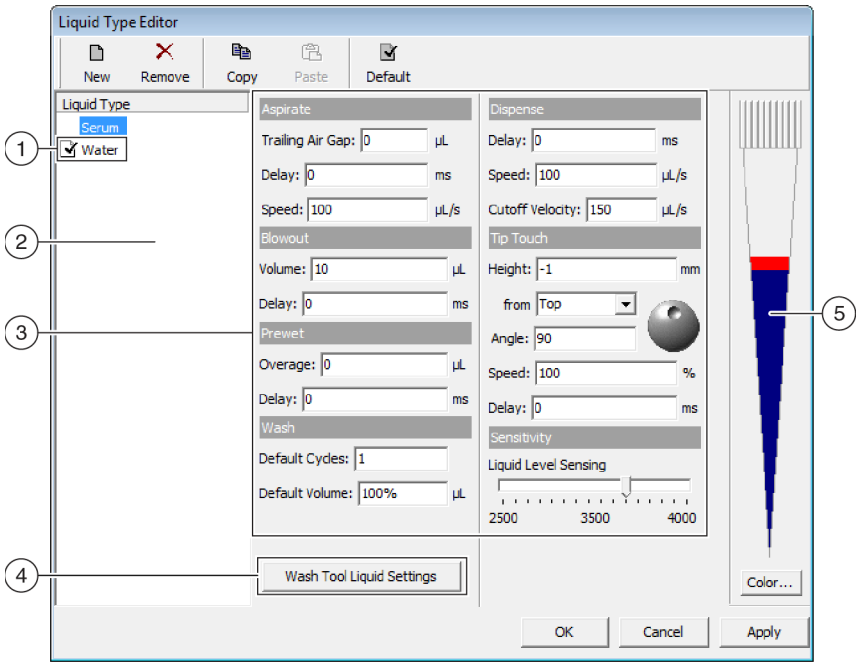
— **Return** — Sets values for volume, speed, and delay for pulling liquid back from a tool just before unloading it.

- **Sensitivity** — **Sensitivity** is *not* applicable to Biomek 4000 instruments.
- **Color** — Changes the color of the graphical representation of the liquid type in Biomek Software.

NOTE When **Override Liquid Type Settings** is selected in the technique, the liquid type settings created in **Liquid Type Editor** are not used (overridden). Refer to CHAPTER 9, *Understanding and Creating Techniques* for more information about creating and editing techniques.

Liquid types, along with information about tip and labware types, well patterns, and pipetting templates and techniques, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to CHAPTER 6, *Understanding and Using Project Files*, for more information on project files.

Figure 8.1 Liquid Type Editor



1. **Default Liquid Type:** A check mark appears next to the default liquid type.
2. **Liquid Type View:** Shows all defined liquid types.
3. **Liquid Type Configuration View:** Shows configuration of selected liquid type, and allows for modification of existing liquid types or the addition of new liquid types.
4. **Wash Tool Liquid Settings**: For liquids used with wash tools, specify settings by selecting this button.
5. **Tip Display:** Graphical representation of **Trailing Air Gap** (at end of tip) and **Blowout** (at top of tip), if applicable. Colors correspond with the Tip Display in the Current Deck Display of the main editor. **Trailing Air Gap** is always green and **Blowout** is always red.

Understanding Liquid Types

Liquid type information is used by techniques to help control the aspirate and dispense operations of a method. Due to liquid characteristics such as viscosity or volatility, each type of liquid may need to be pipetted in a different way. By defining liquid types in the **Liquid Type Editor**, the liquids will pipette consistently among methods. Liquid types containing properties such as **Prewet Delay, Tip Touch**, or **Blowout Volume** may be configured within the **Liquid Type Editor**. Any configured liquid type may be set as the default and used when labware is not configured for any particular liquid type.

Creating New Liquid Types

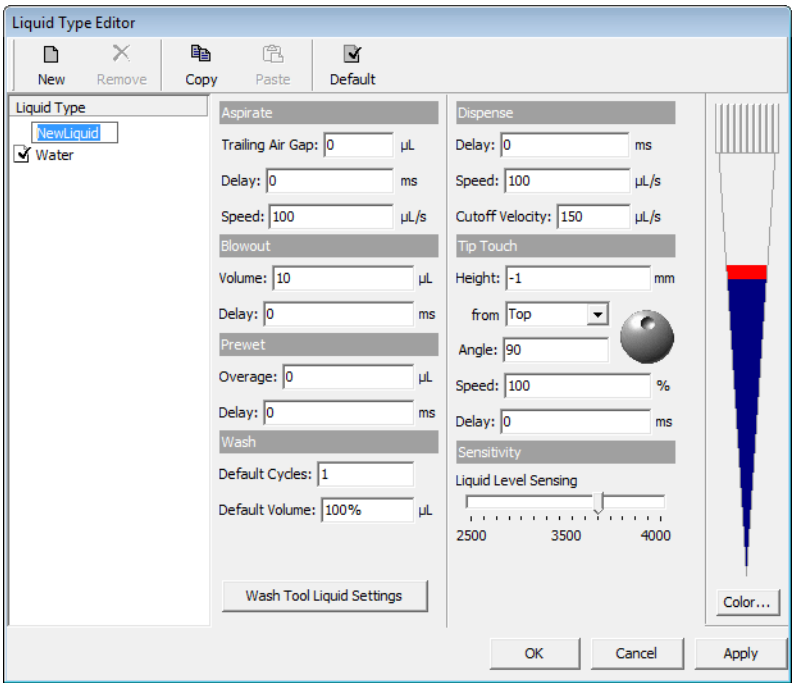
New liquid types are created by setting information in the **Liquid Type Editor**. Liquid type settings are used by Biomek Software in the steps of a method to determine how pipetting operations occur.

To create a new liquid type:

1 Choose **Project > Liquid Type Editor**. **Liquid Type Editor** appears (Figure 8.1).

2 Choose New. The new liquid type appears in the **Liquid Type** with the name "**NewLiquid**" (Figure 8.2)

Figure 8.2 Liquid Type Editor with a New Liquid



3 Enter the name of the new liquid and press **Enter** to save it.

NOTE Liquid type names may contain only alphanumeric characters and the underscore (_).

4 In **Aspirate**, enter the volume of the **Trailing Air Gap** in microliters (µL). After aspirating the liquid, a **Trailing Air Gap** is aspirated to prevent dripping.

5 In **Aspirate**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after an aspirate operation before continuing.

6 In **Aspirate**, enter the desired **Speed** in microliters per second (µL/s). This indicates the speed along the D-axis during aspirate.

7 In **Blowout**, enter the desired **Volume** of the leading air gap to blow out after dispensing the liquid.

8 In **Blowout**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after a blowout before continuing.

9 In **Prewet**, enter the desired **Overage** in microliters. **Overage** is the amount of liquid to be aspirated over the amount specified in the step configuration.

10 In **Prewet**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time from when the **Prewet** volume is completely aspirated until it begins to dispense.

11 In **Dispense**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after a dispense operation before continuing.

12 In **Dispense**, enter the desired **Speed** in microliters per second (µL/s). This indicates the speed along the D-axis during dispense.

13 In **Tip Touch,** enter the desired **Height**.

NOTE **Height**, along with **from** and **Angle**, specify where along the well the **Tip Touch** occurs.

14 In **Tip Touch**, select the desired **from: Top, Bottom**, or **Liquid**. This indicates the location the **Height** is measured from.

NOTE **Top** measures from the top of the well, **Bottom** from the bottom of the well, and **Liquid** from the top of the liquid.

15 In **Tip Touch**, enter the desired **Angle.**

OR

Select the position along the edge on the graphic by positioning the smaller circle at the desired location. The **Angle** adjusts to the current location.

NOTE The **Angle** specifies the location along the well wall where the **Tip Touch** occurs at the specified **Height** and **from** location.

16 In **Tip Touch,** enter the desired **Delay. Delay** specifies the amount of time after the tip touch before continuing.

17 In **Tip Touch**, enter the desired **Speed** as a percentage of the total speed.

18 In **Liquid Level Sensing**, select the desired **Sensitivity. Sensitivity** is the magnitude of change required for LLS to detect the liquid. A larger **Sensitivity** detects smaller changes.

NOTE The **Sensitivity** value is only used if the selected technique has **Inherit From Liquid Type** selected for the technique sensitivity. Refer to CHAPTER 9, *Setting Liquid Level Sensing Values*.

19 Choose **Color...** to designate a new display color for the liquid, if desired.

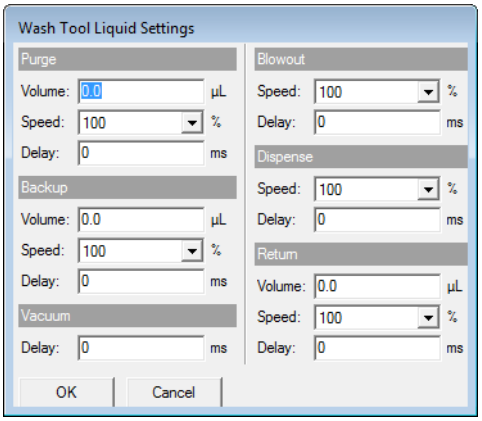
NOTE The color affects only the display of aspirated liquid. The **Trailing Air Gap** is always green and **Blowout** is always red.

20 If the new liquid:

- **Cannot** be used for wash operations, proceed to step 37.
- **Can** be used for wash operations, proceed with the following steps.

21 Select the Wash Tool Liquid Settings button. **Wash Tool Liquid Settings** displays (Figure 8.3).

Figure 8.3 Wash Tool Liquid Settings



22 In **Purge**, enter the desired **Volume** in microliters (µL).

23 In **Purge**, enter the desired **Speed** as a percentage of the total speed.

24 In **Purge**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after a purge operation before continuing (unless it is overridden in the step itself).

25 In **Backup**, enter the desired **Volume in microliters (µL)**.

26 In **Backup**, enter the desired **Speed** as a percentage of the total speed.

27 In **Backup**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after an aspirate backup operation before continuing.

28 In **Vacuum,** enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time to delay after performing the vacuum operation.

29 In **Blowout**, enter the desired **Speed** as a percentage of the total speed.

30 In **Blowout**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after a blowout backup operation before continuing.

31 In **Dispense**, enter the desired **Speed** as a percentage of the total speed.

32 In **Dispense**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after a bulk dispense operation before continuing.

33 In **Return**, enter the desired **Volume in microliters (µL)**.

34 In **Return**, enter the desired **Speed** as a percentage of the total speed.

35 In **Return**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time for pulling liquid back from a tool before unloading it.

36 Select **OK** to save the **Wash Tool Liquid Settings** for the new liquid type.

OR

Select **Cancel** to close **Wash Tool Liquid Settings** without saving changes.

37 Choose **OK** to enter the new liquid type and close the **Liquid Type Editor**.

OR

Choose **Apply** to save the new liquid type without closing **Liquid Type Editor.**

OR

Choose **Cancel** to close the **Liquid Type Editor** without saving changes.

Changing the Aspirate and Dispense Speeds

For typical pipetting operations, the aspirate and dispense speed is expressed in units of microliters per second, and can be changed in the **Liquid Type Editor**. This represents the speed of the plunger in the D-axis on the instrument during pipetting operations. Each tool has a minimum and maximum allowable speed, as shown in Table 8.1

Table 8.1 Minimum and Maximum Pipetting Speeds in D-Axis

Tool	Minimum Speed (µL/s)	Maximum Speed (µL/s)
P20, Single-Tip Pipette Tool	0.04	39.4
P200L, Single-Tip Pipette Tool	0.30	304.0
P1000SL, Single-Tip Pipette Tool	1.80	1780.0
MP20, Multi-Tip Pipette Tool	0.04	39.4
MP200, Multi-Tip Pipette Tool	0.30	304.0
MP1000, Multi-Tip Pipette Tool	1.30	1370.0

Removing Liquid Types

If a liquid type is no longer needed, it can be removed from the project.

NOTE When a liquid type is removed, previous revisions of the liquid type will remain available for validated methods, but will not be available for future method editing tasks.

To remove a liquid type:

1. In the **Liquid Type Editor**, select the liquid type to remove.
2. Select 

.
3. Choose **OK**. The liquid type is removed.

Copying and Pasting Liquid Types Within a Project File

To use the same liquid type with different parameters within a project, copy and paste the liquid type within the **Liquid Type Editor**.

NOTE Liquid types can be exported to and imported from other projects. Refer to CHAPTER 6, *Importing and Exporting Project Files* for information about importing and exporting liquid types.

To copy and paste liquid types:

1. In the **Liquid Type Editor**, select the liquid type to copy.
2. Choose 

.
3. Choose 

. The new liquid appears with the name "**Copy_of_(Liquid Type)**".
4. Rename the liquid type as desired.

   NOTE Liquid type names may contain only alphanumeric characters and the underscore (_).
5. Make any desired changes to the liquid type (refer to *Creating New Liquid Types*).

6 Choose **OK**.

Specifying the Default Liquid Type

Any defined liquid type can be the default. Any labware on the deck not configured with a specific liquid type uses the default liquid type for pipetting operations.

To set the default liquid type:

1 In the **Liquid Type Editor**, select the liquid type to set as default.

2 Choose 

.

NOTE The default liquid type appears with a check mark in the **Liquid Type** list. When the default liquid type is highlighted in the **Liquid Type** list, the **Default** button is toggled on.

CHAPTER 9

Understanding and Creating Techniques

Overview

A technique stores a set of values and properties that instruct the instrument in performing pipetting operations, such as aspirate, dispense, mix, pod height, pod speed, and tip touch. Biomek Software also stores a set of properties related to each technique, such as labware type and liquid type. Based upon these values and properties, the appropriate technique is selected automatically for the pipetting operation.

Techniques, along with information about tip and labware types; liquid types; well patterns; and pipetting templates, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to CHAPTER 6, *Understanding and Using Project Files*, for more information on project files.

NOTE When Beckman Coulter Accounts & Permissions is enabled, only users with the **Develop Projects** permission assigned may open, edit, create, and delete techniques (refer to CHAPTER 1, *Using Accounts and Permissions*).

How Techniques Work

Biomek Software is pre-programmed with a variety of techniques. The properties input during method building are matched with technique properties to select the most appropriate technique for use in the pipetting operation. Techniques are selected automatically based upon the number of properties that match the method. For example, a technique that matches five properties in a method is selected over a technique with four matching properties.

In most instances, one technique will have the closest match with the properties of the current pipetting operation; however, if more than one technique matches the same number of properties, Biomek Software selects the technique with the highest rank. Rank is prioritized such that the lower the number, the higher the rank.

Because Biomek Software selects techniques automatically, any change within a method may result in a new technique selection. When a single value or property is changed in the method, Biomek Software makes sure the technique is still the most appropriate technique to use. When desired, you have the flexibility to override the automatically-selected technique with one of your choosing.

Why Techniques Are Valuable

Techniques are a flexible way to make the pipetting process easier. Techniques allow the pipetting settings to be saved globally and used in multiple methods. Each time a method is created, the technique most appropriate for the pipetting operation is selected with no additional configuration required. When multiple sources and liquids are used in a method, each pipetting operation may use a different technique. This allows for appropriate pipetting throughout the entire method.

Customized techniques may also be created. Once additional techniques are created, they appear and function like predefined techniques.

Accessing the Technique Browser

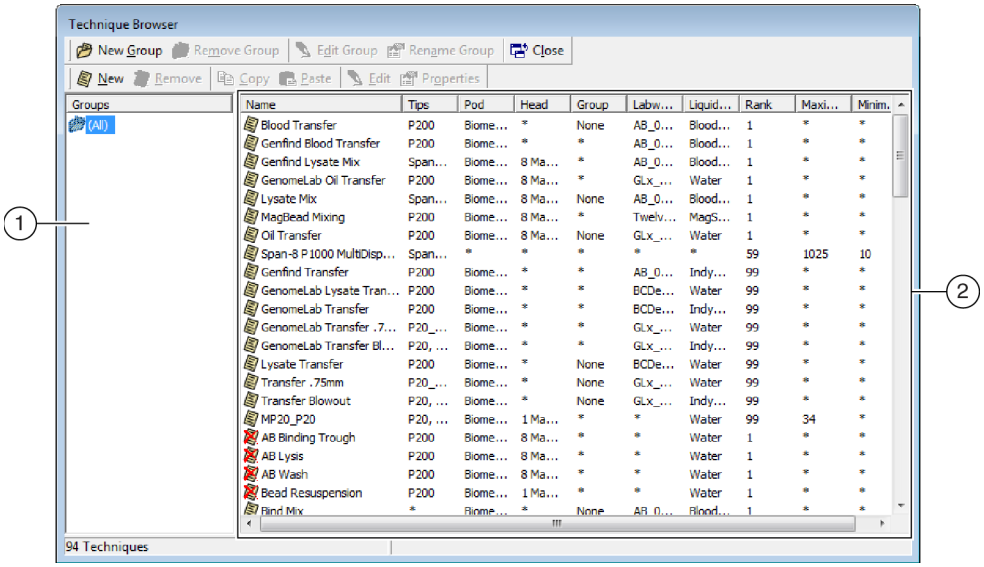
To access the Technique Browser:

1 From the **Project** menu, choose **Technique Browser**.

The **Technique Browser** appears (Figure 9.1). The **Technique Browser** contains two main views:

- **Groups** — Displays all user-created groups that contain a subset of techniques in the project; refer to *Creating Technique Groups* for more information.
- **Techniques View** — Lists all techniques defined in the selected group with their technique properties.

Figure 9.1 Technique Browser

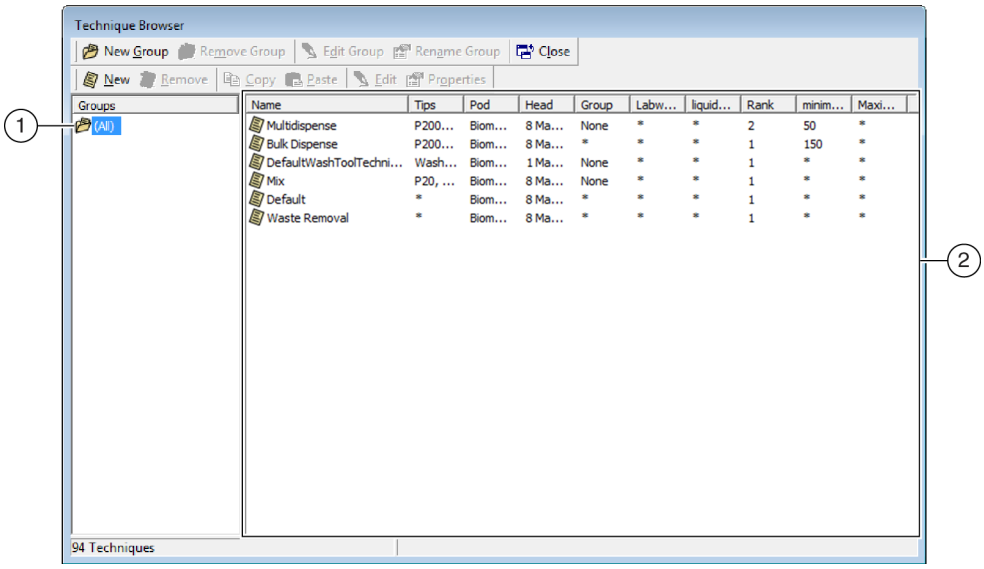


1. **Groups**: selects group to display in the Techniques View.
2. **Techniques View**: shows defined techniques that are part of the selected **Group**.

Identifying Techniques

Techniques are identified by name in the **Technique Browser** (Figure 9.2). Because the name is how the software identifies a particular technique, changing the name of the technique will require modifying the methods that use by specifying the new name in the **Technique** field (Figure 9.19).

Figure 9.2 Technique Browser Where Technique Parameters Are Displayed



1. **Groups**: Filters all techniques to show only those techniques in a selected group.
2. **Techniques View**: Displays all techniques in the selected group and their parameters. Available techniques are selected automatically for different pipetting operations in a method.

Creating New Techniques

The default techniques are sufficient for some pipetting operations and are meant as a starting point; there are instances when additional techniques may be required. For example, a method may call for a technique for a 384-well titerplate that transfers a volume between 5 µL and 10 µL of DMSO. When creating a new technique, the properties of the technique must be configured. For best results, all techniques should be evaluated and fine-tuned for the specific application through experimentation.

Techniques are automatically selected using properties. Properties identify certain aspects of the pipetting operation which might affect how the pipetting operation is performed. For a technique to be available for selection for a specific pipetting operation, all properties for the operation must match the properties in the technique.

The following properties are used to determine the optimal technique to use:

- **Head** — Identifies the tool types for which the technique is applicable; for example, a technique could be created which is only to be used with a specific tool or tools, such as single-channel tools, eight-channel tools, or wash tools. The technique is only used when the tool used for the pipetting operation matches this selection.
- **Labware** — Identifies labware types for which the technique is applicable; for example, a technique could be created which is only to be used when pipetting from a certain type of labware, such as reservoirs, deepwell microplates, or test tube racks. The technique is only used when the labware type used in the pipetting operation matches this selection.
- **Liquid type** — identifies the liquid types for which the technique is applicable; for example, a technique could be created that is only to be used when pipetting a certain liquid type, such as DMSO or water. This can be useful to create special techniques when aspirating or dispensing viscous liquids. The technique is only used when the liquid type used in the pipetting operation matches this selection.
- **Pod** — Identifies the pod performing the pipetting operation.

  NOTE For Biomek 4000 instruments, the **Biomek 4000 Pod** is the only pod.

- **Tips** — Identifies the tip types for which the technique is applicable; for example, a technique could be created which is only to be used with a certain type of tips, such as barrier tips or wash tips. The technique is only used when the tip type used in the pipetting operation matches this selection.
- **Volume** — Identifies the volume range for which a technique is applicable; for example, a technique could be created that is only to be used when pipetting low volumes, such as 0-10 µL. The technique is only used when the volume entered in the step configuration falls within the specified range.
- **Do not Auto-Select** — When checked, excludes the technique from the possible selected techniques for a step when **Auto-Select** has been checked for the step configuration.
- **Rank** — Sets the order for selecting similar techniques.

NOTE If groups have been created (refer to *Creating Technique Groups*), an additional property is listed to allow the new group to be added to an existing group, if desired. **Group** is for organizing techniques only and is not used for selecting the technique to use.

Create additional techniques using the **Technique Browser** (Figure 9.1).

NOTE Automatic selection of techniques may be turned off and new techniques created within a step configuration (refer to *Selecting and Modifying Techniques Manually in a Method*).

To create a new technique and set its properties:

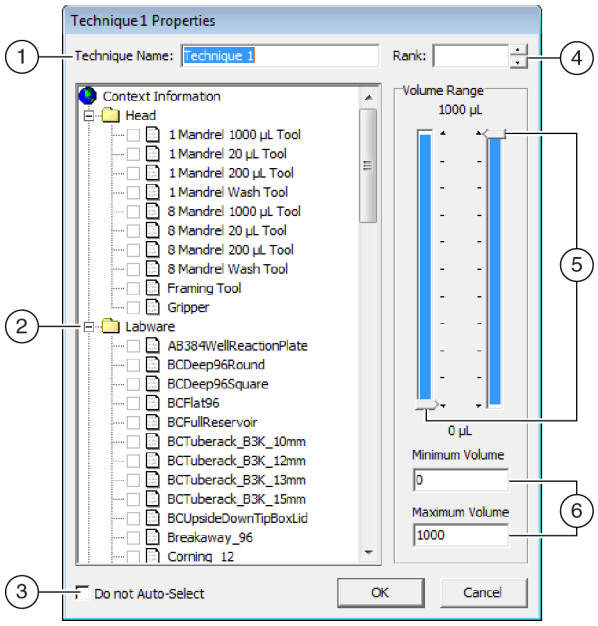
1 From the **Project** menu, choose **Technique Browser. Technique Browser** appears (Figure 9.1).

2 In the **Technique Browser**, choose New. **Technique Properties** appears (Figure 9.3).

OR

Right click on the technique and select **Properties** from the context menu.

Figure 9.3 Setting Technique Properties



1. **Technique Name**: Allows input of a unique name for the new technique or rename for an existing technique.
2. **Context Information**: Specifies the Group (if applicable), Labware, Liquid Type, Pod, Head (Tools), and Tips used for the technique.
3. **Do not Auto-Select**: When checked, excludes the technique from the possible selected techniques for a step when **Auto-Select** has been checked for the step technique configuration.
4. **Rank**: Sets the order for selecting similar techniques. A lower number is chosen preferentially above a higher number.
5. **Graphical Volume Range**: Handles allow adjustment of minimum and maximum pipetting volumes.
6. **Volume Range**: Sets the minimum and maximum volumes that the technique can pipette

NOTE **Graphical Volume Range** and **Volume Range** set the same values. The **Graphical Volume Range** sliders allow for gross adjustments, and text entered into the **Volume Range** fields allow for precise entries.

3 In **Technique Name**, enter a name to identify the technique.

4 In **Rank,** enter a value to set the relative preference of the technique to other techniques with similar properties.

NOTE **Rank** allows Biomek Software to give techniques preference over others. For example, when two techniques (**Technique A** and **Technique B**) are assigned the same properties and the same volume, but **Technique A** has a ranking of **25** and **Technique B** has a ranking of **99**, **Technique A** is selected due to the higher ranking value.

NOTE If the **Rank** field is left blank, the software will assign the lowest priority ranking to this technique. That is, if **Auto-Select** is chosen during method set-up, this technique will be chosen last when there are other techniques matching the same number of properties.

5 In **Context Information**, select the desired **Head (tools), Labware, Liquid Type, Pod,** and **Tips** to use for the technique.

NOTE If no selection is made for a category, the technique is applicable for all items within that category. For example, if no labware types are selected under **Labware**, the technique is available for use with all labware types.

NOTE To remove all current selections from the **Technique Properties**, right click in **Context Information** and select **Clear Selections**. **Clear Selections** removes all selections from all categories.

NOTE If you have created a group, the **Group** category is present in **Context Information**, but it is not used to determine technique selection.

6 In **Volume Range**, enter the **Minimum Volume** and **Maximum Volume** for the technique to aspirate or dispense.

OR

Change the minimum and maximum volumes graphically using the handles on the graphical **Volume Range** (Figure 9.3).

NOTE The left gauge is for **Minimum Volume** and the right gauge is for **Maximum Volume**.

7 Select **Do not Auto-Select** to exclude the new technique from the possible selected techniques for a step, such as **Transfer** or **Combine**, when the **Auto-Select** has been checked for the step technique configuration. The technique will not be automatically selected by Biomek Software for any pipetting operations, but is still available when manually selecting a technique if the properties match (refer to *Selecting and Modifying Techniques Manually in a Method*).

NOTE A technique that has **Do not Auto-Select** selected displays in the **Technique Browser** with a red **x** in the icon next to a technique.

8 Choose **OK**. The technique is created and added to the list in Technique Browser. To access the properties of an existing technique to view or modify them:

Right click on the technique entry in the browser and select **Properties** from the menu.

OR

Click on the technique entry in the browser and select Properties.

Setting Technique Values

After creating a technique and setting the related properties, set the technique values, such as **Tip Touch** or **Mix After Dispense**, in **Technique Editor** before performing a method.

NOTE The **Technique Browser** lists all available techniques. The **Technique Editor** allows for configuration of the technique values for a specific technique.

In the **Techniques Editor**, a drop-down list is used to select the **Pipetting Template** (refer to CHAPTER 10, *Using the Pipetting Template Editor*). When the **Pipetting Template** is selected, the following seven tabs appear.

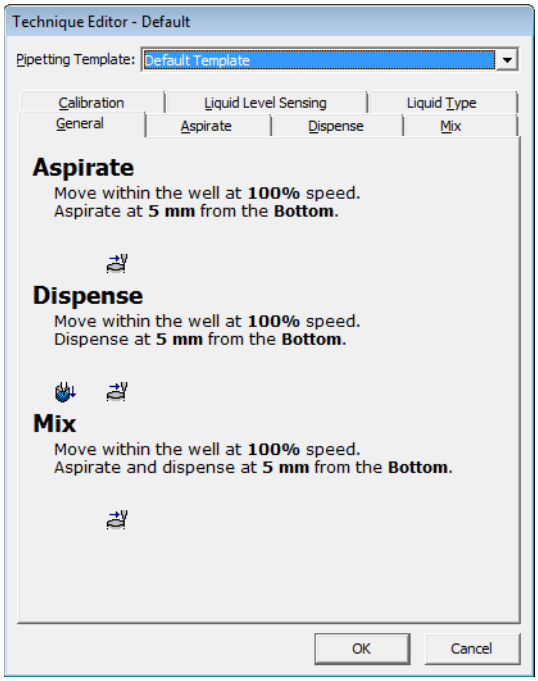
The seven tabs are:

- **General** — *Viewing Technique Description*
- **Aspirate** — *Setting Aspirate Values*
- **Dispense** — *Setting Dispense Values*
- **Mix** — *Setting Mix Values*
- **Calibration** — *Calibrating Techniques*
- **Liquid Level Sensing** — *Setting Liquid Level Sensing Values*
  - Available with P200L or P1000SL Single-Tip Pipette Tool.
- **Liquid Type** — *Overriding Liquid Type Values*

Viewing Technique Description

The **General** tab (Figure 9.4) summarizes the technique configuration on the **Aspirate**, **Dispense**, and **Mix** tabs in sentence form. The icons below each heading identify some of the operations the technique performs (Table 9.1).

Figure 9.4 Technique Editor—General Tab



The icons are:

Table 9.1 Technique Icons

Operation	Icon	Description
Tip Touch		Touches the tip on the side of the well.
Blowout		Aspirates an air gap before the liquid aspirates, and dispenses the air gap after the liquid has been dispensed (used in **Dispense** operations only).
Follow Liquid		Tip follows liquid level during pipetting operations.
Prewet		Quickly aspirates and dispenses liquid before the main aspirate operation occurs (used in **Aspirate** operations only).
Mix		Mixes liquid in wells before aspirate or after dispense.
Trailing Air Gap		Aspirates air after liquid is aspirated to help prevent drips (used in **Aspirate** operations only).

To view technique values in the **General** tab:

1 From the **Project** menu, choose **Technique Browser. Technique Browser** appears.

2 In **Technique Browser**, select the technique to modify.

3 Choose Edit.

OR

Double click on the technique.

OR

Right click in the Techniques View and choose **Edit** from the menu. The **General** tab displays (Figure 9.4).

NOTE Access the **Technique Editor** (Figure 9.4) through the step configuration by choosing **Customize** in the step configuration. This overrides the current technique in the pipetting operation only.

Setting Aspirate Values

Setting aspirate values allows for the technique to perform specific aspirate operations by changing related values, such as **Aspirate Height**, **Pod Speed**, and **Mix Before Aspirate**.

NOTE When setting aspirate values from the **Customize** button in a step configuration, the **Technique Editor** is specific to the operation (Figure 9.5).

To configure **Aspirate** options:

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** appears.

2 In **Technique Browser**, select the technique to modify.

3 Choose Edit.

OR

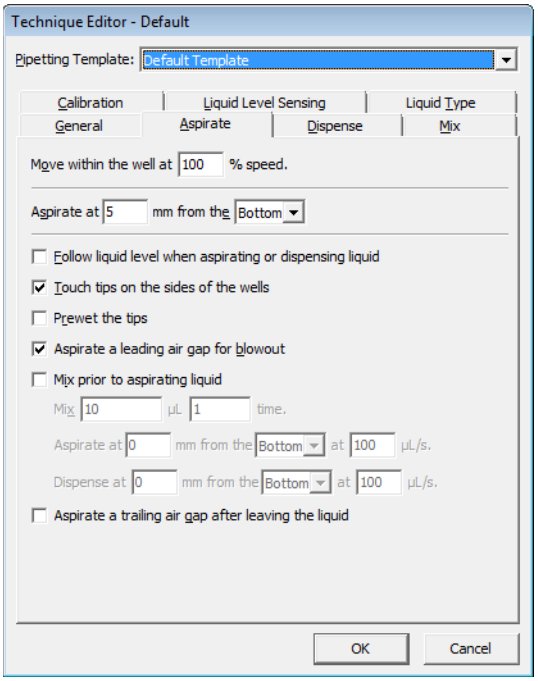
Double click on the technique.

OR

Right click in the Techniques View and choose **Edit** from the menu. The **General** tab displays by default (Figure 9.4).

4 In **Technique Editor,** select the **Aspirate** tab (Figure 9.5).

Figure 9.5 Technique Editor—Aspirate Tab



5 In **Move within the well at**, enter the speed as a percentage of the maximum speed of the pod. This value must be between 0 and 100.

NOTE This controls the speed of the X-, Y-, and Z-axes. This will affect the speed at which the pod moves to the aspirate and dispense heights. The actual aspirate and dispense speeds and the speed for tip touch are controlled by settings in the **Liquid Type Editor** (refer to CHAPTER 9, *Understanding and Creating Techniques*).

6 In **Aspirate at,** enter the distance in millimeters (mm) to measure from the selected position for the aspirate.

7 Select from where to measure the aspirate height: **Top**, **Bottom**, or **Liquid**.

NOTE **Top** measures the aspirate height from the top of the well, **Bottom** from the bottom of the well, and **Liquid** from the top of the liquid. The only time a liquid level is required is when **Aspirate** is set to **Liquid**. It is not necessary to define the liquid level to use **Follow Liquid**.

When a specific height is entered in **Aspirate at**, the aspirate operation occurs at that distance relative to the aspirate position.

NOTE A positive value is measured above the selected location; a negative value is measured below the selected location. For example, to aspirate a liquid 1.0 mm below the liquid level, a value of **-1.0** is entered in **Aspirate at** and **Liquid** is chosen as the aspirate position.

8 Choose **Follow liquid level when aspirating or dispensing liquid** to allow the tip to follow the liquid level during the aspirate operation.

9 Choose **Touch tips on the sides of the wells** to allow tips to rest against the sides of the wells for a specific amount of time after aspirating (refer to CHAPTER 8, *Understanding and Creating Liquid Types*).

10 Choose **Prewet the tips** to perform an aspirate and dispense cycle before performing the actual aspirate operations (refer to CHAPTER 8, *Understanding and Creating Liquid Types*).

11 Choose **Aspirate a leading air gap for blowout** to dispense an air gap on the Dispense operation.

NOTE **Blowout all leading air gaps** must also be chosen on the **Dispense** tab to perform a complete blowout; just choosing **Aspirate a leading air gap for blowout** on the **Aspirate** tab will not perform a complete blowout.

12 Choose **Mix prior to aspirating liquid** to mix liquid before the aspirate occurs, if desired. Refer to *Setting Mix Before Aspirate Values*, for instructions on configuring mix properties.

13 Choose **Aspirate a trailing air gap after leaving liquid** to use the defined **Trailing Air Gap** from the **Liquid Type Editor** or from the **Liquid Type** tab (refer to CHAPTER 8, *Understanding and Creating Liquid Types*).

Setting Mix Before Aspirate Values

Set the **Mix prior to aspirating liquid** values when a mix occurs before the liquid aspirates.

To set the **Mix prior to aspirating liquid** values:

1 Select **Mix prior to aspirating liquid** to activate the associated fields.

2 In **Mix**, enter the amount of liquid to mix, and the number of times to mix.

3 Enter the **Aspirate at** height in millimeters (mm) at which to perform the **Aspirate**.

4 Choose the desired aspirate position: **Top, Bottom**, or **Liquid**.

5 Enter the speed at which to aspirate in µL/s.

6 Enter the **Dispense at** height in millimeters (mm) at which to perform the **Dispense**.

7 Choose the **Dispense** location: **Top, Bottom**, or **Liquid**.

8 Enter the speed at which to dispense in µL/s.

NOTE Mix aspirates and dispenses a specified number of times within a piece of labware.

Setting Dispense Values

Setting the dispense values allows for specific dispense operations to occur by changing related values, such as **Dispense Height, Pod Speed**, and **Mix After Dispense**.

NOTE When setting dispense values from the **Customize** button in a step configuration, the **Technique Editor** is specific to the operation (Figure 9.6).

To set **Dispense** values, complete the following:

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

2 In **Technique Browser**, select the technique to modify.

3 Choose Edit.

OR

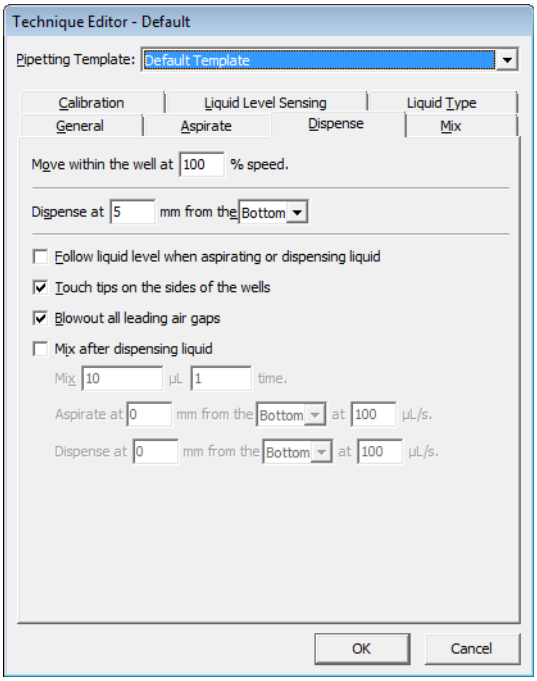
Double click on the technique.

OR

Right click in the Techniques View and choose **Edit** from the menu. The **General** tab displays (Figure 9.4).

4 In **Technique Editor**, select the **Dispense** tab (Figure 9.6).

Figure 9.6 Technique Editor—Dispense Tab



5 In **Move within the well at**, enter the speed as a percentage of the maximum speed of the pod. This value must be between 0 and 100.

NOTE This controls the speed of the X-, Y-, and Z-axes. This will affect the speed at which the pod moves to the aspirate and dispense heights. The actual aspirate and dispense speeds and the speed for tip touch are controlled by settings in the **Liquid Type Editor** (refer to CHAPTER 9, *Understanding and Creating Techniques*).

6 In **Dispense at**, enter the distance in millimeters (mm) to measure from the selected position for the dispense.

7 Select from where to measure the dispense height: **Top**, **Bottom**, or **Liquid.**

NOTE **Top** measures the dispense height from the top of the well, **Bottom** from the bottom of the well, and **Liquid** from the top of the liquid. The only time a liquid level is required is when **Dispense** is set to **Liquid**. The liquid level can be defined by either setting a known volume in the **Labware Properties** (in the **Instrument Setup** step) or by sensing the level with a P200L or P1000SL tool. It is not necessary to define the liquid level to use **Follow Liquid.**

When a specific height is entered in **Dispense at**, the dispense operation occurs at that distance relative to the dispense position.

NOTE A positive value is measured above the selected location; a negative value is measured below the selected location. For example, to dispense liquid 1.0 mm below the liquid level, a value of **-1.0** is entered in **Dispense at** and **Liquid** is chosen as the dispense position.

8 Choose **Follow liquid level when aspirating or dispensing liquid** to allow the tip to follow the liquid level during the dispense cycle.

9 Choose **Touch tips on the sides of the wells** to allow tips to rest against the sides of the wells for a specific amount of time after dispensing.

10 Choose **Blowout all leading air gaps** to dispense an air gap, if necessary (refer to CHAPTER 8, *Understanding and Creating Liquid Types*).

NOTE **Aspirate a leading air gap for blowout** must also be chosen on the **Aspirate** tab to perform a complete blowout; just choosing **Blowout all leading air gaps** on the **Dispense** tab will not perform a complete blowout.

11 Choose **Mix after dispensing liquid** to mix liquid after the dispense occurs. Refer to *Setting Mix After Dispense Values*, for instructions on configuring mix properties

Setting Mix After Dispense Values

Set the **Mix after dispensing liquid** values when a mix occurs after the liquid dispenses.

To set the **Mix after dispensing liquid** values:

1 Select **Mix after dispensing liquid** to activate the associated fields.

2 In **Mix,** enter the amount of liquid to mix, and the number of times to mix.

3 Enter the **Aspirate** height in millimeters (mm) at which to perform the **Aspirate**.

4 Choose the desired aspirate position: **Top**, **Bottom,** or **Liquid.**

5 Enter the speed at which to aspirate liquid in µL/s.

6 Enter the **Dispense** height in millimeters (mm) at which to perform the **Dispense.**

7 Choose the **Dispense** location: **Top**, **Bottom**, or **Liquid.**

8 Enter the speed at which to dispense liquid in µL/s.

Setting Mix Values

Set **Mix** values to create a custom mix. The **Mix** step aspirates and dispenses liquid a specified number of times during a method.

NOTE The number of cycles is configured in the **Mix** step configuration.

To configure **Mix**:

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

2 In **Technique Browser,** select the technique to modify.

3 Choose Edit.

OR

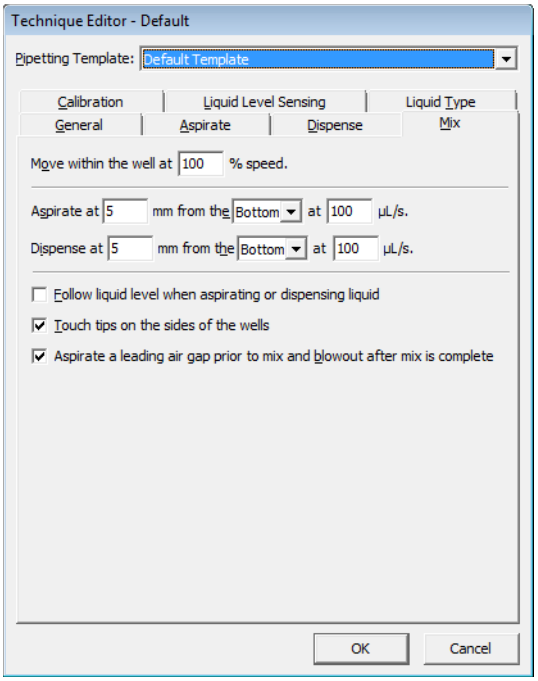
Double click on the technique.

OR

Right click in the Techniques View and choose **Edit** from the menu. The **General** tab displays (Figure 9.4).

4 In **Technique Editor,** select the **Mix** tab (Figure 9.7).

Figure 9.7 Technique Editor—Mix Tab



5 In **Move within the well at,** enter the speed as a percentage of the maximum speed of the pod. This value must be between 0 and 100.

NOTE This controls the speed of the X-, Y-, and Z-axis. This will affect the speed at which the pod moves to the aspirate and dispense heights.

6 Enter the **Aspirate at** height in millimeters (mm) at which to perform the **Aspirate**.

7 Choose the desired aspirate position: **Top**, **Bottom**, or **Liquid**.

8 Enter the speed at which to aspirate liquid in µL/s.

9 Enter the **Dispense at** height in millimeters (mm) at which to perform the **Dispense**

10 Choose the **Dispense** location: **Top**, **Bottom**, or **Liquid**.

11 Enter the speed at which to dispense liquid in µL/s.

12 Choose **Follow liquid level when aspirating or dispensing liquid** to allow the tip to follow the liquid level during the aspirate and dispense cycles.

13 Choose **Touch tips on the sides of the wells** to allow tips to rest against the sides of the wells for a specific amount of time after mixing.

14 Choose **Aspirate a leading air gap prior to mix and blowout after mix is complete** to dispense an air gap, if necessary (refer to CHAPTER 8, *Understanding and Creating Liquid Types*).

Setting Liquid Level Sensing Values

NOTE Liquid Level Sensing is available on P200L and P1000SL Single-Tip Pipette Tools only.

Set **Liquid Level Sensing** values to utilize liquid level sensing to determine the liquid level. Liquid level detection is necessary only if the **Aspirate**, **Dispense**, or **Mix** height is measured from the liquid and the liquid level is unknown. The tool and tips must all be compatible with liquid level sensing to detect the liquid level.

The **Liquid Level Sensing** tab consists of two collapsible sections to configure various aspects of using LLS. Each section is expanded by clicking the down arrow or sentence summary for that section and may then be configured. Only one section may be expanded at a time. When collapsed, each section displays a sentence summary describing the configuration for that section.

The two sections are:

- **General Settings** — Specify the start height and sense speed.
- **Error Handling Settings** — Specify the action to take if LLS fails.

To configure **Liquid Level Sensing**:

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

2 In **Technique Browser**, select the technique to modify.

3 Choose Edit.

OR

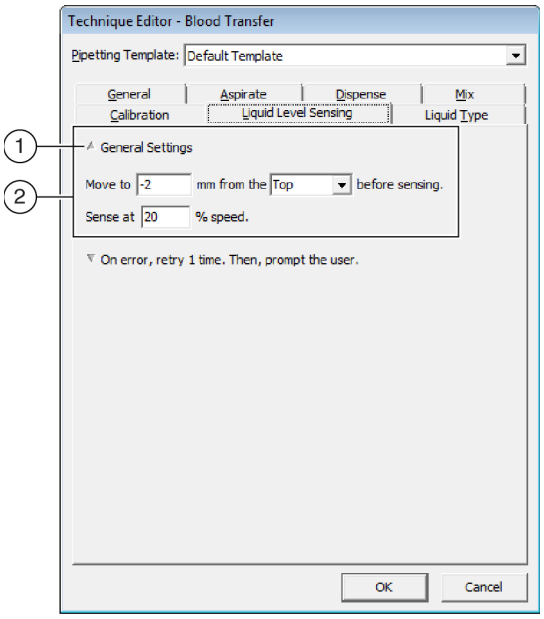
Double click on the technique.

OR

Right click in the Techniques View and choose **Edit** from the menu. The **General** tab displays (Figure 9.4).

4 In **Technique Editor**, select the **Liquid Level Sensing** tab (Figure 9.8).

Figure 9.8 Technique Editor—General Settings on Liquid Level Sensing Tab



1. **Arrow to collapse/expand General Settings.**
2. **General Settings** specify the starting height within the well and pod speed in the Z-axis during liquid level sensing.

Configuring General Settings

General Settings is used to configure the starting height of the tip within the well and the pod speed in the Z-axis during liquid level sense operations.

1 If **General Settings** does not display, click on the topmost sentence summary to expand the **General Settings** configuration (Figure 9.8).

2 Enter the height in millimeters (mm) to **Move to** and start sensing from.

3 Select the **from the** start location: **Top** or **Bottom**. The probe moves to the specified height measured from the top or bottom of the well before sensing.

4 Enter the **Sense at** speed as a percentage of the maximum speed of the pod.

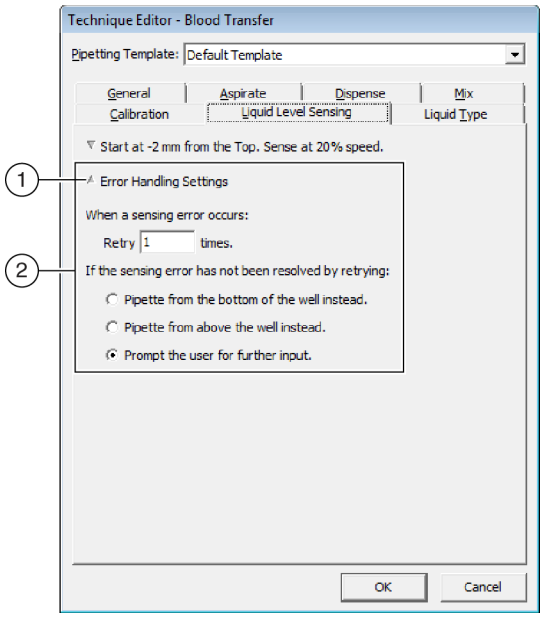
NOTE The speed affects the Z-axis speed only. The default sense speed is 20 percent.

Configuring Error Handling Settings

Error Handling Settings specify the action to take if liquid level sensing fails.

1 If **Error Handling Setting** does not display, click on the last sentence summary to expand the **Error Handling Settings** configuration (Figure 9.9).

Figure 9.9 Technique Editor—Error Handling Settings on Liquid Level Sensing



1. **Arrow to collapse/expand Sensitivity Settings.**
2. **Error Handling Settings** specifies an action to perform if liquid level sensing fails.

2 In **Retry**, enter the number of times to try to detect the liquid level when a sensing error occurs.

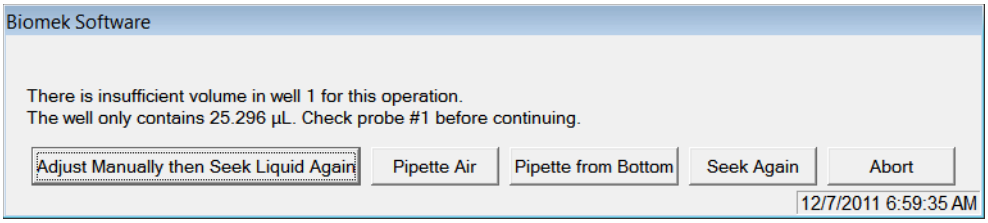
3 In **If the sensing error has not been resolved by retrying,** select the action to perform:

- **Pipette from the bottom of the well instead** — Measures the pipetting height from the bottom of the well instead of from liquid level.

NOTE When pipetting from the bottom of the well, the minimum pipetting height as defined on the **Calibration** tab for the technique (refer to *Calibrating Techniques*) is used.

- **Pipette from above the well instead** — Pipettes from 1.0 mm above the top of the well.
- **Prompt the user for further input** — Prompts the user for further instruction (Figure 9.10) and provides options to pipette from above the well (**Pipette Air**), pipette from the bottom of the well (**Pipette from Bottom**), retry (**Seek Again**), or stop the method (**Abort**).

Figure 9.10 Liquid Level Sensing Error Handling Prompt



Overriding Liquid Type Values

The settings configured on the **Liquid Type** tab override values set in the **Liquid Type Editor** (refer to CHAPTER 8, *Understanding and Creating Liquid Types*). Configure the liquid type override values so specific pipetting characteristics will result, such as the amount of air to use as a blowout, or speeds for aspirate and dispense.

Configuring the **Liquid Type** tab is optional. When overriding liquid type values, the settings entered in the **Liquid Type** tab are used instead of the settings from the particular liquid type. To use the settings from the liquid type, do not select **Override Liquid Type Settings.**

NOTE Use the **Liquid Type tab** only when overriding the liquid type. Create additional liquid types when using common liquid type settings.

To set liquid type override values for this technique:

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

2 In **Technique Browser,** select the technique to modify.

3 Choose Edit.

OR

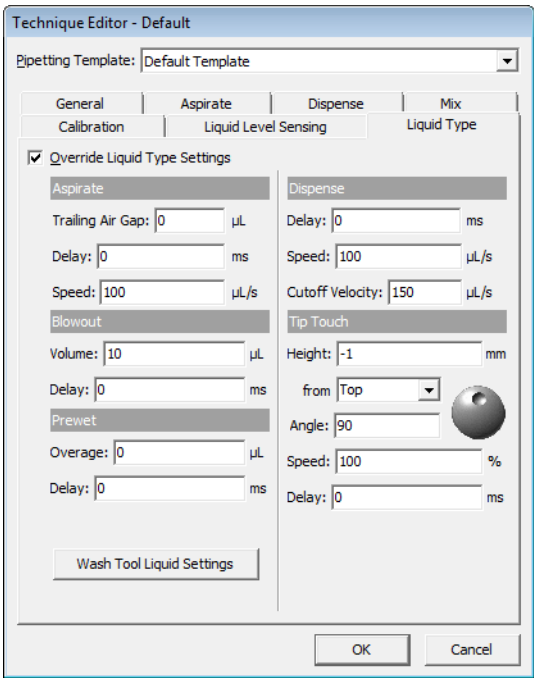
Double click on the technique.

OR

Right click in the Techniques View and choose **Edit** from the menu. The **General** tab displays (Figure 9.4).

4 In **Technique Editor**, choose the **Liquid Type** tab (Figure 9.11).

Figure 9.11 Technique Editor—Liquid Type Tab



5 Select **Override Liquid Type Setting** to activate the Liquid Type tab configuration.

NOTE When overriding liquid type values, the settings entered in the **Liquid Type** tab are used instead of the settings from the particular liquid type. To use the settings from the liquid type, do not select **Override Liquid Type Settings**.

6 In **Aspirate**, enter the volume of the **Trailing Air Gap** in microliters (µL). After aspirating the liquid, a **Trailing Air Gap** is aspirated to prevent dripping.

7 In **Aspirate**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after an aspirate operation before continuing.

8 In **Aspirate**, enter the desired **Speed** in microliters per second (µL/s). This indicates the speed along the D-axis during aspirate.

9 In **Blowout,** enter the desired **Volume** of the leading air gap to blow out after dispensing the liquid.

10 In **Blowout,** enter the desired **Delay** in milliseconds (ms). Delay specifies the amount of time after a blowout before continuing.

11 In **Prewet**, enter the desired **Overage** in microliters. **Overage** is the amount of liquid to be aspirated over the amount specified in the step configuration.

12 In **Prewet**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time from when the Prewet volume is completely aspirated until it begins to dispense.

13 In **Dispense**, enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after a dispense operation before continuing.

14 In **Dispense**, enter the desired **Speed** in microliters per second (µL/s). This indicates the speed along the D-axis during dispense.

15 In **Dispense**, delete the value located in **Cutoff Velocity** field, as this value does not apply to Biomek 4000 instruments.

16 In **Tip Touch**, enter the desired **Height.**

NOTE **Height**, along with **from** and **Angle**, specify where along the well the **Tip Touch** occurs.

17 In **Tip Touch**, select the desired **from: Top**, **Bottom,** or **Liquid**. This indicates the location the **Height** is measured from.

18 In **Tip Touch**, enter the desired **Angle**.

OR

Select the position along the edge on the graphic by positioning the smaller circle at the desired location. The **Angle** adjusts to the current location.

NOTE The **Angle** specifies the location along the well wall where the Tip Touch occurs at the specified **Height** and **from** location.

19 In **Tip Touch**, enter the desired **Delay**. Delay specifies the amount of time after the tip touch before continuing.

20 In **Tip Touch**, enter the desired **Speed** as a percentage of the total pod speed. This indicates the pod speed along the X-, Y-, and Z-axes as the pod moves to the tip touch position.

21 If the technique will be used for wash operations, select **Wash Tool Liquid Settings**, and follow instructions starting at step 22 in CHAPTER 8, *Understanding and Creating Liquid Types*.

Calibrating Techniques

Calibrating techniques improves the accuracy of pipetting operations. All method steps involving aspirating, dispensing, and mixing volumes of liquids use calibration to make sure an accurate volume is aspirated and dispensed. Calibration is also necessary to adjust for liquid properties, such as viscosity.

During a method run, the instrument aspirates and dispenses liquid based on the results of the following equation:

Displaced Volume = Desired Volume * Scaling Factor + Offset Volume

The properties in the equation are:

- **Displaced Volume** — The amount physically aspirated and dispensed
- **Desired Volume** — The amount that is expected to be aspirated and dispensed.
- **Scaling Factor** — The amount to multiply a given volume by to achieve the desired calibration.
- **Offset Volume** — The amount of overage by a specific amount, such as 2 µL.

The results of the equation are displayed in sentence form in the middle section of the **Calibration** tab (Figure 9.12). The displaced volume changes as adjustments are made to the **Scaling Factor** and **Offset** to indicate the result of the equation.

To calibrate techniques:

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

2 In **Technique Browser,** select the technique to modify.

3 Choose Edit.

OR

Double click on the technique.

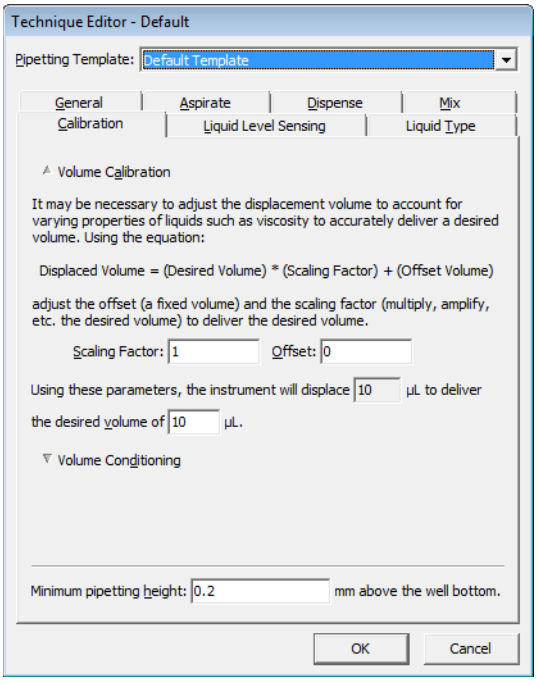
OR

Right click in the Techniques View and choose **Edit** from the menu. The **General** tab displays (Figure 9.4).

4 In **Technique Editor**, select the **Calibration** tab.

5 If the **Volume Calibration** configuration is not displayed, click on **Volume Calibration** to expand the **Volume Calibration** configuration.

Figure 9.12 Technique Editor—Volume Calibration on Calibration Tab



6 Enter the **Scaling Factor** at which to calibrate. The sentence display adjusts accordingly.

NOTE **Scaling Factor** should be greater than 0. A **Scaling Factor** of 1 and an **Offset** of 0 does not alter the volume manipulated during a pipetting operation.

NOTE **Scaling Factor** and **Offset** values are not used in the **DefaultWashToolTechnique**.

7 Enter the desired **Offset**. The sentence display adjusts accordingly.

8 Verify the calibration equation by reading the sentence display. Adjust the **Scaling Factor** and **Offset** as necessary.

9 In **Minimum pipetting height**, enter the number of millimeters from the bottom of the labware that the tip is not allowed to go below.

10 Choose **OK**.

11 Choose **Close** to close **Technique Browser**.

NOTE It is recommended that techniques be tested after calibrating to verify the desired results are achieved.

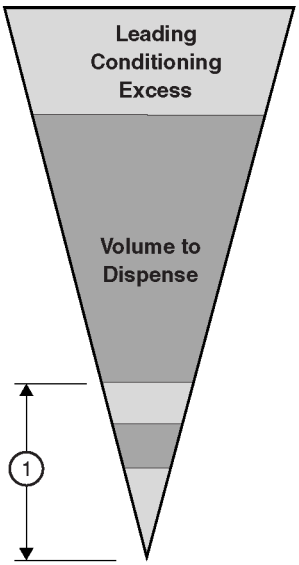
Conditioning Techniques for Multiple Dispense

Conditioning is a specified volume of liquid to dispense when performing multiple dispense operations from a single aspirate operation, and is used to enhance precision when switching from aspirate mode to dispense mode. If a multiple dispense technique is not properly conditioned, the first dispense may be greater than the volume specified in the step.

When using a technique that utilizes volume conditioning, the instrument aspirates and dispenses liquid according to Figure 9.13.

NOTE Volume conditioning is used by a technique only if the associated pipetting template is designed to use volume conditioning. Refer to CHAPTER 10, *Using the Pipetting Template Editor*, for more information on pipetting templates and the **Pipetting Template Editor**.

Figure 9.13 Volume Conditioning Identification



1. **A specified Number of Trailing Volume Sections, each with a specified Trailing Condition Volume.**

The volumes displayed in Figure 9.13 are:

- **Leading Conditioning Excess** — Volume of source aspirated in excess of the sample **Volume to Dispense** that protects from sample dilution. The **Leading Conditioning Excess** is purged after completing all dispense operations.
- **Volume to Dispense** — The total volume of source aspirated for all dispense operations. For example, if dispensing 10 µL across 12 wells of a microplate, the volume aspirated is 120 µL.
- **Trailing Conditioning Volume** — An extra volume of source is aspirated a specified **Number of Trailing Volume Sections** times following the **Volume Aspirated**. Each trailing volume section is dispensed back into the source well separately prior to leaving the well to condition the dispense operation for more precise pipetting. For example, in Figure 9.13, each of the three bottom sections is dispensed back into the source well with three separate dispense actions.

To condition techniques:

---

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

---

2 In **Technique Browser,** select the technique to modify.

3 Choose Edit.

OR

Double click on the technique.

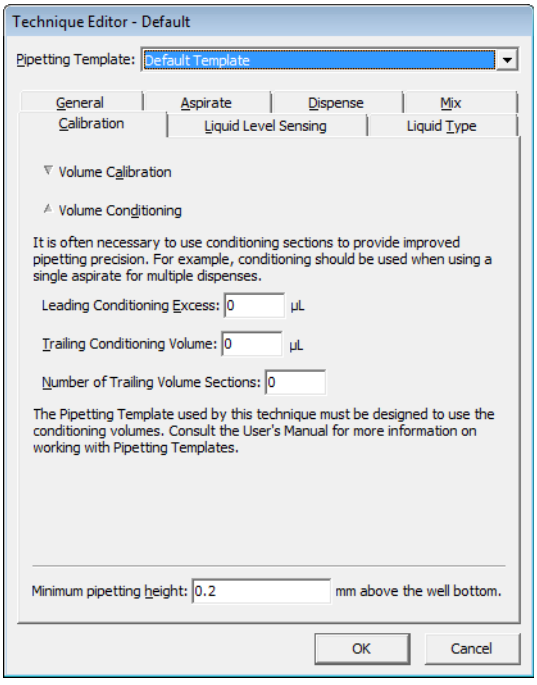
OR

Right click in the Techniques View and choose Edit from the menu. The **General** tab displays (Figure 9.4).

4 In **Technique Editor**, select the **Calibration** tab.

5 If the **Volume Conditioning** configuration is not displayed, click on **Volume Conditioning** to expand the **Volume Conditioning** configuration (Figure 9.12).

Figure 9.14 Technique Editor—Volume Conditioning on Calibration Tab



6 Enter the volume of **Leading Conditioning Excess** to aspirate as an additional buffer in excess of that aspirated automatically as part of the pipetting template.

7 Enter the **Trailing Conditioning Volume** to aspirate for each trailing volume section.

8 Enter the **Number of Trailing Volume Sections** to aspirate.

NOTE After aspirating the volume of source to dispense, an additional volume of source equal to the Number of **Trailing Volume Sections** times the **Trailing Conditioning Volume** is aspirated. Prior to leaving the well, each trailing volume section of **Trailing Conditioning Volume** is dispensed back into the source well in separate dispense actions equal to the specified **Number of Trailing Volume Sections**.

Creating Technique Groups

A Group is a user-created subset of techniques and can be used to organize techniques by their properties via the **Technique Editor** using Groups. Techniques may be in more than one group, if desired.

To create a new group:

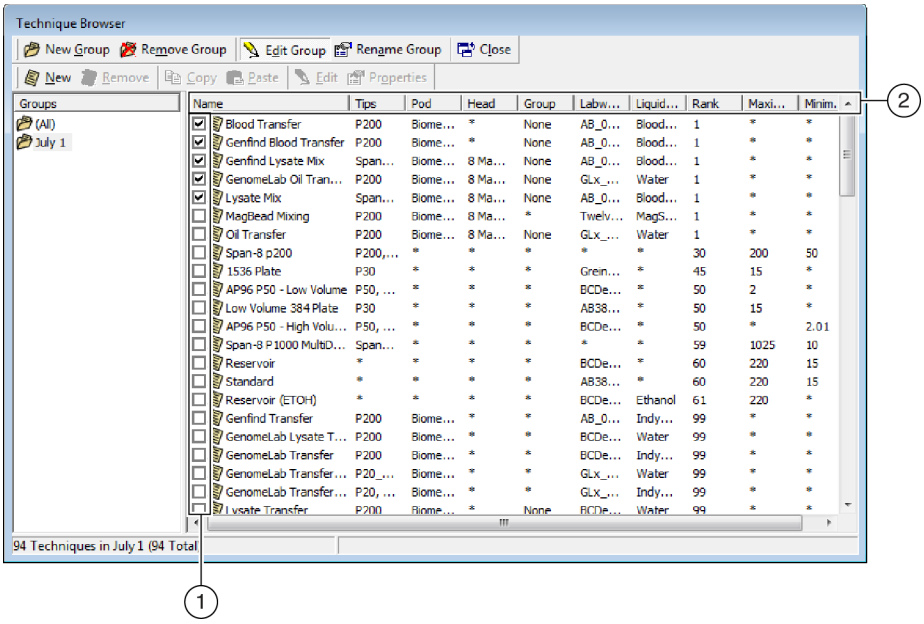
1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

2 Choose New Group.

OR

Right click under **Groups** and select **New Group** from the menu that appears. A new group is added under **Groups** and a check box appears to the left of each technique (Figure 9.15).

Figure 9.15 Creating a New Group in the Technique Browser



1. **Select techniques to include in group by selecting check box.**
2. **Sort techniques by properties by clicking on column headers.**

3 Enter a name for the new group.

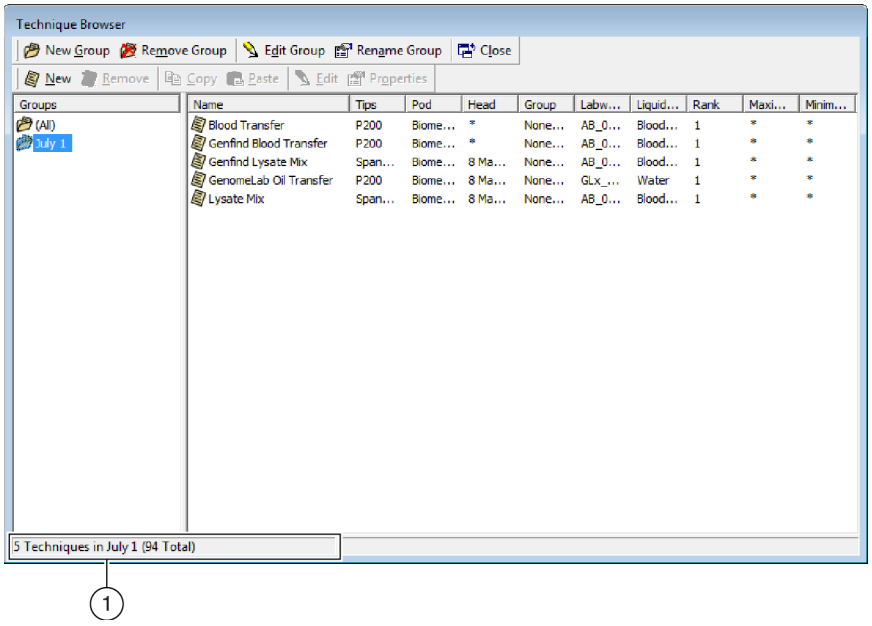
4 In the list of techniques, select the check box to the left of each technique to include that technique in the new group.

NOTE Techniques can be sorted by any of the properties by clicking on the column headings. Selecting a heading once sorts the column in ascending order; clicking on the same heading a second time sorts that column in descending order.

5 Choose Edit Group to exit group editing mode. The check boxes disappear and only the methods that were selected remain in the group.

NOTE The status bar in the **Technique Browser** displays how many techniques are in the selected group and how many techniques there are in the project.

Figure 9.16 New Group Created in the Technique Browser



1. **Status bar displays number of techniques in group and number of techniques in project.**

Renaming Groups

Groups may be renamed at any time, if desired.

To rename a group:

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

2 Select the group to be renamed and choose Rename Group.

OR

Under **Groups**, right click on the group to be renamed and select **Rename Group** from the menu.

3 Enter the desired new name for the group and press the Enter key. The group is renamed.

Adding and Removing Techniques from Groups

Techniques may be added to or removed from a group at any time using the **Edit Group** command.

NOTE Techniques may also be added to a group when they are created by selecting the groups to which the technique is to be added when configuring technique properties (refer to *Creating New Techniques*).

To edit a group:

---

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** displays.

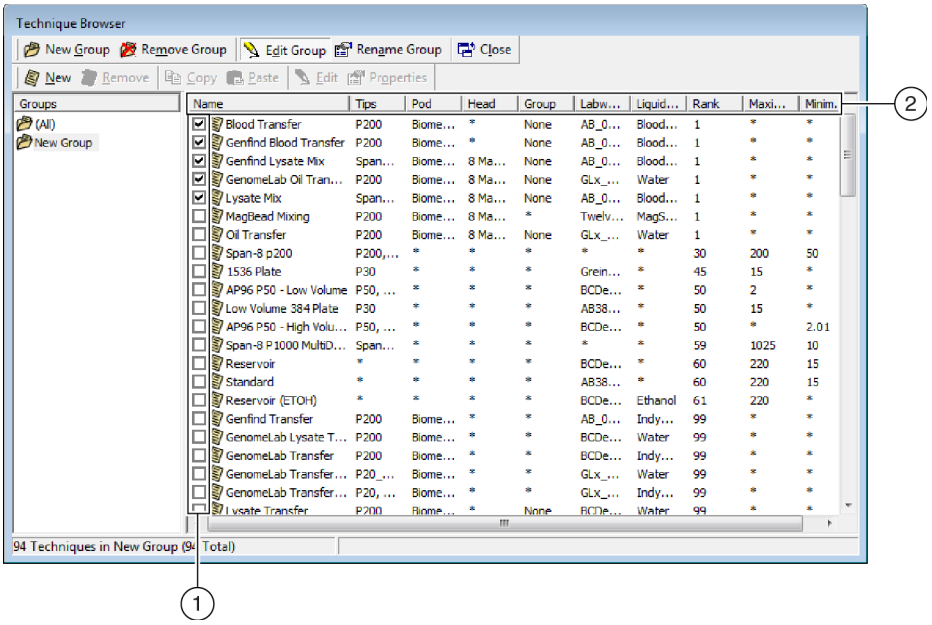
---

2 Select the group to be modified and choose Edit Group.

OR

Under **Groups**, right click on the group to be modified and select **Edit Group** from the menu. A check box displays to the left of each technique (Figure 9.15).

Figure 9.17 Editing a Group in the Technique Browser



1. **Select techniques to include in a group by selecting the check box.**
2. **Sort techniques by properties by clicking on column headers.**

3 In the list of techniques, select the check box to the left of each technique to include in the group, or deselect the check box to the left of each technique to remove that technique from the group.

NOTE Techniques can be sorted by any of the properties by clicking on the column headings. Selecting a heading once sorts the column in ascending order, clicking on the same heading a second time sorts that column in descending order.

NOTE Right clicking on the technique in the techniques list and selecting **Remove** removes the technique from the project, not the group.

4 Choose Edit Group to exit group editing mode. The check boxes disappear and only the methods that were selected remain in the group.

NOTE The status bar in the Technique Browser displays how many techniques are in the selected group and how many techniques there are in the project.

Removing Groups

When a group is no longer needed, it can be removed from the Technique Browser.

To remove a group:

1 From the **Project** menu, choose **Technique Browser**. **Technique Browser** appears.

2 Under **Groups**, select the desired group to remove.

3 Choose Remove Group.

OR

Under **Groups**, right click on the group to be removed and select **Remove Group** from the menu. The group is removed from the list under **Groups**.

Removing Techniques

To prevent Biomek Software from choosing techniques during a method run that may have become obsolete, remove the techniques from the **Technique Browser**.

When a technique is removed, it is no longer available in method building. However, the latest saved revision of the technique remains in the project file and may be restored at any time (refer to CHAPTER 6, *Understanding and Using Project Files*).

To remove techniques:

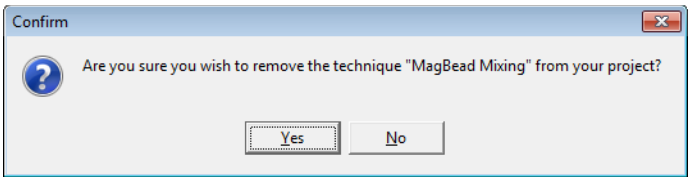
1 In **Technique Browser**, select the technique

2 Choose Remove.

OR

Right click and choose **Remove** from the menu. A **Confirm** prompt displays (Figure 9.18).

Figure 9.18 Remove Technique Confirmation Prompt



3 Choose **Yes** to remove the technique.

Modifying Saved Techniques

When a method uses pipetting requirements that are slightly different from the requirements of previously created techniques, modify the technique that most closely resembles the new pipetting requirements by copying and pasting.

To copy and paste techniques:

1 In **Technique Browser,** select the technique to copy.

2 Choose Copy.

OR

Right click and choose **Copy** from the menu.

3 Choose Paste. The copy appears with the name **Copy of (Technique)**.

OR

Right click and choose **Paste** from the menu.

4 Select the copied technique.

5 Choose Properties.

OR

Right click and choose **Properties** from the menu.

6 Enter a new name for the technique, if desired.

7 Make any changes to the technique properties (refer to *Creating New Techniques*).

8 Choose **OK**.

9 Double click on new technique. **Technique Editor** opens. Update the technique as needed (refer to *Setting Technique Values*).

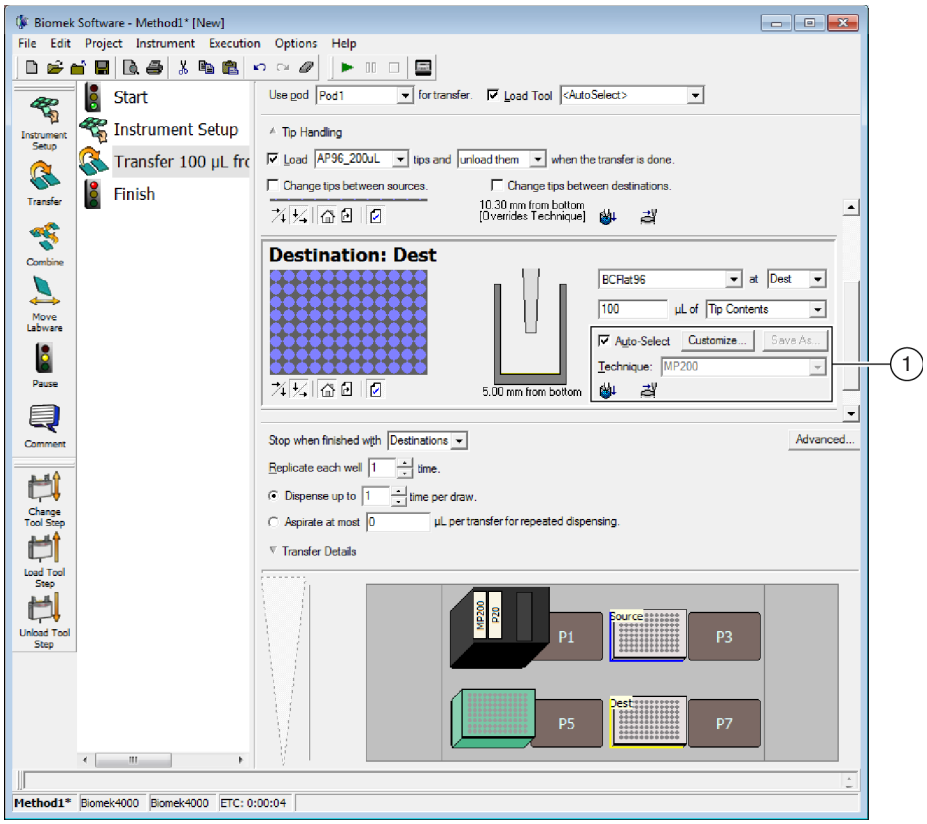
10 Select **OK** to close the **Technique Editor**.

11 Select **Close** to exit the **Technique Browser**.

Selecting and Modifying Techniques Manually in a Method

Automatic selection of techniques is turned on by default; however, there may be instances when manual selection of techniques is desired. When **Auto-Select** is unchecked, manual selection of techniques is possible in the source and destination configuration of a pipetting step, such as **Transfer** or **Combine.** Biomek Software shows all techniques that match the properties of the step configuration (pod, tool, tips, labware type, liquid type, volume) in a drop-down list in the **Technique** field (Figure 9.19)

Figure 9.19 Customize Techniques or Manually Select Techniques from a List in Source or Destination Configurations of a Pipetting Step



1. **Technique Selection**: Techniques are selected automatically, manually from the drop-down list, or customized using the **Customize** button.

Techniques used in methods are normally auto-selected by Biomek Software; however, circumstances may require modifications to techniques due to the current setup or liquid type. Many pipetting steps provide access to the **Technique Editor** during method development.

Modifying a Technique Through a Method Step

Custom techniques created within a method are saved within the current method only and are accessible only in the pipetting operation for which the technique was created. The technique can be saved for global use after configuration, if desired.

When modifying techniques or creating new techniques within a method, only the parameters for the specific operation, along with **Liquid Type**, **Liquid Level Detection**, and **Calibration** settings, may be modified.

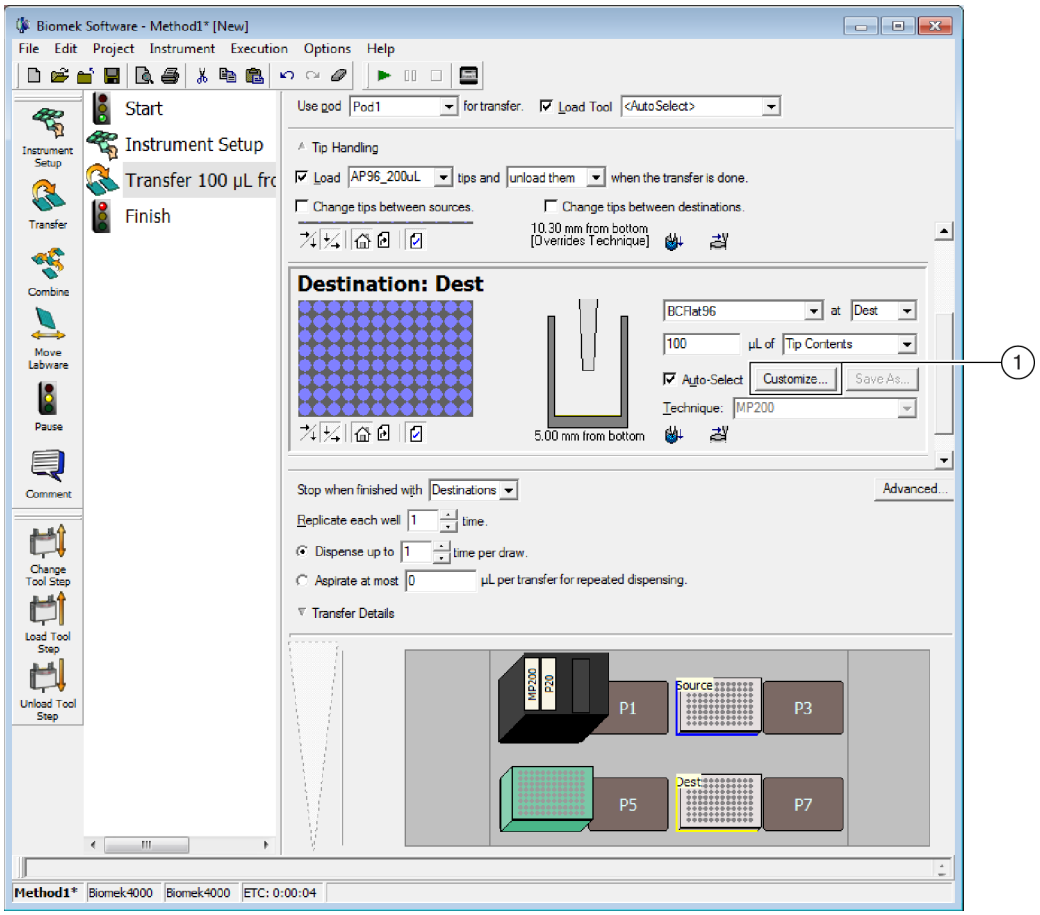
To modify a technique within a step or method:

1 Select the desired step in the method.

2 Select the desired source or destination.

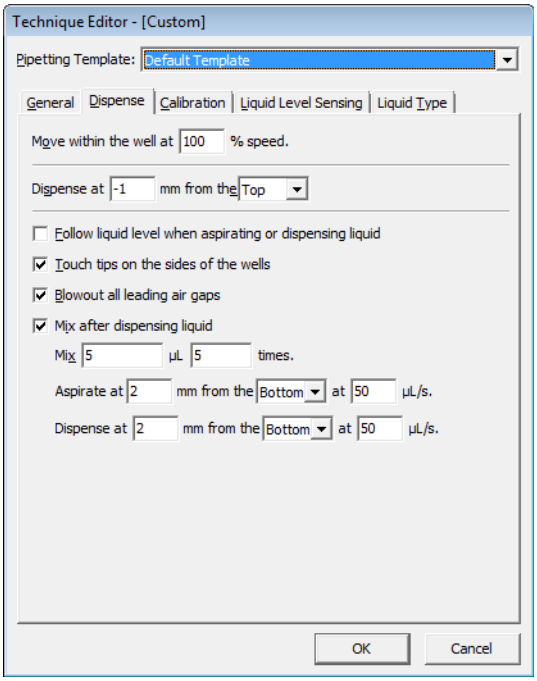
3 Choose Customize... (see Figure 9.20). **Technique Editor** - [**Custom**] displays (Figure 9.21).

Figure 9.20 Technique Selection Within a Method



1. **Custom Technique**: Choose **Customize** to modify the technique.

Figure 9.21 Dispense Tab Appears When Customize is Selected from Destination



4 Customize the technique as needed (refer to *Setting Technique Values*).

NOTE **Technique Properties**, such as **Labware Type, Liquid Type**, and **Tips**, cannot be configured for the custom technique when creating the technique within a method. The technique uses the known properties of the specific operation being customized. **Technique Properties** are configured upon saving the technique for global use (refer to *Saving Custom Techniques*).

5 Choose **OK**. [**Custom**] replaces the technique name.

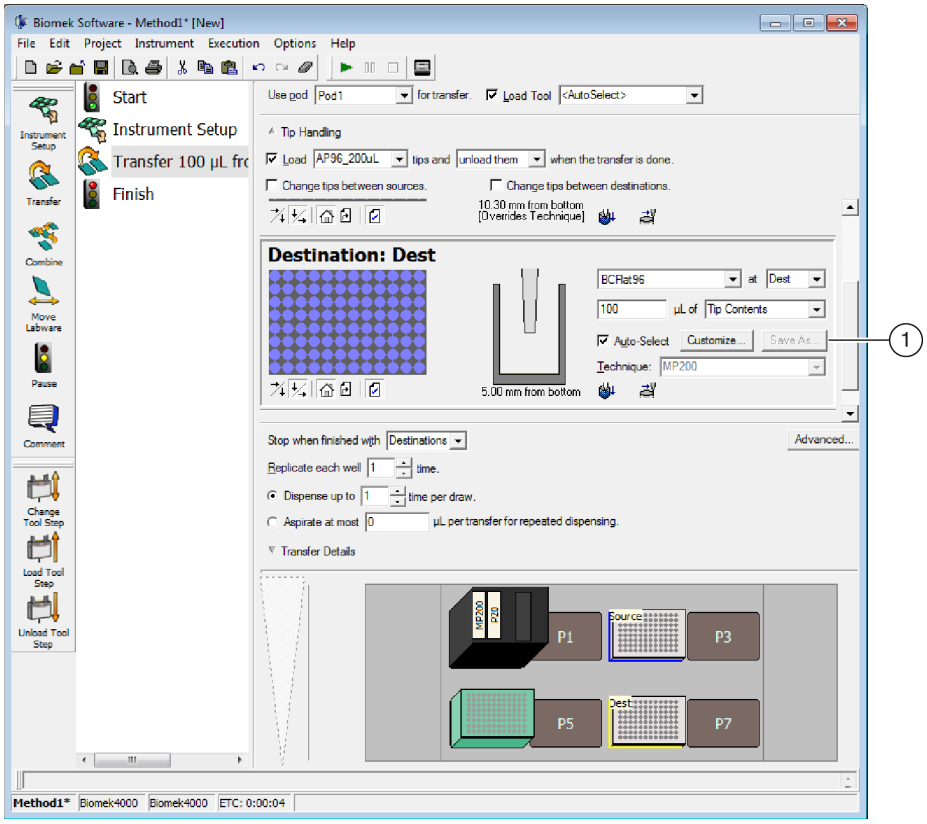
Saving Custom Techniques

A custom technique is saved within the method in which it was created; however, any custom technique can be saved for global use.

To save a custom technique for global use:

1 Choose Save As... in the step configuration (Figure 9.22). **Technique Properties** appears.

Figure 9.22 Save a Custom Technique Within a Step



1. **Custom Technique**: Choose **Save As** to save the technique for global use.

2 Enter the **Technique Name**, then select the properties desired for the technique (refer to *Creating New Techniques*).

3 Choose **OK**. The new technique name appears in **Technique**.

CHAPTER 10

Using the Pipetting Template Editor

Overview

Pipetting operations within steps of a method are configured using techniques. Techniques are associated with a pipetting template that controls how the instrument performs pipetting operations for aspirating, dispensing, and mixing liquids. While using the **Pipetting Template Editor** is not necessary to successfully operate the instrument, it does present the opportunity for finer control over pipetting operations in order to optimize performance for specific applications.

A pipetting template is not used unless it is associated with a technique. Likewise, a technique is useless without the pipetting template that controls it. Biomek Software contains several default pipetting templates by which all predefined techniques are controlled.

Pipetting templates can be modified, or new templates created, using the **Pipetting Template Editor**. Templates are created by configuring a series of steps that dictate the actions the instrument makes, similar to building a method in the Main Editor.

Pipetting templates, along with information about liquid types; labware and tip types; well patterns; and pipetting techniques, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to CHAPTER 6, *Understanding and Using Project Files*, for more information on project files.

NOTE When Beckman Coulter Accounts & Permissions is enabled, only users with the **Develop Projects** permission assigned may open, edit, create, and delete pipetting templates (refer to CHAPTER 1, *Using Accounts and Permissions*)

Creating and Modifying Pipetting Templates

Creating and modifying pipetting templates is achieved with the **Pipetting Template Editor**.

To open the **Pipetting Template Editor**:

1 Choose **Project** > **Pipetting Template Editor**. The **Pipetting Template Editor** displays (Figure 10.1).

Pipetting templates are created in one of the following ways:

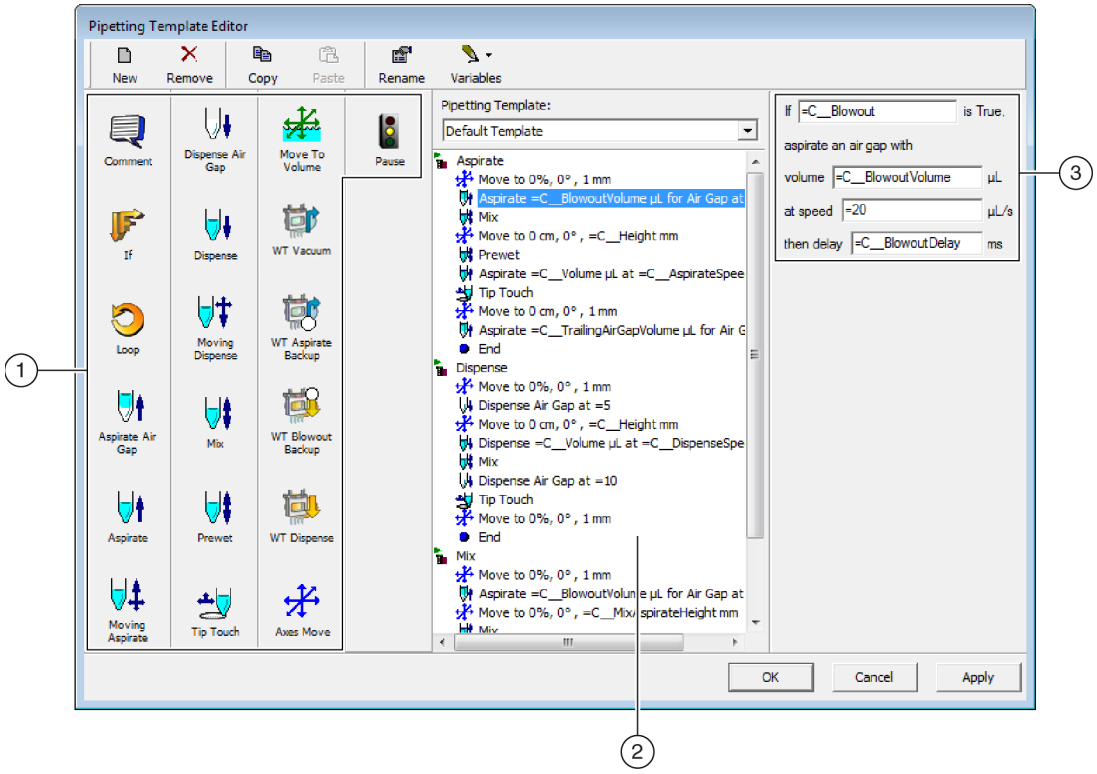
- Create a blank template and insert template steps.
- Copy and paste an existing template and modify as needed.

IMPORTANT Method steps for wash tool operations are created and modified using the **Pipetting Template Editor.** When working with wash tool templates, use these language substitutions for the following operations:

To Create a [ ] Action	Use a [ ] Step	Under [ ] Section in Template
Wash	Combination of **WT Vacuum** and **WT Dispense**	Mix
Bulk Dispense	**WT Dispense**	Dispense
Aspiration	**WT Vacuum**	Aspirate

NOTE The most expedient way to create pipetting templates is to copy and paste the template that most closely resembles the desired operations (refer to *Modifying Existing Pipetting Templates*).

Figure 10.1 Pipetting Template Editor



1. **Pipetting Template Steps**: Template steps used in creating or modifying pipetting templates.
2. **Pipetting Template Method View**: Displays operations in the **Aspirate**, **Dispense**, or **Mix** functions.
3. **Template Steps Configuration**: Context variables are inserted in fields provided for template step configuration.

Viewing Existing Pipetting Templates

A couple of default pipetting templates are included with Biomek Software. These templates have specific operations which they perform, and are associated with each technique to control liquid-handling operations. In order to understand the operations the pipetting template performs, view a pipetting template.

NOTE Refer to *Configuring Pipetting Template Steps*, for more information regarding each template step within the technique.

To view the pipetting template and related operations:

1. Choose **Project > Pipetting Template Editor**. The **Pipetting Template Editor** displays (Figure 10.1).
2. Select the desired **Pipetting Template**.
3. Click on the appropriate step to view the settings for the step.

Creating a New Pipetting Template

New pipetting templates are created using template steps that make up a pipetting procedure (refer to *Configuring Pipetting Template Steps*). The template steps control the order of operations in aspirate, dispense, and mix operations.

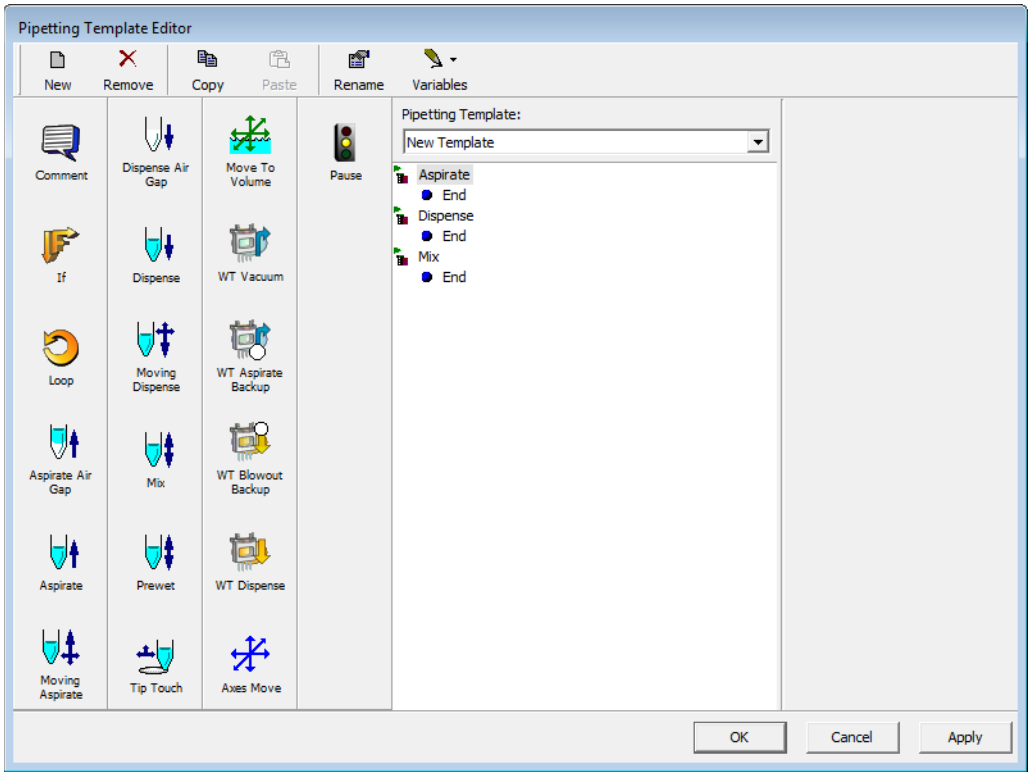
NOTE Before creating or customizing templates, be sure to understand where each of the context variables finds and retrieves the values used in the configured pipetting operations (refer to *Understanding Context Variables*).

To create a new pipetting template:

1. Choose **Project > Pipetting Template Editor**. The **Pipetting Template Editor** displays(Figure 10.1).
2. Choose 

. A blank template with **Aspirate**, **Dispense** and **Mix** steps displays (Figure 10.2).

Figure 10.2 New Pipetting Template

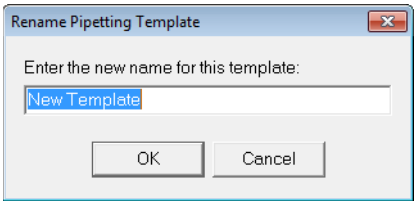


3 Insert and configure the desired template steps (refer to *Configuring Pipetting Template Steps*).

4 Choose 

to change the template name. **Rename Pipetting Template** displays (Figure 10.3).

Figure 10.3 Rename Pipetting Template



5 Enter the name of the new pipetting template and choose **OK.**

6 Choose **OK.** The template is saved and the **Pipetting Template Editor** closes.

OR

Choose **Apply.** The template is saved and the **Pipetting Template Editor** remains open.

OR

Choose **Cancel.** The template is not saved and the **Pipetting Template Editor** closes.

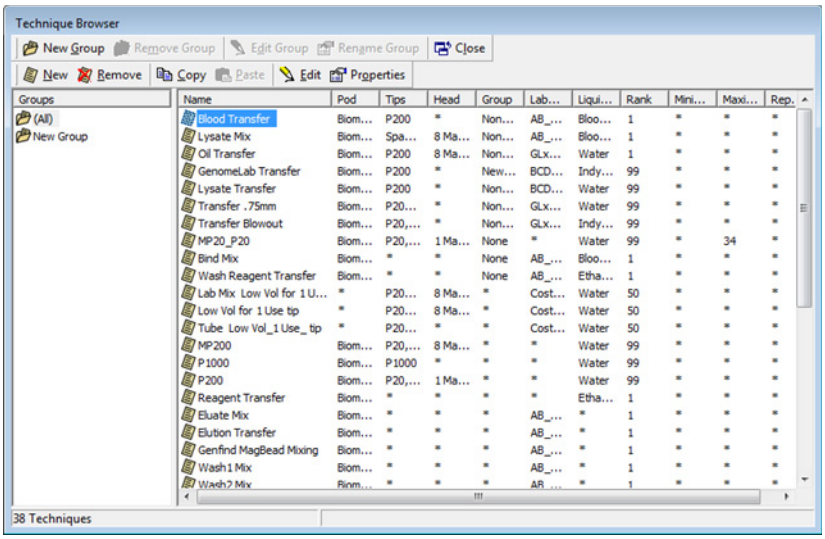
Associating a Pipetting Template with a Technique

A pipetting template is not used by the instrument unless it has been associated with a technique. Every time a pipetting operation occurs in a method that uses a technique with the template assigned, the operations are executed as configured in the pipetting template.

To associate a pipetting template with a technique:

1 Select **Project > Technique Browser.** The **Technique Browser** displays (Figure 10.4).

Figure 10.4 Technique Browser



2 Select the desired technique and choose Edit from the toolbar.

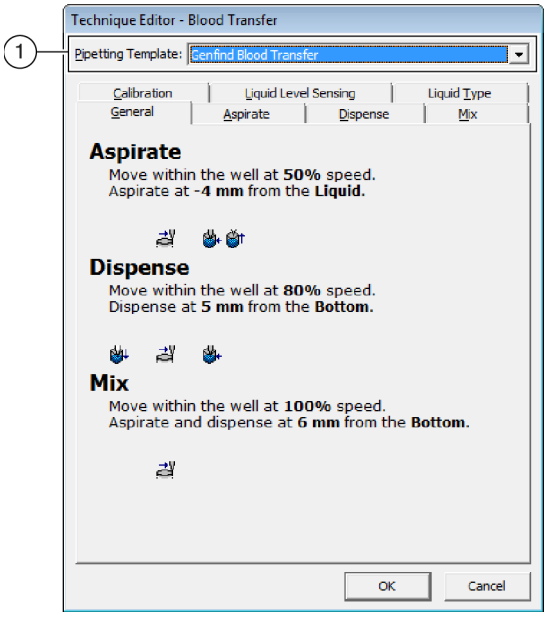
OR

Double click the desired technique on the right side of the **Technique Browser**.

OR

Right click the desired technique and select **Edit** from the menu. The **Technique Editor** displays (Figure 10.5).

Figure 10.5 Technique Editor



1. **Pipetting template associated with the technique is selected here.**

3 Select the appropriate **Pipetting Template** from the list.

4 Choose **OK**. The changes to the technique are saved and the **Technique Editor** closes.

Modifying Existing Pipetting Templates

Copy and paste pipetting templates when making modifications to an existing template. Once the template is copied and pasted as a new template, any changes made do not affect the original.

NOTE Pipetting templates can be exported to and imported from other projects. Refer to CHAPTER 6, *Importing and Exporting Project Files* for information about importing and exporting pipetting templates.

To copy and paste a pipetting template:

1 Choose **Project > Pipetting Template Editor** to open the **Pipetting Template Editor**.

2 In **Pipetting Templat**e, select the template to copy.

3 Choose **Copy**.

4 Choose **Paste** to insert the copied template as a new template. The new template displays with the name **Copy of (Original Template's Name)**.

5 Choose **Rename** to change the template name. **Rename Pipetting Template** displays.

6 Enter the name of the new pipetting template and choose **OK**.

7 Make changes to the pipetting template by inserting and configuring steps (refer to *Configuring Pipetting Template Steps*).

8 Choose **OK**. The template is saved and the **Pipetting Template Editor** closes.

OR

Choose **Apply**. The template is saved and the **Pipetting Template Editor** remains open.

OR

Choose **Cancel**. The template is not saved and the **Pipetting Template Editor** closes.

Understanding Context Variables

Pipetting templates make use of context variables to configure pipetting operations. Context variables are inserted into the template steps configuration and are used to retrieve values from the appropriate technique or liquid type in the **Technique Editor** or **Liquid Type Editor.** For example, **C_DispenseDelay** retrieves the value from **Dispense Delay** of the appropriate liquid type in the **Liquid Type Editor.**

Using context variables gives pipetting templates greater versatility, as the values for context variables are determined by the liquid type or technique used for the specific pipetting operation.

NOTE Variables configured within **Start, Let**, and **Worklist** can be placed into a pipetting template, but doing so may limit the usefulness of the pipetting template. When variables defined in **Start, Let**, and **Worklist** are used in a pipetting template, the template may only be used in methods with the same variable names defined. Be sure that these variables are defined in the method, or an error may occur during method execution.

Inserting Variables and Expressions

Insert variables into the appropriate fields of a pipetting template step, or by using the **Variables** button on the **Pipetting Template Editor.**

Expressions using a combination of variables, numerical constants, and mathematical operators, may also be entered in the fields of the appropriate template steps. For example, an expression could be entered for adding a volume or delay to a variable.

To insert variables in a template step:

---

1 Insert a template step from the **Pipetting Template** step palette into the desired operation: **Aspirate**, **Dispense**, or **Mix**.

OR

Select a template step already configured in the current template.

---

2 Choose the field in which to insert a variable.

---

3 Enter the variable name (Table 10.1).

NOTE When entering context variables into a field, always use a double-underscore (__) between C and the variable name.

OR

Choose 

. Pre-programmed variables arranged by groups display.

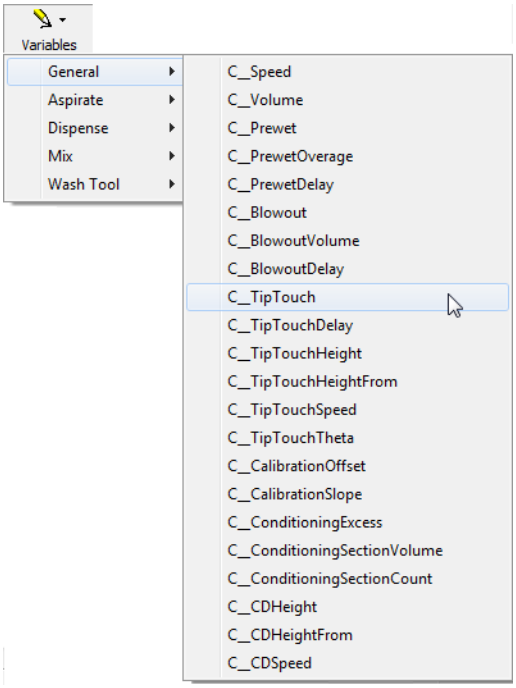
---

4 Choose the desired variable group. The group variables display.

---

5 Choose the desired variable (Figure 10.6). The variables listed depend on the variable group selected.

Figure 10.6 Selecting Variable from the Desired Group



6 Repeat steps 2 to 5 until the template step is configured.

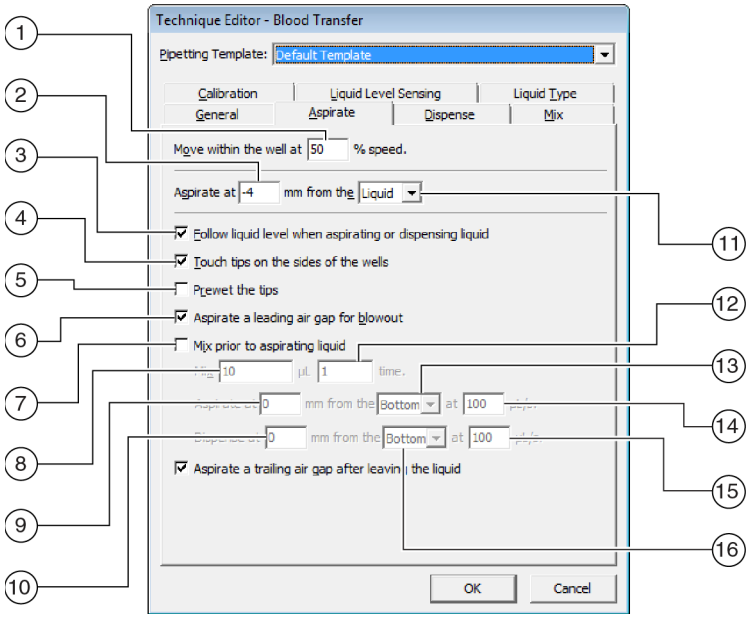
NOTE Refer to *Configuring Pipetting Template Steps*, for more information about inserting and configuring variables in template steps.

Defining Context Variables

To retrieve values, context variables reference fields in the **Technique Editor** and **Liquid Type Editor.** Table 10.1 describes context variables that can be used when creating or modifying a pipetting template. Figure 10.7, Figure 10.8, and Figure 10.9 identify the fields in the **Technique Editor**, **Liquid Type Editor**, and **Wash Tool Liquid Settings** from which the context variables defined in Table 10.1 reference and retrieve values.

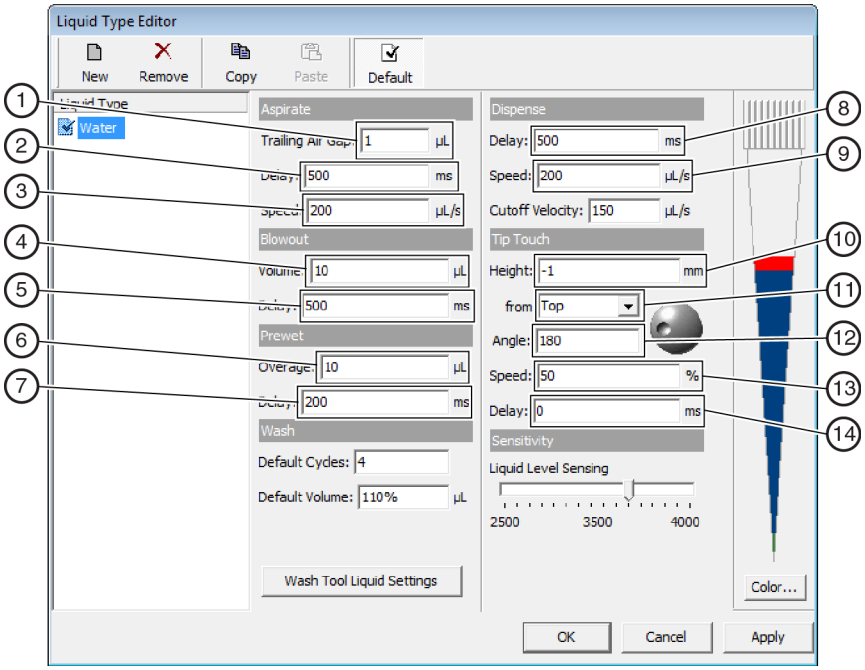
NOTE Template steps default to the most appropriate variable; however, any variable may be used in any field.

Figure 10.7 Identifying the Location of Technique Editor Context Variables



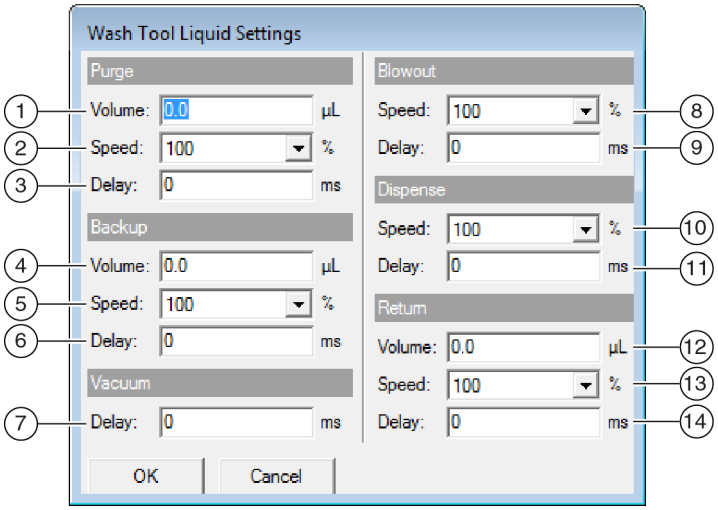
1. **C_Speed**
2. **C_Height**
3. **C_FollowLiquid**
4. **C_TipTouch**
5. **C_Prewet**
6. **C_Blowout**
7. **C_Mix**
8. **C_MixVolume**
9. **C_MixAspirateHeight**
10. **C_MixDispenseHeight**
11. **C_HeightFrom**
12. **C_MixCount**
13. **C_MixAspirateHeightFrom**
14. **C_MixAspirateSpeed**
15. **C_MixDispenseSpeed**
16. **C_MixDispenseHeightFrom**

Figure 10.8 Identifying the Location of Liquid Type Editor Context Variables



1. C__TrailingAirGapVolume
2. C__AspirateDelay
3. C__AspirateSpeed
4. C__BlowoutVolume
5. C__BlowoutDelay
6. C__PrewetOverage
7. C__PrewetDelay
8. C__DispenseDelay
9. C__DispenseSpeed
10. C__TipTouchHeight
11. C__TipTouchHeightFrom
12. C__TipTouchTheta
13. C__TipTouchSpeed
14. C__TipTouchDelay

Figure 10.9 Identifying the Location of Wash Tool Liquid Settings Context Variables



1. **C_WashToolPurgeVolume**
2. **C_WashToolPurgeSpeed**
3. **C_WashToolPurgeDelay**
4. **C_WashToolBackupVolume**
5. **C_WashToolBackupSpeed**
6. **C_WashToolBackupDelay**
7. **C_WashToolVacuumDelay**
8. **C_WashToolBlowoutSpeed**
9. **C_WashToolBlowoutDelay**
10. **C_WashToolDispenseSpeed**
11. **C_WashToolDispenseDelay**
12. **C_WashToolReturnVolume**
13. **C_WashToolReturnSpeed**
14. **C_WashToolReturnDelay**

Table 10.1 Context Variables

Variable Group	Variable	Description	Associates With:
General	C__Blowout	Tells Biomek instrument to perform a blowout.	**Blowout** in technique.
	C__BlowoutDelay	The delay in milliseconds after a blowout.	**Blowout Delay** in liquid type.
	C__BlowoutVolume	The volume of the air gap to blow out.	**Blowout Volume** in liquid type or technique.
	C__CalibrationOffset	Additional volume aspirated or dispensed to accurately deliver the desired volume.	**Offset** in technique calibration.
	C__CalibrationSlope	Scaling factor used to accurately deliver the desired volume	**Scaling Factor** in technique calibration.
	C__ConditioningExcess	Excess volume aspirated as a buffer between the system fluid and source.	**Leading Conditioning Excess** in technique calibration.
	C__ConditioningSectionCount	Number of conditioning sections aspirated following the source.	**Number of Trailing Volume Sections** in technique calibration.
	C__ConditioningSectionVolume	Volume of each conditioning section following the source.	**Trailing Conditioning Volume** in technique calibration.
	C__Prewet	Tells Biomek instrument to perform a prewet cycle.	**Prewet** in technique.
	C__PrewetDelay	The delay in milliseconds from the time the Prewet volume is completely aspirated to the time it begins to dispense.	**Prewet Delay** in liquid type or technique.
	C__PrewetOverage	The volume to add for a prewet cycle.	**Prewet Overage** in liquid type.
	C__Speed	The speed of the pod movement (X, Y, Z axes).	**Pod Speed** % in technique.
	C__TipTouch	Tells Biomek instrument to perform a tip touch operation.	**Tip Touch** in technique.
	C__TipTouchDelay	The delay in milliseconds at the side of wells.	**Tip Touch Delay** in liquid type or technique.
	C__TipTouchHeight	The height of the tip touch.	**Tip Touch Height** in liquid type or technique.
	C__TipTouchHeightFrom	Level — top, bottom, or liquid — from which C__TipTouchHeight is measured.	**Tip Touch Height, from** in liquid type or technique.
	C__TipTouchTheta	Position along well edge tip touch occurs.	**Tip Touch Angle** in liquid type or technique.

Table 10.1 Context Variables

Variable Group	Variable	Description	Associates With:
General (Continued)	C__TipTouchSpeed	The speed of the pod movement.	**Tip Touch Speed** in technique.
	C__Volume	The volume given in the pipetting operation (such as **Transfer** or **Combine**).	**Volume** in step configuration.
Aspirate	C__AspirateDelay	The delay in milliseconds after an aspirate cycle.	**Aspirate Delay** in liquid type.
	C__AspirateSpeed	The speed in µL/sec along the D-axis for an aspirate cycle.	**Aspirate Speed** in liquid type.
	C__TrailingAirGapVolume	The volume of the post-aspirate air gap.	**Aspirate Trailing Air Gap** in liquid type or technique.
	C__TrailingAirGap	Tells Biomek instrument to aspirate a trailing air gap.	**Trailing Air Gap** in technique.
Dispense	C__DispenseDelay	The delay in milliseconds after a dispense operation.	**Dispense Delay** in liquid type or technique.
	C__DispenseSpeed	The speed in µL/sec of the D-axis for a dispense operation.	**Dispense Speed** in liquid type or technique.
Aspirate/ Dispense	C__Height	The height of the aspirate or dispense.	**Aspirate at x mm** in technique.
	C__HeightFrom	Level—top, bottom, or liquid—from which C__Height is measured.	**Aspirate x mm from (Top, Bottom, Liquid)** in technique.

Table 10.1 Context Variables

Variable Group	Variable	Description	Associates With:
Mix	C__Mix	Tells Biomek instrument to perform a mix operation in labware.	**Mix Before Aspirate** or **Mix after Dispense** in technique.
	C__MixAspirateHeight	The height of the mix operation from the relative well location.	**Aspirate at x mm** in technique.
	C__MixAspirateFrom	The location for the mix aspirate to occur.	In **Mix Before Aspirate** or **Mix After Dispense** and **Mix, from (Top, Bottom, Liquid)** in technique.
	C__MixAspirateSpeed	The speed at which to aspirate for the mix cycle.	**Aspirate...at x**% in technique.
	C__MixCount	The number of cycles in a mix.	Number of times to **Mix Before Aspirate** or **Mix After Dispense** in technique.
	C__MixDispenseHeight	The height of the mix dispense.	In **Mix Before Aspirate** or **Mix After Dispense** and **Mix**, from (**Top, Bottom, Liquid**) in technique.
	C__MixDispenseFrom	The height of the mix operation from the relative well location.	In **Mix**, from (**Top, Bottom, Liquid**) in technique.
	C__MixDispenseSpeed	The speed at which to dispense in a mix cycle.	**Dispense...at x**% in technique.
	C__MixVolume	The volume of the mix.	In **Mix before Aspirate** and **Mix After Dispense**, cycles to mix at specific volume in technique.
Wash Tool	C__WashToolPurgeVolume	The amount of liquid to purge when switching liquids or loading a wash tool.	**Purge Volume** in **Wash Tool Liquid Settings** or **Volume** in the **Wash Tool Purge** step.
	C__WashToolPurgeSpeed	The speed to purge the liquid when switching liquids or loading a wash tool.	**Purge Speed** in **Wash Tool Liquid Settings** or **Speed** in the **Wash Tool Purge** step.
	C__WashToolPurgeDelay	The amount of time to delay after purging the liquid prior to performing the next operation.	**Purge Delay** in **Wash Tool Liquid Settings** or **Delay** in **Wash Tool Purge** step.
	C__WashToolBackupVolume	The volume of air aspirated into the tubing to prevent dripping.	**Backup Volume** in **Wash Tool Liquid Settings**.
	C__WashToolBackupSpeed	The desired speed for completing the backup.	**Backup Speed** in **Wash Tool Liquid Settings**.
	C__WashToolBackupDelay	The amount of time to delay operations after aspirating the designated volume of backup.	**Backup Delay** in **Wash Tool Liquid Settings**.
	C__WashToolReturnVolume	The volume of air to aspirate into the tubes to allow a tool to be unloaded.	**Return Volume** in **Wash Tool Liquid Settings**.

Table 10.1 Context Variables

Variable Group	Variable	Description	Associates With:
Wash Tool (Continued)	C__WashToolReturnSpeed	The desired speed to complete the return.	**Return Speed** in **Wash Tool Liquid Settings.**
	C__WashToolReturnDelay	The amount of time to delay the pod after the return is completed.	**Return Delay** in **Wash Tool Liquid Settings**.
	C__WashToolDispenseSpeed	The desired speed at which the wash liquid is dispensed.	**Dispense Speed** in **Wash Tool Liquid Settings**.
	C__WashToolDispenseDelay	The amount of time to delay the pod after dispensing the liquid.	**Dispense Delay** in **Wash Tool Liquid Settings**.
	C__WashToolBlowoutSpeed	The desired speed for dispensing the air gap.	**Blowout Speed** in **Wash Tool Liquid Settings**.
	C__WashToolBlowoutDelay	The amount of time to delay the pod after performing the blowout.	**Blowout Delay** in **Wash Tool Liquid Settings**.
	C__WashToolVacuumToVolume	The volume of liquid to remain in the well.	**Vacuum down to** in the **Wash Tool Vacuum** step and **Wash Tool Wash** step.
	C__WashToolVacuumTime	The amount of time to vacuum the liquid.	**which will take** field in the **Wash Tool Vacuum** step and **Wash Tool Wash** step.
	C__WashToolVacuumDelay	The amount of time to delay the pod after vacuuming the liquid.	**Vacuum Delay** in **Wash Tool Liquid Settings**.

Configuring Pipetting Template Steps

A pipetting template contains template steps that create the pipetting procedure. Steps are configured using context variables (Table 10.1) that retrieve information from the **Technique Editor** or **Liquid Type Editor**, or variables configured in a **Start**, **Let**, or **Worklist** configuration. The following conventions apply:

- All template steps, excluding **Prewet**, may be placed in any part of the pipetting process. **Prewet** is applicable only to **Aspirate** operations and is limited to the **Aspirate** process.
- Any variable defined in the system or method, including those defined in the **Start**, **Let,** or **Worklist** configurations, may be used to configure template steps.
- When using variables defined in **Start**, **Let**, and **Worklist** in a pipetting template, the template is useful only to those methods with the same variable names defined.
- The template steps are available for use in the **Pipetting Template Editor** only.
- When a step is inserted into the pipetting template, each field is configured with the most appropriate context variable by default. These default values may be changed to any desired value, variable, or expression.
- Hovering the mouse pointer over a template step button displays a tool tip with the name of the template step. Some steps also display information about the default configuration for that step.

If, Comment, and Loop

The **If**, **Comment,** and **Loop** steps are available for use in both methods and pipetting templates. When creating a pipetting template using these steps, configure the steps in the same manner as when configuring the step in the Method View.

NOTE For more information, refer to CHAPTER 17, *If Step*; refer to CHAPTER 15, *Comment Step* and refer to CHAPTER 16, *Configuring a Loop Step and Creating a New Variable*.

Aspirate Air Gap

Aspirate Air Gap aspirates an air gap at a specific volume and speed before liquid is aspirated. If a delay between the air gap aspirate and subsequent steps is desired, configure a delay into the template step.

Aspirate Air Gap can be used to aspirate a leading air gap before aspirating liquid, or a trailing air gap after aspirating liquid, depending on where it is inserted in the template.

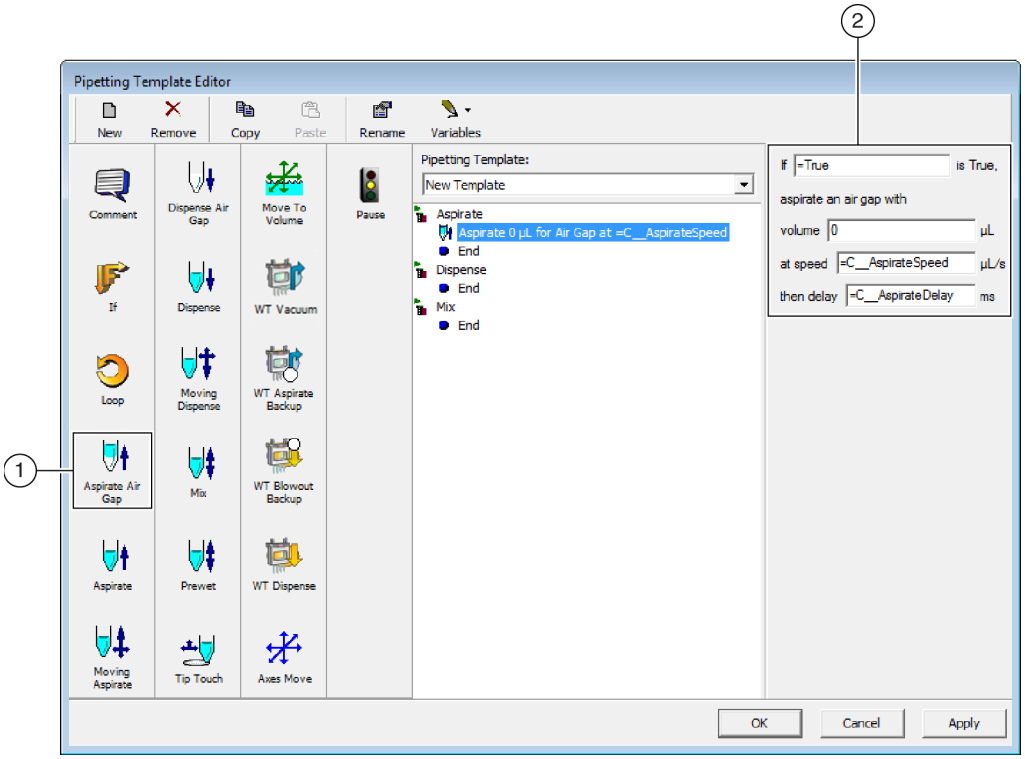
To configure **Aspirate Air Gap**:

---

1 Insert 

in the desired pipetting operation of the template. The template step configuration appears (Figure 10.10).

Figure 10.10 Aspirate Air Gap Step Configuration



1. **Aspirate Air Gap**: Aspirates air at the specified volume and at the specified D-axis speed.
2. **Aspirate Air Gap Configuration**: Aspirate air gap settings are configured here.

2 Enter the variable to configure the **If** condition. When the variable entered is **True**, an air gap is aspirated. The default value, **=True**, always aspirates an air gap.

3 In **volume**, enter the variable or value to specify the amount of air to aspirate for the air gap in microliters (µL). The default value is **0** µL.

4 In **speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µL/sec) during the aspirate operation. The default value is the context variable **C__AspirateSpeed**. (Refer to Table 10.1 for a definition of this variable.)

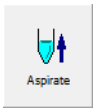
5 In **delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after aspirating an air gap. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C__AspirateDelay**. (Refer to Table 10.1 for a definition of this variable.)

Aspirate

Aspirate aspirates a specific volume at a speed specified in microliters per second (µL/sec). To pause for a specific amount of time after aspirating, add a delay to the **Aspirate** template step.

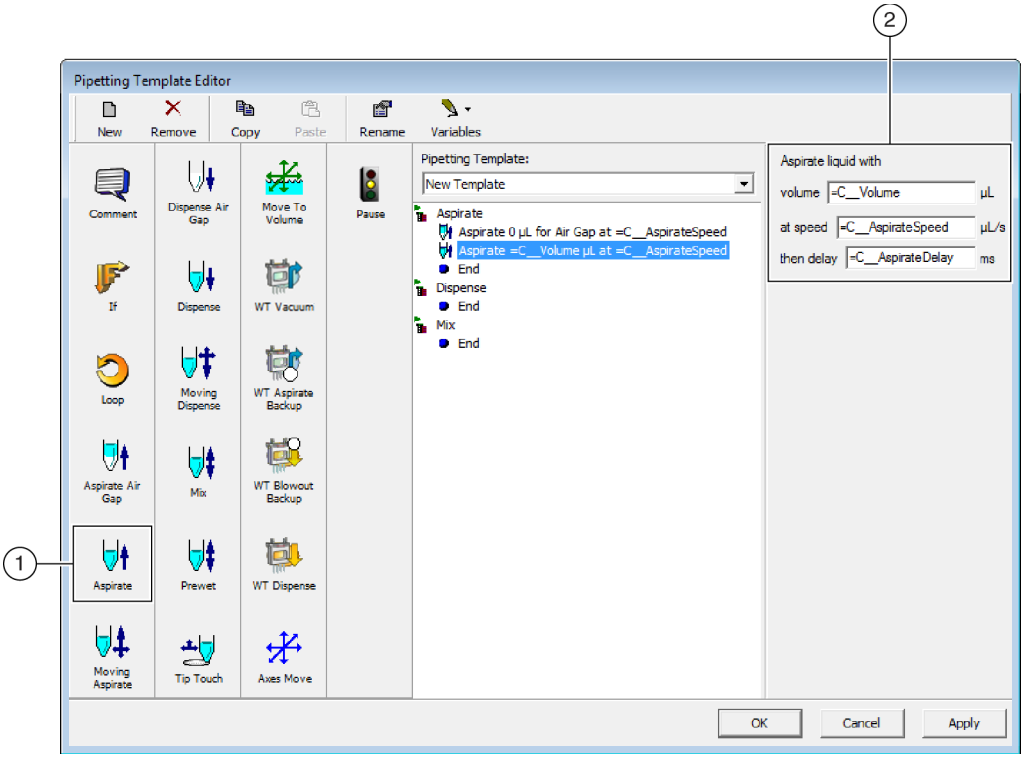
To configure **Aspirate**:

---

1 Insert 

at the desired position. The template step configuration appears (Figure 10.11).

Figure 10.11 Aspirate Step Configuration



1. **Aspirate Step**: Aspirates volume at the specified D-axis speed.
2. **Aspirate Configuration**: Aspirate settings are configured here.

---

2 In **volume**, enter the variable or value to specify the volume of liquid to aspirate in microliters (µL). The default value for this field is the context variable **C__Volume**. (Refer to Table 10.1 for a definition of this variable.)

---

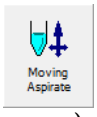
3 In **speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µL/sec) during the aspirate operation. The default value for this field is the context variable **C__AspirateSpeed**. (Refer to Table 10.1 for a definition of this variable.)

4 In **delay,** enter the variable or value to specify the length of the delay in milliseconds (ms) after the aspirate operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C__AspirateDelay**. (Refer to Table 10.1 for a definition of this variable.)

Moving Aspirate

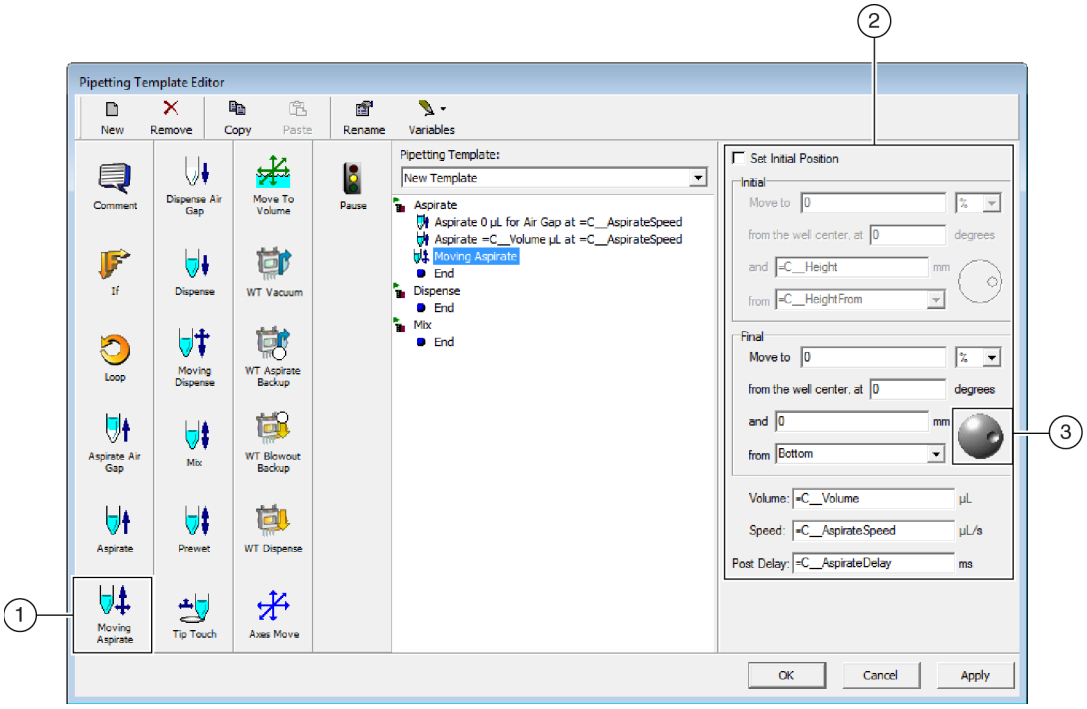
Moving Aspirate aspirates while tips are moving within a well. The template step sets the initial position, final position, and a specific volume for the aspiration.

To configure **Moving Aspirate:**

1 Insert 

into the pipetting method. The template step configuration appears (Figure 10.12).

Figure 10.12 Moving Aspirate Step Configuration



1. **Moving Aspirate Step**: Performs an aspirate operation while moving the tip within the well.
2. **Moving Aspirate Configuration**: **Moving Aspirate** settings are configured here.
3. **Dials for adjusting the angle of movement from the center of the well.** (Number in **degrees** changes accordingly.)

2 Check **Set Initial Position** to set the start position for aspirate, if desired.

NOTE **Set Initial Position** is used if an aspirate must begin at a specific well location on the labware. If this is not set, the pod moves from its current location. **Set Initial Position** is not selected by default.

If **Set Initial Position** is checked, complete the following steps to configure **Initial** position parameters:

1 In **Move to,** enter the variable or value to specify where within the well the aspirate operation begins, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.

2 Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is %.

3 In **from the well center, at**, enter the variable or value to specify the angle at which the **Move to** measurement is performed.

OR

In the graphic representing the well, position the dial at the desired angle at which the **Move to** measurement is performed. The value in **from the well center, at** displays the current angle, in degrees. The default value for the angle is **0** degrees.

4 In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default value for this field is the context variable **C_Height**. (Refer to Table 10.1 for a definition of this variable.)

5 In **from,** enter the variable or value to specify from where the height in **and** is measured. The default value for this field is the context variable **C_HeightFrom.** (Refer to Table 10.1 for a definition of this variable.)

To configure the **Final** position parameters:

1 In **Move to**, enter the variable or value to specify where within the well the aspirate operation moves, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.

2 Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is %.

3 In **from the well center, at**, enter the variable or value to specify the angle at which the **Move to** measurement is performed. The default value for the angle is **0** degrees.

OR

In the graphic representing the well, position the dial at the desired angle at which the **Move to** measurement is performed. The value in **from the well center, at** displays the current angle, in degrees.

4 In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default for this field is **0** mm.

5 In **from**, enter the variable or value to specify from where the height in **and** is measured. The default for this field is **Bottom**.

To complete the **Moving Aspirate** configuration:

1 In **Volume**, enter the variable or value to specify the volume of liquid to aspirate, in microliters (µL). The default value for this field is the context variable **C_Volume**. (Refer to Table 10.1 for a definition of this variable.)

2 In **Speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µL/sec) during the moving aspirate operation. The default value for this field is the context variable **C_AspirateSpeed**. (Refer to Table 10.1 for a definition of this variable.)

3 In **Post Delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the aspirate operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C_AspirateDelay**. (Refer to Table 10.1 for a definition of this variable.)

Dispense Air Gap

Dispense Air Gap dispenses an air gap at a specified speed and allows a delay before further operations occur. Dispensing an air gap is sometimes called a blowout because it blows out the leading air gap.

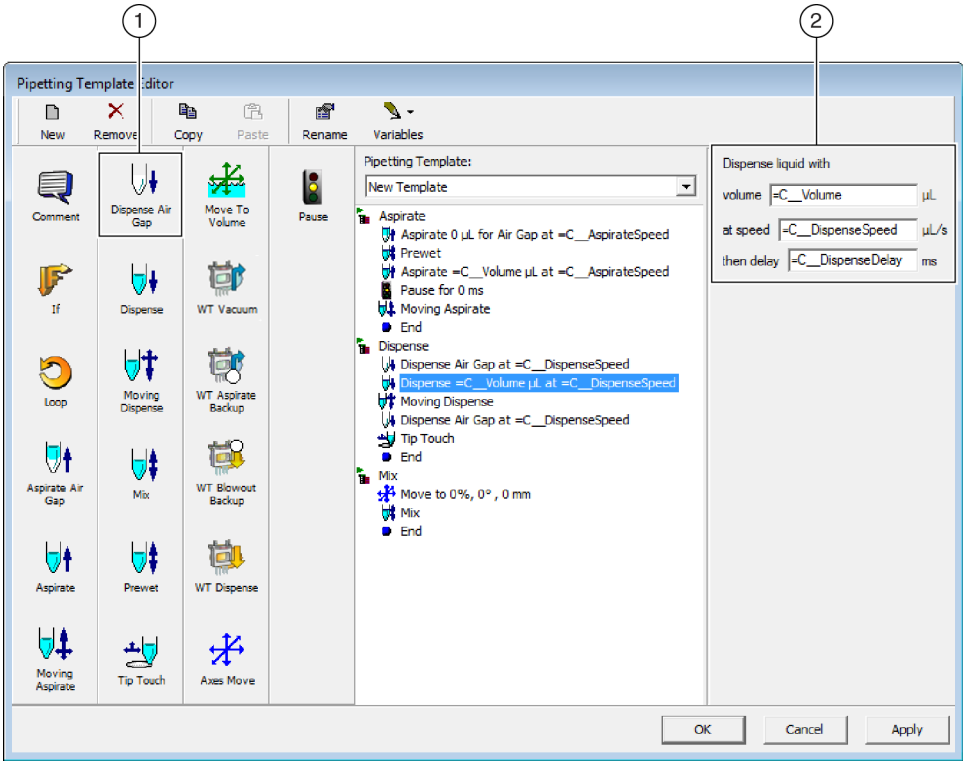
Dispense Air Gap can be used to dispense a trailing or leading air gap, depending on where within the pipetting template it is inserted.

To configure **Dispense Air Gap**:

1 Insert 

into the pipetting method. The template step configuration appears (Figure 10.13).

Figure 10.13 Dispense Air Gap Step Configuration



1. **Dispense Air Gap Step**: Dispenses an air gap at the specified speed.
2. **Dispense Air Gap Configuration**: **Dispense Air Gap** settings are configured here.

2 In **speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µL/sec). during the blowout. The default value for this field is the context variable **C__DispenseSpeed.** (Refer to Table 10.1 for a definition of this variable.)

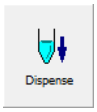
3 In **delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the blowout. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is the context variable **C__DispenseDelay**. (Refer to Table 10.1 for a definition of this variable.)

Dispense

Dispense dispenses a specific volume at a speed specified in microliters per second (µL/sec). To pause for a specific amount of time after dispensing, add a delay to the **Dispense** template step.

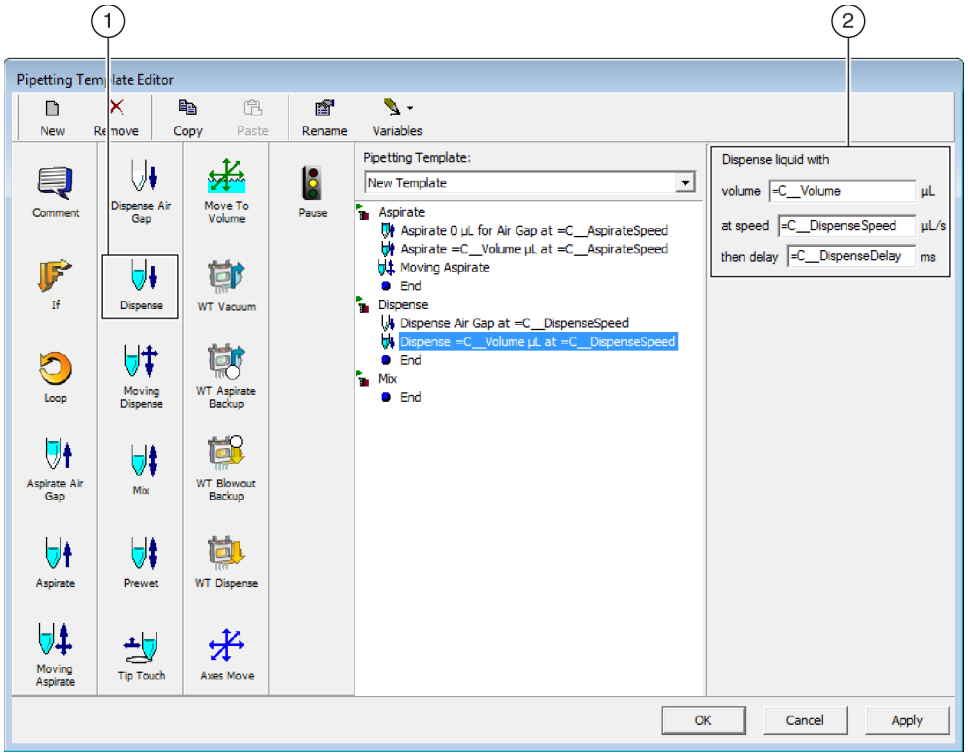
To configure **Dispense**:

---

1 Insert 

into the pipetting method. The template step configuration appears (Figure 10.14).

Figure 10.14 Dispense Step Configuration



1. **Dispense Step**: Dispenses a specific volume at the designated speed.
2. **Dispense Configuration**: Dispense volume settings are configured here.

---

2 In **volume**, enter the variable or value to specify the volume of liquid to dispense in microliters (µL). The default value for this field is the context variable **C__Volume.** (Refer to Table 10.1 for a definition of this variable.)

---

3 In **speed**, enter the variable or value to specify the speed of the pod in the D-axis during the dispense operation in µL/sec. The default value for this field is the context variable **C__DispenseSpeed.** (Refer to Table 10.1 for a definition of this variable.)

4 In **delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the dispense operation. The pod pauses for the specified duration before continuing. The default value for this field is the context variable **C__DispenseDelay**. (Refer to Table 10.1 for a definition of this variable.)

Moving Dispense

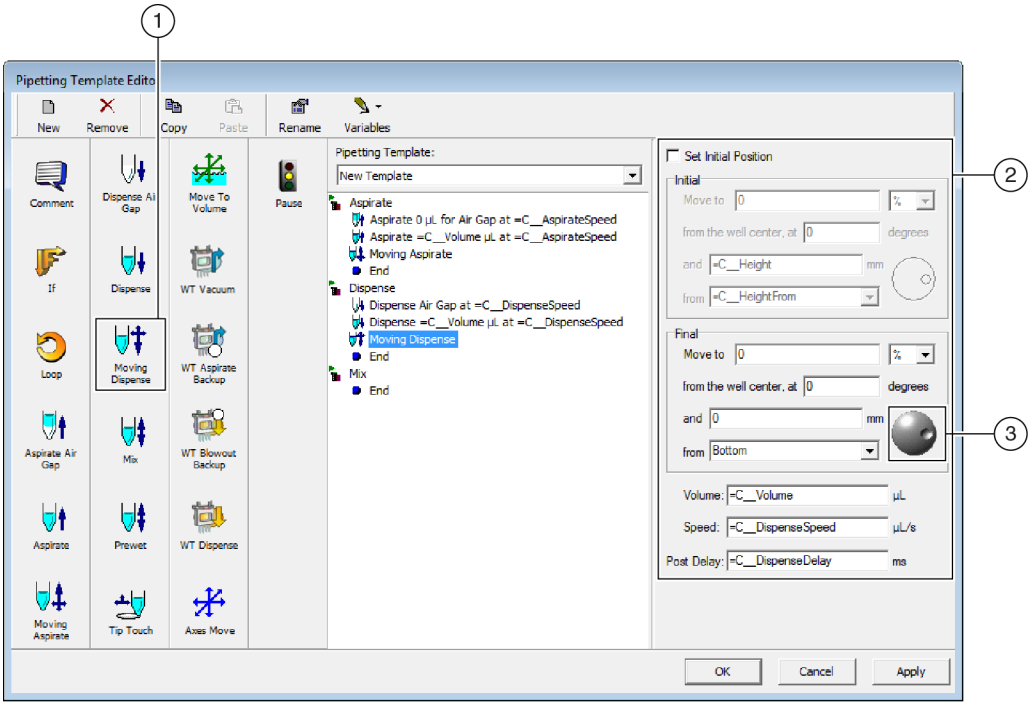
Moving Dispense dispenses a specific volume of liquid while moving between positions relative to the center of the well.

To configure **Moving Dispense**:

1 Insert 

into the pipetting method. The template step configuration appears (Figure 10.15).

Figure 10.15 Moving Dispense Step Configuration



1. **Moving Dispense Step**: Dispenses a specified amount while moving the tips inside the wells.
2. **Moving Dispense Configuration**: Configure **Moving Dispense** settings.
3. **Dials for adjusting the angle of movement from the center of the well.** (The number in **degrees** changes accordingly.)

2 Check **Set Initial Position** to set the start position for dispense, if desired.

NOTE **Set Initial Position** is used if a dispense must begin at a specific location within the well. If this is not set, the pod moves from its current location. **Set Initial Position** is not selected by default.

If **Set Initial Position** is checked, complete the following steps to configure **Initial** position parameters:

1 In **Move to**, enter the variable or value to specify where within the well the dispense operation begins, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.

2 Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is %.

3 In **from the well center, at**, enter the variable or value to specify the angle at which the **Move to** measurement is performed. The default value for the angle is **0** degrees.

OR

In the graphic representing the well, position the dial at the desired angle at which the **Move to** measurement is performed. The value in **from the well center, at** displays the current angle, in degrees.

4 In **and,** enter the variable or value to specify the height of the tip, in millimeters (mm). The default value for this field is the context variable **C_Height.** (Refer to Table 10.1 for a definition of this variable.)

5 In **from**, enter the variable or value to specify from where the height in **and** is measured. The default value for this field is the context variable **C_HeightFrom.** (Refer to Table 10.1 for a definition of this variable.)

To configure the **Final** position parameters:

1 In **Move to,** enter the variable or value to specify where within the well the dispense operation moves, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.

2 Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is %.

3 In **from the well center, at,** enter the variable or value to specify the angle at which the **Move to** measurement is performed. The default value for the angle is **0** degrees.

OR

In the graphic representing the well, position the dial at the desired angle at which the **Move to** measurement is performed. The value in **from the well center, at** displays the current angle, in degrees.

4 In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default for this field is **0** mm.

5 In **from,** enter the variable or value to specify from where the height in **and** is measured. The default for this field is **Bottom.**

To complete the **Moving Dispense** configuration:

1 In **Volume**, enter the variable or value to specify the volume of liquid to dispense, in microliters (µL). The default value for this field is the context variable **C_Volume**. (Refer to Table 10.1 for a definition of this variable.)

2 In **Speed**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µL/sec) during the moving dispense operation. The default value for this field is the context variable **C_DispenseSpeed**. (Refer to Table 10.1 for a definition of this variable.)

3 In **Post Delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the dispense operation. The pod pauses for the specified duration before continuing. The default value for this field is the context variable **C_DispenseDelay**. (Refer to Table 10.1 for a definition of this variable.)

Mix

Mix aspirates and dispenses liquid in wells of labware as a mixing operation.

NOTE This template step performs operations only when **Mix** is selected in the **Technique Editor** for the technique being used during method run.

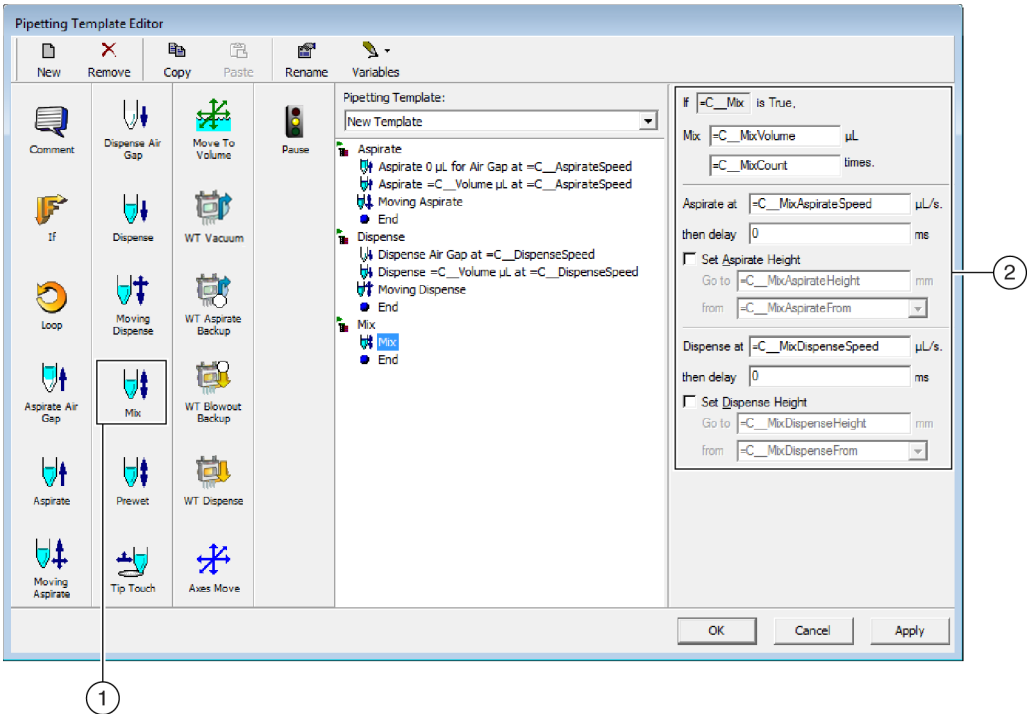
To configure **Mix**:

---

1 Insert 

into the pipetting method. The template steps configuration appears (Figure 10.16).

Figure 10.16 Mix Step Configuration



1. **Mix Step**: performs an aspirate and dispense to mix liquids.
2. **Mix Configuration**: **Mix** settings are configured here.

---

2 In **Mix**, enter the variable or value to specify the volume of liquid to mix, in microliters (µL). The default value for this field is the context variable **C__MixVolume**. (Refer to Table 10.1 for a definition of this variable.)

---

3 In **times**, enter the variable or value to specify the number of times to mix the liquid. The default value for this field is the context variable **C__MixCount**. (Refer to Table 10.1 for a definition of this variable.)

4 In **Aspirate at**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µL/sec) for the aspirate operation. The default value for this field is the context variable **C_MixAspirateSpeed**. (Refer to Table 10.1 for a definition of this variable.)

5 In **then delay,** enter the variable or value to specify the length of the delay in milliseconds (ms) after the mix operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is **0** ms.

6 Check **Set Aspirate Height** to enter the variable or expression for the height of the tips during aspiration.

NOTE If **Set Aspirate Height** is not selected, the mix operation occurs at the current height and the tips do not move vertically before aspirating.

7 In **Go to**, enter the variable or value to specify the height of the tip for the aspirate operations, in millimeters (mm). The default value for this field is the context variable **C_MixAspirateHeight**. (Refer to Table 10.1 for a definition of this variable.)

8 In **from**, enter the variable or value to specify from where the height in **Go to** is measured. The default value for this field is the context variable **C_MixAspirateFrom**. (Refer to Table 10.1 for a definition of this variable.)

9 In **Dispense at**, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µL/sec) for the dispense operation. The default value for this field is the context variable **C_MixDispenseSpeed**. (Refer to Table 10.1 for a definition of this variable.)

10 In **then delay**, enter the variable or value to specify the length of the delay in milliseconds (ms) after the mix operation. The pod pauses for the specified duration before continuing with the next operation. The default value for this field is **0** ms.

11 Check **Set Dispense Height** to enter the variable or expression for the height of the tips during dispense.

NOTE If **Set Dispense Height** is not selected, the mix operation occurs at the current height and the tips do not move vertically before dispensing.

12 In **Go to**, enter the variable or value to specify the height of the tip for the dispense operations, in millimeters (mm). The default value for this field is the context variable **C_MixDispenseHeight**. (Refer to Table 10.1 for a definition of this variable.)

13 In **from**, enter the variable or value to specify from where the height in **Go to** is measured. The default value for this field is the context variable **C__MixDispenseFrom.** (Refer to Table 10.1 for a definition of this variable.)

Prewet

Prewet aspirates, then dispenses the liquid to prepare tips for the main aspiration. **Prewet** should only be used in the **Aspirate** operation of a pipetting template. The delay occurs between the aspirate and dispense of the **Prewet.**

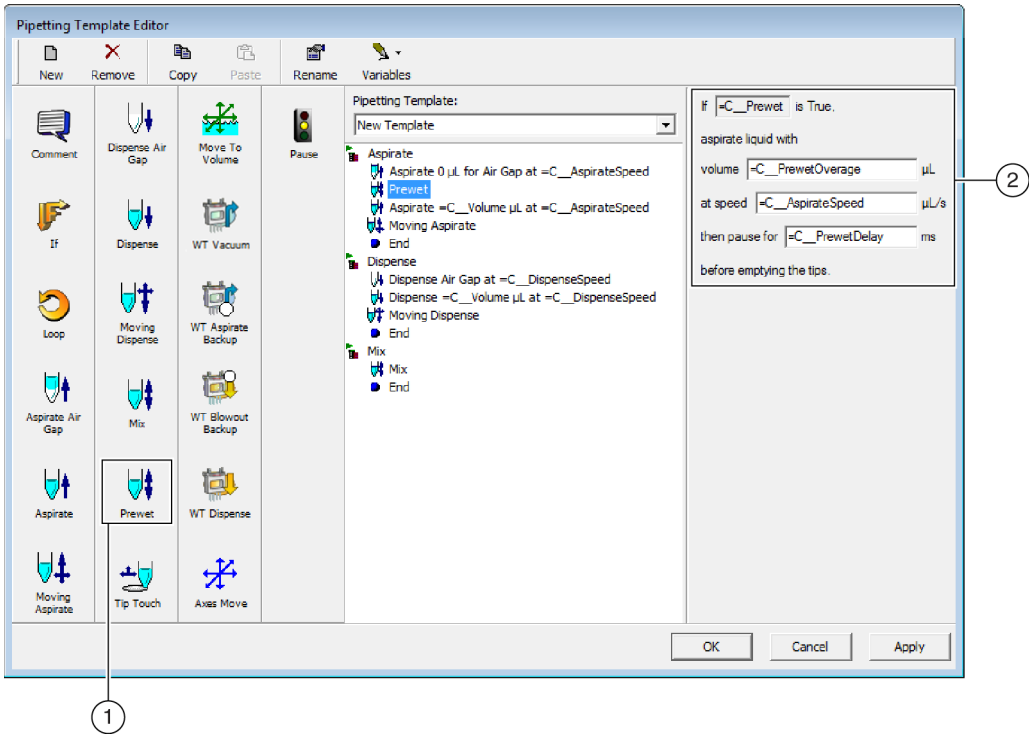
NOTE This template step performs operations only when **Prewet** is selected in the **Technique Editor** for the technique being used during method run.

To configure **Prewet:**

1 Insert 

into the pipetting method. The template steps configuration appears (Figure 10.17).

Figure 10.17 Prewet Step Configuration



1. **Prewet Step**: Performs an aspirate and dispense cycle before the actual aspirate cycle.
2. **Prewet Configuration**: Configure **Prewet** settings here.

2 In **volume**, enter the variable or value to specify the volume of liquid used to prewet the tips. The default value for this field is the context variable **C_PrewetOverage.** (Refer to Table 10.1 for a definition of this variable.)

3 In speed, enter the variable or value to specify the speed of the pod in the D-axis in microliters per second (µL/sec) during the prewet operation. The default value for this field is the context variable **C_AspirateSpeed**. (Refer to Table 10.1 for a definition of this variable.)

4 In **pause**, enter the length of time to delay between aspirating and dispensing the prewet liquid. The pod pauses for the specified duration after aspirating the prewet liquid and before dispensing the prewet liquid. The default value for this field is the context variable **C_PrewetDelay.** (Refer to Table 10.1 for a definition of this variable.)

Tip Touch

If **Tip Touch** is selected in the technique, the tip touches the side of the well and performs any specified delays. The tip then moves back to the center of the well.

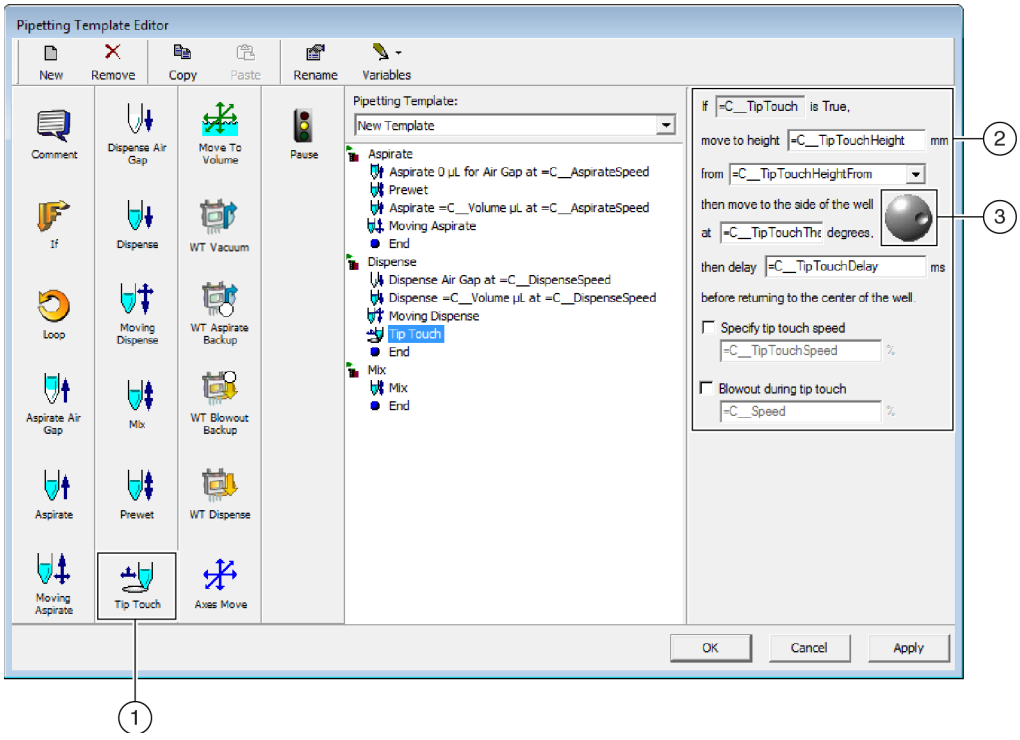
NOTE This template step performs operations only when **Tip Touch** is selected in the **Technique Editor** for the technique being used during method run.

To configure **Tip Touch**:

1 Insert 

into the pipetting method. The template step configuration displays (Figure 10.18).

Figure 10.18 Tip Touch Step Configuration



1. **Tip Touch:** Performs a tip touch to aspirate, delay, then dispense liquids.
2. **Tip Touch Configuration: Tip Touch** settings are configured here.
3. **The dial for adjusting the angle of movement from the center of the well.**

2 In **move to height**, enter the variable or value to specify the desired height, in millimeters (mm), at which to touch the well edge. The default value for this field is the context variable **C__TipTouchHeight**. (Refer to Table 10.1 for a definition of this variable.)

3 In **from,** enter the variable or value to specify from where the **move to height** is measured for the tip touch location. The default value for this field is the context variable **C__TipTouchHeightFrom**. (Refer to Table 10.1 for a definition of this variable.)

4 In **at**, enter the desired variable or value to specify the angle along the well edge at which to touch. The default value for the angle is the context variable **C__TipTouchTheta.** (Refer to Table 10.1 for a definition of this variable.)

OR

In the graphic representing the well, position the dial at the desired angle at which the **Move to** measurement is performed. The value in **from the well center, at** displays the current angle, in degrees.

5 In **then delay**, enter the variable or value to specify the length of the delay before returning to the center of the well. The default value for this field is **0** milliseconds (ms).

6 To control the tip touch speed, check **Specify tip touch speed**.

NOTE If **Specify tip touch speed** is not selected, the tip touch operation occurs at the operation speed as defined in the technique.

7 In the text box below **Specify tip touch speed**, enter the variable or value to specify the speed of the pod during the tip touch operation as a percentage of the maximum speed of the pod. The default value for this field is the context variable **C_TipTouchSpeed**. (Refer to Table 10.1 for a definition of this variable.)

8 To add a blowout, check **Blowout during tip touch**.

NOTE The blowout occurs during the vertical move configured at the beginning of the tip touch.

9 In the text box below **Blowout during tip touch**, enter the variable or value to specify the speed of the pod during the blowout operation as a percentage of the maximum speed of the pod. The default value for this field is the context variable **C_Speed**. (Refer to Table 10.1 for a definition of this variable.)

Axes Move

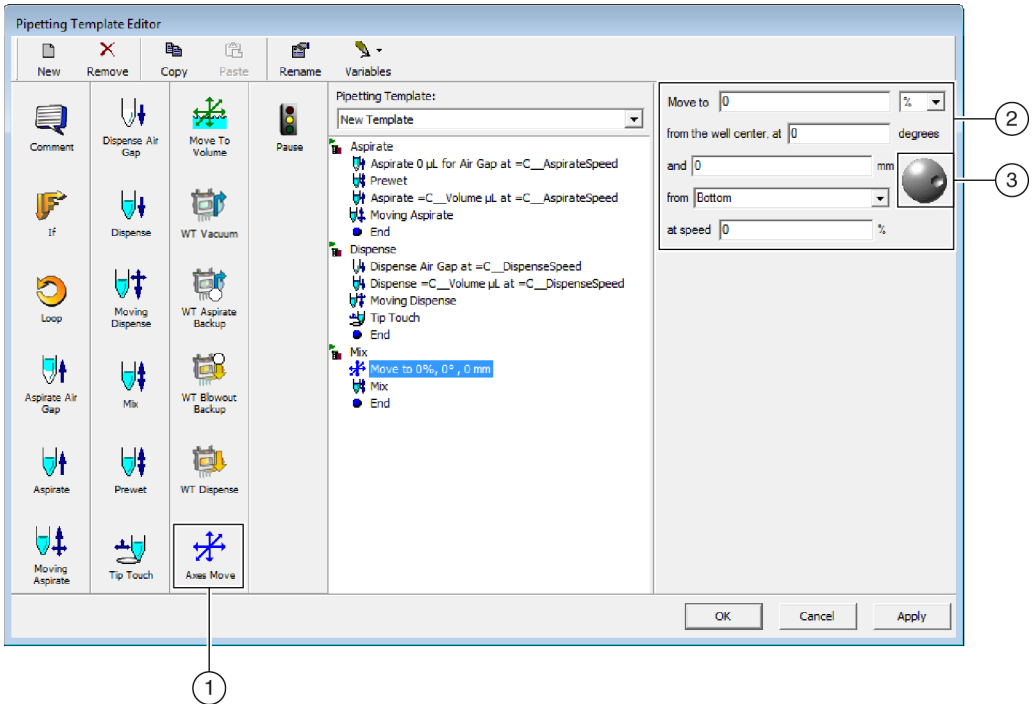
Axes Move moves the tips to a defined place within a well. For example, the template steps may move the tips 10% from the well center and 90 degrees around the edge of the well.

To configure **Axes Move**:

1 Insert 

into the pipetting method. The template step configuration appears (Figure 10.19).

Figure 10.19 Axes Move Step Configuration



1. **Axes Move:** Moves tips within a well the specified distance, degrees, and height.
2. **Axes Move Configuration: Axes Move** settings are configured here.
3. **The dial for adjusting the degree of movement from the center of the well.**

2 In **Move to**, enter the variable or value to specify where within the well to move the tip, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default for this field is **0**.

3 Select the units for the variable or value entered in **Move to**: % (percentage) or cm (centimeters). The default value for this field is %.

4 In **from the well center, at**, enter the variable or value to specify the angle at which the **Move to** measurement is performed. The default value for the angle is **0** degrees.

OR

In the graphic representing the well, position the dial at the desired angle at which the **Move to** measurement is performed. The value in **from the well center, at** displays the current angle, in degrees.

5 In **and**, enter the variable or value to specify the height of the tip, in millimeters (mm). The default value for this field is **0** mm.

6 In **from**, enter the variable or value to specify from where the height in **and** is measured. The default value for this field is **Bottom**.

7 In **at speed**, enter the variable or value to specify the speed of the pod during the axes move as a percentage of the maximum speed of the pod. The default value for this field is **0%**

Pause

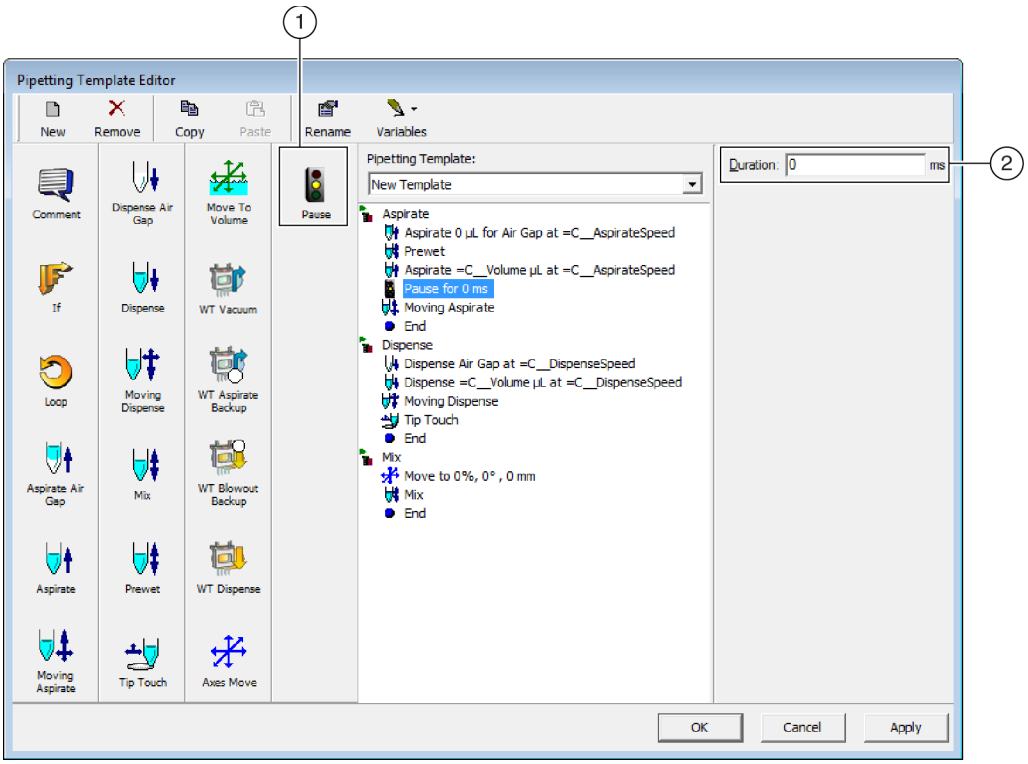
Pause allows the template to stop operations temporarily. **Pause** is configured in milliseconds only.

To configure **Pause**:

1 Insert the 

template step into the pipetting method. The template step configuration appears (Figure 10.20).

Figure 10.20 Pause Step Configuration



1. **Pause:** Places a pause in an operation.
2. **Pause Configuration:** Enter the milliseconds to pause operations.

2 In **Duration**, enter the variable or value for the length of the pause, in milliseconds (ms). The default value for this field is **0** ms.

Move to Volume

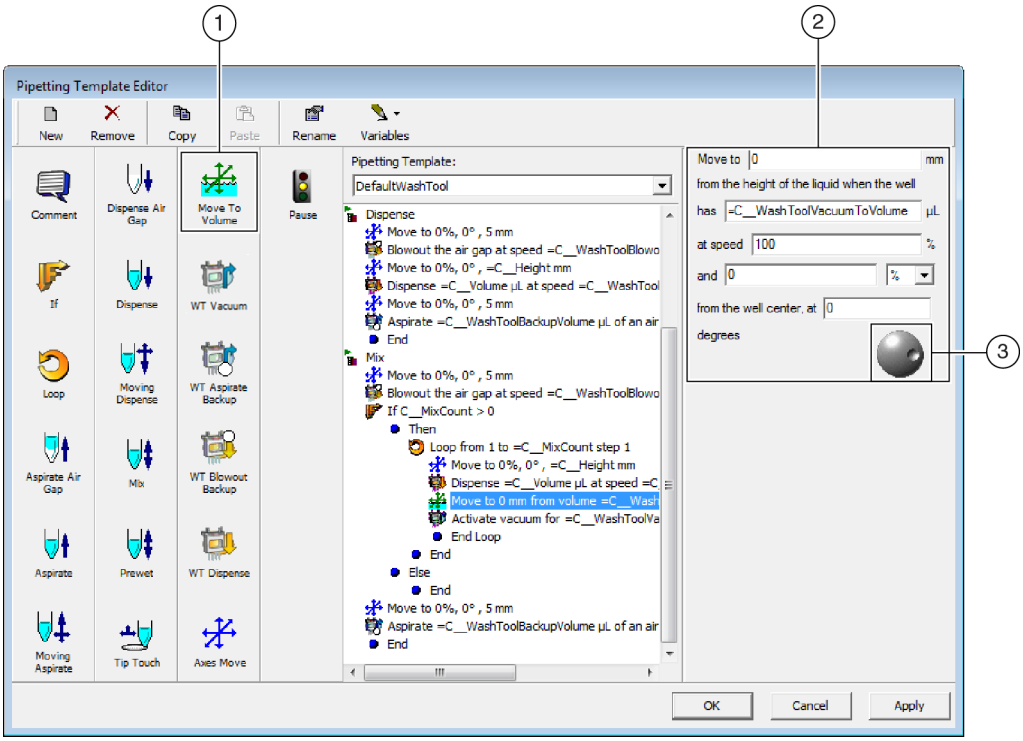
Move to Volume moves the end of wash tips to a defined location within a well.

To configure **Move to Volume**:

1 Insert 

into the wash tool pipetting template. The template step configuration appears (Figure 10.21).

Figure 10.21 Move to Volume Step Configuration



1. **Move to Volume:** Moves tips within a well to the specified height at the specified speed and location.
2. **Move to Volume Configuration: Move to Volume** settings are configured here.
3. **The dial for adjusting the degree of movement from the center of the well.**

2 In **Move to**, enter the variable or value to specify the distance from the liquid to move the wash tip in millimeters (mm). The default for this field is **0**.

NOTE If the tip needs to move below the liquid, enter the value as a negative number.

3 In **from the height of the liquid when the well has**, specify the volume in microliters (µL) of liquid in the wells in which the **Move to** measurement is performed.

4 In **at speed**, enter the variable or value to specify the speed of the pod during the move as a percentage of the maximum speed of the pod. The default value for this field is **0%**.

5 In **and**, enter the variable or value to specify where within the well to move the wash tip, either as a percentage of the distance from the center of the well to the well edge or in centimeters (cm). The default value for this field is **0%**.

6 In the drop-down, specify % or cm for distance from the center of the well.

7 In **from the well center, at**, enter the variable or value to specify the angle at which the **Move to** measurement is performed. The default value for the angle is **0** degrees.

OR

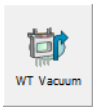
In the graphic representing the well, position the dial at the desired angle at which the **Move to** measurement is performed. The value in **from the well center, at** displays the current angle, in degrees.

Wash Tool Vacuum

Wash Tool Vacuum activates the vacuum on the wash pump for a defined amount of time.

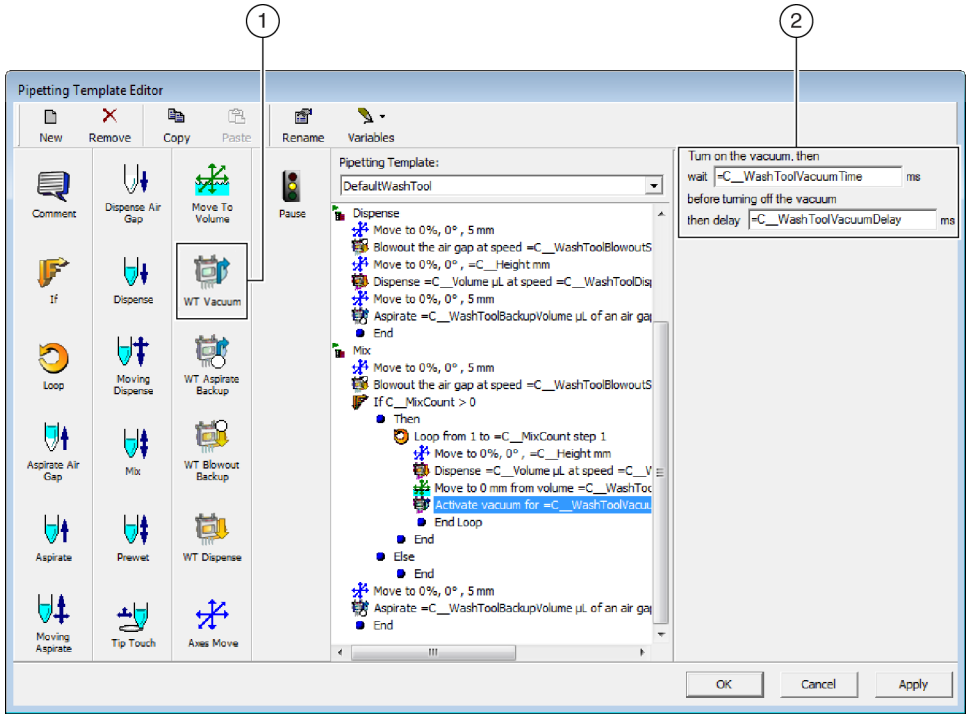
IMPORTANT This step assumes that you have already positioned the tips at the desired location of the vacuum. This operation is normally achieved through the *Move to Volume* step.

To configure **Wash Tool Vacuum**:

1 Insert 

into the wash tool pipetting template. The template step configuration appears (Figure 10.22).

Figure 10.22 Wash Tool Vacuum Step Configuration



1. **Wash Tool Vacuum:** Specifies the amount of time to run the vacuum operation and the amount of time to delay the before beginning the next step.
2. **Wash Tool Vacuum Configuration: Wash Tool Vacuum** settings are configured here.

2 In **Turn on the vacuum, then wait**, enter the variable or value to specify the amount of time in milliseconds (ms) to run the vacuum operation before turning off the vacuum. The default value is the context variable **=C__WashToolVacuumTime**. (Refer to Table 10.1 for a definition of this variable.)

3 In **then delay**, enter the variable or value to specify the amount of time in milliseconds (ms) to delay after the vacuum has been turned off. The pod pauses for the specified duration before continuing with the next operation. The default value is the context variable **=C__WashToolVacuumDelay**. (Refer to Table 10.1 for a definition of this variable.)

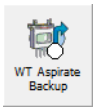
Wash Tool Aspirate Backup

Wash Tool Aspirate Backup aspirates an air gap into the tubing to allow the wash tool to move between wells without dripping liquid onto unintended locations on the labware. Through this step, the volume of air to backup, as well as the speed and delay time is defined for this operation. This is generally the last step in the dispense part of a wash tool pipetting operation or bulk dispense operation template.

IMPORTANT This step assumes that the tips are located above the liquid level, as air needs to be aspirated, not liquid.

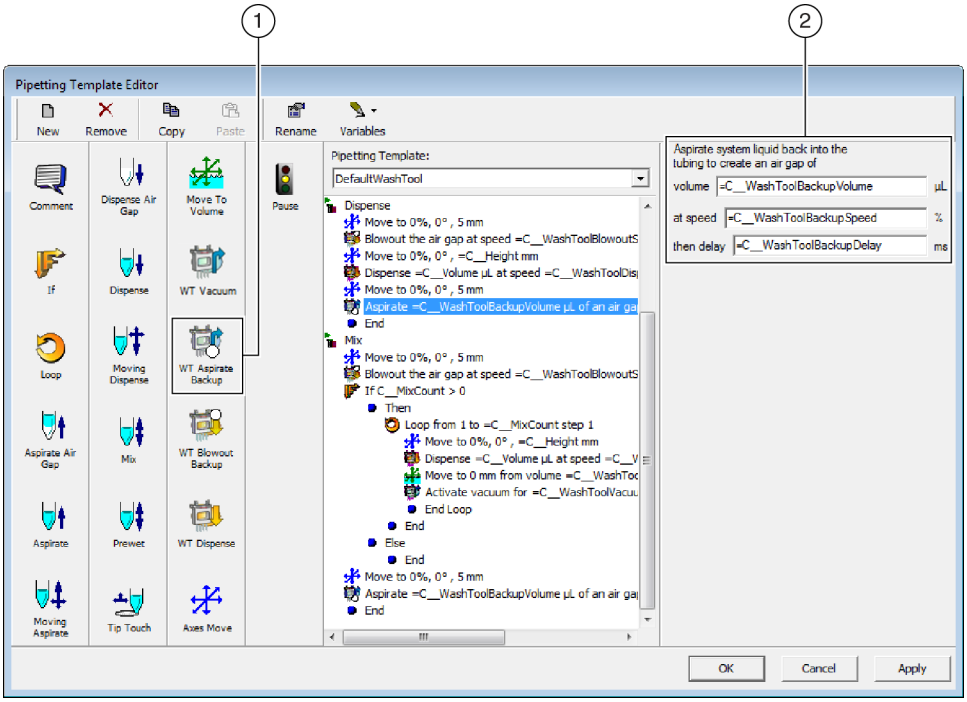
To configure **Wash Tool Aspirate Backup**:

---

1 Insert 

into the wash tool pipetting template. The template step configuration appears (Figure 10.23).

Figure 10.23 Wash Tool Aspirate Backup Step Configuration



1. **Wash Tool Aspirate Backup:** Specifies the volume, speed, and the length of time to delay after aspirating the air gap prior to performing the next operation.
2. **Wash Tool Aspirate Backup Configuration: Wash Tool Aspirate Backup** settings are configured here.

---

2 In **Aspirate system liquid back into the tubing to create an air gap of volume**, enter the variable or value to specify the amount of air in microliters (µL) to aspirate into the tubing. The default value is the context variable **=C__WashToolBackupVolume**. (Refer to Table 10.1 for a definition of this variable.)

---

3 In **at speed**, enter the variable or value to specify the speed at which the air gap aspiration occurs as a percentage of the maximum speed of the pod. The default value is the context variable **=C__WashToolBackupSpeed**. (Refer to Table 10.1 for a definition of this variable.)

4 In **then delay**, enter the variable or value to specify the amount of time in milliseconds (ms) to delay after aspirating the air gap. The pod pauses for the specified duration before continuing with the next operation. The default value is the context variable **=C_WashToolBackupDelay**. (Refer to Table 10.1 for a definition of this variable.)

Wash Tool Blowout Backup

Wash Tool Blowout Backup step dispenses any backed up air gap from the tubing. The amount of air that has been backed up is remembered by the system and is not needed as a parameter. Only speed and delay inputs are needed for this step.

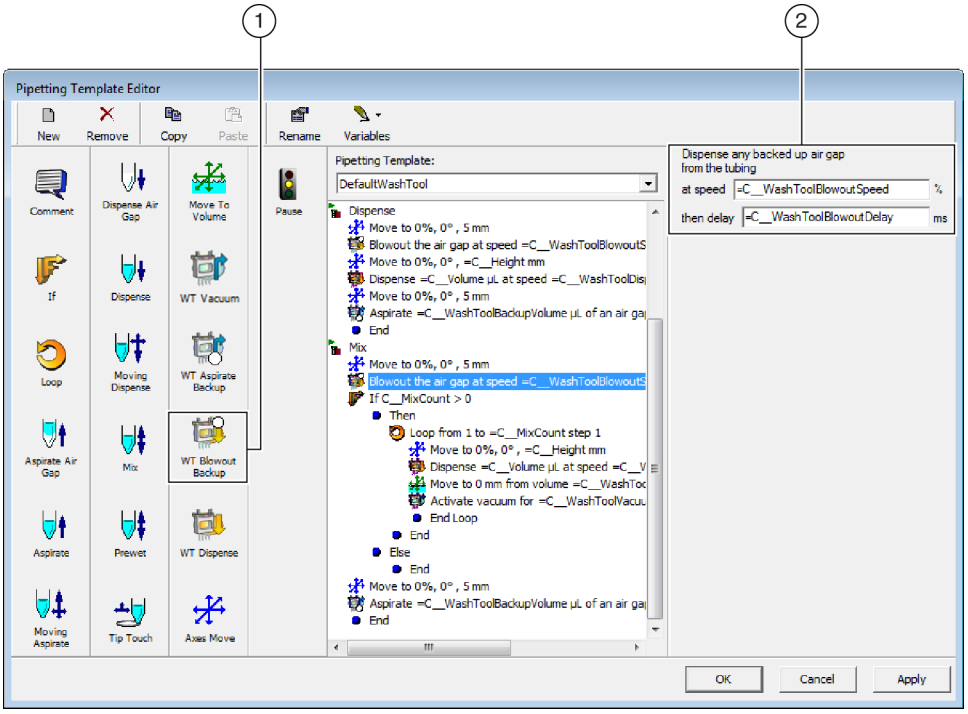
IMPORTANT This step assumes the tips have been moved out of the well to a safe location prior to beginning this step. Doing so ensures bubbles will not be produced in the labware while dispensing air.

To configure **Wash Tool Blowout Backup**:

1 Insert 

into the wash tool pipetting template. The template step configuration appears (Figure 10.24).

Figure 10.24 Wash Tool Blowout Backup Step Configuration



1. **Wash Tool Blowout Backup:** Specifies the speed at which to dispense the air gap and the length of time to hold the pod prior to performing the next operation.
2. **Wash Tool Blowout Backup Configuration: Wash Tool Blowout Backup** settings are configured here.

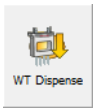
2 In **Dispense any backed up air gap from the tubing at speed**, enter the variable or value to specify the speed at which the air gap is dispensed as a percentage of the maximum speed of the pump. The default value is the context variable **=C__WashToolBlowoutSpeed**. (Refer to Table 10.1 for a definition of this variable.)

3 In **then delay**, enter the variable or value to specify the amount of time in milliseconds (ms) to delay after dispensing the air gap. The pod pauses for the specified duration before continuing with the next operation. The default value is the context variable **=C__WashToolBlowoutDelay**. (Refer to Table 10.1 for a definition of this variable.)

Wash Tool Dispense

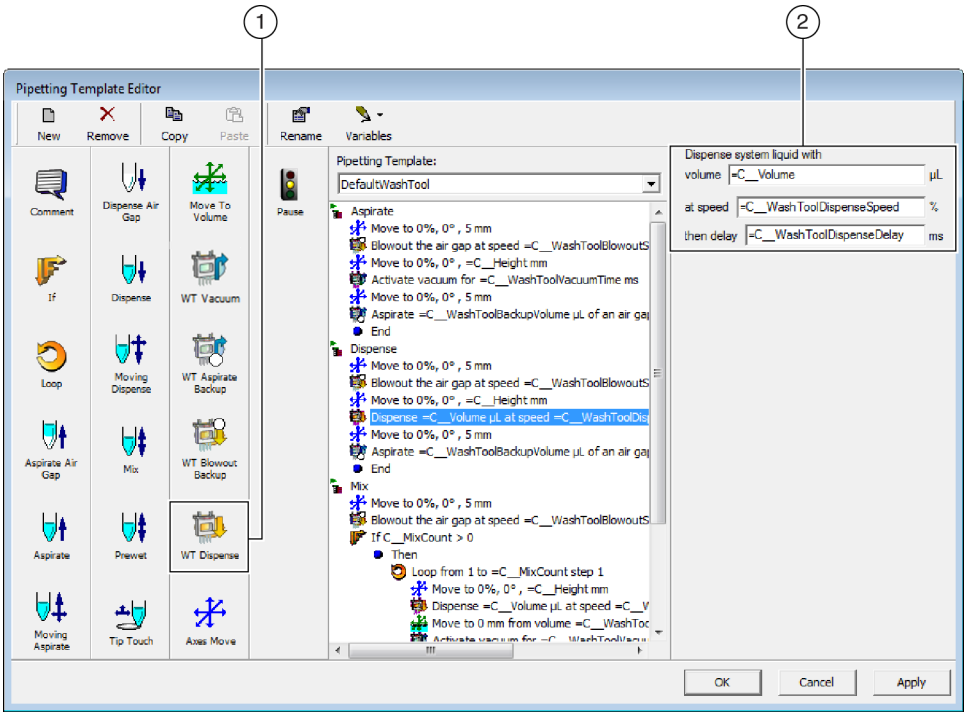
Wash Tool Dispense dispenses liquid from the currently selected valve. Volume, speed, and the length of time for the delay after dispensing are the parameters for this step.

To configure **Wash Tool Dispense**:

1 Insert 

into the wash tool pipetting template. The template step configuration appears (Figure 10.25).

Figure 10.25 Wash Tool Dispense Step Configuration



1. **Wash Tool Dispense:** Specifies the speed at which to dispense the liquid of the currently selected valve, the amount to dispense, and the length of time to hold the pod prior to performing the next operation.
2. **Wash Tool Dispense Configuration: Wash Tool Dispense** settings are configured here.

2 In **Dispense system liquid with volume**, enter the variable or value to specify the volume of liquid in microliters (µL) to dispense into the wells. The default value is the context variable **=C__Volume**. (Refer to Table 10.1 for a definition of this variable.)

3 In **at speed**, enter the variable or value to specify the speed at which the liquid is dispensed as a percentage of the maximum speed of the pump. The default value is the context variable **=C__WashToolDispenseSpeed**. (Refer to Table 10.1 for a definition of this variable.)

4 In **then delay**, enter the variable or value to specify the amount of time in milliseconds (ms) to delay after dispensing the liquid. The pod pauses for the specified duration before continuing with the next operation. The default value is the context variable **=C__WashToolDispenseDelay**. (Refer to Table 10.1 for a definition of this variable.)

CHAPTER 11

Creating Well Patterns

Overview

Creating certain methods requires the tips to access specific wells in labware. **Well Patterns** (Figure 11.1) is an editor that allows patterns for accessing specific wells to be created and stored. There are also well patterns already created in the editor which may be used, copied, or revised to create new patterns. Any well pattern stored in **Well Patterns** may be renamed or deleted.

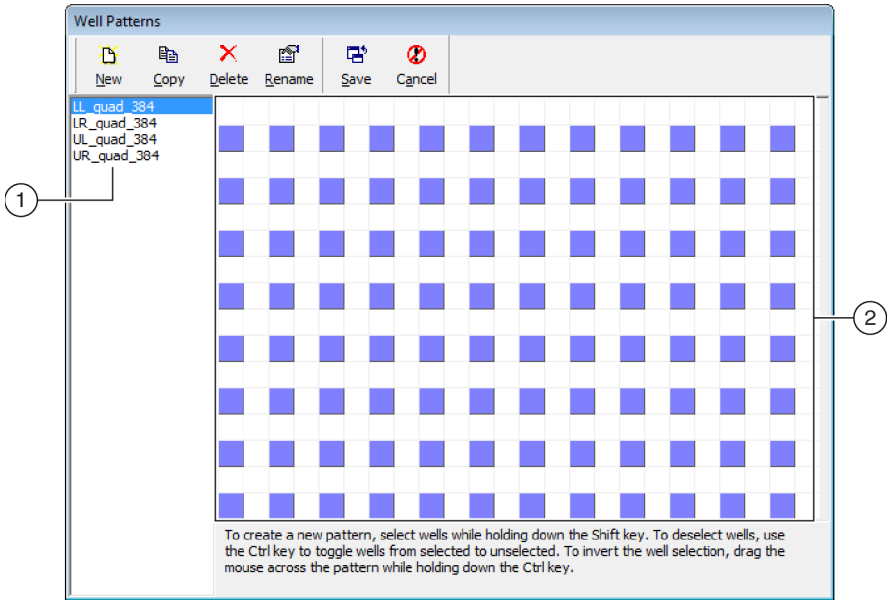
The patterns created and stored in **Well Patterns** are accessible in the **Transfer** and **Combine** steps (refer to CHAPTER 15, *Configuring Transfer and Combine Steps*). Well patterns may also be created in the **Transfer** and **Combine** steps and then stored in **Well Patterns**.

Well patterns, along with information about tip and labware types; liquid types; and pipetting templates and techniques, are stored as part of a project file. Project files store a history of all changes, additions, and deletions of items from the project file. Refer to CHAPTER 6, *Understanding and Using Project Files*, for more information on project files.

NOTE When Beckman Coulter Accounts & Permissions is enabled, only users with the **Develop Projects** permission assigned may open, edit, create, and delete well patterns (refer to CHAPTER 1, *Using Accounts and Permissions*).

To access the **Well Pattern Editor**, choose **Project > Well Pattern Editor**. **Well Patterns** display. (Figure 11.1).

Figure 11.1 Well Patterns



1. **Well Pattern List:** Lists the available patterns.
2. **Displays the highlighted pattern from Well Pattern List.**

Use the Well Pattern Editor for:

- *Creating a New Well Pattern*
- *Copying a Well Pattern*
- *Deleting a Well Pattern*
- *Renaming a Well Pattern*

Creating a New Well Pattern

New well patterns are created based on the type of labware accessed by the specific tips.

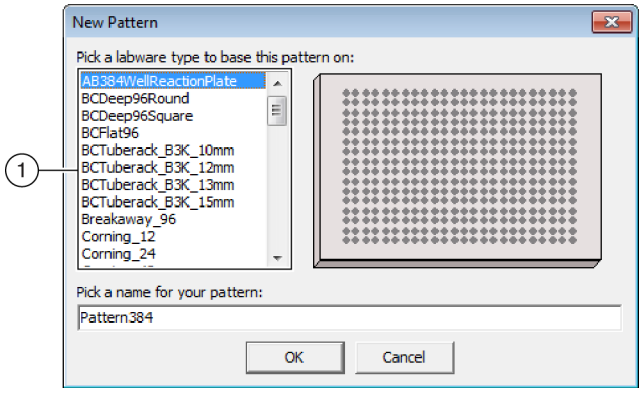
NOTE To make sure the desired pattern is not already created, view the patterns in **Well Patterns** by highlighting the well pattern in the list displayed in **Well Patterns** (Figure 11.1).

To create a new well pattern:

---

1 From **Well Patterns** (Figure 11.1), choose **New**. **New Pattern** displays (Figure 11.2).

Figure 11.2 New Pattern



1. **List of labware on which to base a new pattern.**

2 From the list of labware, choose a labware type on which to base the new pattern.

3 In **Pick a name for your pattern:**, rename the new pattern, if desired.

NOTE By default, the first new pattern is named after the number of wells on the labware type. Subsequent patterns using the same labware type are named after the number of wells plus a number. For example, the first new pattern created for a 96-well would be **Pattern96**, the second new pattern would be **Pattern96_1,** and the third new pattern would be **Pattern96_2.**

4 Choose **OK**. The labware grid based on the labware type appears in **Well Patterns**.

5 Create the new pattern from the labware grid by clicking and dragging the mouse and using Ctrl and Shift on the keyboard.

NOTE To create a new pattern, select wells while holding down the Shift key. To deselect wells, use the Ctrl key while clicking the wells to toggle the wells from select to deselect. To invert the well selection, drag the mouse across the pattern while holding down the Ctrl key.

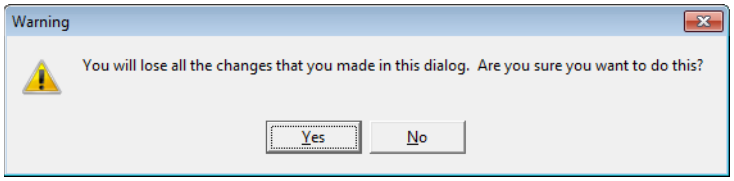
NOTE If Shift or Ctrl is not held down when clicking and dragging, the previous selection will be deleted when subsequent selections are made.

6 Choose **Save** to save the changes. **Well Patterns** closes and all the changes made in the dialog are saved.

OR

Choose **Cancel** to cancel the changes. A **Warning** (Figure 11.3) appears. Choose **Yes. Well Patterns** closes and all the changes made in the dialog are cancelled.

Figure 11.3 Warning When Cancel is Chosen



Copying a Well Pattern

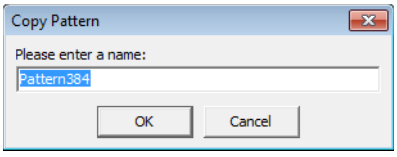
Copying a well pattern creates an exact copy of it. The copied well pattern can be modified to create a new well pattern.

To copy a well pattern:

1 From **Well Patterns** (Figure 11.1), highlight the desired pattern from the Well Pattern List.

2 Choose **Copy. Copy Patter**n (Figure 11.4) displays.

Figure 11.4 Copy Pattern



3 Rename the pattern, if desired.

NOTE By default, the first new pattern is named after the number of wells on the labware type. Subsequent patterns using the same labware type are named after the number of wells plus a number. For example, the first new pattern created for a 96-well would be **Pattern96**, the second new pattern would be **Pattern96_1,** and the third new pattern would be **Pattern96_2**.

4 Choose **OK**. The copied pattern appears in **Well Patterns**.

5 If desired, modify the well pattern. Refer to step 5 of *Creating a New Well Pattern* for details.

6 Choose **Save** to save the changes. **Well Patterns** closes and all the changes made in the dialog are saved.

OR

Choose **Cancel** to cancel the changes. A **Warning** (Figure 11.3) appears. Choose **Yes. Well Patterns** closes and all the changes made in the dialog are cancelled.

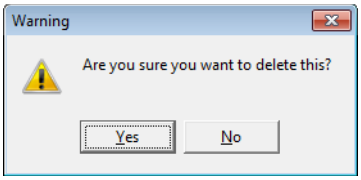
Deleting a Well Pattern

To delete a well pattern stored in **Well Patterns**:

1 From **Well Patterns** (Figure 11.1), highlight the desired pattern from the **Well Pattern List**.

2 Choose **Delete**. A **Warning** (Figure 11.5) displays, confirming the deletion.

Figure 11.5 Warning Confirming Deletion of a Pattern



3 Choose **Yes**. The pattern is deleted from the list of patterns in **Well Patterns**.

4 Choose **Save** to save the changes. **Well Patterns** closes and all the changes made in the dialog are saved.

OR

Choose **Cancel** to cancel the changes. A **Warning** (Figure 11.3) appears. Choose **Yes. Well Patterns** closes and all the changes made in the dialog are cancelled.

Renaming a Well Pattern

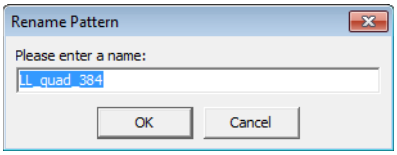
Renaming a well pattern provides the opportunity to assign a descriptive name to a well pattern for easy identification.

To rename a well pattern in **Well Patterns**:

1 From **Well Patterns** (Figure 11.1), highlight the desired pattern from the Well Pattern List.

2 Choose **Rename**. **Rename Pattern** (Figure 11.6) appears.

Figure 11.6 Rename Pattern



3 Type a new name for the pattern.

4 Choose **OK**. The pattern is renamed in the list of patterns in **Well Patterns.**

5 Choose **Save** to save the changes. **Well Patterns** closes and all the changes made in the dialog are saved.

OR

Choose **Cancel** to cancel the changes. A **Warning** (Figure 11.3) appears. Choose **Yes**. **Well Patterns** closes and all the changes made in the dialog are cancelled.

CHAPTER 12

Creating and Using Methods

Overview

A method is a series of steps controlling the operations of the instrument. When steps are inserted into a method, they represent operations performed during the method run. The steps available for insertion into a method are located on the left of the Biomek Software main editor in the step palettes (Figure 12.1).

NOTE When Beckman Coulter Accounts & Permissions is enabled, only users with **Develop Methods** permission may develop, open, and edit methods (refer to CHAPTER 1, *Using Accounts and Permissions*).

Biomek Software does a substantial amount of the method-building work while at the same time allowing direct and precise control over the building of method.

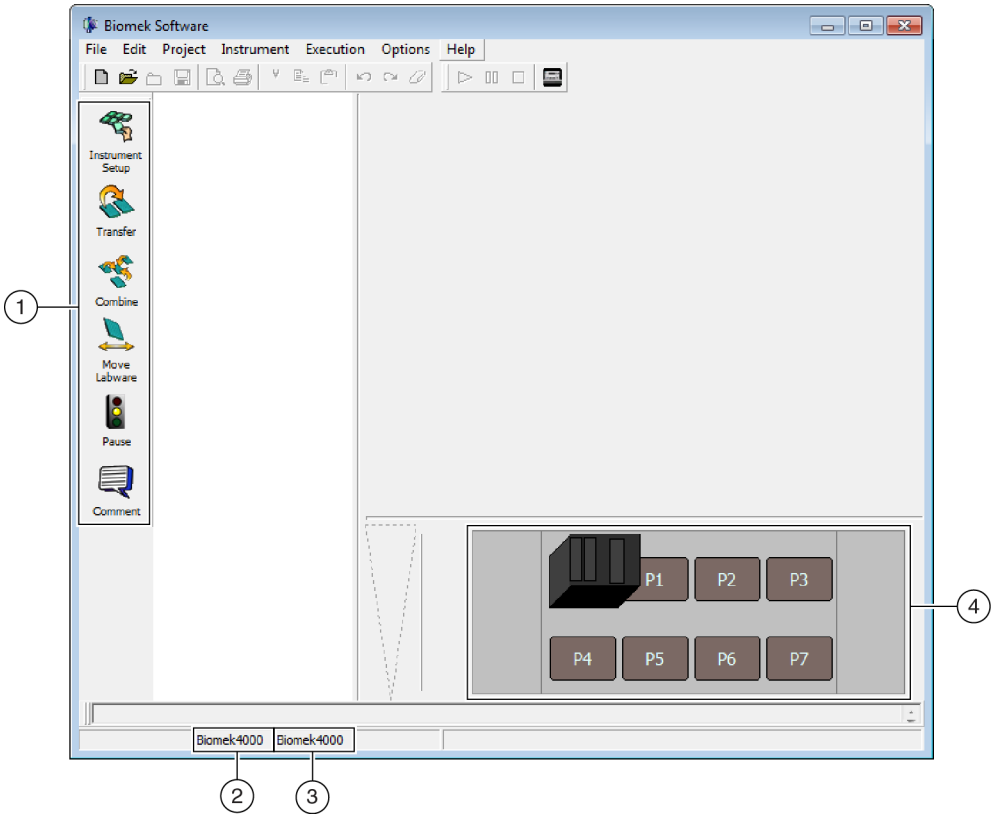
Methods are stored in projects, which contain all of the items required to perform the method; for example, labware classes or techniques. Saving a method automatically checks in the method, creating a record of the revision that preserves the method configuration at the time it was saved. Revisions may be accessed from the revision history at a later time and used as a template for a new revision, if desired.

⚠ CAUTION

Incorrectly created Biomek Software methods can cause system crashes, resulting in equipment damage, or hazardous waste spills. Verify all methods are properly created prior to executing the method run.

NOTE The appearance of the main editor (Figure 12.1), such as the Current Deck Display and step palettes, varies based on the current instrument file and project file. The current instrument and project file names are displayed in the status bar of the main editor.

Figure 12.1 Biomek Software Main Editor for Method Creation



1. **Step palettes**
2. **Current instrument**
3. **Current project**
4. **Current Deck Display:** Displays the status of the deck upon completion of the previous step.

Using methods to control the operations of the instrument includes:

- *Creating a New Method*
- *Inserting Steps in a Method*
- *Using Additional Step Palettes*
- *Copying, Cutting, and Pasting Steps in a Method*
- *Deleting Steps in a Method*
- *Using Undo and Redo in Method Building*
- *Entering and Viewing Method Properties*
- *Saving a Method*
- *Validating a Method*
- *Signing a Method*
- *Viewing Method History*
- *Checking Out a Revision of a Method*
- *Opening a Saved Method*
- *Importing and Exporting Methods*

- *Deleting and Restoring Methods*
- *Running, Pausing, and Stopping a Method*
- *Printing a Method*
- *Improving a Method*

Creating a New Method

The main editor (Figure 12.1) is the starting point for creating a liquid-handling method using the instrument. Method steps from the step palette are inserted into the Method View in a linear fashion.

When steps are inserted into a method, the configuration associated with that step appears on the right side of the Biomek Software main editor (Figure 12.2).

NOTE Steps not configured appropriately generate errors when the method is validated or run.

To create a new method:

1 Launch **Biomek Software**. The main editor displays (Figure 12.1).

2 From the toolbar, select the icon.

OR

From the **File** menu, choose **New**.

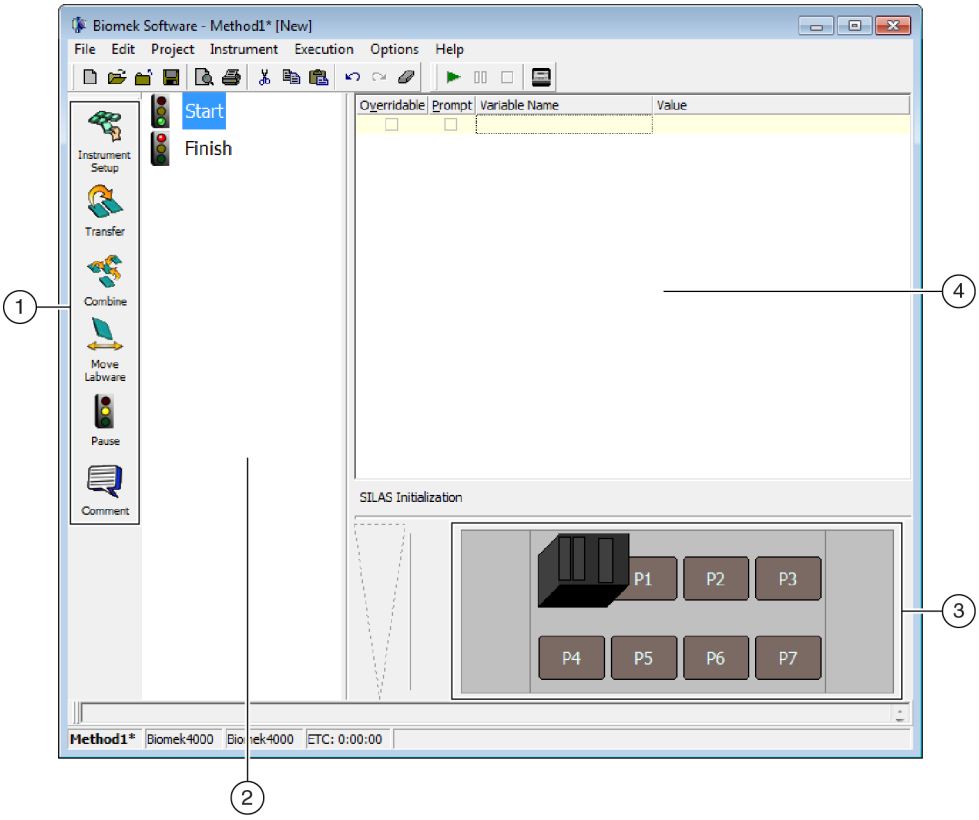
OR

Drag and drop a step, such as **Instrument Setup**, into the Method View.

A new method is created and assigned the default name **Method# [New]** (Figure 12.2).

NOTE The **Start** and **Finish** steps appear automatically in a new method.

Figure 12.2 Biomek Software Main Editor



1. **Basic Step Palette:** Displays the steps available for insertion into a method. Additional steps are available through other step palettes or the **Step Palette Builder** (refer to CHAPTER 28, *Using the Step Palette Builder*).
2. **Method View:** The method is built step by step in this area.
3. **Current Deck Display:** Displays the status of the deck upon completion of the previous step.
4. **Step configuration area:** When a step is highlighted in the Method View, the corresponding configuration appears in this area.

There are two steps automatically present in every method created and executed by Biomek Software:

- Start — The first step in a method; allows creation of global variables that are applicable to the entire method, as opposed to a variables applicable only to one step within the method.
- Finish — The final step in a method; provides options to clear the deck, clear the devices on the deck, unload tips from the pod, unload tools from the pod, clear all global variables, and generate a report on data sets.

Configuring the Start Step

Use the **Start** step to define variables used throughout the entire method, as opposed to variables defined within individual steps. A variable is a value that has been assigned a name (Figure 12.3).

NOTE Variables defined in individual steps, such as the **Let** step, are applicable only to that step and any nested substeps. Refer to CHAPTER 17, *Let Step*, for more information about the **Let** step.

To use a variable created in the **Start** step, that variable name is entered into the configuration of the step using the variable. In the example shown in Figure 12.4, the variable **AspValue**, created in the Start configuration is entered in the **µL** (volume) field of the **Transfer** step.

The Biomek Software internally substitutes the name with its value, but the name remains in the field. In Figure 12.4, **AspValue** is substituted internally by the value '10'. The value of '10' is never displayed, only the variable name **AspValue**. The method can be run subsequently with a different value for **AspValue**, and the software automatically replaces **AspValue** with the new value.

Variables created in the **Start** step can also give a prompt at the start of a method run allowing new values to be entered for each variable at runtime.

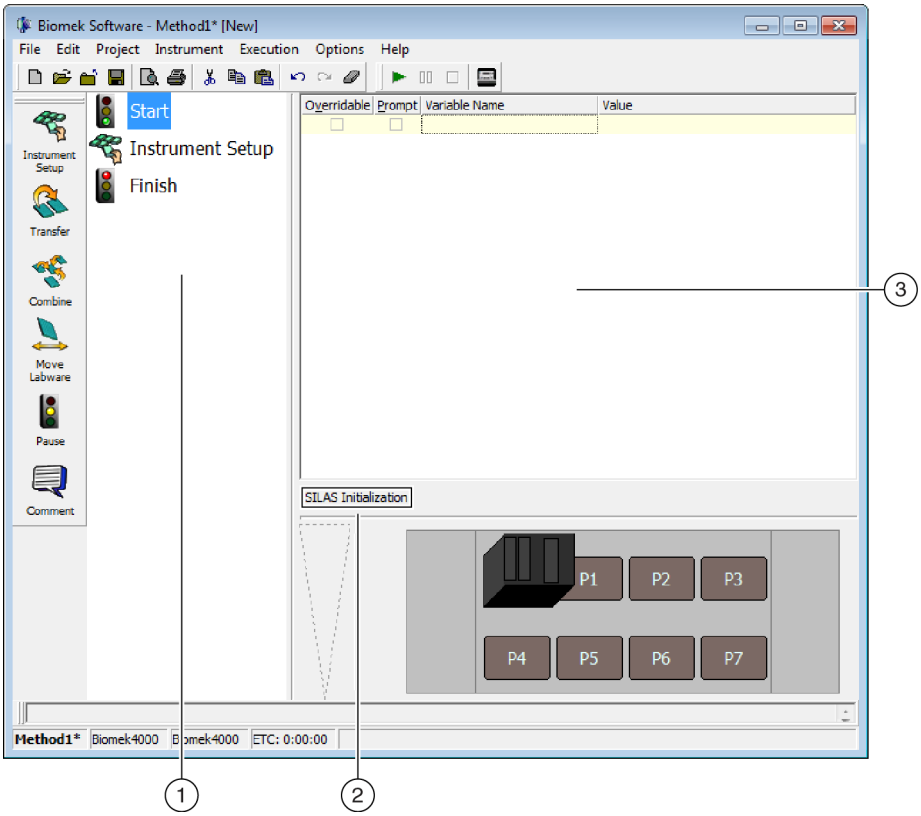
NOTE Refer to CHAPTER 13, *Using Variables in a Method*, for more information on using variables in a method.

To configure a variable in the **Start** step:

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1 Select **Start** in the **Method View**. The **Start** step configuration displays (Figure 12.3).

Figure 12.3 Start Step and Configuration

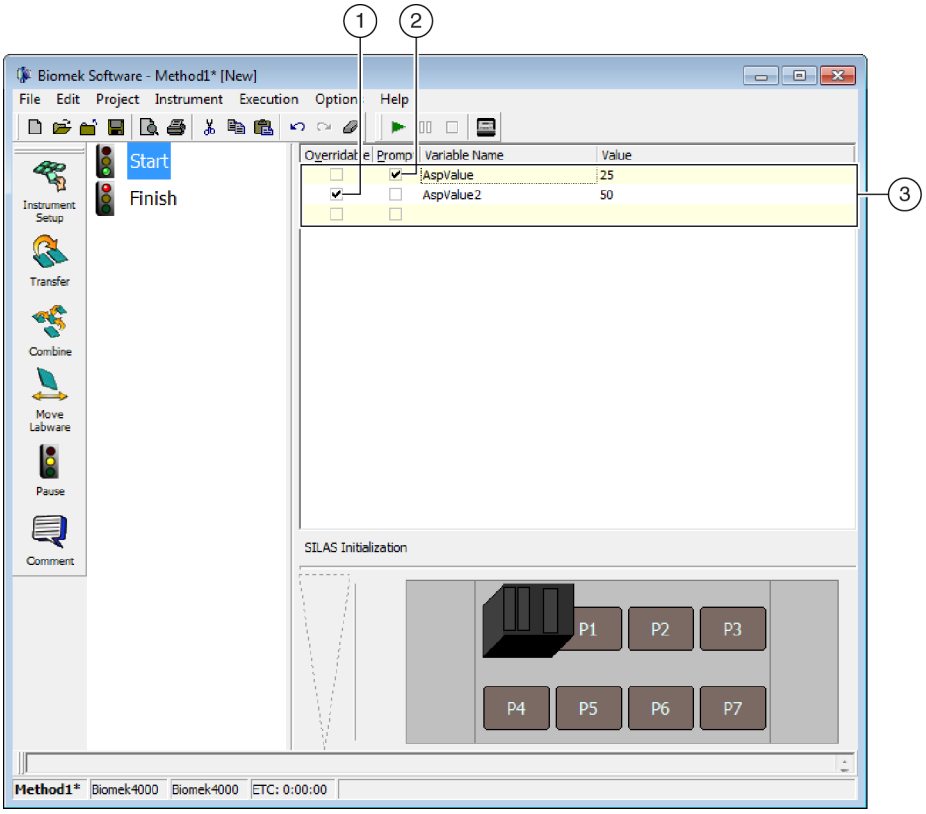


1. **Method View**: Every method contains the **Start** and **Finish** steps which appear automatically when a new method is created.
2. **SILAS Initialization**: Used to initialize SILAS modules or consumers at the beginning of a run.
3. **Start step configuration**: Variables defined in the **Start** step configuration can be used throughout the method.

---

2 Click under **Variable Name** (Figure 12.4) to position the cursor in the **Variable Name** field.

Figure 12.4 Start Step with Variables Configured



1. **Select this check box to allow the variable to be overwritten by a previously defined value.**
2. **Select this check box to be prompted at runtime to enter a value for this variable.**
3. **Examples of variables defined in the Start step configuration.**

3 Enter a **Variable Name**.

NOTE Variable names must begin with a letter, may only use alphanumeric characters (0-9, A-Z) and the underscore (_), and may not exceed 255 characters. Variable names are not case sensitive.

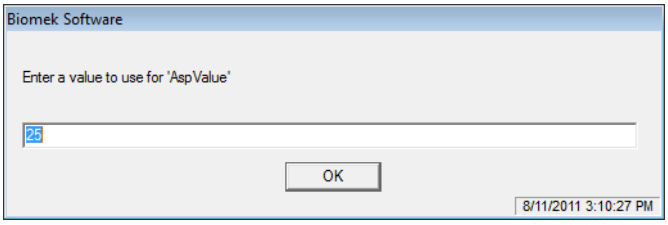
4 Click in the **Value** field and enter the desired default value for the variable.

5 Check the box under **Overridable** (Figure 12.4) if the variable can be overridden by a subsequently defined value. For example, a variable **Test** is created in the **Start** step with a value of 10. A **Let** step later in the method assigns a value of 15 to the **Test** variable. If **Overridable** is selected in the **Let** step, the previously existing value from the **Start** step of 10 overrides the value in the **Let** step. If **Overridable** is not selected in the **Let** step, however, the variable is assigned the value of 15 define in the **Let** step.

6 Check the box under **Prompt** (Figure 12.4) to activate a prompt for the variable at run time. Each time the method is run, a prompt similar to the one shown in Figure 12.5 asks for verification of the variables and their values. Verification of the variables provides an opportunity to change the default values associated with the variables each time the method is run, if desired.

NOTE A separate prompt appears for each variable that has **Prompt** selected.

Figure 12.5 Prompt to Enter Value for Variable at Runtime



7 Repeat steps 2-6 for each variable.

NOTE To get a new line for another variable, press Enter with the cursor in the **Value** field of the last defined variable.

Configuring the Finish Step

The **Finish** step is the last step in every Biomek method. The **Finish** step indicates the end of a method and provides opportunities to control pod, deck, and device status upon completion of a method.

When highlighted in the Method View:

- The **Finish** step configuration is displayed on the right side of the Biomek Software main editor.
- The software runs an internal validation to check for errors in the method.
- An **Estimated Time to Completion (ETC)** of the method is displayed in the status bar at the bottom of the Biomek Software main editor.

NOTE When the **Finish** step is highlighted in the Method View, the software estimates the real time required to complete the entire method. When any other step is highlighted in the Method View, the length of time displayed in the **ETC** field represents the time required to complete the method up to the selected step. If an error is found in validation, **ETC** displays as **Failed.**

Use the **Finish** step to re-initialize the software state of the deck and external hardware devices, and to physically remove tips and tools from the pod when a method is completed.

The default configuration for the **Finish** step is all options selected (Figure 12.6). If the options are not selected, errors may occur due to conflicts between the labware in a new method and the

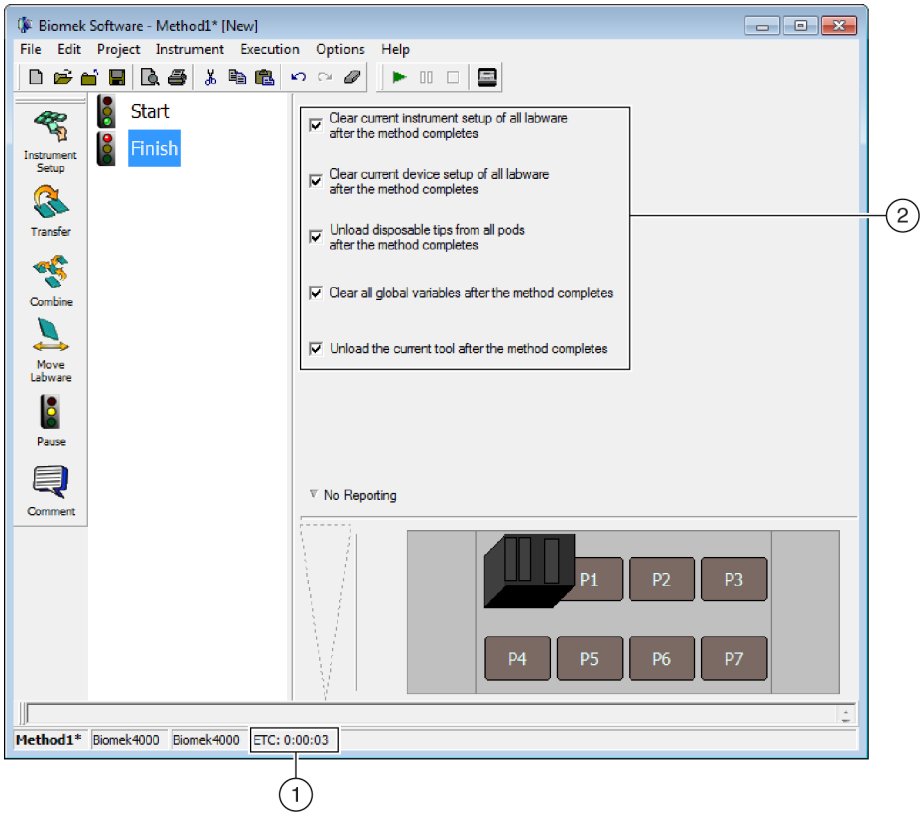
labware from the previous method. The error occurs because software and hardware remain in their final state after a method is run, unless told otherwise.

NOTE Each of the **Finish** step options is independent of the others, so any combination of the options may be selected.

NOTE If the **Finish** step configuration options are not used, steps must be added to the new method to reset the software and hardware.

The options of the **Finish** step reset the hardware and software so a new method can populate the deck as required, without encountering labware errors. The **Finish** step also allows for reports to be generated on labware data from data sets (refer to CHAPTER 14, *Using Sample Tracking and Data Sets in a Method*).

Figure 12.6 The Finish Step Configuration



1. **Estimated Time to Completion** appears only when a step is highlighted in the **Method View**.
2. **Finish step configuration**: The **Finish** step configuration informs the software that the Instrument Setup and any external hardware devices are clear of labware and physically removes any tips and tools loaded on the pod.

Clear Current Instrument Setup of All Labware After the Method Completes

The Current Deck Display represents the status of the labware on the deck upon completion of a method run (Figure 12.6). Typically, a clear deck is needed at the start of a method.

To clear the deck in the software after a method, select **Clear current instrument setup of all labware after method completes** in the **Finish** step configuration. This ensures a clear deck for the next method.

NOTE To use the same deck setup for a subsequent method, do not select **Clear current instrument setup of all labware after method completes** in the **Finish** step configuration. The labware positions, volumes, and marks carry over to the next method. Use the **As Is** option in the **Instrument Setup** step in the subsequent method to leave those positions in their current state.

Clear Current Device Setup of All Labware After the Method Completes

The **Device Setup** remembers the contents of the devices on the deck at completion of a method run (Figure 12.6). Typically, devices are clear of labware at the start of a method.

To clear all devices of labware, select **Clear current device setup of all labware after method completes** in the **Finish** step configuration. This ensures clear devices for the next method.

NOTE Insert an **Instrument Setup** step at the beginning of the next method to specify where labware is located on the deck (refer to CHAPTER 15, *Instrument Setup Step*). Use the **Deck Editor** to specify the location of devices on the deck (refer to CHAPTER 5, *Preparing and Managing the Deck*), and use the **Device Setup** step to configure the contents of the external devices. Refer to CHAPTER 21, *Using External Devices with Biomek Laboratory Automation Workstations*, and CHAPTER 21, *Device Setup Step*, for more information about configuring external devices.

Unload Disposable Tips After the Method Completes

Tips remain on the tools unless they are removed during a step or in the **Finish** step (Figure 12.6). Typically, the tool needs to be clear of tips at the start of a method.

NOTE Disposable tips can be removed from any pipetting tool.

To clear the tool of disposable tips, select **Unload disposable tips from all pods after method completes** in the **Finish** step configuration.

Clear All Global Variables After the Method Completes

Global variables are set in the **Start** or **Set Global** steps. A variable is a value that has been assigned a name and can be referenced repeatedly during a method. Global variables are carried over into subsequent methods unless they are cleared in the **Finish** step.

To clear all global variables, select **Clear all global variables after the method completes** in the **Finish** step configuration.

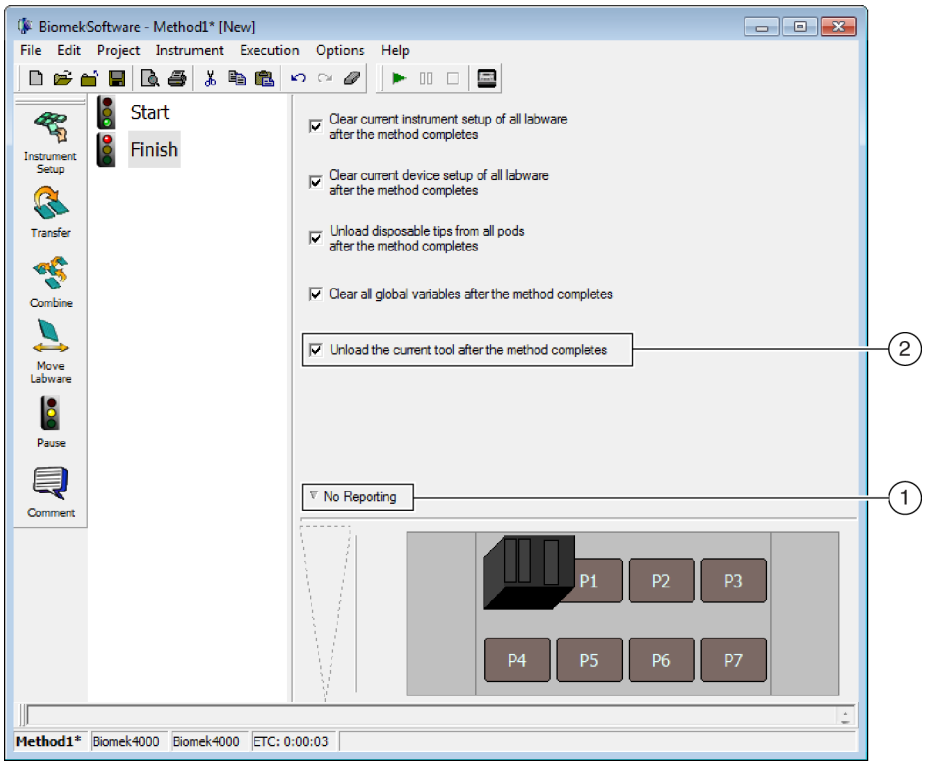
Unload the Current Tool After the Method Completes

An option to unload whatever tool is installed on the pod at the end of the method is available (Figure 12.7). Selecting this option instructs the instrument to unload any tool installed on the pod upon completion of the method to ensure no tool is installed at the start of the next method.

If **Unload the current tool after method completes** is not selected, it may be necessary to add additional steps to the start of any subsequent methods to unload or change the tool on the pod.

To unload the tool at the end of the method, select **Unload the current tool after the method completes** in the **Finish** step configuration. Any tool loaded onto the pod is removed and placed back onto the tool rack at the conclusion of the method.

Figure 12.7 Finish Step Options



1. **No Reporting**
2. **Option to unload a tool from the pod at the end of a method.**

Configuring a Report in the Finish Step

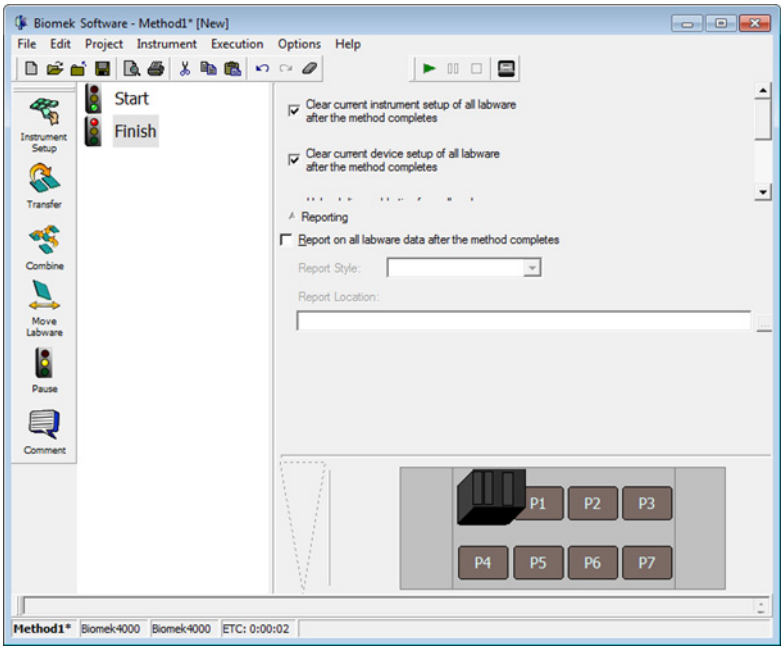
The **Finish** step can be configured to create a report on data sets at the end of the method. Refer to CHAPTER 14, *Using Sample Tracking and Data Sets in a Method*, for more information on using data sets in a method.

NOTE To create a report on data sets after any transfer or pipetting operation, a **Reporting** step can be inserted into a method at any time (refer to CHAPTER 23, *Configuring the Reporting Step*).

To choose the report style and location of a report at the end of a method:

1 From the **Finish** step, select **No Reporting** (Figure 12.7) to open the **Reporting** configuration (Figure 12.7).

Figure 12.8 Reporting Enabled on Finish Step



2 Select **Report on all labware data after the method completes** to enable reporting.

3 From **Report Style**, choose one of the following:

- **Text File**
- **Per-Plate HTML Files**
- **Per-Plate Text Files**
- **SQL Server** (refer to CHAPTER 23, *Configuring a SQL Server Report Style*)

NOTE Refer to CHAPTER 23, *Report Styles*, for examples and information on the types of reports that may be generated.

4 Select … (browse) to navigate to the location where you wish to save the files. If you are saving:

- **Text Files:** Navigate to the desired location, and then enter a file name and select **Save**.
- **Per-Plate HTML Files** or **Per-Plate Text Files**: Navigate to the appropriate folder, and then select **OK**.

- To a **SQL Server**: In the **SQL Server Connection** window, either:
  - Enter the **User** and **Password** information

    OR
  - Select **Use NT Authentication**.

  Select **Connect**. In **Databases**, choose the desired database, and select **OK** to close the window. In the **Finish** step configuration, enter a table name into the **Table Name** field.

Reporting on the **Finish** step is configured.

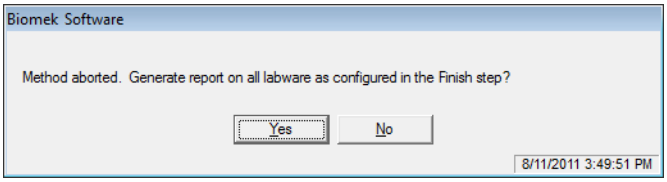
Generating a Report When a Method Stops

When a method is stopped or aborted and reporting is configured in the **Finish** step, a prompt appears asking if a report should be generated as configured in the **Finish** step (Figure 12.9) (refer to *Configuring a Report in the Finish Step*).

To generate a report when a method stops:

1 From Figure 12.9, choose **Yes**. The report generates as configured in the **Finish** step.

Figure 12.9 Prompt When Method is Aborted



Completing Finish Step Configuration

Once all the desired options on the **Finish** step have been selected, the method can be run. When the method is completed, any actions selected in the **Finish** step are performed.

Inserting Steps in a Method

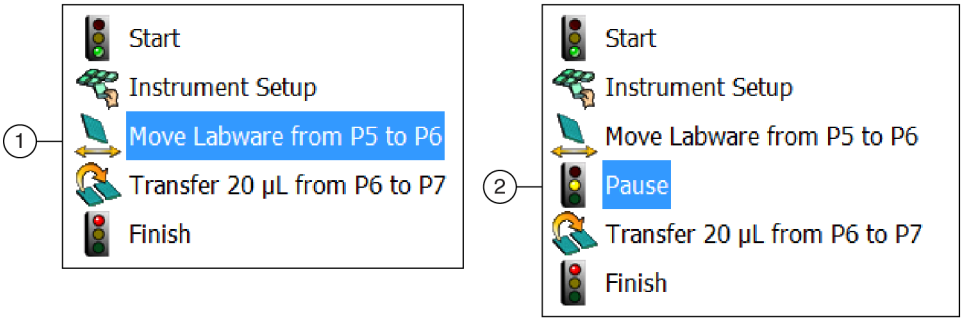
Steps can be added to a method in a sequential order or inserted at any location in the Method View during the method building process; however, steps must represent the desired order of execution when the method is run.

To insert a step in a method, choose one of the following procedures:

1 Select the step above the desired insertion point (Figure 12.10).

2 Click the desired step on the step palette. The step is inserted below the selected step.

Figure 12.10 Inserting a Step Into a Method

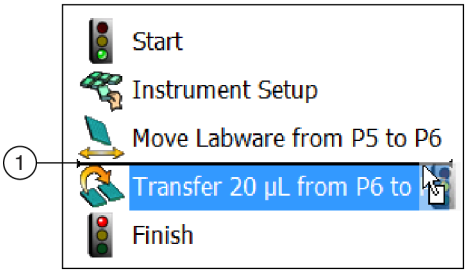


1. **Select the step above the desired insertion point.**
2. **Choose the desired step from the Step Palette. The step automatically inserts into the method.**

OR

Drag and drop the desired step from the step palette into the desired location in the **Method View.** A black bar displays at the insertion point (Figure 12.11).

Figure 12.11 Inserting a Step by Drag and Drop



1. **Insertion bar:** The insertion bar indicates the target point where the step will be inserted into the method.

Understanding Techniques

All pipetting operations in a method are controlled using techniques. A technique instructs the instrument in performing pipetting operations, such as aspirate, dispense, and mix. Technique selections are made anytime liquid needs to be aspirated or dispensed during a method.

A technique stores a set of values, such as aspirate and dispense height, pod speed, and tip touch, used in pipetting operation. Biomek Software also stores a set of properties, such as labware type and liquid type, related to each technique. Based upon these values and properties, the appropriate technique is selected automatically for the pipetting operation. This auto-selection can be overridden and a technique selected manually for each operation, if desired.

Pipetting options used in the selected technique are represented visually under the Technique field in the step configuration. These pipetting options are included in Figure 12.1.

Table 12.1 Pipetting Options

Option	Icon	Description
Prewet the tips		Aspirates and dispenses a specified volume of liquid before pipetting to prewet the tips.
Tip touch		Allows tips to touch a designated location briefly in a well after aspirating or dispensing. **NOTE** Movement of a tip touch first centers the tip in the well, performs the pipetting operation, moves to the side of the well, performs a specified delay, and returns to the center of the well for dispensing.
Mix prior to aspirating liquid or Mix after dispensing liquid		Mixes the liquid before aspirating or after dispensing.
Follow liquid level when aspirating or dispensing		Accomplished with calculations that determine the difference in height of a liquid level after an aspirate or dispense operation is completed. The Z- and D-axis are coordinated according to that liquid level.
Aspirate a trailing air gap after leaving the liquid		Draws air into tips after aspirating liquid, and blows out that air before dispensing.
Blowout all leading air gaps		Draws air into tips before aspirating liquid, and blows out that air after dispensing to ensure all liquid has been dispensed.

NOTE Refer to CHAPTER 9, *Understanding and Creating Techniques*, for more information on pipetting techniques.

Using Additional Step Palettes

Additional steps, other than those displayed on the **Basic** step palette, may be added to a method by displaying one of the existing step palettes or creating a new step palette using the **Step Palette Builder** (refer to CHAPTER 28, *Using the Step Palette Builder*).

To display an existing step palette:

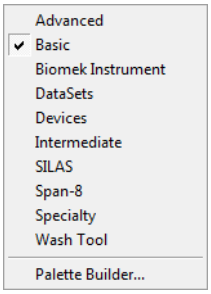
1 From the **Options** menu, select **Toolbars** and then select the desired step palette to display.

NOTE The step palettes available depend on instrument type and configuration.

OR

Right click any empty palette space, and select the desired step palette to display from the step palette menu (Figure 12.12).

Figure 12.12 Step Palette Menu



NOTE To create a custom step palette or add steps to existing step palettes, select **Palette Builder** to open the **Step Palette Builder**.

Copying, Cutting, and Pasting Steps in a Method

One or more steps can be copied, cut, and pasted within a method or between methods in a sequential order. Steps can be inserted at any location in the Method View during the method building process; however, they must represent the desired order of execution when the method is run.

The originating method and the destination method must use the same deck and instrument setups when copying, cutting, and pasting steps between methods. Verifying that the deck and instrument setups are the same in both methods ensures that Biomek Software knows where labware is physically located on the deck. If the decks do not match, steps copied from another method may need to be modified to work in the new method.

To copy, cut, and paste one or more steps in a method:

1 Highlight a step in the Method View for copy (or cut).

2 To select multiple steps to copy (or cut):

- While holding down (Shift), select the final step in the series to copy (or cut). All the steps between the first and second steps selected are now highlighted.
- While holding down (Ctrl), select additional steps to copy (or cut). All the selected steps are highlighted.

3 From the **Edit** menu, select **Copy** (or **Cut**).

OR

Right click on any of the selected steps and select **Copy** (or **Cut**) from the menu that displays.

NOTE If **Cut** is selected, the highlighted step(s) are removed from the Method View. If any other step is **Copied** or **Cut** before **Pasting** the first step in the Method View, the first copied or cut step is lost or overwritten.

4 If the step is to be pasted in a different method, open the desired method (refer to *Opening a Saved Method*).

5 Highlight the step below where the copied or cut step(s) are to be pasted.

6 From the **Edit** menu, select **Paste.**

OR

Right click the step below where the copied or cut step(s) are to be pasted and select **Paste** from the menu that displays. The step(s) are inserted above the highlighted step.

Deleting Steps in a Method

Steps can be deleted from a method during the method-building process if they are no longer desired.

To delete a step from a method:

1 Highlight the step in the Method View.

2 To select multiple steps to delete:

- While holding down (Shift) , select the final step in the series to delete. All the steps between the first and second steps selected are now highlighted.
- While holding down (Ctrl) , select additional steps to delete. All the selected steps are highlighted.

3 Press **Delete** on the keyboard.

OR

From the **Edit** menu, select **Clear.** The highlighted step(s) are deleted.

OR

Right click on any of the selected steps and select **Clear** from the menu that displays.

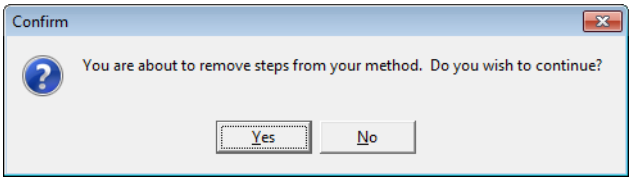
4 If **Ask for confirmation before removing a step from a method** is selected in **Preferences** (CHAPTER 28, *Changing Display Preferences*), a prompt displays asking for confirmation each time a step is deleted from a method (Figure 12.13).

5 Choose **Yes** to delete the step from the method.

OR

Choose **No** to cancel the deletion.

Figure 12.13 Confirmation to Delete Steps in a Method



Using Undo and Redo in Method Building

The Biomek Software maintains a history of actions performed during method building. By using the **Undo** and **Redo** features located on the toolbar, this history can be accessed and the actions undone or redone while building a method. Hovering the mouse over the **Undo** or **Redo** button on the toolbar displays a tool tip indicating what action will be undone or redone.

The following actions are stored in the history and may be undone and redone while building a method:

- Adding a step.
- Removing a step.
- Moving a step.
- Configuring a step.
- Changing active selection.

NOTE The active selection is the currently selected (highlighted) step within the method. Selecting another step in the method changes the active selection.

Using Undo

Undo is used to undo the most recent method-building action. Multiple actions may be undone by performing consecutive **Undo** actions; there is no limit to how many actions can be undone.

To undo an action:

1 Select **Undo** from the **Edit** menu.

OR

Click on the toolbar.

NOTE When **Undo** is used while configuring a step, it undoes all actions made to the configuration. For example, while configuring **Instrument Setup** step and placing labware on deck positions, choosing **Undo** will undo the entire **Instrument Setup** step and not just the last deck position that was configured.

Using Redo

Redo is used to redo an action that has been undone using the **Undo** feature. By performing consecutive **Redo** actions, multiple actions can be redone if multiple actions were undone.

NOTE If another action is performed after undoing an action, **Redo** is disabled and the previously undone action cannot be redone.

To redo an undone action:

1 Select **Redo** from the **Edit** menu.

OR

Click on the toolbar.

Entering and Viewing Method Properties

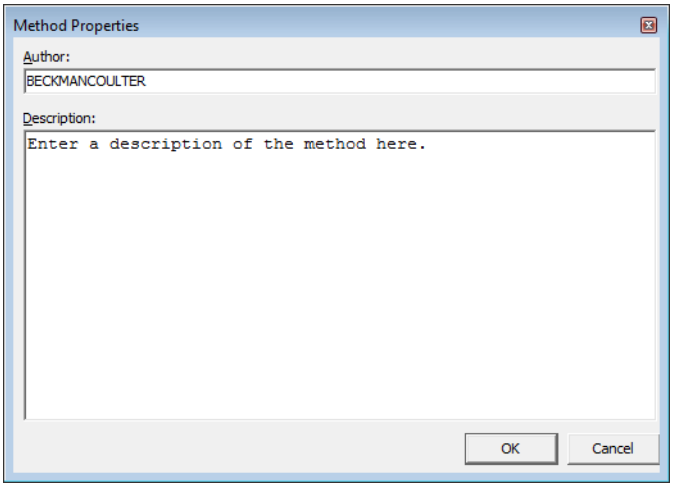
Method Properties allows for entry of a description of the method that can be viewed or modified.

NOTE Method properties can be viewed, but not modified when running a method in validated mode (refer to *Opening a Saved Method*). Validated mode is available only when Beckman Coulter Accounts & Permissions is enabled (refer to CHAPTER 1, *Using Accounts and Permissions*).

To enter or view **Method Properties**:

1 From the **File** menu, select **Properties. Method Properties** displays (Figure 12.14).

Figure 12.14 Method Properties



2 In **Author**, enter the name or user name of the method designer.

3 In **Description**, enter a description of the method.

4 Choose **OK** to save changes and close **Method Properties**.

OR

Choose **Cancel** to close **Method Properties** without saving changes.

Saving a Method

Methods may be saved at any time during their development. Saving a method automatically checks in the method, creating a record of the revision that preserves the method configuration at the time it was saved. Revisions may be accessed from the revision history at a later time.

If any of the project items, such as labware class definitions or techniques, changes after the method is saved, when the method is opened next, the latest definitions are used. Methods are saved as elements of the project file, not as separate files. To use a method in another project file or on another system, it must be exported to a Biomek method file (*.bmf) and imported into the desired project (refer to *Importing and Exporting Methods*).

Methods may be saved in and moved between folders from **Save Method** or **Open Method** (refer to *Using Folders When Saving Methods*).

To save a method:

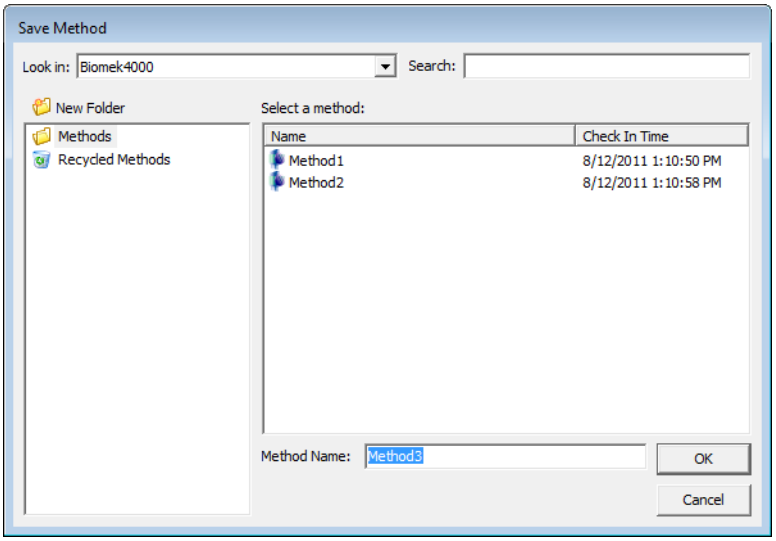
1 Choose (**Save Method**) on the toolbar.

OR

From the **File** menu, choose **Save. Save Method** displays (Figure 12.15).

NOTE **Save Method** displays only the first time the method is saved; subsequent saves to the method do not prompt for a new file name. To save an existing method with a different file name, choose **Save As...** from the **File** menu.

Figure 12.15 Save Method



NOTE If Accounts & Permissions is enabled, **Last Checked In By** and the name of the person who checked in the method displays.

NOTE To quickly display a desired method, choose the project from **Look in** where methods are stored and enter the name of the method in **Search**.

2 In **Method Name**, enter the name under which the method is saved.

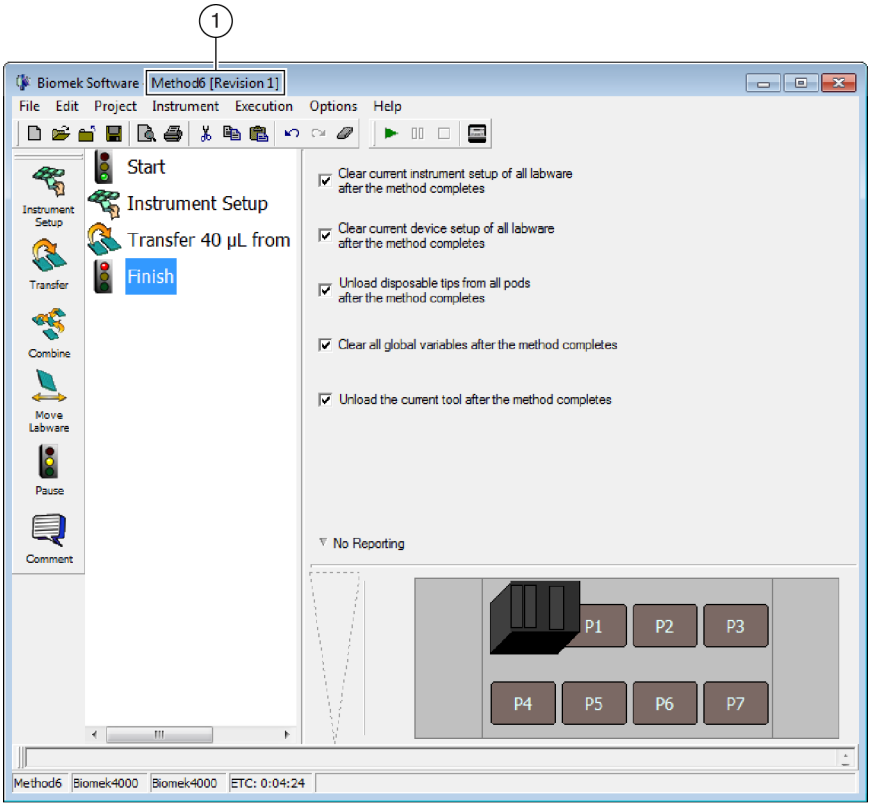
3 Choose **OK**. The method is saved with the specified method name and **Save Method** closes. The title bar of the Biomek Software main editor displays the method name as **MethodName [Revision #]** (Figure 12.16).

NOTE Each time the method is saved, the method name changes the **Revision #** to the next number.

OR

Choose **Cancel. Save Method** closes without saving the method.

Figure 12.16 Biomek Software Main Editor After Saving Method6



1. **Method name and revision number displayed in title bar.**

Saving a Method with Accounts & Permissions Enabled

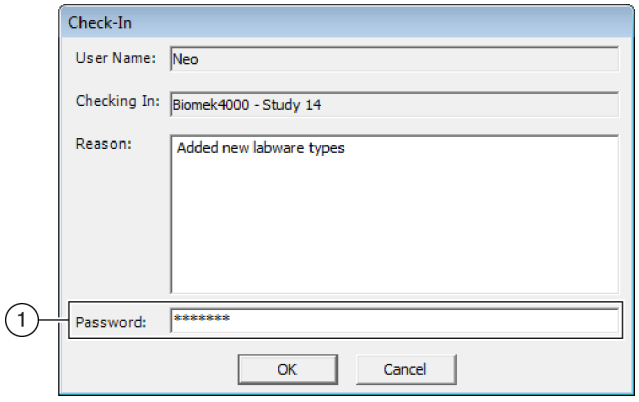
When Accounts and Permissions is enabled, **Check-In** displays after **Save Method** displays and is configured. A **Reason** for the method change or check-in and, if Accounts & Permissions is configured to require password checks, a **Password** must be entered before the method can be saved.

To save a method with Accounts & Permissions enabled:

1 Follow the three steps in *Saving a Method*. **Check-In** displays (Figure 12.17). In **Reason**, enter a reason for the method being checked in. Text entered in Reason is date and time stamped, and stored in the audit log of all user activity.

2 If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password**.

Figure 12.17 Check-In



1. **Password:** Appears only when Accounts & Permissions is configured to require password checks (refer to CHAPTER 1, *Setting the Level of Support for Accounts and Permissions*).

3 Choose **OK** to check in the method. If project items were modified, **Check-In** displays to check in the project items.

OR

Choose **Cancel** to close **Check-In** without checking in the method.

Using Folders When Saving Methods

Methods can be saved in previously created folders, saved in new folders, and moved between folders.

To save a method in a previously created folder:

1 Complete steps 1 and 2 in *Saving a Method*.

2 Click on the desired folder.

3 Choose **OK**. The method is saved in the folder.

To save a method in a new folder:

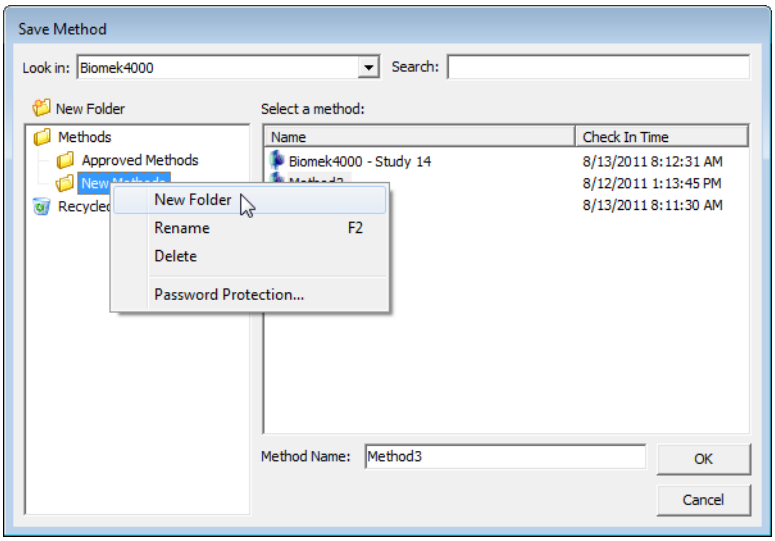
1 Complete steps 1 and 2 in *Saving a Method*.

2 Right click on the desired folder and choose **New Folder** to create a subfolder (Figure 12.18).

OR

Choose New Folder to create a new folder.

Figure 12.18 Creating a New Subfolder



NOTE Folders may be renamed or deleted by right clicking on the folder name (Figure 12.18). Methods and folders may be locked by using **Password Protection** (refer to CHAPTER 2, *Using Password Protection*).

3 Choose **OK**. The method is saved in the new folder.

To move methods between folders:

1 Click the desired folder to display the enclosed methods in **Select a method**

2 From **Select a method**, highlight the desired method to move and drag it to the desired folder. The method is moved to the desired folder.

Validating a Method

When Beckman Coulter Accounts & Permissions is enabled, methods may be validated. A validated method is a revision of a method that is saved, approved with an electronic signature, and protected from further modification. Revisions of project items required to run the validated method are checked in and protected from further modification. This ensures that validated method runs are reproducible.

Validating a revision of a method is not the same as validating a method before a run to internally test for errors before the method is actually run. To validate a method to test for errors before it is run, check **Validate the current method before running it** in **Preferences** (refer to CHAPTER 28, *Changing Display Preferences*).

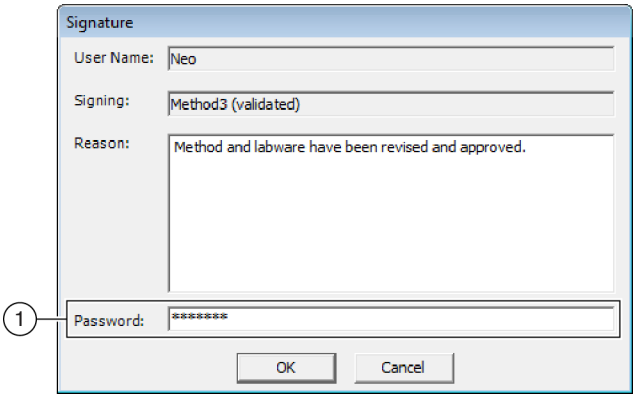
NOTE Only users with **Validate Method**s permission can validate methods. Refer to CHAPTER 1, *Using Accounts and Permissions* for more information about Beckman Coulter Accounts & Permissions. Permissions can be configured so that a user may be permitted to run only validated methods (refer to *Opening a Saved Method*).

To validate a method:

1 From the **File** menu, choose **Validate**. If the method has changed since the last revision, **Check-In** displays (Figure 12.17).

2 Refer to *Saving a Method with Accounts & Permissions Enabled*, to complete the steps necessary to save the method with the changes. **Signature** displays (Figure 12.9).

Figure 12.19 Signature



1. **Password:** Appears only when Accounts & Permissions is configured to require password checks (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

3 In **Reason**, enter a reason for the signature for the method being validated. Text entered in **Reason** is date and time stamped, and stored in the audit log of all user activity.

4 If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password** (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

5 Choose **OK** to validate the method.

OR

Choose **Cancel** to close **Signature** without validating the method.

NOTE After validating a method, it remains in development mode. To use the method in validated mode, it must be closed and then opened in validated mode. Refer to *Opening a Saved Method* for more information about opening methods in validated mode.

Signing a Method

When Beckman Coulter Accounts & Permissions is enabled, methods that are saved or validated may be signed. Signing allows users to add comments with an electronic signature to the audit trail for the method open in the editor. Signing is useful when laboratory policies require personnel to review and sign off on procedures; for example, a supervisor could approve a new validated method via the electronic signature generated by signing the method in Biomek Software.

NOTE Refer to CHAPTER 1, *Using Accounts and Permissions* for more information about Beckman Coulter Accounts & Permissions.

To sign a method:

1 Ensure the method has been saved (refer to *Saving a Method*).

2 From the **File** menu, choose **Sign. Signature** appears (Figure 12.20).

Figure 12.20 Signature



1. **Password:** Appears only when Accounts & Permissions is configured to require password checks (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

3 In **Reason**, enter a reason for the signature for the method being signed. Text entered in **Reason** is date and time stamped, and stored in the audit log of all user activity.

4 If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password** (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

5 Choose **OK** to sign the method.

OR

Choose **Cancel** to close **Signature** without signing the method.

Viewing Method History

Revision and run history for the current method can be viewed at any time. Method history is viewed in two windows:

- **History** — View all checked in and validated revisions of the current method (refer to *Viewing Revision History*).
- **Validated Run History** — View information about each validated run of the current method (refer to *Viewing Validated Run History*).

NOTE Validated methods and **Validated Run History** are available only when Beckman Coulter Accounts & Permissions is enabled (refer to CHAPTER 1, *Using Accounts and Permissions*).

NOTE Refer to *Checking Out a Revision of a Method*, to check out and run a revision of a method.

Viewing Revision History

A revision history that tracks each time the current method has been checked in or validated can be viewed when the method is open.

NOTE Methods can be validated only when Beckman Coulter Accounts & Permissions is enabled (refer to CHAPTER 1, *Using Accounts and Permissions*).

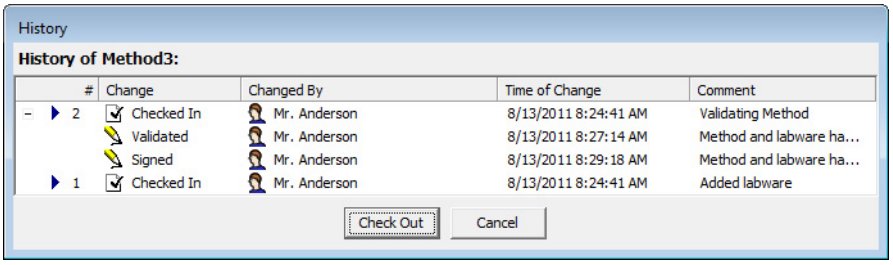
To view the history for a method:

1 From the **File** menu, choose **History. History** displays (Figure 12.21).

NOTE Revision history details are listed in a tree structure that lists information by run and type. Branches may be expanded or collapsed using the + and - buttons to the left.

The **Changed By** and **Comment** columns appear only when Accounts & Permissions is enabled.

Figure 12.21 Method History



2 When finished viewing the history, choose **Cancel** to close **History**.

Viewing Validated Run History

Validated methods run in validated mode generate a run history that can be viewed when the method is open. A run history includes access to all dialog alerts, log reports, worklists, and other files associated with or generated by the method during the run.

Many of the files listed in the run history can be viewed, saved, and printed (refer to *Viewing, Saving, and Printing Run History Details*).

NOTE Validated methods and their run history are available only when Beckman Coulter Accounts & Permissions is enabled. Refer to CHAPTER 1, *Using Accounts and Permissions* and *Validating a Method*.

NOTE Text files, such as *.csv files used by the **Worklist**, **Define Pattern**, and **Transfer From File** steps, appear in the run history and may be opened directly from the window. However, when a project or validated method is exported, they are excluded from the Biomek import (*.imp) or method (*.bmf) file. To use a *.csv file in a method exported to another system, it must be copied to the system along with the Biomek import or method file.

IMPORTANT Run information appearing in the **Validated Run History** window cannot be altered.

To view the validated run history for a method:

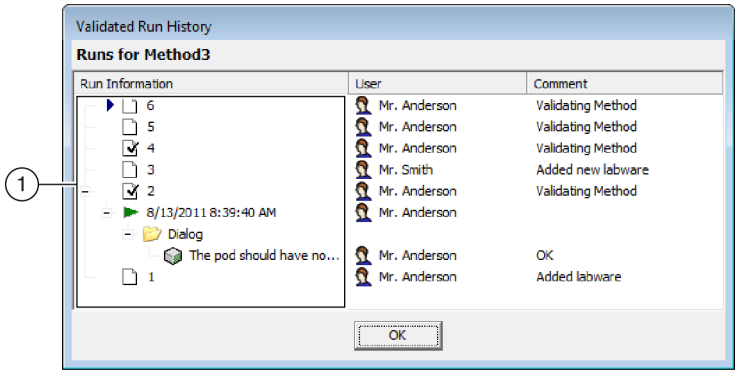
1 From the **File** menu, choose **Open** to open the method.

2 Select the method, and choose **OK**.

3 From the **File** menu, choose **Run History**. **Validated Run History** displays (Figure 12.22).

NOTE Run history details are listed in a tree structure that lists information by run and type. Branches may be expanded or collapsed using the + and - buttons to the left.

Figure 12.22 Validated Run History Displayed in Validated Mode



1. **Run History details**

4 When finished viewing the history, choose **OK** to close **History**.

Viewing, Saving, and Printing Run History Details

Many of the files listed in the run history details can be viewed, saved, and printed.

IMPORTANT Text files created using the procedures in this section are **not** protected from tampering, and, therefore, are not 21 CFR Part 11 compliant. Compliant records are available by viewing the **Validated Run History** (see *Viewing Validated Run History* for complete details).

To view and print log and other text files:

1 While in the **Validated Run History** window, right click on the desired file and choose **Open** from the menu. The file opens in **Print Preview** with printing and viewing options (Figure 12.23).

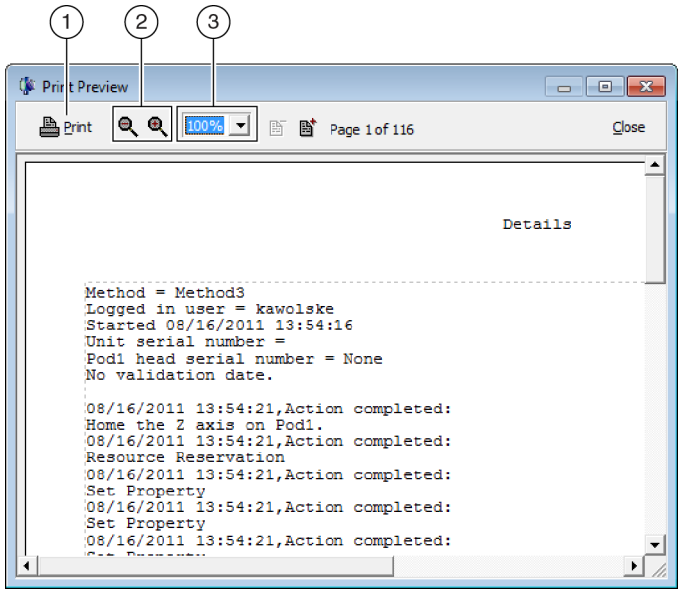
To save a file listed in the run history:

NOTE **Dialog** details cannot be viewed or saved.

1 While in the **Validated Run History** window, right click on a file and choose **Save** from the menu that appears.

2 Save files in text format by appending **.txt** to the end of the filename for best file compatibility.

Figure 12.23 Print Preview



1. **Print**
2. **Zoom in and out**
3. **Change view magnification**

Checking Out a Revision of a Method

The revisions of a method may be checked out and opened in the main editor through the revision history that tracks each time the method has been checked in or validated. The revision history of a method can only be viewed when the method is opened.

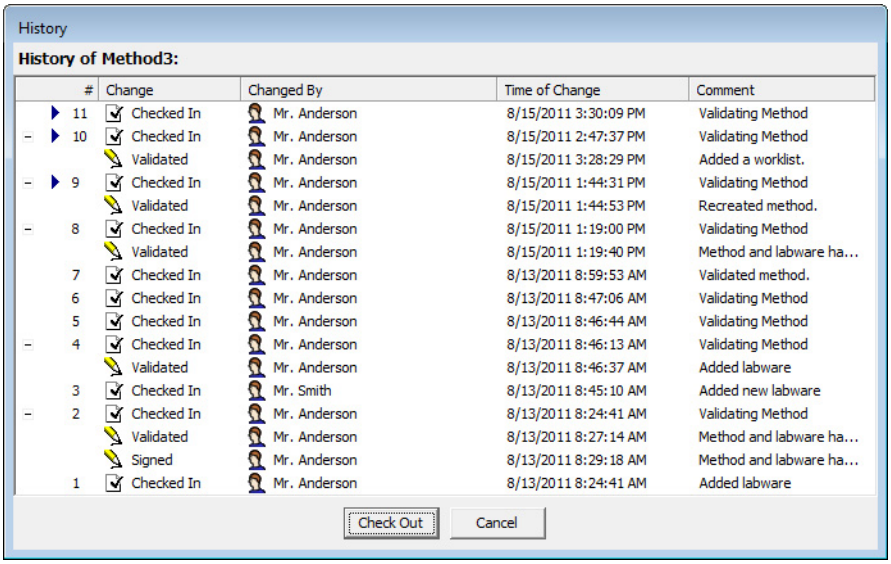
To check out a revision of a method:

1 With the method open, choose **File > History**. **History** displays (Figure 12.24).

NOTE Revision history details are listed in a tree structure that lists information by run and type. Branches may be expanded or collapsed using the + and - buttons to the left.

The **Changed By** and **Comment** columns appear only when Accounts & Permissions is enabled.

Figure 12.24 Method History



2 Click on the desired revision of the method and choose **Check Out.** The desired revision of the method opens in the main editor.

NOTE If the checked out method is revised and checked in, the revision number advances in the method title and another revision is recorded in **History**. If a validated method is checked out and a **Reason** is not entered in **Check-In** when the revision is saved, **Validating Method** displays in the **Comment** column.

Opening a Saved Method

Methods saved in a project file can be opened only in that project file. Opening a method using the Open command opens it in development mode using the current revision for all project items.

NOTE Methods may also be opened from **Recent Methods** on the **File** menu. A deleted method may be opened from the **Recycled** folder. Opening a deleted method automatically restores it.

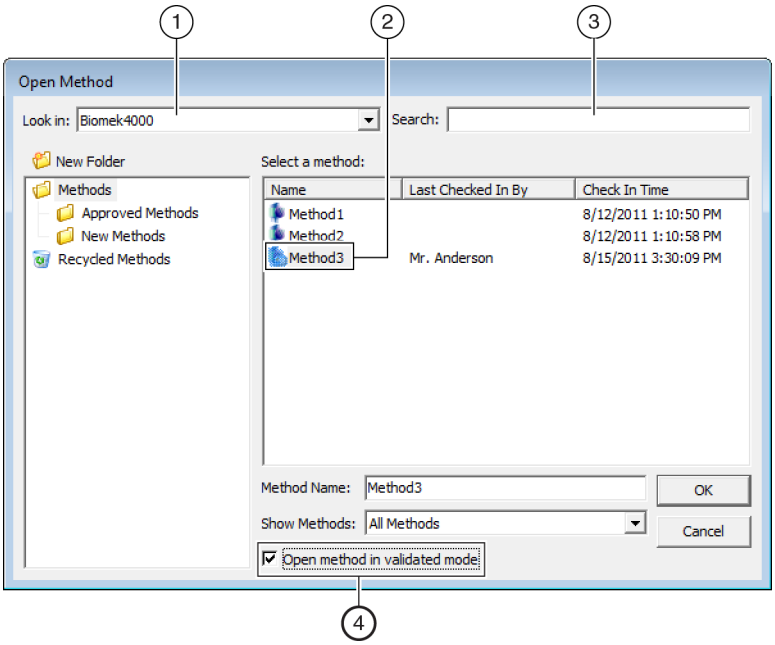
To open a saved method:

1 Choose **Open Method** on the toolbar.

OR

From the **File** menu, choose **Open**. **Open Method** displays, listing all saved methods (Figure 12.25).

Figure 12.25 Open Saved Methods



1. **Look in**: Choose the project where the desired method is stored.
2. **Validated Methods**: Available only when Accounts & Permissions is enabled.
3. **Search**: To quickly locate a method, enter the name here.
4. **Open method in validated mode**: Allows applicable methods to be opened in validated mode by users with appropriate permissions.

2 Select the desired method to open.

NOTE To quickly locate a method, enter the name in **Search** and the project under which the method is stored in **Look in**.

NOTE When Accounts & Permissions is enabled, validated methods are denoted with an ID card to represent validation (Figure 12.25). Only validated methods appear in Open Method for users that only have **Run Validated Methods** permission.

Users with **Develop Methods** permission have the option to **Open method in validated mode**. Only previously validated methods can be opened in validated mode. Methods opened in validated mode are locked and cannot be modified.

3 Choose **OK.** The selected method is opened in the main editor.

OR

Choose **Cancel** to close **Open Method** without opening a method.

Importing and Exporting Methods

Methods can be freely shared between projects or transferred between computers by exporting and importing Biomek method files. A method file is created by exporting a method from the active project, and contains the method and all records required to execute the method. This allows the method to execute correctly when the method file is imported into a different project.

NOTE When Beckman Coulter Accounts & Permissions is enabled, users with the **Run Validated Methods** or **Develop Methods** permission may export methods, but only those with the **Develop Methods** permission may import methods into a project (refer to CHAPTER 1, *Using Accounts and Permissions*).

NOTE Projects may also be imported and exported. Refer to CHAPTER 6, *Importing and Exporting Project Files*, for more information.

NOTE Unless the password is provided, methods locked via **Password Protection** may not be exported or imported (refer to CHAPTER 2, *Using Password Protection*).

This section covers:

- *Exporting a Method*
- *Exporting a Method to the Desktop*
- *Exporting All Methods Associated With a Project File*
- *Importing Methods*
- *Importing a Method from the Desktop*

Exporting a Method

The method currently open in Biomek Software can be exported to a Biomek method file (*.bmf). The method file contains all records necessary to allow the method to be imported into another project file and executed.

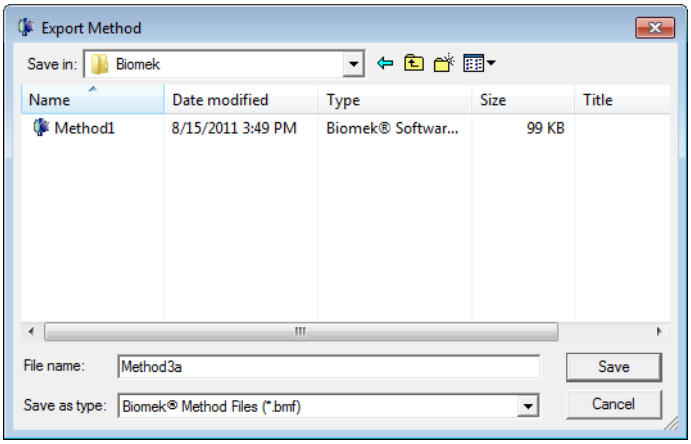
NOTE When Accounts & Permissions is enabled, users with **Run Validated Methods** or **Develop Methods** permission may export the currently open method. However, when validated methods are exported and later imported into different projects, they are no longer considered validated and open in development mode. After being imported, they can then be validated by users with **Validate Methods** permission

NOTE Text files, such as *.csv files used by the **Worklist**, **Define Pattern**, and **Transfer From File** steps, appear in the run history and may be opened directly from the window. However, when a project or validated method is exported, they are excluded from the Biomek import (*.imp) or method (*.bmf) file. To use a *.csv file in a method exported to another system, it must be copied to the system along with the Biomek import or method file.

To export the currently open method:

1 From the **File** menu, choose **Export**. **Export Method** displays (Figure 12.26).

Figure 12.26 Export Method



2 In **Save in**, browse to the desired location to save the exported Biomek method file.

3 In **File name,** enter a name for the method file.

4 Choose **Save** to export and save the method file.

Choose **Cancel** to close **Export Method** without exporting the method.

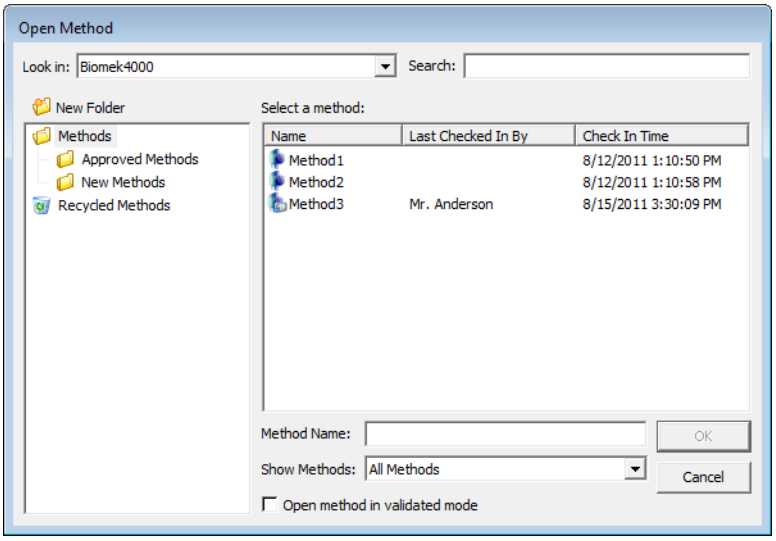
Exporting a Method to the Desktop

A method may be exported to the desktop via **Open Method**.

To export a method to the desktop:

1 From **File,** choose **Open**. **Open Method** displays (Figure 12.27).

Figure 12.27 Dragging a Method from Open Method to the Desktop



2 Highlight the desired method and drag it to the desktop. The method is exported to the desktop.

NOTE The desired folder may be exported to the desktop by dragging and dropping it from **Open Method** to the desktop.

Exporting All Methods Associated With a Project File

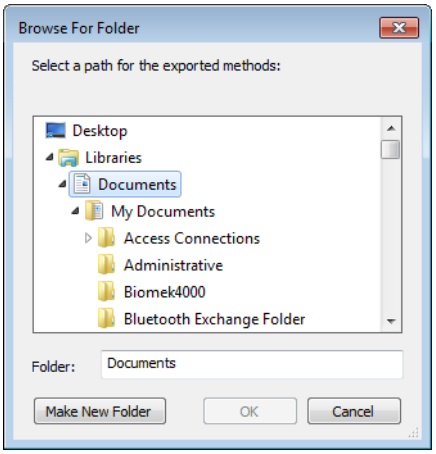
All methods associated with the currently open project file may be exported at the same time. Method files are exported to a folder selected or created by the user.

NOTE When Accounts & Permissions is enabled, users with **Run Validated Methods** or **Develop Methods** permission may export the currently open method. However, when validated methods are exported and later imported into different projects, they are no longer considered validated and open in development mode. After being imported, they can then be validated by users with **Validate Methods** permission.

To export all saved methods:

1 From the **File** menu, choose **Export All**. **Browse For Folder** displays (Figure 12.28).

Figure 12.28 Browse for Folder



2 Use the tree view to browse to the folder where the exported method files will be saved.

OR

Choose **Make New Folder** to create a new folder for the method files. The new folder appears in the tree view with the name highlighted.

3 If a new folder has been created, enter a new name for it.

OR

To change the name of an existing folder, select the folder, click on the folder name a second time, and enter the new name.

4 Choose **OK** to export all methods to the selected folder.

OR

Choose **Cancel** to stop the operation without exporting any methods.

Importing Methods

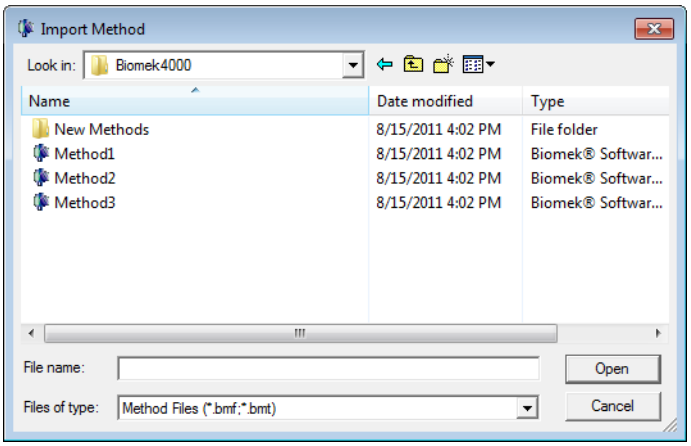
Biomek method files previously exported from a project file can be imported into the currently active project file. Importing a method file also imports all the necessary records to execute the method.

Multiple methods can be selected and imported simultaneously.

To import methods into the project file:

1 From the **File** menu, choose **Import**. **Import Method** displays (Figure 12.29).

Figure 12.29 Import Method



2 In **Look in**, browse to the location where the desired Biomek method file(s) is saved.

3 Select the desired method file(s) to import. To import several method files, hold the Ctrl key while selecting each method desired to import.

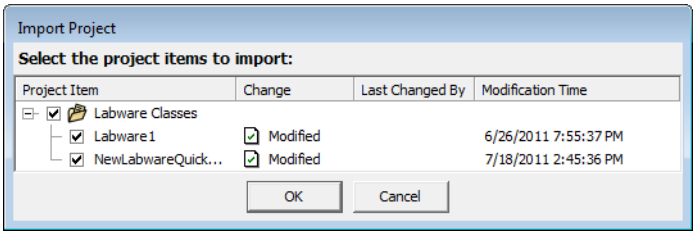
4 Choose **Open** to import the selected method file(s).

OR

Choose **Cancel** to close **Import Method** without importing the method file.

5 Choose **Yes** to confirm the desired method file is selected. If new project items have been added or project items have changed, **Import Project** displays (Figure 12.30).

Figure 12.30 Importing Project Items



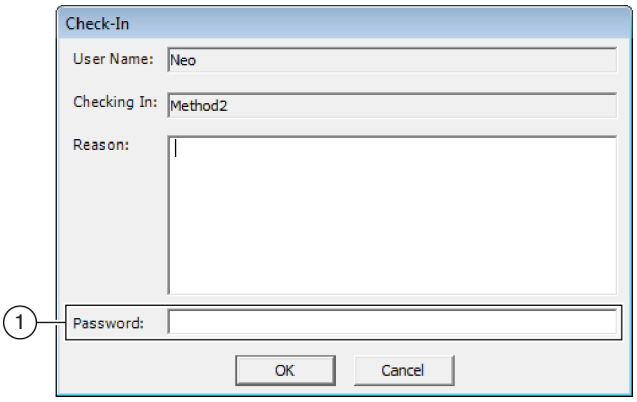
6 Choose **OK** to import all of the checked project items.

OR

Uncheck the project items that are not to be imported and choose **OK**. If Accounts & Permissions is enabled, **Check-In** displays (Figure 12.31).

NOTE To deselect all project items, right click in **Import Project** and choose **Select None**.

Figure 12.31 Checking in a Method



1. **Password:** Appears only when Accounts & Permissions is configured to require password checks (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

7 In **Reason**, enter a reason for the check-in. Text entered in **Reason** is date and time stamped, and stored in the audit log of all user activity.

8 If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password** (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

9 Choose **OK** to import the method.

OR

Choose **Cancel** to close **Check-In** without importing the method.

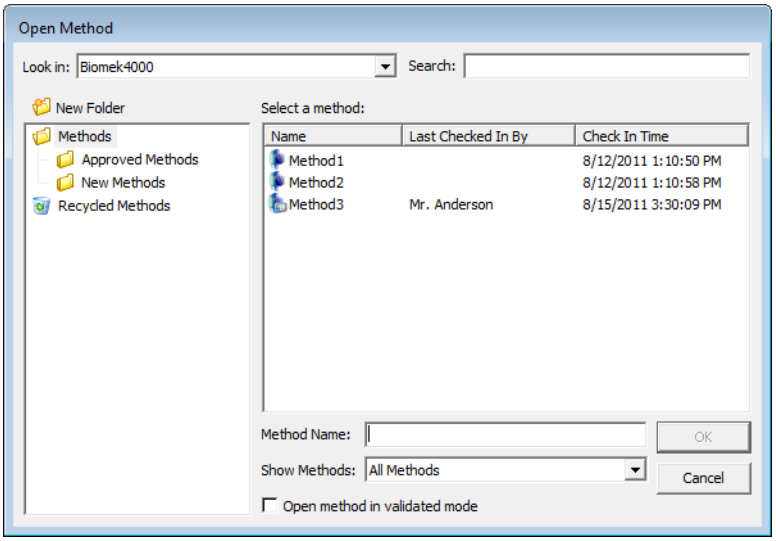
Importing a Method from the Desktop

A method may be imported from the desktop via **Open Method.**

To import a method from the desktop

1 From **File,** choose **Open. Open Method** displays (Figure 12.32).

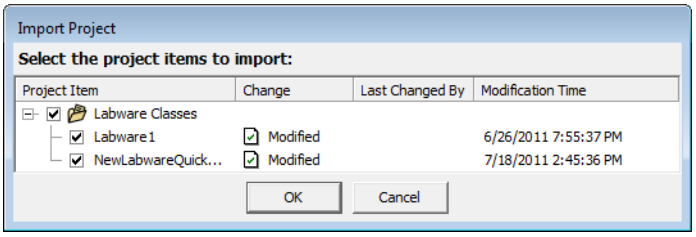
Figure 12.32 Dragging a Method from the Desktop to Open Method



2 From the desktop, choose the desired method and drag and drop it to **Open Method.** If new project items have been added or project items have changed, **Import Project** displays (Figure 12.33).

NOTE The desired folder may be imported from the desktop by dragging and dropping it from the desktop to **Open Method**.

Figure 12.33 Importing Project Items



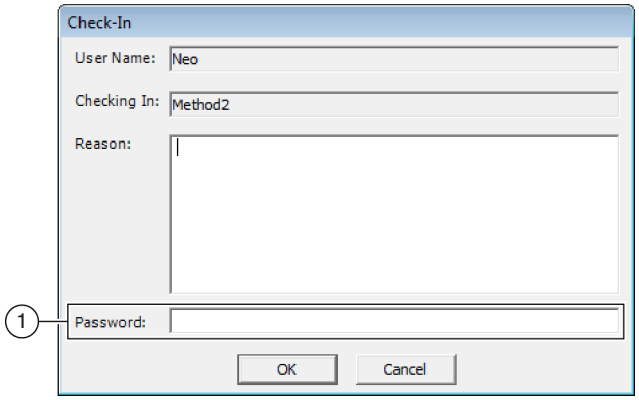
3 Choose **OK** to import all of the checked project items.

OR

Uncheck the project items that are not to be imported and choose **OK**. If Accounts & Permissions is enabled, **Check-In** displays (Figure 12.34).

NOTE To deselect all project items, right click in **Import Project** and choose **Select None.**

Figure 12.34 Checking in a Method



1. **Password:** Appears only when Accounts & Permissions is configured to require password checks (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

4 In **Reason,** enter a reason for the check-in. Text entered in **Reason** is date and time stamped, and stored in the audit log of all user activity.

5 If Accounts & Permissions is configured to require password checks for signing and check-in, enter the user **Password** (refer to CHAPTER 1, *Installing and Setting the Level of Support for Accounts and Permissions*).

6 Choose **OK** to import the method.

OR

Choose **Cancel** to close **Check-In** without importing the method.

Deleting and Restoring Methods

Methods may be deleted, but are not completely removed and may be restored at any time.

Deleting Methods

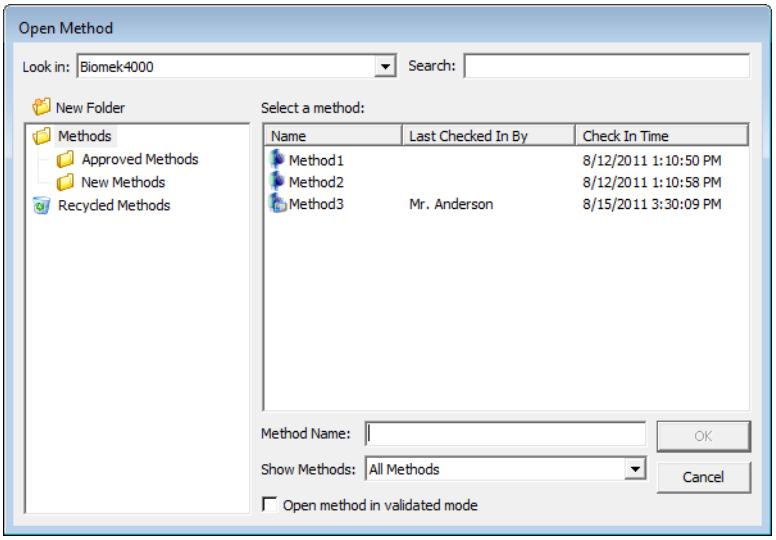
To delete a saved method:

1 Choose **Open Method** on the toolbar.

OR

From the **File** menu, choose **Open**. **Open Method** displays, listing all saved methods (Figure 12.35).

Figure 12.35 Open Saved Methods



2 Right click the desired method to delete and select **Delete**. The method is placed in **Recycled Methods**.

OR

Drag the desired method to delete to **Recycled Methods**.

Restoring Methods

To restore a deleted method:

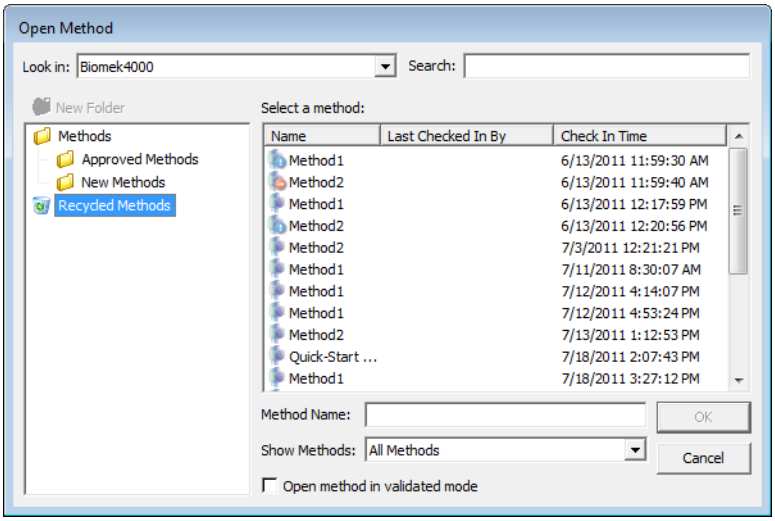
1 Choose **Open Method** on the toolbar.

OR

From the **File** menu, choose **Open. Open Method** displays, listing all methods saved in the project file (Figure 12.35).

2 Choose **Recycled Methods** on the left side of **Open Method** to display all the methods that have previously been deleted (Figure 12.36).

Figure 12.36 Recycled Methods



3 Right click the desired method to restore and choose **Restore**. The method is moved from **Recycle Methods** to **Methods**.

OR

Drag the method to the desired folder.

NOTE A method may be opened directly from the **Recycled** folder by selecting the method and choosing **OK**.

Running, Pausing, and Stopping a Method

Methods may be run on the instrument or in simulation mode immediately after they are built. If desired, methods may be configured to check for internal errors and confirm that labware on the instrument deck matches the layout specified in the method before every run.

This section covers:

- *Running a Method*
- *Pausing a Method in Progress*
- *Stopping a Method in Progress*
- *Disabling Steps Within a Method*

Running a Method

After a method has been built, it may be run immediately on the instrument or in **Simulate** mode. In simulate mode, the software runs the method and checks for configuration errors in each step. While the method is running, the Biomek Simulator shows an animated 3-D model of the instrument performing the method.

When simulate mode is chosen, validated methods run in validated mode are recorded in **Run History**. Validated methods run in development mode are not logged. Validated methods are only available when Accounts & Permissions is enabled.

NOTE When Beckman Coulter Accounts & Permissions is enabled, only users with **Develop Methods** or **Run Validated Methods** permission may run methods. Users with **Develop Methods** permission may run any method saved on the system; users with **Run Validated Methods** permission may only run validated methods. Refer to CHAPTER 1, *Biomek Software Permissions* for more information about the permissions available to users of Biomek Software.

To run a Biomek 4000 method:

1 From **Hardware Setup** in **Port**, choose:

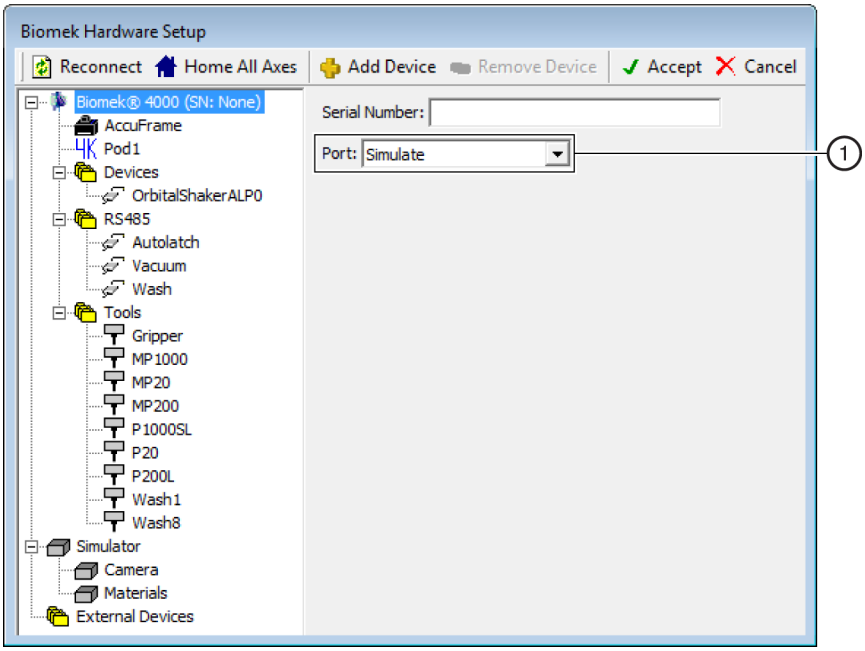
- **Simulate** to run the method in simulated mode (Figure 12.37).

  OR

- **COM(x)** (where *x* is the port number to which the Biomek 4000 instrument is connected, for example, "COM5") to run the method on the instrument.

  NOTE The list of communication ports will vary depending on the number of available ports on your instrument.

Figure 12.37 Port Field in Hardware Setup



1. **Port** field

2 If running the method on the instrument, from the **Instrument** menu, choose **Home All Axes** to home the pod, if necessary. The pod must be homed before performing methods each time the instrument is powered on.

NOTE Refer to the instrument hardware manual for more information about homing the pod.

3 To start the method run, on the toolbar, click the **green arrow** button.

OR

From the **Execution** menu, choose **Run**.

The method run begins. Depending on how Biomek Software is configured, two events may precede the execution of steps in the method:

- If **Validate Before Run** is selected in **Options > Preferences**, the method is validated internally to check for errors (refer to CHAPTER 28, *Configuring General Options*).

  NOTE Validating the method for errors is a different process from validating a revision of a method when Accounts & Permissions is enabled. Refer to *Validating a Method* for more information about validating a revision of a method.

- If **Pause to confirm setup?** is selected in the **Instrument Setup** step, a deck confirmation prompt displays (Figure 12.38).

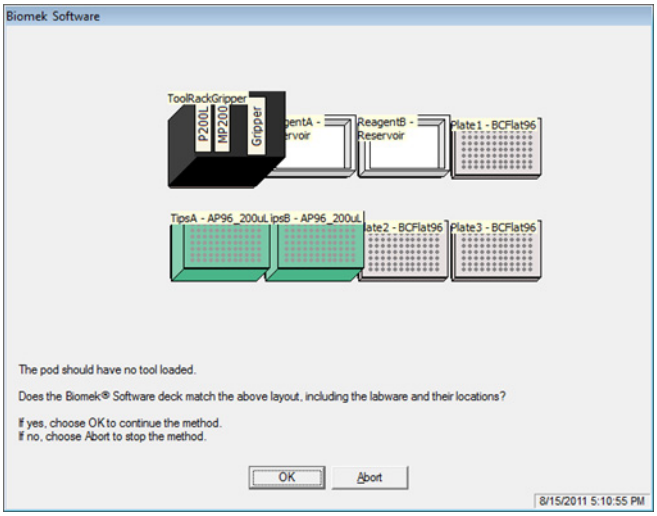
⚠ CAUTION

Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose each ALP correctly in the software may result in collisions between the pod and ALPs during operation.

To confirm that the deck setup is correct:

1 Visually confirm the deck setup on the instrument matches the display.

Figure 12.38 Deck Layout Confirmation Prompt for a Biomek 4000 Method



2 Choose **OK** if the setup is acceptable.

OR

Choose **Abort** to close the deck confirmation prompt and cancel the method run.

NOTE To set up the deck correctly, either set up labware on the instrument deck to match the layout displayed in the deck confirmation prompt, or change the Deck Layout in the **Instrument Setup** step (refer to CHAPTER 15, *Populating the Deck with Labware and Tools*).

The method runs as soon as the deck setup is confirmed. The method run can be visually followed in the Method View; steps are highlighted in green as they are executed.

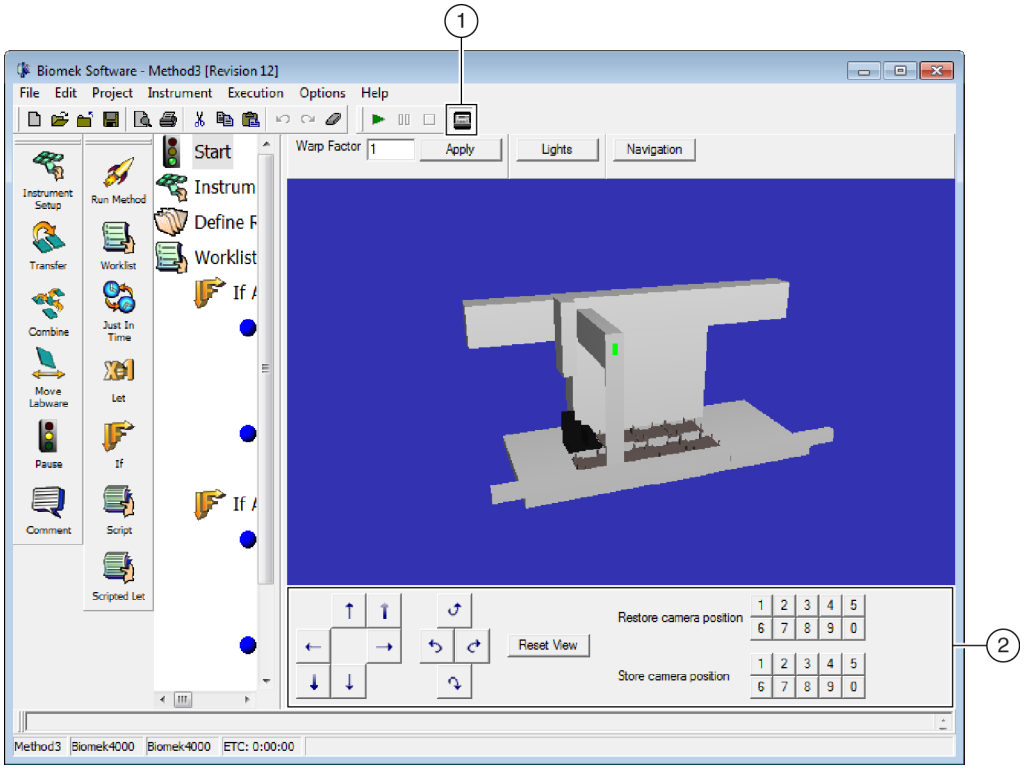
When a method runs in simulate mode, the Simulator appears and shows a 3-D animation of the method being performed (refer to *Viewing the Method Run In the Biomek Simulator*).

NOTE If Accounts & Permissions is configured to automatically log off users after a set period of operating system inactivity, the possibility exists that a user may be logged off automatically during a method run. When a user is logged off, the method run continues, but any prompts, such as the deck layout confirmation (Figure 12.38), are hidden from view until the same user, or another user with permission to run methods, logs on.

Viewing the Method Run In the Biomek Simulator

When a method is run in simulate mode, the Biomek Simulator appears and shows an animated 3-D model of the instrument performing the method (Figure 12.39).

Figure 12.39 The Biomek 4000 Simulator Showing a Method Run



1. **Simulation Display:** Toggles the Biomek 4000 Simulator on and off during a method run.
2. **Camera Navigation:** Buttons appear when enabled in **Hardware Setup** or when toggled on in the simulator controls (refer to *Using the Simulator Controls*).

Five methods of controlling the simulator view are available:

- From the toolbar, choose (**Simulation Display**) to toggle the Biomek 4000 Simulator on and off while the method is executing.

  NOTE The simulator automatically launches when the method run begins and closes when it is finished. If the animation does not run smoothly, try reducing the image quality setting in **Hardware Setup** (refer to CHAPTER 4, *Configuring Simulator Settings*).

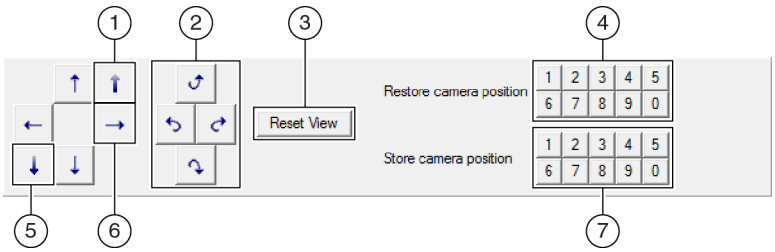
- Change the view by placing the cursor in the simulator display, then clicking and dragging the mouse in the desired direction of rotation.
- Change the view by clicking the cursor in the simulator display and using the keyboard control keys defined in **Camera** (refer to CHAPTER 4, *Configuring Camera Controls*).

- Use the camera navigation controls to change, save, and reset the view (Figure 12.40). The navigation controls are displayed when enabled in **Hardware Setup** or when toggled on using the simulator controls (refer to *Using the Simulator Controls*).

  NOTE Additional simulator parameters may also be configured in **Hardware Setup** (refer to CHAPTER 4, *Configuring the Biomek 4000 Simulator*).

- Press the tilde **(~)** key to access the simulator controls (refer to *Using the Simulator Controls*). The simulator controls provide the ability to change the simulation playback speed, toggle the camera navigation controls on and off, and modify the lighting that illuminates the simulated instrument.

Figure 12.40 Camera Navigation Buttons



1. **Move In**: Moves the instrument closer.
2. **Rotate camera position**: Rotates the camera in the indicated direction
3. **Reset View**: Restores the default view.
4. **Restore camera position**: Choose a position to show the view stored in that position.
5. **Move out**: Moves the instrument further away.
6. **Move camera position**: Moves the camera position in the indicated direction.
7. **Store camera position**: Choose a position to save the current view. Up to ten positions may be saved.

Using the Simulator Controls

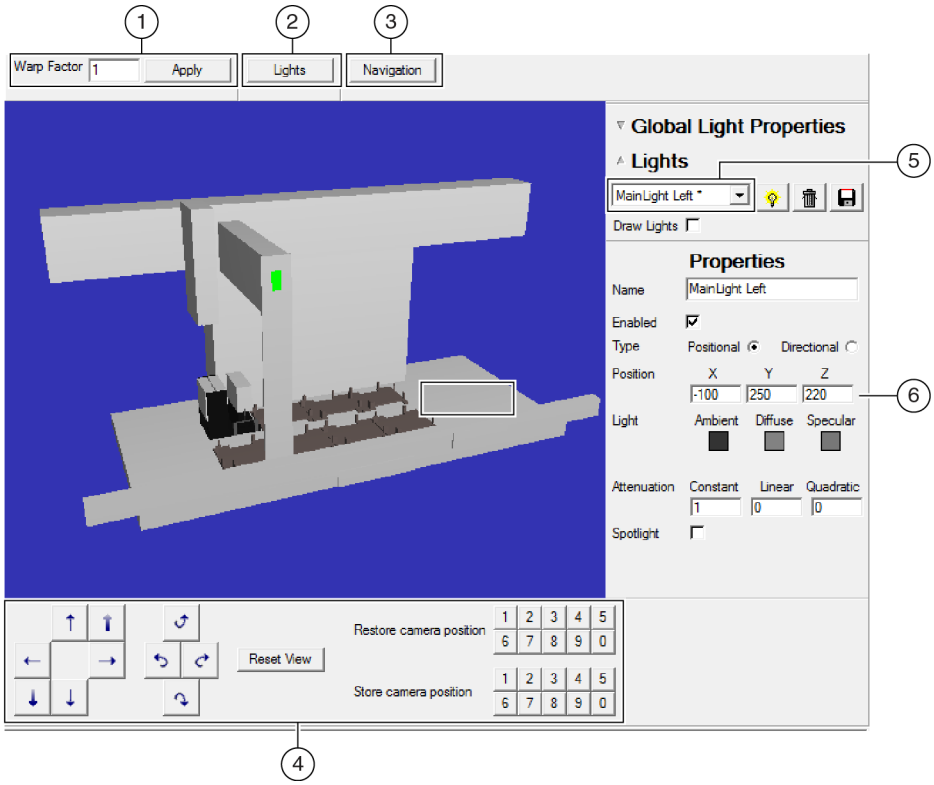
The simulator controls provide the ability to change the simulation playback speed, toggle the camera navigation controls on and off, and modify the lighting that illuminates the simulated instrument.

To access and use the simulator controls:

---

1 During a simulated method run, press the tilde **(~)** key to toggle the simulator controls on. The simulator controls appear (Figure 12.41).

Figure 12.41 Biomek Simulator with All Simulator Controls Enabled



1. **Warp Factor**
2. **Lights**
3. **Navigation**
4. **Navigation Controls**
5. **Light currently being configured**
6. **Lighting Controls**

---

2 Enter a new **Warp Factor** and choose **Apply** to change the simulator playback speed, if desired. **Warp Factor 1** runs the simulation in real time, **Warp Factor 2** at twice normal speed, and so on.

---

3 Choose **Lights** to toggle the lighting controls on, if necessary.

4 Create a new light or choose an existing light from the pull-down menu, and use the lighting controls to modify the lighting properties as desired. Table 12.2 provides a description of each lighting control.

NOTE Modifying the lighting parameters is not recommended because the default parameters cannot be restored if changed or deleted.

5 Choose **Navigation** to toggle the camera navigation controls on, if necessary. Refer to *Viewing the Method Run In the Biomek Simulator*, for detailed information about using the navigation controls.

6 Press the tilde **(~)** key to toggle the simulator controls off, if desired.

Table 12.2 Stimulator Lighting Controls

Control	Description	Additional Information
Global Light Properties		
Local View	Select to subtly change the intensity of light.	
Global Ambient	Choose the color of ambient light present in the simulator view.	
Lights		
 (**new light**)	Create a new light.	
 (**delete light**)	Delete the light currently selected in the pull-down menu.	A light that has been deleted cannot be restored.
 (**save light**)	Save the configuration of the light currently selected in the pull-down menu.	
Draw Lights	Select to display the light sources in the simulator view.	
Properties		
Name	Change or enter a new name for the selected light.	
Enabled	Select to enable (turn on) the selected light.	
Type	Choose the type of light: **Positional** or **Directional**.	Positional light radiates from the source in all directions; directional light radiates from the source in a single direction.

Table 12.2 Stimulator Lighting Controls *(Continued)*

Control	Description	Additional Information
Direction	Enter X, Y, and Z coordinates for the direction from which the selected light is directed at the instrument.	
Light	Choose colors for the **Ambient**, **Diffuse**, and **Specular** properties of the light.	**Ambient** and **Diffuse** define the color of the 3-D model of the instrument when the light is enabled. **Specular** defines the color of specular highlights (glare).
Attenuation	Enter values in each field to define the fall off from the center of the light.	Available only when **Positional** is the type of light selected. Entering higher values causes the light to fall off quicker.
Spotlight	Choose to cast a tightly focused beam of light at the 3-D model of the instrument.	Available only when **Positional** is the type of light selected
Spot Direction	Enter **X, Y**, and **Z** coordinates for the direction from which the spotlight is directed at the instrument.	Available only when **Spotlight** is the type of light selected.
Spot Exponent	Enter a value to set the focus of the spotlight.	Available only when **Spotlight** is the type of light selected. A low value distributes the light evenly across the illuminated area; a high value concentrates more light in the center of the spotlight.
Spot Cutoff	Enter a value to set the size of the spotlight cone, which determines the total surface area covered by the spotlight.	Available only when **Spotlight** is the type of light selected.

Pausing a Method in Progress

Pause causes the method to halt after the instrument has completed the move in progress. For example, if the instrument is in the process of loading tips when **Pause** is selected, it finishes loading the tips before the system halts. When the method is resumed, it continues as though it were never halted.

NOTE A method cannot be edited during a pause.

Use one of the following procedures to pause a method:

⚠ CAUTION

To avoid equipment damage and/or hazardous waste spills, no changes to the Biomek 4000 state are permitted while a method is paused. Changes can be made to the labware contents, but not the deck or the devices.

1 From the **Execution** menu, choose **Pause**.

OR

Choose  on the toolbar. The instrument completes the move in progress and stops.

Stopping a Method in Progress

Use **Stop** to halt a method during its run when there is no intent to resume method execution. If the pod is in the process of a move, the operation is not completed. Since the method is halted, this option allows edits to the method or changes to the hardware and deck.

NOTE **Stop** may not halt operations already in progress on external devices.

Use one of the following procedures to stop a method during a run:

1 From the Execution menu, choose **Stop**.

OR

Choose  on the toolbar.

OR

Press the STOP button on the front of the instrument.

NOTE Use standard procedures to rerun the method.

Disabling Steps Within a Method

Individual steps within a method can be disabled for execution. When the method is run, Biomek Software ignores any disabled steps.

Disabling steps is useful for experimenting with the configuration of certain steps during method development, or when only a subset of the steps in a method needs to be executed in a method run for an assay.

NOTE If a method is checked out in validated mode, steps cannot be disabled or enabled.

To disable a step in a method:

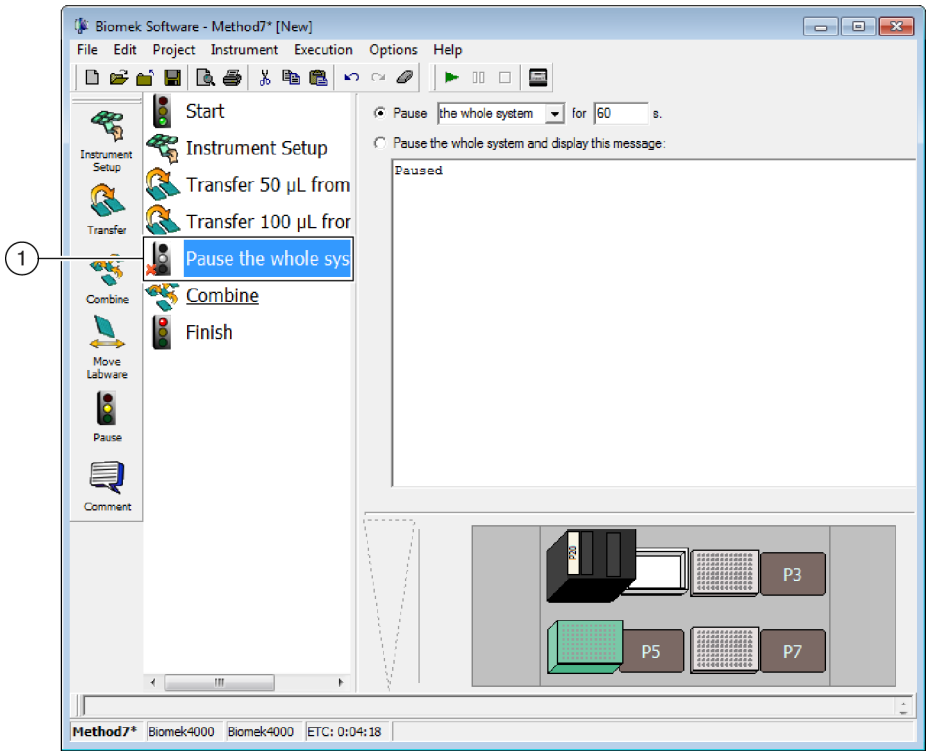
1 Select the desired step to disable.

2 From the **Edit** menu, choose **Disable step**.

OR

Right click the step and choose **Disable step** from the menu. The step icon changes to grayscale with a red **X** to indicate the step is disabled.

Figure 12.42 Step Disabled in Method View



1. **Disabled step**: Disabled step icon displayed in grayscale with red X.

To enable a previously disabled step:

1 Select the disabled step to enable.

2 From the **Edit** menu, choose **Enable step**.

OR

Right click the step and choose **Enable step** from the menu. The red **X** disappears and the step icon changes to color to indicate the step is enabled.

Printing a Method

Printing a hard copy of a method is useful if a computer monitor is some distance from the instrument, it is necessary to show the method steps to someone away from the lab, or a hard-copy record of the method is needed to recreate the method. All of the step configurations are listed in the hard copy.

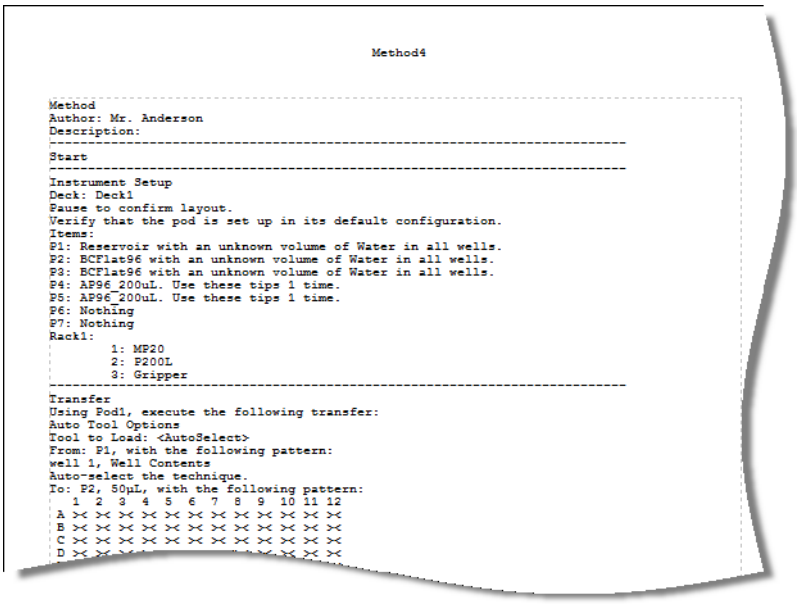
To print a Biomek method in sequential text form:

1 Select the **File** menu.

2 Choose **Print**. A print-out similar to Figure 12.43 is produced at the default printer.

NOTE Use **Print Preview** from the **File** menu to open a dialog which displays how the method appears when printed.

Figure 12.43 Printed Method



Improving a Method

Biomek provides procedures that allow a method to be observed in order to make adjustments to improve the way it runs.

Here are two procedures to improve the way a method runs:

- *Running the Method at Slow Speed*
- *Using Logging*

Running the Method at Slow Speed

To slow down the pod speed to provide more time to examine the method in progress:

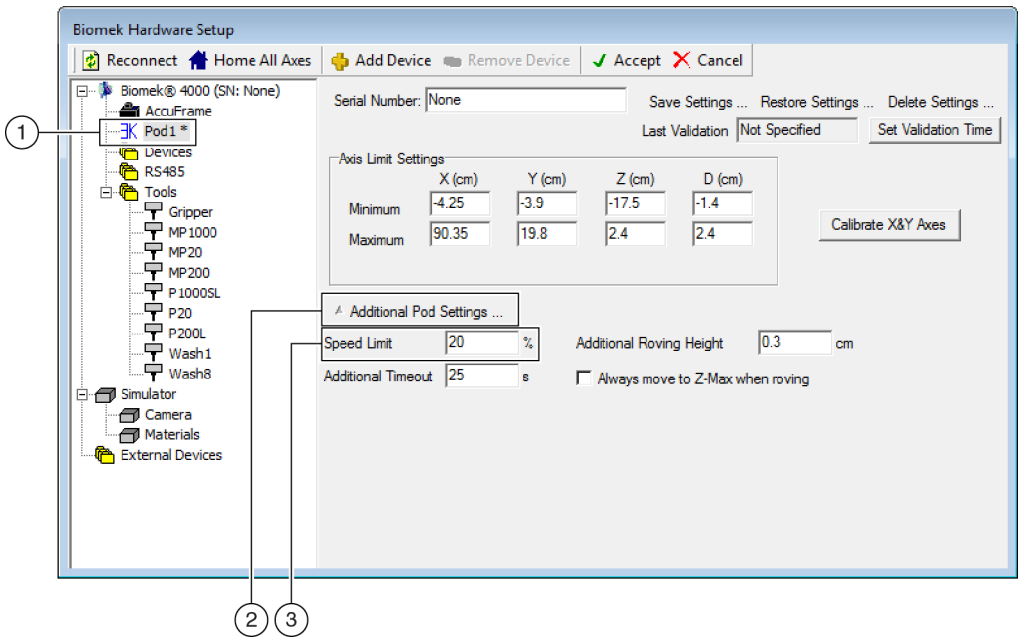
1 From the **Instrument** menu, choose **Hardware Setup. Hardware Setup** displays (Figure 12.44).

2 On the left side of **Hardware Setup**, select the desired pod.

3 Expand the **Additional Pod Settings.**

4 Set the **Speed Limit** to **20%.** This is the recommended speed for observing a method as it runs (Figure 12.44).

Figure 12.44 Changing the Method Speed in Hardware Setup



1. **Selected Pod**
2. **Additional Pod Settings (expanded)**
3. **Speed Limit**

5 Choose **Accept** to save the changes and close **Hardware Setup.**

6 From the **Execution** menu, choose **Run** to start the method.

NOTE Another way to run the method slowly is to use **Single Step** on the **Execution** menu. **Single Step** allows the unit to move one operation at a time by clicking the launch button for each move. Refer to CHAPTER 24, *Performing Single Operations Within Steps*, for more information about using **Single Step**.

Using Logging

Text format logs are used for close examination of every operation that occurs during method execution in order to modify the run to improve the method. These generated logs give detailed information, including the date and time.

There are several logs available in Biomek Software:

- **Details** — Provides comprehensive information on every operation the instrument performs.
- **Errors** — Lists errors for a method, if any.
- **Pipetting** — Lists aspirate and dispense operations.
- **UnifiedPipetting** — Captures pipetting operations, along with Sample IDs for wells, including information on where the aspirate or dispense operation occurs.
- **UnifiedTransfer** — Captures transfer operations, along with Sample IDs for wells, including information on the source and destination labware.

To turn logging on or off:

1 From the toolbar, choose **Options**.

2 Choose **Log Configuration**.

3 Check or uncheck the desired **Log(s)**.

NOTE Refer to CHAPTER 25, *Generating and Using Log Data*, for more information on generating and using log data.

CHAPTER 13

Using Variables and Expressions in a Method

Overview

A variable is a value that has been assigned a name. A value can contain text strings, arrays, expressions, objects, operators, or numerical constants. Any value assigned a name can be referenced repeatedly during a method by inserting the variable name in any applicable field in a step configuration.

An expression is a one-line combination of alphanumeric characters and/or variables combined using mathematical operations. An expression can be used anywhere a variable can be used, and it may use one or more variables.

Advantages to using variables include:

- Several variables can be created in one step; for example, the **Start** step can be used to define multiple variables that are available to every step within a method, while the **Let** and **Worklist** steps can be used to create multiple variables that can be used by their substeps.
- Several variables can be used in one step.
- A name can be entered as a variable or expression in any step configuration field where the value associated with the variable or expression is required. Biomek Software then interprets the variable or expression and replaces it with the associated value.
- A variable can be used as many times as necessary; for example, multiple steps within **Let** and **Loop** steps can all use the same variable.

  NOTE To make variables available to all steps in a method, define the variables in the **Start** step.

- Variables used extensively in a method need only be changed in the step in which they are defined to change the value in every step in the method that uses the variable.
- When a method is run more than once, the value associated with that variable can be changed in the step, and the associated values within the method automatically change accordingly.

Using Variables

A variable consists of a name and a value. To use a variable, enter an equal sign (=) followed by the variable name into the step configuration requiring the variable. For example, in Figure 13.1, the variable **=AspValue**, created in the **Start** step configuration of the method (Figure 13.2), is entered in the **Volume** field.

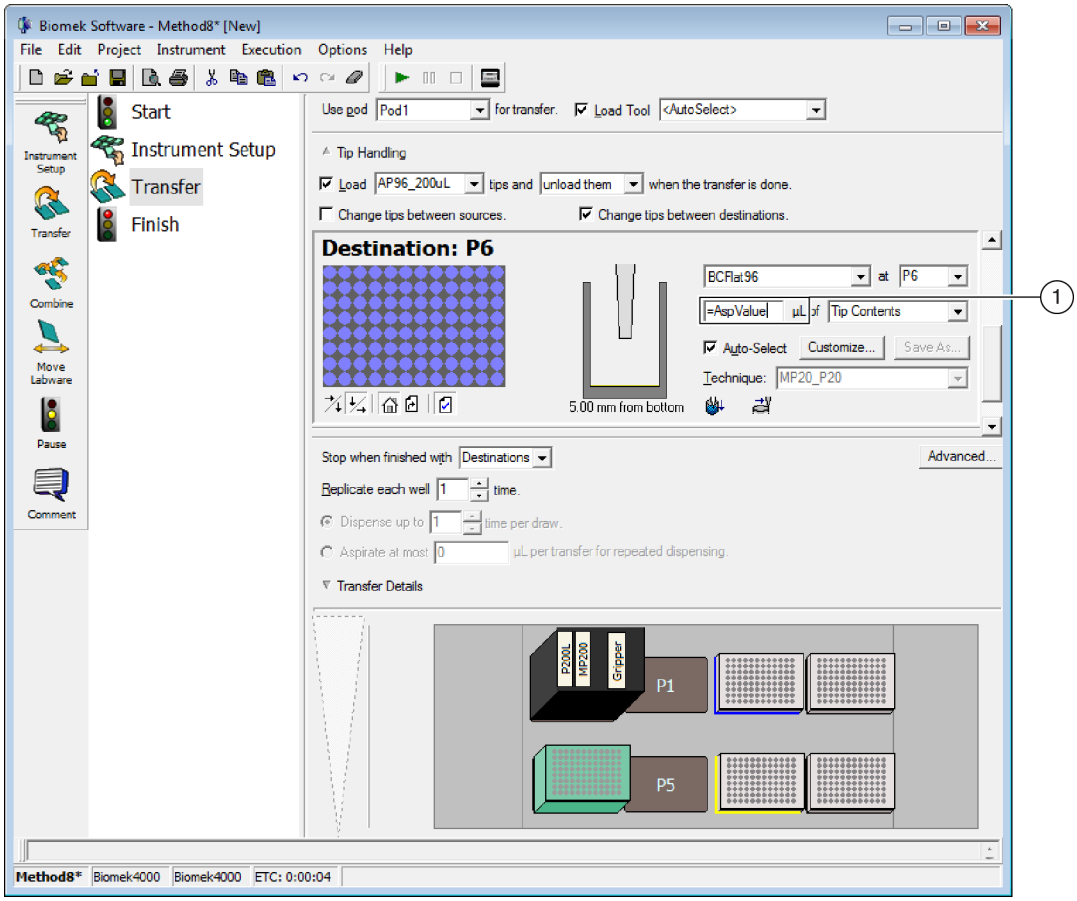
Biomek Software internally substitutes the name with its value, but the name remains in the field. In the example, the variable **AspValue** is substituted internally by the value 25. The value of 25 is never displayed, only the variable name.

Variable values are not assigned a unit of measure. When a variable is identified in a step, the unit of measure is defined by the requirements of the step. For example, if a variable named **AspValue** is assigned a value of 5, and **=AspValue** is entered in a field that requires microliters, the software interprets the value of 5 as 5 microliters; likewise, if **=AspValue** is entered in a field that requires seconds, the software interprets the value as 5 seconds.

NOTE If a variable is used in a pipetting step with an auto-selected technique, and the value of the variable changes such that a new technique would be selected, the technique is automatically updated when the step is executed.

NOTE Enter the variable name preceded by the equal (=) sign in any field where the value it represents is appropriate.

Figure 13.1 Transfer Step Using the AspValue Variable



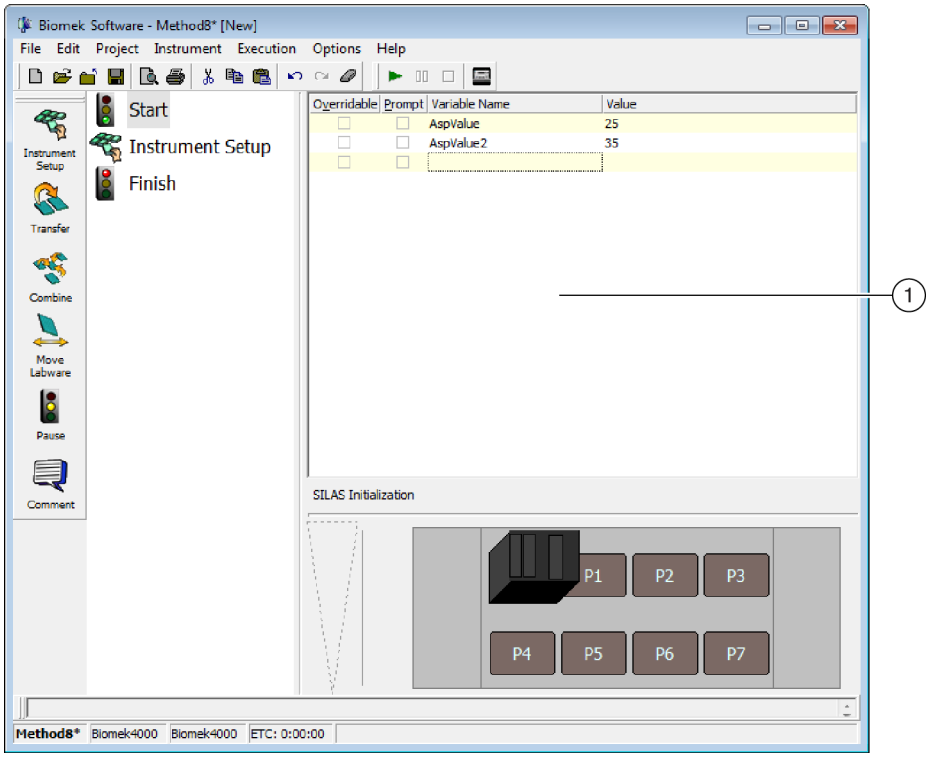
1. **Using a variable to specify volume**

Creating Variables

Variables may be created in several steps. Refer to the section for the step for more specific information on creating variables with that step:

- CHAPTER 12, *Configuring the Start Step*
- CHAPTER 16, *Loop Step*
- CHAPTER 17, *Run Method Step*
- CHAPTER 17, *Worklist Step*
- CHAPTER 17, *Let Step*
- CHAPTER 20, *Create Group Step*
- CHAPTER 20, *Set Global Step*
- CHAPTER 20, *Define Procedure Step*
- CHAPTER 20, *Run Program Step*

Figure 13.2 Variables Configured in the Start Step



1. **Variables defined in the Start step can be used in any step within the method.**

Using Variables in a Method

To use a variable created previously in the method, the variable name is entered into the configuration of the step. In the example, the variable **AspValue**, created in the **Start** configuration (Figure 13.2), is entered in the **µL** (volume) field of the **Transfer** step (Figure 13.3).

NOTE Enter the **Variable Name** in any field where the value it represents is appropriate.

Biomek Software internally substitutes the name with its value, but the name remains in the field. In the example (Figure 13.2), **AspValue** is substituted internally by the value **25**. The value of **25** is never displayed, only the variable name **AspValue**.

Variables previously configured in any step may be used in any field where the value of the variable is a valid value for the field. For example, a variable with a value of 50 would be appropriate in a **Volume** field, but not in a field asking for a deck position.

Any variables used in a method must be defined prior to the step in which they are used, or an error occurs. For example, if the variable **AspValue** is not defined when it is entered in the **Transfer** step, an error results.

NOTE Keep this in mind when writing a method that will be run in another method using the **Run Method** step. If the **Run Method** step in the other method specifies any variable values, those variables must be created in the method for method validation. When the method is run through the **Run Method** step, it is run using the variable values specified in the **Run Method** step.

NOTE Variables created with some steps are only applicable for that step and its substeps. For example, a variable created with a **Let** step may only be used for substeps of the **Let** step.

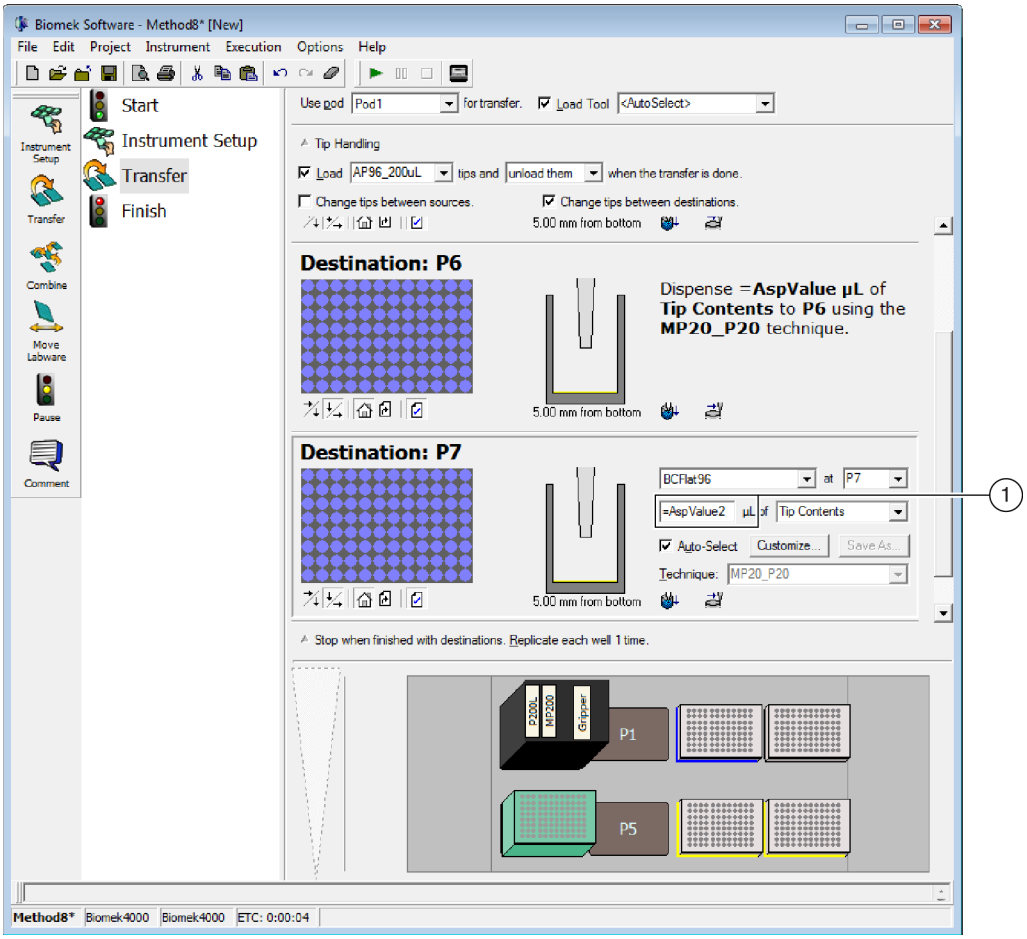
To use a previously created variable in a step configuration:

1. Select the appropriate field in the desired step configuration.

2. Enter the variable name, preceded by an equal sign. For example, **=AspValue** in the **Volume** field of the **Transfer** step (Figure 13.3) indicates that a volume equal to the value of the variable **AspValue** is dispensed in the selected destination labware.

   NOTE Variables may be used in any field which the value is a valid entry. For example, a variable that has a text value cannot be entered in a field that is expecting a numerical input.

Figure 13.3 Transfer Step Using the AspValue and AspValue2 Variables Defined in the Start Step



1. **Using variables defined in the Start Step.**

Using Expressions

An expression is a one-line combination of variables, such as **AspValue**; mathematical operators, such as addition (+); string constants, such as "P4"; and numeric constants. An expression can be used anywhere a variable can be used and may contain one or more variables; for example, the variable **ReservoirVolume** can be calculated from the number of samples. The variable **ReservoirVolume** is an expression, such as, "**Samples*50**" or "**Samples*SampleVol+DeadVolume.**"

Like variables, expressions start with an equal sign. Expressions can contain operators allowed in VBScript programming, such as addition (+), division (/), exponentiation (^), concatenation of strings (&), and functions like random (Rnd), rounding (Round), or absolute value (Abs).

An expression can be entered in any step configuration field where the value associated with the expression is appropriate. Biomek Software interprets the expression and replaces it with the associated value.

Three examples of expressions are:

- If a variable called **my_volume** is defined, transferring from a 96-well microplate to each quadrant of a 384-well microplate could be accomplished by placing **=my_volume / 4** in the volume field.
- If the three variables **VolumeA**, **VolumeB**, and **VolumeC** are defined to represent the volumes transferred to a destination microplate from three different sources, mixing the entire contents of the destination microplate could be accomplished by configuring a **Mix** step using the expression **= VolumeA + VolumeB + VolumeC** in the volume field.
- In a **Loop** step, a variable called **count** is created and appended to the letter "P" in a step configuration as the expression **= "P" & count**. If the **Loop** is configured to start at 1 and end at 10, the **Loop** results would be P1, P2, ..., P10. This could be used to perform the same operation on multiple plates located at ALP positions named P1, P2, ..., P10.

CHAPTER 14

Using Sample Tracking and Data Sets in a Method

Overview

Sample tracking means the contents of the plate or tube are known at any time in the method and decisions may be made during transfer or pipetting operations based on the contents of the plate or tube.

Sample tracking is possible in Biomek Software using data sets, which store specific information about wells or tubes (refer to *Data Set Definition*).

Sample Tracking

Sample tracking allows information about a sample in an individual well to be moved along with the sample when it is moved to another well. Sample tracking is enabled through the following functions of Biomek Software:

- association of a sample ID with wells or tubes through data sets.
- automatic copying of the **SampleID** data set (and any other data sets) during transfer and pipetting operations.
- reporting of information.

Data Set Definition

Data sets allow information about a sample in an individual well or tube to be tracked when the sample is moved to another well or tube. During any transfer or pipetting operation, all data sets associated with a plate are automatically copied from the source plate to the destination plate; however, only the wells in the data set affected by the transfer or pipetting operation are copied to the destination plate. The information in the data set can be used in decision-making; for example, during a **Transfer** or **Combine** step, a data set can be used to determine from which wells or tubes liquid should be aspirated or to which wells or tubes liquid should be dispensed.

Data Set Steps

Four steps in Biomek Software allow data sets to track samples. Knowledge of these steps is necessary to understand how data sets are used in Biomek Software to track samples:

- **Create Data Set** — Specifies data in a data set (refer to CHAPTER 23, *Configuring the Create Data Set Step*).
- **Data Set Management** — Renames, removes, copies, or modifies the properties of a data set (refer to CHAPTER 23, *Configuring the Data Set Management Step*)
- **Data Set Processing** — Applies a transformation expression to an existing data set to create a new data set (refer to CHAPTER 23, *Configuring the Data Set Processing Step*).
- **Reporting** — Generates a report on data sets at any point during a method (refer to CHAPTER 23, *Configuring the Reporting Step*).

NOTE Refer to CHAPTER 23, *Using the DataSets Step Palette*, for complete information on displaying the **DataSets** step palette and configuring the data sets steps.

Example of Sample Tracking Using Data Sets

While there are numerous ways in which sample tracking can be implemented using data sets, the following is an example of using data sets to track sample ID:

If a sample ID is associated with a tube and an amount is transferred from the tube to specified wells on a microplate, the **Sample ID** data set for the tube is copied to the specified wells on the microplate. The report will show the sample ID in the tube and the sample ID in the specified wells.

Understanding How Data Sets Are Created

The information contained in a data set is chosen in the **Create Data Set** step (refer to CHAPTER 23, *Configuring the Create Data Set Step*); however, some data sets may be generated in other ways through the software.

Biomek Software creates data sets in several ways:

- automatically (refer to *Understanding the Volume Data Set*)

  NOTE The **Volume** data set is created automatically

- using the **Instrument Setup** step (refer to CHAPTER 15, *Creating the SampleID Data Set Using the Instrument Setup Step*).
- using the **Create Data Set** step (refer to CHAPTER 23, *Configuring the Create Data Set Step*).

- using the **Script** or **Scripted Let** step (refer to CHAPTER 27, *Scripting Data Sets*).

  NOTE Creating data sets using scripting requires prior knowledge of Visual Basic scripting.

NOTE While Biomek Software retains information on all data sets and allows the information to be used anytime during the method, the specific information on a data set can only be viewed in a report configured in the **Reporting** (refer to CHAPTER 23, *Configuring the Reporting Step*) or **Finish** steps (refer to CHAPTER 12, *Configuring the Finish Step*).

Understanding the Volume Data Set

The volume of each well or tube is automatically tracked and stored for each piece of labware in a data set called **Volume**. The **Volume** data set is read-only and cannot be changed or manipulated, but may be used in other steps in the method to specify well patterns or volumes.

The **Volume** data set is reported when reports on data sets are generated and configured in the **Reporting** step (refer to CHAPTER 23, *Configuring the Reporting Step*). The **Volume** data set allows the volume of a well or tube to be known at any time during a method by inserting a **Reporting** step after any transfer or pipetting operation.

Using Data Sets in a Transfer or Combine Step

Not only are data sets automatically copied from the source plate to the destination plate during all transfer and pipetting operations, data sets may also be used in a **Transfer** or **Combine** step to define patterns for aspirating and dispensing liquid or to specify transfer volumes to specific wells. However, to use data sets to define well patterns for the **Transfer** and **Combine** steps, a data set must first be created for the source or destination labware in the **Create Data Set** step (refer to CHAPTER 23, *Configuring the Create Data Set Step*).

NOTE The well patterns defined using data sets are for use during the transfer operation for the specific **Transfer** or **Combine** step; they cannot be saved in the **Well Pattern Editor**.

Data sets can be used in a **Transfer** or **Combine** step for:

- *Defining Well Patterns Using Data Sets*
- *Specifying Volumes Using Data Sets*

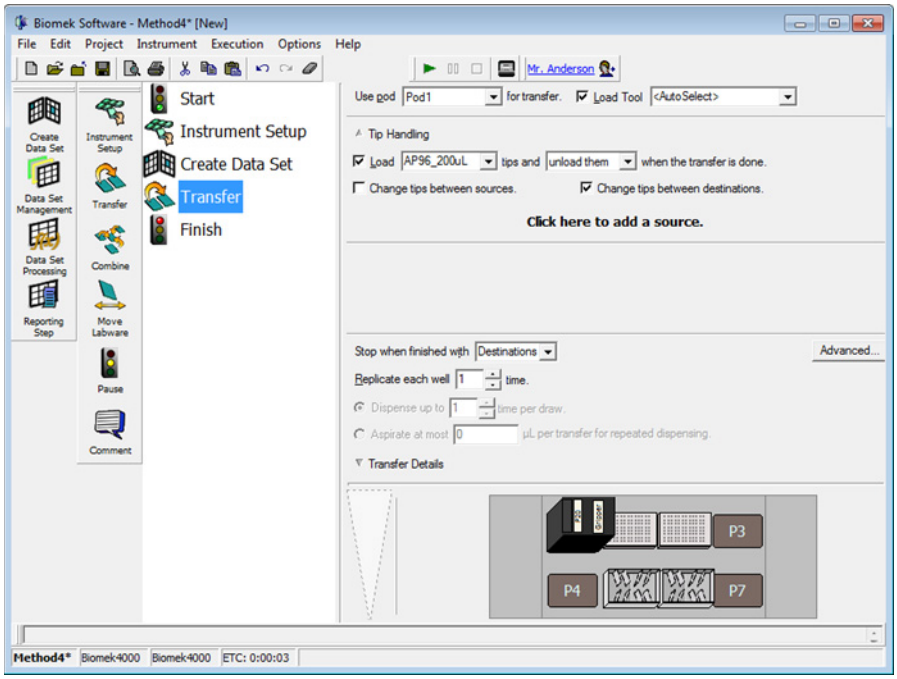
Defining Well Patterns Using Data Sets

Data sets may be used in a method to define well patterns for aspirating and dispensing liquid using the **Transfer** and **Combine** steps.

To use data sets to configure source or destination labware in a **Transfer** or **Combine** step:

1 Insert a **Transfer** or **Combine** step into the Method View anywhere after the specific data set that is used has been created (Figure 14.1).

Figure 14.1 Transfer Step in Method View After Data Set is Created



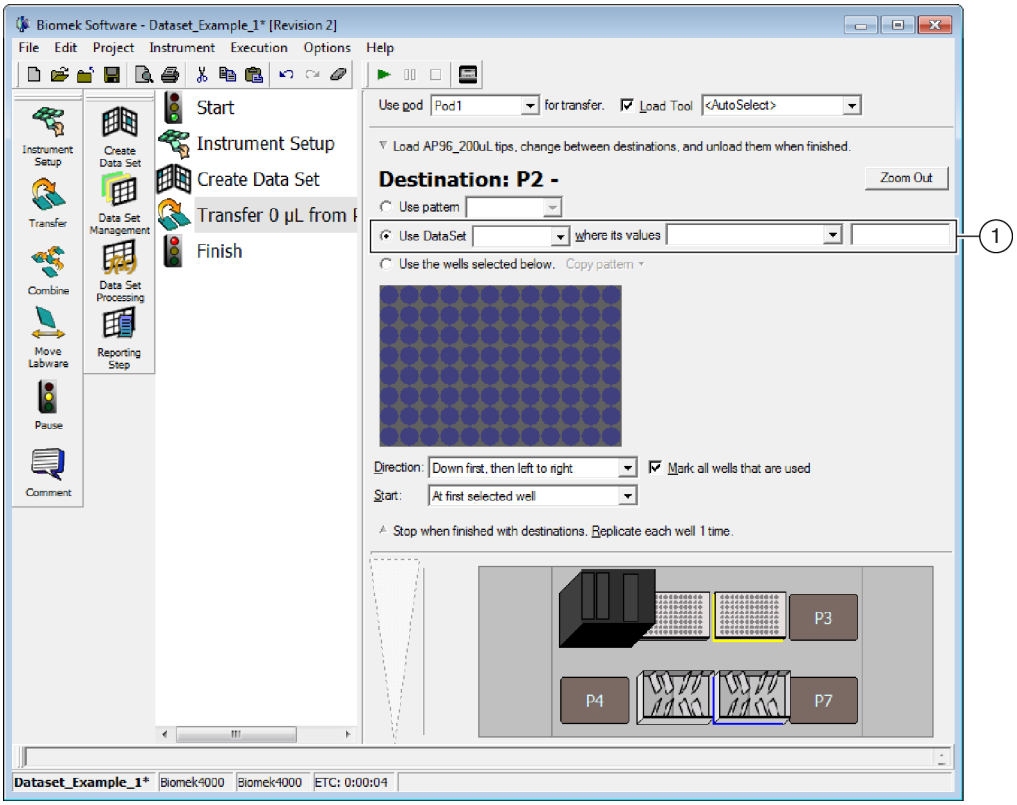
2 Configure the **Tip Handling** as desired.

NOTE Refer to CHAPTER 15, *Configuring Tip Handling*, for information on configuring **Tip Handling**.

3 Select the Source or Destination labware.

4 Double click on the graphic of the labware to zoom in (Figure 14.2).

Figure 14.2 Transfer Step—Zoomed-In Destination Labware



1. **Use Data Sets**: Select this option and configure the expression to define a well pattern using a data set.

5 Select **Use Data Set** to define a pattern using a data set.

NOTE All data sets defined for the specified Source or Destination labware are available for selection.

6 In **where its values**, select the desired option:

- **are equal to** — wells that have a value for the selected data set that are equal to a specified value or string are included in the pattern.

  NOTE Strings used with **are equal to** must be entered as **=“string”**.

- **are greater than** — wells that have a value for the selected data set that are greater than a specified value are included in the pattern.
- **are greater than or equal to** — wells that have a value for the selected data set that are greater than or equal to a specified value are included in the pattern.
- **are less than** — wells that have a value for the selected data set that are less than a specified value are included in the pattern.

- **are not equal to** — wells that have a value for the selected data set that are not equal to a specified value or string are included in the pattern.

  NOTE Strings used with **are not equal to** must be entered as **=“string”**.

- **contain** — wells that contain a specified numeric or text string within their value for the selected data set are included in the pattern.

  NOTE Strings used with **contain** must be entered as **=“string”**

7 Enter a value to complete the expression.

8 Double click the graphic of the labware or choose **Zoom Out** to return to the **Transfer** step configuration.

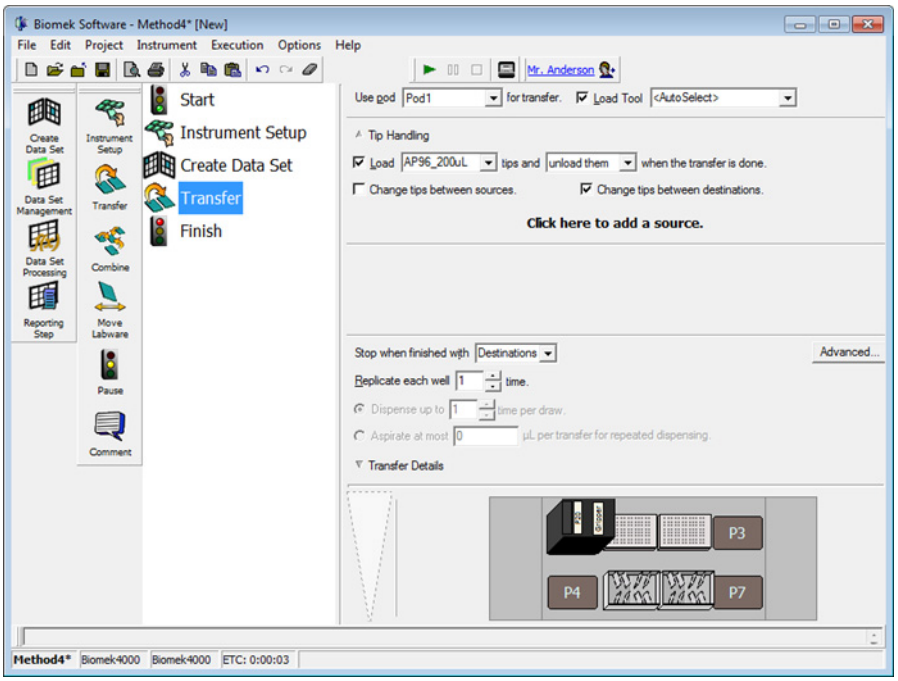
Specifying Volumes Using Data Sets

Data sets may be used in a method to specify transfer volumes using the **Transfer** and **Combine** steps

To use data sets to configure volumes in a **Transfer** or **Combine** step:

1 Insert a **Transfer** or **Combine** step into the Method View anywhere after the specific data set that is used has been created (Figure 14.3).

Figure 14.3 Transfer Step in Method View After Data Set is Created



2 Configure the **Tip Handling** as desired.

NOTE Refer to CHAPTER 15, *Configuring Tip Handling*, for information on configuring **Tip Handling**.

3 Select the Source or Destination labware.

NOTE For a **Transfer** step, **Volume** is configured in the destination labware; for a **Combine** step, **Volume** is configured in the source labware.

4 In **Volume**, enter **=positions.PositionName.labware.DataSets("name")("A1")**, where "A1" is the position in the data set of the desired value.

CHAPTER 15

Using the Basic Step Palette

Overview

The **Basic** step palette incorporates the basic steps that provide essential functionality for the Biomek 4000 system, including general instrument setup, pipetting operations, and labware manipulation.

⚠ CAUTION

Make sure the correct ALP is chosen when configuring the deck setup in the Deck Editor. ALPs vary in height and failure to choose each ALP correctly in the software may result in collisions between ALPs during operation.

The steps available in the **Basic** step palette are shown in Table 15.1:

Table 15.1 Basic Step Palette

Step	Icon	Description
Instrument Setup		Specifies the type of labware used for a liquid transfer, the position the labware occupies on the deck, and some labware content configuration. **NOTE** The type and position of ALPs and other hardware on the deck is specified in the **Deck Editor**.
Transfer		Comprises tool load, tip load, aspirate, dispense, and unload tip functions in one step to transfer liquid from a single source to one or more destinations.
Combine		Similar to a **Transfer** step, except **Combine** transfers liquids from one or more sources to a single destination.
Move Labware		Moves labware via automatic manipulation using the gripper tool.
Pause		Halts instrument interaction with a position for a specified amount of time or the entire deck for an indefinite period of time.
Comment		Documents the method or adds instructions in the Method View.

Instrument Setup Step

⚠ CAUTION

Always verify that the physical instrument setup matches the instrument setup in Biomek Software. Inaccurate instrument setup can result in inappropriate pipetting or pod collision, resulting in equipment damage or hazardous waste spills.

When preparing the instrument for a method, it is important to understand a critical concept that applies every time the instrument is set up: obstacle avoidance. When building a method, always tell the software what labware and ALPs are on the deck, and the deck position each occupies. In the **Instrument Setup** step, labware and tools are selected and positioned on the instrument deck.

As the bridge and pod move during method execution, the pod rises just enough to clear the objects sitting on the deck, and not much higher; therefore, if the software is not aware of what and where objects are on the deck, a hardware crash may occur.

Insert an **Instrument Setup** step to specify the labware, devices, and ALPs that are on the deck and the deck position each occupies. The **Instrument Setup** step can be inserted immediately after the **Start** step (Figure 15.1), or at any point in the method flow.

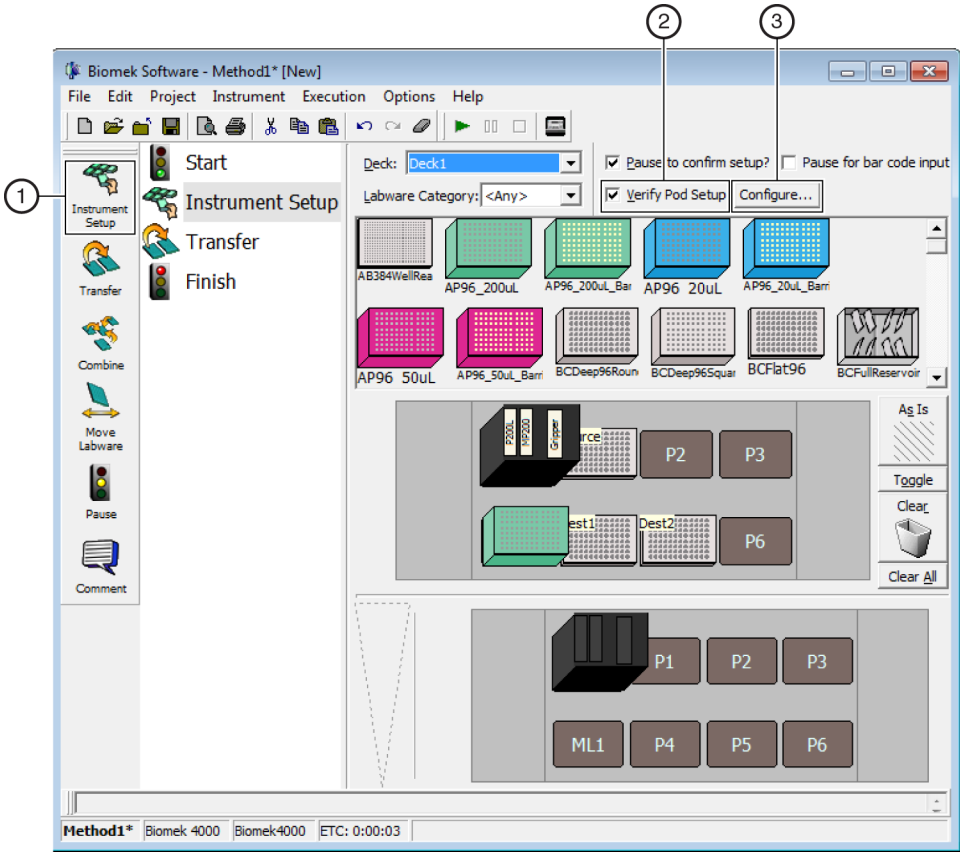
The **Sample ID** data set is also created in the **Instrument Setup** step by configuring the option **Pause for bar code input?** (refer to *Creating the SampleID Data Set Using the Instrument Setup Step*).

To insert an **Instrument Setup** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 15.1).

Figure 15.1 Instrument Setup Step and Configuration



1. **Instrument Setup Step icon**
2. **Verify Pod Setup option**
3. **Configure Pod Setup**

⚠ CAUTION

To make sure the pod avoids all obstacles during its travel, in Biomek Software, always specify the labware, ALPs, and devices that are on the deck, and the deck position each occupies. Failure to do so can cause pod collision, resulting in equipment damage or hazardous waste spills.

Configuring the **Instrument Setup** step includes:

- *Selecting a Deck Layout*
- *Verifying Deck Layout*
- *Configuring Pod Setup Options*
- *Populating the Deck with Labware and Tools*
- *Configuring Tip and Labware Properties*
- *Creating the SampleID Data Set Using the Instrument Setup Step*
- *Creating Custom Labware*

Selecting a Deck Layout

⚠ CAUTION

Make sure the correct ALP is chosen when configuring the deck setup in the Biomek Software "Deck Editor." ALPs vary in height, and failure to choose the correct ALP in the "Deck Editor" can result in collisions, causing equipment damage and/or hazardous waste spills.

The **Instrument Setup** step uses a Deck Layout as a map for the placement of labware, ALPs, and external hardware devices.

A Deck Layout is a blueprint, or map, of the instrument deck. Biomek Software provides two predefined Deck Layout options: **Deck1** and **Standard**. These two deck layouts represent the basic deck layout for the instrument with only standard deck positions.

NOTE The **Standard** deck layout is read-only and may not be modified.

When an **Instrument Setup** step is inserted into a method, the default Deck Layout set in the **Deck Editor** is automatically selected. If another deck layout other than the default deck is desired, choose any existing Deck Layout in **Deck** from the drop-down list.

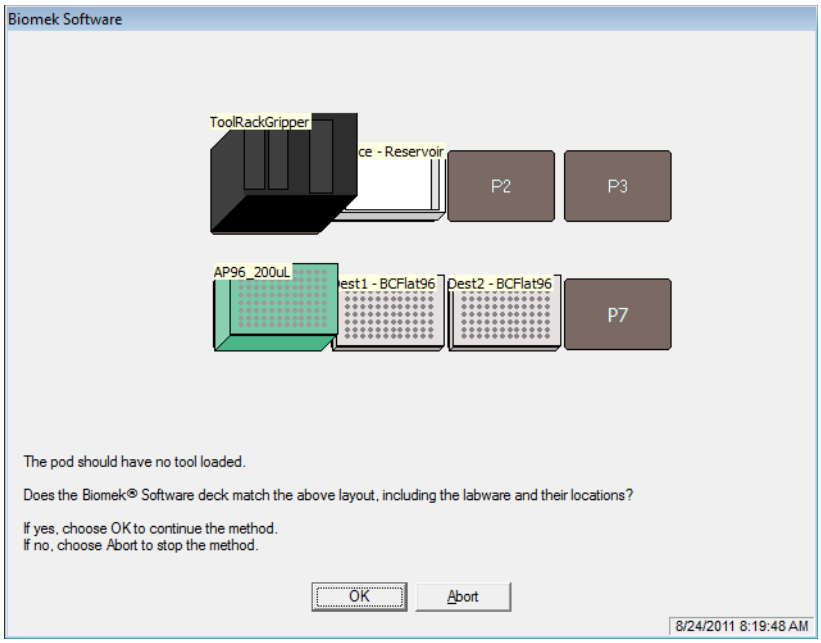
NOTE Refer to CHAPTER 5, *Preparing and Managing the Deck*, for more information on creating and modifying a deck layout and setting the default deck layout.

Verifying Deck Layout

It is possible to verify the Deck Layout selected for a method before the method is run by selecting the **Pause to Confirm Setup**? option (Figure 15.2). The default selection for the **Pause to Confirm Setup**? option is **On**.

Verification of the Deck Layout is recommended when a method is run repeatedly, or when modifications have been made to a method. A prompt appears (similar to the one in Figure 15.2) when **Pause to Confirm Setup?** is selected prior to running the method. The prompt displays the deck layout and the labware type and name (if assigned a name in **Labware Properties**) of the labware on each position.

Figure 15.2 Pause to Confirm Setup? Deck Layout Confirmation Prompt



Configuring Pod Setup Options

Verify Pod Setup? is used to configure the current state of the pod or tool on the instrument at the beginning of the **Instrument Setup** step. However, selecting **Tips Loaded** or **Tool Loaded** informs Biomek Software that tips or a tool are loaded on the instrument; it does not instruct the instrument to load tips or a tool.

Verify Pod Setup? is recommended when multiple methods are run one following another, when a single method is run repeatedly, or when tips are not loaded during the method.

There are two options for **Verify Pod Setup**.

- **Tool Loaded** informs software that a tool is loaded on the pod at the time of the **Instrument Setup** step. The default setting is **Off**.
- **Tips Loaded** informs the software that tips are loaded onto the tool at the time of the **Instrument Setup** step, if **Tool Loaded** is **On** and a pipetting tool is selected. The default setting is **Off.**

NOTE A pod setup verification (Figure 15.2) only appears when **Pause to confirm setup?** is selected. If **Pause to confirm setup?** is not selected, but **Verify Pod Setup** is selected, the dialog does not appear.

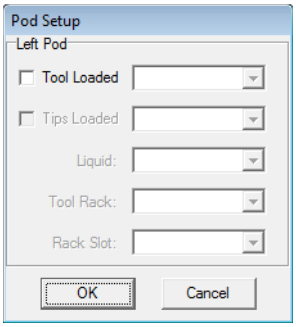
To verify the pod setup:

1 Select **Verify Pod Setup**.

2 Select **Pause to confirm setup?**.

3 Choose Configure... to change the **Pod Setup**, if desired. **Pod Setup** displays (Figure 15.3).

Figure 15.3 Pod Setup Prompt



4 Select **Tool Loaded,** if a tool must be loaded at the beginning of the method. The **Tool Loaded** field has three states:

- **Checked** — Indicates tool is loaded
- **Unchecked** — Indicates tool is not loaded
- **Gray-checked** — Instructs the software to leave the tool in its current state, whether a tool is loaded or not loaded

5 If **Tool Loaded** is selected:

a. Select the tool type loaded that the beginning of the method from the **Tool Loaded** drop-down.

b. If the loaded tool is a wash tool (Wash1 or Wash8), in **Liquid**, select the liquid type used with the tool.

c. In **Tool Rack**, select the deck position of the tool rack where the tool is to be returned.

d. In **Rack Slot**, choose the slot number where the tool is to be returned.

6 Select **Tips Loaded,** if tips must be loaded at the beginning of the method. The **Tips Loaded** field has three states:

- **Checked** — Indicates tips are loaded
- **Unchecked** — Indicates tips are not loaded
- **Gray-checked** — Instructs the software to leave the tips in their current state, whether tips are loaded or not loaded

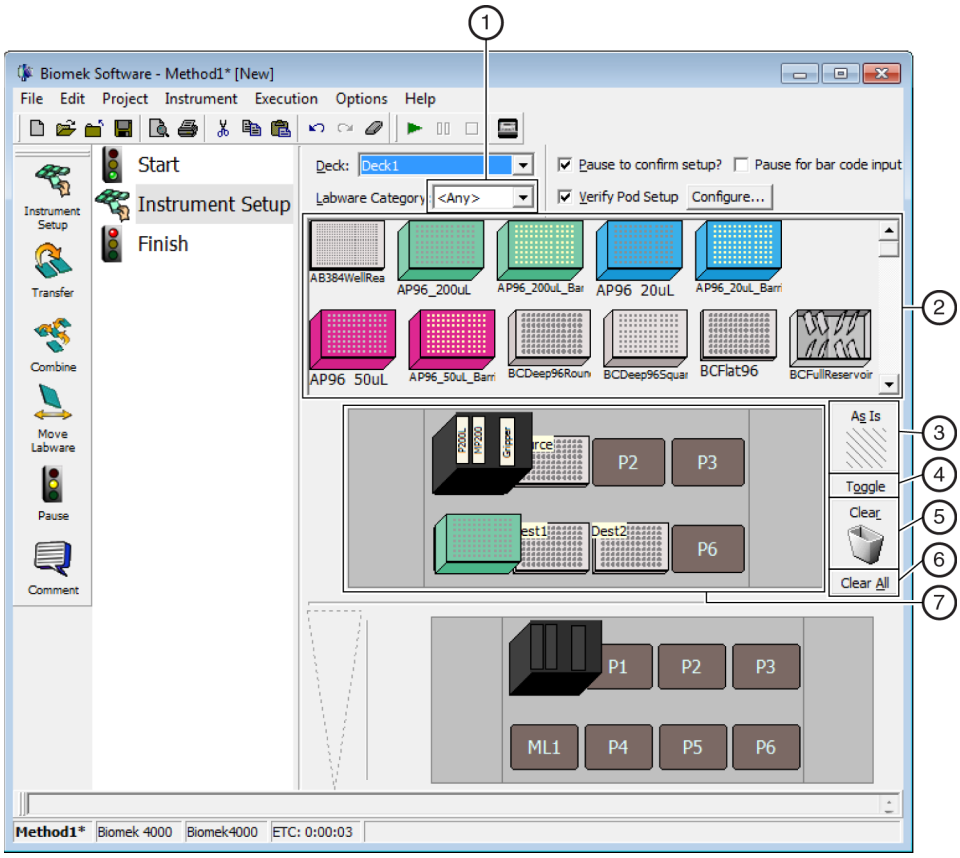
7 If **Tips Loaded** is selected, select the tip type loaded at the beginning of the method.

8 Choose **OK** to save the changes made to the **Pod Setup**.

Populating the Deck with Labware and Tools

The labware available for selection is displayed graphically below **Labware Category** (Figure 15.4). A specific type of labware can be viewed in the graphical display, or all types of labware available can be viewed simultaneously, using the **Labware Category** filter.

Figure 15.4 Populating the Deck Layout



1. **Labware Category selection.**
2. **Labware Category Graphical Display**: Graphical representation of the types of labware available for populating the Deck Layout. The labware displayed here is based on the **Labware Category** selected above.
3. **As Is**: Individual deck positions retain their current state, whether empty or occupied by labware or a device.
4. **Toggle**: Toggles all empty deck positions to the **As Is** state and from the **As Is** state to their initial status, allowing those deck positions to retain their empty state.
5. **Clear**: Drag a piece of labware from the deck position to the trash to remove it.
6. **Clear All**: Clears all deck positions, whether empty or occupied by labware or a device.
7. **Instrument Setup Display**: Displays the setup of the deck. Once labware is added to the deck, it is displayed here. If names have been assigned to labware, the names are displayed.

To populate the Deck Layout with labware:

NOTE When populating the deck with labware, consider the tip to labware accessibility of the tool as described in the *Biomek 4000 Hardware Manual*.

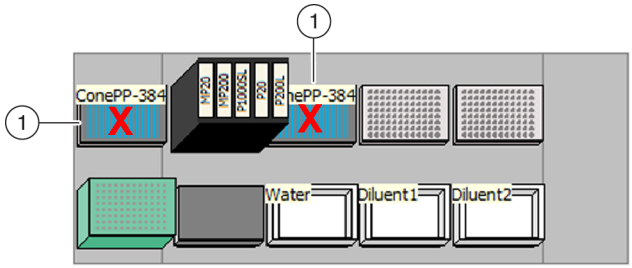
1 To display labware, select the type of labware desired in **Labware Category**. **Labware Category** choices include:

- **Any** — Lists all types of labware available, including lids and deck positions reserved for swapping labware.
- **Custom** — Lists any labware stored with defined properties (refer to *Creating Custom Labware*).
- **Lid** — Lists lids associated with labware available.
- **Reservation** — Reserves deck positions for specific purposes; for example, to enable swapping of labware between positions.
- **Reservoir** — Lists reservoirs available.
- **TipBox** — Lists types of tips available.
- **Titerplate** — Lists types of microplates available
- **Tuberack** — Lists types of tube racks available.

NOTE Labware types and their characteristics are defined in the **Labware Type Editor.** Refer to CHAPTER 7, *Creating and Modifying Tip and Labware Types*, for information using the **Labware Type Editor.** If the **Hide Labware** option was chosen while defining a labware type, it will not be displayed in the **Instrument Setup** step.

⚠ CAUTION

Do not place 384-well plates on either side of a tool rack, as this poses a risk of equipment damage when pipetting to the columns adjacent to the tool rack. The figure below is an example of an at-risk deck setup. Place the 384-well plates on another available deck position to avoid damage.



1. At-risk locations for 384-well plates.

⚠ CAUTION

Do not place tip boxes on positions other than ManualLatch or AutoLatch positions (designated as ML# or AL# in Biomek Software). If a tip box is placed on a positioner other than latch, the instrument might have problems loading or unloading tips.

2 To place labware on the Deck Layout, drag and drop each desired labware graphic to the desired position on the Deck Layout display.

OR

Click on the labware graphic, and then on the desired position in Deck Layout display. The same type of labware can be added to as many deck positions as required by continuing to click on deck positions.

OR

Click on the labware graphic, and then click and drag the mouse over multiple deck positions in the Deck Layout display. This places the labware in all the highlighted positions.

NOTE To move labware to a different position, drag the desired labware to the new position in the Deck Layout.

3 To remove unwanted labware from the Deck Display during setup, drag and drop the labware to the **Clear** (trash) icon (Figure 15.4).

OR

Select **Clear** and then click on all the labware that needs to be removed.

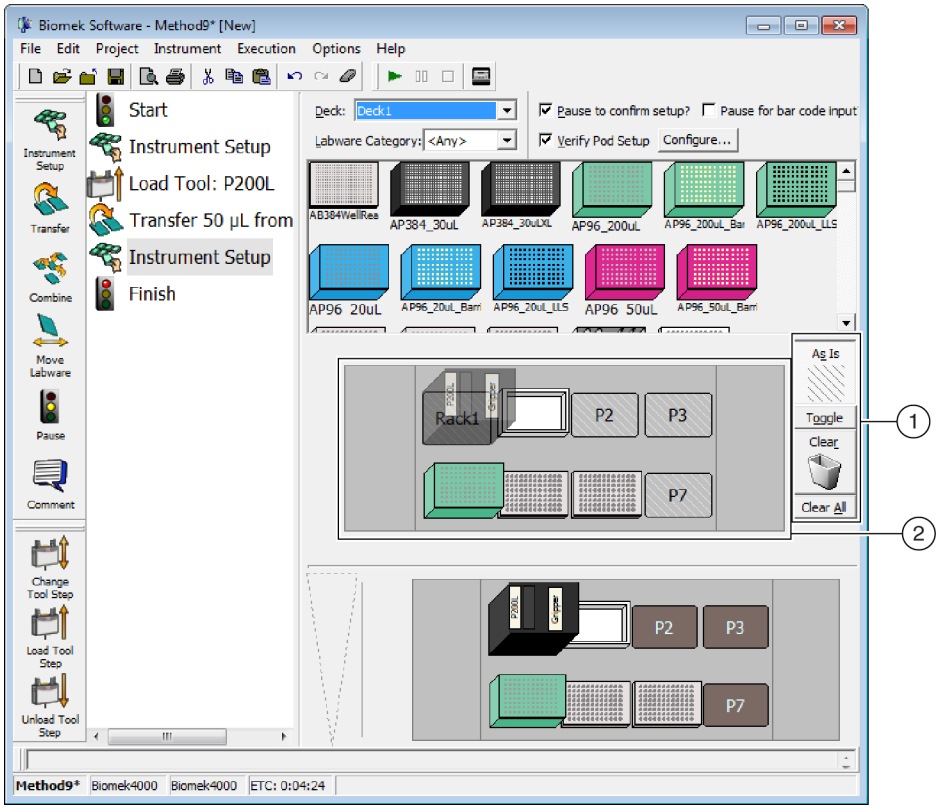
OR

Right click the unwanted labware and select **Delete** from the menu that displays.

Changing Instrument Setup During a Method

When changing the instrument setup during a method, a second **Instrument Setup** step must be added. The additional **Instrument Setup** step reflects modifications to the current state of the deck (Figure 15.5).

Figure 15.5 A Second Instrument Setup Step with Deck Positions Specified As Is



1. **Instrument Setup Options**: Allows manipulation of the deck positions for addition and removal of labware during a method run.
2. **Instrument Setup Display**: Displays the setup of the deck. Once labware is added to the deck, it is displayed here. If names have been assigned to labware, the names are displayed.

Additional **Instrument Setup** steps can be inserted into a method as many times as necessary to complete a liquid-handling process, and to accommodate the addition of labware to the deck throughout a method.

The following options are available to help modify all instrument setups, either globally or by individual deck positions. These options are:

- **As Is** — Individual deck positions retain their current state, whether empty or occupied by labware or a device.
- **Toggle** — Toggles all empty deck positions to the **As Is** state and from the **As Is** state to their initial status, allowing those deck positions to retain their empty state.
- **Clear** — Clears individual deck positions, whether empty or occupied by labware.
- **Clear All** — Clears all deck positions, whether empty or occupied by labware or a device.

As Is and Toggle

As Is indicates that a deck position retains its current state, whether empty or occupied by labware or a device. Previously populated deck positions are indicated with the **As Is** option in the subsequent **Instrument Setup** step configuration. When **As Is** is applied to a deck position, the position becomes grayed out in the Deck Layout display (Figure 15.5).

As Is may also be used at the start of a method to indicate that deck positions retain their state from a previously run method that did not clear the deck of all labware in the **Finish** step.

To indicate that a deck position retains its current state:

1 Click 

.

2 Click any deck position on the Deck Layout, and it is displayed **As Is**.

3 Repeat step 2 for each desired deck position.

OR

Click on a deck position, and then click and drag the mouse over multiple deck positions in the Deck Layout display. This toggles all the highlighted positions to the **As Is** state.

Toggle toggles all empty deck positions in the Instrument Setup Display between **As Is**, preserving the deck position's current state (Figure 15.6), and **Clear**, which empties a deck position. When **Toggle** is selected, deck positions labeled **As Is** revert to **Clear**.

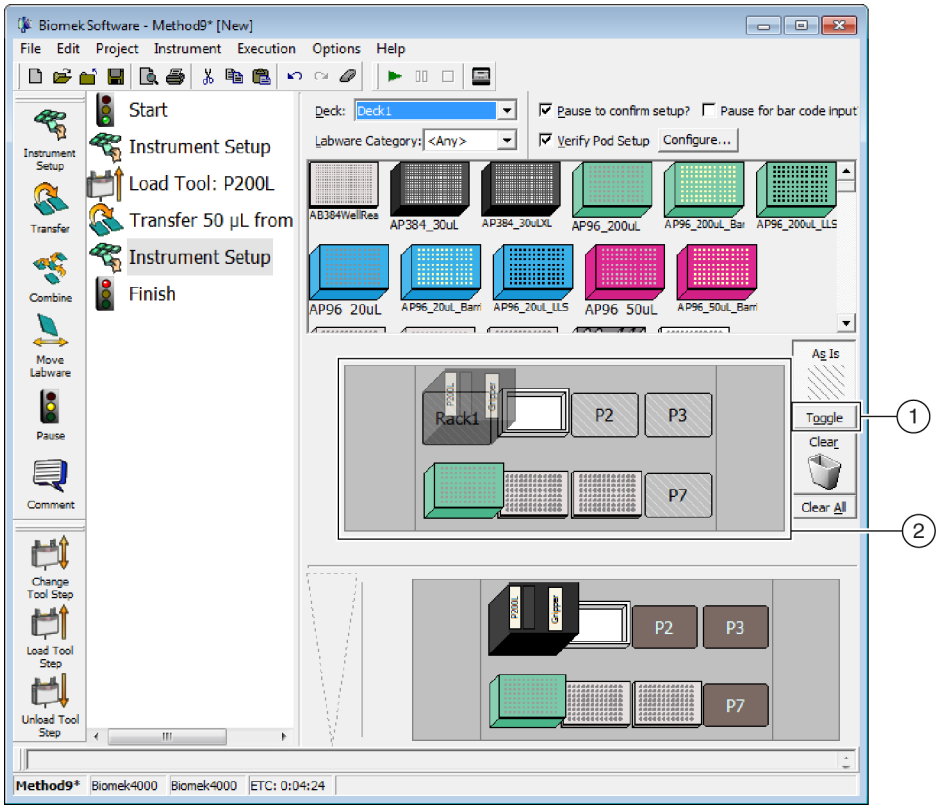
NOTE Adding labware to a deck position that is set to **As Is** removes the **As Is** status and replaces that position with the added labware. Any labware at that position is assumed to be removed from the deck and replaced with the new labware.

To indicate that a deck position retains its current state:

1 Click 

, and any deck position not occupied by a piece of labware in the **Instrument Setup** display is toggled to the **As Is** state.

Figure 15.6 Toggle Applied to the Deck Layout

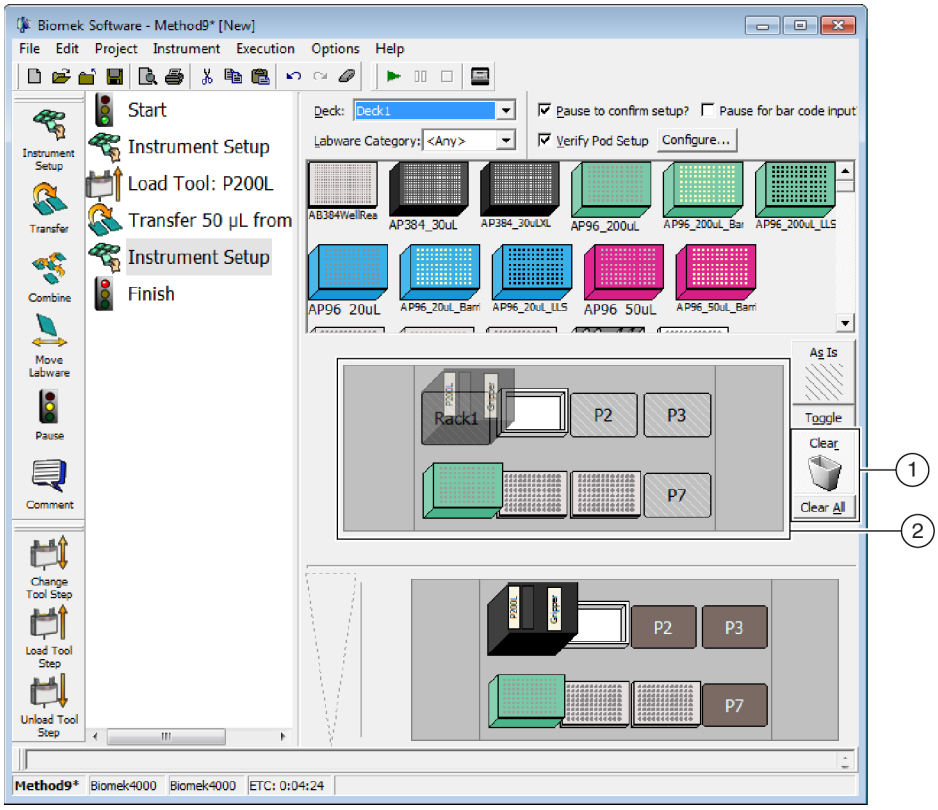


1. **Toggle:** Changes all unpopulated deck positions to the **As Is** state.
2. **Instrument Setup Display**

Clear and Clear All

Clear removes labware or the **As Is** designation from individual deck positions. There is no confirmation for **Clear**, so once **Clear** is chosen, and a deck position is selected, the position is cleared of any labware or the **As Is** option (Figure 15.7).

Figure 15.7 Clear Deck Layout Designation Applied to Rack1



1. **Clear and Clear All**
2. **Instrument Setup Display**

The **Clear All** option removes all labware and **As Is** designations from the Instrument Setup. **Clear All** displays a prompt before the deck is cleared of all labware and **As Is** designations.

NOTE If a deck position that contained labware from a previous **Instrument Setup** step is set to **Clear**, the labware is assumed to have been removed from the deck and that position no longer contains any labware.

To remove labware from the **Instrument Setup** configuration:

---

1 Choose 

to clear a single deck position of labware or an **As Is** designation.

---

2 Click on the deck position in the Deck Layout display.

3 Continue to click on individual deck positions to empty them.

OR

Drag and drop labware from Deck Layout into **Clear**.

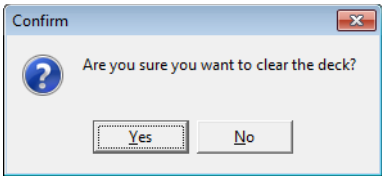
OR

Right click on the labware in the Deck Layout display and select **Delete**.

4 To clear the entire deck at one time, choose Clear All.

5 A confirmation prompt asking for verification appears. Choose **Yes** to remove all labware from the deck (Figure 15.8).

Figure 15.8 Confirmation Prompt to Clear All Labware from the Deck Layout



Configuring Tip and Labware Properties

Labware Properties is used to configure properties for each piece of labware added to the Deck Layout. The information provided in **Labware Properties** is used when a pipetting technique is selected, and when tips are loaded and unloaded.

To access **Labware Properties**:

1 Double click on a piece of labware in the Deck Layout.

NOTE Double-clicking on a stack of labware at the selected position opens the **Properties** for the top piece of labware only.

OR

Right click on a piece of labware in the Deck Layout and choose **Properties** to open **Labware Properties**.

NOTE If there is a stack of labware at the selected position, a submenu appears from **Properties** listing labware from bottom to top.

The configuration options in **Labware Properties** provide the following information, if it applies to the type of labware selected:

- Name assigned to a piece of labware, if desired
- Labware type
- Maximum volume per well
- Bar code
- Sense liquid level options
- Volume for each well, if known. The default volume for a labware type may be set in the **Labware Type Editor** (refer to CHAPTER 7, *Editing Labware Type Properties*).
- Liquid type(s). Liquid type can be assigned on a per-well basis.
- Where to dispose of tips
- Where to dispose of tip boxes
- Maximum number of times tips may be loaded
- Available tips

NOTE Variables and expressions may be entered in any field that can be configured. Refer to CHAPTER 13, *Using Variables*, and CHAPTER 13, *Using Expressions*, for more information on using variables and expressions.

Configuring Labware Properties for Tips

When the labware selected for configuration is a tip box, **Labware Properties** provides the ability to configure the following information:

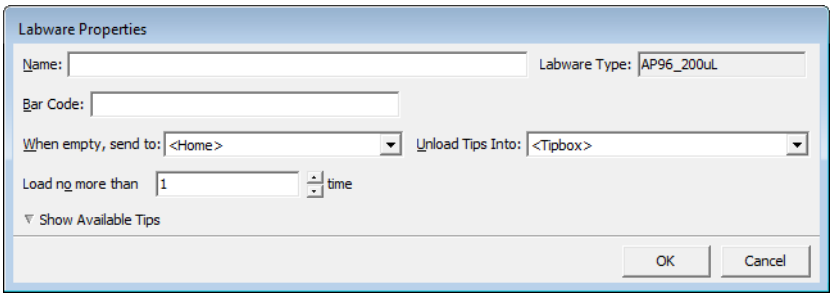
---

1 Double click the tip box to configure in the Deck Layout.

OR

Right click the tip box to configure in the Deck Layout and select **Properties** from the menu. **Labware Properties** for tips displays (Figure 15.9).

Figure 15.9 Labware Properties for Tips



2 In **Name**, enter the name assigned to the tip box, if applicable. Naming a tip box forces the instrument to look for the specific box of tips, rather than any tip box on the deck that contains the specified tip type.

NOTE Multiple tip boxes can be given the same name. This is useful for creating a pool of tip boxes for a specific use.

OR

Leave **Name** blank. When **Name** is blank, tips are accessed by the information displayed in the **Labware Type** field.

3 In **Labware Type**, verify the tip type.

4 In **Bar Code**, enter the bar code. Use the bar code field to identify a specific tip box in certain methods, such as plate replication. This field may be left blank.

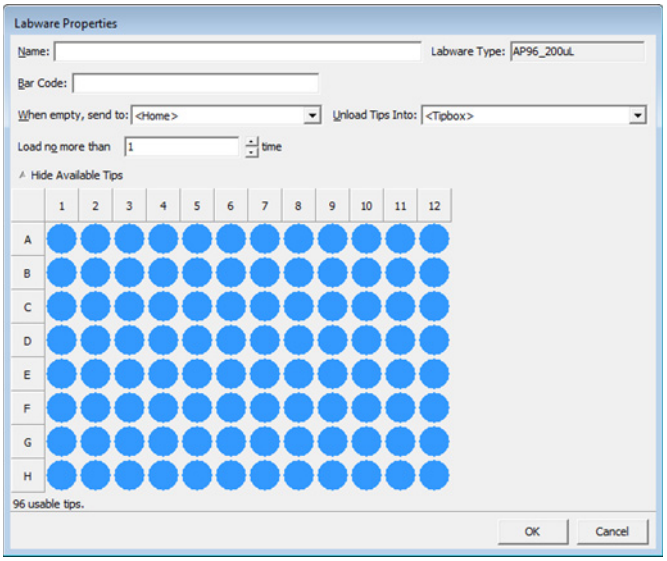
5 In **When empty, send to**, select a final destination for the tip box at the end of the method.

6 In **Unload Tips Into**, select the location reserved for tip disposal, or select **<tipbox>** to shuck the tips back into the box for later reuse or disposal.

7 In **Load no more than**, enter the number of times tips can be loaded onto the tool during the method.

8 Choose **Show Available Tips** to display a graphic of the tip box (Figure 15.10).

Figure 15.10 Labware Properties for Tips with Available Tips Shown



9 On the graphic of the tip box, select the usable tips. By default, all tips are selected. This can be used to indicate missing tips or tips that are otherwise not used in the method.

10 Choose **Hide Available Tips** to collapse the graphic of the tip box.

11 Choose **OK** to save **Labware Properties** and return to the **Instrument Setup** step configuration.

Configuring Labware Properties of Microplates, Reservoirs, and Tube Racks

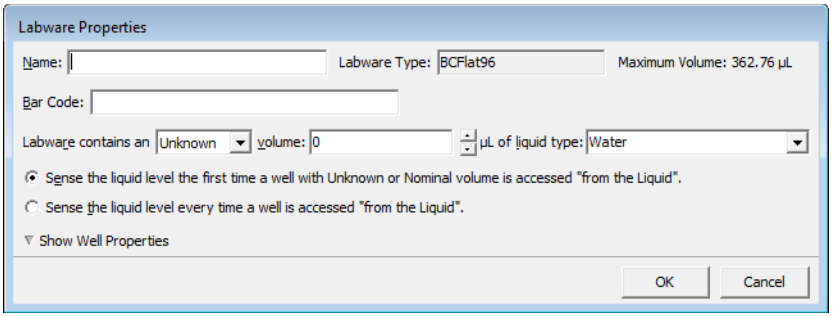
When the labware selected for configuration is a microplate, reservoir, or tube rack, **Labware Properties** provides the opportunity for configuration (Figure 15.11).

1 Double click the piece of labware to configure in Deck Layout.

OR

Right click the piece of labware to configure in Deck Layout and select **Properties** from the menu. **Labware Properties** for microplates, reservoirs, and tube racks displays (Figure 15.11).

Figure 15.11 Labware Properties for Microplates, Reservoirs, and Tube Racks



2 Verify the **Labware Type.**

3 In **Name**, enter a name for the labware.

NOTE When a deck is populated by numerous pieces of labware, naming labware is recommended. Names should be descriptive of the contents of the labware or the work being accomplished during the method. Naming labware in a meaningful fashion may reduce confusion.

4 In **Bar Code**, enter the bar code to identify a specific plate in certain methods, such as plate replication. This field may be left blank.

5 Make a selection in **Labware contains.** This information is used by many of the techniques supplied with Biomek Software that aspirate or dispense at a certain offset from the liquid level.

NOTE Some tools can detect the liquid level using liquid-level sensing technology.

- If **Known** is selected, the liquid level is not detected during method run and the entered value is used during validation and method run. **Known Volume** should be supplied whenever possible.
- If **Unknown** is selected, the liquid level is detected during method run if required by the technique, and the wells are assumed to be full when validating the method.
- If **Nominal** is selected, the liquid level is detected during method run, but the volume in the wells is assumed to be the entered value when validating the method.

6 Enter the **Volume**, if **Nominal** or **Known** volume is selected. A value entered in **Volume** is assigned to each well on the selected labware.

7 Select the **Liquid Type** contained in the labware. Specifying liquid type is useful when Biomek Software auto-selects a pipetting technique for any aspirate and dispense operations on this piece of labware. This technique is auto-selected based on the physical factors of the liquid, as well as the physical attributes of the labware, and the tool performing the operation. If the labware contains more than one liquid type, see step 9 below. For more information on liquid types, refer to CHAPTER 8, *Understanding and Creating Liquid Types*.

8 Select **Sense the liquid level the first time a well with Unknown or Nominal volume is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level only the first time the system accesses a well with an **Unknown** or **Nominal** volume from the liquid. When the same well on the piece of labware is accessed, the liquid level is calculated internally based on the result of the earlier liquid level sense and the amount aspirated or dispensed to the well in previous steps.

OR

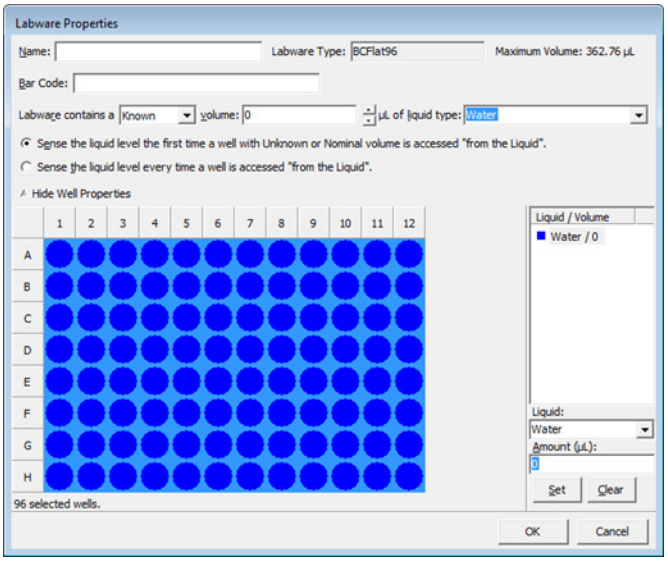
Select **Sense the liquid level every time a well is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level every time it accesses a well with an **Unknown** or **Nominal** volume from the liquid.

NOTE Liquid level sensing options apply only if the tool accessing the labware is liquid level sensing capable (P1000SL and P200L). If not, the selected option is ignored.

9 If the labware does not contain uniform volumes and/or liquids, choose **Show Well Properties** to display a graphic of the labware (Figure 15.12) and assign two or more volumes/liquids to wells on the same piece of labware.

NOTE If a volume for all wells is specified in step 6, proceed to step 16.

Figure 15.12 Labware Properties for a 96-Well Microplate with Well Properties Shown



NOTE **Show Well Properties** may appear different depending on the number of wells on the selected labware.

10 Select the desired wells on the graphic.

NOTE Hold down (Ctrl) to toggle wells between selected and deselected without affecting the selection status of other wells. Click a column or row heading to select all wells of a column or row.

NOTE By right-clicking on the graphic and selecting **Invert Selection**, you can simultaneously deselect the wells that are currently selected, while selecting all previously deselected cells.

11 In **Liquid**, enter the liquid type to assign to the currently selected wells.

12 Enter the volume to assign to the currently selected wells in **Amount**.

13 Choose **Set** to assign the current **Liquid** and **Amount** to the currently selected wells. The wells are given a color code that corresponds to the list of set volumes under **Liquid/Volume**.

14 Repeat steps 10-13 until all desired wells have been assigned the desired volume and liquid type. **Clear** sets the liquid to the default and volume for all wells back to zero.

15 Choose **Hide** to collapse the graphic of the labware.

16 Choose **OK** to save **Labware Properties** and return to the **Instrument Setup** step configuration.

Configuring Labware Properties for a Tool Rack

The instrument tool rack stores various interchangeable tools for the pod on the instrument deck during a method. The Biomek 4000 instrument can load and unload tools from the tool rack to give the instrument different capabilities. The tools available to the pod are configured from **Labware Properties** in an **Instrument Setup** step.

Since a gripper tool may be placed physically on the Gripper Tool Rack or the Off-Deck Gripper Rack only (refer to the *Biomek 4000 Hardware Manual)*, it must be configured in **Instrument Setup** using a Gripper Tool Rack or Off-Deck Gripper Tool Rack.

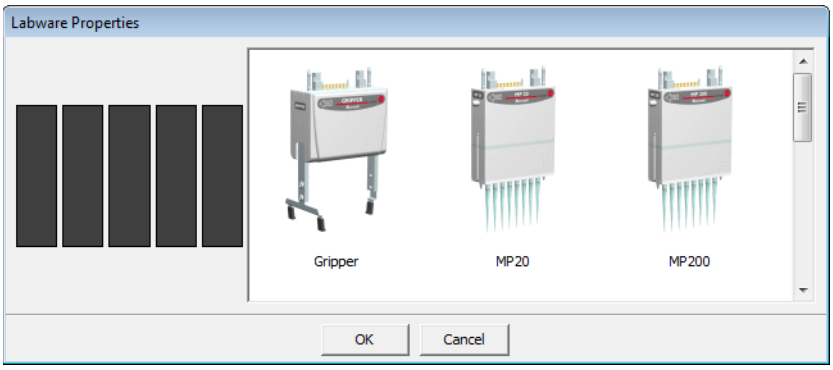
To configure the tools available at a tool rack in **Instrument Setup**:

1 Double click the tool rack to configure it in **Instrument Setup**

OR

Right click the tool rack to configure it in **Instrument Setup** and select **Properties** from the menu. **Labware Properties** for the Biomek 4000 tool rack appears (Figure 15.13).

Figure 15.13 Labware Properties for a Biomek 4000 Tool Rack



2 Locate the desired tool on the right side of **Labware Properties** and drag it to one of the unoccupied (black) positions on the tool rack. The selected tool is placed in the position (Figure 15.14).

Figure 15.14 Labware Properties for a Biomek 4000 Tool Rack With Tools Loaded

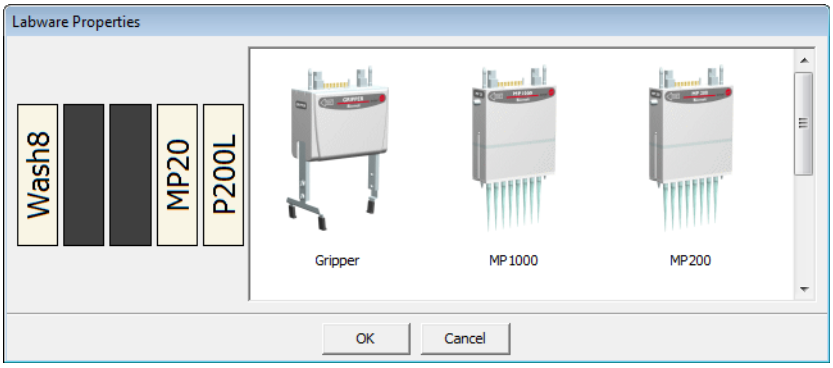
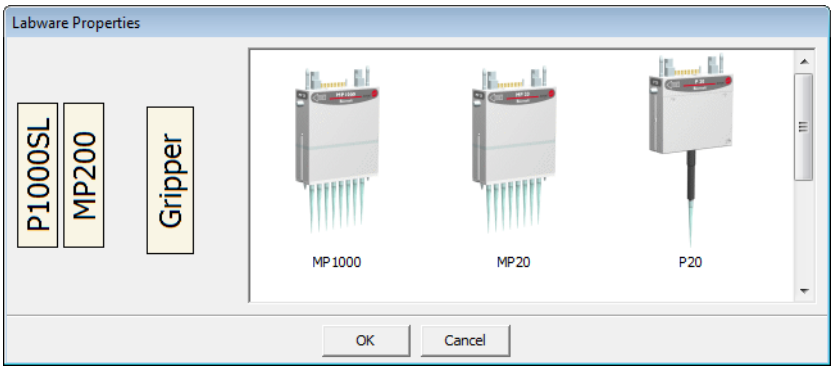


Figure 15.15 Labware Properties for a Biomek 4000 Gripper Tool Rack With Tools Loaded



NOTE The Gripper tool requires a larger slot, and can only be placed into tool racks that are specifically designed to store the tool.

3 Repeat step 2 until the rack is full or all desired tools have been placed on the tool rack.

To make changes to the rack:

- **To completely remove a tool from the rack**, select the tool from the rack position and drag it to the right side of **Labware Properties**.
- **To move a tool to a different rack position**, select the tool and drag it to the desired position. If the position is currently occupied, the tool replaces the tool in that position, and the position from which the tool was removed becomes available.

⚠ CAUTION

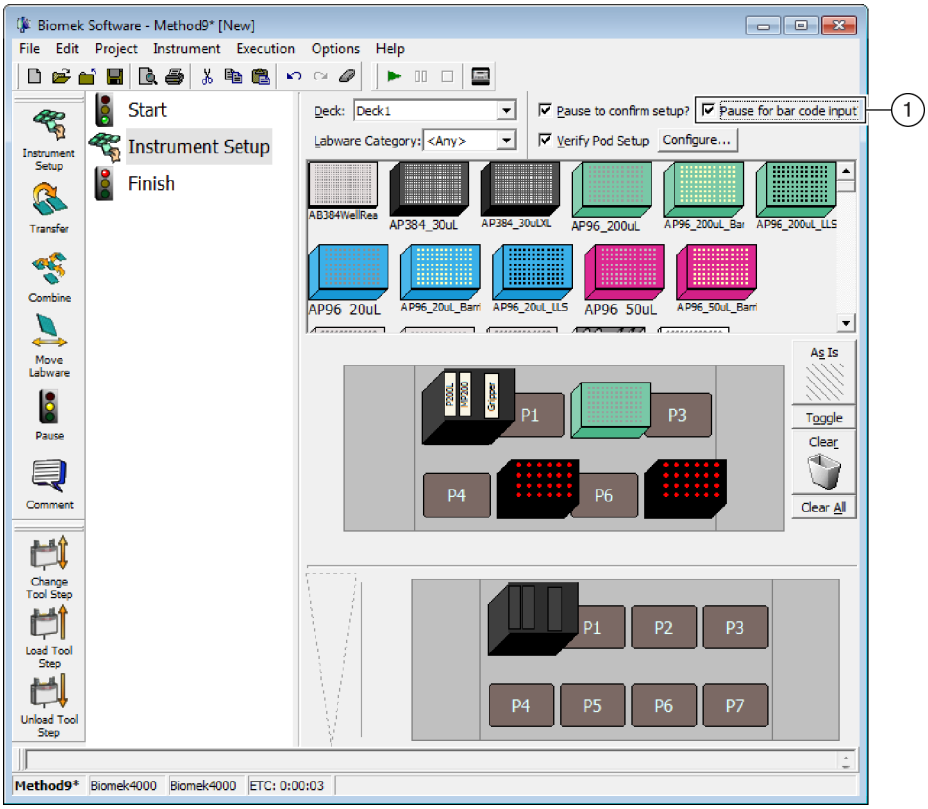
Inaccurate Biomek Software representation of tool placement in the tool rack can cause hardware crashes and instrument and/or tool damage. Ensure that Biomek Software is updated each time tool placement is physically changed on the deck.

4 Choose **OK** to save the **Labware Properties** for the tool rack.

Creating the SampleID Data Set Using the Instrument Setup Step

The **Instrument Setup** step contains an option to **Pause for bar code input?** during a method run (Figure 15.16). When this option is selected, the method pauses at the **Instrument Setup** step and allows for per-well or per-tube bar codes to be entered for all labware on the deck. Using the specified bar codes, a data set called **SampleID** is created for each piece of labware.

Figure 15.16 Enabling Bar Code Input in the Instrument Setup Step

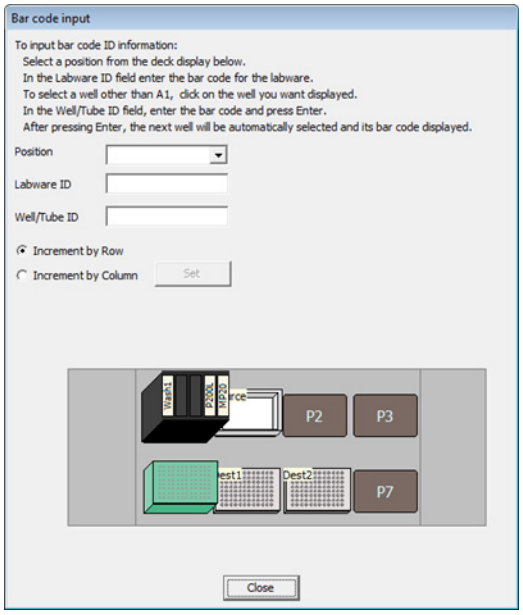


1. **Select to enable bar code input.**

When **Pause for bar code input?** is selected, **Bar code input** (Figure 15.17) displays during the method run at the **Instrument Setup** step.

If **Pause to confirm setup?** is also selected, **Bar code input** displays after the Deck Confirmation prompt (refer to *Verifying Deck Layout*).

Figure 15.17 Bar Code Input



If desired, only labware IDs or only sample IDs may be entered in **Bar code input**. It is not necessary to enter both labware and sample IDs for any piece of labware.

NOTE Labware must be unstacked to assign Labware ID and/or Well/Tube ID in Bar code input. When labware is stacked, only the topmost plate in the stack can have IDs assigned.

To enter labware and sample IDs:

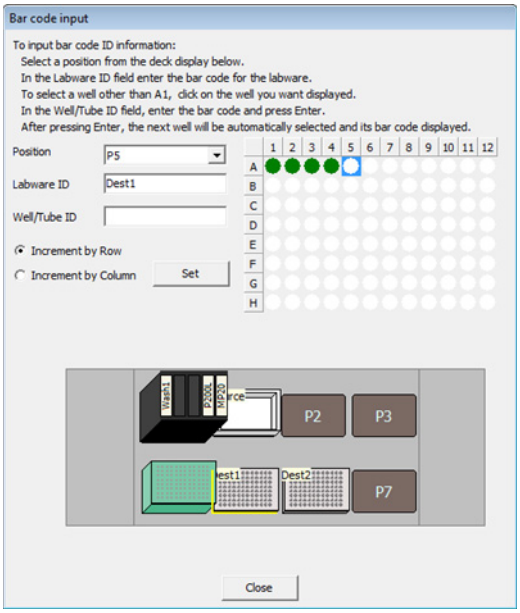
---

1 In **Position**, select the deck position of the labware to specify labware or sample IDs.

OR

Click on the desired piece of labware in the Deck Display. A graphic of the selected labware type appears (Figure 15.18).

Figure 15.18 Entering Sample IDs for Labware in Bar Code Input



2 In **Labware ID**, enter the plate bar code or name.

3 Select **Increment by Row** to enter sample IDs by row.

OR

Select **Increment by Column** to enter sample IDs by column.

NOTE The Increment selection determines which well is automatically selected when a sample ID is set by choosing **Set** or pressing **Enter**.

4 Select the well or tube in the labware graphic to assign a sample ID.

5 In **Well/Tube ID**, enter the bar code or sample ID to assign to the selected well or tube.

6 Press Enter or choose **Set** to assign the **Labware ID** and **Well/Tube ID** to the selected labware and well or tube. The well or tube is assigned the sample ID and turns green to indicate a sample ID has been assigned to that well or tube. The next well or tube on the labware is automatically selected.

NOTE If using a handheld bar code reader, ensure the bar code reader is configured to transmit a carriage return and line feed.

7 Repeat steps 4-6 to assign a sample ID to all desired wells or tubes of the labware.

8 Repeat steps 1-6 to assign labware and/or sample IDs to each desired piece of labware.

9 After sample IDs have been entered to all desired labware, choose **Close**. The SampleID data set is created for every piece of labware on the deck with a specified Sample ID.

Each **Instrument Setup** step with **Pause for bar code input?** selected allows wells or tubes to be assigned IDs. If a new ID is assigned to a well or tube that previously had a **SampleID** created, the new value overwrites the old value. To maintain a record of all **SampleIDs** for a well or tube, use the **Data Set Management** step to rename or create a copy of the **SampleID** data set before the additional **Instrument Setup** step assigns the new sample ID (refer to CHAPTER 23, *Configuring the Data Set Management Step*).

Creating Custom Labware

The **Custom** labware category offers the option to create and reuse labware with defined and stored **Labware Properties**. New labware stored in the **Custom** labware category maintains the **Labware Properties** defined when the labware was added to the Custom Labware category, including the name, bar code, liquid type, and volume information.

Custom labware creates an instance of the labware type containing the attributes of the working revision of the labware type it is based on at the time the custom labware is created and the configured **Labware Properties.** Custom labware is saved to the project file.

NOTE The default volume for a labware type can be specified in the labware definition stored in the **Labware Type Editor** (refer to CHAPTER 7, *Editing Labware Type Properties*).

To create **Custom** labware:

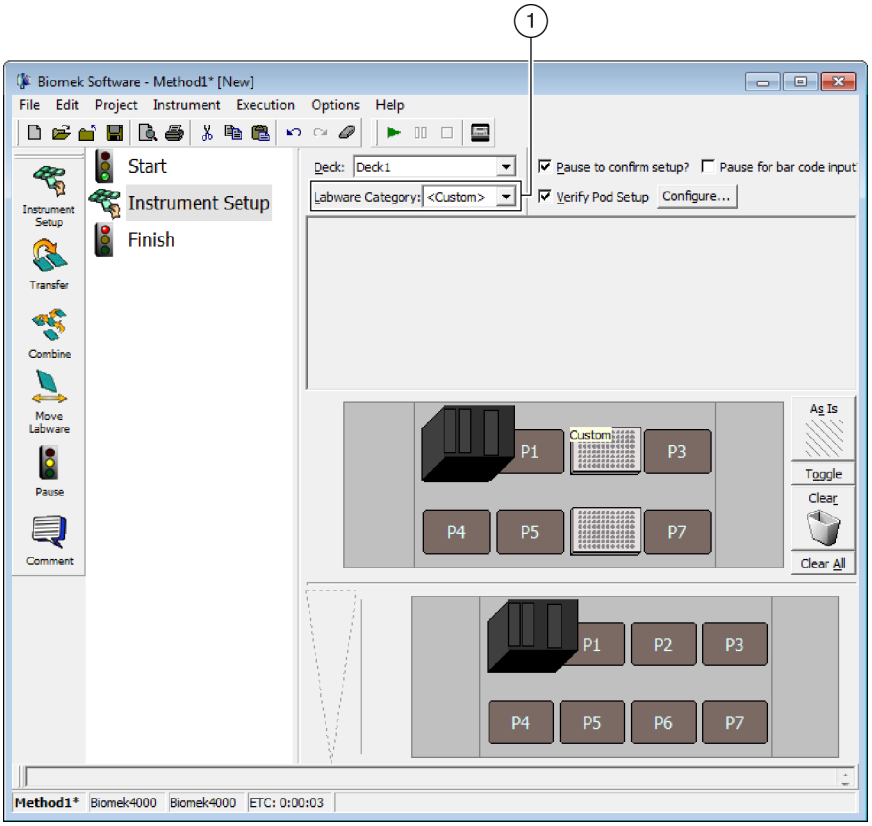
1 Highlight the **Instrument Setup** step.

2 Add the desired labware to create the custom labware from to the deck; for example, if creating a custom reservoir, add a reservoir to the deck. (Refer to *Populating the Deck with Labware and Tools*).

3 Configure the **Labware Properties** for that piece of labware. (Refer to *Configuring Labware Properties for Tips* and *Configuring Labware Properties of Microplates, Reservoirs, and Tube Racks* to configure **Labware Properties**.)

4 In **Labware Category**, display the **<Custom>** labware category. If no custom labware has been created, no labware displays.

Figure 15.19 Custom Labware Category Displayed



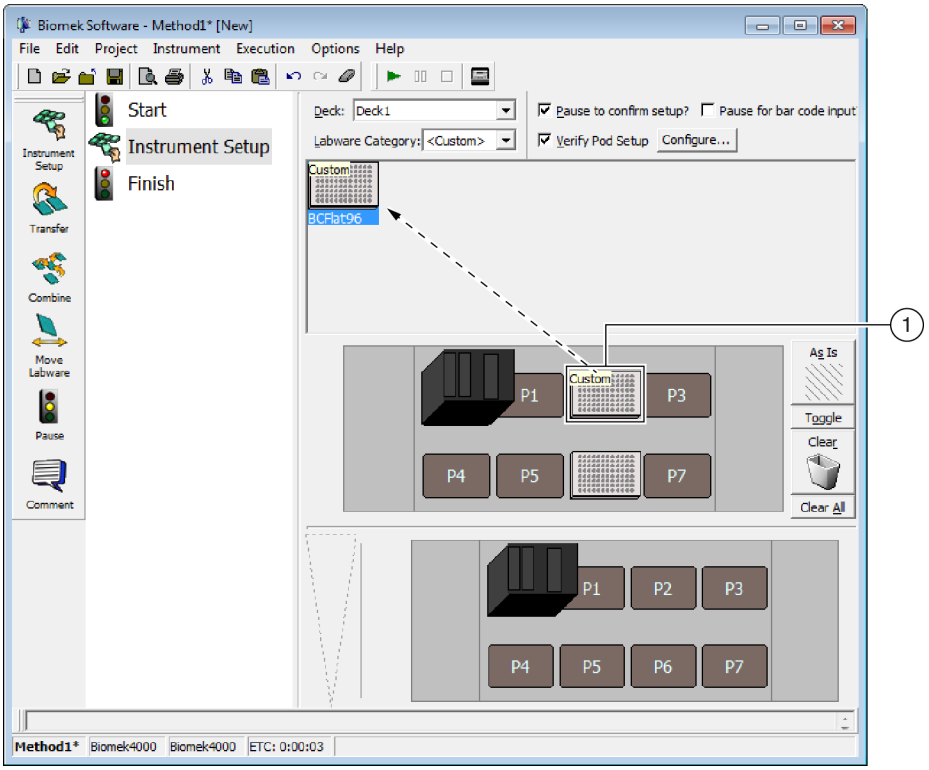
1. **Custom must be selected in Labware Category to create custom labware.**

---

5 Drag and drop the labware graphic from the Deck Layout to the **<Custom> Labware Category** display. If the **<Custom>** labware category is not visible, dragging and dropping the labware has no effect.

NOTE Multiple pieces of labware, or stacks of labware, cannot be added to the **<Custom>** labware category simultaneously; each piece of labware must be added individually. If a stack of labware is dragged to the Custom category, only the top labware in the stack is added.

Figure 15.20 Custom Labware Created



1. **Drag configured labware from the deck layout configuration to the graphical labware display with Custom selected in Labware Category to create a custom labware.**

---

6 To delete a piece of labware from the **< Custom >** labware category, drag the labware from the **< Custom>** labware category display to **Clear**.

NOTE Custom labware added to the **< Custom >** labware category in the **Instrument Setup** step is visible in the **Device Setup** (refer to CHAPTER 21, *Device Setup Step*).

Configuring Transfer and Combine Steps

The **Transfer** and **Combine** steps configure multiple aspirate and dispense operations using the selected tool to transfer liquid from all specified source wells to all specified destination wells. The **Transfer** step transfers liquid from a single source to one or more destinations, while the **Combine** step transfers liquid from one or more sources to a single destination.

The pipetting tool aspirates from all channels at once (one for a single-channel tool or eight for an eight-channel tool). The tool transfers the same volume from each channel in each aspirate and dispense cycle.

NOTE If there are multiple sources or destinations, each source or destination may have a different volume transferred, but all wells on any single source or destination must have the same volume transferred. To transfer different volumes to or from wells on the same piece of labware, configure multiple sources or destinations using the same labware but specify different wells and volumes or use a **Transfer From File** step (see CHAPTER 18, *Transfer From File Step*).

The **Transfer** and **Combine** steps perform five liquid-handling functions through the step configuration, eliminating the need to insert multiple steps to complete the liquid transfer:

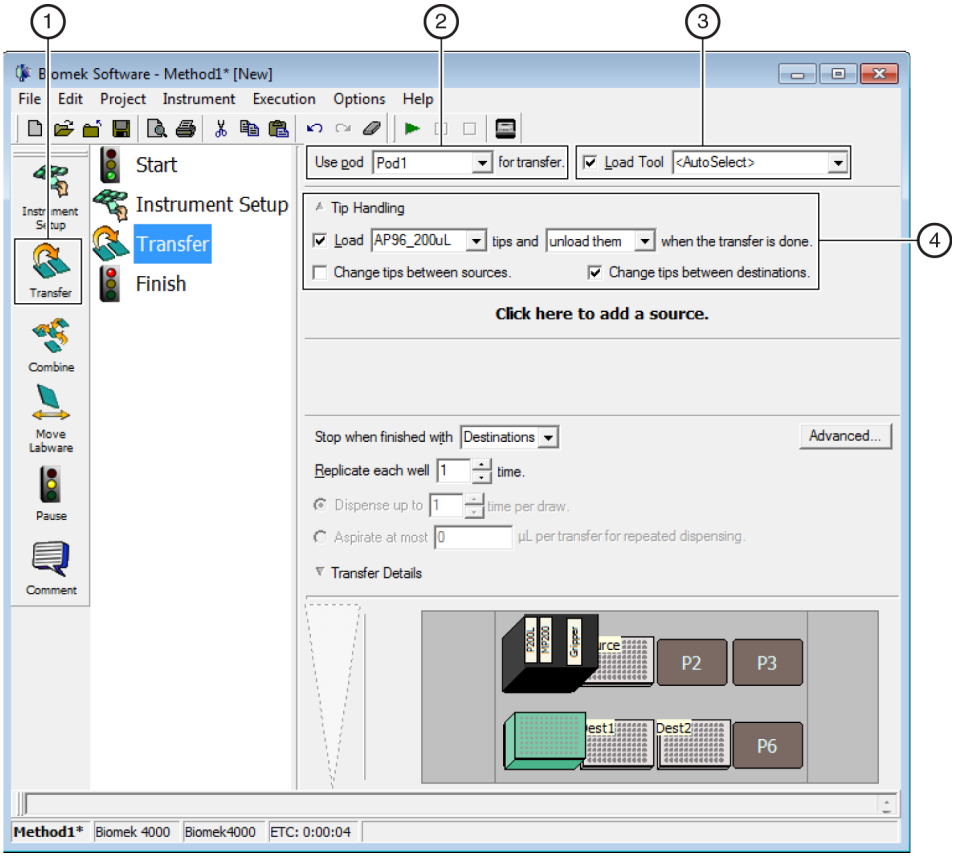
- Load a tool.
- Load tips onto the tool.
- Aspirate liquid from source(s).
- Dispense liquid to destination(s).
- Unload tips from tool.

The **Transfer** and **Combine** step configuration includes:

- *Configuring Tool Handling*
- *Configuring Tip Handling*
- *Configuring Source Labware*
- *Configuring Destination Labware*
- *Configuring Transfer Details*

Insert a **Transfer** or **Combine** step into the Method View (Figure 15.21).

Figure 15.21 Transfer Step Configuration



1. **Transfer** step
2. **Pod Configuration**: Because the Biomek 4000 instrument only has one pod, the default **Pod1** is displayed.
3. **Load Tool**: Select a specific tool from the drop-down or keep the default as **<AutoSelect>** where the software chooses the appropriate tool for the step.
4. **Tip Handling Configuration**: **Tip Handling** parameters specify tip type, whether tips remain on the pod at the end of the liquid transfer, when to change tips, and tip wash options.

Configuring Tool Handling

Tool usage for a transfer process can be set up either by choosing a specific tool or allowing the software to automatically select the most appropriate tool for the transfer. For details on configuring **<AutoSelect>** to your preference, see CHAPTER 7, *Editing Compatible Tools*.

To configure tool handling, determine whether you wish to specify a tool for the transfer process or use the default **<AutoSelect>** feature, allowing the software to choose the appropriate tool. If you wish to manually select the tool, select the **Load Tool** drop-down arrow (Figure 15.21), and choose the appropriate tool.

IMPORTANT Automatic tool-selection is determined by two factors, including the volume of liquid specified for a transfer and the capacity of a tool. Because the additional volume of an air gap is not considered when the software selects a tool, when large air gaps are needed for pipetting operations, the total volume required for pipetting opertations could exceed the capacity of a tool, resulting in a validation error similar to the examples below:

- "*Error trying to aspirate from P5: Error in the aspirate operation of the "Default Template" pipetting template: Move of Pod to D of 37.0000 µL violates D tool maximum of 34*"
- "*Error trying to aspirate from P5: Error in the aspirate operation of the "Default Template" pipetting template: Move of Pod1 to D of 2.8519 violates D axis maximum of 2.4000.*"

To prevent a validation errors similar to those listed above, either:

- Select a larger tool from the **Load Tool** drop-down.
- Designate a lower volume of liquid to transfer (see *Configuring Destination Labware* and, for **Combine** steps, also see *Configuring Source Labware*).
- Designate a smaller air gap (see CHAPTER 9, *Understanding and Creating Techniques*).

Configuring Tip Handling

Configuring **Tip Handling** in the **Transfer** and **Combine** steps is not required, because the default **Tip Handling** configuration locates and loads clean tips automatically every time a **Transfer** or **Combine** steps are initiated and unloads them when the step is completed. It is recommended, however, that **Tip Handling** configuration be supplied if cross contamination or conserving consumables is a concern, or a specific tip type should be used.

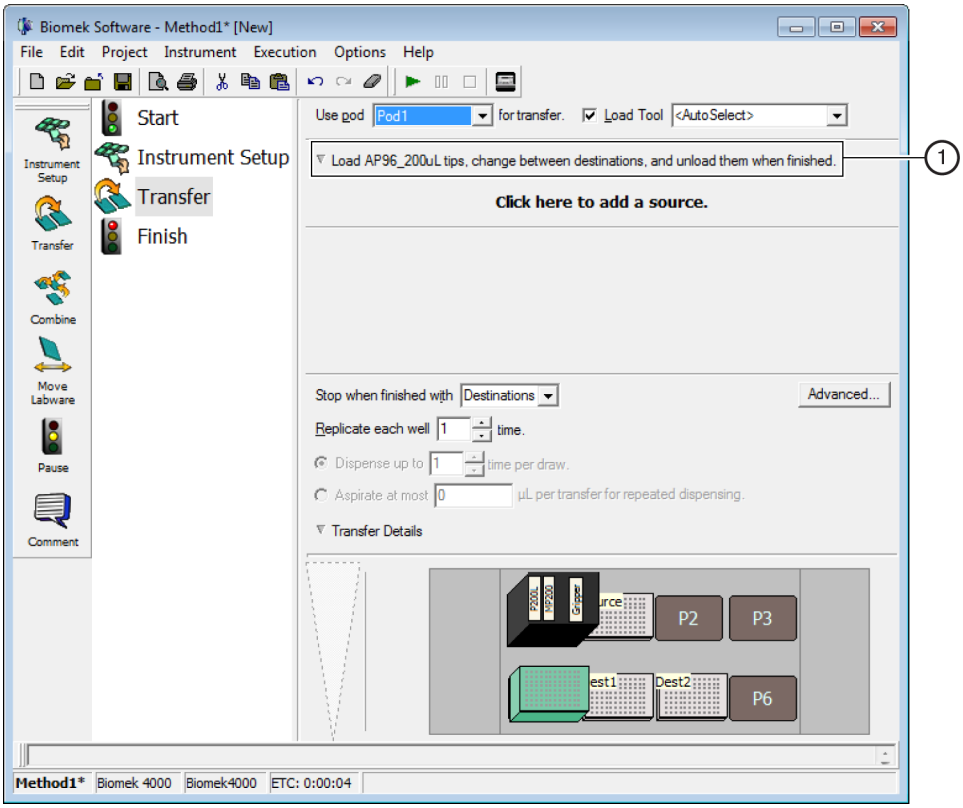
Tip Handling is also used to configure changing tips between transfer operations. Tips may be changed between sources or between destinations.

To configure **Tip Handling** (Figure 15.21) for the **Transfer** or **Combine** steps:

---

1 If **Tip Handling** is not already displayed, click the arrow or sentence summary to expand the **Tip Handling** configuration (Figure 15.21).

Figure 15.22 Tip Handling Collapsed



1. **Tip Handling**: A sentence summary is displayed when **Tip Handling** is collapsed. To expand **Tip Handling**, select the down arrow or the sentence summary.

---

2 Select **Load** to load new tips at the start of the **Transfer** or **Combine** step.

NOTE If **Load** is not selected, the **Transfer** or **Combine** step uses previously loaded tips, rather than loading new tips at the start of the step.

If **Load** is selected and the tips loaded on the tool have been used, an error may occur. To increase the number of uses allowed for tips, increase the **Load no more than X times** count in the **Labware Properties** configuration in the **Instrument Setup** step (refer to *Configuring Tip and Labware Properties*).

---

3 If **Load** is selected, select the type of tips to load from the drop-down list, or from the Current Deck Display.

NOTE If tips are selected from the Current Deck Display, and the tips are named, **Load** displays the name, not the tip type. If a name was not assigned to the tips, the tip type is displayed in **Load**.

Naming tips in the **Instrument Setup** step limits when tips will automatically be selected (see *Configuring Tip and Labware Properties* for additional information). In general, if you are not using this functionality, it is recommended that tips not be named in the **Instrument Setup** step because this could restrict the instrument from locating available tips.

4 To return tips to the tip box after the **Transfer** or **Combine** step is completed, select **unload them**.

OR

To leave tips on after the **Transfer** or **Combine** steps is completed, select **leave them on**.

NOTE To conserve tips when using the **Transfer** or **Combine** steps within a **Loop** step, uncheck **Load** and select **leave them on** (steps 4 and 6 above). Add **Load Tool** step and a **New Tips** step to the method prior to the **Loop** step, and an **Unload Tips** step after the **Loop**. This loads new tips before the **Loop** step, uses the same set of tips for all **Transfer** or **Combine** steps completed as part of the **Loop**, and unloads the tips when the **Loop** step is completed.

5 Select **Change tips between sources.**, to change tips each time a new source well is accessed.

NOTE **Change tips between sources** changes tips any time it is required to aspirate liquid from a different well or wells than the previous aspirate operation. For example, if transferring a full 96-well plate using the MP200 tool, the instrument instructs the instrument to use new tips when aspirating from each column.

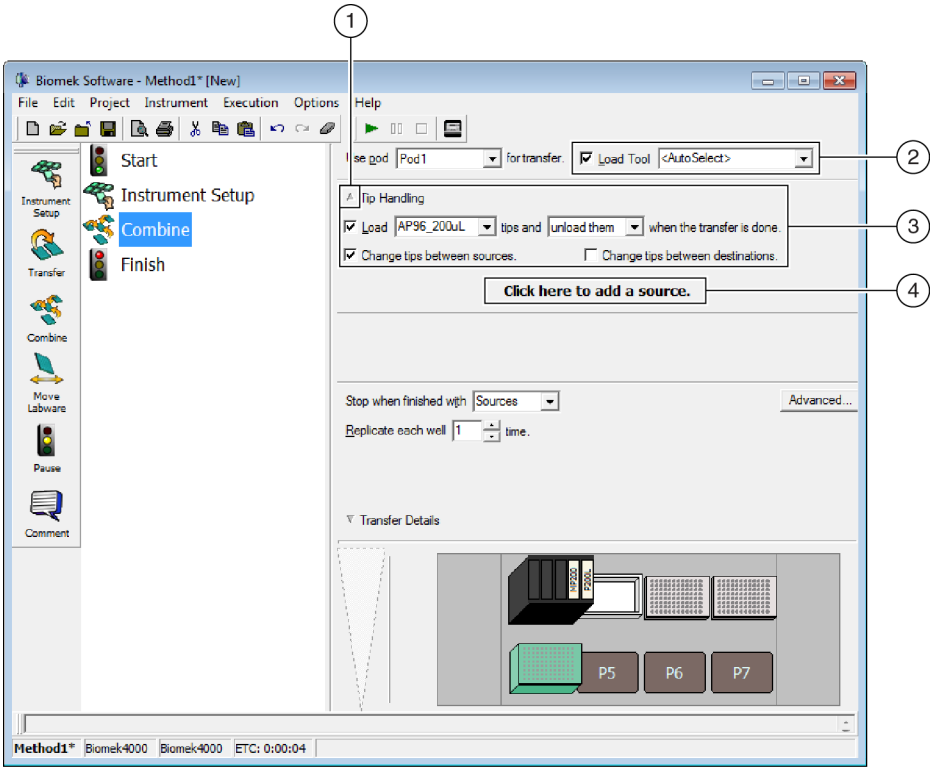
6 Select **Change tips between destinations.**, to change tips each time a new destination well is accessed.

NOTE **Change tips between destinations** changes tips after all dispense operations, except the last. Tips are removed after the last dispense operation only if **unload them** is selected in **Tip Handling**. If there is only one **Destination Well** (for P tools) or Destination Column (for MP tools) configured, **Change tips between destinations** does not change tips.

The **Tip Handling** configurations can be collapsed to allow more room during **Source** and **Destination Labware** configuration. When collapsed, the tip handling configuration is displayed as a sentence summary (Figure 15.22). Use the sentence summary to verify that tip handling has been configured appropriately.

To collapse or expand the **Tip Handling** configuration, click the arrow to the left of **Tip Handling** or the textual display (Figure 15.23).

Figure 15.23 Combine Step—Adding Source Labware



1. **Arrow to collapse/expand Tip Handling.**
2. **Tool configuration.**
3. **Expanded Tip Handling configuration.**
4. **Click here to add a source. The Source Labware configuration opens.**

Configuring Source Labware

A 'source' is a group of wells accessed at one time by the instrument to aspirate liquid; for example, depending on the tool loaded onto the pod, it aspirates from either 1 or 8 wells at a time.

NOTE If there are multiple sources in the **Combine** step, each source may have a different volume transferred, but all wells on each source must have the same volume transferred. To transfer different volumes from wells on the same microplate, configure multiple sources using the same source plate but specifying different wells and volumes.

The **Source Labware** configuration for the **Transfer** and **Combine** steps includes specifying:

- Labware type
- Labware location
- Liquid amount to transfer (for **Combine** step only)
- Liquid type
- Well pattern
- Technique selection
- Pipetting height

NOTE A single source is configured for the **Transfer** step, because the **Transfer** step moves liquid from a single source to one or more destinations. Multiple sources can be configured for the **Combine** step, because the **Combine** step moves liquid from multiple sources to a single destination.

To configure **Source Labware** for the **Transfer** and **Combine** steps:

1 Select **Click here to add a source** (Figure 15.23). **Source:** configuration appears.

2 Click on the desired piece of labware in the Current Deck Display. The labware type and position for that piece of labware is entered automatically into the **Source Labware** configuration.

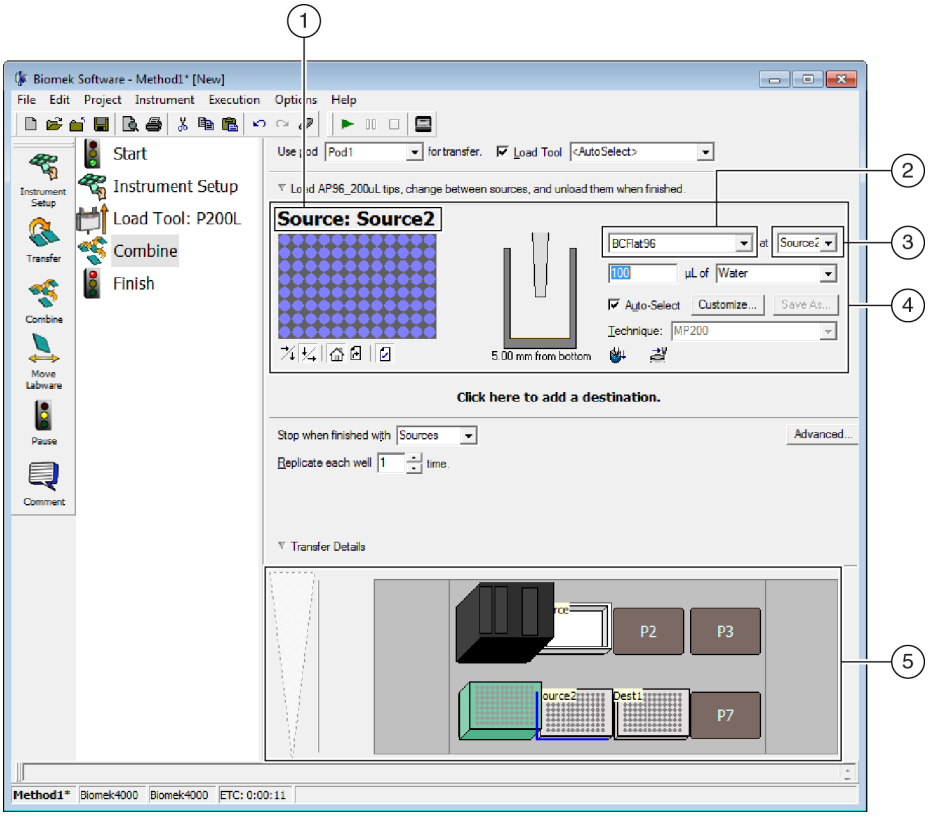
NOTE If the selected labware is named, the name of the labware appears instead of the deck position.

OR

Select a **Source Labware** (Figure 15.24) type and specify the deck position.

NOTE To configure additional **Source Labware** for a **Combine** step, select **Click here to add a source**, and then select another piece of labware from the Current Deck Display. A Destination labware must be configured before configuring additional source labware. If an incorrect piece of labware is selected, right click on the labware title and select **Delete** on the menu that appears, or change the Source Labware selection by clicking anywhere in the source labware configuration area, and selecting another piece of labware.

Figure 15.24 Combine Step—Source Labware Configuration



1. **Source Labware title.**
2. **Source Labware type selection.**
3. **Deck position selection.**
4. **Source Labware configuration.**
5. **Current Deck Display**: The Current Deck Display is used for labware selection, and it displays the status of the deck upon completion of the previous step.

---

3 Verify the deck position of the labware.

NOTE A bright blue outline appears in the Current Deck Display around the labware designated as the **Source Labware**.

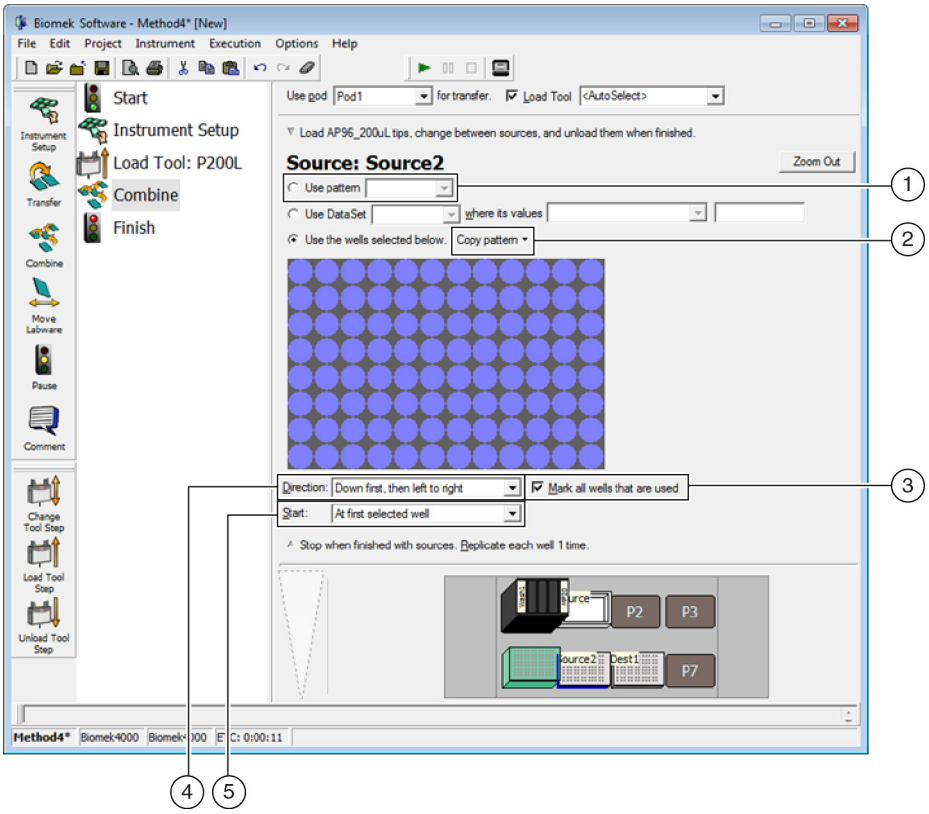
---

4 To specify the wells in a microplate to access, double click the source labware in the step configuration to zoom in on the labware (Figure 15.25).

NOTE To call up a menu for **Zoom In** and a **Specify Selection as Text** option, right click on the labware.

Specify Selection as Text allows selection of wells as targets for aspirate and dispense operations. **Specify Selection as Text** may also be used to enter variables or expressions.

Figure 15.25 Transfer Step—Zoomed-In Labware Configuration



1. **Use pattern**: Use a well pattern created using the **Define Pattern** step or using the **Well Pattern Editor**.
2. **Copy pattern**: Use a well pattern created in the **Well Pattern Editor**. The option of creating a unique pattern in the graphic as also available.
3. **Mark all wells that are used**: This option will mark all wells accessed when the step is completed.
4. **Direction**: Select the direction in which wells are accessed.
5. **Start**: Select the first well accessed.

---

5 Select the wells from which to transfer by using one of the following techniques:

NOTE A multi-tip pipette tool always selects groups of wells in columns of 8 while a single-tip pipette tool can select individual wells.

- Choose **Copy Pattern** to use a previously defined well pattern created using the **Well Pattern Editor** (refer to CHAPTER 11, *Creating Well Patterns*). Select the desired pattern.

  NOTE The pattern must be compatible with the tool selected and the labware type.

  The software automatically selects a tool based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired tool.

- Select **Use pattern** and choose the previously defined pattern from the list to use a pattern created in a **Well Pattern Editor** or **Define Pattern** step.

  NOTE Refer to CHAPTER 18, *Define Pattern Step*, for more information about creating patterns using the **Define Pattern** step.

- Define a well pattern using data sets (refer to CHAPTER 14, *Defining Well Patterns Using Data Sets*).
- Create a custom well pattern from the labware grid by dragging the mouse and using Ctrl and Shift on the keyboard.

  NOTE Hold Shift and click a well to select additional wells without deselecting any wells. Hold Ctrl and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted.

NOTE To save the new pattern, right click the labware graphic and select **Save Pattern** from the menu. Enter a name for the pattern in **New Pattern** and choose **OK**.

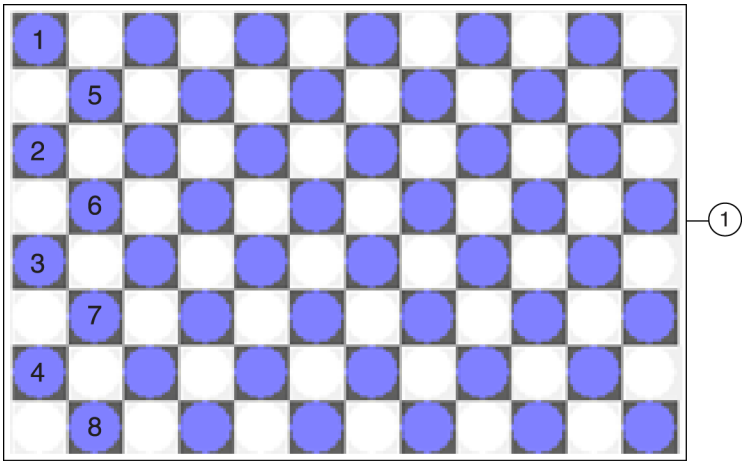
---

6 Select the **Direction** in which source wells are mapped to destinations. **Down first, then left to right** is the default selection.

NOTE **Direction** controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The **Transfer** step automatically determines the most efficient way to complete the transfer.

- **Down first, then left to right** - goes down each column from top to bottom, then goes right to the next column (Figure 15.26)

Figure 15.26 Wells Accessed Down First, Then Left to Right

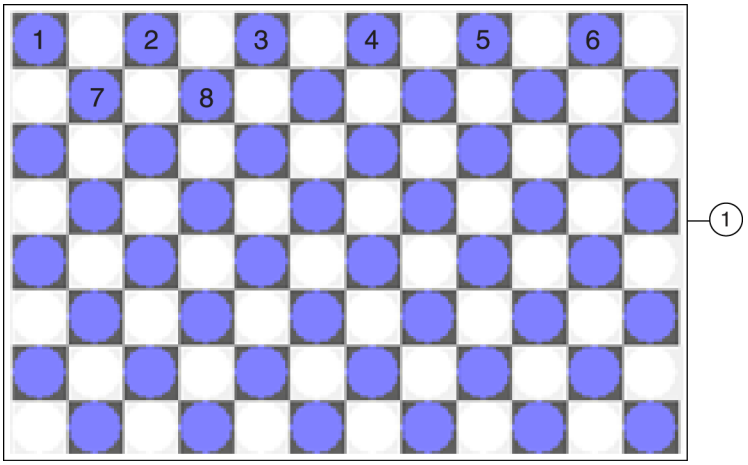


1. **Down first, then left to right**: Wells are mapped to destination labware in the order indicated, going down each column and then moving to the right to the next column.

OR

- **To the right first, then top to bottom** - goes across each row from left to right, then goes down to the next row (Figure 15.27)

Figure 15.27 Wells Accessed to the Right First, Then Top to Bottom



1. **To the right first, then top to bottom**: Wells are mapped to the destination labware in the order indicated, going across each row and then moving down to the next row.

NOTE The direction can also be selected when the labware is zoomed out by using the icon (**Down, then right**) or icon (**Right, then down**) beneath the labware.

---

7 Select the first well accessed in **Start**. **At first selected well** is the default selection.

NOTE **Start** controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The **Transfer** step automatically determines the most efficient way to complete the transfer.

- **At first selected well** - moves in the selected **Direction**, starting from the first well selected on the labware.

  OR

- **At first unmarked well** - moves in the selected **Direction**, starting at the first unmarked well on the labware.

NOTE The selected labware must have marks from a previous **Transfer** or **Combine** step with **Mark all wells that are used** selected.

NOTE The start location can also be selected when the labware is zoomed out by using the icon (**Start at selection**) or the icon (**Start at last mark**) buttons beneath the labware.

8 De-select **Mark all wells that are used**, if it is not desired to mark wells. This option must be selected to use any options later in the method that make use of marks. For example, if **Mark all wells that are used** is selected and the **Transfer** step runs out of sources before using all destinations, it marks the wells that have liquid transferred to them. Another **Transfer** step is transferring liquid to the same plate. By selecting **At first unmarked well** as the **Start** condition, the first source well will be transferred to the first unused destination well and continue according to the specified **Direction. Mark all wells that are used** is selected by default.

NOTE **Mark all wells that are used** can also be selected when the labware is zoomed out by using the (**Set mark**) icon beneath the labware.

9 Choose **Zoom Out** to return to the step configuration screen.

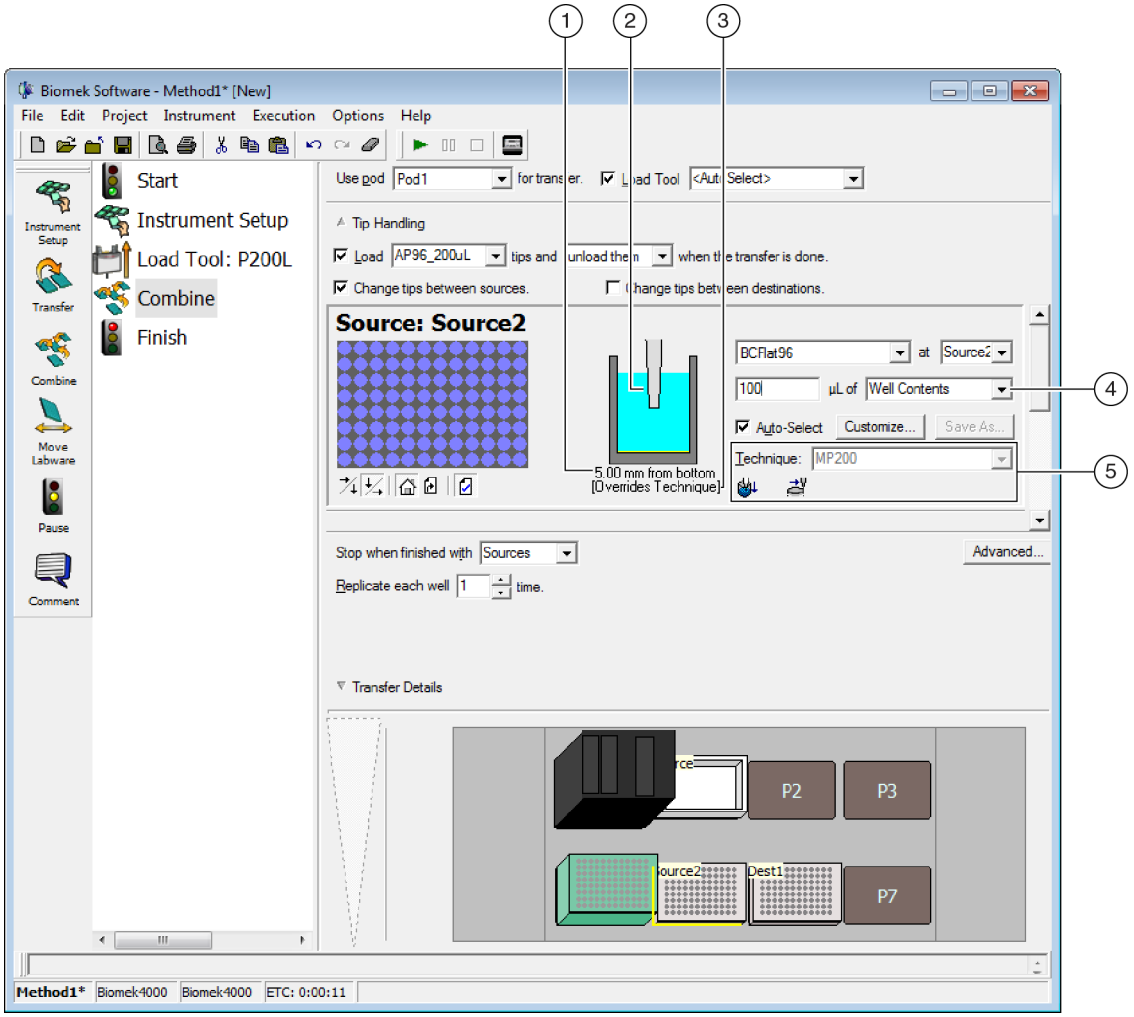
10 For a **Combine** step, enter the amount of liquid (µL) to aspirate from the **Source Labware**. This will also be the amount of liquid dispensed into the destination labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue**.

NOTE Refer to CHAPTER 14, *Specifying Volumes Using Data Sets*, for information on specifying volumes using data sets.

11 In **Using liquid type**, select the type of liquid in the **Source Labware** (Figure 15.28). Keeping the default selection, **Well Contents**, allows the software to identify the liquid type based on other properties defined elsewhere in the method.

NOTE The **Using liquid type** selection is one of the criteria the software uses to choose the technique that best applies to the operation.

Figure 15.28 Combine Step—Source Labware Configuration



1. **Adjust aspirate height**
2. **Tip height**
3. **Overrides Technique**: Indicates that the height of the tip has been manipulated.
4. **Liquid type selection**
5. **Technique selection**

---

12 Keep the auto-selected **Technique** (refer to *Auto-Selection of a Technique*).

NOTE The software automatically selects a **Technique** based on the liquid type, labware type, tip type, and volume being aspirated.

OR

Manually select the desired **Technique**, or customize the selected **Technique** (refer to *Customizing and Saving a Technique*).

13 Leave the height as is to use the settings specified in the pipetting technique.

OR

Set the aspirate height manually using one of the following techniques:

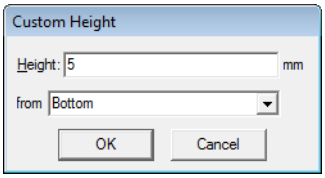
- Set the aspirate height by positioning the cursor over the graphic of a tip inside a well (Figure 15.28). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

NOTE The cursor changes to a  when positioned over the graphic.

- Click in the graphic of a tip inside a well, and adjust the height using the PgUp and PgDn and the up and down arrow keys. PgUp and PgDn change the height by 1 mm at a time; the up and down arrow keys change the height by 0.1 mm at a time.
- Right click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and **Custom Height** appears (Figure 15.29). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

NOTE The phrase (**Overrides Technique**) appears below the graphic when the tip height is changed by manipulating the graphic (Figure 15.28), or when the technique is changed with the **Customize** option.

Figure 15.29 Custom Height Prompt



14 For a **Combine** step, repeat steps 1 to 13 for each **Source Labware** desired.

NOTE A **Destination Labware** must first be selected before additional **Source Labware** can be configured.

Auto-Selection of a Technique

Auto-Select option is the default setting in the **Transfer** and **Combine** steps configuration. Disabling **Auto-Select** provides access to a list of predefined techniques, as well as allowing access to the **Technique Editor** so changes can be made to existing techniques.

NOTE For more information on creating, editing, and saving techniques, refer to *Customizing and Saving a Technique* in this chapter, and CHAPTER 9, *Understanding and Creating Techniques*.

Customizing and Saving a Technique

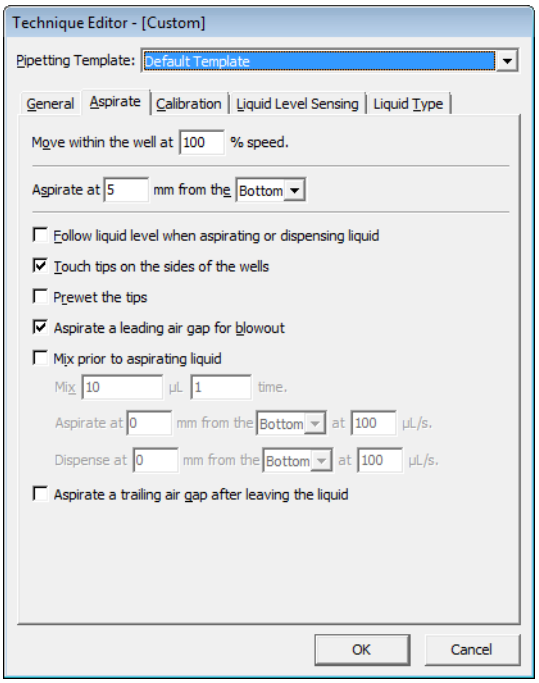
To select a **Technique** other than the technique selected automatically by Biomek Software:

1 Uncheck **Auto-Select**. The **Technique:** field is activated.

2 Select a **Technique:** from the list of predefined techniques.

3 Click **Customize** to modify the technique, if desired. The **Technique Editor** appears (Figure 15.30).

Figure 15.30 Technique Editor - Dispense Options



NOTE The **Aspirate** tab is virtually the same as the **Dispense** tab, with the exception of the **Aspirate a trailing air gap after leaving the liquid** and **Prewet the tips** pipetting options which appear on the **Aspirate** tab. When dispense operations are being configured, only the **Dispense** tab is displayed, while the **Aspirate** tab is displayed only when configuring aspirate operations. The **Liquid Level Sensing** tab only appears if the pod or tool supports liquid level detection.

4 Make desired changes in the applicable tabs of the **Technique Editor**.

5 Click **OK** to save the edited technique and return to the **Transfer** and **Combine** steps.

6 Click **Save As** to save an edited technique for use in this method and others.

NOTE If **Save As** is not selected, the technique is saved with the current method, but is not accessible to other methods or other steps within the current method.

Configuring Destination Labware

A 'destination' is a group of wells accessed at one time by the instrument to dispense liquid. Depending on the tool loaded onto the pod, it aspirates from either 1 or 8 wells at a time.

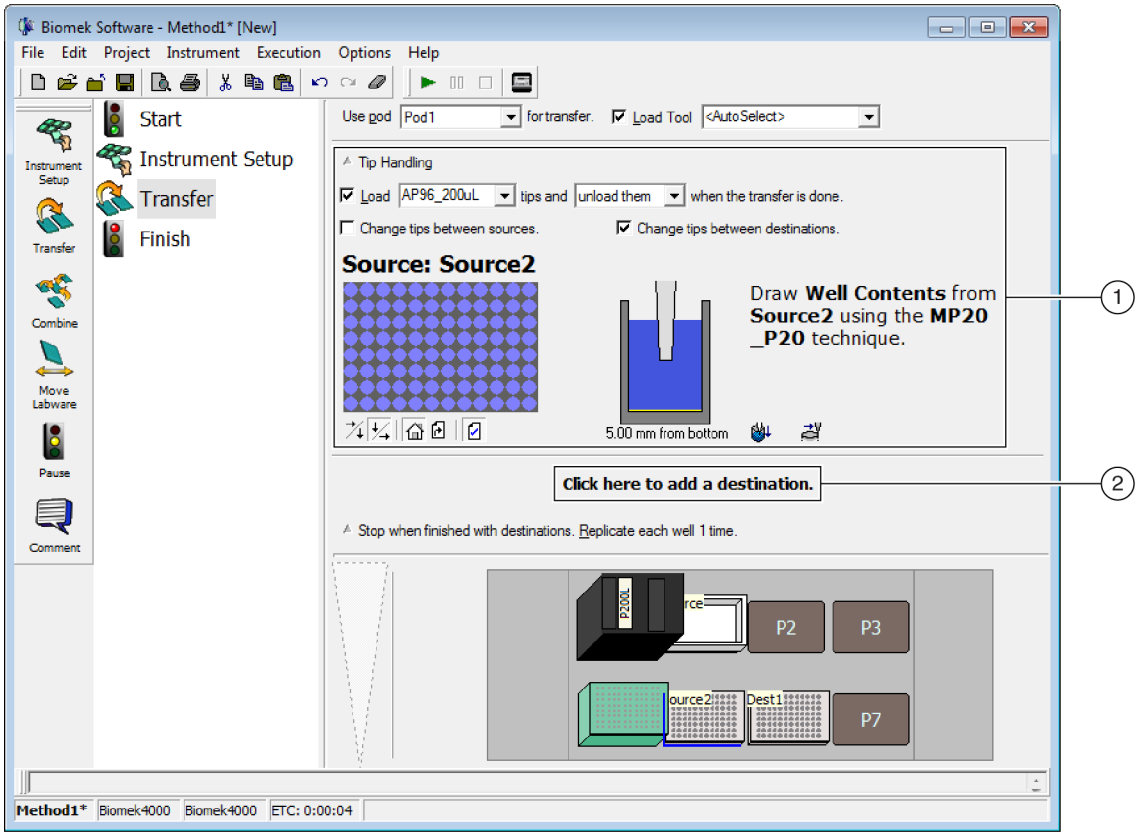
NOTE If there are multiple destinations, each destination may have a different volume transferred, but all wells on each destination must have the same volume transferred. For example, to transfer different volumes to different wells on the same 96-well plate, configure multiple destinations using the same destination plate, but specifying different wells and volumes.

The **Destination Labware** configuration for the **Transfer** and **Combine** steps includes specifying:

- Labware type
- Labware location
- Liquid amount to transfer (for **Transfer** step only)
- Liquid type
- Well pattern to access
- Technique selection
- Pipetting height

NOTE Multiple destinations can be configured for the **Transfer** step, because the **Transfer** step moves liquid from a single source to one or more destinations. A single destination is configured for the **Combine** step, because the **Combine** step moves liquid from one or more sources to a single destination.

Figure 15.31 Transfer Step—Addition Destination Labware



1. **Configured Source Labware.**
2. **Click this button to add Destination Labware and open the Destination Labware configuration.**

To configure **Destination Labware** for the **Transfer** and **Combine** steps:

---

1 Select **Click here to add a destination** (Figure 15.31). The **Destination Labware** configuration appears.

NOTE **Transfer** steps can also be used to dispense liquids to waste by selecting the **WasteAlp** as the **Destination Labware**. For additional details on using the Liquid Waste Station, see the *Biomek 4000 ALPs and Accessories Manual*.

⚠ WARNING

Risk of contamination. The Liquid Waste Station can be contaminated from method solutions. Follow the appropriate decontamination procedures outlined by your laboratory safety officer.

2 Click on the desired piece of labware in the Current Deck Display. The labware type and position for that piece of labware is entered automatically into the **Destination Labware** configuration.

NOTE If the selected labware is named, the name of the labware appears instead of the deck position.

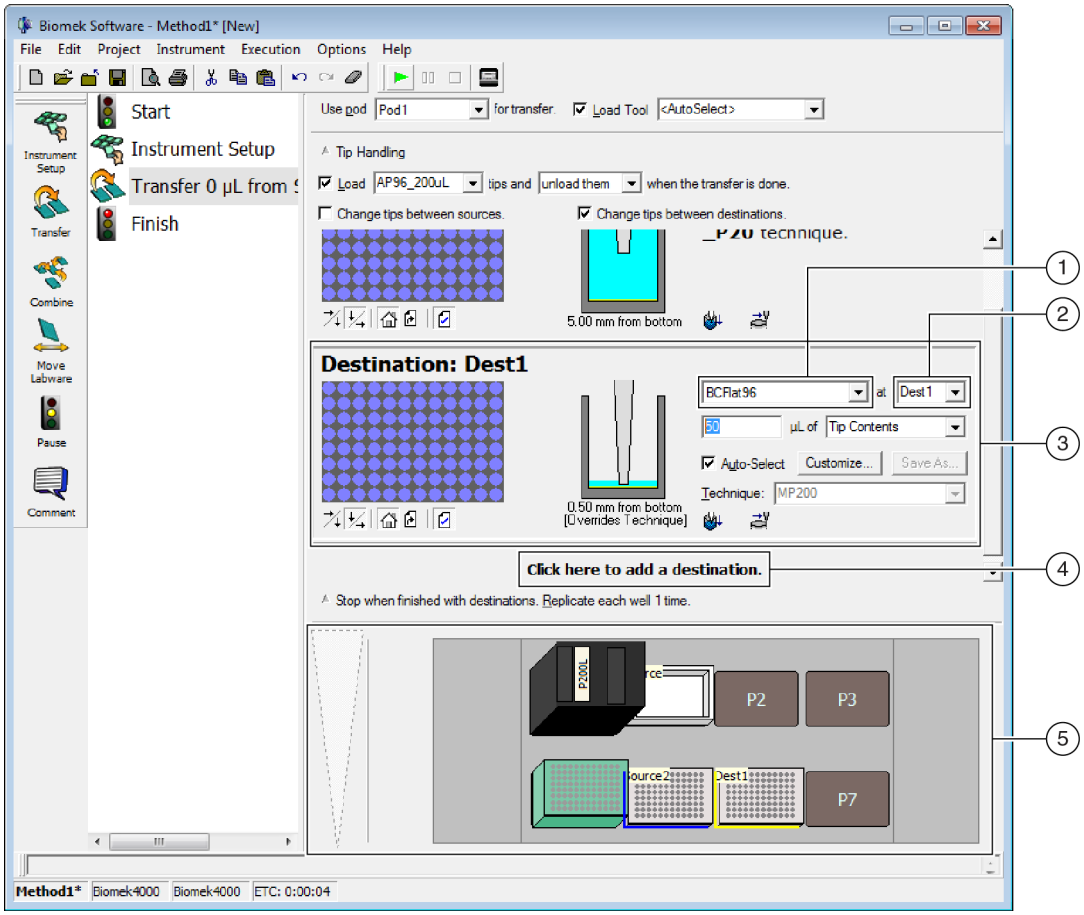
OR

Select a **Destination Labware** (Figure 15.32) type and deck position.

NOTE Once the first **Destination Labware** has been selected, the **Source Labware** parameters are collapsed to display a sentence summary. To reopen the **Source Labware** parameters, click anywhere in the **Source Labware** configuration area.

NOTE Subsequent labware selections modify the active **Source** or **Destination** Labware configuration. To configure additional **Destination Labware**, select **Click here to add a destination**, or select outside a labware configuration, and then select another piece of labware from the Current Deck Display. If an incorrect piece of labware is selected, right click on the labware title and select **Delete** on the menu that appears.

Figure 15.32 Transfer Step—Destination Labware Configuration



1. **Select Destination Labware type.**
2. **Deck position selection.**
3. **Destination Labware configuration.**
4. **Additional Destination Labware: Continue addition Destination Labware by clicking this button, or by selecting more labware in the Current Deck Display.**
5. **Current Deck Display**: Displays the status of the deck upon completion of the previous step. Also useful for labware selection.

---

3 Verify the deck position of the labware.

NOTE A bright yellow outline appears in the Current Deck Display around the labware designated as the **Destination Labware**.

---

4 To specify the wells of a microplate to access, double click the destination labware in the step configuration to zoom in on the labware.

NOTE To call up a menu for **Zoom** and a **Specify Selection as Text** option, right click on the labware.

Specify Selection as Text allows selection of wells as targets for aspirate and dispense operations. **Specify Selection as Text** may also be used to enter variables or expressions.

5 Select the wells from which to transfer using one of the following techniques:

NOTE A multi-tip pipette tool always selects groups of wells in columns of 8 while a single-tip pipette tool can select individual wells.

- Choose **Copy Pattern** and select the desired pattern to use a previously defined well pattern created using the **Well Pattern Editor** (refer to CHAPTER 11, *Creating Well Patterns*).

  NOTE The pattern must be compatible with the tool.

  The software automatically selects a tool based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired tool.

- Select **Use pattern** and choose the previously defined pattern from the list to use a pattern created in a **Well Pattern Editor** or **Define Pattern** step.

  NOTE Refer to CHAPTER 18, *Define Pattern Step*, for more information about creating patterns using the **Define Pattern** step.

- Define a well pattern using data sets (refer to CHAPTER 14, *Defining Well Patterns Using Data Sets*).
- Create a custom well pattern from the labware grid by dragging the mouse and using Ctrl and Shift on the keyboard.

  NOTE Hold Shift and click a well to select additional wells without deselecting any wells.

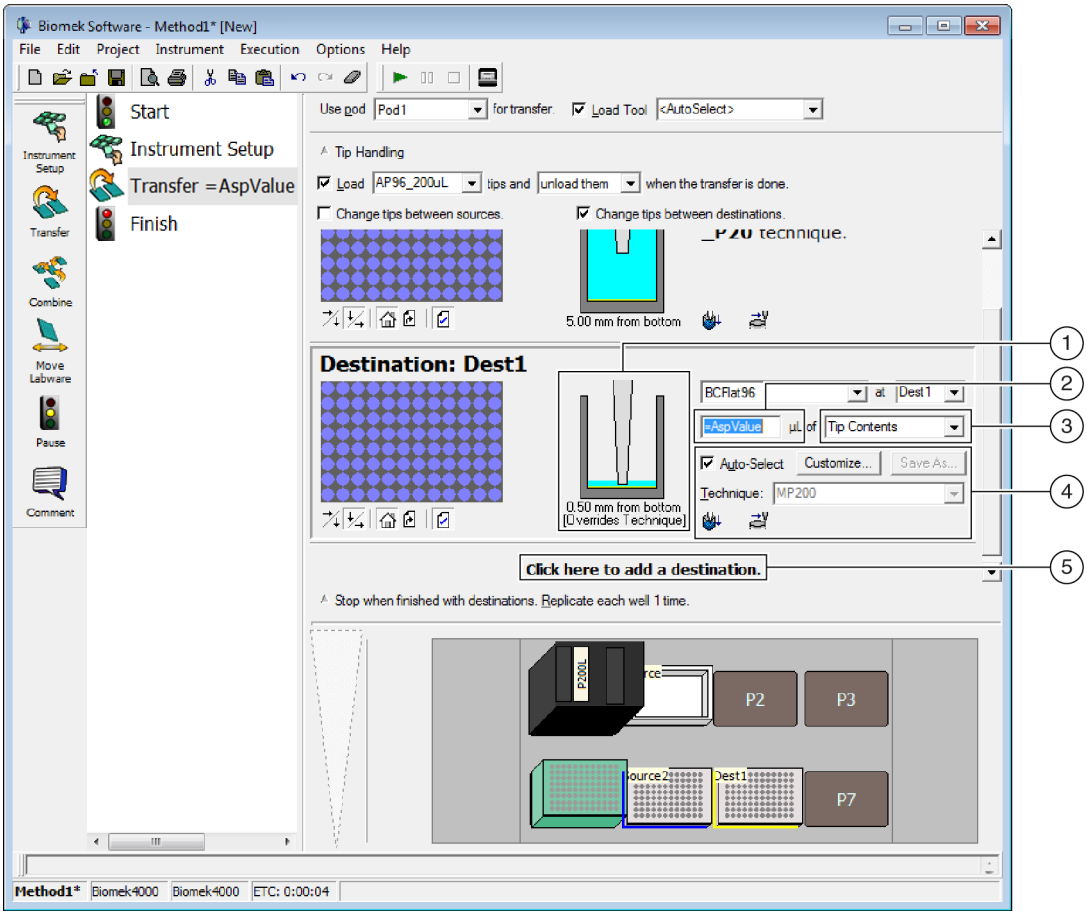
  Hold Ctrl and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted.

NOTE To save the new pattern, right click the labware graphic and select **Save pattern** from the menu. Enter a name for the pattern in **New Pattern** and choose **OK**.

6 Choose **Zoom Out** to return to the step configuration screen.

7 For a **Transfer** step, enter the amount of liquid (µL) to dispense into the **Destination Labware**. This will also be the amount of liquid aspirated from the source labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue** (Figure 15.33).

Figure 15.33 Transfer Step—Destination Labware Technique Configuration



1. **Adjust dispense height.**
2. **Amount to dispense.**
3. **Liquid type selection.**
4. **Technique selection.**
5. **Continue addition of Destination Labware by clicking this button, or by selecting more labware in the Current Deck Display.**

---

8 Verify that the liquid type indicated is correct. The liquid type dispensed to the **Destination Labware** should match the liquid type in the **Source Labware** configuration. Keeping the default selection, **Tip Contents**, allows the software to identify the liquid type based on other properties defined elsewhere in the method.

NOTE The liquid type selection is one of the criteria the software uses to choose the technique that best applies to the operation.

9 Keep the auto-selected **Technique** (refer to *Auto-Selection of a Technique*).

NOTE The software automatically selects a **Technique** based on the liquid type, labware type, tip type, and volume being aspirated.

OR

Manually select the desired **Technique** and customize the selected Technique (refer to *Customizing and Saving a Technique*).

10 Leave the height as is to use the settings specified in the pipetting technique.

OR

Set the dispense height manually using one of the following techniques:

- Set the dispense height by positioning the cursor over the graphic of a tip inside a well (Figure 15.33). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

  NOTE The cursor changes to a  when positioned over the graphic.

- Position the cursor in the graphic of a tip inside a well, and adjust the height using the PgUp and PgDn and the up and down arrow keys. PgUp and PgDn change the height by 1 mm at a time; the up and down arrow keys change the height by 0.1 mm at a time.

- Right click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and **Custom Height** appears (Figure 15.29). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

NOTE The phrase (**Overrides Technique**) appears below the graphic when the tip height is changed by manipulating the graphic, or when the technique is changed with the **Customize** option.

11 For a **Transfer** step, repeat steps 1 to 13 for each additional piece of **Destination Labware**.

Auto-Selection of a Technique

Auto-Select option is the default setting in the **Transfer** and **Combine** steps configuration. Disabling **Auto-Select** provides access to a list of predefined techniques, as well as allowing access to the **Technique Editor** so changes can be made to existing techniques.

NOTE For more information on creating, editing, and saving techniques, refer to *Customizing and Saving a Technique*, and CHAPTER 9, *Understanding and Creating Techniques*.

Customizing and Saving a Technique

Disabling **Auto-Select** provides access to a list of predefined techniques, as well as allowing access to the **Technique Editor** so changes can be made to existing techniques.

NOTE For more information on creating, editing, and saving techniques, refer to CHAPTER 9, *Understanding and Creating Techniques*.

To select a **Technique** other than the technique selected automatically by Biomek Software:

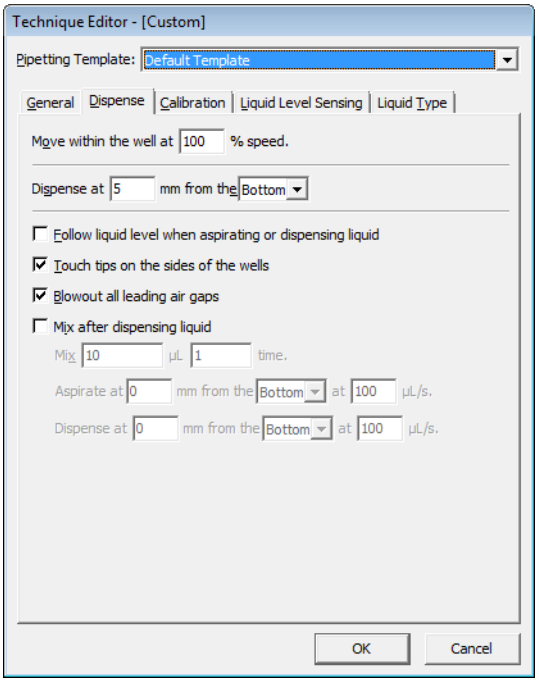
1. Uncheck **Auto-Select**. The **Technique:** field is activated.

2. Select a technique from the list of predefined techniques.

3. Click **Customize** to modify the technique, if desired. The **Technique Editor** appears (Figure 15.34).

   NOTE refer to CHAPTER 9, *Understanding and Creating Techniques*, for more information about the **Technique Editor**.

   Figure 15.34 Technique Editor—Dispense Options



   NOTE The **Aspirate** tab is virtually the same as the **Dispense** tab, with the exception of the **Aspirate a trailing air gap after leaving the liquid** and **Prewet the tips** pipetting options which appear on the **Aspirate** tab. When dispense operations are being configured, only the **Dispense** tab is displayed, while the **Aspirate** tab is displayed only when configuring aspirate operations.

4. Make desired changes in the applicable tabs of the **Technique Editor**.

5 Click **OK** to save the edited technique and return to the **Transfer** and **Combine** steps.

6 Click **Save As** to save an edited technique for use in this method and others.

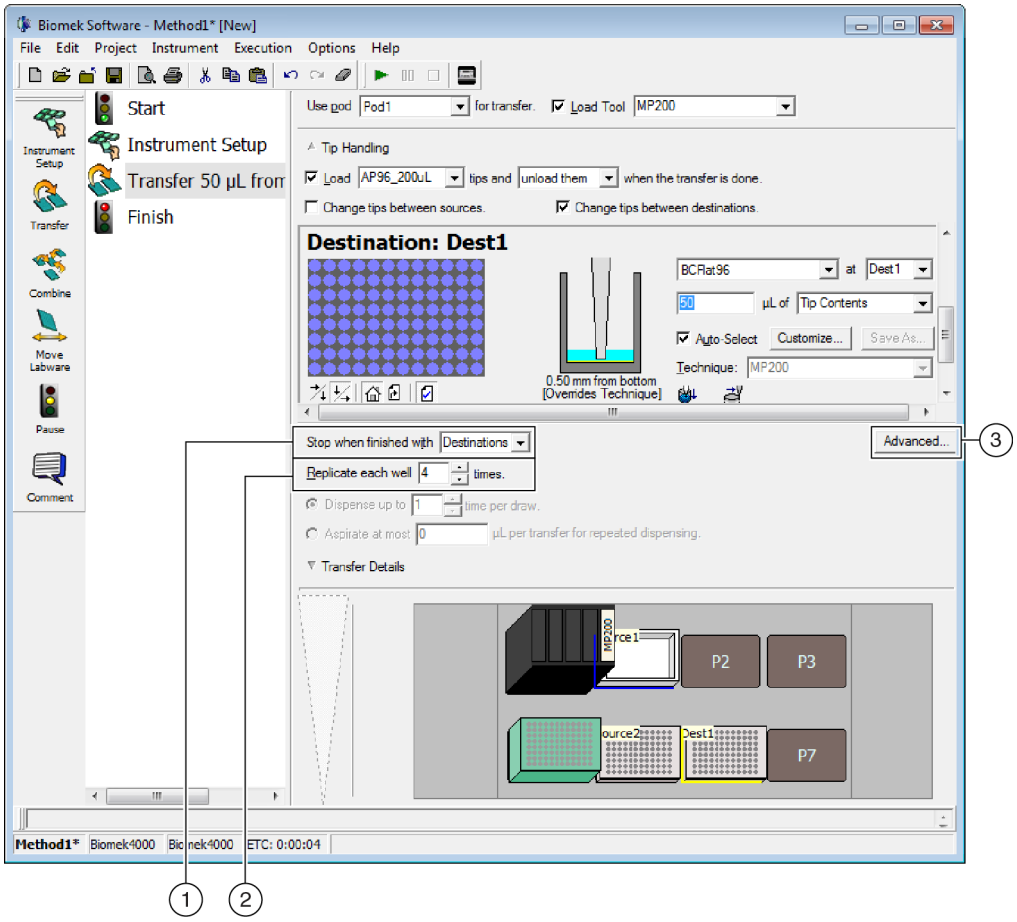
NOTE If **Save As** is not selected, the technique is saved with the current method, but is not accessible to other methods or other steps within the current method.

Configuring Transfer Details

Transfer Details (Figure 15.35) includes specifying:

- a stop condition for transfer operations
- a repeat pipetting configuration
- a maximum tolerance in timing between transfer operations (Figure 15.35)

Figure 15.35 Transfer Step—Additional Transfer Details



1. **Stop condition**: The stop option controls when the liquid transfer operation stops: after all destination wells or tubes have been used, or after all source wells or tubes have been used.
2. **Replicate**: The number of destination wells to which each source well is transferred.
3. **Advanced option**: The **Advanced...** option provides access to a **Just-In-Time (JIT)** configuration option for the **Transfer** and **Combine** steps. **JIT** specifies the maximum tolerance in timing between transfer operations.

To configure **Transfer Details** for the **Transfer** and **Combine** steps:

---

1 Click the arrow or sentence summary below the labware configuration section to expand **Transfer Details.**

---

2 In **Stop when finished with**, choose to determine when the liquid transfer operation stops: after **Sources, Destinations**, or **Either**.

- **Sources** - the **Transfer** or **Combine** is complete when it runs out of sources
- **Destinations** - the **Transfer** or **Combine** is complete when it runs out of destinations

- **Either** - the **Transfer** or **Combine** is complete when it runs out of either sources or destinations

  NOTE The default setting for **Stop when finished with** is **Destinations** to avoid cross contamination.

  NOTE If there are more source wells than destination wells and **Stop when finished with** is set to **Sources**, after dispensing to the final destination it will go to the first selected destination and continue until it runs out of sources. If **Destinations** is selected, it will stop after dispensing to the last destination and not use the remaining sources. If **Either** is selected, it will stop after dispensing to the last destination and not use the remaining sources.

  If marks are being used, the sources and/or destination wells used will be marked. Future **Transfer** or **Combine** operations may continue with the unmarked wells.

---

3 Select one of the repeat pipetting configuration options: **Dispense up to** or **Aspirate at most.**

NOTE If **Tip Handling** is configured to **Change tips between destinations**, the repeat pipetting options are unavailable for selection.

NOTE Only one repeat pipetting option may be selected. Either **Dispense up to** or **Aspirate at most** may be selected, but not both.

---

4 In **Dispense up to**, select the number of times the instrument is allowed to dispense per draw (aspirate). For example, if dispensing 75 µL to each of six microplates, three aspirate operations of 150 µL can each dispense into two destinations. In this case, **Dispense up to** is set to no fewer than two.

NOTE The default setting in **Dispense up to** is one, which does not allow a repeat pipetting operation. Settings of two or more allow repeat pipetting.

OR

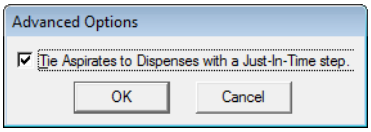
In **Aspirate at most**, select the maximum volume to aspirate from the source for repeat pipetting. For example, if dispensing 75 µL to each of six microplates, three aspirate operations of 150 µL can each dispense into two destinations. In this case, **Aspirate at most** is set to no less than 150 µL.

---

5 In **Replicates**, enter the number of times each source well should be transferred to the destination labware. For example, if **Replicates** is set at **3**, the first source well is transferred to the first three destination wells; the second source well is transferred to the next three destination wells; and so forth.

6 Select **Advanced** to change the default setting of applying a **Just-In-Time (JIT)** block to aspirate and dispense operations. **Just In Time** synchronizes the execution of the substeps within the **Transfer** or **Combine** step. The **Advanced Options** prompt appears (Figure 15.36).

Figure 15.36 Advanced Button - JIT Block



7 Uncheck Tie **Aspirate to Dispense with a JIT Block** to deactivate the **JIT** block.

8 Click **OK** to save any changes.

The **Transfer Details** configuration can be collapsed to allow more room during **Source** and **Destination Labware** configuration. When collapsed, the **Transfer Details** configuration is displayed as a sentence summary. Use the sentence summary to verify that **Transfer Details** have been configured appropriately.

To collapse or expand the **Transfer Details** configuration, click the arrow to the left of **Transfer Details** or the textual display.

Move Labware Step

NOTE The gripper tool is required to move labware.

The **Move Labware** step moves labware from one position on the instrument deck to another position. **Move Labware** can also remove labware from the deck by placing it in an appropriate disposal position, or to an external hardware device without halting the instrument or the method.

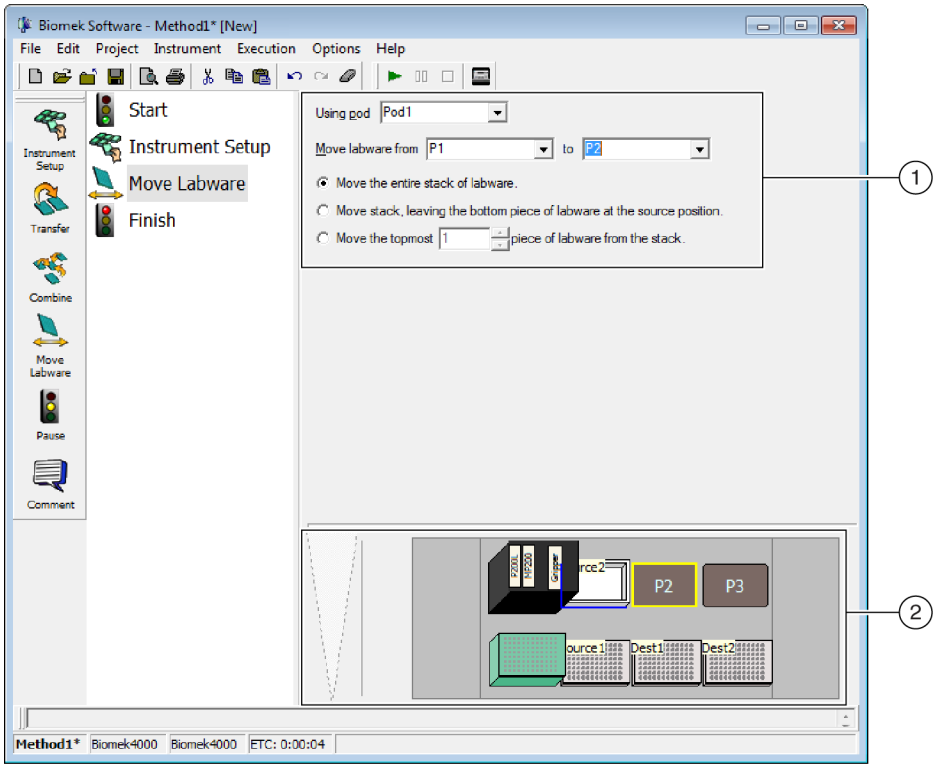
Inserting a Move Labware Step

To insert a **Move Labware** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 15.37).

Figure 15.37 Move Labware Step and Configuration



1. **Move Labware step configuration**: The stacking options configure how labware is moved from stacks on the deck.
2. **Current Deck Display**: The origination position is outlined in blue. The destination location is outlined in yellow.

Configuring the Move Labware Step

⚠ CAUTION

Make sure the correct ALP is chosen when configuring the deck setup in the Biomek Software "Deck Editor." ALPs vary in height, and failure to choose the correct ALP in the "Deck Editor" can result in collisions, causing equipment damage and/or hazardous waste spills.

To configure a **Move Labware** step, complete the following steps:

NOTE To use the **Move Labware** step, a gripper tool must be added and configured in **Hardware Setup** (refer to the *Biomek 4000 Hardware Manual*) and placed on a tool rack in an **Instrument Setup** step (refer to *Instrument Setup Step*).

---

1 In **Move labware from**, select the original deck position for the labware from the drop-down.

OR

Select the labware from the Current Deck Display.

This instructs the instrument to move labware from a specific deck position in preparation for leaving it at a final destination.

2 In **to**, select the final deck position from the drop-down.

OR

Select the position from the Current Deck Display.

This instructs the instrument to move the labware to a final deck position.

3 Select the desired option for moving stacked labware:

NOTE Gripper tool can move up to three microplates at a time.

- **Move the entire stack of labware** - moves all labware in the stack; this option should be selected when moving a single unstacked piece of labware or when moving an entire stack.
- **Move stack, leaving the bottom piece of labware at the source position** - moves all labware in the stack except for the bottom piece.

  NOTE Selecting **Move stack, leaving the bottom piece of labware at the source position** when the source deck position contains only one piece of labware results in an error.

- **Move the topmost...piece(s) of labware from the stack** - moves only the specified number of labware from the top of the stack.

NOTE Refer to CHAPTER 7, *Biomek Stacking Rules*, for complete information on using stacks on Biomek instruments.

Pause Step

The **Pause** step is used to either halt a deck position or device during a method for a specified amount of time, or pause the instrument for an indefinite period of time. During the pause of a deck position or device, the instrument may still move and act on other deck positions. Depending on the purpose of the pause, the step can be configured in one of two ways:

- To incubate a piece of labware in a specific position for a specific amount of time, configure the desired time in seconds to hold that position idle and unavailable for interaction with the instrument (Figure 15.38). Refer to *Configuring a Pause for Specific Deck Position or Pod*.
- To manipulate the deck by hand during a method, configure the step to pause the instrument for an indefinite period of time (Figure 15.40). When the **Pause** step halts the instrument, the amber indicator lights on the front of the unit are activated, and a prompt appears. The prompt

displays the text inserted in the **Pause** step configuration and requires acknowledgement before the method continues. Refer to *Pausing the Whole System and Displaying a Message*.

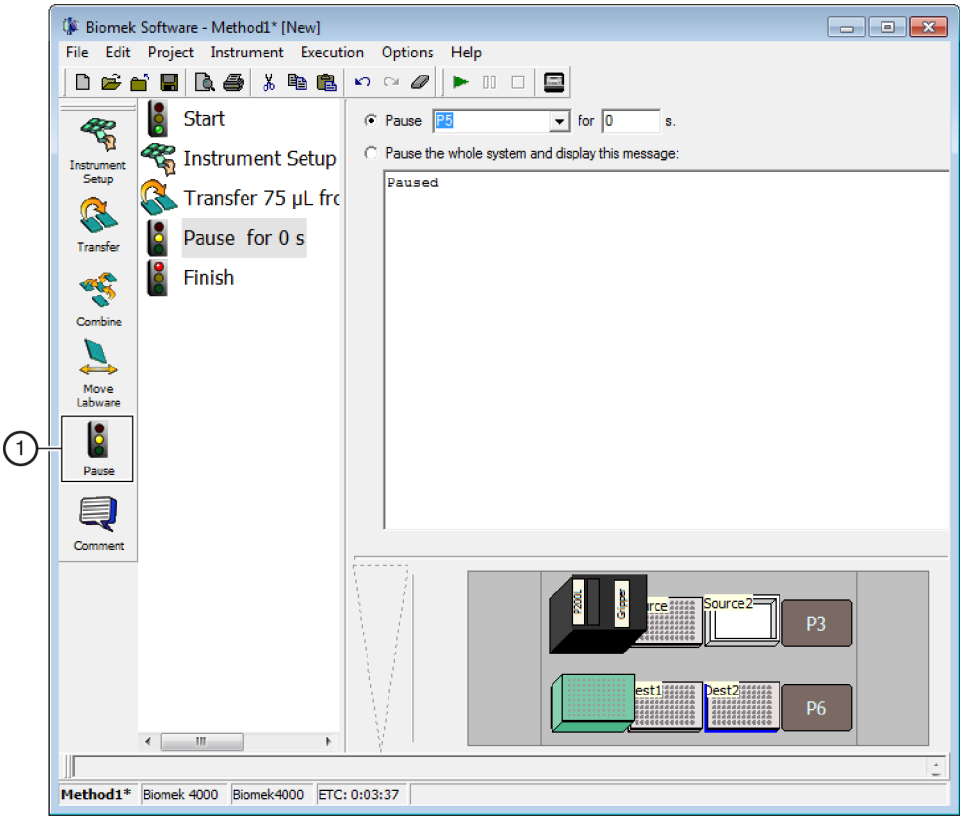
NOTE When the **Pause** step occurs during a method run, the pod remains in the position of the last action competed before the pause. If the purpose of the **Pause** step is to move labware on or off the deck, a **Move Pod** step must be inserted in the method prior to the **Pause** step so that the pod is out of the way (refer to CHAPTER 16, *Move Pod Step*).

To insert a **Pause** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 15.38).

Figure 15.38 Inserting a Pause Step in a Method



1. **Pause** step: When pausing a specific deck position, the **Pause** step indicates the deck position affected and the length of the pause.

Configuring a Pause for Specific Deck Position or Pod

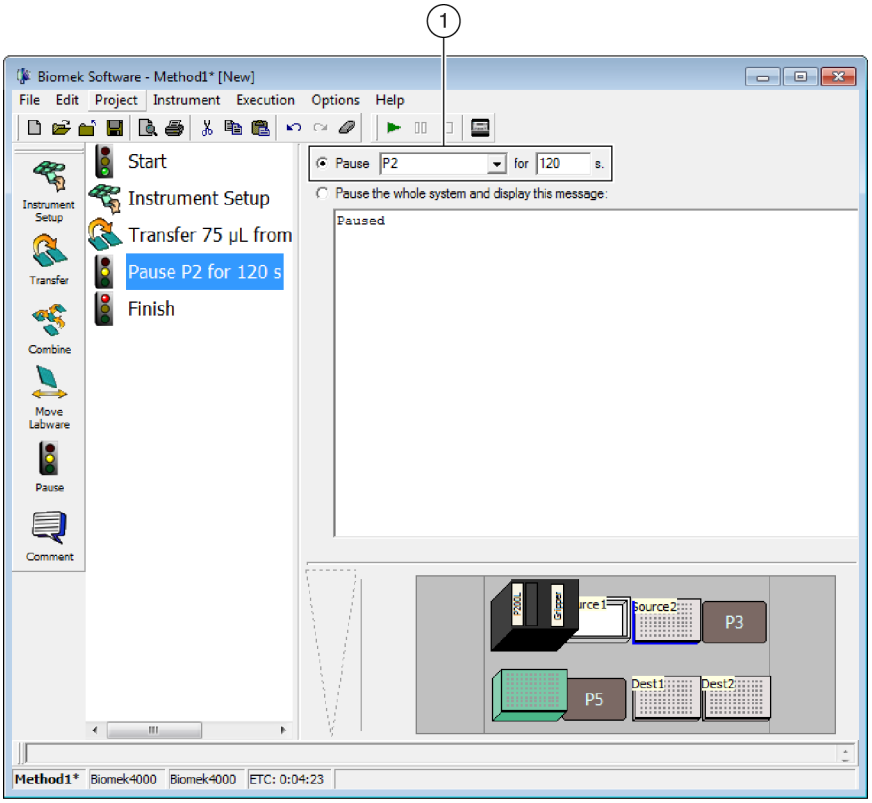
To configure a **Pause** for a specific deck position:

1 Choose **Pause** in the **Pause** step configuration (Figure 15.38).

2 In **Pause**, select the deck position or pod in the Current Deck Display or from the drop-down list (Figure 15.39).

NOTE To pause the instrument for a specified length of time, select **the whole system** in **Pause**.

Figure 15.39 Pausing a Deck Position for a Specified Length of Time



1. **Pause a deck position**: To stop action on a piece of labware in a specific position for a specific amount of time (for example, to incubate), configure the desired time in seconds to hold that position idle and unavailable for interaction with the instrument.

3 Choose the **length of the pause**, in seconds.

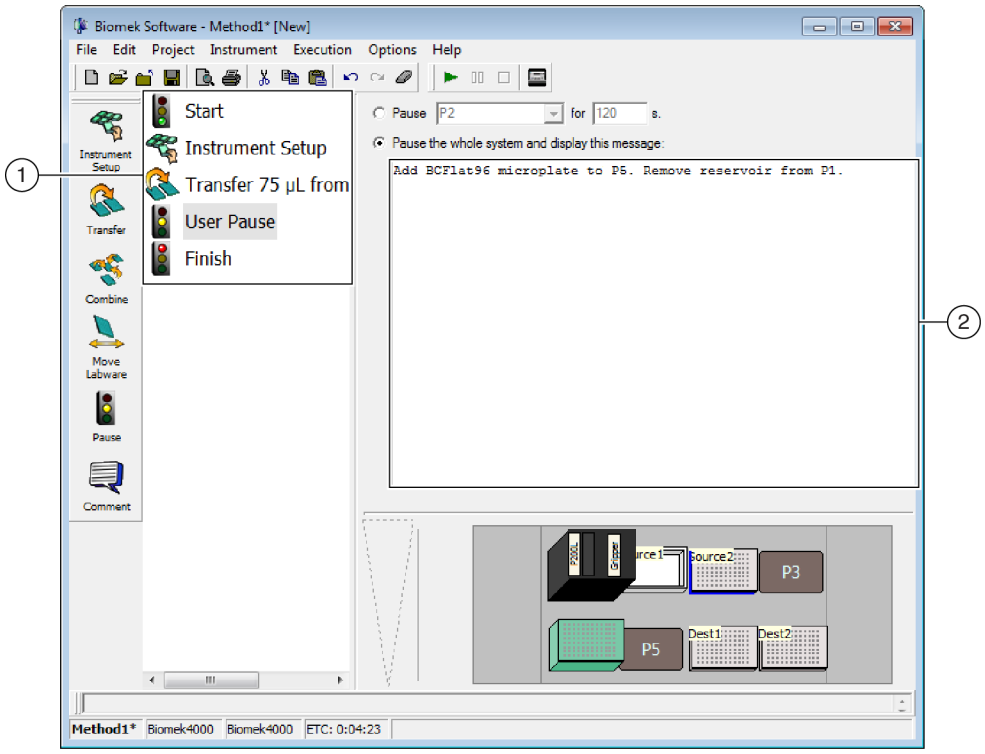
NOTE The method continues with operations not affected by the **Pause**, when possible. If the next step is dependent upon the deck position or pod paused, the method waits until the **Pause** has been completed.

Pausing the Whole System and Displaying a Message

To configure a **Pause** for the entire Biomek instrument and display a message:

1 Select **Pause the whole system and display this message:** in the **Pause** step configuration (Figure 15.40).

Figure 15.40 Pause Step That Provides Instruction

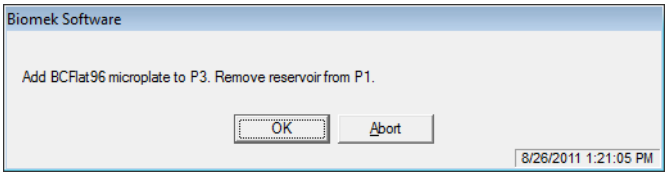


1. **Method View**: When pausing the entire system, the **Pause** step indicates that a pause has been requested by the "user." A prompt appears when the method reaches the **Pause** step, asking for verification that the method can continue.

2 Enter the message to display when the **Pause** is initiated.

NOTE When **Pause the whole system and display this message**: is selected, a prompt (Figure 15.41) appears in Biomek Software with the text entered in the **Pause** step configuration. When the action requested is complete, click **OK** to continue the method, or select **Abort** to halt the method without completing it.

Figure 15.41 Pause Message Prompt



Comment Step

The **Comment** step documents a method and/or adds instructions in the Method View. Text inserted into the **Comment** step configuration may indicate the purpose of a segment of a method, prompt for an action, or convey any other desired information in the Method View. The **Comment** step does not initiate any actions on the instrument and is used only to provide descriptive information and notes to a method.

NOTE Comments are printed when a method is printed. Chose **Print** from the **File** menu to print a method (refer to CHAPTER 12, *Printing a Method*).

To configure **Comment**:

1. Drag and drop the 

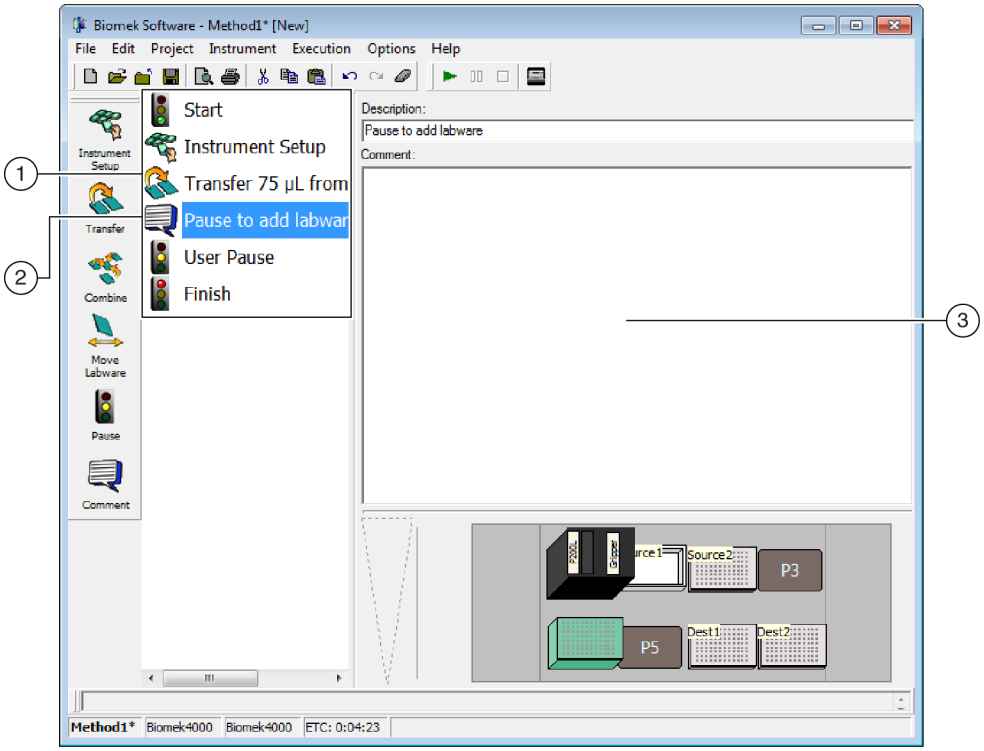
icon into the Method View (Figure 15.42).

2. In **Description**, enter a short summary of the comment. The text entered in **Description** is used as the step caption in the Method View.

3. In **Comment**, enter the full text for the comment.

4. Click the next step, and the **Comment** step in the **Method View** displays the text entered in **Description** (Figure 15.42).

Figure 15.42 Comment Step After Text is Inserted



1. **Method View**: The text entered in the **Comment** step configuration appears in the Method View.
2. **Configured Comment step**.
3. **Comment step configuration**: Any text can be inserted into the **Comment** step configuration.
   The text inserted can be a directive, an identifier, a reminder, or descriptive.

CHAPTER 16

Using the Intermediate Step Palette

Overview

Steps on the **Intermediate** step palette provide individual control over liquid-handling functions outside the **Transfer** and **Combine** steps, including tip handling operations, flow of control, tip and tip box relocation options, and pod movement.

⚠ CAUTION

Make sure the correct ALP is chosen when configuring the deck setup in the Biomek Software "Deck Editor." ALPs vary in height, and failure to choose the correct ALP in the "Deck Editor" can result in collisions, causing equipment damage and/or hazardous waste spills.

The steps available in the **Intermediate** step palette are shown in Table 16.1.

Table 16.1 Intermediate Step Palette

Step	Icon	Description
Aspirate		Aspirates a specified amount of liquid from a single source in preparation for the **Dispense** step.
Dispense		Dispenses a specified amount of liquid into a single destination, following the **Aspirate** step.
Mix		Mixes the contents of a piece of labware using repeated aspirate and dispense.
New Tips		Loads new tips onto the tool.
Unload Tips		Unloads tips from the tool.
Loop		Executes one or more steps a configured number of times.

Table 16.1 Intermediate Step Palette

Step	Icon	Description
Cleanup		Places tips and tip boxes at specified locations.
Move Pod		Moves the pod to a specified deck location.
Group		Groups a series of steps in a nested fashion under a logical name that appears in the Method View.

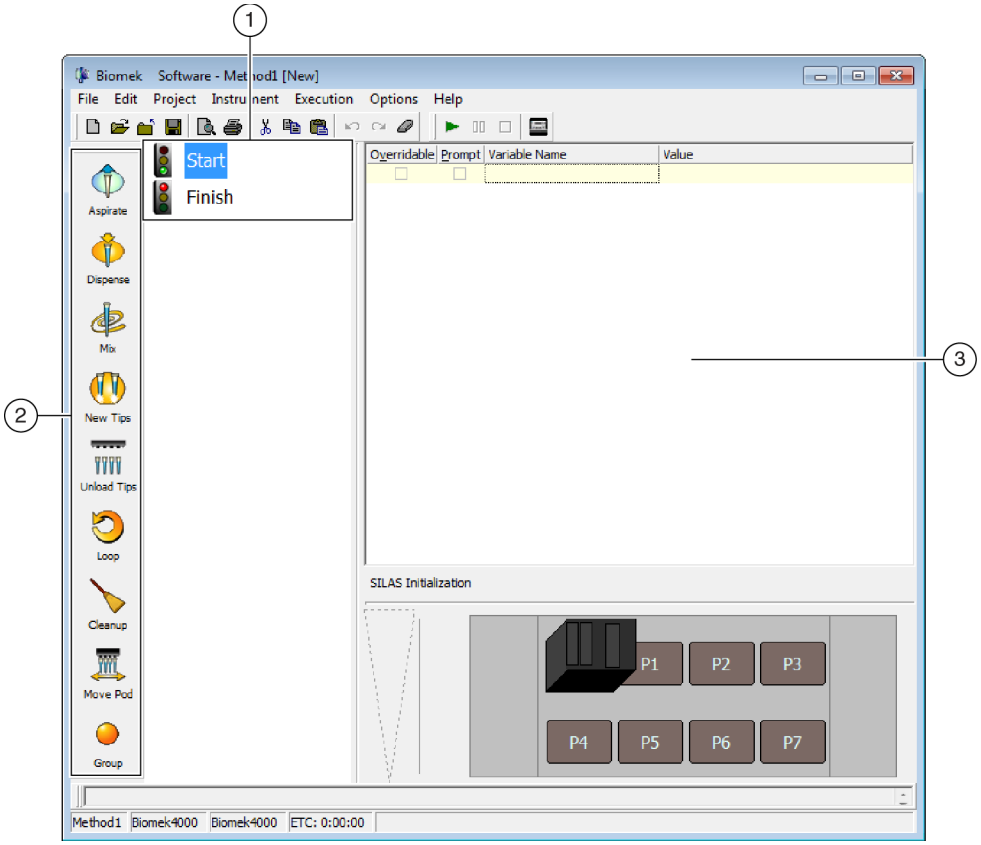
When one of the above steps is added to a method, the configuration associated with that step appears on the right side of the Biomek Software main editor, in step configuration (Figure 16.1).

NOTE Steps not configured appropriately generate errors when the method is validated or run.

Displaying the Intermediate Step Palette

In order to add intermediate steps to a method, display the **Intermediate** step palette (Figure 16.1).

Figure 16.1 Biomek Software Main Editor with Intermediate Step Palette Displayed



1. **Method View**: The method is built step by step in the Method View.
2. **Intermediate Step Palette**
3. **Step Configuration**: When a step is highlighted in the Method View, the corresponding configuration appears in this area.

To display the **Intermediate** step palette, complete the following:

1 Right click any empty palette space, and the step palette menu displays. Select **Intermediate**.

OR

From the toolbar, select **Options** > **Toolbars** > **Intermediate**.

Aspirate Step

The **Aspirate** step removes liquid from source labware in preparation for dispensing to destination labware. Each tip of the tool descends into the wells of the source labware and aspirates the desired volume. The **Aspirate** step is often used in conjunction with the **Dispense, New Tips**, and **Unload Tips** steps (Figure 16.2), but it can be used with any combination of steps. **Aspirate** provides more direct control over pipetting operations than the **Transfer** or **Combine** steps because any step or combination of steps can complete the liquid transfer operation started with the **Aspirate** step.

NOTE A **Load Tool** or **Change Tool** step must be inserted and configured to load an appropriate pipetting tool prior to an **Aspirate** step in the method (refer to CHAPTER 19, *Load Tool Step* or CHAPTER 19, *Change Tool Step*). Depending on the tool loaded, either a single well or eight wells in a column are selected when aspirating.

NOTE A **Loop** step and variable can be used to aspirate from more wells on a microplate or tubes in a rack (refer to *Loop Step*).

The **Aspirate** step configuration includes specifying:

- Labware type accessed during aspirate
- Position of the labware on the deck
- Type of liquid to aspirate
- Volume to aspirate
- Pod that performs aspirate
- Tip refresh, if desired, and the type of tips used
- Technique selection
- Well(s) accessed, if applicable

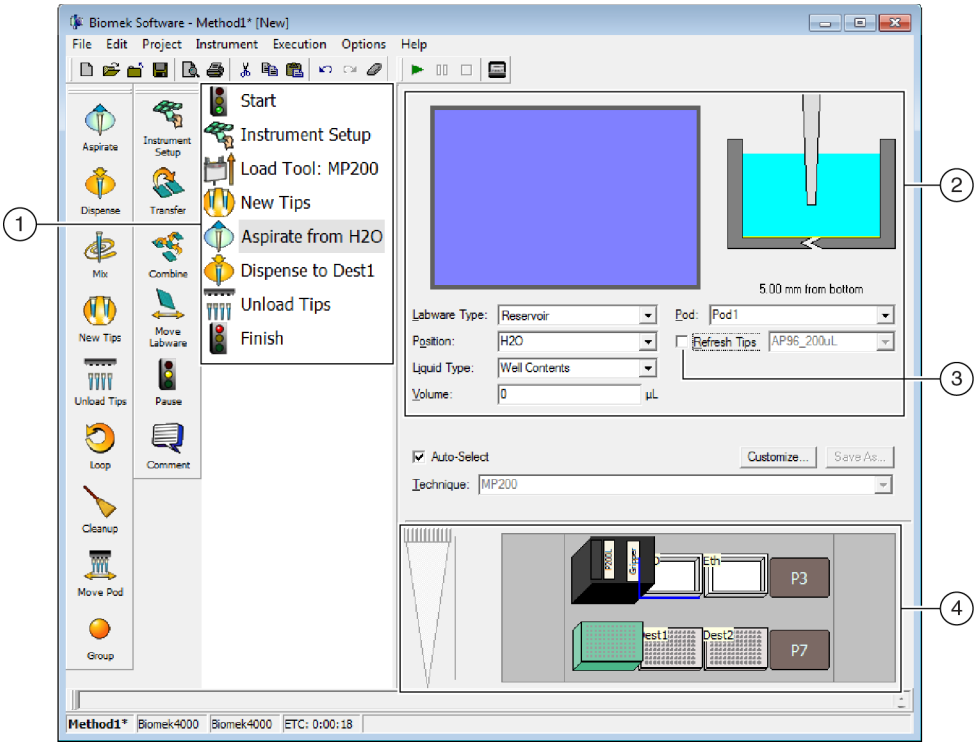
NOTE Either a single well or eight wells in a column are selected, depending on the tool loaded. If a tool is not loaded prior to inserting the **Aspirate** step into the method, the software defaults to a single-tip pipetting tool. Specify the tool prior to adding the **Aspirate** step if you intend to use a multi-tip pipetting tool for pipetting operations.

To insert an **Aspirate** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 16.2).

Figure 16.2 Aspirate Step and Configuration



1. **Method View**: Note that tips are loaded prior to the **Aspirate** step and unloaded after the **Dispense** step.
2. **Aspirate step configuration**
3. **Refresh Tips**: **Refresh Tips** is unchecked when loading tips prior to the **Aspirate** step. **Refresh Tips** loads new tips prior to the **Aspirate** operation.
4. **Current Deck Display**: The Current Deck Display is used for labware selection, and it displays the status of the deck upon completion of the previous step.

Configuring the Aspirate Step

When an **Aspirate** step is added to a method, the **Aspirate** step configuration displays (Figure 16.2).

To configure the **Aspirate** step:

---

1 Click on the desired piece of labware in the Current Deck Display from which to aspirate. Information for that piece of labware is entered automatically into the **Aspirate** step configuration.

OR

Select a **Labware Type** (Figure 16.2).

---

2 Verify the **Position** of the labware.

NOTE A bright blue outline appears in the Current Deck Display around the selected labware.

---

3 Indicate the **Liquid Type** contained in the selected labware.

NOTE The liquid type defaults to **Well Contents**.

---

4 Enter the **Volume** aspirated from the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue**.

---

5 Select the well(s) to aspirate from by highlighting the desired area(s) on the labware graphic. Either a single well or eight wells in a column are selected, depending on the tool loaded.

NOTE To zoom in on the labware, double click on the labware. To call up a menu for **Zoom In** and a **Specify Selection as Text** option, right click on the labware. **Specify Selection as Text** allows the selection of wells using a numeric list as a target for the aspirate operation.

---

6 Check **Refresh Tips**, if desired, and specify the **tip type**. **Refresh Tips** loads new tips to the tool whether tips are currently loaded or not.

NOTE If Biomek Software determines that tips are already loaded, the default setting for **Refresh Tips** is **Off**. If Biomek Software determines that tips are not loaded, the default setting for **Refresh Tips** is **On**.

---

7 The software automatically selects a **Pipetting Technique** based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

OR

Choose **Customize** and configure the technique as desired in the **Technique Editor**.

NOTE For more information on customizing, configuring, and saving a technique, refer to CHAPTER 9, *Understanding and Creating Techniques*.

8 In some cases, it may be necessary to override the aspiration height. Leave the height as is to use the settings specified in the pipetting technique.

OR

Set the aspirate height manually using one of the procedures listed below.

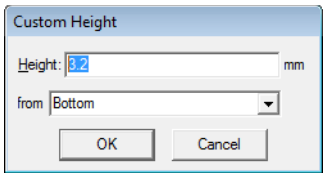
- Set the aspirate height by positioning the cursor over the graphic of a tip inside a well (Figure 16.5). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

  NOTE The cursor changes to a  when positioned over the graphic.

  (**Overrides Technique**) appears below the graphic when the tip height is changed by manipulating the graphic (Figure 16.5) or when the technique is changed with the **Customize** option. For more information on selecting and editing a technique for this method, refer to CHAPTER 9, *Understanding and Creating Techniques*.

- Right click on the graphic of a tip inside a well, and a menu displays. Select **Custom Height**, and the **Custom Height** prompt displays (Figure 16.3). Insert the **height** in millimeters and, in **from**, select a reference point from the drop-down list. Click **OK** to save the edits and return to the **Aspirate** step configuration.

  Figure 16.3 Custom Height Prompt

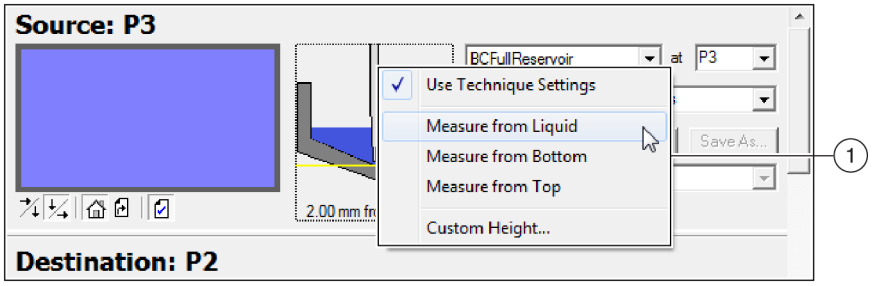
- Click in the graphic of a tip inside a well, and adjust the height using the PgUp and PgDn and the up and down arrow keys. PgUp and PgDn change the height by 1 mm at a time; the up and down arrow keys change the height by 0.1 mm at a time.

NOTE Changes made using the options listed above can be reset to the technique default height by right clicking on the graphic of the tip and selecting **Use Technique Settings**.

To change the point of reference from where aspirations are measured, right click on the graphic of the tip, and, from the pop-up menu (Figure 16.4), select the option you prefer. Options include the following:

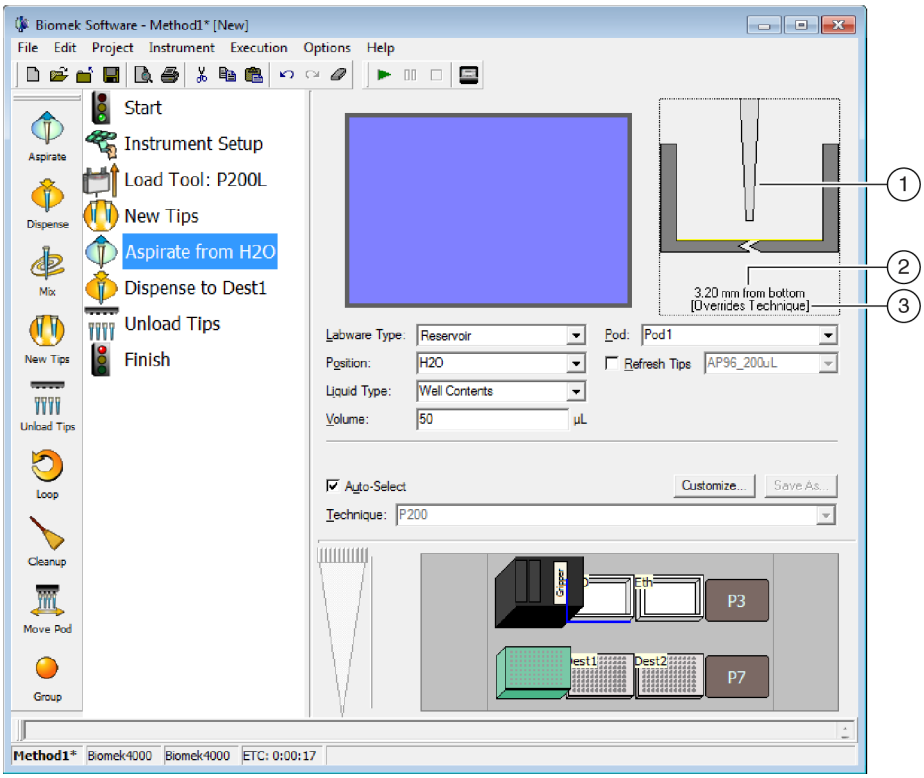
- **Measure from Liquid**—The surface of the liquid is the reference point. The value should be negative, as this indicates that the aspiration occurs below the surface of the liquid.
- **Measure from Bottom**—The bottom of the source labware is the reference point for the aspiration height.
- **Measure from Top**—The top of the source labware is the reference point for aspiration height. The value should be a negative number, as this indicates that the liquid is aspirated from below the top of the well.

Figure 16.4 Aspiration Measurement Options—Menu



1. Select the option to use as a reference point for measuring aspiration height.

Figure 16.5 Adjusting the Aspirate Height



1. **Adjust the tip height for Aspirate, if needed.**
2. **Height display.**
3. **Notifies that the step is not using the technique settings.**

For more information on creating, editing, and saving techniques for use with other methods, refer to CHAPTER 9, *Understanding and Creating Techniques*.

9 Select a step that occurs after the **Aspirate** step or the **Finish** step to validate the step configuration.

Dispense Step

The **Dispense** step dispenses liquid into a single destination labware following **Aspirate.** Each tip of the tool descends into the wells of the destination labware and dispenses the desired volume. The **Dispense** step is often used in conjunction with the **Aspirate**, **New Tips,** and **Unload tips** steps, but it can be used with any combination of steps. **Dispense** provides more direct control over pipetting operations than the **Transfer** or **Combine** steps because any step or combination of steps can initiate the liquid transfer operation.

NOTE Tips must be loaded and have liquid in them from a previous step, such as an **Aspirate** step, prior to using a **Dispense** step.

NOTE A **Loop** step and variable can be used to dispense to more wells on a microplate or tubes in a tube rack (refer to *Loop Step*).

The **Dispense** step configuration includes specifying:

- Labware type accessed during dispense
- Position of the labware on the deck
- Type of liquid to dispense
- Volume to dispense
- Pod that performs dispense
- Empty tips, if desired
- Technique selection
- Well(s) accessed, if applicable

  NOTE Either a single well or eight wells in a column are selected, depending on the tool loaded. If a tool is not loaded prior to inserting the **Dispense** step into the method, the software defaults to a single-tip pipetting tool. Specify the tool prior to adding the **Dispense** step if you intend to use a multi-tip pipetting tool for pipetting operations.

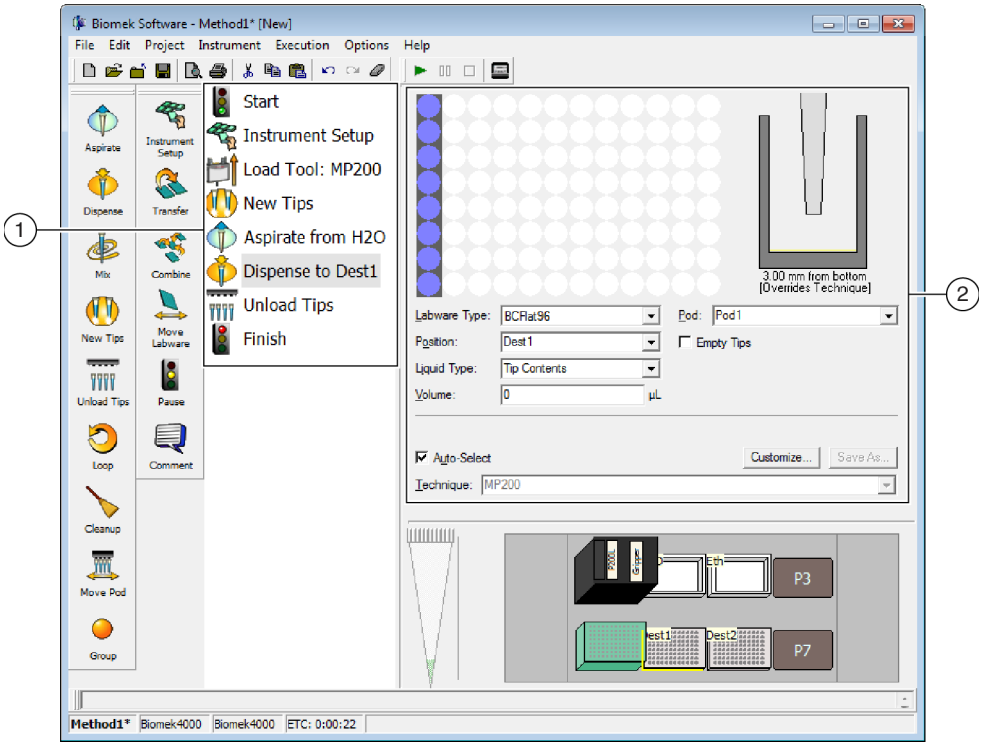
To insert a **Dispense** step into a method:

---

1 Drag and drop the 

icon into the Method View (Figure 16.6).

Figure 16.6 Dispense Step and Configuration



1. **Method View**: The method displayed contains a **Dispense** step. The location of the dispense operation is specified in the **Dispense** caption in the Method View. Note that tips are loaded prior to the **Aspirate** step and unloaded after the **Dispense** step.
2. **Dispense step configuration.**

Configuring the Dispense Step

When a **Dispense** step is added to a method, the **Dispense** step configuration appears (Figure 16.6).

To configure the **Dispense** step:

1 Click on the desired piece of labware in the Current Deck Display. Information for that piece of labware is entered automatically into the **Dispense** step configuration.

OR

Select a **Labware Type** (Figure 16.6).

NOTE **Dispense** steps can also be used to dispense liquids to waste by selecting the **WasteAlp** as the dispense **Labware Type**. For additional details on using the Liquid Waste Station, see the *Biomek 4000 ALPs and Accessories Manual*.

⚠ WARNING

The Liquid Waste Station can be contaminated from method solutions. Follow the appropriate decontamination procedures outlined by your laboratory safety officer.

---

2 Verify the **Position** of the labware.

NOTE A bright yellow outline appears in the Current Deck Display around the selected labware.

---

3 Indicate the **Liquid Type** to be dispensed to the selected labware.

NOTE The liquid type defaults to **Tip Contents**.

---

4 If the tips contain liquid, enter the **Volume** dispensed to the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue.**

NOTE This step is not necessary if **Empty Tips** is selected.

---

5 Select the well or column to dispense to by highlighting the desired well or column on the labware graphic.

NOTE To zoom in on the labware, double click on the labware. To call up a menu for **Zoom In** and a **Specify Selection as Text** option, right click on the labware.

Specify Selection as Text allows the selection of wells or tubes as a numeric list as a target for the dispense operation. It may also be used to enter variables or expressions. Wells are numbered left to right and down (for example, the first row contains wells 1-12, the second row, wells 13-24, etc., for a 96-well microplate).

---

6 Check **Empty Tips**, if desired. **Empty Tips** expels the **Trailing Air Gap**, the fluid contained in the tip, and the **Blow Out** all at one time, rather than as separate operations.

NOTE The default setting for **Empty Tips** is **Off**.

7 The software automatically selects a **Pipetting Technique** based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique.**

OR

Choose **Customize** and configure the technique as desired in the **Technique Editor**.

NOTE For more information on customizing, configuring, and saving a technique, refer to CHAPTER 9, *Understanding and Creating Techniques*.

8 In some cases, it may be necessary to override the dispense height. Leave the height as is to use the settings specified in the pipetting technique.

OR

Set the dispense height manually using one of the following techniques:

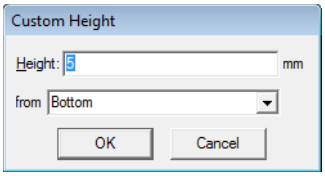
- Set the dispense height by positioning the cursor over the graphic of a tip inside a well (Figure 16.9). Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

  NOTE The cursor changes to a  when positioned over the graphic.

  The phrase (**Overrides Technique**) appears below the graphic when the tip height is changed by manipulating the graphic (Figure 16.9) or when the technique is changed with the **Customize** option. For more information on selecting and editing a technique for this method, refer to CHAPTER 9, *Understanding and Creating Techniques*.

- Click in the graphic of a tip inside a well, and adjust the height using the PgUp and PgDn and the up and down arrow keys. PgUp and PgDn change the height by 1 mm at a time; the up and down arrow keys change the height by 0.1 mm at a time.
- Right click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and the **Custom Height** prompt appears (Figure 16.7). Insert the **height** in millimeters and, in **from**, select a reference point from the drop-down list. Click **OK** to save the edits and return to the **Dispense** step configuration.

Figure 16.7 Custom Height Prompt



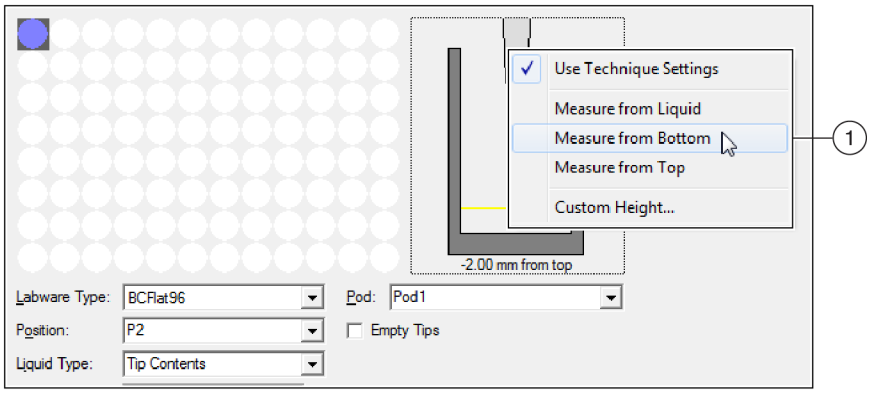
NOTE Changes made using the options listed above can be reset to the technique default height by right clicking on the graphic of the tip and selecting **Use Technique Settings**.

To change the point of reference from where aspirations are measured, right click on the graphic of the tip, and, from the pop-up menu (Figure 16.8), select the option you prefer. Options include the following:

- **Measure from Liquid**—If liquid is present, the surface of the liquid is the reference point.

- **Measure from Bottom**—The bottom of the destination labware is the reference point for the dispense height.
- **Measure from Top**—The top of the destination labware is the reference point for dispense height.

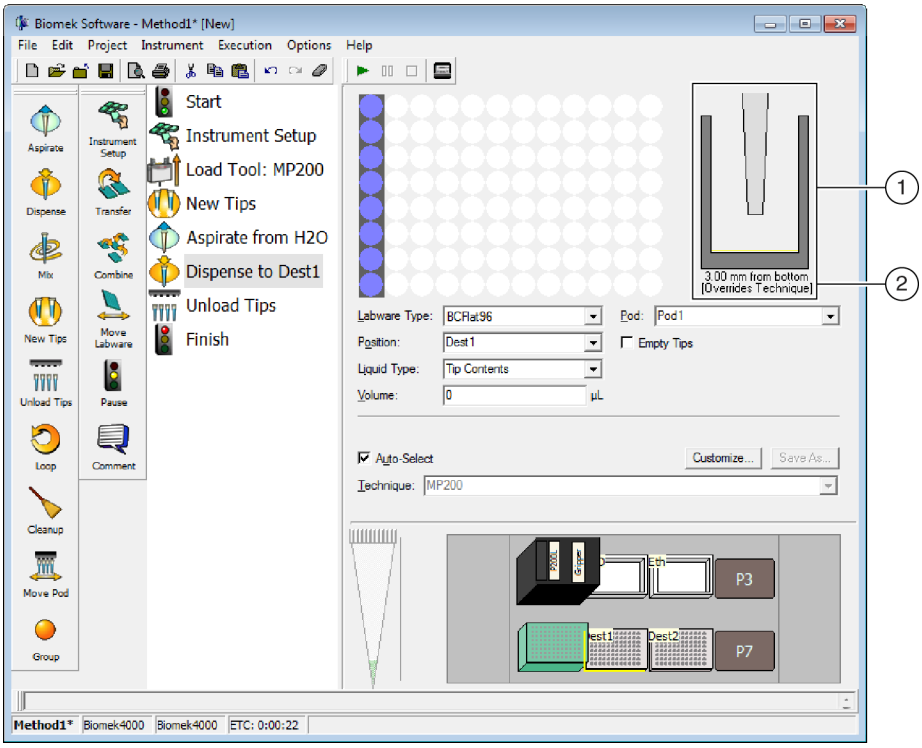
Figure 16.8 Dispense Measurement Options—Menu



1. Select the option to use as a reference point for measuring dispense height.

For more information on creating, editing, and saving techniques for use with other methods, refer to CHAPTER 9, *Understanding and Creating Techniques*.

Figure 16.9 Dispense Step—Adjusting the Dispense Height



1. **Adjust the height for the Dispense operation.**
2. **Notifies that the step is not using the technique settings.**

9 Select a step that occurs after the **Dispense** step or the **Finish** step to validate the step configuration.

Mix Step

The **Mix** step provides a mixing motion for the contents of a piece of labware by performing one or more aspirate and dispense operations within a single well, tube, or column. The **Mix** step can be used to mix the contents of a piece of labware that has been inactive for an extended length of time, prior to aspirating, or to mix the contents in the well following a dispense.

A **Load Tool** or **Change Tool** step must be configured with an appropriate pipetting tool prior to a **Mix** step in the method (refer to CHAPTER 19, *Load Tool Step* or CHAPTER 19, *Change Tool Step*). Depending on the tool loaded, either a single well or eight wells in a column are selected when mixing.

NOTE If a tool is not loaded prior to inserting the **Mix** step into the method, the software defaults to a single-tip pipetting tool. Specify the tool prior to adding the **Mix** step if you intend to use a multi-tip pipetting tool for pipetting operations.

NOTE A **Loop** step and variable can be used to mix more wells on a microplate or tubes in a tube rack (refer to *Loop Step*).

The **Mix** step configuration includes specifying:

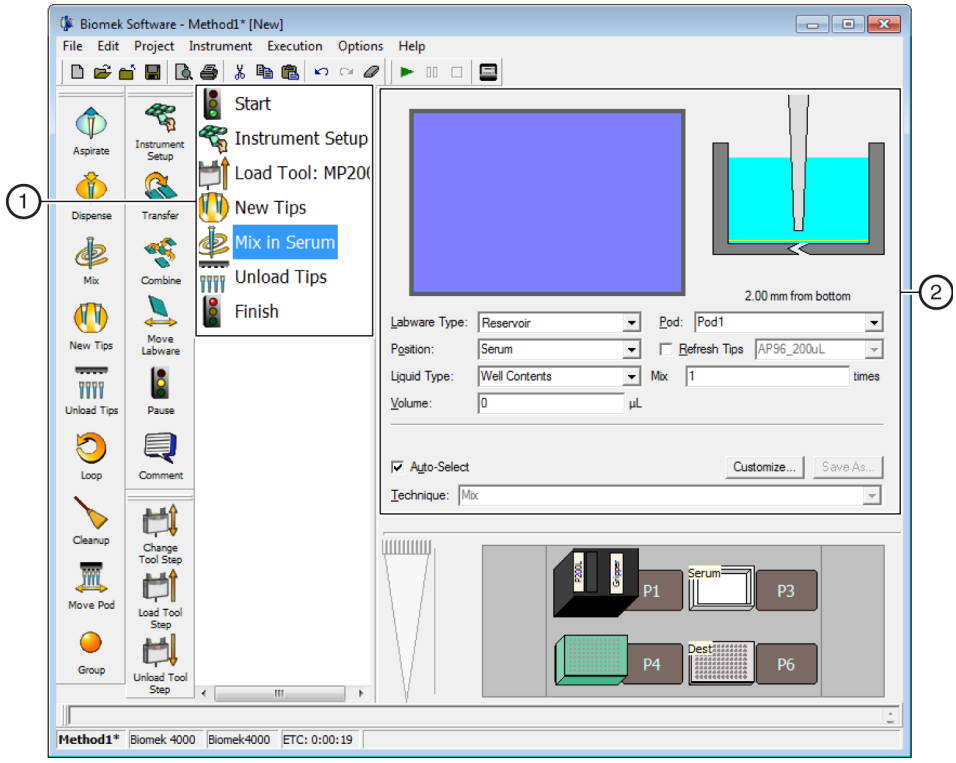
- Labware type accessed during mix
- Position of the labware on the deck
- Type of liquid mixed
- Volume mixed
- Pod performing the mix
- Tip refresh, if desired, and the type of tips to load
- Number of aspirate and dispense cycles to perform during the mix process
- Technique selection
- Wells accessed — either a single well or eight wells in a column are selected, depending on the tool loaded.

To insert a **Mix** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 16.10).

Figure 16.10 Mix Step and Configuration



1. **Method View**: The location of the mix operation is specified in the **Mix** caption in the Method View. Note that tips are loaded prior to and unloaded after the **Mix** step.
2. **Mix step configuration.**

Configuring the Mix Step

When a **Mix** step is added to a method, the **Mix** step configuration appears (Figure 16.10).

To configure the **Mix** step:

1 Click on the desired piece of labware in the Current Deck Display (Figure 16.10). Information for that piece of labware is entered automatically into the **Mix** step configuration.

OR

Select a **Labware Type** from the drop-down list.

2 Verify or select the **Position** of the labware.

NOTE A bright green outline appears in the Current Deck Display around the selected labware.

3 Select the well(s) to mix by highlighting the desired well(s) on the labware graphic.

NOTE Either a single well or eight wells in a column are selected when mixing wells, depending on the tool loaded.

NOTE To zoom in on the labware, double click on the labware. To call up a menu for **Zoom In** and a **Specify Selection as Text option**, right click on the labware.

Specify Selection as Text allows the selection of wells or tubes in a numeric list as a target for the mix operation.

4 Indicate the **Liquid Type** contained in the selected labware.

5 Enter the **Volume** mixed in the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue**.

6 View the tip graphic to ensure the mix height is appropriate for the operation. The mix height cannot be changed using the graphic, as it could with **Aspirate** and **Dispense** steps. If you wish to change the mix height, select **Customize**, and make changes using the **Technique Editor** (see CHAPTER 9, *Setting Mix Values* for details).

7 Ensure **Pod1** is visible in the **Pod** field.

NOTE On the Biomek 4000 instrument, there is only one pod; therefore, **Pod1** is the only option available in the **Pod** drop-down.

8 Check **Refresh Tips**, if desired, and specify the **tip type**. **Refresh Tips** loads new tips to the tool whether tips are currently loaded or not.

NOTE If Biomek Software detects that tips are already loaded, the default setting for **Refresh Tips** is **Off**. If Biomek Software detects that tips are not loaded, the default setting **Refresh Tips** is **On**.

9 In **Mix**, enter the number of times the mix operation is performed.

10 The software automatically selects a **Pipetting Technique** based on the liquid type, labware type, tip type, and volume being mixed. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

OR

Choose **Customize** and configure the technique as desired in the **Technique Editor**.

NOTE For more information on customizing, configuring, and saving a technique, refer to CHAPTER 12, *Understanding Techniques*.

11 Select a step that occurs after the **Mix** step or the **Finish** step to validate the step configuration.

New Tips Step

The **New Tips** step instructs the instrument to load new tips at a specific point in a method. **New Tips** is used when precise tip control is required. **New Tips** is used in conjunction with the **Unload Tips** step. Also, since tips must be loaded prior to aspirate and mix, the **New Tips** step should be positioned prior to any **Aspirate** or **Mix** steps if tips have not been previously loaded.

The **New Tips** step is used in place of the **Refresh Tips** option in the **Mix** and **Aspirate** steps or the **Load Tips** option in the **Transfer** and **Combine** steps, when more tip control is desired. **New Tips** is particularly useful with the **Loop** and **Worklist** steps; for example, when a **Worklist** step is performing a transfer that accesses the same tips repeatedly at different points throughout the worklist, the tips can be loaded and unloaded as many times as their tip configuration allows.

Loading new tips is recommended when:

- The current tips have manipulated a caustic fluid.
- The current tips have been loaded the maximum number of times allowed in their **Labware Properties**.

  NOTE To increase the number of uses allowed for each set of tips, increase the **Load no more than** count in the **Labware Properties** configuration in the **Instrument Setup** step.

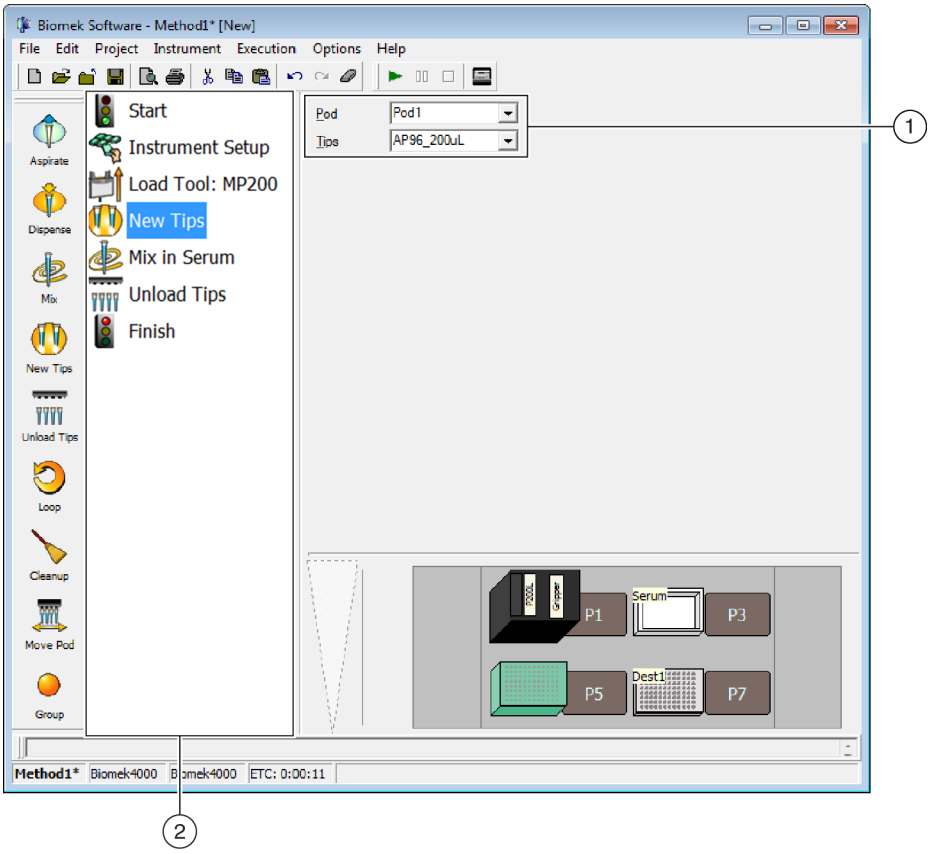
- Clean tips are required to avoid cross-contamination.

To insert a **New Tips** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 16.11).

Figure 16.11 New Tips Step and Configuration



1. **New Tips step configuration**.
2. **Method View**

To configure **New Tips:**

1 Ensure **Pod1** is visible in the **Pod** field.

NOTE On the Biomek 4000 instrument, there is only one pod; therefore, **Pod1** is the only option available in the **Pod** drop-down.

2 Select the **Tips** to be loaded in the **New Tips** step from the drop-down list.

OR

Select the tip box from the Current Deck Display. Selecting tips from the Current Deck Display automatically updates **Tips** in the step configuration.

NOTE The name of a specific tip box can be entered in **Tips** if tip boxes were assigned names in the **Instrument Setup** step. If a name is specified, the **New Tips** step only uses tip boxes with that name. However, if the tip type is used, **New Tips** uses any available tip of that type.

3 Select a step that occurs after the **New Tips** step or the **Finish** step to validate the step configuration.

Unload Tips Step

The **Unload Tips** Step instructs the instrument to unload tips at a specific point in a method. **Unload Tips** is used when precise tip control is required. **Unload Tips** is often used in conjunction with the **New Tips** steps, but it can be used with any combination of steps. It is acceptable to use the **Unload Tips** step multiple times throughout a method.

Unload Tips is used when tip integrity is in question or when cross-contamination between labware is a concern. **Unload Tips** can be used in place of the **Unload (Tips)** option in the **Transfer** and **Combine** steps, and is particularly useful with **Loop** and **Worklist** steps; for example, when a **Worklist** step performs a transfer accessing the same tips repeatedly, the tips can be loaded and unloaded as many times as the tip configuration allows with the **New Tips** and **Unload Tips** steps.

Unloading tips is recommended when:

- The current tips have manipulated a caustic fluid.
- The current tips have been loaded the maximum number of times allowed in the **Labware Properties**.

  NOTE To increase the number of uses allowed for each set of tips, increase the **Load no more than** count in the **Labware Properties** configuration in the **Instrument Setup** step.

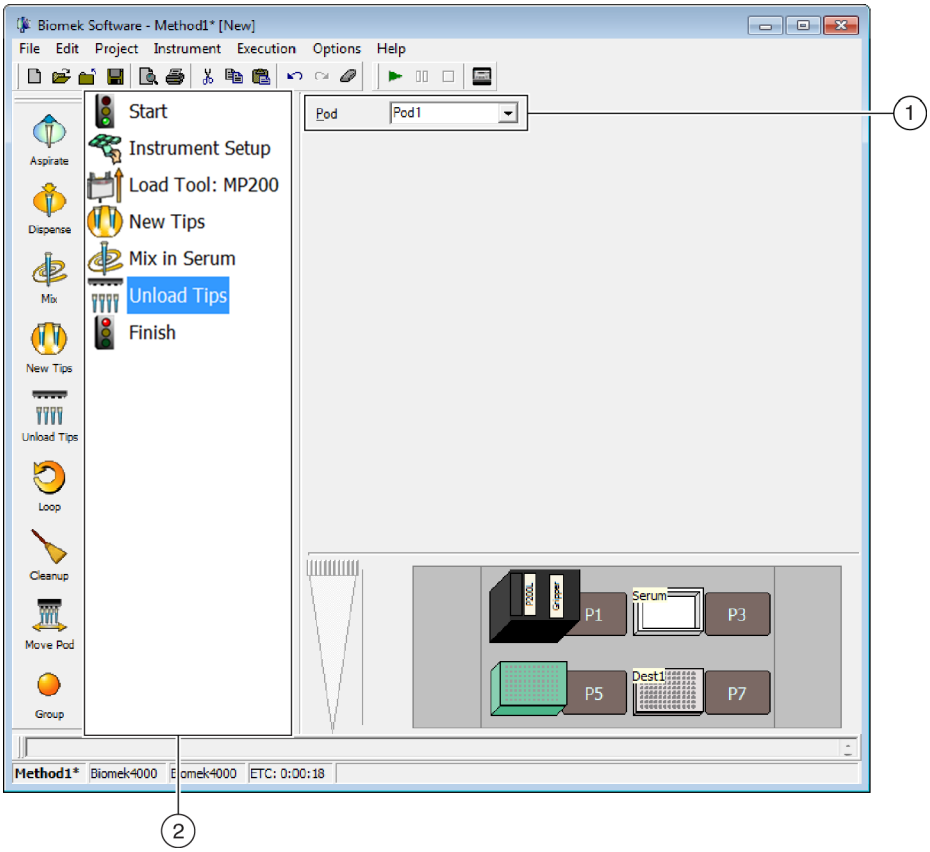
- The integrity of the current tips is in question.
- To avoid cross-contamination of samples.

To insert a **Unload Tips** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 16.12).

Figure 16.12 Unload Tips Step and Configuration



1. **Unload Tips configuration**.
2. **Method View**

To configure **Unload Tips:**

1 Ensure **Pod1** is visible in the **Pod** field.

NOTE On the Biomek 4000 instrument, there is only one pod; therefore, **Pod1** is the only option available in the **Pod** drop-down.

2 Select a step that occurs after the **Unload Tips** step or the **Finish** step to validate the step configuration.

Loop Step

The **Loop** step executes any steps located between the **Loop** and **End Loop** icons as many times as specified in the **Loop** step configuration; for example, if a method required multiple repetitions of the same aspirate and dispense operations, the **Loop** step allows the repetition of those steps as many times as required. The steps requiring repetition, in this case the **Aspirate** and **Dispense** steps, are 'substeps' of the **Loop** step.

When the **Loop** step is added to a method, the **Loop** icon appears in the Method View, as well as the **End Loop** icon. All steps placed between the **Loop** and **End Loop** icons are contained within the **Loop** and are repeated as many times as indicated in the **Loop** step configuration (Figure 16.13).

NOTE While the **Loop** step is executing, a number appears in parentheses behind each substep within the **Loop** step, indicating the current iteration of the loop.

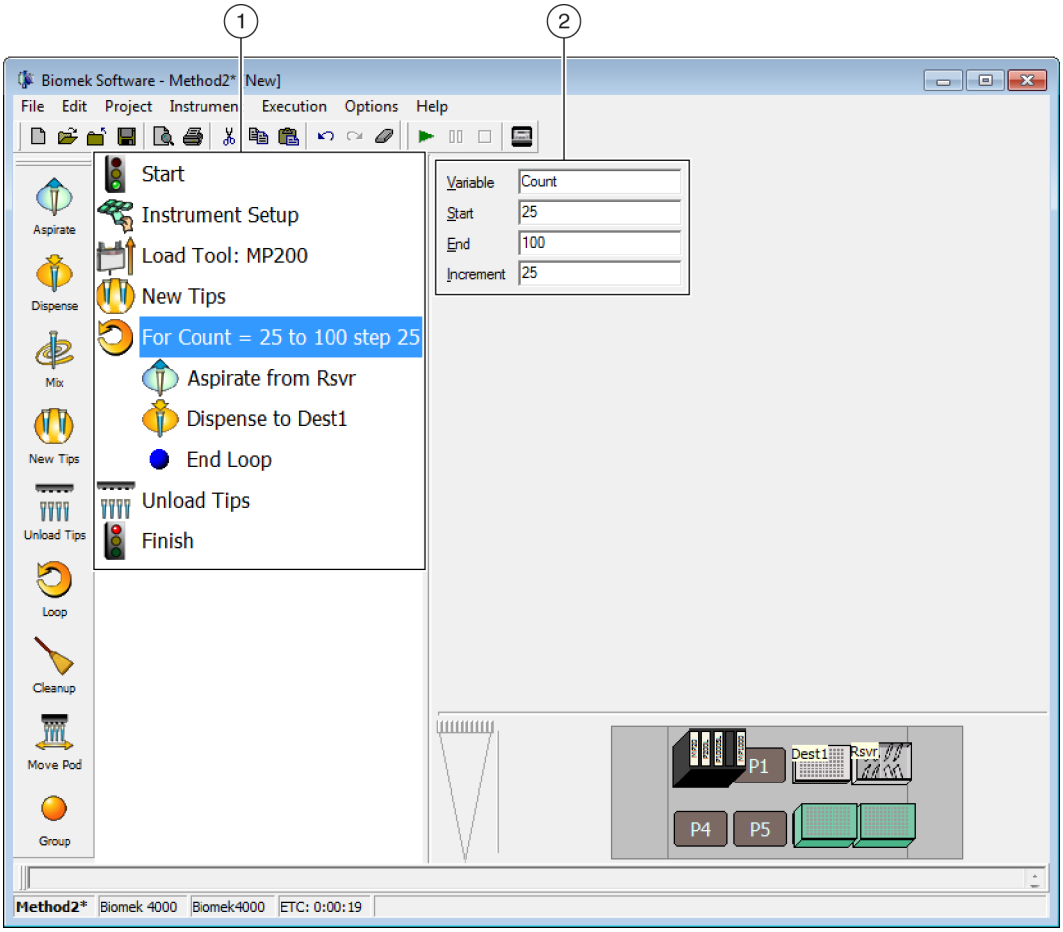
NOTE Variables defined in a **Loop** step apply only to the **Loop** and its substeps.

To insert a **Loop** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 16.13).

Figure 16.13 Loop Step and Configuration



1. **Method View**: The method displayed contains a **Loop** step. Note that the **Aspirate** and **Dispense** steps are positioned between the **Loop** icon and the **End Loop** icon. The configured **Variable, Start, End**, and **Increment** values are displayed in the **Loop** caption in the Method View.
2. **Loop step configuration**: The **Loop** step configuration is used to specify an optional variable used by the substeps within the **Loop** step, the **Start** and **End** count numbers, and the **Increment** used to proceed from the start number to the end number.

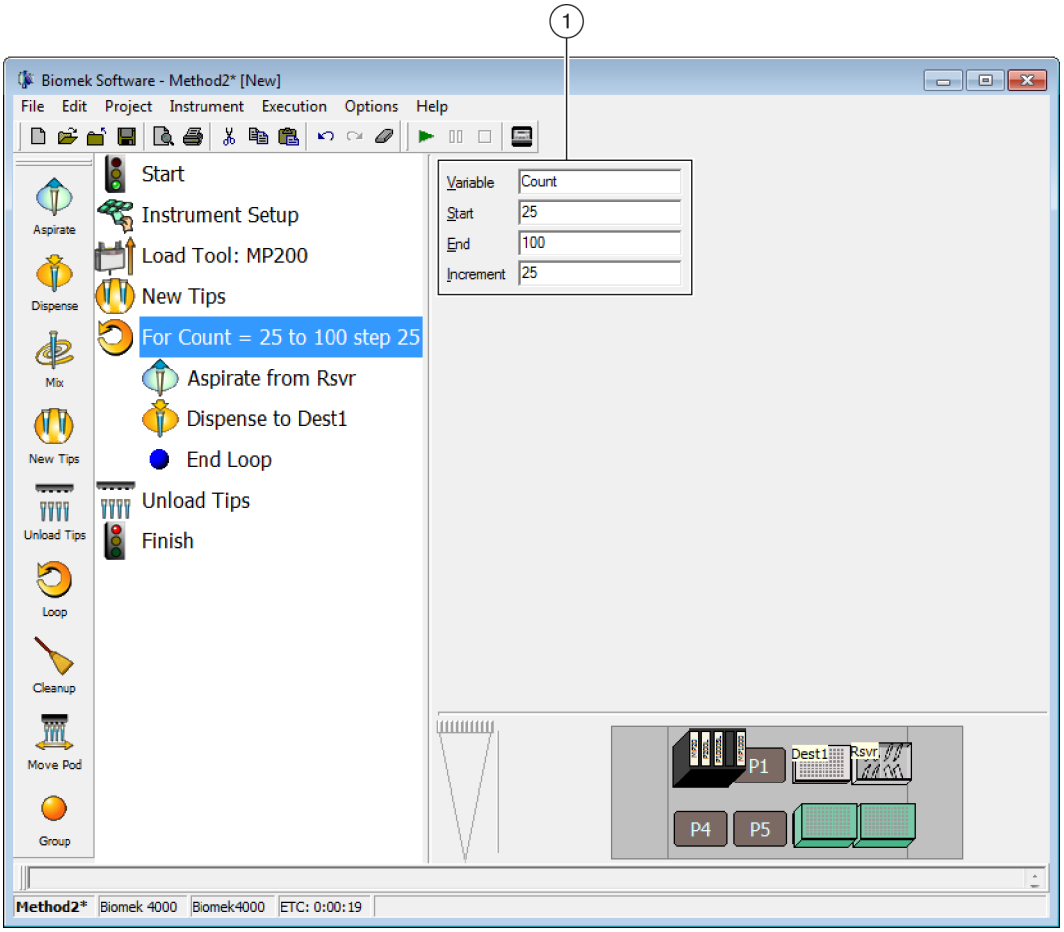
Configuring a Loop Step and Creating a New Variable

To configure a **Loop** step and create a new variable:

1 In **Variable**, insert a variable for the **Loop** step that may be used in substeps (Figure 16.14), if desired. **Variable** creates a variable that can be used in the step configurations for any substep of the **Loop** (Figure 16.15). A variable name cannot contain a space or a punctuation mark, such as a period (.), a comma (,) or an ampersand (&).

NOTE An entry in **Variable** is optional. The **Loop** step can function without a **Variable**.

Figure 16.14 Loop Step—Variable Created in Variable



1. **The variable "Count" has been created for the Loop.**

---

2 Insert the **Start** value for the **Loop** count (Figure 16.14).

NOTE A **Loop** usually begins counting at '1'; for example, if the **Increment** is '25', **Start** is '1', and **End** is '100', four passes of the loop are completed for the **Count** values of 1, 26, 51 and 76. It is occasionally desirable, however, to start the count at a different value; for example, if the **Start** value is changed from '1' to '25', four passes of the loop are completed for the **Count** values of 25, 50, 75 and 100.

---

3 Insert the **End** value for the **Loop** count.

NOTE Each time the method completes a loop, its count is advanced. The method drops out of the **Loop** when the next pass would exceed the **End** number; for example, if the **Increment** is '25', **Start** is '1', and **End** is '100', four passes of the loop are completed for the **Count** values of 1, 26, 51 and 76. The **Loop** stops at 76 because the value of the next pass would be 101, which exceeds the **End** value of 100.

4 Insert an **Increment** value for the **Loop** count. The **Increment** advances the iteration of the **Loop** from the **Start** value to the **End** value. Variables can be used in **Increment**; however, the variable must be preceded by an equal (=) sign (Figure 16.15).

NOTE When the variable is accessed in the substeps, the value of the variable is incremented until the value reaches the **End** value, without going over. For example, you can define a variable 'Inc,' and then set **Increment** for **Count** to '=Inc'. In that case, if Inc=25, and if **Start** is '1,' **End** is '100,' four iterations of the loop are completed for the values 1, 26, 51, and 76. If Inc=10, 10 iterations of the loop are completed, for values 1,11,21,31,41,51,61,71,81,91.

5 Select **End Loop** in the Method View to add steps to the **Loop**.

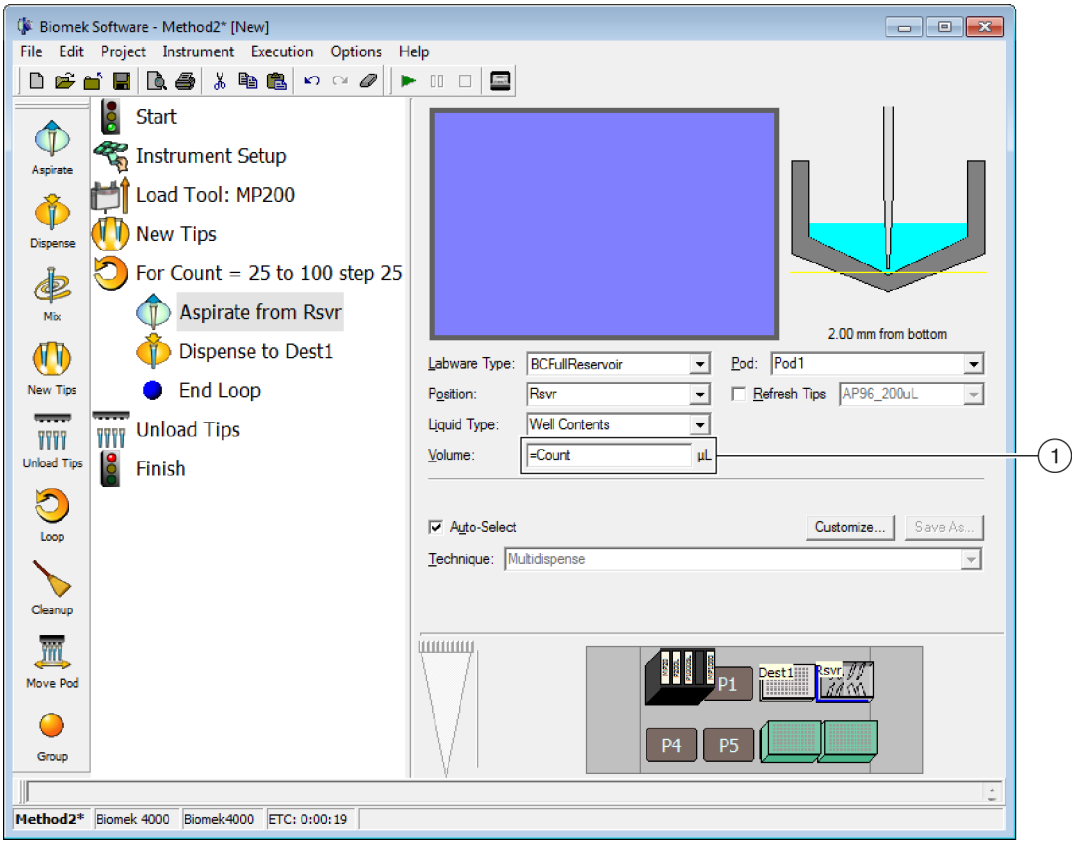
6 Insert the desired substeps between **Loop** and **End Loop**.

OR

Drag and drop existing steps from the method between the **Loop** and **End Loop**.

7 Configure the substeps, using the variable created in **Variable** where applicable.

Figure 16.15 Loop Step Variable 'Count' Used in an Aspirate Substep



1. **The variable "Count" used in the Aspirate step within a Loop step.**

NOTE In the example, the variable '**Count**' is used in the volume fields of the **Aspirate** and **Dispense** substeps of the **Loop** step (Figure 16.15).

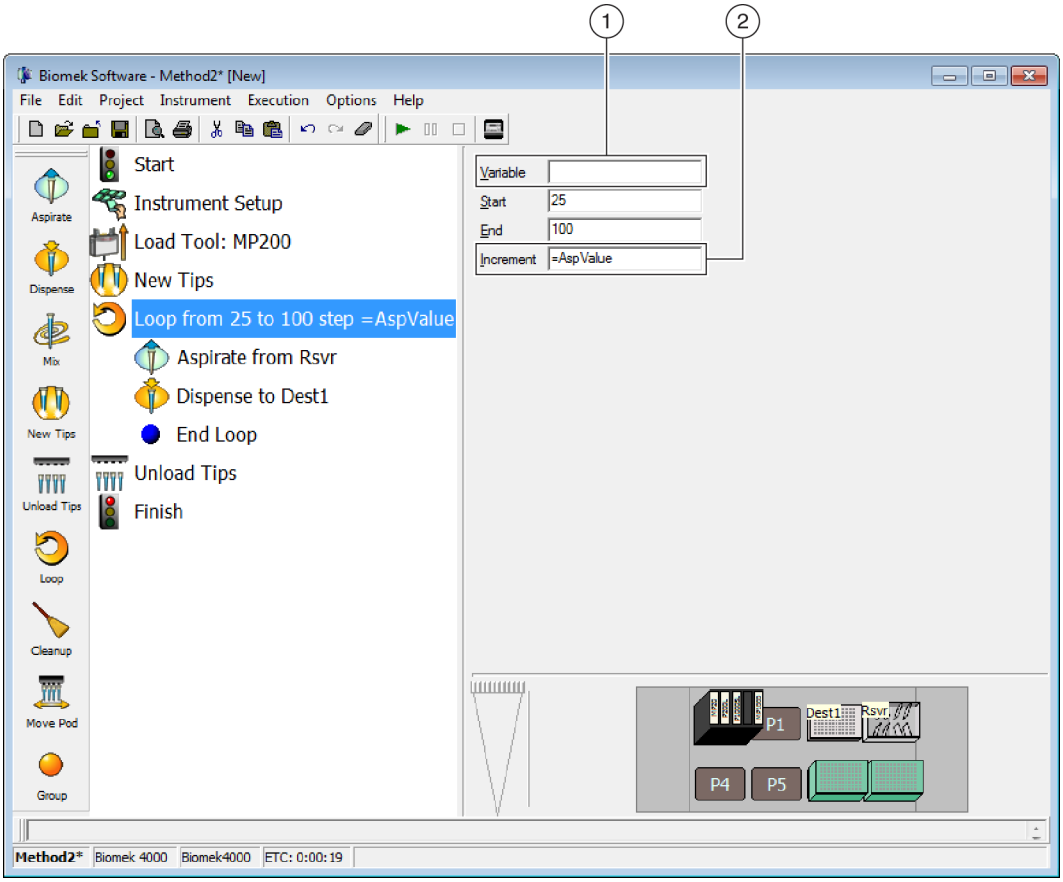
Configuring a Loop Step Using an Existing Variable

To configure a **Loop** step without creating a new variable, but using an existing variable:

1 Leave **Variable** blank (Figure 16.16).

NOTE An entry in **Variable** is optional. The **Loop** step can function without an entry in **Variable**.

Figure 16.16 Loop Step—Using a Previously Created Variable as the Increment



1. **Variable is left blank.**
2. **The variable "AspValue" is being used as an Increment for the Loop step.**

2 Insert the **Start** value for the **Loop** count.

NOTE A **Loop** usually begins counting '1'; for example, if **Increment** is '**=AspValue2**' and **AspValue2** has an assigned value of 25, and if **Start** is '1' and **End** is '100', four iterations of the loop are completed for the values 1, 26, 51, and 76. It is occasionally desirable, however, to start the count at a different value; for example, if the **Start** value is changed from '1' to '25', four passes of the loop are completed for the values of 25, 50, 75, and 100.

3 Insert the **End** value for the **Loop** count.

NOTE Each time the method completes a loop, its count is advanced. The method drops out of the **Loop** when the next pass would exceed the **End** number; for example, if **Increment** is '**=AspValue2**' and **AspValue2** has an assigned value of 25, and if **Start** is '1' and **End** is '100', four iterations of the loop are completed for the values 1, 26, 51, and 76. The **Loop** stops at 76 because the value of the next pass would be 101, which exceeds the **End** value of 100.

4 Insert a previously created variable in **Increment** (Figure 16.16). The value of the variable is used as the **Increment** to advance the iterations of the **Loop** from the **Start** value to the **End** value. Variables must be preceded by an equal (=) sign in the **Loop** step configuration, as well as in the substep configurations.

NOTE When the variable is accessed in the substeps, the value of the variable is incremented until the value reaches the **End** value, without going over. For example, if **Increment** is '**=AspValue2**' and **AspValue2** has an assigned value of 25, and if **Start** is '1' and **End** is '100', four iterations of the loop are completed for the values 1, 26, 51, and 76.

5 Select **End Loop** in the Method View to add steps to the **Loop**.

6 Insert the desired substeps between **Loop** and **End Loop**.

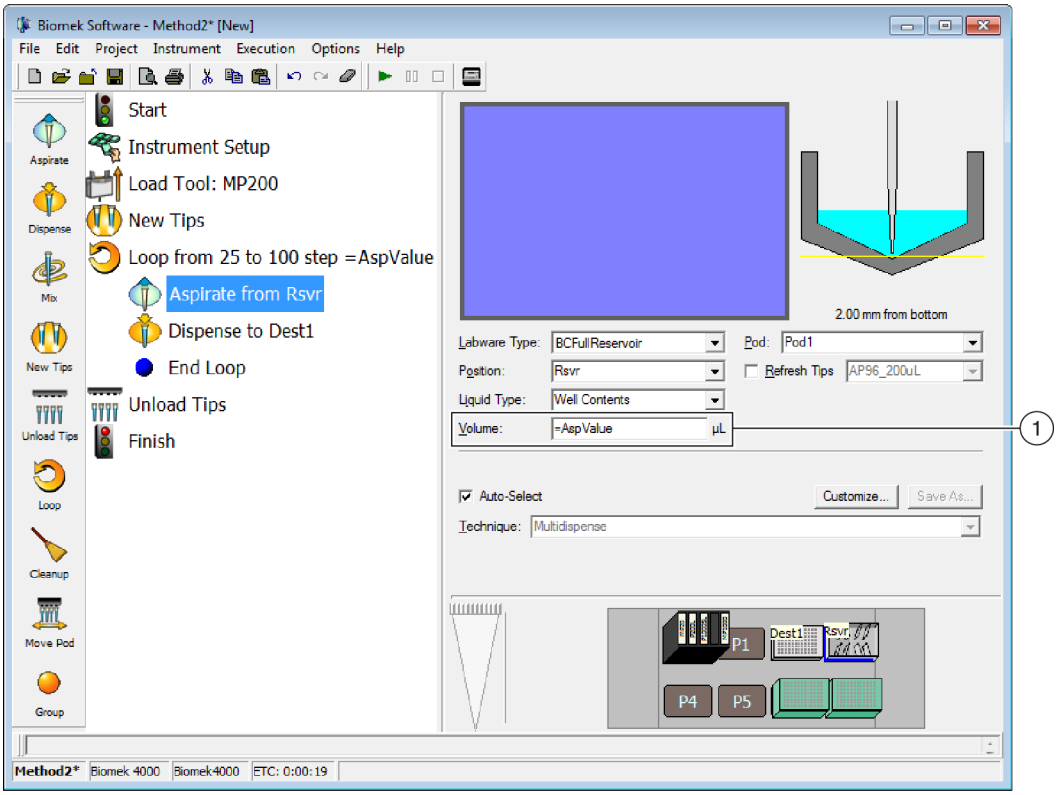
OR

Drag and drop existing method steps into the loop by placing them between the **Loop** and **End Loop** steps.

7 Configure the substeps using the previously created variable where applicable.

NOTE The variable '**AspValue**' is used in the volume fields of the **Aspirate** and **Dispense** substeps of the **Loop** step (Figure 16.17).

Figure 16.17 Loop Step - The 'AspValue' Variable is Used as the Volume for the Substeps



1. **The variable "AspValue" is used in the volume field of the substeps.**

Cleanup Step

The **Cleanup** step is used to direct the instrument to dispose of tips and tip boxes. Normally, when a method is completed, tips and tip boxes are left in their final positions, regardless of their originating positions. The **Cleanup** step can return tips and tip boxes to their original deck position or hardware device; place them in a trash receptacle; or leave them wherever they are when the method is completed.

The **Cleanup** step configuration includes:

- With no configuration options selected, all tips are sent to their configured location at the end of the method.
- When **Send tip boxes to their configured final destinations** is checked, all the tip boxes that came from off deck and all those that were configured to go to trash are sent to those final destinations.
- When **Send boxes that started on deck back to their original locations** is checked, in addition to the operations resulting from the box checked above, any tip boxes that started on the deck are

returned to their starting position. (This option is activated only when **Send tip boxes to their configured final destinations** is selected.)

Cleanup resets the hardware by physically returning tips and tip boxes to their original positions, while the **Finish** step only unloads tips and resets the software to its original state at the completion of the method. Use the **Cleanup** step with the **Finish** step to reset both the hardware and the software to the state they were in at the onset of the method, or to clear the deck of used tips and tip boxes. The **Cleanup** step is useful when the same method is run repeatedly, one time after another, and when trying to track which tips and tip boxes were used for which fluids and labware.

To insert a **Cleanup** step into a method:

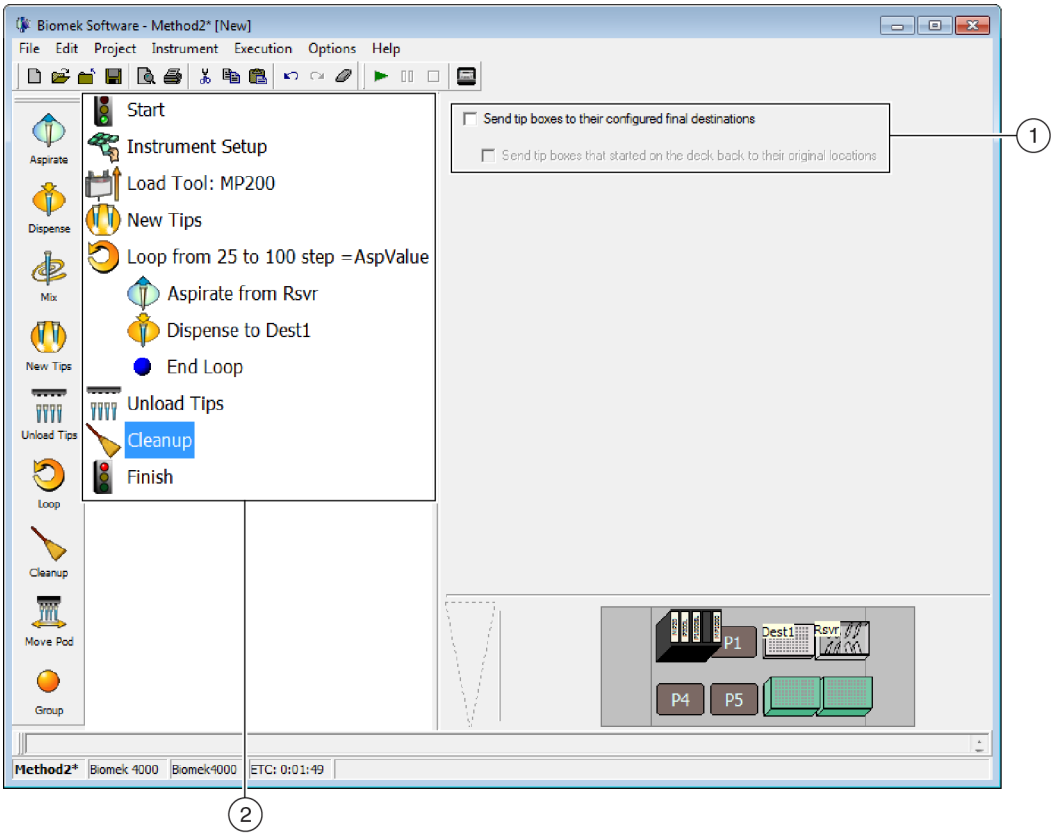
---

1 Drag and drop the 

icon into the Method View (Figure 16.18).

NOTE Tip boxes loaded in Manual Latch positions cannot be moved.

Figure 16.18 Cleanup Step and Configuration



1. **Cleanup Configuration**: The **Cleanup** step configuration provides the options to **Send tip boxes to the final destinations** configured in the **Labware Properties** for that tip box. Return the tip boxes to their starting location, regardless of whether they originated on the deck or in an external hardware device.
2. **Method View**

To configure the **Cleanup** step:

1 Select **Send tip boxes to the configured final destination**, if desired. This sends the tip boxes to the final destination configured in the **Labware Properties** for that tip box.

NOTE The default setting for the **Cleanup** step is both options **Unchecked**. Inserting the **Cleanup** step without selecting either option instructs the instrument to unload any tips currently on the pod to the final destination configured in **Labware Properties** for those tips.

2 Select **Send tip boxes that started on deck back to their original locations**, if desired. This returns the tip boxes to their starting location, regardless of whether they originated on the deck or in an external hardware device.

NOTE **Send tip boxes that started on the deck back to their original locations** is only available when **Send tip boxes to their configured final destination** is selected.

3 Select a step that occurs after the **Cleanup** step or the **Finish** step to validate the step configuration.

Move Pod Step

The **Move Pod** step moves the pod to a deck position that does not hamper access to the labware, ALPs, and devices on the deck.

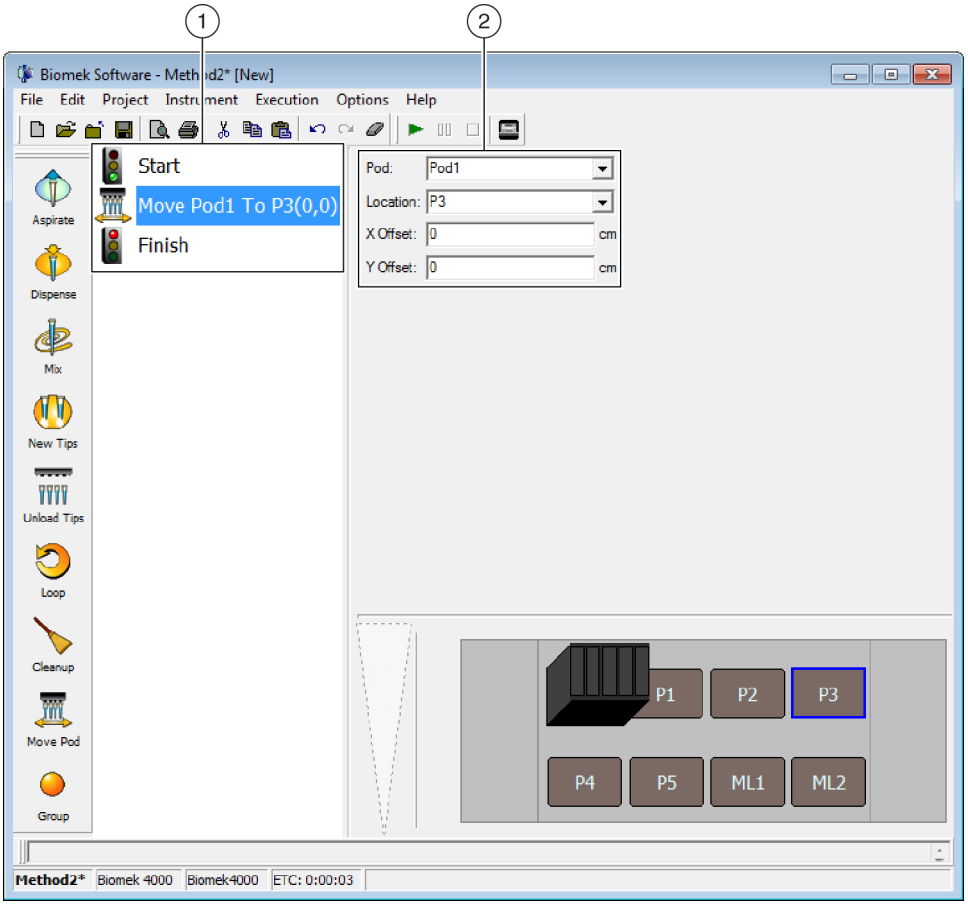
Use **Move Pod** to ensure that the pod does not interfere with activities taking place on the deck, such as the addition, removal, or relocation of labware or devices.

To insert a **Move Pod** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 16.19).

Figure 16.19 Move Pod Step and Configuration



1. **Method View**
2. **Move Pod Configuration**: The **Move Pod** step configuration indicates the pod being moved, the deck position the selected pod is moved to, and any offset values required to provide an accurate position. Note that in the Method View, the step is labeled as a "Move" of "Pod1" to deck position "P3" with offset values of "0,0."

To configure the **Move Pod** step:

1 Ensure **Pod1** is visible in the **Pod** field.

NOTE On the Biomek 4000 instrument, there is only one pod; therefore, **Pod1** is the only option available in the **Pod** drop-down.

2 In **Location**, select the deck position from the drop-down list.

OR

Select **Location** from the Current Deck Display. Selecting a location from the Current Deck Display automatically updates **Location** in the step configuration.

NOTE A bright blue outline appears in the Current Deck Display around the selected location.

3 Insert the **X Offset** value in centimeters (cm).

4 Insert the **Y Offset** value in centimeters (cm).

NOTE Selecting the deck position without offset values is usually sufficient to relocate the pod; however, **X** and **Y Offset** values can be used to provide a more specific position.

The final position of the pod when using **X** and **Y Offsets** is the deck position specified in **Location** *Plus* the values inserted into the **X** and **Y Offsets**. For example, when framing an ALP, the labware positioned on the ALP is 'offset' from the zero (0) point, or back-left corner, of the ALP to the actual edge of the labware itself.

5 Select a step that occurs after the **Move Pod** step or the **Finish** step to validate the step configuration.

Group Step

The **Group** step gathers steps performing similar functions or steps achieving a specific result together. **Group** reduces the confusion that can arise when viewing large methods by consolidating and applying a single label to a number of steps. Multiple **Group** steps can be used within a method, and they can be placed in a **Group** step together to further abbreviate the steps displayed in the Method View.

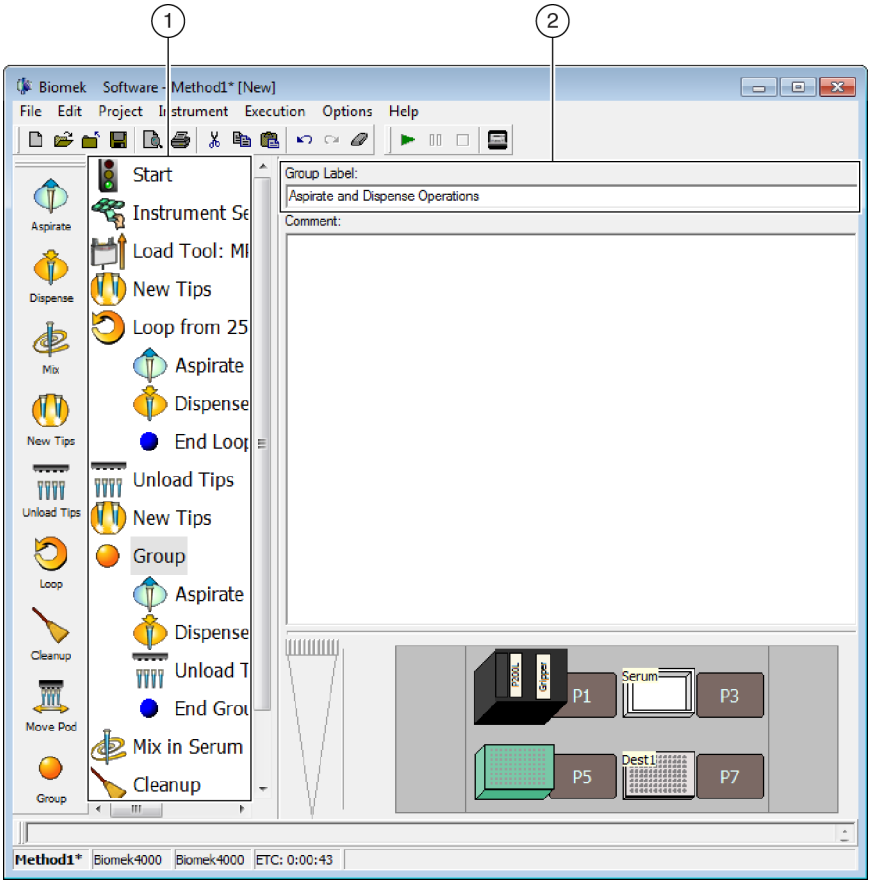
Advantages to grouping steps are:

- The steps contained the **Group** step are hidden from the Method View by collapsing the **Group** step.
- The **Group** step is collapsed by default when a method is opened. This means long methods appear shorter and more concise.
- Multiple steps can be identified by a single label.
- All steps related to a specific operation can be grouped together under a single label to identify the operation they perform.

To insert a **Group** step into a method:

1 Drag and drop the Group icon into the Method View (Figure 16.20).

Figure 16.20 Group Step and Configuration



1. **Method View**: The method displayed contains a **Group** step. The **Group** is labeled "Aspirate and Dispense Operations" because that phrase is inserted in the **Group** step configuration.
2. **Group step configuration**: The **Group** step configuration provides the label applied to the steps grouped together.

When a **Group** step is added to a method, the **Group** step configuration appears (Figure 16.20).

To configure the **Group** step:

1 Double click on the **Group** step to expand it so that the End Group icon is visible.

2 In **Group Label**, enter text to identify the group.

NOTE The text inserted in **Group Label** appears in the **Group** steps caption in the Method View.

3 Insert steps between the **Group** and **End** icons.

4 Double click on the **Group** step to collapse it so that the steps contained within the **Group** step are hidden from view.

NOTE The **Group** step is collapsed by default when the method opens.

CHAPTER 17

Using the Advanced Step Palette

Overview

The steps presented in the **Advanced** step palette (Figure 17.1) provide tools for more complex management of methods. These steps are used to perform the following:

- Repeat a series of steps using a list of specified values without entering and configuring the steps individually.
- Access and run a method within a method.
- Conditionally execute steps based on an aspect of the environment, such as the volume in a microplate.

The steps available in the **Advanced** step palette are listed in Table 17.1:

Table 17.1 Advanced Step Palette

Step	Icon	Description
Run Method		Accesses and runs a method within a method.
Worklist		Fills in variables based on a worklist file.
Just In Time		Synchronizes the execution of steps.
Let		Defines variables for its substeps.
If		Evaluates a condition within a method and runs either the “then” substeps or the “else” substeps according to the condition.

Table 17.1 Advanced Step Palette

Step	Icon	Description
Script		Runs a list of commands providing customized control over the instrument.
Scripted Let		Similar to **Script** step, with the exception that it allows variables to be extended outside the script and used in the method.

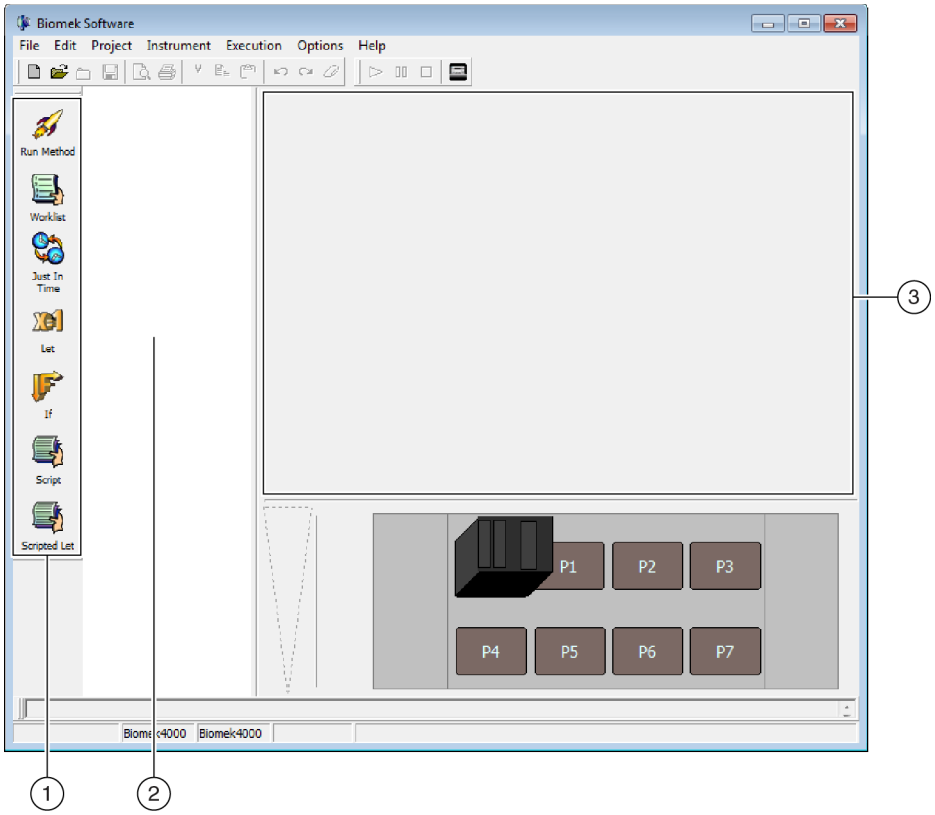
When one of the above steps is inserted into a method, the configuration options associated with that step appear on the right side of the Biomek Software main editor, in step configuration.

NOTE Steps not configured appropriately may generate errors when the method is validated or run.

Displaying the Advanced Step Palette

In order to add advanced steps to a method, display the **Advanced** step palette (Figure 17.1).

Figure 17.1 Biomek Software Main Editor with Advanced Step Palette Displayed



1. **Advanced Step Palette**: Displays the steps available for insertion into a method.
2. **Method View**: The method is built step by step in this area.
3. **Step Configuration**: When a step is highlighted in the Method View, set the corresponding configuration in this area.

To display the **Advanced** step palette:

1 Right click any empty palette space, and select **Advanced** from the menu.

OR

From the toolbar, select **Options > Toolbars > Advanced**.

Run Method Step

The **Run Method** step executes a previously created method within the method in progress. **Run Method** saves time by assigning variables accessible by the previously created method and by preventing unnecessary duplication of steps. If the same series of steps is used in a number of methods, a method can be created containing only those steps and accessed using a **Run Method** step. Multiple **Run Method** steps can be used within a method. Methods referenced by a **Run Method** step must be stored in the active project file.

Although it is not visible in the Method View, the **Run Method** step 'inserts' all of the steps from the referenced method into the current method at the point the **Run Method** step displays. All of the steps contained in the submethod are completed as a part of the current method; they are not completed as a separate method.

NOTE A 'submethod' is a method run within another method. It is recommended that the submethod use the same **Instrument Setup** step configuration as the method in progress. If the submethod and the method in progress do not use the same **Instrument Setup**, an **Instrument Setup** step must be added to the method in progress to ensure that all labware for both methods is visible to the instrument.

The advantages of using **Run Method** are:

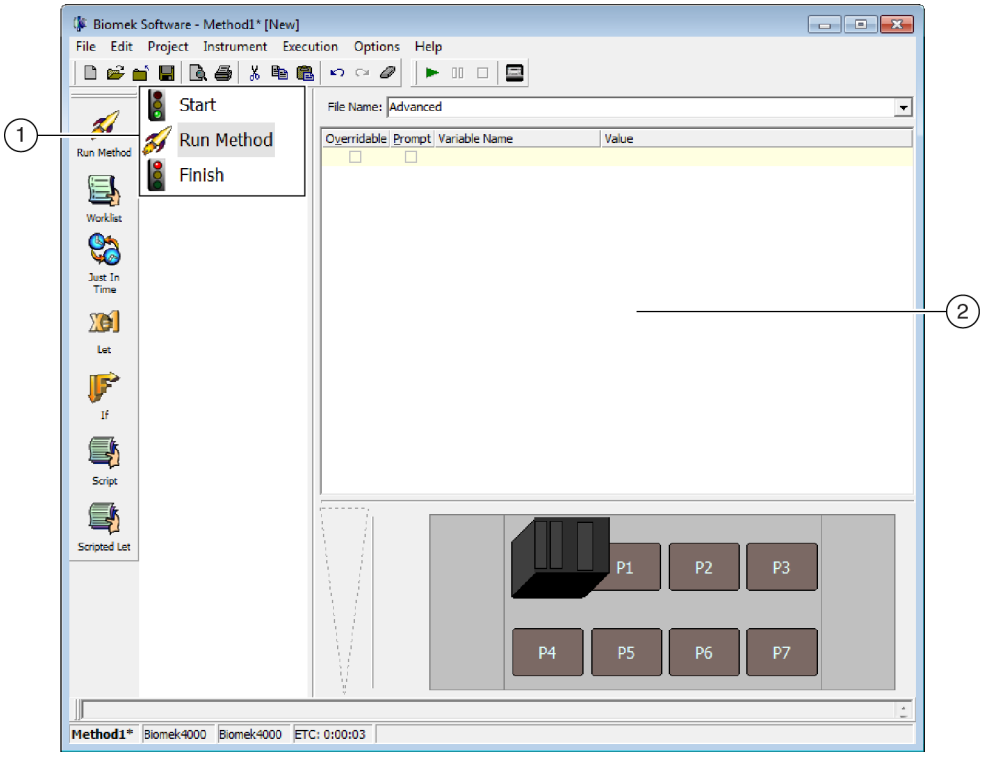
- The ability to run a method within a method.
- Allows repetition of steps configured in a previously created method without recreating those steps.
- Variables assigned in the **Run Method** step are accessible by the submethod.
- Controls the size of the current method and reduces confusion by listing only the **Run Method** step in the Method View, not all of the steps accessed by the **Run Method** step.

To insert a **Run Method** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 17.2).

Figure 17.2 Run Method Step and Configuration



1. **Method View**: The method displayed contains a **Run Method** step. Note that the **Run Method** step shows the name of the submethod.
2. **Run Method Step Configuration**: The **Run Method** step configuration allows the selection of a previously created method and then runs it as a submethod within the current method. Variables configured in the **Run Method** step configuration are accessible by the submethod.

Configuring the Run Method Step

To configure the **Run Method** step:

1. In **File Name**, select a submethod to run within the method in progress. The **Run Method** step shows the name of the submethod.

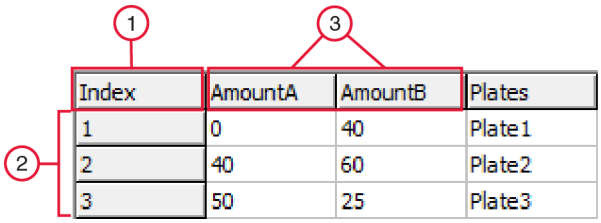
   NOTE Only submethods stored in the same project file as the method in progress are available. To access a submethod stored in another project file, import the desired submethod into the project (refer to CHAPTER 6, *Importing and Exporting Project Files*).

2. Configure any variables as needed (refer to CHAPTER 13, *Using Variables and Expressions in a Method*).

Worklist Step

The **Worklist** step uses a text file to supply multiple values for one or more variables (Figure 17.3). **Worklist** is useful when repetition of the same step(s) is required, but a variable, or variables, needs to change each time the step(s) is executed. When a group of steps using the variable(s) defined in a text file are placed inside a **Worklist** step, **Worklist** automatically performs each step once for each line in the text file. The steps using the variable(s) defined in the text file are substeps within the **Worklist** step in the Method View.

Figure 17.3 Worklist Example



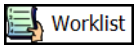
1. **Loop variable**: The variable assigned in the Worklist configuration that holds the current iteration of the Worklist 'loop.'
2. **Rows of data**: Each row of data represents a pass for the step(s) nested within the **Worklist** step.
3. **Values Used (During the Worklist Step)**: Value assigned during each pass of the worklist for each of the steps within the **Worklist** step.

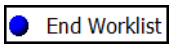
NOTE Values read from the text file must be formatted correctly in order for Biomek Software to create the worklist with the desired row and column formatting. Each row in the text file represents a row in the worklist. In each row, columns are designated by separating individual values with commas.

Worklist text files may be created in a database, spreadsheet, or text editor. When creating a worklist in a database or spreadsheet, save the file in comma-separated values (*.csv) format. When using a text editor or word processor, manually separate values on a single line with commas and save the file in text (*.txt) format.

NOTE Quotation marks may be used in the text file, but they must come in pairs. The **Worklist** step looks at the first set of quotation marks and interprets that everything after them is included as a row of data up to the second set of quotation marks. If quotation marks are desired in a row of data, use another set of quotation marks around the data within the quotations marks. For example, type ""this is a comment"" in the text file and "this is a comment" will appear in the row of data in the **Worklist** step.

The **Worklist** step operates like a combined **Let/Loop** step because it 'lets' a variable in the **Worklist** text file use different values for each pass of the **Worklist** 'loop'. **Worklist** 'loops' through the substeps until each step has used each line of the **Worklist** text file specified.

When **Worklist** is added to a method, the 

and the 

icons display in the Method View. Any step(s) inserted between the **Worklist** and **End Worklist** icons use the variables contained in the **Worklist** text file configured in the **Worklist** step.

Advantages of using a **Worklist** include:

- Data in a text file is accessible by any Biomek Software method.
- Selecting the text file in the **Worklist** step configuration copies all of the variable data from the text file into the **Worklist** step configuration without individually entering all of the variables and their values in each of the steps performed inside the **Worklist** step (Figure 17.4).
- A dynamic link exists between the method and the text file. The **Worklist** step accesses the text file each time the method is run; therefore, any updates made to the text file are included in the next method run.

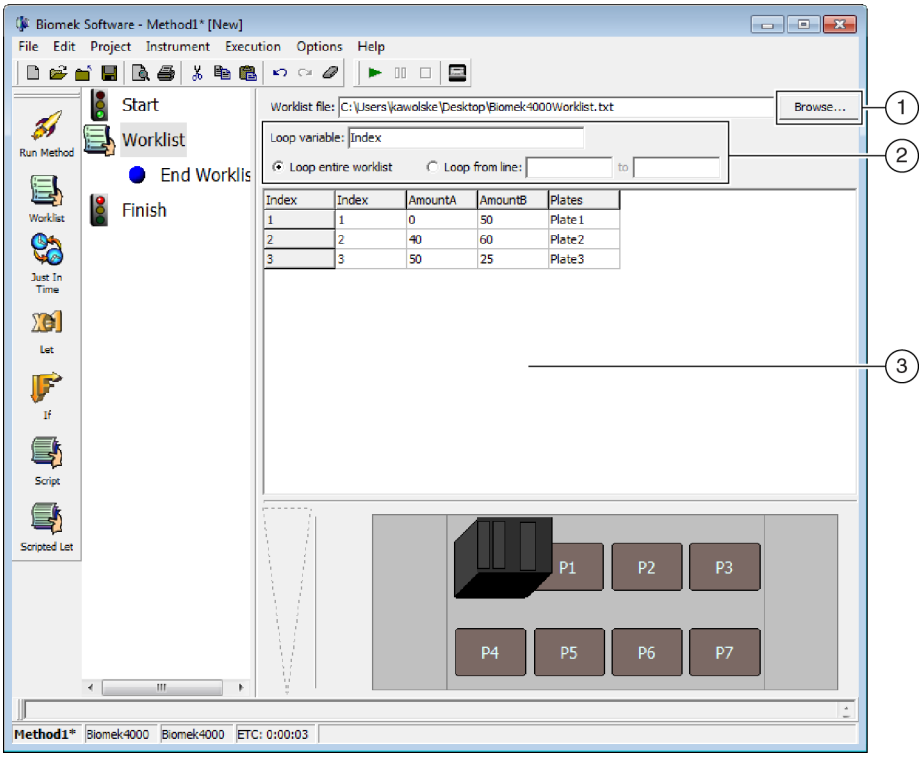
  NOTE The text file configured in the **Worklist** step must maintain its original file path, or the method will not be able to find the text file. If the text file path changes, update the **Worklist** step configuration to reflect the new file path.

To insert a **Worklist** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 17.4).

Figure 17.4 Worklist Step and Configuration



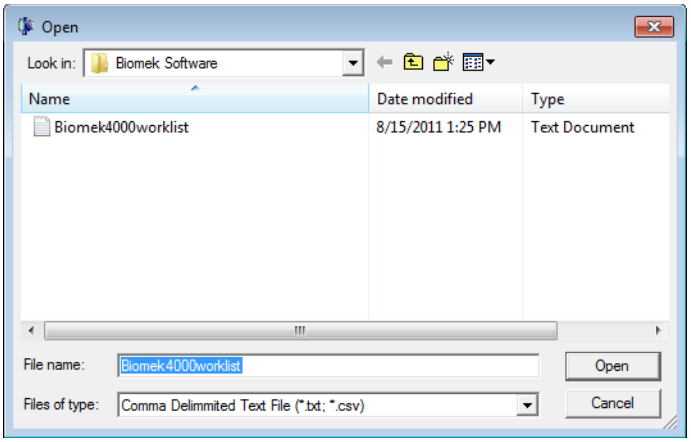
1. **Browse**: Allows the selection of a text file that can be used by the method under development.
2. **Loop Variable**: Specify the **Loop variable** name and assigned values here.
3. **Worklist Step Configuration**: When a file is selected, the Worklist configuration updates to display the contents of the specified file; however, the Worklist configuration cannot edit the contents of the file.

Configuring the Worklist Step

Complete the following to configure the **Worklist**:

1 Click the **Browse** button following **File Name**. **Open** appears (Figure 17.5)

Figure 17.5 Worklist—Text File Selection



2 Browse to and select the text file accessed during the method run.

NOTE The file path and the file name of the text file are included in the **Worklist** step in the **Method View**.

3 Click **Open** to add the file to the **Worklist** configuration and return to the main Biomek Software window.

4 Enter a name for the **Loop Variable.** The loop variable holds the current iteration number of the worklist.

5 Select **Loop entire worklist** to use all rows of the worklist.

OR

Select **Loop from line** and enter the start and end row numbers to use a specific range of rows from the worklist.

Just In Time Step

Just In Time synchronizes the execution of the substeps within the **Just In Time** step (Figure 17.6).

The steps within the **Just In Time** step are queued in the order in which they appear in the Method View, but it is possible to execute two or more steps simultaneously. In Figure 17.6, for example, the first two substeps are completed, then deck position P5 is paused. While the pause on P5 is in process, the next four steps are completed because they do not require access to deck position P5. Finally, the last two steps are completed once the pause is finished because they require access to deck position P5.

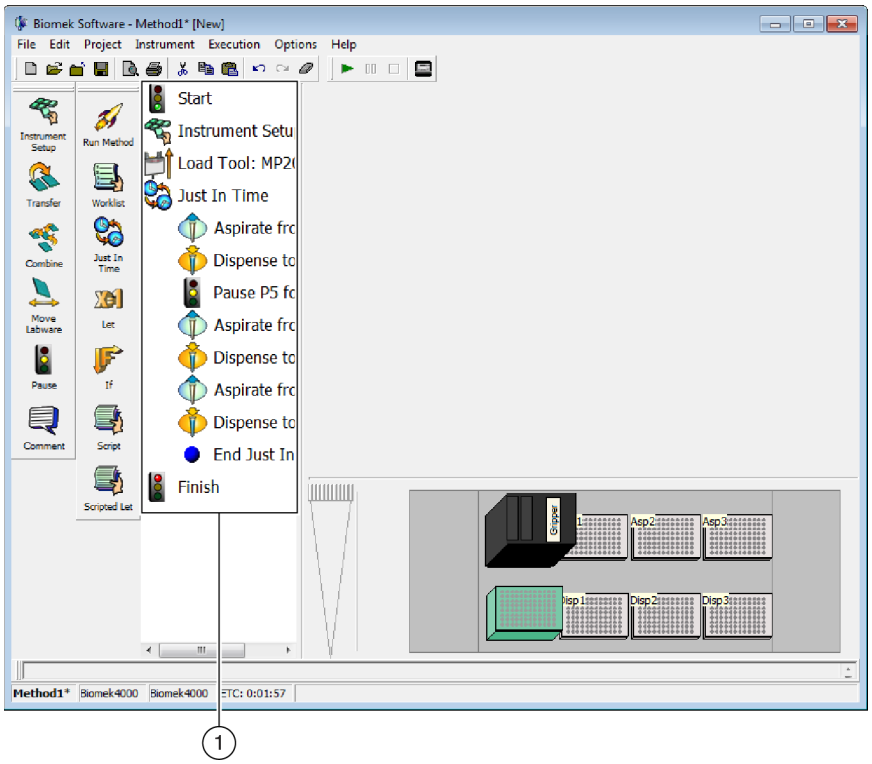
NOTE An incubation period is accomplished using the **Pause** step (refer to CHAPTER 15, *Pause Step*).

Since **Just In Time** is a part of the **Transfer**, **Combine**, and **Move Labware** steps, it is not necessary to use these steps in conjunction with the **Just In Time** step.

Use **Just In Time** when an **Aspirate** operation and its subsequent **Dispense** operation must occur immediately following an incubation period (Figure 17.6) or when a method requires that a preparatory operation should not occur too early with respect to another related operation.

NOTE Any steps placed between the **Just In Time** and **End Just In Time** icons are configured in their individual step configurations, but they are completed when appropriate within the **Just In Time** step.

Figure 17.6 Just In Time Step

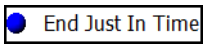


1. **Method View**: The method displayed contains a **Just In Time** step. Note that the **Just In Time** step contains nested steps, which can be hidden from view to control the size of the method displayed in the Method View.

To insert a **Just In Time** step into a method:

1 Drag and drop the 

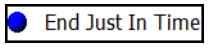
icon into the Method View. The 

step appears in the method, as well as an 

step (Figure 17.6).

To configure **Just In Time**:

1 Enter the steps requiring synchronized timing between the 

and 

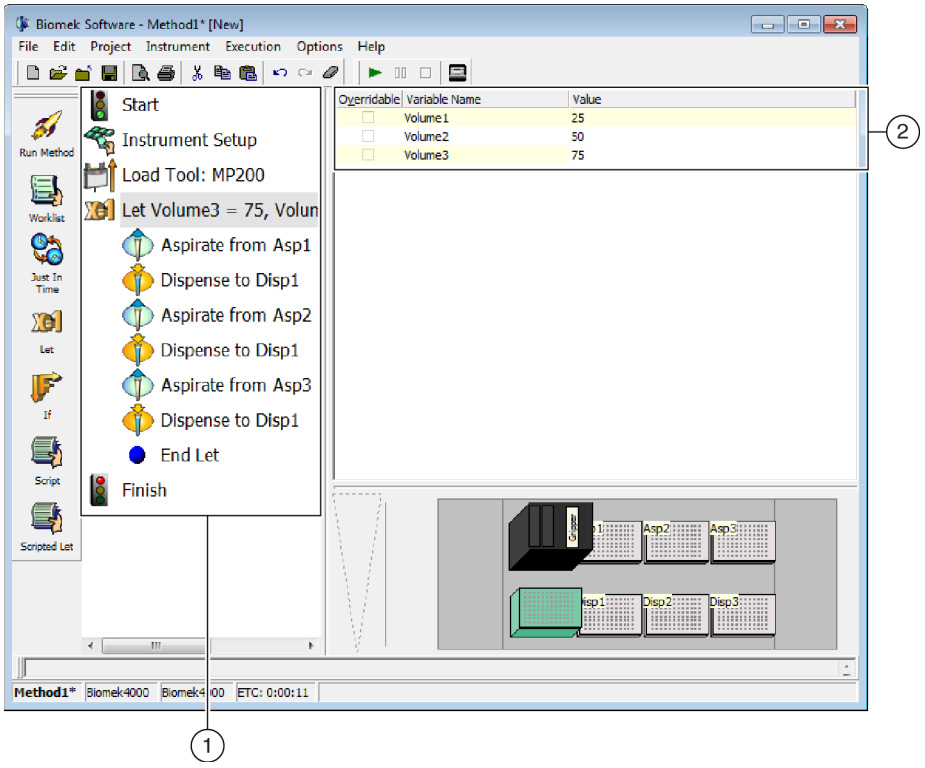
steps.

NOTE The **Just In Time** step does not affect the **Estimated Time to Completion** for the method when its substeps are already synchronized steps, such as the **Transfer**, **Combine**, or **Move Labware** steps.

Let Step

The **Let** step is used to create variables accessible only to the sub-steps of the **Let** step (Figure 17.7). The variables can be used by multiple steps within the **Let** step, and they allow configuration of the steps by specifying explicit values for things like volumes and heights. For example, instead of typing the number of microliters into the volume field of an **Aspirate** step, the name of a variable is inserted. Every time the **Aspirate** step is executed, the current value of that variable is used as the volume.

Figure 17.7 Let Step and Configuration



1. **Method View**: The method displayed contains a **Let** step. Variables assigned in the **Let** step configuration can appear in the **Let** step caption in the **Method View**; however, if numerous variables are assigned and they cannot all be displayed in the **Let** step caption, an ellipsis appears in the caption instead.
2. **Let configuration**: The **Let** configuration assigns a **Name** and **Value** to variables used by the steps nested within the **Let** step. Variables assigned in the **Let** step are only available to the substeps within the **Let** step; they are not available to steps outside the **Let** step.

When the **Let** step is added to a method, the Let and End Let steps appear (Figure 17.7). Any steps placed between the Let and End Let steps are substeps controlled by the **Let** step, but they are configured through their individual step configurations. Substeps are enqueued for execution in the order of appearance in the Method View; however, it is possible to execute two or more steps simultaneously.

Any of the substeps within the **Let** step can use variables created in the **Let** step configuration. Only the **Name** displays in the step configuration, not the **Value** associated with that **Name**. Biomek Software automatically uses the associated **Value** when the step is executed.

Configuring the Let Step

Configuring the **Let** step involves creating the variables used by the substeps within the **Let** step (Figure 17.7).

To insert a **Let** step into a method:

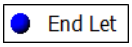
1 Drag and drop the 

icon into the Method View (Figure 17.7).

To configure the **Let** step:

1 Insert the variables desired (refer to CHAPTER 13, *Using Variables and Expressions in a Method*).

2 Enter desired steps between 

and 

steps.

3 Configure the substeps between **Let** and **End Let**.

If Step

The **If** step controls which steps in a method execute based on a condition, such as the volume of liquid in a piece of labware. When **If** is run, Biomek Software tests the **If** condition, then processes the appropriate block of substeps based on the results of the test.

The substeps of **If** include:

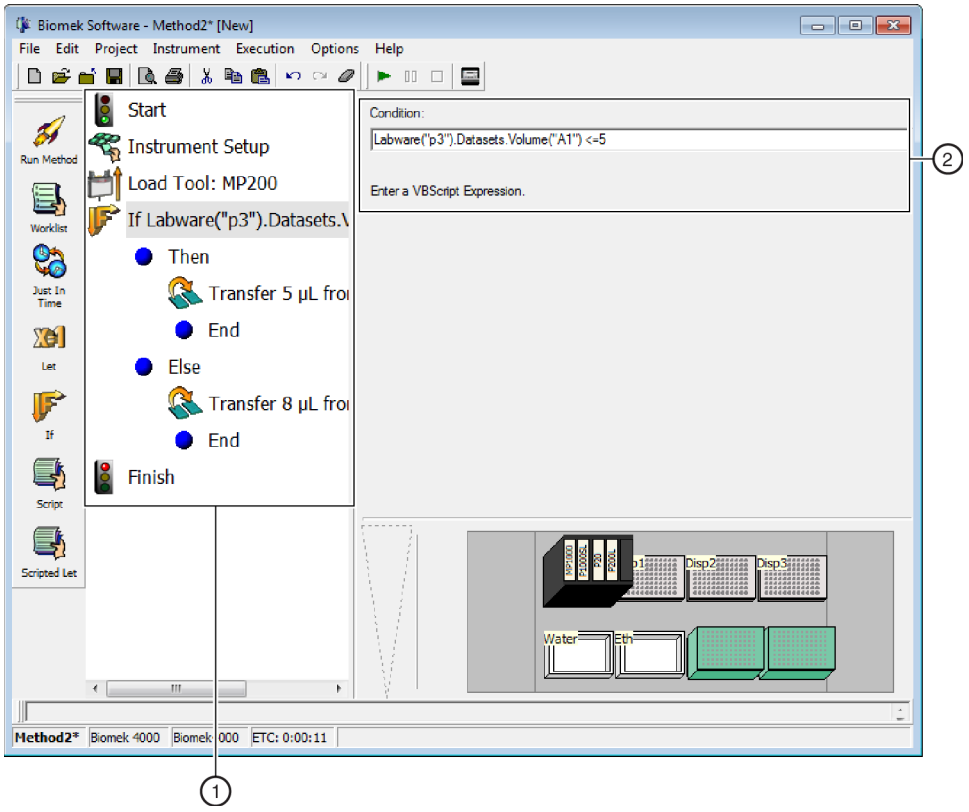
- **Then** — Substeps following **Then** are processed if the condition is true.
- **Else** — Substeps following **Else** are processed if the condition is false.
- **End** — The **End** substep terminates each **If, Then**, and **Else** block of steps (Figure 17.8).

To insert an **If** step into a method:

1 Drag and drop an 

icon into the Method View. The **If** step configuration displays (Figure 17.8).

Figure 17.8 If Step and Configuration



1. **Method View**: The condition being tested appears in the **If** step command in the Method View. Note the nested **Then** and **Else** steps which are completed, depending on the results of the condition tested.
2. **If Step Configuration**: The condition being verified and acted upon is input in the **If** step configuration.

Configuring the If Step

To configure the **If** step:

1 Enter the **Condition** in the configuration.

NOTE A **Condition** must be a valid VBScript expression and can refer to variables defined in other steps.

2 Highlight **End** under the **Then** substep.

3 Add and configure the steps performed if the condition is true.

4 Highlight **End** under the **Else** substep.

5 Add and configure the steps to perform if the condition is false.

NOTE Any steps placed between the **Then** and **End** or **Else** and **End** icons are configured in their individual step configurations using the same procedures as though they were a main step in the method.

Script Step

NOTE The information in this section is intended only to assist in gaining an understanding of what the scripting function does. It is not intended to be a tutorial on scripting. The **Script** step is provided only for the use of methods developed within Beckman Coulter at this time. This function is not currently supported for end-user applications.

NOTE Refer to CHAPTER 27, *Scripting*, for other information on scripting.

While the editors and templates in Biomek Software provide the means to perform most operations, it is possible that some highly specialized liquid-handling applications are beyond this scope. Although not an activity typically required by users, Biomek Software uses the **Script** step for writing script to accommodate these advanced needs.

A Biomek Software script consists of lines of code that provide instructions for instrument operations. The lines of code, or commands, may be typed into the **Script** step configuration. Running the method invokes a Visual Basic script interpreter that evaluates each line of code and performs the requested operation.

Dragging a **Script** step from the Method View to the step palette makes it available as a step to any method (refer to CHAPTER 28, *Changing Window Appearance*). To make the values defined in a **Let** step available to the **Script** step, place the **Script** step within the **Let** step.

The **Script** step provides a configuration area in which a description of the script step may be entered and lines of code may be written (Figure 17.9).

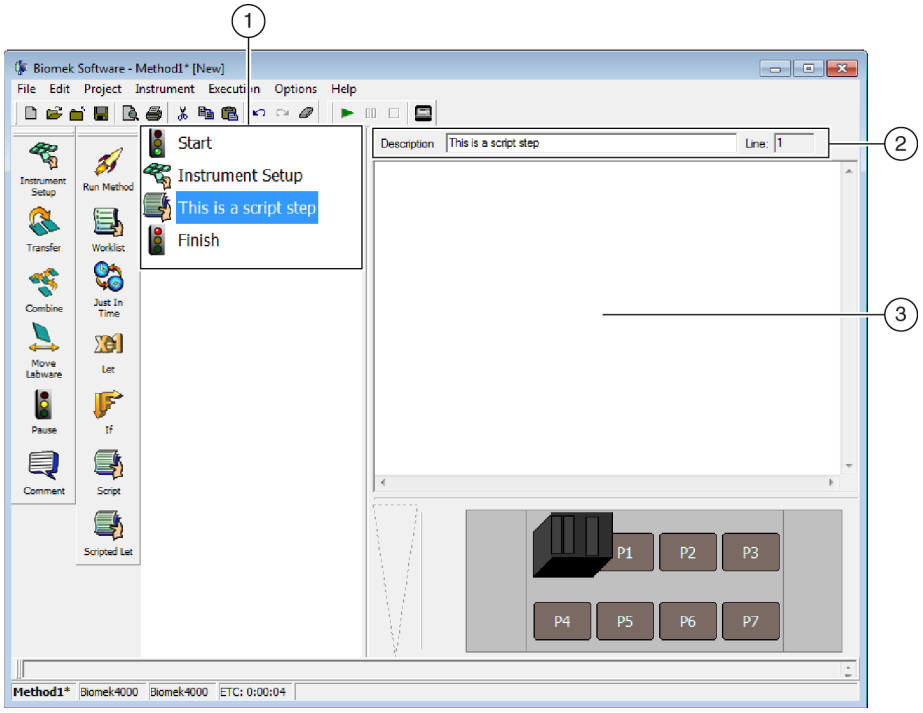
To insert a **Script** step into a method:

1 Drag and drop a 

icon into the Method View (Figure 17.9).

NOTE Place the **Script** step within a **Let** block of steps (refer to *Let Step*) to use the variables defined in the **Let** step in the **Script**.

Figure 17.9 Script Step and Configuration



1. **Method View**: The **Description** entered in the **Script** step configuration appears in the method.
2. **Enter the description here.**
3. **Script Step Configuration**: Code is entered here in this **Script** step configuration area.

Configuring the Script Step

To configure the **Script** step:

---

1 In **Description**, enter a description for the operation or purpose of the **Script** step.

NOTE The **Description** replaces the word "Script" in the **Script** step caption in the Method View.

---

2 Position the cursor in the **Script** step configuration.

NOTE The lines of code can be entered in a word processor and then copied and pasted into the **Script** Step Configuration using standard Windows procedures. Use standard Windows techniques for editing scripts.

3 Write and edit the script.

NOTE The Biomek Software scripting feature is based on Visual Basic Scripting, a subset of the Microsoft Visual Basic programming language. Any code interpreted by Visual Basic Scripting can be interpreted by the instrument and may be included in a method. More Visual Basic Scripting information is available at

http://msdn.microsoft.com/scripting and in the book, *VBScript in a Nutshell*, 2nd Edition, Matt Childs, Paul Lomax, and Ron Petrusha 2003, O'Reilly & Associates, Inc. For more specific Biomek Software scripting help, contact Beckman Coulter Technical Support.

Scripted Let Step

NOTE The information in this section is intended only to assist in gaining an understanding of what the scripting function does. It is not intended to be a tutorial on scripting. The **Scripted Let** step is provided only for the use of methods developed within Beckman Coulter at this time. This function is not currently supported for end-user applications.

NOTE Refer to CHAPTER 27, *Scripting*, for other information on scripting.

The **Scripted Let** step is similar to the **Script** step (refer to *Script Step*), except it allows for variables created within a Script to be extended outside the Script and used in the method like variables created in a **Let** step (refer to *Let Step*). Two additional commands are available to set variables — **Extend** and **WeakExtend**.

- **Extend** — Sets the variable name to the specified value for all steps contained within the **Scripted Let**. The proper syntax for **Extend** is **Extend "Variable Name", Value.**
- **WeakExtend** — Sets the variable name to the specified value for all steps contained within the **Scripted Let** step if the specified variable does not already have a value. This is similar to a **Let** variable with **Overridable** selected. The proper syntax for **WeakExtend** is **WeakExtend "Variable Name", Value.**

The **Scripted Let** step provides a configuration area in which a description of the script step may be entered and lines of code may be written.

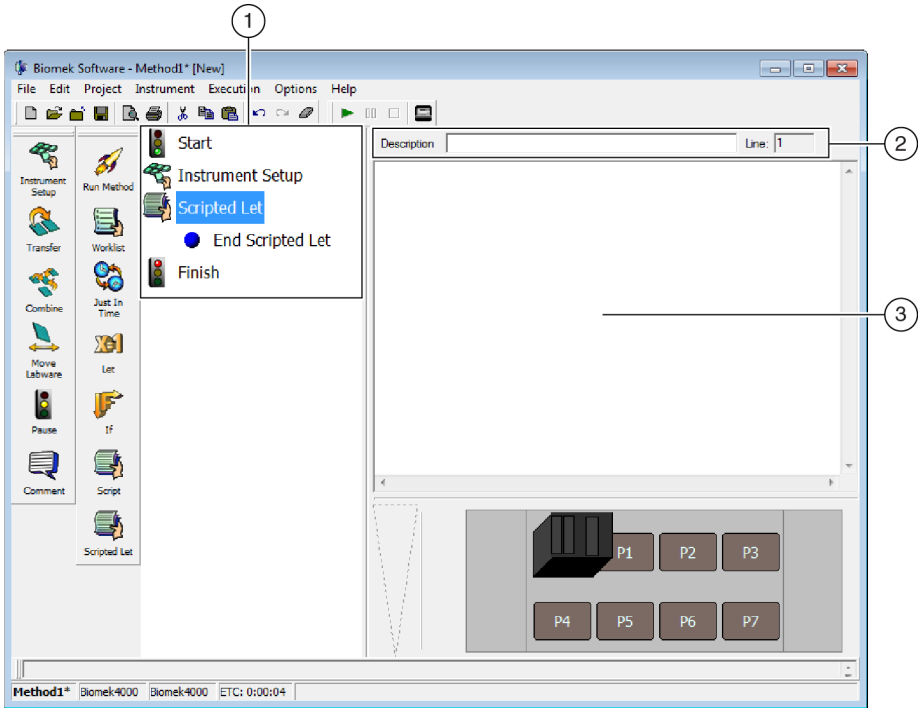
To insert a **Scripted Let** into a method:

1 Drag and drop the 

icon into the Method View (Figure 17.10).

NOTE Place the **Scripted Let** step within a **Let** block of steps (refer to *Let Step*) to use the variables defined in the **Let** step in the Script.

Figure 17.10 Scripted Let Step and Configuration



1. **Method View**: The **Description** entered in the **Script** step configuration appears in the method.
2. **Enter the description here.**
3. **Scripted Let step configuration**: Code is entered here in this **Scripted Let** step configuration area.

Configuring the Scripted Let Step

To configure the **Scripted Let** step:

---

1 In **Description**, enter a description for the operation or purpose of the **Scripted Let** step.

NOTE The **Description** replaces the words "Scripted Let" in the **Scripted Let** step caption in the Method View.

---

2 Position the cursor in the **Scripted Let** step configuration.

NOTE The lines of code can be entered in a word processor and then copied and pasted into the **Scripted Let** step configuration using standard Windows procedures. Use standard Windows techniques for editing scripts.

3 Write and edit the script.

NOTE The Biomek Software scripting feature is based on Visual Basic Scripting, a subset of the Microsoft Visual Basic programming language. Any code interpreted by Visual Basic Scripting can be interpreted by the instrument and may be included in a method.

4 Insert any substeps between **Scripted Let** and **End Scripted Let** that utilize any variables defined in the **Scripted Let.**

NOTE Variables extended outside of a script in the **Scripted Let** step are only available to the substeps within the **Scripted Let**.

CHAPTER 18

Using the Span-8 Step Palette

Overview

Steps on the **Span-8** step palette provide individual control over liquid-handling functions, including tip handling and pipetting operations outside the **Transfer** and **Combine** steps. Additional steps, such as **Serial Dilution** and **Transfer From File**, configure larger operations involving multiple liquid-handling functions.

The **Serial Dilution**, **Transfer From File**, and **Define Pattern** steps can all be used with pipetting tools on the Biomek 4000 instrument.

The steps available in the **Span-8** step palette are listed in Table 18.1.

Table 18.1 Span-8 Step Palette

Step	Icon	Description
Serial Dilution		Performs a series of dilutions on a single microplate.
Transfer From File		Performs well-to-well transfers using a comma-separated data file.
Define Pattern		Create a method-specific well pattern manually or by reading well information from a file.

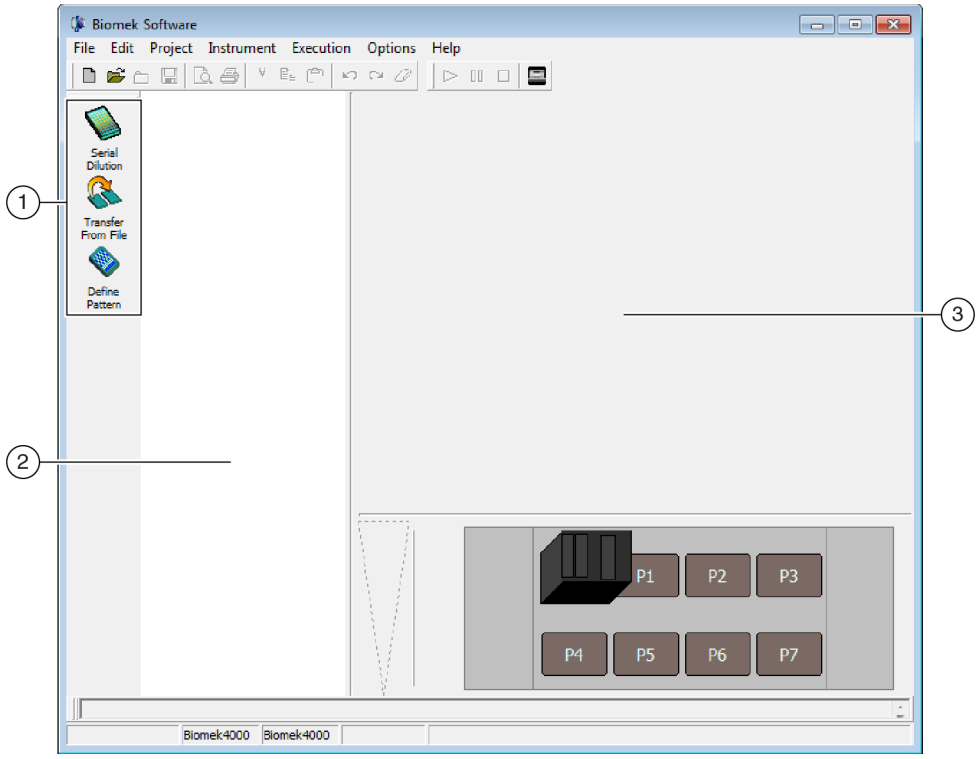
When one of the above steps is added to a method, the configuration associated with that step appears on the right side of the Biomek Software main editor, in step configuration (Figure 18.1).

NOTE Steps not configured appropriately in step configuration generate errors when the method is validated or run.

Displaying the Span-8 Step Palette

In order to add **Span-8** steps to a method, display the **Span-8** step palette (Figure 18.1).

Figure 18.1 Biomek Main Editor with Span-8 Step Palette Displayed



1. **Span-8 Step Palette**
2. **Method View**: The method is built step by step in the Method View.
3. **Step Configuration**: When a step is highlighted in the Method View, the corresponding configuration appears in this area.

To display the **Span-8** step palette:

1 Right click any empty palette space, and the step palette menu displays. Select **Span-8**.

OR

From the menu bar, select **Options > Toolbars > Span-8**.

Serial Dilution Step

The **Serial Dilution** step is used to perform multiple dilutions of a sample on a single microplate. The **Serial Dilution** step transfers liquid from wells on a microplate to other wells on the same microplate and may also add diluent to those wells. The liquid(s) within the microplate can be set up using the **Serial Dilution** step or in the same method prior to the **Serial Dilution** step.

Serial dilution completes multiple dilutions by performing the following actions in sequence:

1. Transfer a volume of diluent from the diluent labware to all selected wells except the first row or column (unless specified otherwise).
2. Transfer a volume of sample from the first selected well to the next selected well.
3. Mix the solution, if indicated by the technique.

   NOTE The **Serial Dilution** step does not automatically mix the solution. Select **Customize** to add mixing to the technique or create a new technique in the **Technique Editor**. Refer to CHAPTER 9, *Creating New Techniques*, for information on creating and modifying techniques.

4. Transfer a volume of solution to the next selected well.
5. Mix the solution, if indicated by the technique.
6. Repeat transfer and mix operations until all selected wells are used.

   NOTE The labware may be previously prepared, either by hand or by using the instrument, with a specific volume of diluent in the selected wells. If the labware is previously prepared, skip the step that adds diluent to the wells.

The **Serial Dilution** step specifies:

- Pod that performs the dilution.
- Tool to load.
- Tips used during dilution.
- Labware type accessed during serial dilution.
- Position of the labware on the deck.
- Liquid type in the labware.
- Wells in the selected labware to use for dilution.
- Volume being diluted.
- Direction in which wells are accessed during dilution.
- Technique.
- Diluent labware type accessed during serial dilution.
- Position of the diluent labware on the deck.
- Liquid type in the diluent labware.
- Wells in the selected diluent labware to use for dilution.
- Dilution ratio.
- Discard extra volume from last wells.
- Change tips (timing).

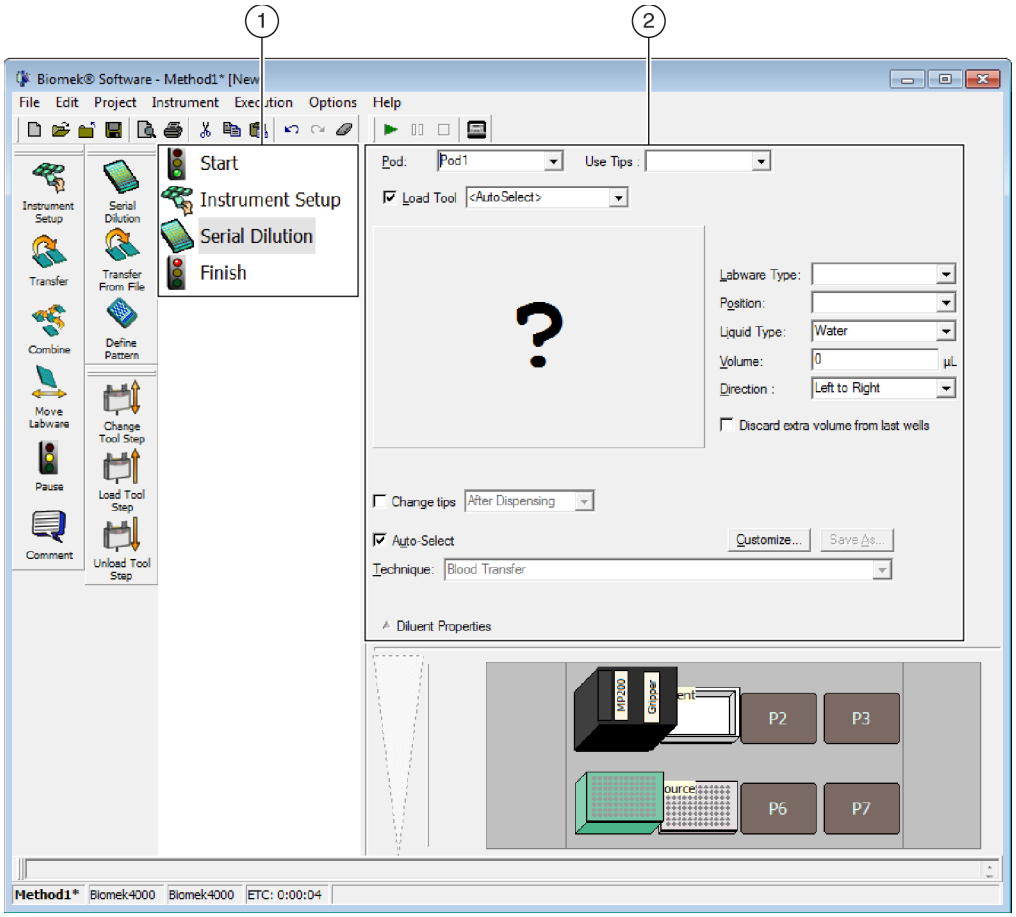
- Whether to add diluent before transfer.
- Changing tips between diluent transfers.
- Technique for diluent transfers.

To insert a **Serial Dilution** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 18.2).

Figure 18.2 Serial Dilution Step and Configuration



1. **Method View**: The method displayed contains a **Serial Dilution** step.
2. **Serial Dilution step configuration**

Configuring the Serial Dilution Step

When a **Serial Dilution** step is added to a method, the **Serial Dilution** step configuration displays (Figure 18.2).

NOTE If it is desired to have diluent in any unused wells as a standard, tips can be conserved by using a **Transfer** step to transfer diluent to the unused wells and selecting **Leave them on** in the **Tip Handling** configuration.

To configure **Serial Dilution:**

---

1 In **Use Tips**, select the tip type loaded from the drop-down list.

OR

Select the tip box from the Current Deck Display with the desired tip type. Selecting tips from the Current Deck Display automatically updates **Tips** in the step configuration.

NOTE If tip boxes were assigned names in the **Instrument Setup** step, enter that name in **Use Tips**. If tips were not assigned names, select the tip type. It is recommended that tips not be named in the **Instrument Setup** step because this could restrict the step from locating available tips.

---

2 If the appropriate tool is not already loaded through a **Load Tool** or **Change Tool** step (from the **Biomek Instrument** step palette), select the tool from the **Load Tool** drop-down, or keep the default selection as **<Auto Select>**, which allows the software to choose the most appropriate tool for the operation.

NOTE Refer to CHAPTER 19, *Change Tool Step* or CHAPTER 19, *Load Tool Step* for information about configuring the desired step.

---

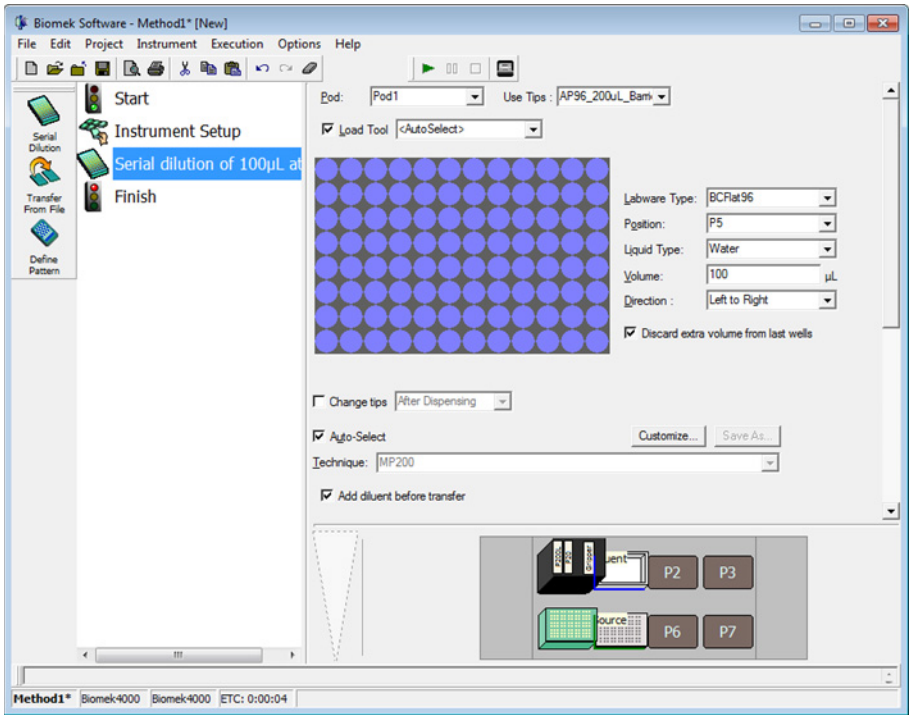
3 Click on the desired piece of labware in the Current Deck Display in which the serial dilution is performed. Information for that piece of labware is entered automatically into the **Serial Dilution** step configuration.

OR

Select a **Labware Type** from the list (Figure 18.3).

NOTE The labware contains the sample that is diluted in the first row or column of selected wells, depending on the direction of dilution selected.

Figure 18.3 Serial Dilution Step Configuration with Labware Configured



4 Verify the **Position** of the labware.

NOTE A green outline appears in the Current Deck Display around the selected labware.

5 Select the **Liquid Type** being diluted in the selected labware.

6 Select the wells on the labware to use in the serial dilution.

NOTE To zoom in on the labware, double click on the labware. To call up a menu for **Zoom In** and a **Specify Selection as Text** option, right click on the labware.

Specify Selection as Text allows the selection of wells in a microplate as a target for the dilution operations. **Specify Selection as Text** can also be used to enter variables or expressions. Wells are numbered left to right and down (for example, the first row contains wells 1-12, the second row, wells 13-24, etc., for a 96-well microplate).

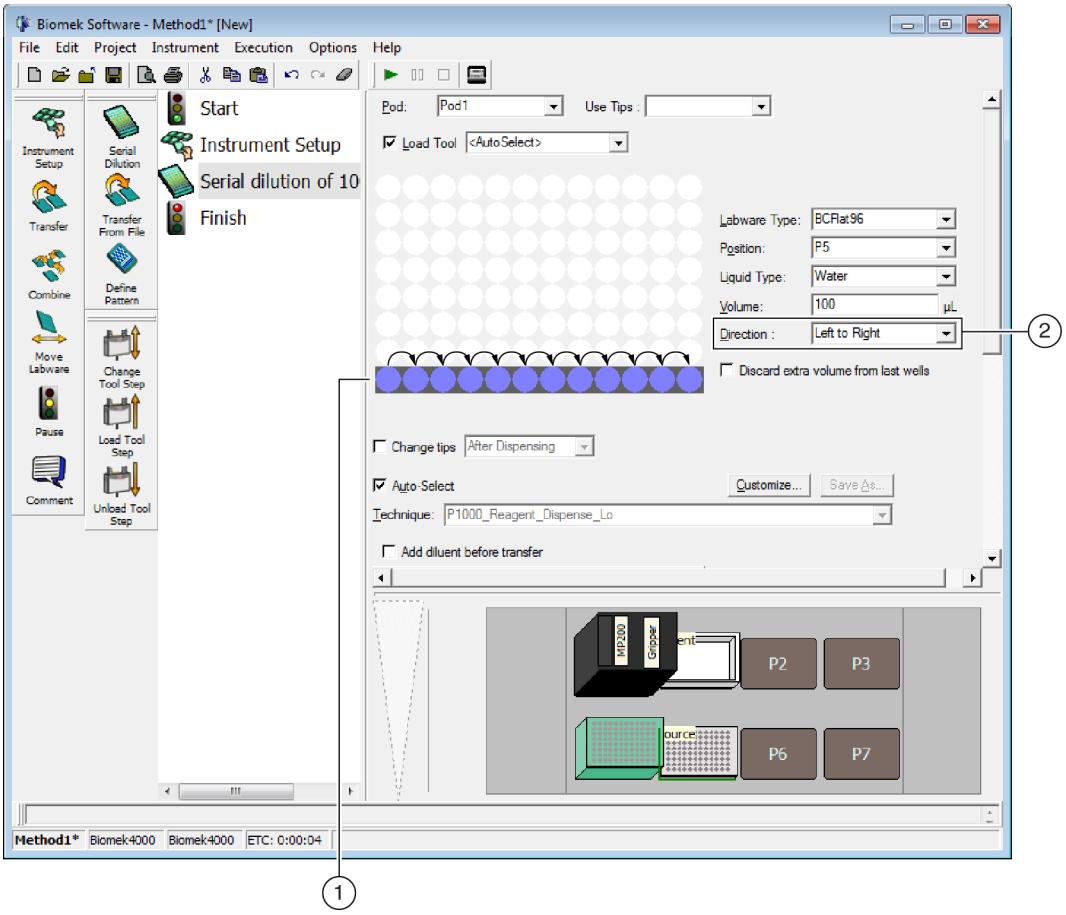
7 Enter the **Volume** diluted in each well of the selected labware. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue**. Otherwise, just enter the desired value.

NOTE This is the volume of each diluted solution that is transferred to the next well for the next dilution.

8 Select the **Direction** to dilute. The specified **Volume** is transferred from each well to the next selected well in the chosen Direction for the next dilution. Available options are:

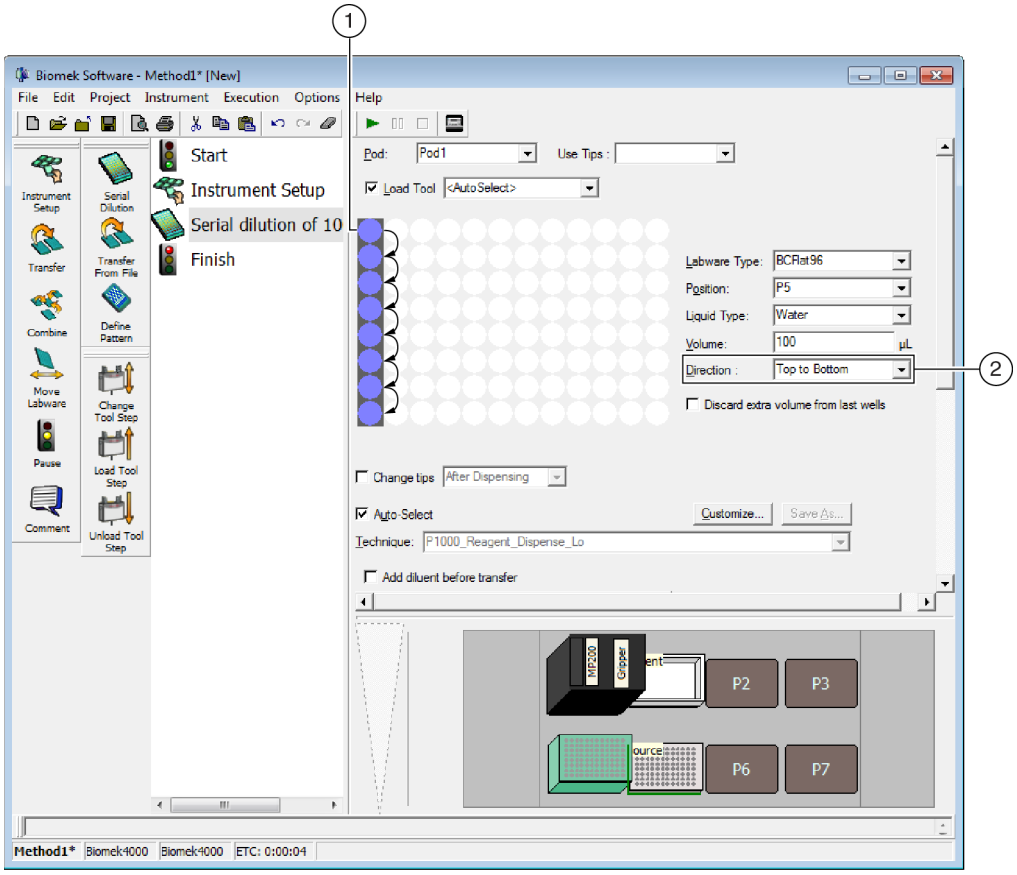
- **Left to right** — dilutes across rows of microplate (Figure 18.4).
- **Top to bottom** — dilutes down columns of microplate (Figure 18.5)

Figure 18.4 Serial Dilution from Left to Right



1. **Leftmost selected well**: Contains sample to dilute.
2. **Diluted sample is transferred in direction of arrows, as indicated in Direction.**

Figure 18.5 Serial Dilution from Top to Bottom



1. **Topmost selected well**: Contains sample to dilute.
2. **Diluted sample is transferred in direction of arrows, as indicated in Direction.**

---

9 Select **Discard extra volume from last wells** to aspirate the extra **Volume** from the last wells and discard it so that each well contains the same volume of solution.

NOTE The extra liquid is typically discarded with the tips when they are shucked back into the tip box. Liquid can also be discarded by transferring the liquid to the Liquid Waste Station; this can be done by setting up a **Transfer** step after the **Serial Dilution** step. For details on setting up a **Transfer** step, see CHAPTER 15, *Configuring Transfer and Combine Steps*.

⚠ WARNING

The Liquid Waste Station can be contaminated from method solutions. Follow the appropriate decontamination procedures outlined by your laboratory safety officer.

10 The software automatically selects a **Technique** based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

OR

Choose **Customize** and configure the technique as desired in the **Technique Editor**.

NOTE For more information on customizing, configuring, and saving a technique, refer to CHAPTER 9, *Understanding and Creating Techniques*.

NOTE It is recommended that the technique used for serial dilution includes mixing for best results. Select **Customize** to add mixing to the technique or create a new technique in the **Technique Editor**. Refer to CHAPTER 9, *Creating New Techniques*, for information on creating and modifying techniques.

11 If the labware is previously prepared with diluent, select a step that occurs after the **Serial Dilution** step or the **Finish** step to validate the step configuration.

OR

If the labware is not previously prepared with diluent, configure **Diluent Properties**. Proceed to *Configuring Diluent Properties*.

Configuring Diluent Properties

Diluent Properties are configured if the sample microplate is not previously prepared with diluent. The **Diluent Properties** configuration allows for diluent to be transferred from a piece of labware to the wells used for the dilution.

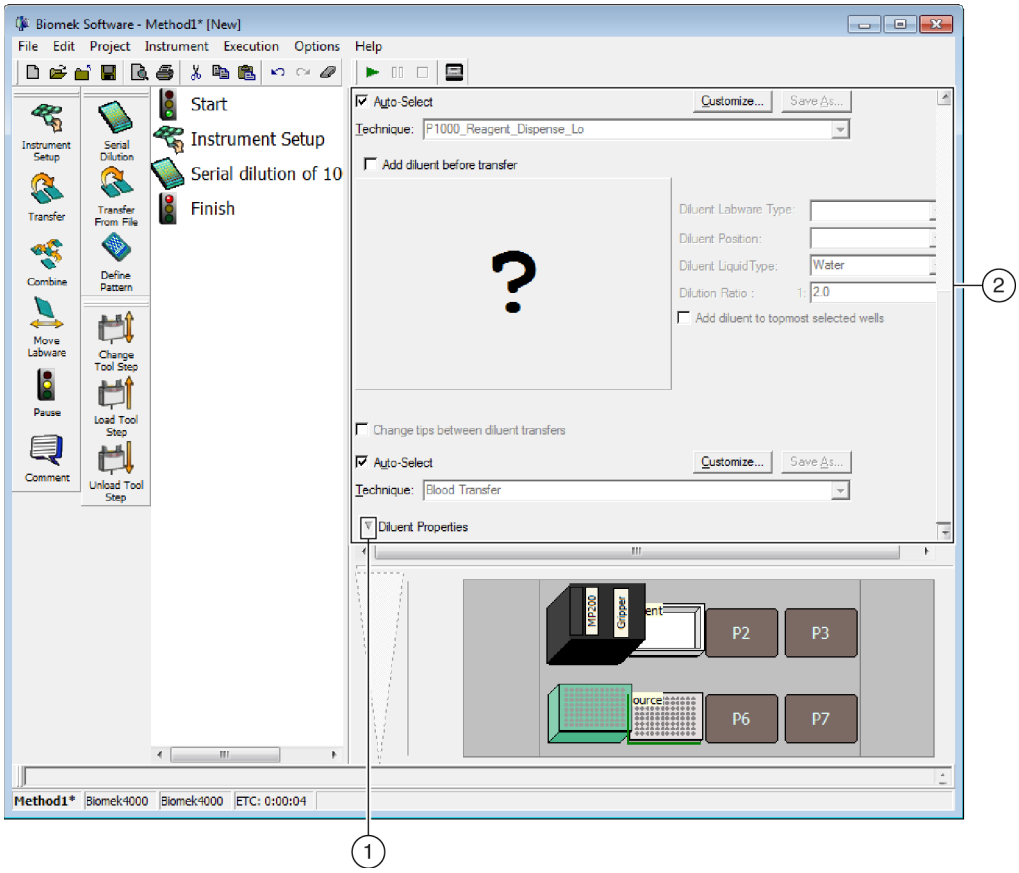
The **Diluent Properties** configuration can be collapsed to allow more room during configuration. When collapsed, the diluent properties configuration is displayed as the text **Diluent Properties**.

To collapse or expand the **Diluent Properties** configuration, click the arrow to the left of **Diluent Properties** or the textual display.

To configure **Diluent Properties** for the **Serial Dilution** step:

1 Click the arrow to the left of **Diluent Properties** or the textual display to expand the **Diluent Properties** configuration (Figure 18.6).

Figure 18.6 Serial Dilution — Diluent Properties Configuration



1. **Arrow to collapse/expand Diluent Properties.**
2. **Diluent Properties**: Diluent labware is configured in the expanded **Diluent Properties** section.

2 Select **Add diluent before transfer** to activate the **Diluent Properties** configuration.

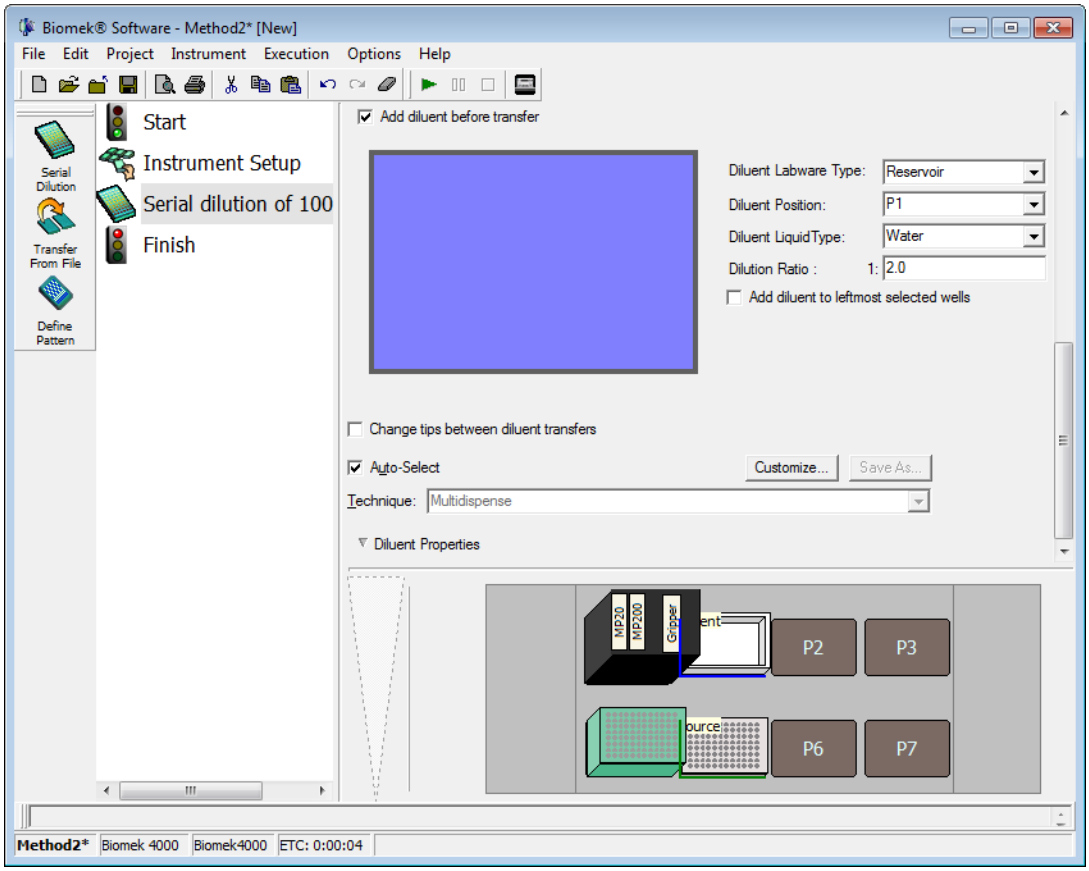
3 Click on the desired piece of labware in the Current Deck Display to select the labware with the diluent. Information for that piece of labware is entered automatically into the **Diluent Properties** configuration.

OR

Select a **Diluent Labware Type** from the list (Figure 18.7).

NOTE Reservoirs are the only labware type valid for diluent retrieval.

Figure 18.7 Serial Dilution Step Configuration with Diluent Labware



4 Verify the **Diluent Position** of the diluent labware.

5 Select the **Diluent Liquid Type** of the diluent in the diluent labware.

6 Enter the desired **Dilution Ratio**. If using a variable, enter an equal sign (=) followed by the variable name; for example, **=AspValue**. Otherwise, just enter the desired value.

NOTE The **Dilution Ratio** is set up as a ratio of volume of sample to total solution (sample plus diluent) volume. For example, a **Dilution Ratio** of 1:2 indicates that for every microliter of sample there are two microliters of solution, or a 50 percent dilution (one microliter of diluent added).

7 Select the wells on the labware from which to aspirate diluent. Wells should be selected according to the procedures described in CHAPTER 15, *Configuring Transfer and Combine Steps*.

NOTE To zoom in on the labware, double click on the labware. To call up a menu for **Zoom In** and a **Specify Selection as Text** option, right click on the labware. **Specify Selection as Text** allows the selection of wells in a microplate as a target for the dilution operations. **Specify Selection as Text** may also be used to enter variables or expressions. Wells are numbered left to right and top to bottom (for example, the first row contains wells 1-12, the second row, wells 13-24, etc., for a 96-well microplate)

NOTE Selecting more than one well for diluent indicates that the same diluent is held within multiple wells, and Biomek Software aspirates by alternating between the selected wells. This behavior is especially useful when using a modular reservoir for the diluent, and more liquid than one well can hold is needed for diluting the samples.

8 Select **Add Diluent to leftmost/topmost selected wells** if it is desired to use the first selected wells for the first dilution. Enough diluent to achieve the entered **Dilution Ratio** is added to the first selected wells.

NOTE If the dilution **Direction** is configured as **Left to Right**, **Add diluent to leftmost selected wells** is available (Figure 18.4). If the dilution **Direction** is configured as **Top to Bottom**, **Add diluent to topmost selected wells** is available (Figure 18.5).

9 Choose **Change tips between diluent transfers** to change tips between each diluent transfer.

10 The software automatically selects a **Technique** based on the liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

OR

Choose **Customize** and configure the technique as desired in the **Technique Editor**.

NOTE For more information on customizing, configuring, and saving a technique, refer to CHAPTER 12, *Understanding Techniques*.

NOTE It is recommended to use a technique that includes mixing for best results. Select **Customize** to add mixing to the technique or create a new technique in the **Technique Editor**.

11 Select a step that occurs after the **Serial Dilution** step or the **Finish** step to validate the step configuration.

Transfer From File Step

Transfer From File allows a specified volume to be transferred from a specified source well to a specified destination well by reading data from a comma-delimited text file (.txt or .csv). A comma-delimited text file is a text file that specifies the values of a table by separating each column with a comma and each row with a return.

NOTE **Transfer From File** may only be used with a single-tip pipette tool.

The **Transfer From File** configuration specifies:

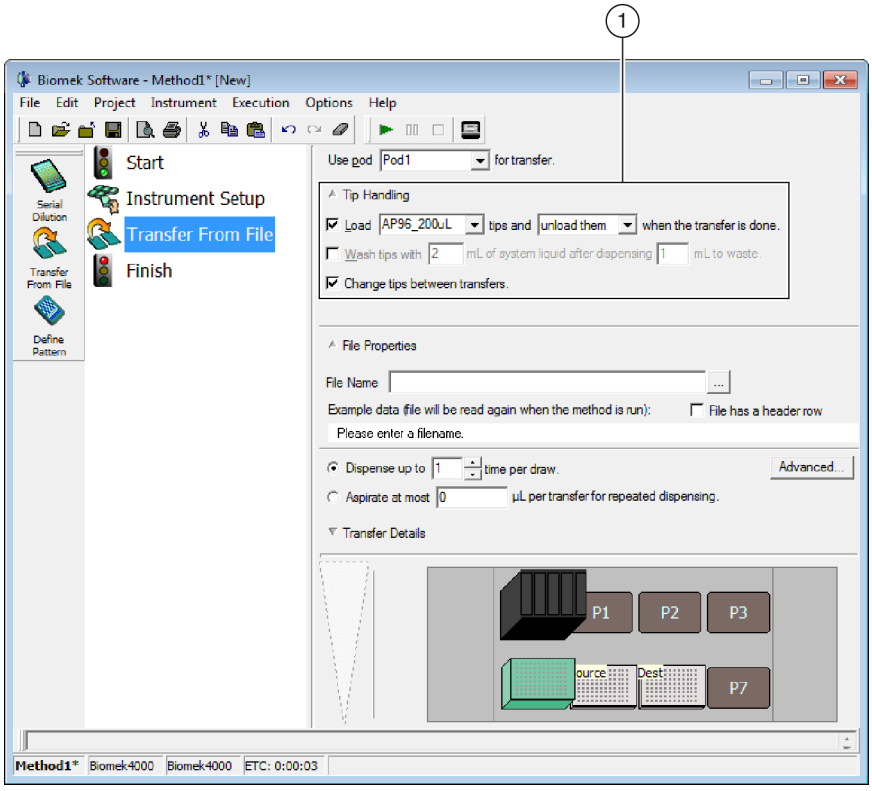
- Tip handling
- File properties
- Source labware
- Destination labware
- Transfer details

To insert a **Transfer From File** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 18.8).

Figure 18.8 Transfer From File Step and Configuration



1. **Tip Handling Configuration**: Tip Handling parameters specify tip type, whether tips remain on the tool at the end of the liquid transfer and when to change tips.

Configuring Tip Handling

Configuring **Tip Handling** in the **Transfer From File** step is optional, because the instrument locates and loads clean tips automatically every time a **Transfer From File** step is initiated. It is recommended, however, that **Tip Handling** configuration be supplied if cross contamination or conserving consumables is a concern.

To configure **Tip Handling** (Figure 18.8) for the **Transfer From File** step:

---

1 If **Tip Handling** is not already displayed, click the arrow or sentence summary to expand the **Tip Handling** configuration.

2 Check **Load** and select the type of tips used in the transfer to load tips at the start of the **Transfer From File** step. If **Load** is unchecked, the **Transfer From File** steps uses previously loaded tips, rather than loading new tips at the start of the **Transfer From File** step. Unchecking **Load** deactivates initial tip loading for the **Transfer From File** step.

NOTE Tips are selected from the drop-down list, or from the Current Deck Display. If tips are selected via the Current Deck Display, and the tips are unused, **Load** displays the name, not the tip type. If a name was not assigned to the tips, the tip type is displayed in **Load**.

It is recommended that tips not be named in the **Instrument Setup** step, because this could restrict the instrument from locating available tips.

NOTE If **Load** is checked and the tips loaded on the tool have been used, an error may occur. To increase the number of uses allowed for tips, increase the **Load no more than** count in the **Labware Properties** configuration in the **Instrument Setup** step.

3 To discard tips after the **Transfer From File** step is completed, select unload them.

OR

To leave tips on after the **Transfer From File** step is completed, select leave them on.

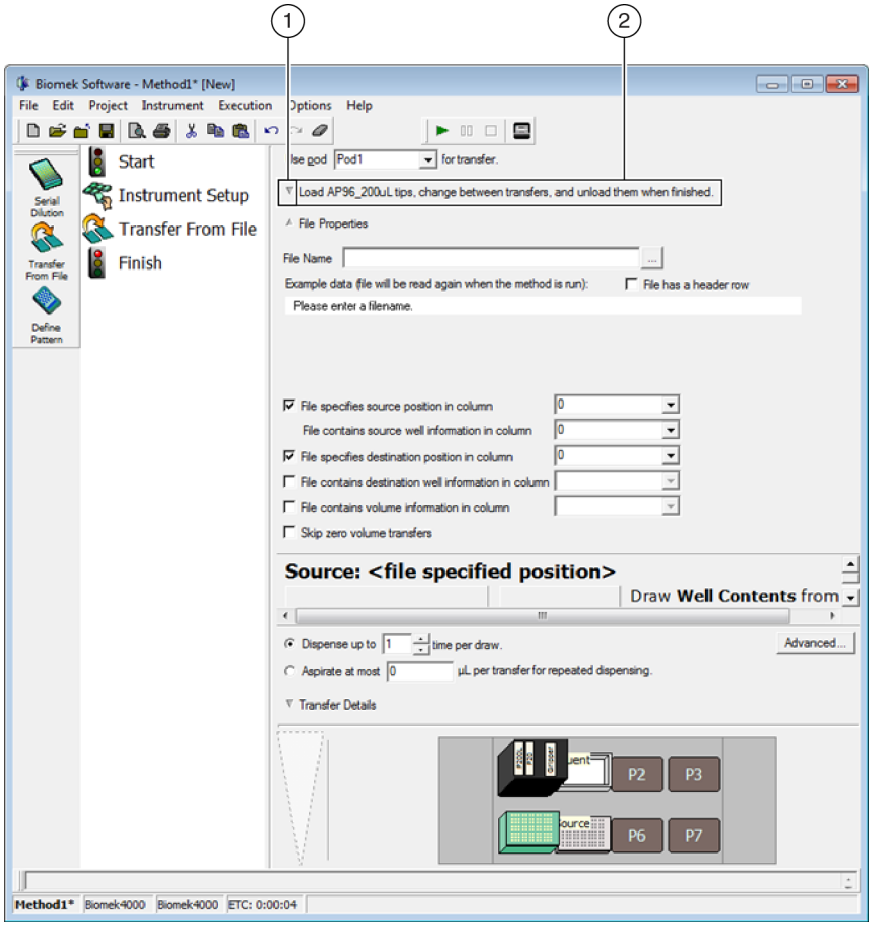
NOTE The **Load** and **unload them/leave them on fields** (this step and step 2 above) are useful when multiple **Transfer From File** steps are used within a method; for example, in the first **Transfer From File** step, check **Load** and select **leave them on**. In the second **Transfer From File** step, uncheck **Load** and select **leave them on**. In the third **Transfer From File** step, uncheck **Load** and select **unload them**. This loads new tips for the first **Transfer From File** step, uses the same set of tips for all three **Transfer From File** steps, and unloads the tips when the third **Transfer From File** step is completed. This is useful when trying to conserve consumables.

4 Select **Change tips between transfers** to change tips between liquid transfers, if desired.

The **Tip Handling** configuration can be collapsed to allow more room during **File Properties**, **Source Labware**, and **Destination Labware** configuration. When collapsed, the **Tip Handling** configuration is displayed as a sentence summary (Figure 18.9). Use the sentence summary to verify that **Tip Handlin**g has been configured appropriately.

To collapse or expand the **Tip Handling** configuration, click the arrow to the left of **Tip Handling** or the textual display (Figure 18.9).

Figure 18.9 Transfer From File Step—Tip Handling Collapsed



1. **Arrow to collapse/expand Tip Handling.**
2. **Collapsed Tip Handling configuration.**

Configuring File Properties

Transfer From File uses a comma-separated value file to configure parts of the transfer operation. The **File Properties** configuration is needed to specify the file to use and which columns indicate what information.

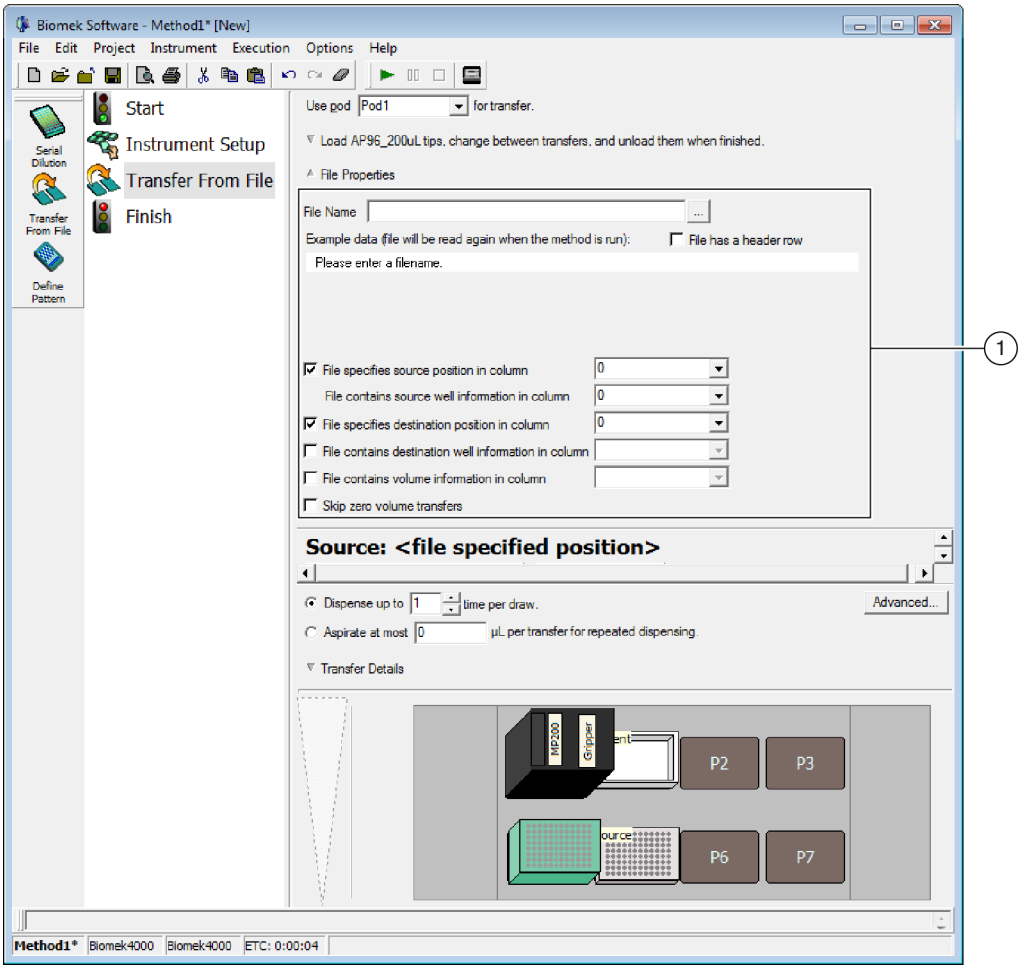
The file must contain at least information on source wells accessed, but may also specify the position on deck or name of source labware, position on deck or name of destination labware, destination wells accessed, and volume transferred. If all information is specified by the data file, each row is a single well-to-well transfer.

To configure **File Properties** for the **Transfer From File** step:

---

1 If **File Properties** is not already displayed, click the arrow or textual display to expand the **File Properties** configuration (Figure 18.10).

Figure 18.10 Transfer From File—File Properties



1. **File Properties Configuration**: File Properties specifies the file to use for the transfer information and the type of information stored in each column.

---

2 If **File Name**, enter the full path and file name of the data file from which to read the transfer information.

OR

Choose the ... (browse) button next to **File Name** and select the directory and file from which to read the transfer information in **Open** (Figure 18.11). The selected file is read and **Example data** is displayed (Figure 18.12).

NOTE The data file must be a comma-delimited text file (.txt or .csv).

Figure 18.11 Open Dialog

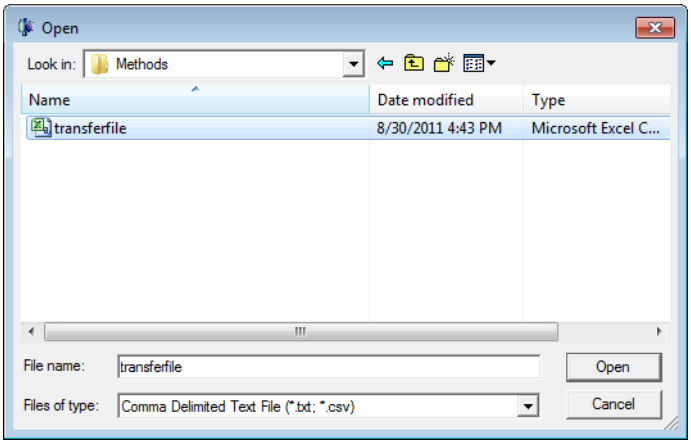
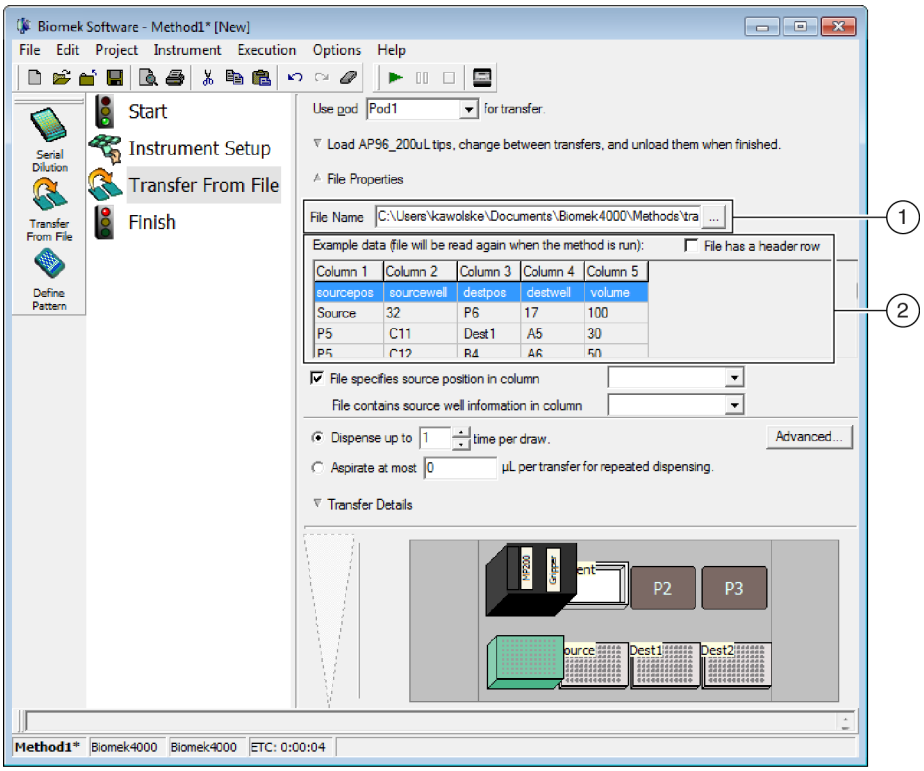


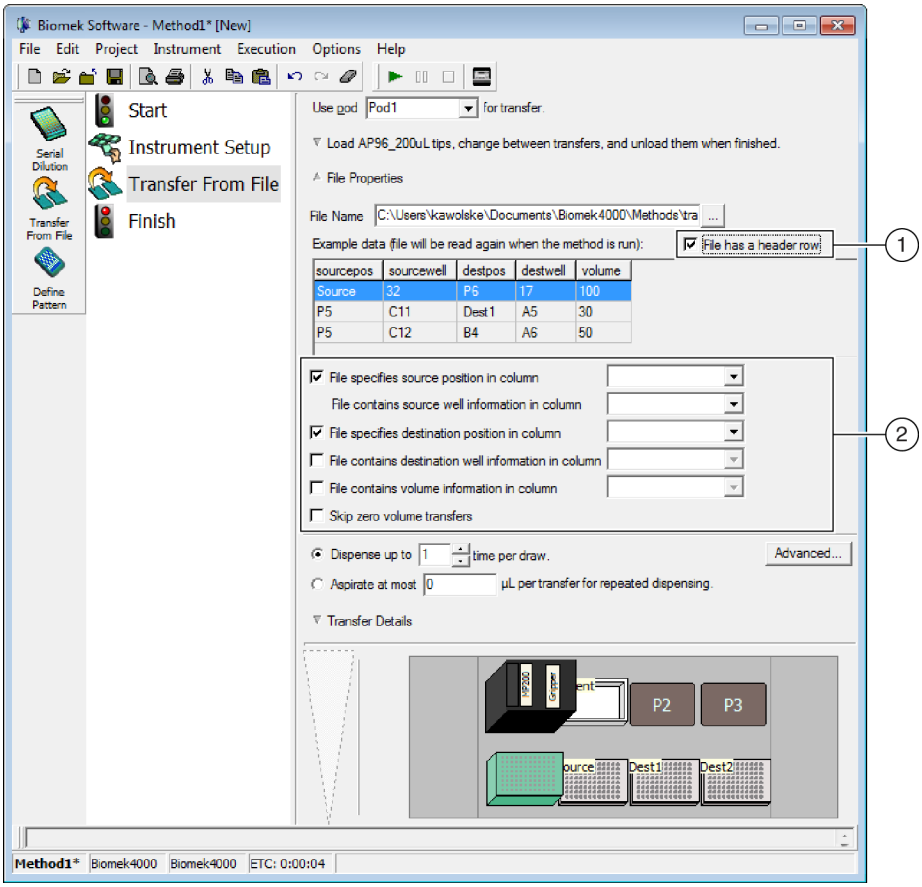
Figure 18.12 Transfer From File - Example Data Displayed



1. **File Name**: Select the file from which to read.
2. **Example Data**: Data is read from the file selected in **File Name** and displayed here.

3 If the file read has a header row identifying the columns, select **File has a header row.** The first row of the data file is used to identify the columns (Figure 18.13).

Figure 18.13 Transfer From File - Example Data with Header Row



1. **File has a header row**: Uses the first row of the data file to identify columns.
2. **Specify the type of information stored in each column.**

---

4 Select **File specifies source position in column** if a column of the data file stores information about the position of source labware and select the desired column from the list.

NOTE The source position column may contain deck positions (P4, P7, etc.) or labware names (Source1, Dest1, etc.). If information is stored as labware names, there must be a labware on the deck with the specified labware name (Figure 18.13).

---

5 In **File contains source well information in column**, select the column of the data file that stores information about source wells from which to transfer from the list.

NOTE The source well column may specify wells with either alphanumeric well addresses (A1-H12 for a 96-well plate) or numeric well numbers (1-96 on a 96-well plate). The same data file may contain both alphanumeric and numeric well information (Figure 18.13).

6 Select **File specifies destination position in column** if a column of the data file stores information about the position of destination labware and select the desired column from the list.

NOTE The destination position column may contain either deck positions (P4, P7, etc.) or labware names (Source1, Dest1, etc.) If information is stored as labware names, there must be labware on the deck with the specified labware name (Figure 18.16).

7 Select **File contains destination well information in column** if a column of the data file stores information about destination wells to which to transfer and select the desired column from the list.

NOTE The destination well column may specify wells with either alphanumeric well addresses (A1-H12 for a 96-well plate) or numeric well numbers (1-96 on a 96-well plate). The same data file may contain both alphanumeric and numeric well information.

8 Select **File contains volume information in column** if a column of the data file stores information about the volume to transfer and select the desired column from the list.

NOTE All volumes are specified in microliters (µL).

9 Select **Skip zero volume transfers** to ignore any rows that specify a volume of 0 when performing the **Transfer From File** step.

The **File Properties** configuration can be collapsed to allow more room during **Source Labware** and **Destination Labware** configuration. When collapsed, the **File Properties** configuration is displayed as text.

To collapse or expand the **File Properties** configuration, click the arrow to the left of the **File Properties** or the textual display.

Configuring Source Labware

A 'source' is a group of wells accessed at one time by the instrument to aspirate liquid. For example, using a single-tip pipette tool, the Biomek 4000 instrument aspirates from a single well at a time.

The **Transfer From File** step configures multiple aspirate and dispense operations using the selected probes to transfer all source wells to the destination labware.

The **Source Labware** configuration for the **Transfer From File** step includes choosing:

- the labware type
- the labware location, if not specified by the file
- the liquid type
- the technique
- the pipetting height

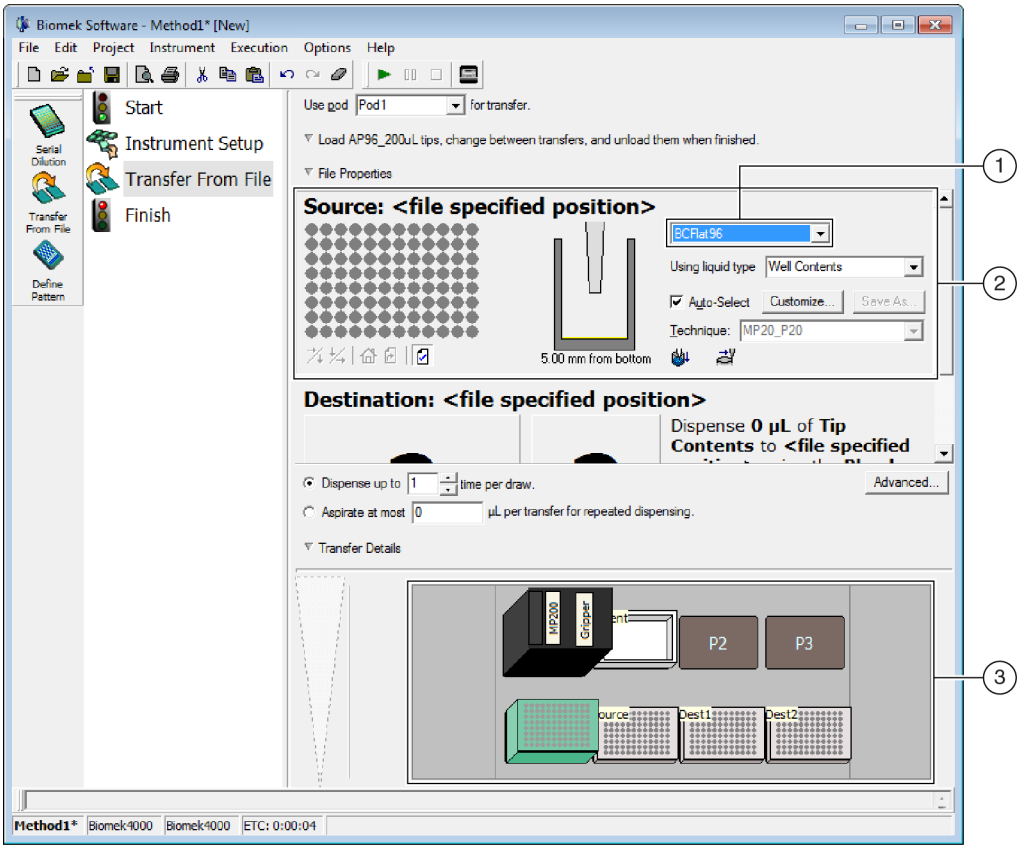
NOTE Only one piece of **Source Labware** is configured, because the **Transfer From File** step moves liquid from a single source to one or more destinations. However, if the source position is specified by the file, multiple sources are accessed for the transfer, but all sources are configured by a single source configuration.

To configure **Source Labware** for the **Transfer From File** step:

---

1 Click on the **Source** configuration area to activate it (Figure 18.14).

Figure 18.14 Transfer From File Step—Source Labware Selection



1. **Source labware type selection**
2. **Source Labware configuration**: If the position is specified by the file, the source labware title displays **<file specified position>**.
3. **Current Deck Display**: The Current Deck Display is used for labware selection, and it displays the status of the deck upon completion of the previous step.

2 If the source position is not specified by the file, click on the desired piece of labware in the Current Deck Display (Figure 18.14). Information for the piece of labware is entered automatically into the **Source Labware** configuration.

OR

If the source position is specified by the data file, select the labware type of the source labware. All sources must use the same labware type.

NOTE Once **Source Labware** has been selected any subsequent selections become **Destination Labware**. If an incorrect piece of labware is selected, right click on the labware title and select **Delete** on the menu that appears. If the **Source Labware** is incorrect, activate the **Source Labware** configuration by clicking anywhere in the source labware configuration area, and select another piece of labware.

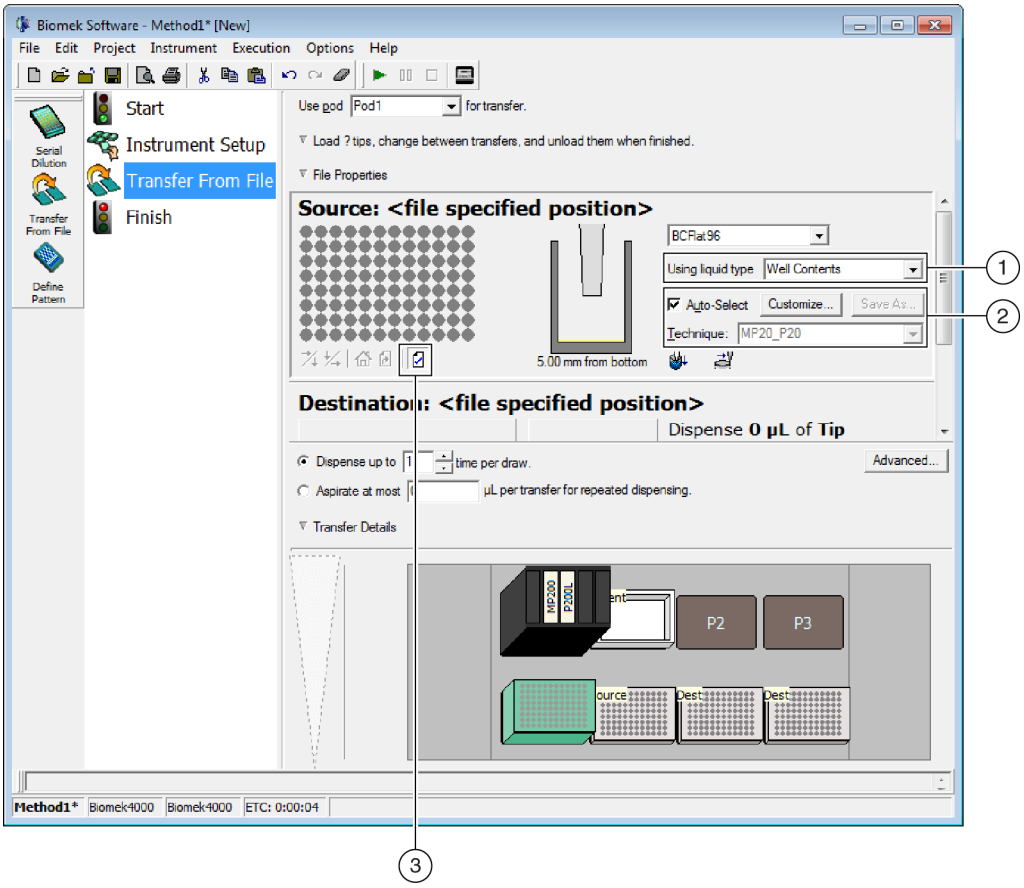
3 Verify the deck position of labware, if not specified by the data file.

NOTE A bright blue outline appears in the Current Deck Display around the labware designated as the **Source Labware**.

4 In **Using liquid type**, select the type of liquid in the **Source Labware** (Figure 18.15). Keeping the default selection, **Well Contents**, allows the software to predict the liquid type based on other properties defined elsewhere in the method.

NOTE The **Using liquid type** selection is one of the criteria the software uses to choose the technique that best applies to the operation.

Figure 18.15 Transfer From File Step—Source Labware Configuration



1. **Liquid type selection**
2. **Technique selection**
3. **"Set mark" icon**

5 De-select **Mark all wells that are used**, if it is not desired to mark wells. This option must be selected to use any options later in the method that make use of marks. For example, if **Mark all wells that are used** is selected and the **Transfer From File** step runs out of sources before using all destinations, it will mark the last well that had liquid transferred to it. Another **Transfer From File** step is transferring liquid to the same plate. By selecting **At first unmarked well** as the **Start** condition, the first source well will be transferred to the first unused destination well.

NOTE **Mark all wells that are used** can also be selected when the labware is zoomed out by using the (**Set Mark**) button beneath the labware.

NOTE **Mark all wells that are used** is selected by default.

6 Keep the auto-selected technique (refer to CHAPTER 15, *Auto-Selection of a Technique*).

NOTE The software automatically selects a **Technique** based on the liquid type labware type, tip type, and volume being aspirated.

OR

Manually select the desired **Technique**, or customize the selected **Technique** (refer to CHAPTER 15, *Customizing and Saving a Technique*).

7 Leave the height as is to use the settings specified in the pipetting technique.

OR

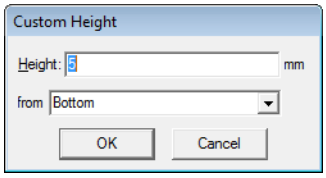
Set the aspirate height manually using one of the following techniques:

- Set the aspirate height by positioning the cursor over the graphic of a tip inside a well. Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

  NOTE The cursor changes to a when positioned over the graphic.

- Click in the graphic of a tip inside a well, and adjust the height using the PgUp and PgDn and the up and down arrow keys. PgUp and PgDn change the height by 1 mm at a time; the up and down arrow keys change the height by 0.1 mm at a time.
- Right click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and **Custom Height** appears (Figure 18.19). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

Figure 18.16 Custom Height Prompt



NOTE The phrase (**Overrides Technique**) appears below the graphic when the tip height is changed by manipulating the graphic, or when the technique is changed with the **Customize** option.

NOTE Changes made using the options listed above can be reset to the technique default height by right clicking on the graphic of the tip and selecting **Use Technique Settings**.

To change the point of reference from where aspirations are measured, right click on the graphic of the tip, and, from the pop-up menu, select the option you prefer. Options include the following:

- **Measure from Liquid**—The surface of the liquid is the reference point. The value should be negative, as this indicates that the aspiration occurs below the surface of the liquid.
- **Measure from Bottom**—The bottom of the source labware is the reference point for the aspiration height.
- **Measure from Top**—The top of the source labware is the reference point for aspiration height. The value should be a negative number, as this indicates that the liquid is aspirated from below the top of the well.

Configuring Destination Labware

A 'destination' is a group of wells accessed at one time by the instrument to dispense liquid; for example, using a single-tip pipette tool, the instrument dispenses to a single well at a time.

The **Transfer From File** step configures multiple aspirate and dispense operations to transfer all selected source wells to the destination labware.

The **Destination Labware** configuration includes choosing:

- the labware type
- the labware location, if not specified in the data file
- the wells on labware used, if not specified in the data file
- the liquid amount to transfer, if not specified in the data file
- the liquid type
- the technique

- the pipetting height

NOTE Multiple pieces of **Destination Labware** can be configured for the **Transfer From File** step, because the **Transfer** step can move liquid from a single source to one or more destinations. However, if the destination position is specified in the data file, all destinations are configured by a single destination configuration.

To configure **Destination Labware** for the **Transfer From File** step:

---

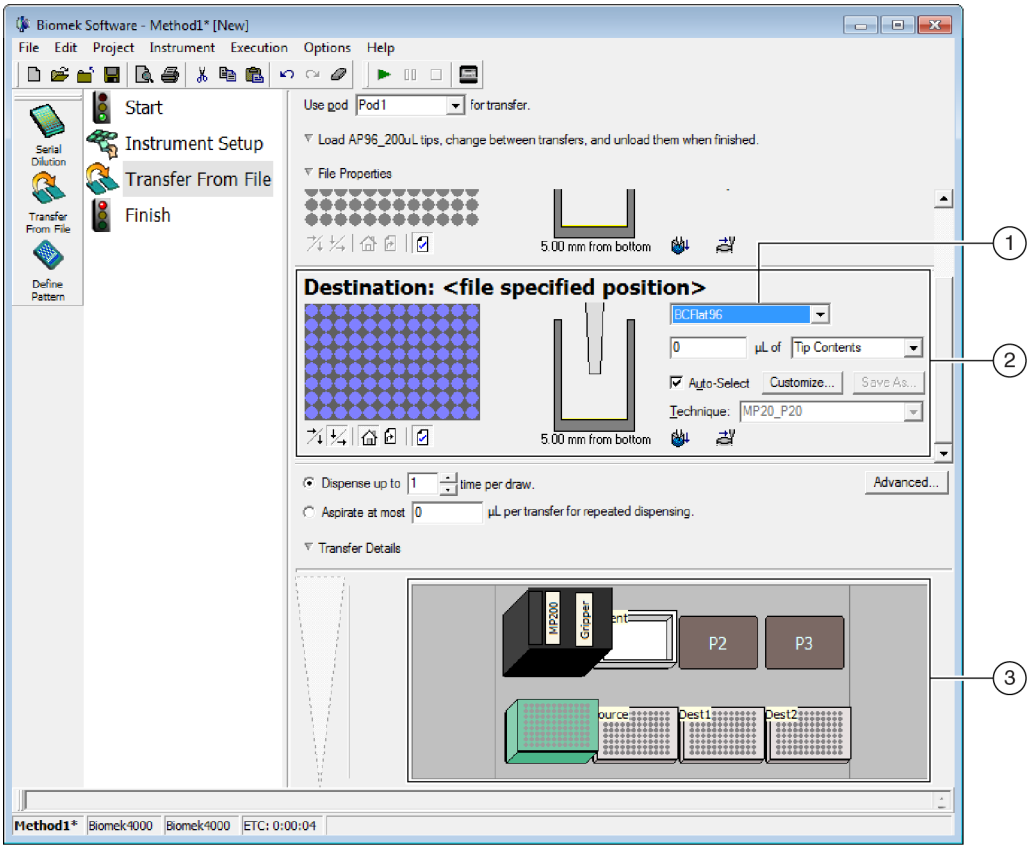
1 Select the **Destination Labware** type of the destination labware. All destinations must use the same labware type.

NOTE Once the first **Destination Labware** has been selected, the **Source Labware** parameters are collapsed to display a sentence summary. To reopen the **Source Labware** parameters, click anywhere in the **Source Labware** configuration area.

NOTE Subsequent labware selections modify the active **Source** or **Destination Labware** configuration. To configure additional **Destination Labware**, select **Click here to add a destination**, or select outside a labware configuration, and then select another piece of labware from the Current Deck Display. If an incorrect piece of labware is selected, right click on the labware title and select **Delete** on the menu that appears.

If either the destination position or destination wells are specified by the data file, additional destinations cannot be configured.

Figure 18.17 Transfer From File Step—Destination Labware Selection



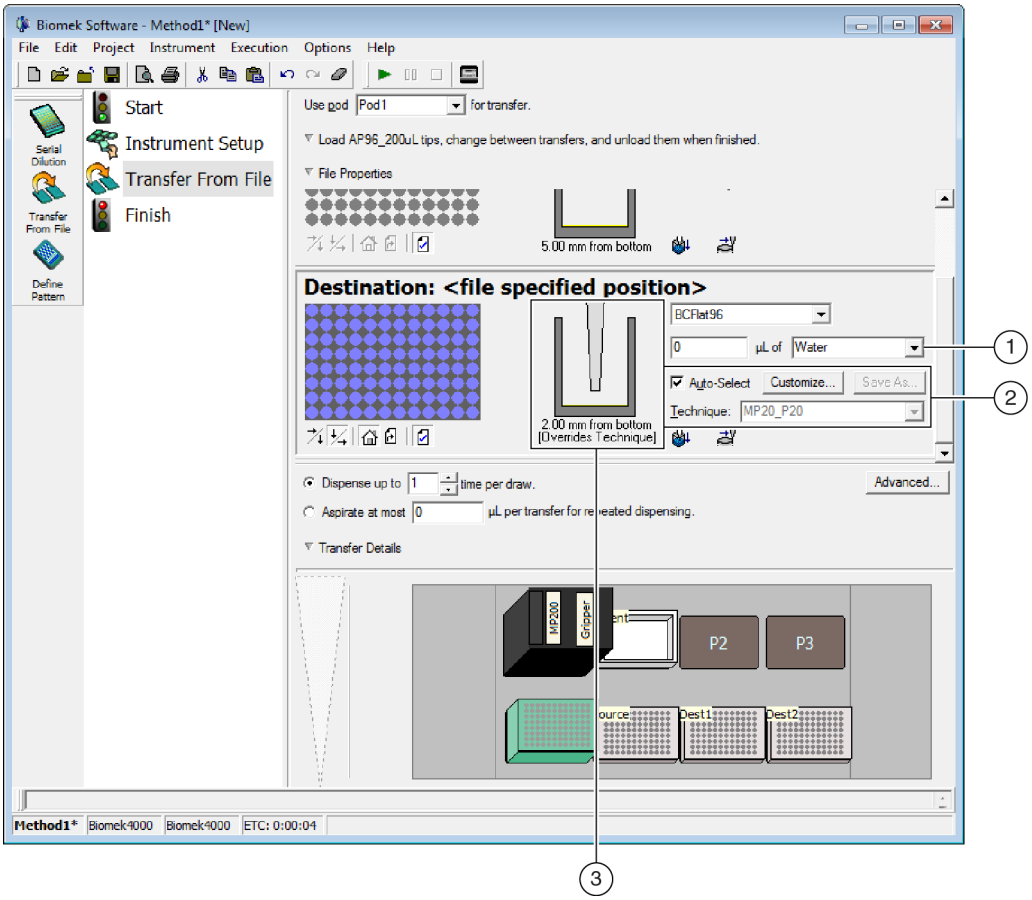
1. **Destination Labware type selection**
2. **Destination Labware configuration**: If the position is specified by the file, the **Destination Labware** title displays **<file specified position>**.
3. **Current Deck Display**: The Current Deck Display is used for labware selection, and it displays the status of the deck upon completion of the previous step.

---

2 Verify the deck position of the labware, if not specified by the data file.

NOTE A bright yellow outline appears in the Current Deck Display around the labware designated as the **Destination Labware**.

Figure 18.18 Transfer From File Step—Destination Labware Configuration



1. **Liquid type selection**
2. **Technique selection**
3. **Adjust dispense height**

3 Enter the amount of liquid (µL) dispensed into the **Destination Labware**, if not specified by the data file. If using a variable or expression, enter an equal sign (=) followed by the variable name or expression; for example, **=AspValue** (Figure 18.18).

4 Verify that the liquid type indicated is correct. The liquid type is dispensed to the **Destination Labware** should match the liquid type in the **Source Labware** configuration.

OR

Keeping the default selection, **Tip Contents**, allows the software to predict the liquid type based on other properties defined elsewhere in the method.

NOTE The liquid type selection is one of the criteria the software uses to choose the technique that best applies to the operation.

5 Deselect **Mark all wells that are used**, if it is not desired to mark wells. This option must be selected to use any options later in the method that make use of marks. For example, if **Mark all wells that are used** is selected and the **Transfer From File** step runs out of sources before using all destinations, it will mark the last well that had liquid transferred to it. Another **Transfer From File** step is transferring liquid to the same plate. By selecting **At first unmarked well** as the **Start** condition, the first source well will be transferred to the first unused destination well. **Mark all wells that are used** is selected by default.

NOTE **Mark all wells that are used** can also be selected when the labware is zoomed out by using the (**Set mark**) button beneath labware.

6 Keep the auto-selected **Technique** (refer to CHAPTER 15, *Auto-Selection of a Technique*).

NOTE The software automatically selects a **Technique** based on the liquid type, labware type, tip type, and volume being aspirated.

OR

Manually select the desired **Technique**, or customize the selected **Technique** (refer to CHAPTER 15, *Customizing and Saving a Technique*).

7 Leave the height as is to use the settings specified in the pipetting technique.

OR

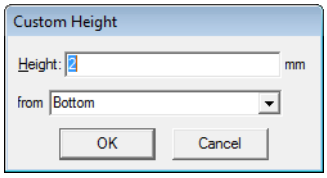
Set the dispense height manually using one of the following techniques:

- Set the dispense height by positioning the cursor over the graphic of a tip inside a well. Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

  NOTE The cursor changes to a when positioned over the graphic.

- Click in the graphic of a tip inside a well, and adjust the height using the PgUp and PgDn and the up and down arrow keys. PgUp and PgDn change the height by 1 mm at a time; the up and down arrow keys change the height by 0.1 mm at a time.
- Right click on the graphic of a tip inside a well, and a drop-down menu appears. Select **Custom Height**, and **Custom Height** appears (Figure 18.19). Insert the **Height** in millimeters (mm) and, in **from**, select a reference point from the drop-down list.

Figure 18.19 Custom Height Prompt



NOTE The phrase (**Overrides Technique**) appears below the graphic when the tip height is changed by manipulating the graphic, or when the technique is changed with the **Customize** option.

NOTE Changes made using the options listed above can be reset to the technique default height by right clicking on the graphic of the tip and selecting **Use Technique Settings**.

To change the point of reference from where aspirations are measured, right click on the graphic of the tip, and, from the pop-up menu, select the option you prefer. Options include the following:

- **Measure from Liquid**—The surface of the liquid is the reference point. The value should be negative, as this indicates that the aspiration occurs below the surface of the liquid.
- **Measure from Bottom**—The bottom of the source labware is the reference point for the aspiration height.
- **Measure from Top**—The top of the source labware is the reference point for aspiration height. The value should be a negative number, as this indicates that the liquid is aspirated from below the top of the well.

8 If destination wells are not specified by the data file, go to *Configuring Destination Wells*.

9 Repeat steps 1-8 for each additional piece of **Destination Labware** if neither destination positions nor destination wells are specified by the data file.

Configuring Destination Wells

If destination wells were not specified by the data file, further configuration of the destination labware is required.

To complete the **Destination Labware** configuration:

1 Double click the **Destination Labware** graphic in the step configuration to zoom in on the labware.

NOTE To call up a menu for **Zoom In** and **Specify Selection as Text** option, right click on the labware.

Specify Selection as Text allows the selection of wells in a microplate as targets for the transfer operation as comma-delimited text. Wells are numbered left to right and down (for example, the first row contains wells 1-12, the second row, wells 13-24, etc., for a 96-well plate). **Specify Selection as Text** may also be used to enter variables or expressions.

2 Select the wells that are destinations for the transfer using one of the following techniques:

NOTE A single-tip pipette tool can select individual wells.

- Choose **Copy Pattern** and select the desired pattern to use a previously defined well pattern created using the **Well Patterns Editor** (refer to CHAPTER 11, *Creating Well Patterns*).

  NOTE The pattern must be compatible with the tool installed.

- Select **Use pattern** and choose a previously defined pattern from the list to use a pattern created in the **Well Patterns Editor** or a **Define Pattern** step.

  NOTE Refer to *Define Pattern Step*, for more information about creating patterns using the **Define Pattern** step.

- Define a well pattern using data sets (refer to CHAPTER 14, *Defining Well Patterns Using Data Sets*).
- Create a custom well pattern from the labware grid by dragging the mouse and using (Ctrl) and (Shift) on the keyboard.

  NOTE Hold (Shift) and click a well to select additional wells without deselecting any wells. Hold (Ctrl) and click a well to toggle the selection status of selected wells without affecting the status of other wells. If (Shift) or (Ctrl) is not held down when selecting wells, any previous selection is deleted.

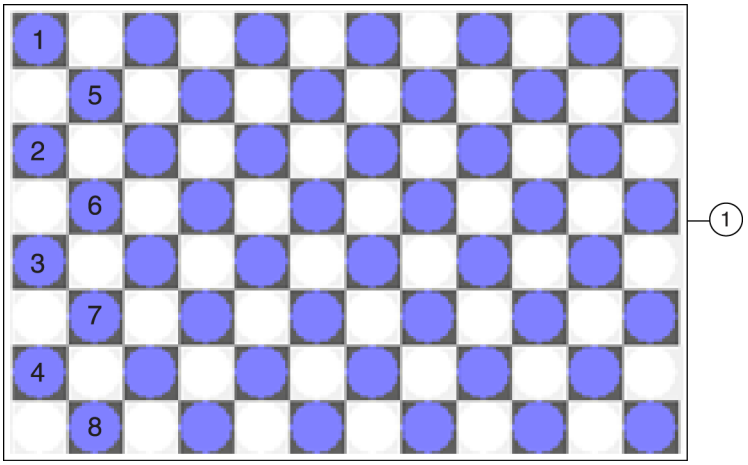
NOTE To save the pattern, right click the labware graphic and select **Save Pattern** from the menu. Enter a name for the pattern in **New Pattern** and choose **OK**.

3 Select the **Direction** in which destination wells are mapped to sources. **Down first, then left to right** is the default selection.

NOTE **Direction** controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The **Transfer From File** step automatically determines the most efficient way to complete the transfer.

 (**Down first, then left to right**) - goes down each column from top to bottom, then goes right to the next column (Figure 18.20).

Figure 18.20 Wells Accessed Down First, Then Left to Right

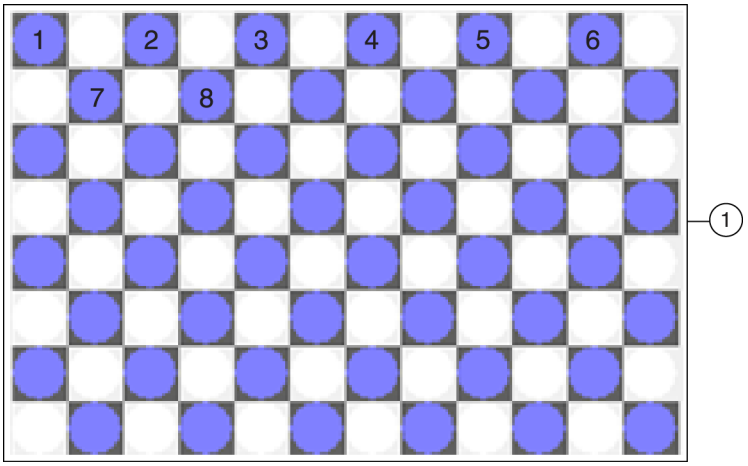


1. **Down first, then left to right**: Wells are mapped to destination labware in the order indicated, going down each column and then moving to the right to the next column.

OR

(**To the right first, then top to bottom**) - goes across each row from left to right, then goes down to the next row (Figure 18.21).

Figure 18.21 Wells Accessed to the Right First, Then Top to Bottom



1. **To the right first, then top to bottom**: Wells are mapped to the destination labware in the order indicated, going across each row and then moving down to the next row.

NOTE The direction can also be selected when the labware is zoomed out by using the **Down, then right** or **Right, then down** buttons beneath the labware.

4 Select the first well accessed in **Start**. **At first selected well** is the default selection.

NOTE **Start** controls how source wells are mapped to the destination, not the physical order in which wells are transferred. The **Transfer From File** step automatically determines the most efficient way to complete the transfer.

At first selected well - moves in the selected **Direction** starting from the first well selected on the labware.

OR

At first unmarked well - moves in the selected **Direction** starting from the first selected well on the labware after the marked well.

NOTE The selected labware must have a mark from a previous **Transfer From File** step with **Mark all wells that are used** selected.

NOTE The start location can also be selected when the labware is zoomed out by using the **Start at selection** or **Start at first unmarked well** buttons beneath the labware.

NOTE When transferring liquid, the source well in the first row of the data file is transferred to the first accessed destination well, the second source well is transferred to the second accessed destination well, and so forth.

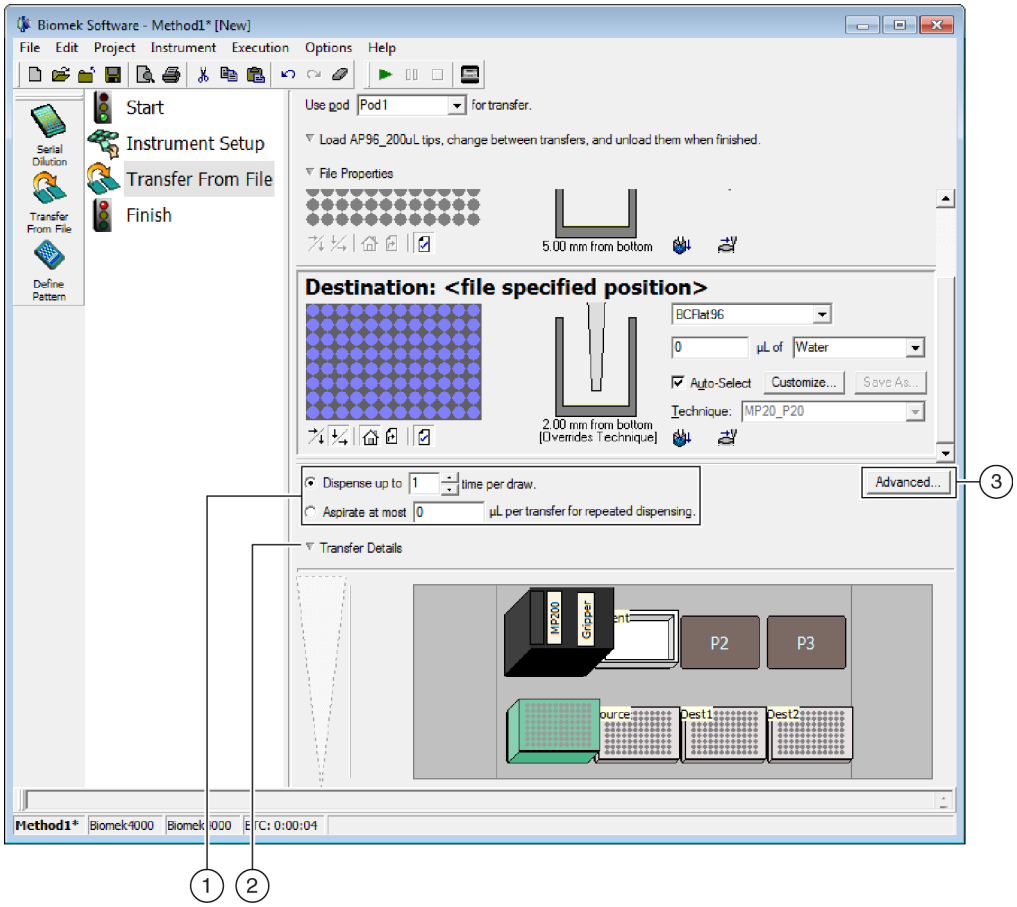
5 Choose **Zoom Out** to return to the step configuration screen.

Configuring Transfer Details

Transfer Details includes specifying:

- a repeat pipetting configuration (Figure 18.22).
- the maximum tolerance in timing between transfer operations (Figure 18.23).

Figure 18.22 Transfer From File Step - Configuring Additional Transfer Details



1. **Repeat pipetting configuration**: The repeat pipetting options control how many dispense operations are allowed per aspirate operation.
2. **Arrow to collapse/expand Transfer Details**
3. **Advanced Option**: The **Advanced** option provides access to a **Just-In-Time (JIT)** configuration option for the **Transfer From File** step. **JIT** specifies the maximum tolerance in timing between transfer operations.

To configure **Transfer Details** for the **Transfer From File** step:

---

1 Click the arrow or sentence summary below the labware configuration section to expand **Transfer Details.**

---

2 Select one of the repeat pipetting configuration options: **Dispense up to** or **Aspirate at most.**

NOTE Only on repeat pipetting option may be selected. Either **Dispense up to** or **Aspirate at most** may be selected, but not both.

---

3 In **Dispense up to**, select the number of times the instrument is allowed to dispense per aspirate. For example, if dispensing 75 µL to each of six microplates, three aspirate operations of 150 µL can each dispense into two destinations. In this case, **Dispense up to** is set to **no fewer than two**.

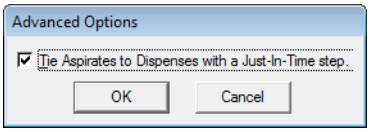
OR

In **Aspirate at most**, select the maximum volume to aspirate from the source for repeat pipetting. For example, if dispensing 75 µL to each of six microplates, three aspirate operations of 150 µL can each dispense into two destinations. In this case, **Aspirate at most** is set to no less than 150 µL.

NOTE The default repeat setting is **Dispense up to one time per draw**, which does not allow a repeat pipetting operation. Settings of two or more allow repeat pipetting.

4 Click **Advanced** to change the default setting of applying a **Just-In-Time (JIT)** block to aspirate and dispense operations. The **Advanced Options** prompt appears (Figure 18.23).

Figure 18.23 Advanced Button - JIT Block



5 Uncheck **Tie Aspirate to Dispense with a JIT Block** to deactivate the **JIT** block.

6 Click **OK** to save any changes.

The **Transfer Details** configuration can be collapsed to allow more room during **Source** and **Destination Labware** configuration. When collapsed, the **Transfer Details** configuration is displayed as a sentence summary. Use the sentence summary to verify that **Transfer Details** has been configured appropriately.

To collapse or expand the **Transfer Details** configuration, click the arrow to the left of **Transfer Details** or the textual display (Figure 18.22).

Define Pattern Step

Define Pattern is used to create patterns and assign names to them for use in other steps in the method, such as a **Transfer** or **Combine** step. Well patterns defined using the **Define Pattern** step are method specific and embedded as part of the method.

Embedding the well patterns as part of the method has several advantages:

- Sharing methods among other users is simpler because the pattern information is stored in the method, not in the project.
- Common well patterns can be modified for individual methods without changing the well pattern in the project.

- The pattern definition can be changed while keeping the same pattern name, making it simple to modify methods by changing the well pattern definition. Since the **Transfer** and **Combine** steps use the pattern name, changes to the pattern are automatically updated in the **Transfer** and **Combine** steps.

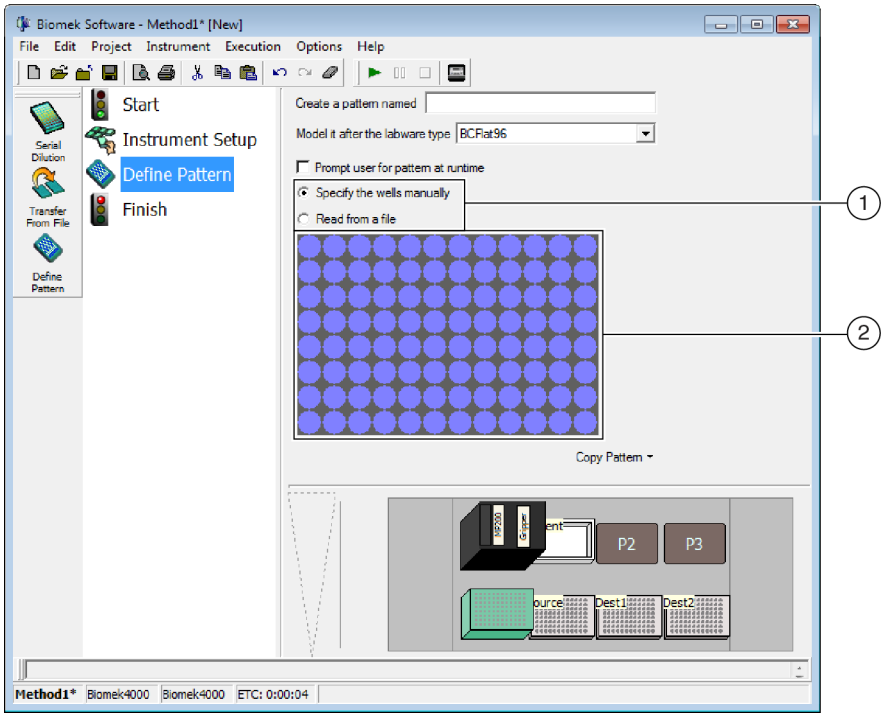
  NOTE This is particularly useful when the pattern is defined by a file using rows that match a bar code or other value. In a **Loop** step, the pattern could change based on the bar code of the current labware in a group created with a **Create Group** step. Each iteration of the **Loop** would transfer using a different pattern as defined by the file in the **Define Pattern** step.

To insert a **Define Pattern** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 18.24).

Figure 18.24 Define Pattern Step and Configuration



1. **Define Pattern configuration options**: The pattern has two options for selecting the wells in a pattern, **Specify the wells manually** or **Read from a file**.
2. **Specify the wells manually**: Used to manually specify the wells in a pattern.

Define Pattern has two different configuration options. It can define a pattern by manually specifying wells or reading from a file.

Configuring the Define Pattern Step by Specifying the Wells Manually

To configure the **Define Pattern** step by manually specifying the wells:

1. In **Create a pattern named**, enter a name for the pattern.
2. In **Model it after the labware type**, select the labware type for the pattern.
3. Select **Specify the wells manually**.
4. On the graphic representing the labware, select the wells to be included in the pattern. All wells are selected by default (Figure 18.24).

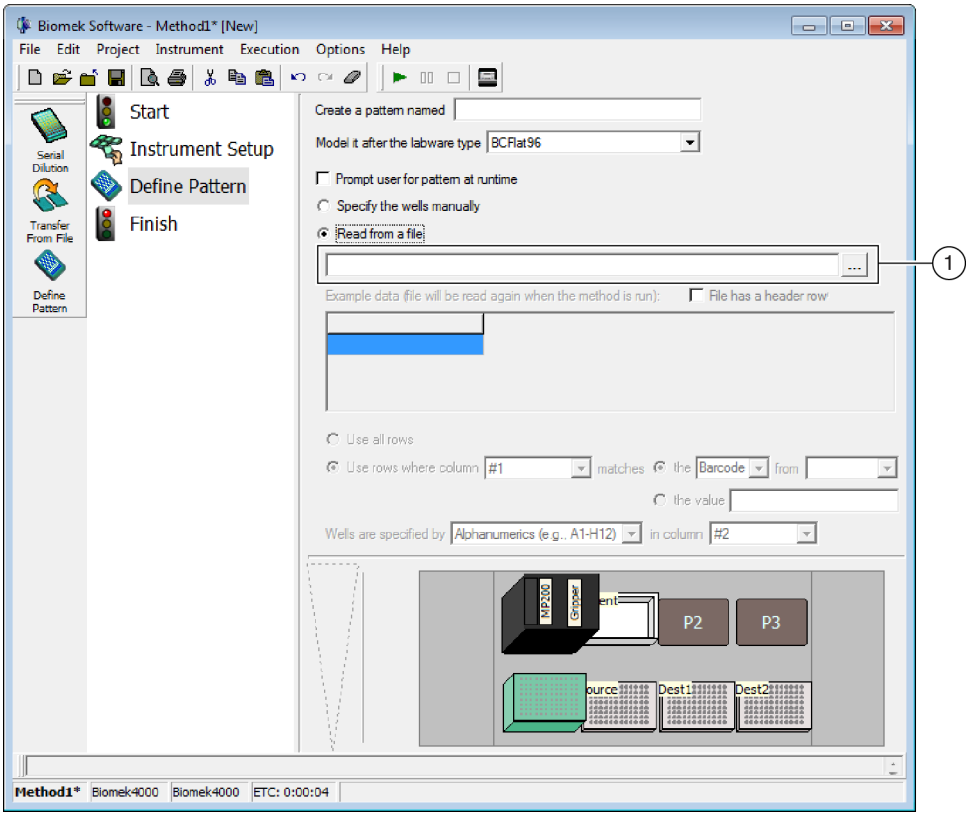
   NOTE Click on a well to select it and deselect the current selection. Hold down Shift and click on additional wells to select wells without affecting the current selection. Hold down Ctrl and click on wells to toggle wells between selected and deselected without affecting the current selection.
5. To use or modify a well pattern defined in the **Well Patterns Editor**, select **Copy Pattern** and choose the pattern from the list.

Configuring the Define Pattern Step Reading from a File

To configure the **Define Pattern** step by reading well information from a file:

1. In **Create a pattern named**, enter a name for the pattern.
2. In **Model it after the labware type**, select the labware type for the pattern.
3. Select **Read from a file**. The **Read from a file** configuration options appear (Figure 18.25).

Figure 18.25 Define Pattern Step - Read From a File Configuration



1. **File selection**: Used to select the file to read to create the pattern.

---

4 Enter the full path and file name of the data file from which to read the pattern information.

OR

Choose ... and select the directory and file from which to read the pattern information in **Open** (Figure 18.26). The selected file is read and **Example data** is displayed (Figure 18.27)

NOTE The data file must be a comma-delimited text file (.txt or .csv).

Figure 18.26 Open Dialog

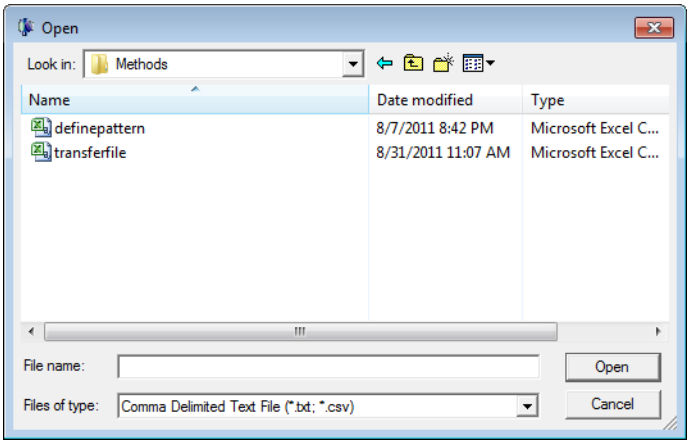
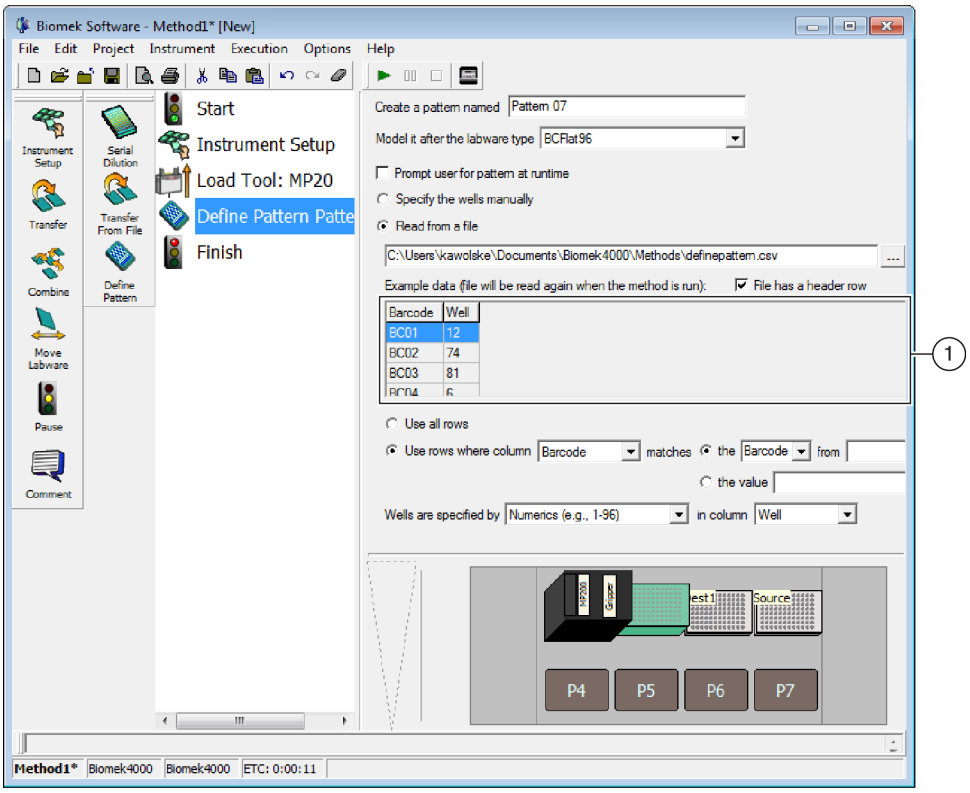


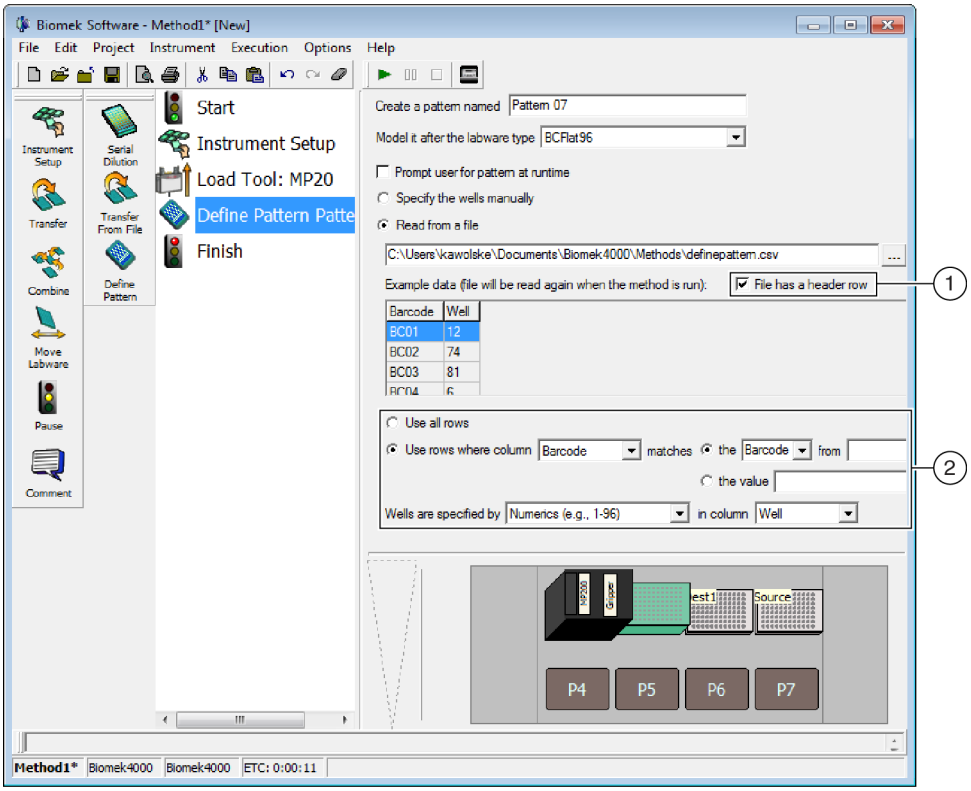
Figure 18.27 Define Pattern Step - Example Data Displayed



1. **Example Data**: The selected file is read and data displayed in the **Example data** section.

5 If the file read has a header row identifying the columns, select **File has a header row.** The first row of the data file is used to identify the columns (Figure 18.28).

Figure 18.28 Define Pattern Step - Example Data with Header Row



1. **File has a header row**: Uses the first row of the data file to identify columns.
2. **Specify the lines of the data file to use.**

6 Beneath the **Example data**, select which lines from the data file to use when defining the pattern.

- To use all rows of the data file, select **Use all lines**.
- To use specific wells where a certain column matches a specified bar code or value, refer to *Specifying Lines to Use*.

7 In **Well are specified by**, select whether wells are identified using alphanumeric well addresses (for example, A1-H12 for a 96-well plate) or numeric well numbers (for example, 1-96 for a 96-well plate), and specify the column that contains the well information.

8 Choose a step that occurs after the **Define Pattern** step or the **Finish** step to validate the step configuration.

Specifying Lines to Use

Sometimes it may be desired to only use specific rows from the data file. For example, if a data file contains information on several plates, the file can be configured to use only the rows pertaining to the current plate using the bar code, deck position, or other factor.

To use selected lines from the data file:

1 Select **Use lines where column** to activate the configuration.

2 In **column matches**, select the column from the data file that must match the specified value to use the row.

3 Select whether the selected column must match the **Bar code** or **Name** of the labware selected in **from** and specify a deck position or labware name to match against in **from**.

OR

Select **the value** and enter a variable or expression that must match the column selected.

The rows that match the specified condition are used to define the well pattern using the column that specifies the well information.

Using a Defined Pattern in a Transfer or Combine Step

Once a pattern has been created using a **Define Pattern** step, it may be used in any **Transfer** or **Combine** step within a method that uses a pipetting tool.

To use a defined pattern in a **Transfer** or **Combine** step:

1 Select the desired **Transfer** or **Combine** step in the Method View. The step configuration appears.

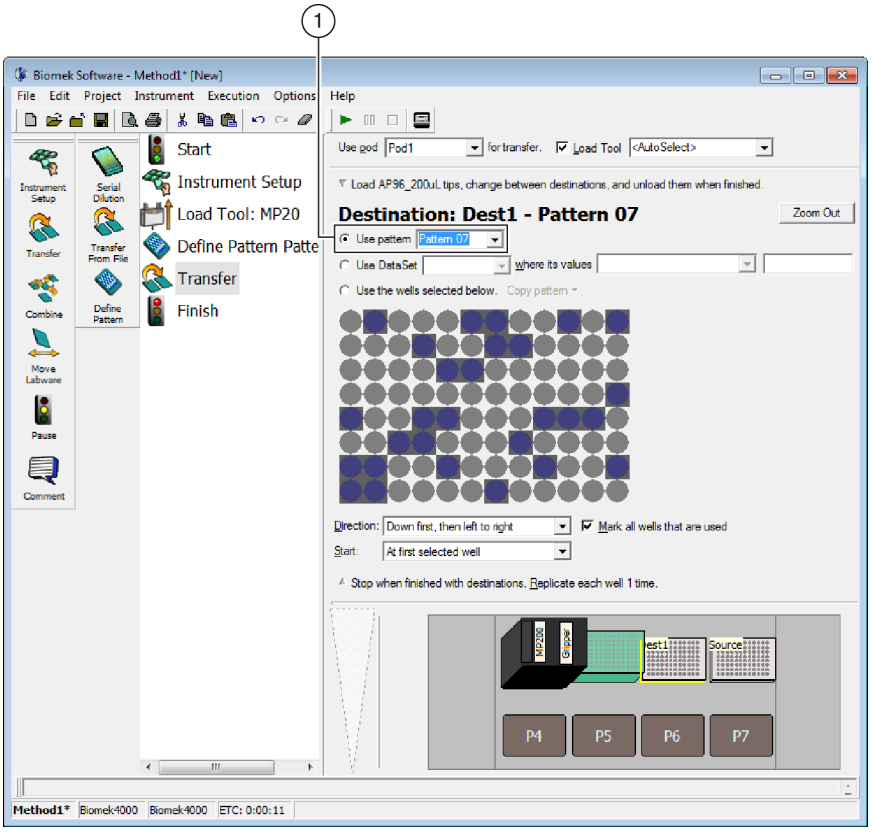
2 Select the desired **Source** or **Destination** configuration to display the configuration for the selected labware.

3 Double click the graphic of the labware to zoom in on it.

4 Select **Use pattern** to use a pattern created in a **Define Pattern** step.

5 Choose the desired pattern created in a **Define Pattern** step from the list (Figure 18.29). During method run, the configured step uses the specified pattern.

Figure 18.29 Transfer Step Using Sample Pattern



1. **Use Pattern**: Specify the pattern to use for the selected labware. The current definition of the selected pattern is displayed on the labware graphic. Pattern 07 is selected for the Destination.

NOTE Only patterns that are defined in the current method or from a previously run method that did not clear global variables appear in the list.

6 Choose a step that occurs after the configured **Transfer** or **Combine** step or the **Finish** step to validate the step configuration.

Configuring Runtime Patterns

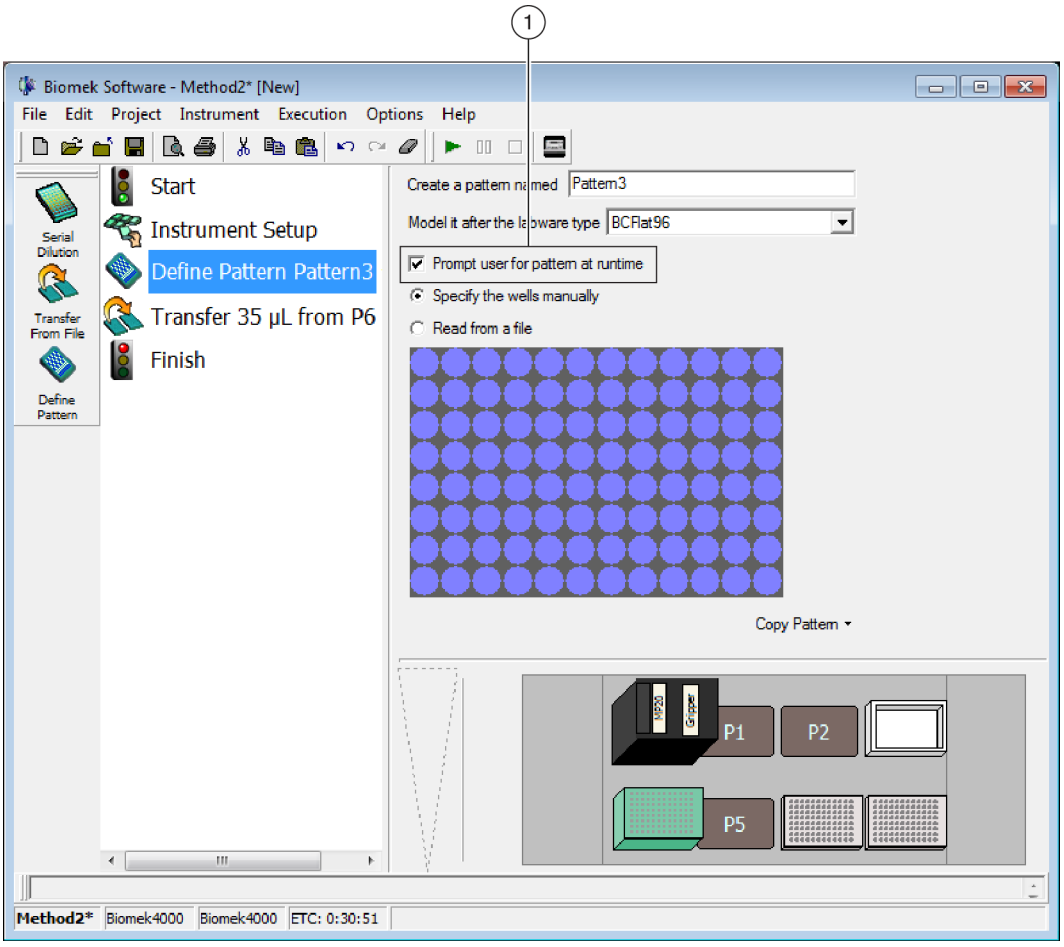
The **Runtime Pattern** feature prompts you to alter the pattern on the labware when the run is initiated.

To enable a **Runtime Pattern:**

1 Add a **Define Pattern** step to the method.

2 Select the **Prompt user for pattern at runtime** check box to enable the **Runtime Pattern** feature (Figure 18.30).

Figure 18.30 Runtime Pattern Prompt



1. Select this check box to enable the **Runtime Pattern** feature.

3 Once all method setup activities are completed, and the method run is prompted, you will receive the **Please Select Wells in Pattern:** dialog.

- If well selection was specified manually in the **Define Pattern** step, you will be prompted to specify wells manually at runtime.
- If well selection was specified by a file in the **Define Pattern** step, you will have the option to change the file at runtime.

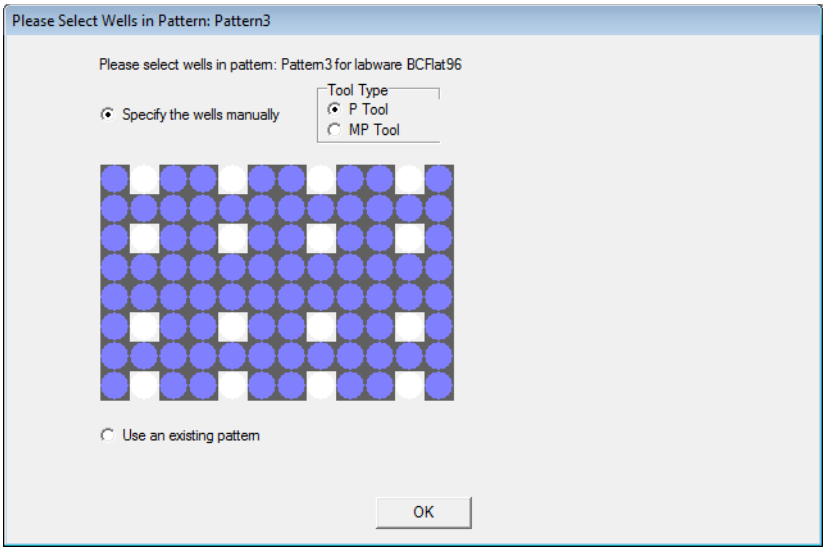
Make the required selections, and select **OK** when completed.

NOTE To select multiple wells, press the Ctrl key while clicking on desired each well.

NOTE If a **Define Pattern** step is located within a **Loop** step, the runtime pattern prompt (Figure 18.31) appears during each pass of the loop. If the step is located outside of the **Loop** step, the runtime pattern prompt occurs only once in the run, even if the pattern is used multiple times in the method.

Figure 18.31 is an example of selections made at runtime.

Figure 18.31 Runtime Pattern Selections



CHAPTER 19

Using the Biomek Instrument Step Palette

Overview

The **Biomek Instrument** step palette provides steps for use specifically with a Biomek 4000 workstation, including tool changing, loading, and unloading.

The steps available in the **Biomek Instrument** step palette are shown in Table 19.1.

Table 19.1 Biomek Instrument Step Palette

Step	Icon	Description
Change Tool		Unloads the tool currently loaded on the Biomek 4000 pod to an empty tool rack position and loads the specified tool.
Load Tool		Locates the specified tool on the deck and loads it to the Biomek 4000 pod.
Unload Tool		Unloads the tool currently loaded on the Biomek 4000 pod to an empty tool rack position.

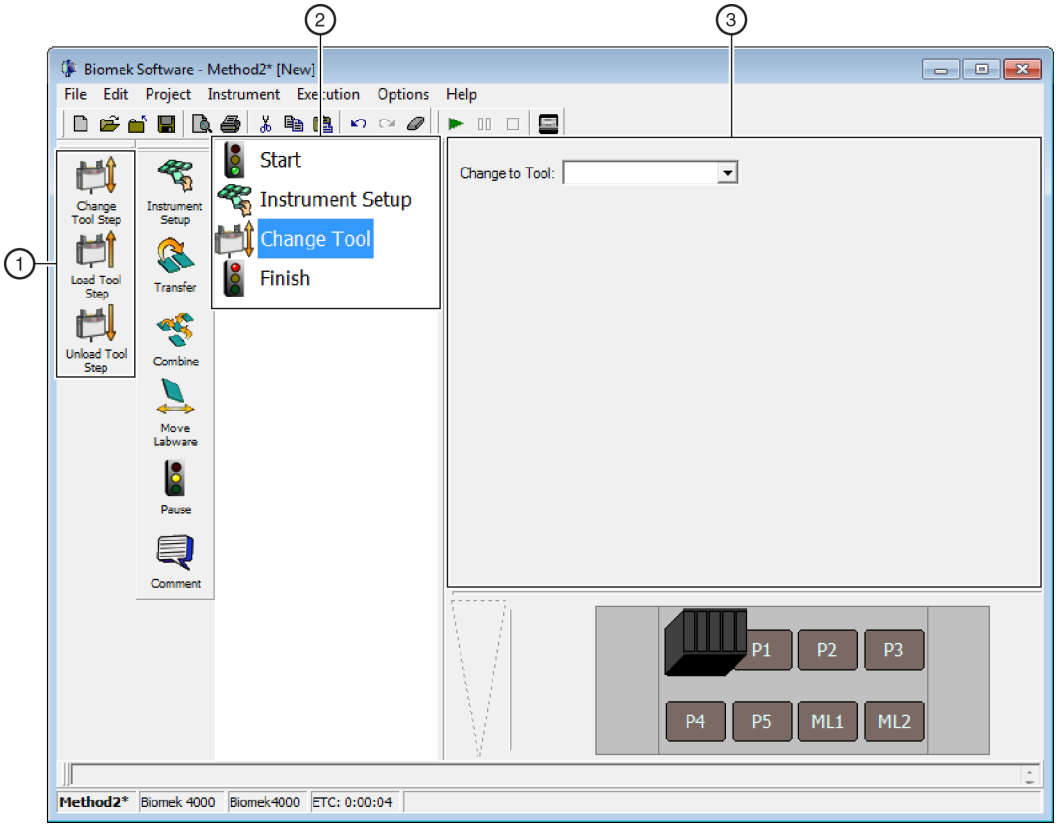
When one of the above steps is added to a method, the configuration for the step appears on the right side of the Biomek Software main editor, in step configuration (Figure 19.1).

NOTE Steps not configured appropriately in **Step Configuration** generate errors when the method is validated or run.

Displaying the Biomek Instrument Step Palette

In order to add Biomek Instrument steps to a method, display the **Biomek Instrument** step palette (Figure 19.1).

Figure 19.1 Biomek Software Main Editor With Biomek Instrument Step Palette Displayed



1. **Biomek Instrument Step Palette**
2. **Method View**: The method is built step by step in the Method View.
3. **Step Configuration**: When a step is highlighted in the Method View, the corresponding configuration appears in this area.

To display the **Biomek Instrument** step palette:

1 Right click any empty palette space, and the step palette menu displays. Select **Biomek Instrument**.

OR

From the toolbar, select **Options > Toolbars > Biomek Instrument**.

Change Tool Step

The **Change Tool** step is used to instruct the instrument to unload the tool installed on the pod and load a different tool. The instrument automatically returns the currently-installed tool to the original location from where it was loaded.

NOTE The **Transfer**, **Combine**, and **Move Labware** steps include the option to automatically change to an appropriate tool to perform the operation, by choosing **<AutoSelect>** from the **Load Tool** drop-down. If a **Change Tool** step is inserted prior to a **Transfer** or **Combine** step, it does not guarantee that the transfer or combine process will actually use the tool selected in that **Load Tool** step; this is because the **Transfer** or **Combine** step could override the **Load Tool** step, depending on whether the **Load Tool** option is selected in the **Transfer** or **Combine** step configuration.

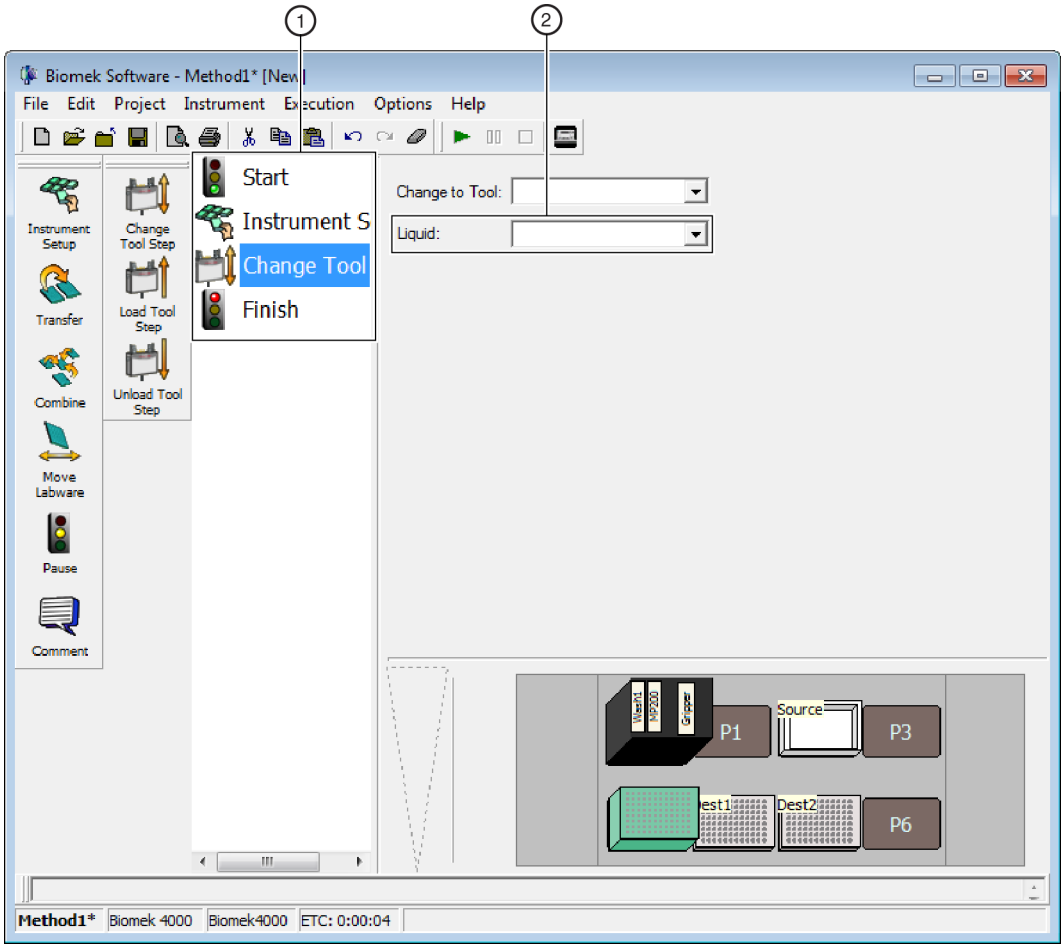
NOTE The **Aspirate**, **Dispense**, **Transfer From File**, and **Mix** steps do not have the automatic tool-loading feature, thus requiring the appropriate tool to be loaded prior to execution.

To insert a **Change Tool** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 19.2).

Figure 19.2 Changing Tools During a Method



1. **Method View**
2. **Liquid** field: Displays only when the six port valve is installed.

To configure the **Change Tool** step:

1 In **Change to Tool**, specify the tool to load after unloading the current tool. All tools located on the deck in a tool rack (as configured in **Labware Properties** for the tool rack in an **Instrument Setup** step) are available for selection.

2 If the tool selected in **Change to Tool** is a wash tool, and the six port valve is installed, in **Liquid**, select the liquid type to purge the tubing and wash tool with after loading the tool. Biomek Software automatically performs a purge operation similar to a **Wash Tool Purge** step with the selected **Liquid** when the tool is loaded.

3 Select a step that occurs after the **Change Tool** step or the **Finish** step to validate the step configuration.

Load Tool Step

The **Load Tool** step is used to instruct the workstation to load a tool to the pod. If a tool is currently installed, the instrument automatically returns the loaded tool to the original location from where it was loaded.

NOTE The **Transfer**, **Combine**, and **Move Labware** steps include the option to automatically change to an appropriate tool to perform the operation, by choosing **<AutoSelect>** from the **Load Tool** drop-down. If a **Load Tool** step from the Biomek Instrument step palette is inserted prior to a **Transfer** or **Combine** step, and **<AutoSelect>** is selected in the **Transfer** or **Combine** step, and alternate tool can be automatically selected and used instead of the tool selected in the **Load Tool** step. To ensure that a specific tool is used, either specify the tool to load in the **Transfer** or **Combine** step, or uncheck **Load Tool** in the **Transfer** or **Combine** step and use the **Load Tool** step.

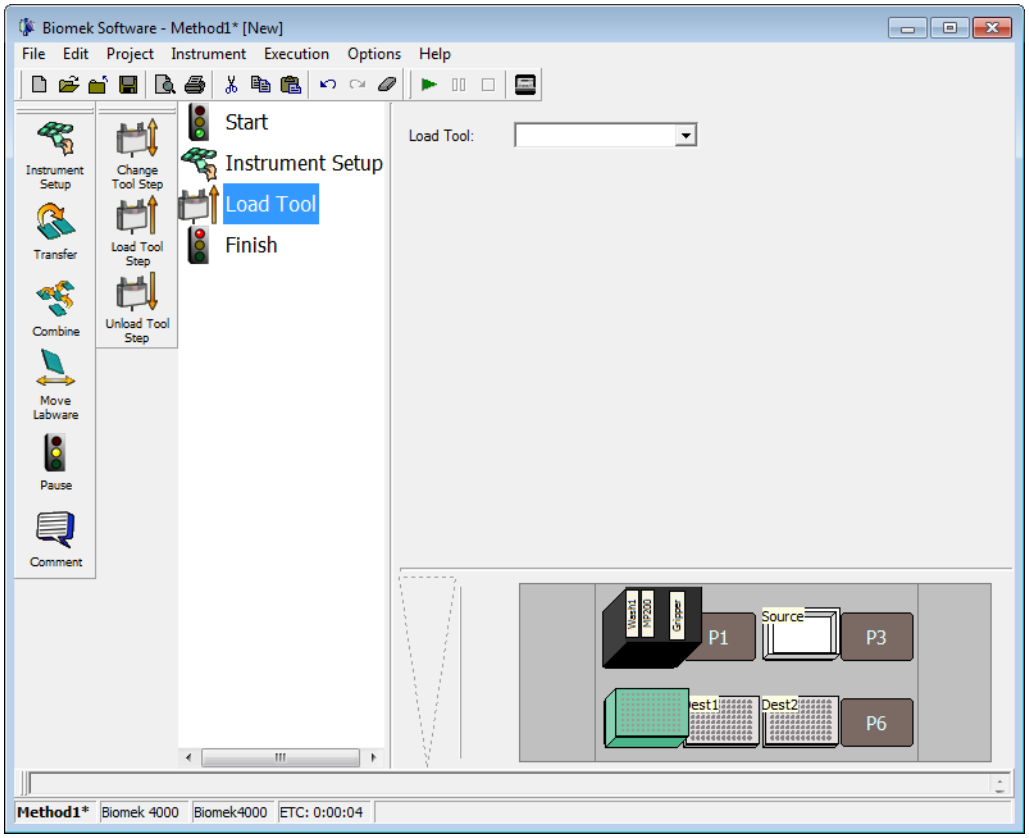
NOTE The **Aspirate**, **Dispense**, **Transfer From File**, and **Mix** steps do not have the automatic tool-loading feature, thus requiring the appropriate tool to be loaded prior to execution.

To insert a **Load Tool** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 19.3).

Figure 19.3 Loading Tool During a Method



To configure the **Load Tool** step configuration:

1. In **Load Tool**, specify the tool to load to the pod. All tools that are located on the deck in a tool rack (as configured in the **Labware Properties** for the tool rack in an **Instrument Setup** step) are available for selection.

2. If the tool selected in **Load Tool** is a wash tool, and the six port valve is installed, in **Liquid**, select the liquid type to purge the tubing and wash tool with after loading the tool. Biomek Software automatically performs a purge operation similar to a **Wash Tool Purge** step with the selected **Liquid** when the tool is loaded.

3. Select a step that occurs after the **Load Tool** step or the **Finish** step to validate the step configuration.

Unload Tool Step

The **Unload Tool** step is used to instruct the instrument to unload the tool installed on the pod. The instrument automatically returns the currently-installed tool to the original location from where it was loaded.

A tool must be unloaded before loading a new tool. Many steps, such as **Transfer**, **Combine**, and **Move Labware** automatically unload the current tool and load a more appropriate tool for the operation. It is only necessary to use an **Unload Tool** step when it is desired to unload the current tool prior to loading a specific tool to the pod using a **Load Tool** step.

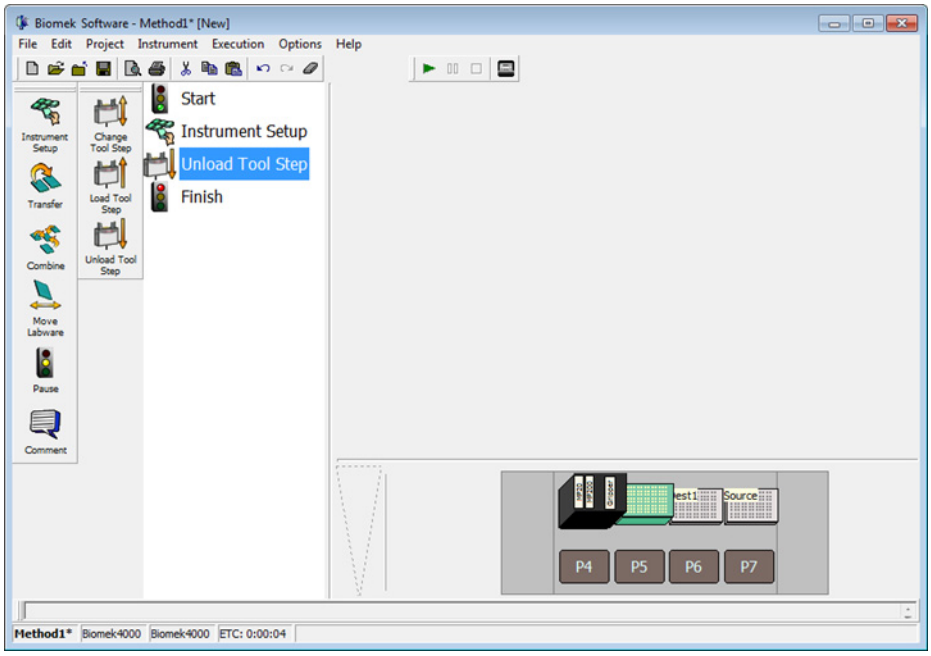
NOTE The Biomek 4000 pod can be instructed to automatically unload any tools installed at the end of a method in the **Finish** step.

To insert an **Unload Tool** step into a method:

1. Drag and drop the 

icon into the Method View (Figure 19.4).

Figure 19.4 Unloading a Tool During a Method



The **Unload Tool** step requires no additional configuration. Select a step that occurs after the **Unload Tool** step or the **Finish** step to validate the step configuration.

CHAPTER 20

Using the Specialty Step Palette

Overview

The steps presented in the **Specialty** step palette allow more control over methods. These steps are used to:

- Set variables and make non-incremental changes to variables.
- Break out of loops.
- Create and use groups of labware.
- Run executables.
- Define and run procedures.

NOTE The steps available in the **Specialty** step palette do not use the pod directly and may be used with any configuration.

The steps available in the **Specialty** step palette are shown in Table 20.1:

Table 20.1 Specialty Step Palette

Step	Icon	Description
Create Group		Creates a group of labware.
Next Labware		Accesses the next piece of labware in a group of labware created using **Create Group**.
Run		Runs any executable file during a method.
Next Item		Names a global variable, provides a list of VB script expressions, and specifies behavior when the list is exhausted.
Set Global		Defines a global variable that can be used in subsequent steps of a method.

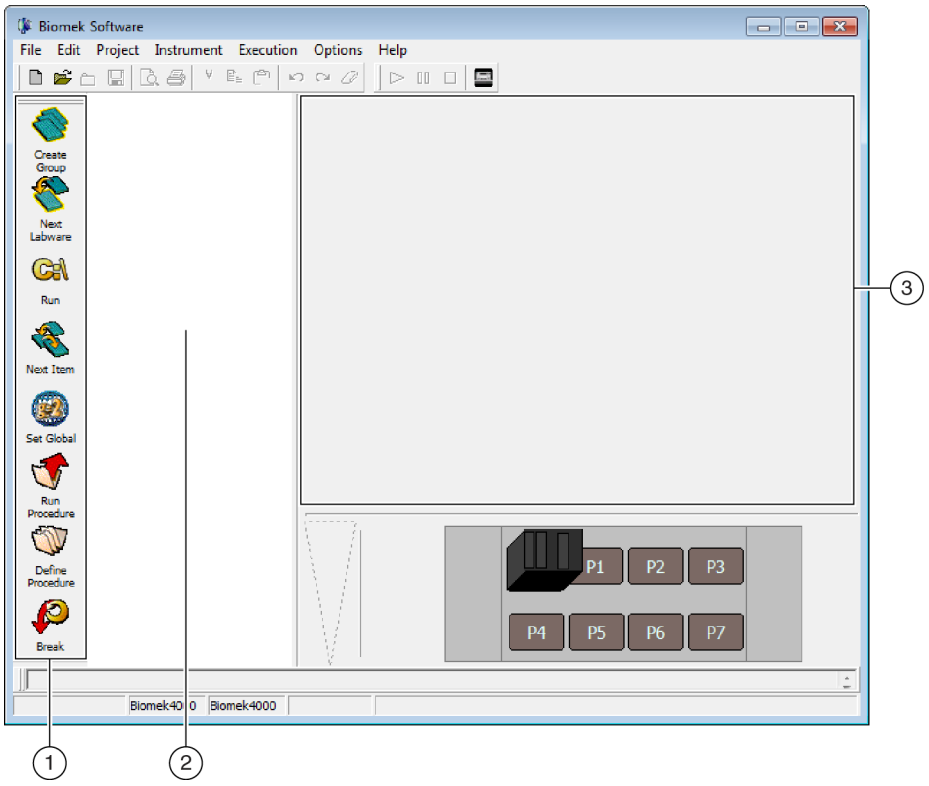
Table 20.1 Specialty Step Palette

Step	Icon	Description
Run Procedure		Runs a series of steps previously created in a **Define Procedure** step.
Define Procedure		Creates a series of steps that can be run at any point during a method using a **Run Procedure** step.
Break		Breaks out of one or more loops.

Displaying the Speciality Step Palette

To add specialty steps to a method, display the **Specialty** step palette (Figure 20.1).

Figure 20.1 Biomek Software Main Editor with Specialty Step Palette Displayed



1. **Specialty Step Palette**: Displays the steps available for insertion into a method.
2. **Method View**: The method is built step by step in this area.
3. **Step Configuration**: When a step is highlighted in the Method View, set the corresponding configuration in this area.

To display the **Specialty** step palette:

1 Right click any empty palette space, and select **Specialty** from the menu.

OR

From the toolbar, select **Options > Toolbars > Specialty.**

Create Group Step

The **Create Group** step creates and names a group of labware that may be accessed during a method run using a **Next Labware** step.

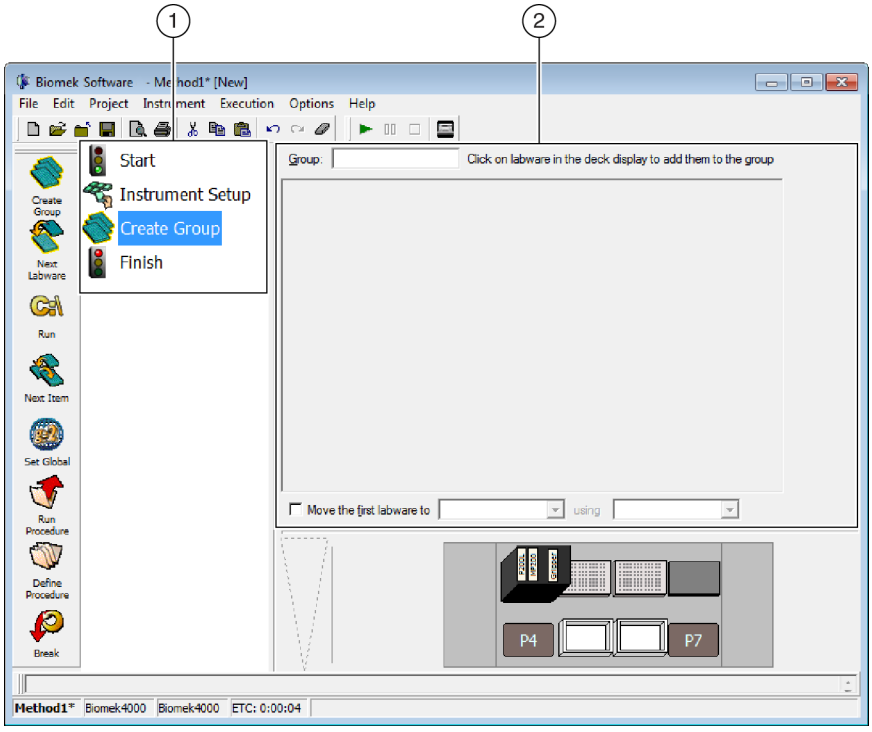
Configuring the Create Group Step

To insert an **Create Group** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 20.2).

Figure 20.2 Create Group Step and Configuration



1. **Method View**: The method displayed contains a **Create Group** step. After configuring, the group name appears in the step caption.
2. **Create Group configuration**: **Create Group** is used to create a group a labware and assign a name to that group.

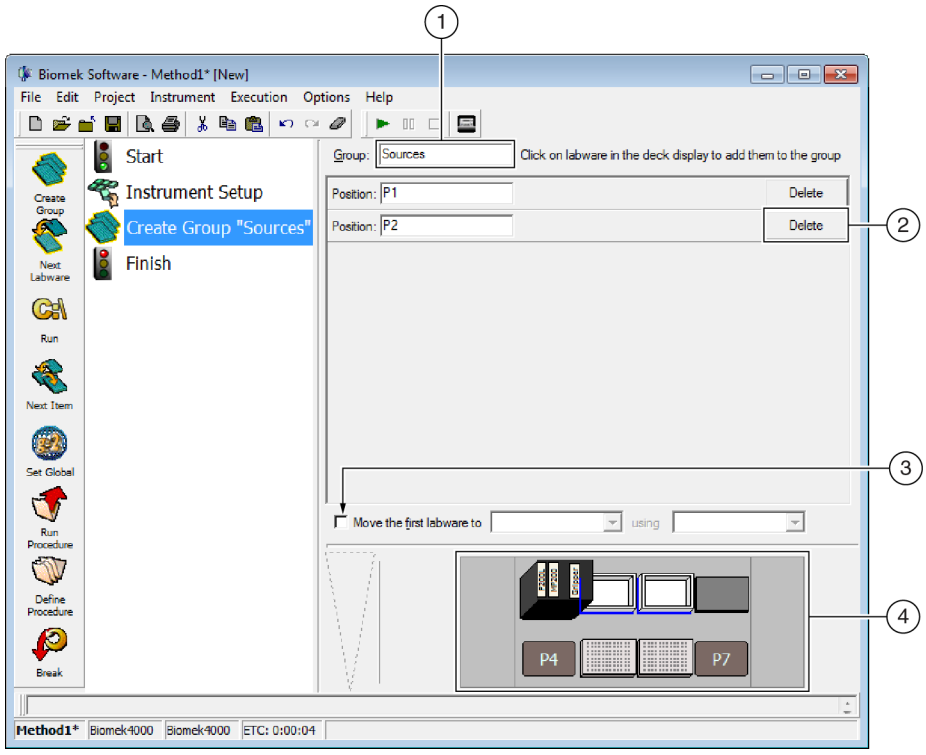
To configure the **Create Group** step:

1 In **Group**, enter a name for the group of labware (Figure 20.3).

2 Click on labware in the Current Deck Display to add them to the group.

NOTE Choose **Delete** to remove the labware from the group.

Figure 20.3 Create Group Step Configuration with Labware Added



1. **Enter the name of the group here.**
2. **Delete labware from the group here.**
3. **Provides an option to allow a Gripper tool to move labware to the appropriate deck position.**
4. **Current Deck Display**: Clicking on labware here adds them to the group.

3 Choose **Move the first labware to** to allow the pod to move labware to a specific position, if desired.

NOTE Selecting **Move the first labware** to is equivalent to inserting a **Next Labware** step right after the **Create Group** step. The group variable is assigned the value of the first labware in the group and is moved to the specified position.

NOTE To use a gripper tool, it must be installed in **Hardware Setup**, configured in **Instrument Setup**, and available on the deck.

4 If **Move the first labware to** is selected, select the deck position to which to move the first labware.

NOTE Click on any empty deck position in Current Deck Display. **Move the first labware to** is selected, and the deck position chosen in the Current Deck Display is selected.

If a deck position is not selected, it leaves the labware at its current location.

5 If **Move the first labware to** is selected, select **Pod1** in the **using** drop-down to move the first labware to the selected position.

NOTE To use a gripper tool, it must be installed in **Hardware Setup**, configured in **Instrument Setup**, and available on the deck.

Next Labware Step

Next Labware is used to select the next labware, which was configured in the **Create Group** step. As the first **Next Labware** step is added to the method, Biomek Software automatically creates a global variable defined as the name of the group (specified in the **Create Group** step). This global variable can be used in other steps of the method (e.g., a **Transfer** step). The **Next Labware** step also has options to get the next labware only when a pattern is completed or to break out of the current loop when all labware is used.

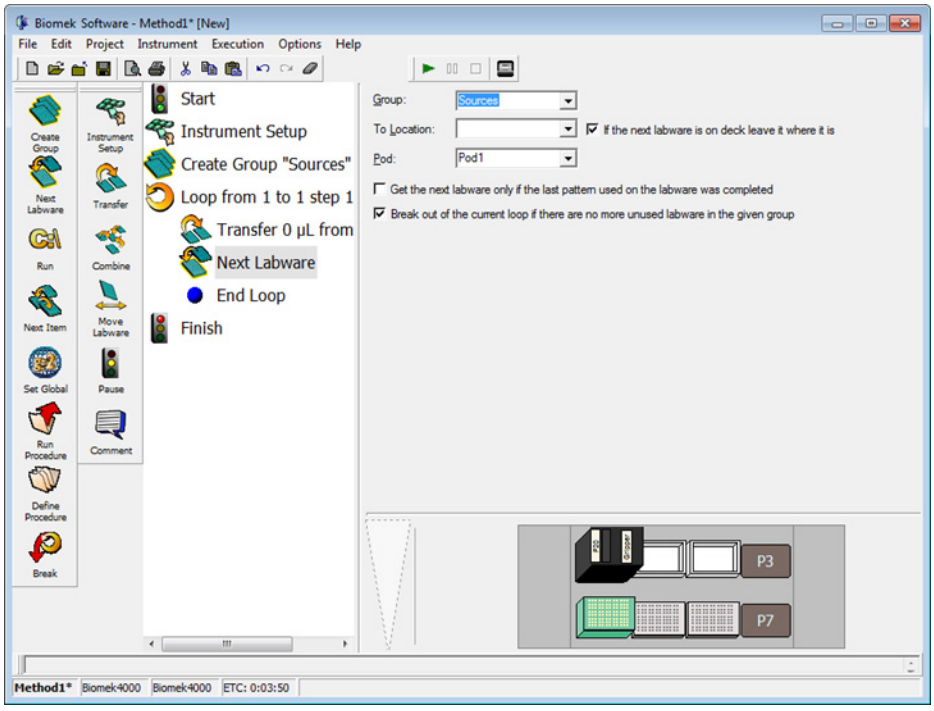
Configuring the Next Labware Step

To insert an **Instrument Setup** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 20.4).

Figure 20.4 Next Labware Step and Configuration



To configure the **Next Labware** step:

---

1 Choose the **Group** from the pull-down menu.

---

2 In **To Location**, choose the deck position to which the next listed labware in the selected **Group** is moved by selecting from the list.

OR

Click on the empty deck position in the Current Deck Display.

---

3 Check **If the labware is on deck leave it where it is** to leave the labware in its current location instead of moving it to the **To Location**, if desired.

NOTE To use a gripper tool, it must be installed in **Hardware Setup**, configured in **Instrument Setup**, and available on the deck.

---

4 Choose **Get the next labware only if the last pattern used on the labware was completed** to allow the next piece of labware in the group to be accessed only if all the selected wells on the current piece of labware have been accessed in a **Transfer** or **Combine** step.

5 Choose **Break out of the current loop if there are no more unused labware in the given group** to break out of the current loop and allow the method to continue when all the labware in the group has been accessed.

Using Group Variables in a Method

Group names configured in a **Create Group** step and assigned a value with a **Next Labware** step may be used in any deck position field in any step within the method.

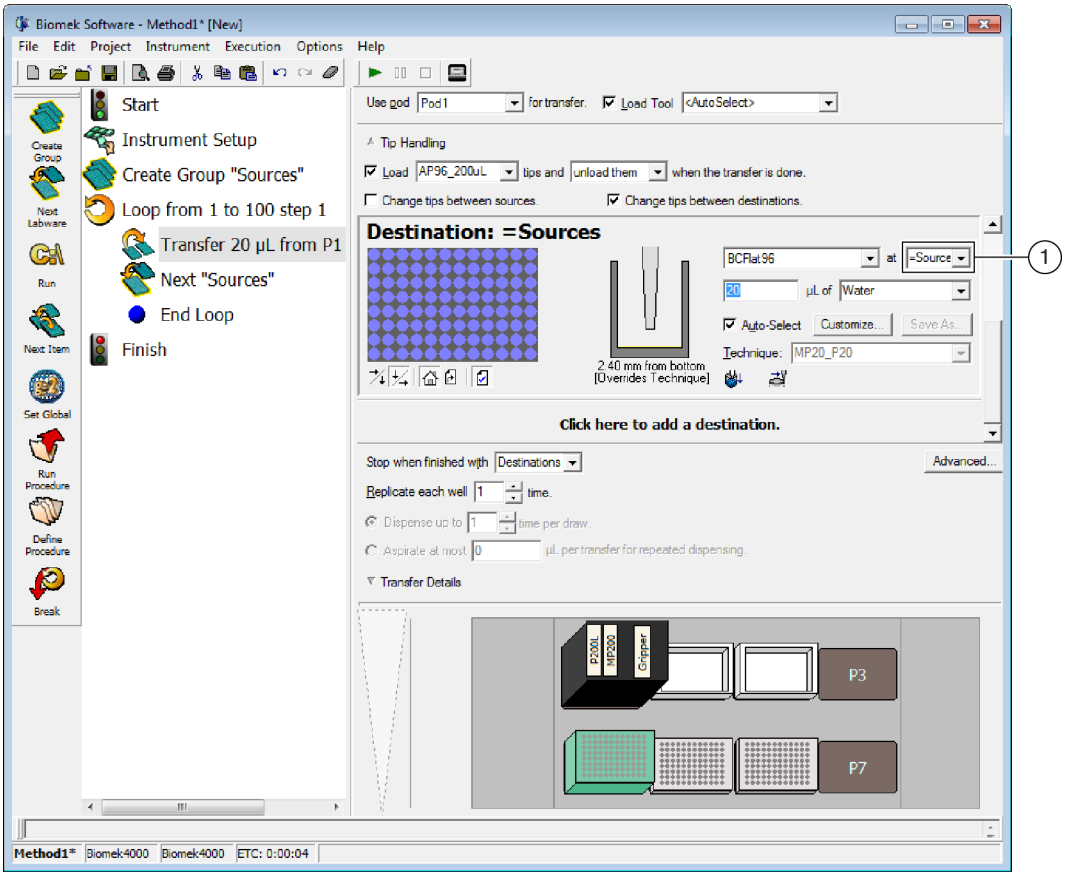
To use a group variable in another step:

1 Select a field that requires a deck position in the desired step configuration. For example, the group **Sources** is used to specify the deck location of the destination for the **Transfer** step (Figure 20.5).

2 Enter the group name, preceded by an equal sign. For example, **=Sources** in the **at** field of the destination in the **Transfer** step indicates a volume is transferred to the labware at the deck position indicated by the group variable **Sources.**

NOTE **Group** names may be used in any field where a deck position is a valid value for that field.

Figure 20.5 Transfer Step Using the Sources Group Defined in a Create Group Step



1. **Using a group defined in the Create Group step.**

Run Program Step

Run Program executes any application within a method. It can be used, for example, to run a custom data logger, display a read-me file or special instructions at specified times during a method, or access a database.

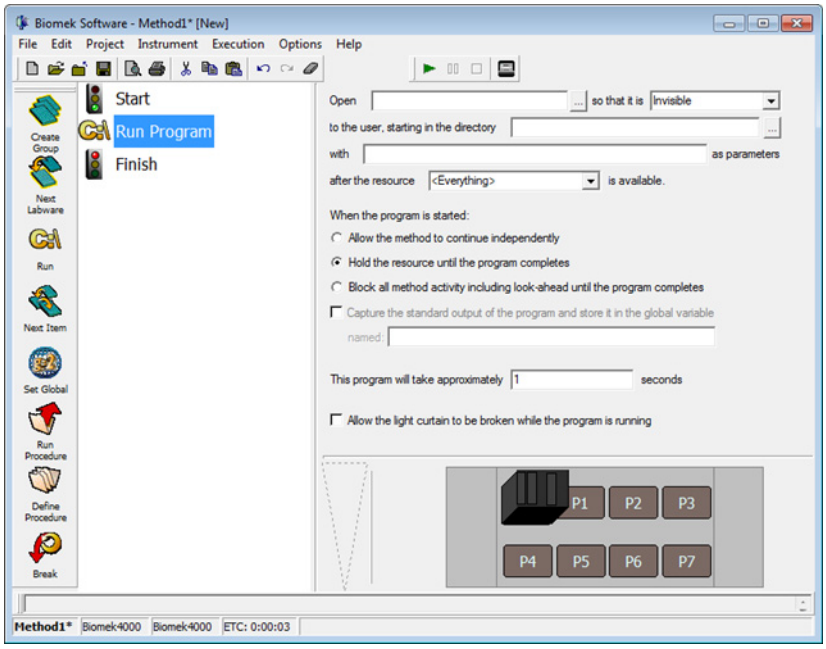
Configuring the Run Program Step

To insert an **Run Program** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 20.6).

Figure 20.6 Run Program Step and Configuration



To configure the **Run Program** step:

1 In **Open**, enter the full path and file name for the program to execute during method run.

OR

Choose ... and select the desired program from **Open**.

NOTE Any executable file (.exe, .bat, etc.) in any accessible directory (local or network) may be selected in the **Run Program** step. Websites can be accessed (http://www.beckmancoulter.com) or email (mailto:jdoe@example.com) sent.

2 Select how the program should be run in **so that it is.** Options are **Visible** or **Invisible.**

NOTE Any application that is Visible is run and displayed in a visible window. Any application that is **Invisible** is run in the background with no visual display. Certain executables, such as Notepad or Calculator, cannot be executed as **Invisible**.

3 In **starting in the directory**, specify the directory to search for the parameter entered in **with.**

NOTE When the **Run Program** step is executed, it searches the indicated directory for the specified parameter. Results depend on the application run and whether or not the specified parameter is found.

4 In **with**, enter any parameters used when running the program. For example, if the selected program is Microsoft Word, the full path and file name of a Word document can be entered as a parameter. The program runs and opens the Word file entered as a parameter in **with.**

5 In **after the resource**, select a pod, deck position, or ALP. The program executes when the selected resource is available.

NOTE Select **<Everything>** to run the program when everything on the deck is available.

6 Make a selection in **When a program is started:**

- **Allow the method to continue independently** — After starting the program, the method continues independent from the program; that is, it does not wait for the program to finish before continuing with the method. This is useful for displaying information that does not require immediate attention.
- **Hold the resource until the program complete**s — The selected resource is paused while the program is running and may not be accessed until the program is finished and closed.
- **Block all method activity including look-ahead until the program completes** — The method pauses and waits for the program to finish before enqueueing the next step and continuing with the method. This is useful when data from the executable is used to make choices in a Biomek method; for example, a LIMS system driving a hit picking method.

7 In **This program will take approximately**, enter the estimated length of time to run the program in seconds.

NOTE The time entered in **This program will take approximately** is only used to calculate the **ETC** and does not affect the method run or actual run time for the method.

8 To pause the instrument while the program is running, select **Allow the light curtain be broken while the program is running.** This lowers the speed of the instrument fans and initiates the light to flash, alternating green and yellow, indicating a paused instrument state.

NOTE Selecting this option disables **Allow the method to continue independently** described in Step 6 above.

9 Select a step that occurs after the **Run Program** step or the **Finish** step to validate the step configuration.

Next Item Step

The **Next Item** step is used to iterate over a sequence of values. When configured, the **Next Item** step names a global variable, provides a list of **VB** script expressions, and specifies behavior when the list is exhausted.

When the **Next Item** step is used in a method, the named global variable may be assigned a new value. Each expression is evaluated to form a list of values.

If the named global variable is not assigned a value, it is assigned the first value of the list. If the global variable is assigned a value, the step searches for a matching value in the list and performs one of the following actions based on the results of the search:

- If a match is found, the global variable is assigned the next value in the list.
- If the matching value is the last value in the list, the action to take when the list is exhausted is applied.
- If no match is found, the global variable is assigned the first value in the list.

NOTE Use a **Set Global** step prior to the first appearance of a **Next Item** step to create the variable used in the **Next Item** step and assign it no value (leave the **Value field** empty). This guarantees that the first **Next Item** step assigns the first value in the list to the variable.

The **Next Item** step is often used with a **Loop** step, with the value of the variable changing with each iteration of the loop.

NOTE Refer to CHAPTER 16, *Loop Step*, for more information on using the **Loop** step.

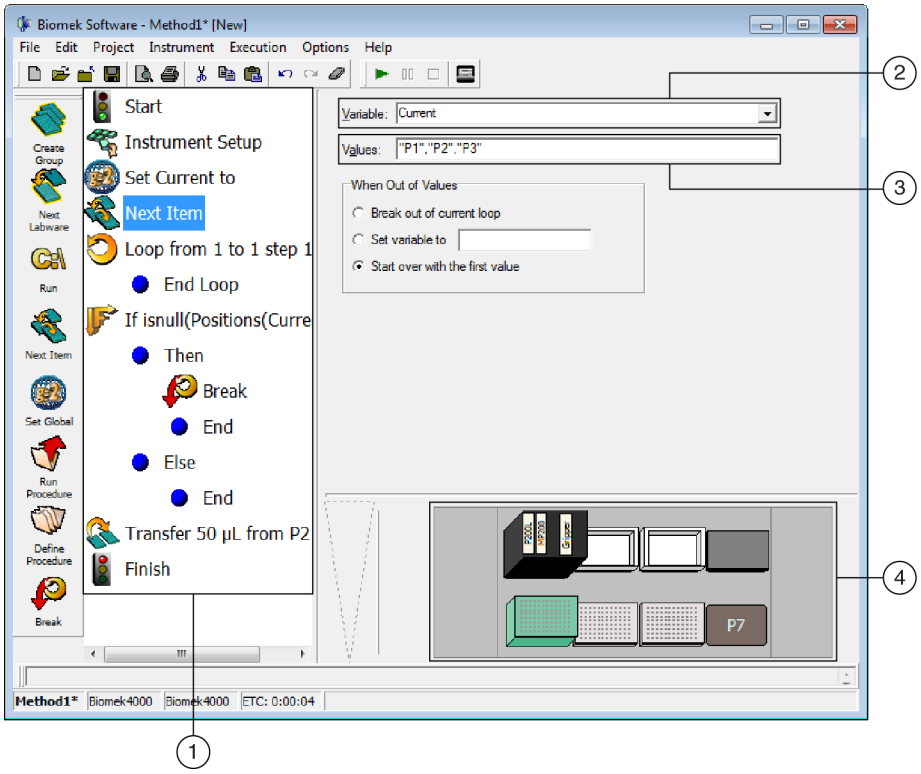
Configuring the Next Item Step

To insert an **Next Item** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 20.7).

Figure 20.7 Next Item Step and Configuration



1. **Method View**
2. **Variable**: Select a previously created variable or create a new variable here. The **Current** variable, created in the **Set Global** step, is selected here.
3. **Values**: Enter the list of values here, separated by commas.
4. **Current Deck Display**: Clicking on deck positions adds them to the list of **Values**.

To configure the **Next Item** step:

1 Select a previously defined **Variable**

OR

Enter a new **Variable** name.

2 Enter the **Values** of the **Variable**, separating each with a comma.

NOTE Deck positions must be entered in double quotes. For example, deck position P4 is entered as "**P4**" in **Values**. Deck positions may also be entered by clicking on each position in the Current Deck Display.

NOTE All **Values** must be unique. If a value is repeated in the list, an error occurs during validation.

3 Indicate the action to take when all values have been used:

- **Break out of current loop** — Ends the current loop and continues with the method; **Next Item** must be placed inside a **Loop** step or a procedure that is run from inside a **Loop** step to use this option.
- **Set variable to** — Sets the variable to a specified value and uses that value for the variable.
- **Start over with the first value** — Sets the variable to the first value and continues; loops the **Next Item** values.

Set Global Step

The **Set Global** step is used to create a global variable accessible to all steps following the **Set Global** step in a method. It allows steps to be parameterized by specifying the value of a variable for fields such as volumes and heights. For example, instead of typing the number of microliters into the volume field of an **Aspirate** step, the name of a variable is inserted. Every time the **Aspirate** step is executed, the current value of that variable is used as the volume.

Any of the steps following the **Set Global** step can use variables created in the **Set Global** step configuration. A step uses a global variable by referencing it in its step configuration. Biomek Software automatically uses the associated value when the step is executed.

NOTE For information on variables and expressions, refer to CHAPTER 13, *Using Variables and Expressions in a Method*.

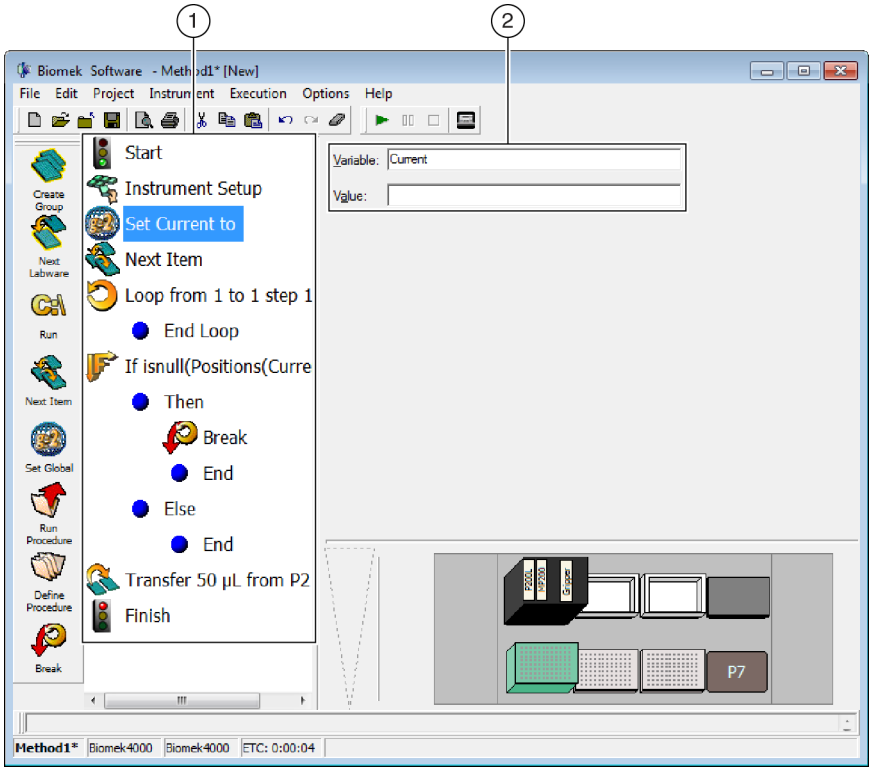
Configuring the Set Global Step

To insert a **Set Global** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 20.8).

Figure 20.8 Set Global Step and Configuration



1. **Method View**: The method displayed contains a **Set Global** step. The variable assigned in **Set Global** appears in the step caption.
2. **Set Global configuration**: The **Set Global** configuration consists of a variable name and value. Variables assigned in a **Set Global** step are available to all steps following the **Set global** step and may be used in any field instead of entering a value. Here, the variable **Current** is created and is later used in a **Next Item** step.

Configuring the **Set Global** step involves naming the variable and setting its initial value.

To configure the **Set Global** step:

---

1 Select **Set Global** in the Method View. The **Set Global** step configuration displays.

---

2 Enter the **Variable** name (refer to CHAPTER 13, *Using Variables and Expressions in a Method*).

3 Enter the desired **Value** for the **Variable**.

NOTE The value of the variable is assigned the appropriate units when used in a step configuration. For example, if a variable **AspValue** with a value of 10 is used in the **Volume** field of a **Transfer** step, the software interprets this as 10 microliters (µL).

NOTE Deck positions must be entered in double quotes. For example, deck position P4 is entered as "**P4**" in **Values**.

Defining and Running Procedures

The **Define Procedure** and **Run Procedure** steps are used to create a series of steps that may be used multiple times in a method. A procedure is created by adding and configuring steps within a **Define Procedure** step.

Variables may be created in the **Define Procedure** step and used to configure the steps in the procedure. Variables created in the **Define Procedure** step configuration can be overridden in the **Run Procedure** step configuration.

Multiple procedures can be defined in a method, and a procedure can be run multiple times within a method.

The advantages of using procedures are:

- The ability to run the same steps multiple times within a method but configure them only once.
- The size of the current method is controlled, which reduces confusion by listing only the **Run Procedure** step in the Method View, not all of the steps accessed by the **Run Procedure** step.

Define Procedure Step

The **Define Procedure** step is used to create procedures that may be called any time during a method with a **Run Procedure** step.

To insert a **Define Procedure** step into a method:

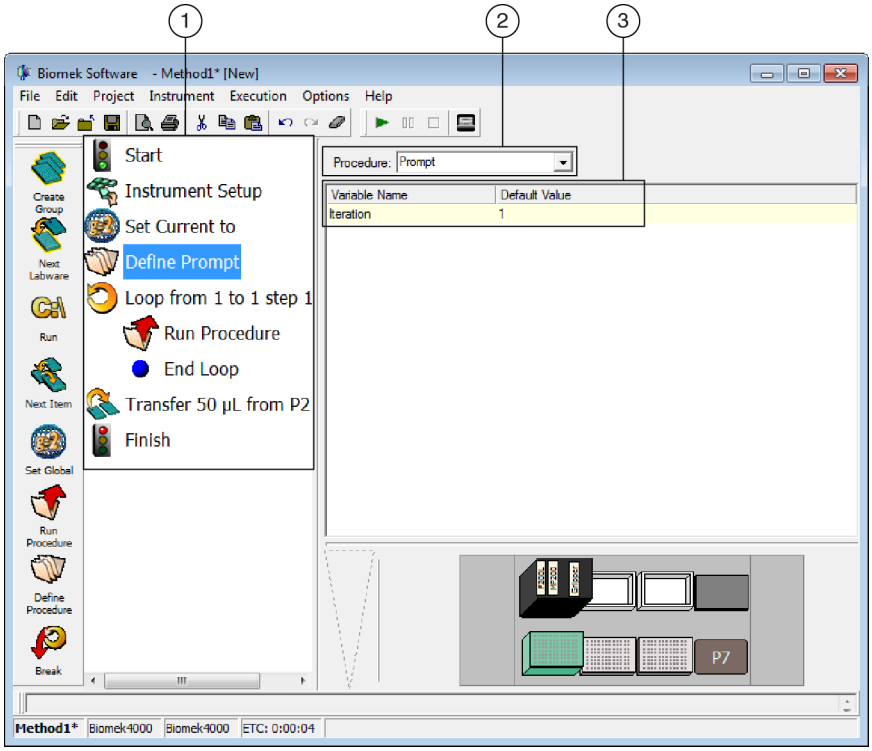
1 Drag and drop the 

icon into the Method View (Figure 20.9).

2 **Define Procedure** is added to a method collapsed. Double click the Define Procedure icon to expand the procedure and display the  End Procedure icon.

Any steps placed between the **Define Procedure** and **End Procedure** icons are run when the procedure is called with a **Run Procedure** step. These steps are configured through their individual step configurations.

Figure 20.9 Define Procedure Step and Configuration



1. **Method View**: The method displayed contains a **Define Procedure** step. The name assigned to the procedure appears in the step caption.
2. **Procedure**: Assign a name to the procedure.
3. **Variables**: Insert any variables used in the procedure here. The values for the variables may be assigned new values when the procedure is run in a **Run Procedure** step.

Configuring the Define Procedure Step

To configure the **Define Procedure** step:

1 In **Procedure**, enter a name for the procedure.

NOTE The procedure name may contain only alphanumeric characters and the underscore (_), and are not case-sensitive.

2 Insert the variables desired (refer to CHAPTER 13, *Using Variables and Expressions in a Method*).

NOTE Variables created in a **Define Procedure** step are accessible only to the substeps within that procedure.

3 Double click the **Define Procedure** icon in the Method View to open the procedure. The **End Procedure** icon appears below the **Define Procedure** icon.

4 Insert the desired steps between **Define Procedure** and **End Procedure**.

5 Configure the steps between **Define Procedure** and **End Procedure** as desired.

6 Double click the **Define Procedure** icon to collapse the procedure and hide all steps between the **Define Procedure** and **End Procedure** icons.

7 Validate the step by inserting a **Run Procedure** step into the method and configuring it to run the newly defined procedure (see *Run Procedure Step* for complete instructions).

IMPORTANT **Define Procedure** steps are not recognized as official steps by Biomek Software until *after* a **Run Procedure** step that uses that procedure is added to the method. Therefore, the **Define Procedure** step cannot be validated, and the Current Deck Display will not reflect the changes to the deck, until *after* the **Run Procedure** step is added.

Run Procedure Step

The **Run Procedure** step executes a procedure previously created with the **Define Procedure** step. The step inserts all of the steps from the referenced procedure into the current method at the point the **Run Procedure** step displays. The called procedure then behaves exactly as if the steps were configured at the point where the procedure is called.

The **Run Procedure** step may also assign new values to variables created in the called procedure. These values override any value configured in the **Define Procedure** step. This allows a procedure to be used as a template that can be customized each time it is performed by a **Run Procedure** step by changing the values of the variables.

Configuring the Run Procedure Step

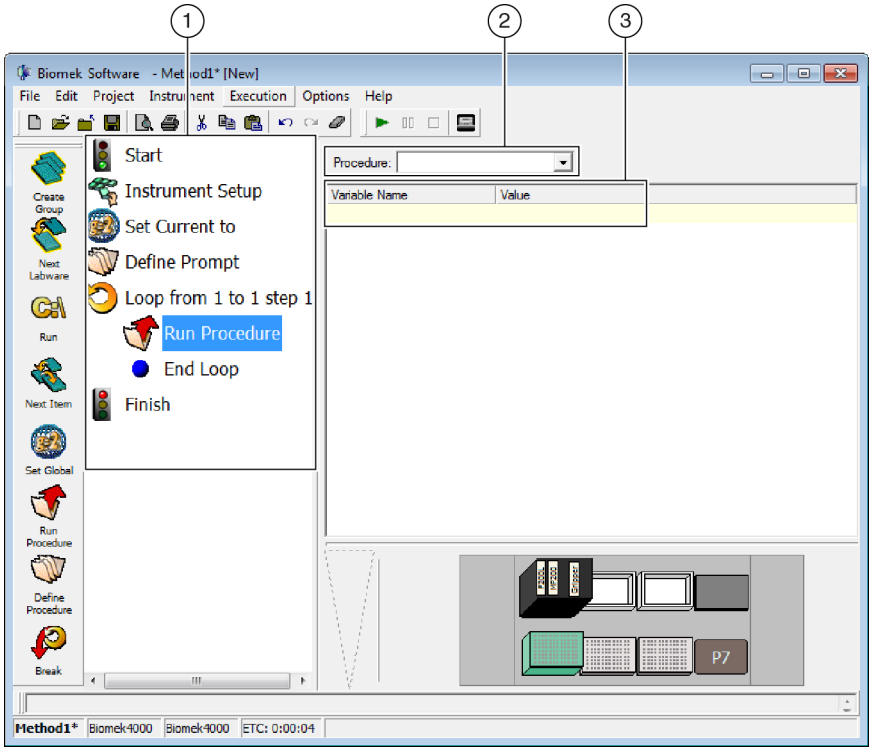
To insert a **Run Procedure** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 20.10).

NOTE The procedure to run in a **Run Procedure** step must be defined in a **Define Procedure** step earlier in the method, or in a previously run method that did not clear all global variables in the **Finish** step.

Figure 20.10 Run Procedure Step and Configuration



1. **Method View**: The method displayed contains a **Run Procedure** step. The name of the procedure to execute appears in the step caption once a procedure is selected.
2. **Procedure**: Select a previously defined procedure.
3. **Variables**: Assign new values to the procedure variables, if desired.

To configure a **Run Procedure** step:

---

1 Select the desired procedure from the list of defined procedures. The variables used in that procedure are displayed.

---

2 Enter the desired values for the variables (refer to CHAPTER 13, *Using Variables and Expressions in a Method*).

NOTE Variables in a **Run Procedure** step are accessible only to the called procedure.

---

3 Select the **Finish** step to validate the **Define Procedure** step, as well as the other steps in the method.

IMPORTANT The procedure used in this newly created **Run Procedure** step cannot be validated until *after* the **Run Procedure** step is validated. Therefore, it could be necessary to make corrections to the **Define Procedure** step once this step is validated.

Break Step

The **Break** step is used to break out of one or more loops during a method. **Break** is usually used as part of an **If** step to break out of a **Loop** under certain conditions. When **Break** is placed under the **Then** substep, and the **If** statement is true, the **Break** step ends the **Loop**.

NOTE The **Break** step must be placed inside of a **Loop** step or a procedure run from inside a **Loop** step or errors are generated during validation or method run.

NOTE Refer to CHAPTER 16, *Loop Step*, for more information on using a **Loop** step. Refer to CHAPTER 17, *If Step*, for more information on using an **If** Step.

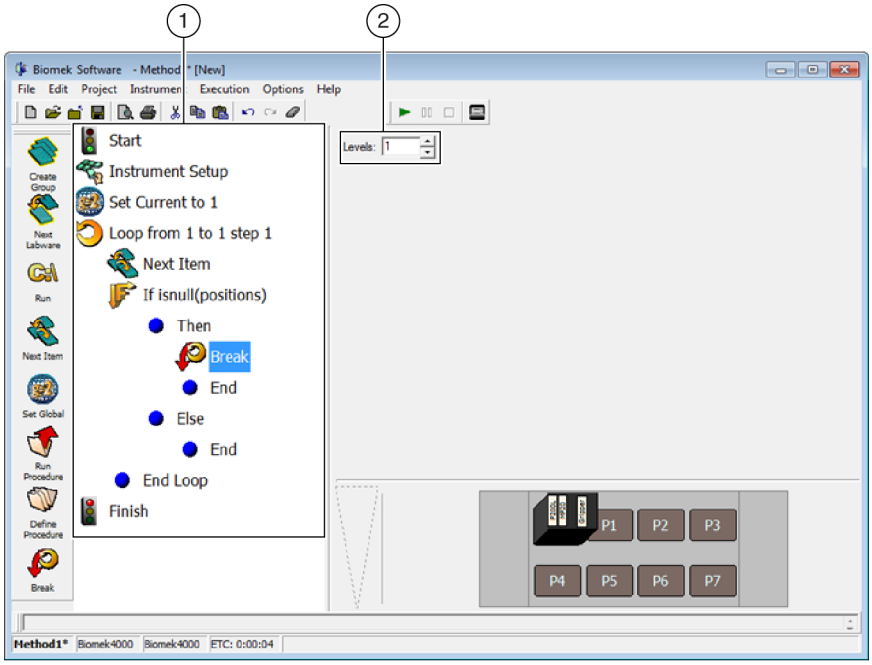
Configuring the Break Step

To insert a **Break** step into a method:

1 Drag and drop the 

icon inside a **Loop** step in the Method View (Figure 20.11).

Figure 20.11 Break Step and Configuration



1. **Method View**: The method displayed includes a **Break** step inserted inside a **Loop** in an **If** step. When the **If** condition is true, the **Loop** step ends even if all iterations have not been completed.
2. **Levels**: The number of nested **Loop** steps to break out of. This value must be less than or equal to the total number of nested loops in which the **Break** step is found.

To configure the **Break** step:

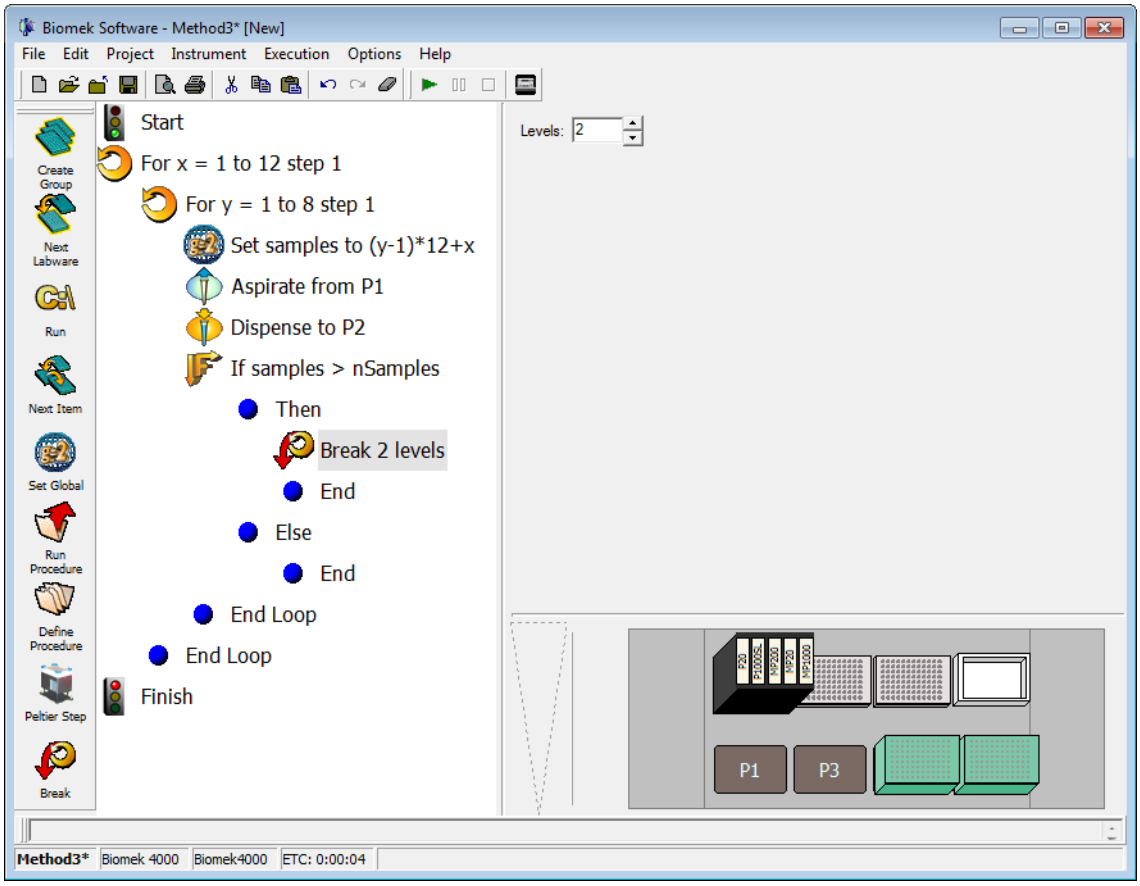
1 In **Levels**, select the number of levels to break out of.

NOTE **Levels** refers to the number of nested **Loop** steps that are discontinued. **Break** terminates the number of **Loop** steps specified in **Levels** and continues with the method.

For example, the method shown in Figure 20.12 contains a **Loop** step that contains a second **Loop** step nested. Within the second **Loop** step is an **If** step with a **Break** step with **Levels** set at **2** under the **Then** branch. When the **If** statement in the second **Loop** step is true, the **Break** step terminates both **Loop** steps and continues with the method. If **Levels** was set to **1**, the **Break** step terminates the second **Loop** step and continues with the first **Loop** step.

NOTE There must be a number of nested **Loop** steps greater than or equal to the number of **Levels,** or an error occurs during method validation and run.

Figure 20.12 Break Step Example



CHAPTER 21

Using the Devices Step Palette

Overview

The steps presented in the **Devices** step palette (Figure 21.1) integrate active ALPs and other devices with the instrument. The integration allows Biomek Software to control the device.

After an active ALP or device is integrated, Biomek Software understands the attributes of the device, displays the configuration for the device, and receives information for operating the device.

NOTE Devices must be installed and configured in **Hardware Setup**. Refer to the *Biomek 4000 Hardware Manual* for more information.

NOTE Devices must also be configured on the deck in the **Deck Editor** (refer to CHAPTER 5, *Preparing and Managing the Deck*).

The steps displayed on the **Devices** step palette are included in Table 21.1:

Table 21.1 Devices Step Palette

Step	Icon	Description
SPE		Allows a method to easily assemble and disassemble the stack for the SPE (Solid Phase Extraction) ALP.
Device Setup		Configures labware contained in external devices that hold multiple pieces of labware.
Device Action		Controls devices such as the Orbital Shaker, AutoLatch, vacuum, and active ALPs during a method run.

The step in Table 21.2 appears when a SILAS device and the software associated with it are installed on the system:

Table 21.2 SILAS Step Palette

Step	Icon	Description
SILAS Consumer Setup		Controls operation of the associated SILAS Module, such as a barcode reader or a SILAS consumer that has been added to a step palette.

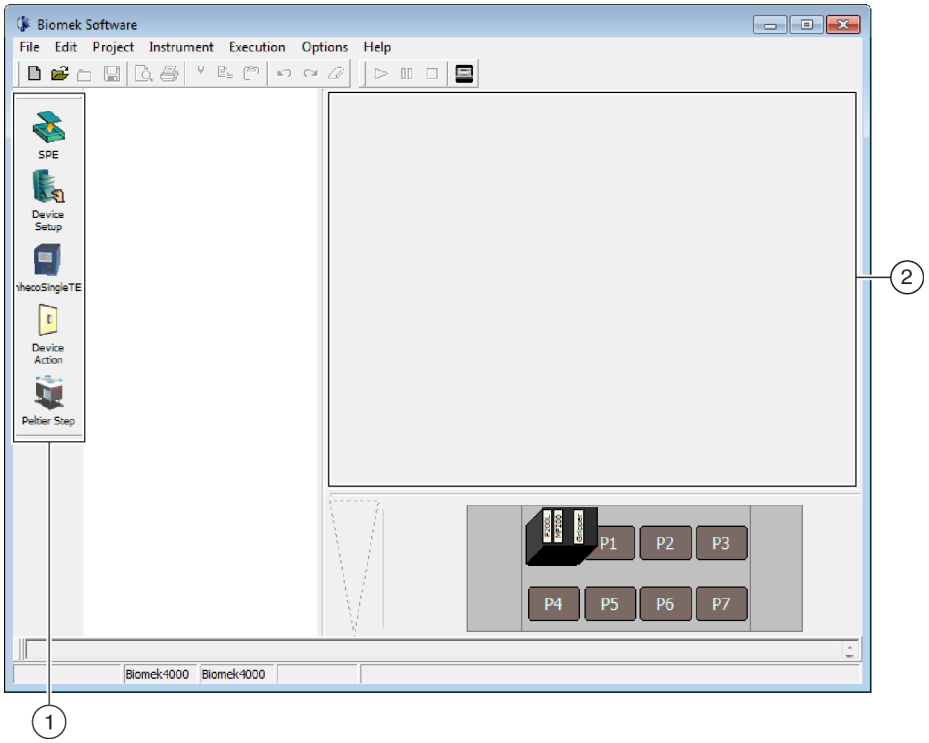
NOTE The icon for a **SILAS Module** step varies according to the device the step represents; for example, a **Barcode Reader SILAS Module** step displays an icon of a barcode reader.

When a device integration step is added to a method, the configuration associated with that step appears on the right side of the main editor in step configuration. Steps not configured appropriately can generate errors when the method is validated or run. For additional information, refer to the manual provided with your device.

Displaying the Devices Step Palette

In order to add device steps to a method, the **Devices** step palette must be displayed (Figure 21.1).

Figure 21.1 Main Editor with Devices Step Palette Displayed



1. **Devices Step Palette**
2. **Step Configuration**: When a step is highlighted in the Method View, set the corresponding step configuration in this area.

To display the **Devices** step palette, complete the following:

1 Right click any empty palette space, and the step palette menu appears. Select **Devices** from the menu.

OR

From the toolbar, select **Options > Toolbars > Devices**.

SPE Step

The SPE ALP applies a vacuum to remove liquid from a filter microplate. The **SPE** step is a convenient way of executing the assembly and disassembly of the SPE ALP system. The configuration for the **SPE** step informs Biomek Software of the:

- Operation required of the **SPE** step (Figure 21.2)
- Location of the filtered microplate used by the SPE ALP
- Locations of the SPE vacuum manifold and receiver
- Location of the SPE ALP on the deck
- Pod constructing/destroying the SPE stack

NOTE A gripper tool must be installed and configured on the deck.

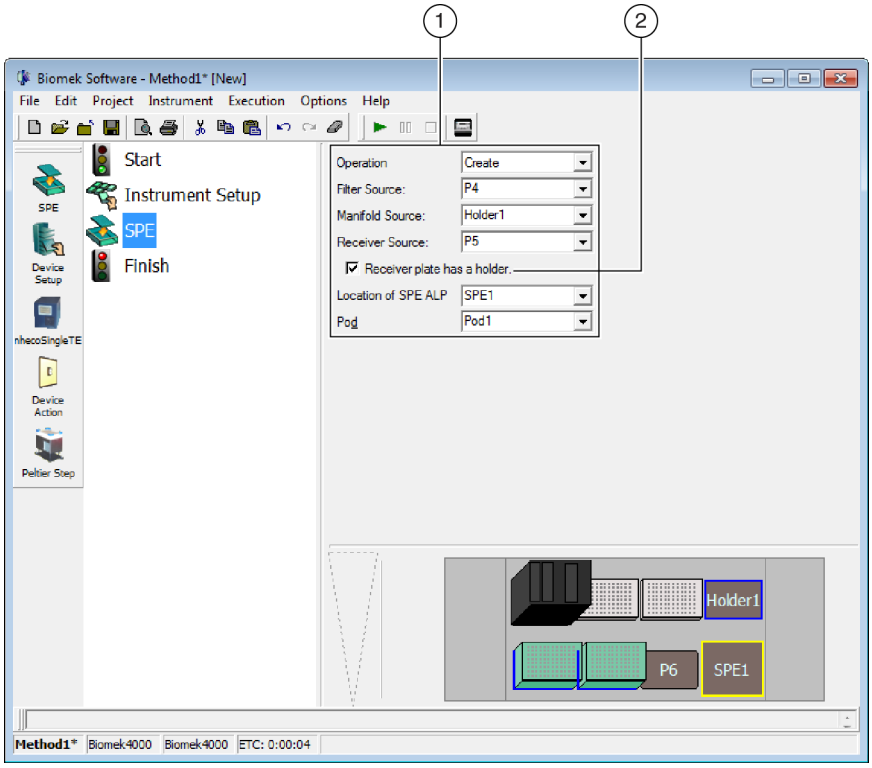
NOTE The SPE ALP occupies two deck positions.

To insert a **SPE** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 21.2).

Figure 21.2 SPE Step and Configuration



1. **SPE step configuration**: The operation performed by the **SPE** step, as well as the position and identity of the components of the SPE ALP are provided in the **SPE** step configuration.
2. **Receiver Plate configuration**: When the receiver microplate is positioned in a microplate holder, the presence of the holder must be indicated by selecting **Receiver plate has a holder**.

Configuring the SPE Step

When an **SPE** step is added to a method, the SPE step configuration appears (Figure 21.2)

To configure the **SPE** step:

1 Select the **Operation** performed by the SPE ALP from the options listed below:

- **Create** — Assembles the various pieces of an SPE stack.
- **Destroy** — Disassembles an SPE stack.

2 Select the location of the **Filter Source** used by the SPE stack. The **Filter Source** is the location on the deck of the filtered microplate that is placed on top of the SPE ALP stack.

3 Select the location of the **Manifold Source** for the SPE stack. The **Manifold Source** is the location of the Manifold, which is referred to as the Collar in the *Biomek 4000 ALPs and Accessories Manual.*

4 Select the location of the **Receiver Source** for the SPE stack. The **Receiver Source** is the location of any microplate that is to be positioned inside the SPE Collar and the SPE ALP. If no receiver microplate is defined, the fluid flows through the source filtered microplate into the SPE ALP Base. The fluid is removed from the base via the vacuum hose (refer to the *Biomek 4000 ALPs and Accessories Manual*).

NOTE **Filter Source, Manifold Source**, and **Receiver Source** all change to **Destination** when **Operation** is set to **Destroy**.

5 Select **Receiver plate has a holder** if the receiving microplate is positioned in a Filter Holder. The Filter Holder is used to keep the tips of a filtered microplate from touching the base of an ALP stand or labware holder. A filter microplate without a Filter Holder can be positioned inside a 1x1 ALP without damaging the microplate.

NOTE Labware, including the Filter Holder, is positioned on the Deck Layout in the **Instrument Setup** step.

6 Select the **Location of SPE ALP** on the deck.

7 Specify the **Pod** accessing the SPE stack. For the Biomek 4000 instrument, the only option is **Pod1**.

8 Select a step that occurs after the **SPE** step or the **Finish** step to validate the step configuration.

Using External Devices with Biomek Laboratory Automation Workstations

External devices may be used during a method run. In order to use these devices in a method, there are three components that must be configured for proper operation of the device. These components are:

- **Device Editor** — Sets the attributes of the device within Biomek Software (refer to *Configuring Devices Using the Device Editor*).
- **Device Setup Step** — Configures the labware within a device for use in a method (refer to *Device Setup Step*).
- **SILAS Module** — Configures the operation of the device for the method. Refer to the manual provided with your device for additional information.

Configuring Devices Using the Device Editor

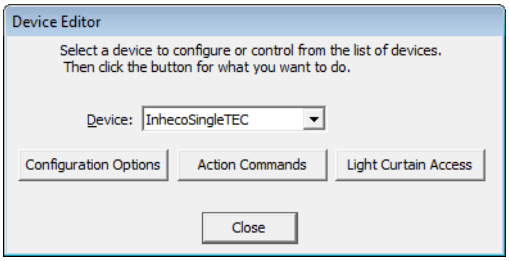
Use the **Device Editor** to configure external devices for use with the instrument. Each external device may contain different setup options, such as the number and type of labware the device is capable of holding. In order to use the device, this information must be provided through the **Device Editor**.

NOTE For specific operating instructions for external devices, refer to the user's manual for each specific device.

To open the **Device Editor**:

1 Choose **Instrument > Device Editor**. **Device Editor** appears (Figure 21.3)

Figure 21.3 Device Editor



To configure a device for use with the instrument:

1 In **Device**, select an installed device.

2 Choose the desired option:

- **Configuration Options** — Configures the device to be used with the instrument. Available options vary, depending on the device being configured. Refer to the device user's manual for more information about available options.
- **Action Commands** — Select and manually operate individual device operations. Available options vary, depending on the device being configured. Refer to the device user's manual for more information about available operations.
- **Light Curtain Access** — Not applicable on Biomek 4000 instruments.

Device Setup Step

The **Device Setup** step is used to configure the labware contained in multiple slot external devices (Figure 21.4). A **Device Setup** step only configures one device, so multiple **Device Setup** steps must be used when multiple external devices are used.

Device Setup is used to select the type of labware contained in each slot in the device, and it allows the **Labware Properties** to be set for each piece of labware in the device.

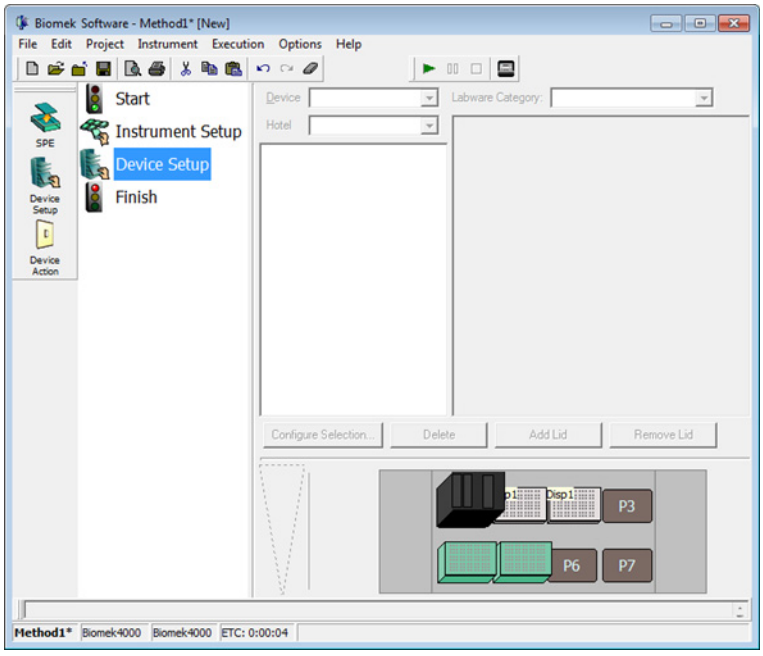
NOTE The software included with an external device must be installed before the device can be configured in the **Device Setup** step and accessed by the instrument.

To insert a **Device Setup** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 21.4).

Figure 21.4 Device Setup Step and Configuration



Configuring the Device Setup Step

When a **Device Setup** step is inserted into a method, the **Device Setup** step configuration appears (Figure 21.4). The **Device Setup** step configuration includes:

- **Configure Selection** — Displays the Labware Properties for the selected piece of labware.
- **Delete** — Removes labware from the selected slot.
- **Add Lid** — Communicates to the software that a lid is included with a piece of labware, such as a tip box or microplate with a lid. When **Add Lid** is applied to any piece of labware, an asterisk appears next to the labware indicating that a lid is present.
- **Remove Lid** — Communicates to the software that a lid has been removed from the labware. When **Remove Lid** is applied to any piece of labware with an asterisk next to its name, the asterisk disappears indicating that a lid is no longer present.

To configure the **Device Setup** step:

1 From the **Device** drop-down, select the device from the options listed. The configuration for the device is displayed in step configuration.

2 From the **Labware Category** drop-down, select the appropriate labware category.

3 Select a position, or multiple positions, within the configuration of the device to populate with labware.

4 Select a piece of labware from the graphical labware display.

OR

a. Select the **Device** from the options listed. The configuration for the device is displayed in step configuration.

b. Select a **Labware Category**.

c. Select a position, or multiple positions, within the configuration of the device to populate with labware.

d. Select a piece of labware from the graphical labware display.

OR

Drag and drop a piece of labware from the graphical labware display to the desired position in the device.

e. Right click a piece of labware in the step configuration and select **Configure Selection**. **Labware Properties** appears for the type of labware being configured (Figure 21.5 and Figure 21.6). Use **Labware Properties** to configure each piece of labware within the device (refer to *Configuring Labware Properties for Tips and Labware*).

f. Choose **OK** to save **Labware Properties** and return to the **Device Setup** step configuration.

g. Use **Add Lid** and **Remove Lid** as necessary to configure the lid status for the labware in the device.

NOTE When **Add Lid** is selected, it indicates that a lid is included with a piece of labware. An asterisk appears next to the labware in the graphical representation of the stack (Figure 21.4).

Configuring Labware Properties for Tips and Labware

Specific tips and labware used in a method can be configured using Labware Properties. The information provided in Labware Properties is used when a pipetting technique is selected, and when tips are loaded and unloaded.

To access **Labware Properties**:

1 Double click on a piece of labware in the **Device Setup** step configuration.

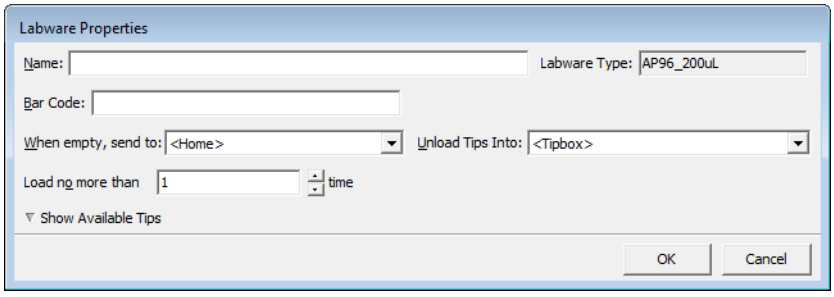
OR

Choose **Configure Selection**.

OR

Right click on a piece of labware in the **Device Setup** step configuration, and choose **Configure Selection**. **Labware Properties** appears (Figure 21.5).

Figure 21.5 Labware Properties for Tips



Configuring Labware Properties for Tips

When the labware selected for configuration is tip box, **Labware Properties** provides the ability to configure (Figure 21.5):

- Name assigned to the tip box
- Bar code
- Where to dispose of tips
- Where to dispose of tip boxes
- Maximum number of times tips can be loaded
- Available tips

NOTE Variables and expressions may entered in any field that can be configured. Refer to CHAPTER 13, *Using Variables and Expressions in a Method*, for more information on using variables and expressions.

To configure Labware Properties:

---

1 In **Labware Type**, verify the tip type.

---

2 In **Name**, enter name for the tip box, if applicable.

OR

Leave **Name** blank. When **Name** is blank, tips are accessed by the information displayed in the Labware Type field

NOTE Naming tip boxes causes the instrument to look for a specific box of tips, rather than any tip box containing the specified tip type, located anywhere on the deck. Multiple tip boxes can be given the same name. This is used to create a pool of tip boxes for a specific use.

---

3 In **Bar Code**, enter the bar code.

NOTE Use the bar code field to identify a specific tip box in certain methods, such as plate replication. This field may be left blank.

---

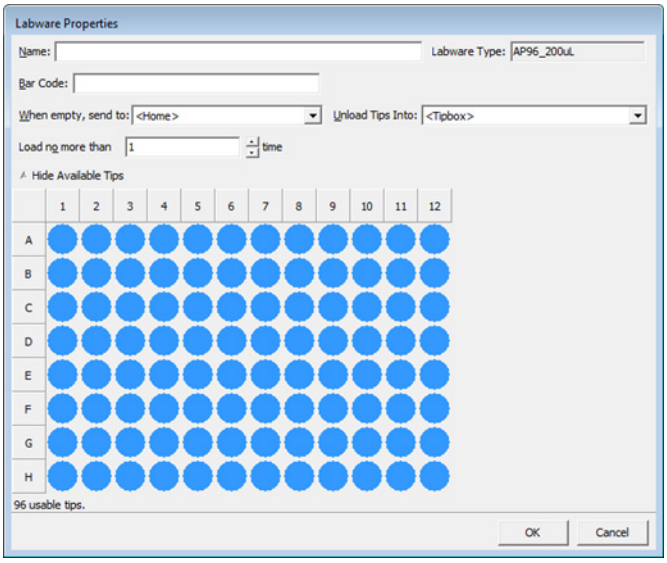
4 In **When empty, send** to, select a final destination for the tip box at the end of the method.

5 In **Unload Tips Into**, select the location reserved for tip disposal.

6 In **Load no more than**, enter the number of times tips can be loaded onto a tool during the method.

7 Choose **Show Available Tips** to display a graphic of the tip box (Figure 21.6).

Figure 21.6 Labware Properties for Tips with Available Tips Shown



8 On the graphic of the tip box, select the usable tips. This can be used to indicate missing tips or tips that are otherwise not used in the method. By default, all tips are selected.

9 Choose **Hide Available Tips** to collapse the graphic of the tipbox.

10 Choose **OK** to save Labware Properties and return to the **Device Setup** step configuration.

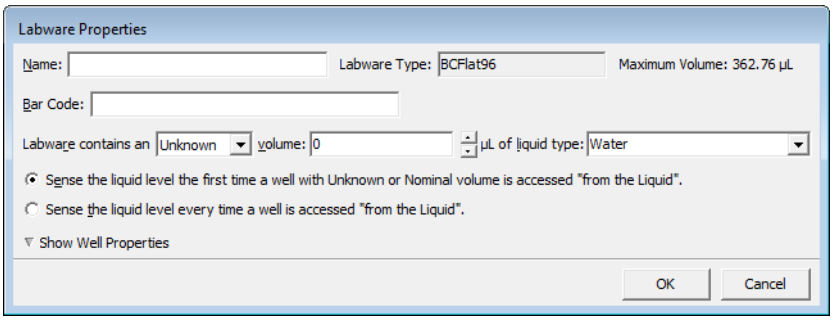
Configuring Labware Properties for Labware

For labware other than tip boxes, **Labware Properties** provides the ability to configure (Figure 21.7):

- Name assigned to the labware
- Bar code
- Volume status (known, unknown, nominal)
- Volume for each well, if known
- Liquid type

NOTE Variables and expressions may entered in any field that can be configured. Refer to CHAPTER 13, *Using Variables and Expressions in a Method*, for more information on using variables and expressions.

Figure 21.7 Labware Properties for Microplates, Reservoirs, and Tube Racks



To configure **Labware Properties**:

1 Verify the **Labware Type**.

2 In **Name**, enter a name for the labware.

NOTE When a deck is populated by numerous pieces of labware, naming labware is recommended. Names should be descriptive of the contents of the labware or the work being accomplished during the method. Naming labware in a meaningful fashion may reduce confusion.

3 In **Bar Code,** enter the bar code.

NOTE Use the bar code field to identify a specific plate in certain methods, such as plate replication. This field may be left blank.

4 Make a selection in **Labware contains**. Options are **Unknown, Nominal**, and **Known**. This information is used by many of the techniques supplied with Biomek Software which aspirate or dispense liquid a certain offset from the liquid level. Some tools can detect the liquid level using liquid-level sensing technology.

- If **Known** is selected, the liquid level is not detected during method run and the entered value is used during validation and method run. **Known Volume** should be supplied whenever possible.

- If **Unknown** is selected, the liquid level is detected during method run if required by the technique, and the wells are assumed to be full when validating the method.
- If **Nominal** is selected, the liquid level is detected during method run, but the volume in the wells is assumed to be the entered value when validating the method.

5 Enter the **Volume**, if **Nominal** or **Known Volume** is selected. A value entered in **Volume** is assigned to all wells.

6 Select the **Liquid Type** contained in the labware. The liquid type is useful information when Biomek Software auto-selects a technique for any aspirate and dispense operations acted upon this piece of labware. The technique auto-selected to aspirate and dispense the liquid is selected based on the physical factors of the liquid, as well as the physical attributes of the labware. For more information on liquid types, refer to CHAPTER 8, *Understanding and Creating Liquid Types*.

7 Select **Sense the liquid level the first time a well with Unknown or Nominal volume is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level only the first time it accesses a well with an **Unknown** or **Nominal** volume from the liquid. In any instance when the same well on the piece of labware is accessed, the liquid level is calculated internally based on the result of the earlier liquid level sense and the amount aspirated or dispensed to the well in previous steps.

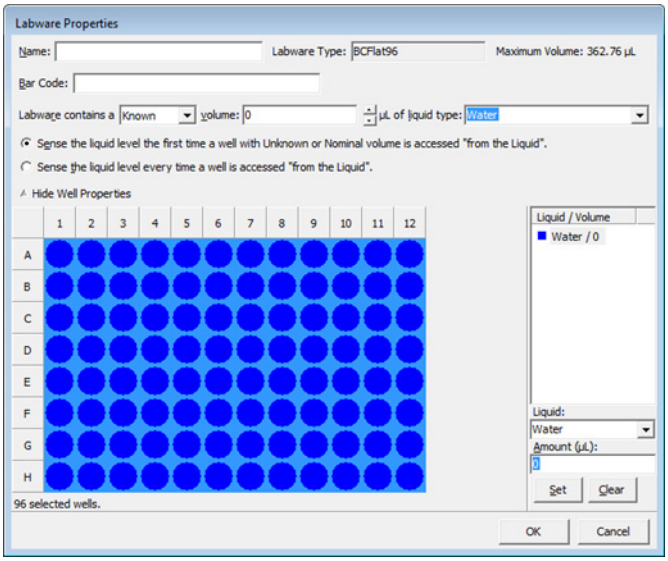
OR

Select **Sense the liquid level every time a well is accessed "from the Liquid"** to use liquid level sensing to determine the liquid level every time it accesses a well with an **Unknown** or **Nominal** volume from the liquid.

NOTE Liquid level sensing options only apply if the pod or tool accessing the labware is capable of sensing the liquid level. If not, the option selected is ignored.

8 If the labware does not contain uniform volumes and liquid types, choose **Show Well Properties** to display a graphic of the labware (Figure 21.8).

Figure 21.8 Labware Properties for 96-Well Microplate Well Properties Shown



9 Select the desired wells on the graphic.

NOTE Hold down (Ctrl) to toggle wells between selected and deselected without affecting the selection status of other wells.

10 In **Liquid**, enter the liquid to assign to the currently selected wells.

11 Enter the volume to assign to the currently selected wells in **Amount**.

12 Choose **Set** to assign the current **Liquid** and **Amount** to the currently selected wells. The wells are given a color code that corresponds to the list of set volumes under **Volume**.

NOTE **Clear** sets the volume for all wells back to zero and changes the liquid type back to the default.

13 Repeat steps 9-12 until all desired wells have been assigned the desired volume and liquid type.

14 Choose **Hide Well Properties** to collapse the graphic of the labware.

15 Choose **OK** to save **Labware Properties** and return to the **Device Setup** step configuration.

Device Action Step

The **Device Action** step is used to configure the actions of devices such as the autolatch, vacuum, and active ALPs.

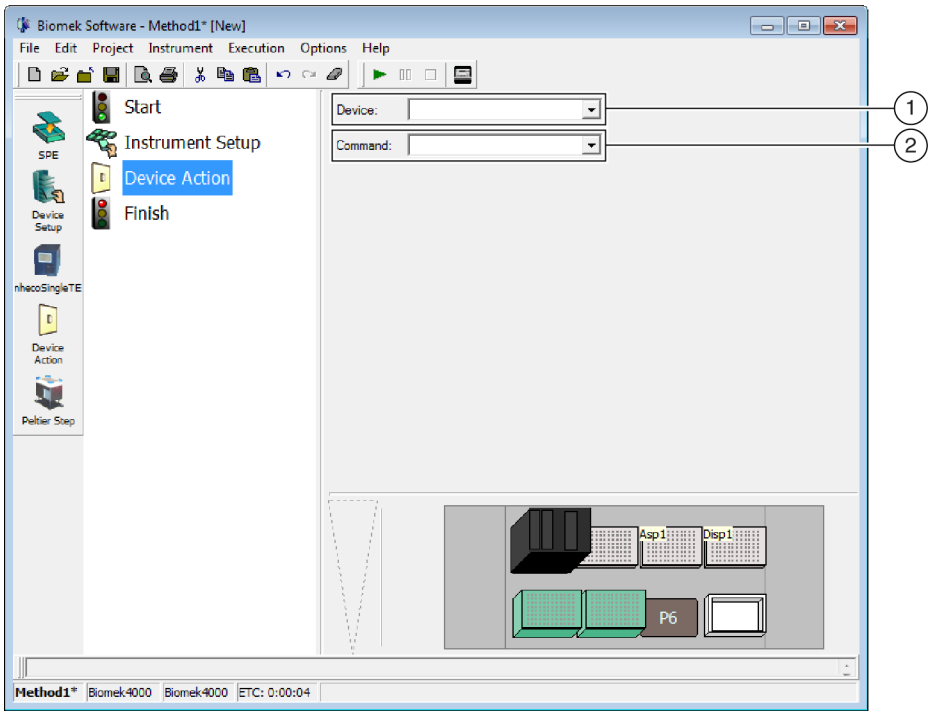
NOTE Any devices installed in **Hardware Setup**, except Device Controllers, are listed under **Device** in the **Device Action** step configuration.

To insert a **Device Action** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 21.9).

Figure 21.9 Device Action Step and Configuration



1. **Device**: Select the device to control here.
2. **Command**: Select the action for the device to execute here. Some commands require further configuration.

Configuring the Device Action Step

When **Device Action** is added to a method, the associated configuration appears.

The configuration options available for the **Device Action** step depend upon the device selected for configuration.

⚠ WARNING

Risk of contamination. Improper Biomek Software configuration of "Hardware Setup," the "Device Action" step, or AutoLatch "Position Properties" in the Deck Editor can cause tip boxes or tips to collide with labware containing biologically or chemically hazardous material, resulting in spills on the Biomek 4000 deck. Always test the system configuration and associated device operations with water before using biological or chemical agents.

The **Device Action** step is used to control the following ALPs and devices:

- *Configuring the Device Action Step for an AutoLatch*
- *Configuring the Device Action Step for the Vacuum*
- *Configuring the Device Action Step for an Orbital Shaker ALP*

Configuring the Device Action Step for an AutoLatch

If an AutoLatch is associated with a deck position, the AutoLatch automatically opens when a tip box is moved and automatically closes when loading or unloading tips (for additional details on associating an AutoLatch to a deck position, see CHAPTER 5, *Preparing and Managing the Deck*). Setting up the **Device Action** step for the AutoLatch provides options to more precisely control these movements.

To configure the **Device Action** step for the Auto-Latching Tip Rack Holder or AutoLatch:

---

1 From **Device,** select the autolatch performing the required operation.

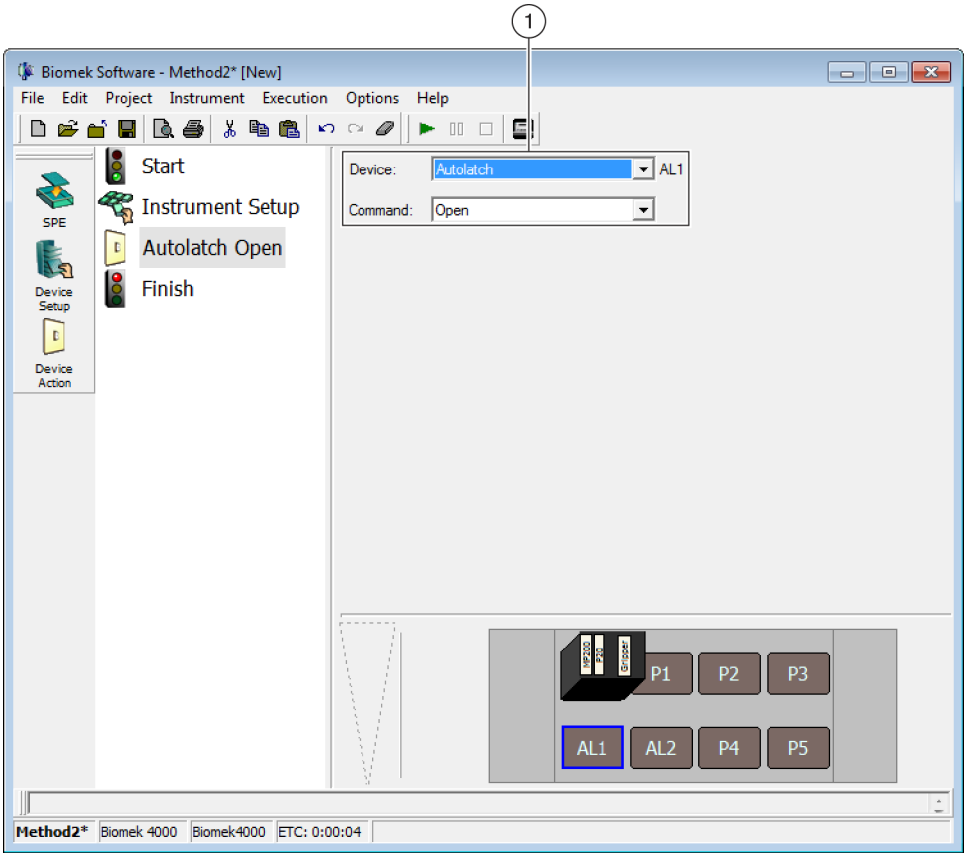
OR

Click on the autolatch in the Current Deck Display to select it.

The configuration for the autolatch appears (Figure 21.13).

NOTE The deck position has a blue border in the Current Deck Display and is displayed to the right of **Device**.

Figure 21.10 Device Action Step for the Autolatch



1. **Device Action Step Configuration**: The **Device Action** step configuration specifies an operation performed by the AutoLatch.

2 In **Command**, indicate the desired state for the autolatch: **Open** or **Close**.

Configuring the Device Action Step for the Vacuum

To configure the **Device Action** step for the vacuum:

1 From **Device**, select the vacuum performing the required operation.

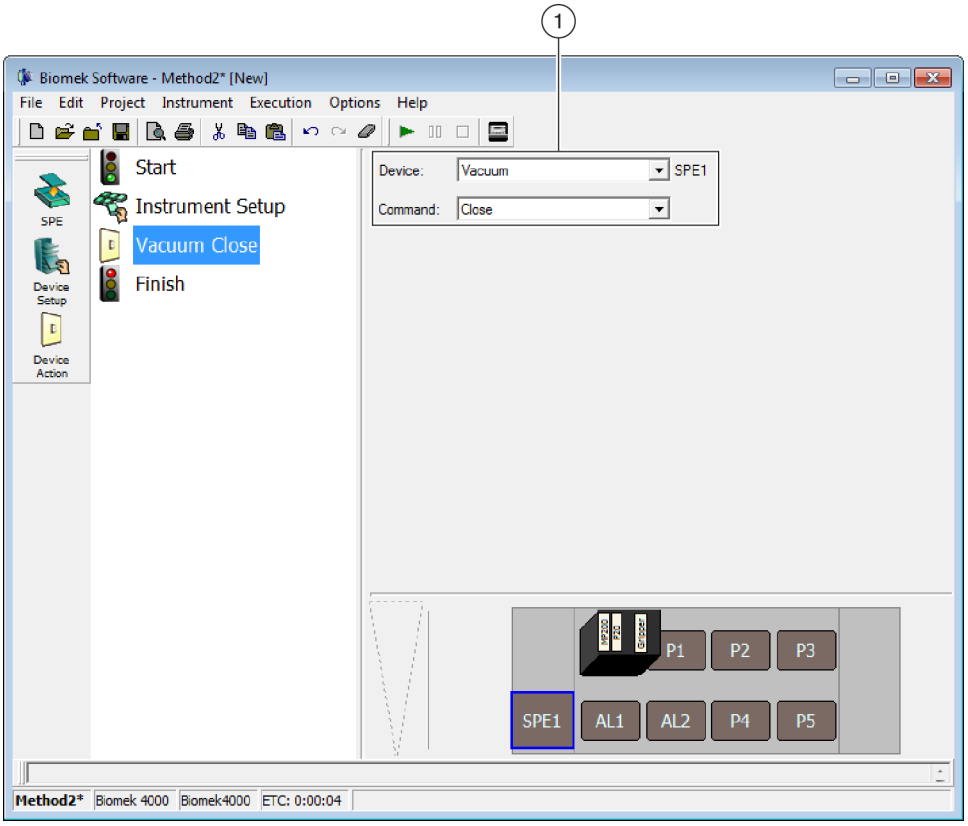
OR

Click on the vacuum in the Current Deck Display to select it.

The configuration for the vacuum appears (Figure 21.11).

NOTE The deck position has a blue border in the Current Deck Display and is displayed to the right of **Device**.

Figure 21.11 Device Action Step for the Vacuum



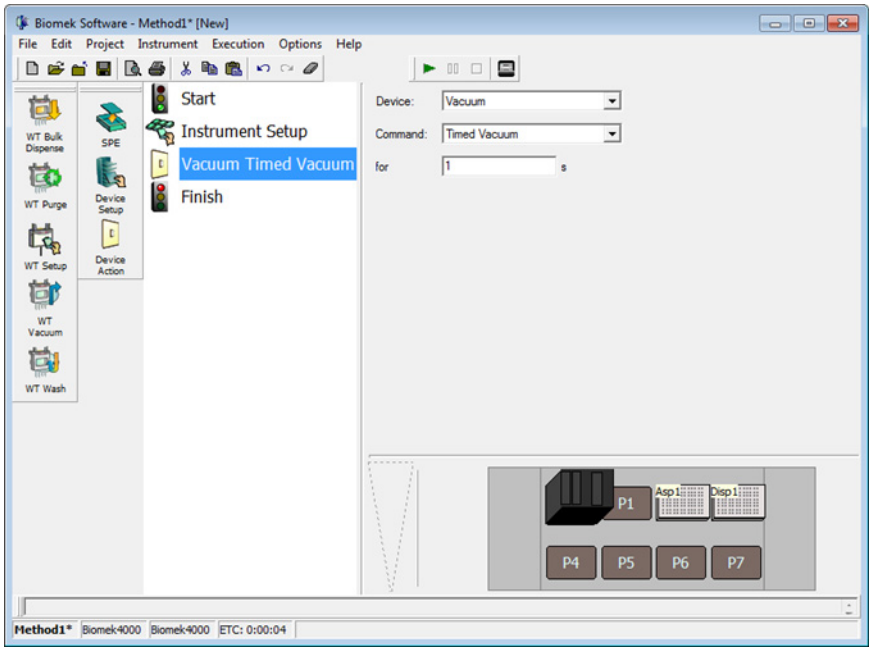
1. **Device Action Step Configuration**: The **Device Action** step configuration specifies an operation performed by the vacuum.

---

2 In **Command**, choose:

- **Close** — To close the vacuum.
- **Open** — To open the vacuum.
- **Timed Vacuum** — To select the vacuum time in seconds. Figure 21.12 appears.

Figure 21.12 Device Action for the Vacuum with Timed Vacuum Chosen



Configuring the Device Action Step for an Orbital Shaker ALP

To configure the **Device Action** step for the Orbital Shaker ALP (for complete instructions on setting up and configuring the Orbital Shaker ALP in Biomek Software, refer to the *Biomek 4000 ALPs and Accessories Manual*):

IMPORTANT Prior to using the Orbital Shaker, follow all precautions described in *Orbital Shaker Safety Information*.

1 From **Device,** select the Orbital Shaker ALP performing the required operation.

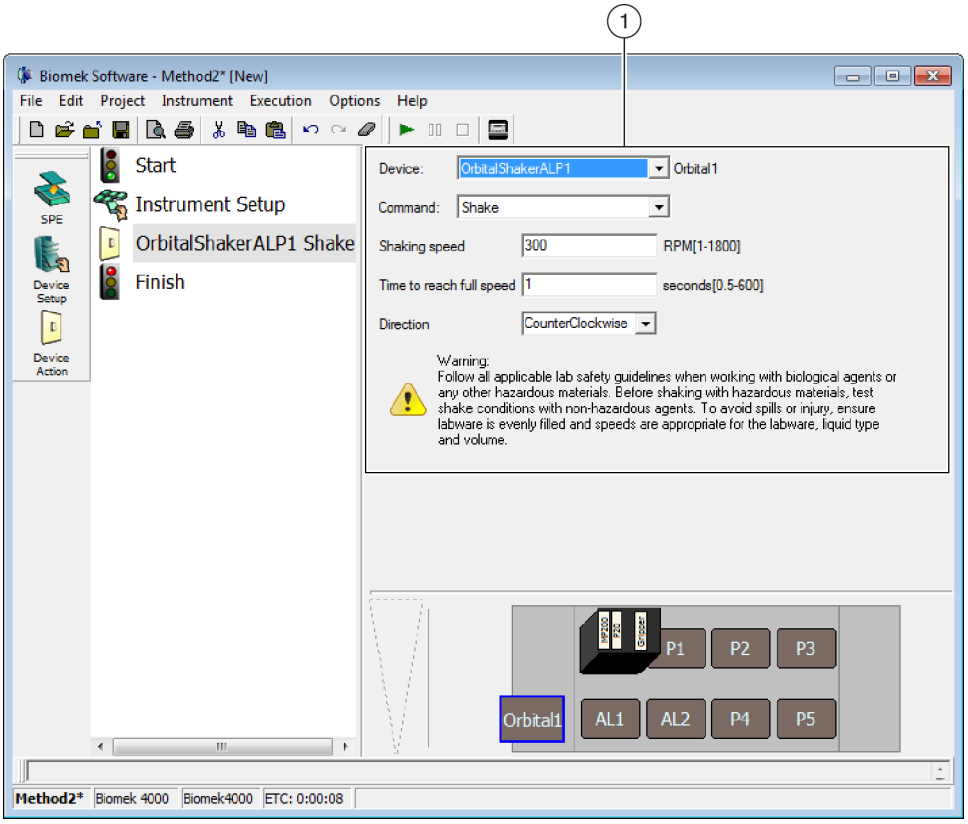
OR

Click on the Orbital Shaker ALP in the Current Deck Display to select it.

The configuration for the Orbital Shaker ALP appears (Figure 21.13).

NOTE The deck position has a blue border in the Current Deck Display and is displayed to the right of **Device**.

Figure 21.13 Device Action Step for the Orbital Shaker



1. **Device Action Step Configuration**: The **Device Action** step configuration specifies an operation performed by the Orbital Shaker.

2 In **Command**, indicate the desired action for the Orbital Shaker.

3 Configure any required parameters for this action. Refer to the *Biomek 4000 ALPs and Accessories Manual* for details.

Orbital Shaker Safety Information

Follow all safety precautions for each device used with the instrument, including, but not limited to, the following preventative measures related to the Orbital Shaker ALP.

⚠ WARNING

Risk of personal injury or equipment damage. Turn off power to the Biomek 4000 Laboratory Automation Workstation before attaching or removing the Orbital Shaker ALP. Failure to do so can cause electrical shock or equipment damage.

Establishing a Safe Maximum Shaking Speed for Orbital Shaker ALPs

The Orbital Shaker ALP supports most labware used on the instrument, although not all labware should be shaken at the same speed. The maximum shaking speed appropriate for each type of labware is of particular concern since fluid in labware may splash or spill at different shaking speeds due to labware parameters and fluid viscosity.

⚠ CAUTION

Risk of Equipment Damage. Non-compliant labware might not be securely grasped by the ALP or might cause physical damage to the ALP. Only labware meeting the ANSI/SBS Microplate Standards listed below is recommended for use on the Orbital Shaker ALP.

- **ANSI/SBS 1-2004: Microplates - Footprint Dimension**
- **ANSI/SBS 2-2004: Microplates - Height Dimensions**
- **ANSI/SBS 3-2004: Microplates - Bottom Outside Flange Dimensions**

⚠ WARNING

Do not shake tip boxes, tip box lids, or reservoirs on the Orbital Shaker ALP. The clamps on the ALP cannot hold tip boxes, tip box lids, or reservoirs securely during a shaking procedure.

Recommended Maximum Shaking Speeds

Recommended maximum shaking speeds were determined for a variety of labware from each class of labware supported by the instrument. A variety of fluids and shaking parameters were used to establish a recommended maximum shaking speed.

⚠ WARNING

Risk of contamination. Do not exceed the recommended maximum shaking speed to ensure labware stays securely clamped on the Orbital Shaker ALP.

Testing on each piece of labware was conducted by filling the labware with the specified liquid to a percentage of the labware's maximum well capacity and executing a shaking operation. The maximum shaking speeds presented in Table 21.3 show the results of testing.

NOTE Table 21.3 should be used only as general reference material. Conduct testing according to the procedures outlined by the laboratory safety officer to determine the safe maximum shaking speed for all labware, liquid, and shaking sequence combinations.

⚠ WARNING

The type and amount of fluid being shaken will impact the maximum shaking speed for all types of labware. Conduct testing according to the procedures outlined by the laboratory safety officer to determine the safe maximum shaking speed for any type and amount of liquid.

⚠ WARNING

Risk of personal injury or property damage. Always observe appropriate cautionary procedures as defined by your safety officer when using flammable solvents or toxic, pathological, or radioactive materials.

⚠ WARNING

Risk of contamination. Uneven fluid distribution could compromise the ability of the clamping mechanism to securely hold the labware. Ensure liquid is distributed evenly prior to using the Orbital Shaker ALP. Maximum recommended shaking speed values in Table 21.3 assume fluid is distributed evenly throughout the plate.

Table 21.3 Recommended Maximum Labware Shaking Speeds

Labware Type	Liquid	With Fluid			Default Maximum Shaking Speed (Empty)[4/]
		Volume in µL[1/]	Volume as %[2/]	Shaking Speed (RPM)[3/]	
10 mm test tubes	Water	2136	51	800	1000
12 mm test tubes	Water	3100	50	400	400
13 mm test tubes	Water	4984	49	700	800
AB384Well Reaction	Water	20	50	1800	1800
BCFlat96	Water	100	27	1700	1800
BCDeep96Round	Water	712	54	1100	1600
BCDeep96Square	Water	1200	50	1100	1400
CostarCone96Round	Water	178	56	1200	1800
CostarCone96Round	Water	100	31	1700	1800

1/**Volume in µL** provides the number of µL of liquid added to each of the wells of the specified labware.
2/**Volume as** % provides the percent of each well filled by the value in **Volume in µL**.
3/**Shaking Speed (RPM)** is the recommended maximum speed the specified piece of labware should be shaken when the labware contains fluid. Exceeding this speed may spill or splash fluid out of the labware.
4/**Default Maximum Shaking Speed (Empty)** is the maximum shaking speed for the specified labware when it is empty. Exceeding this speed may compromise the ability of the clamping mechanism to securely hold the labware (Refer to the *Biomek 4000 ALPs and Accessories Manual*, for additional information on Maximum Shaking Speeds.)

Table 21.3 Recommended Maximum Labware Shaking Speeds *(Continued)*

Labware Type	Liquid	With Fluid			Default Maximum Shaking Speed (Empty)[4/]
		Volume in µL[1/]	Volume as %[2/]	Shaking Speed (RPM)[3/]	
CostarFlat384Square	Water	100	82	1170	1800
Greiner96Ubottom	Water	239	75	1000	1800
Greiner96Ubottom	Water	100	31	1600	1800
GreinerFlat384Square	Water	100	71	1170	1800
GreinerShallow384Round	Water	15	52	1000	1800
Microfuge Tubes	Water	890	40	900	900
NuncFlat384Square	Water	100	64	1170	1800
CostarDeep96Square	Cell Pellet plus buffer	90 + pellet	4	950	1400
CostarDeep96Square	Cell Pellet plus buffer	210 + cells	8	1000	1400
CostarDeep96Square	Cell Pellet plus buffer	330 + cells	13	1000	1400
CostarDeep96Square	Cell Pellet plus buffer plus MagneSil Blue	355 + cells	15	1000	1400
Greiner96Ubottom	MagneSil Blue	30	9	720	1800
Greiner96Ubottom	MagneSil Red	55	17	720	1800
Greiner96Ubottom	MagneSil Red plus buffers	145	46	1000	1800
Greiner96Ubottom	MagneSil Red plus Ethanol	150	47	800	1800
Greiner96Ubottom	MagneSil Red plus water	150	47	1000	1800
Greiner96Ubottom	MagneSil Yellow plus Ethanol	100	31	800	1800
Greiner96Ubottom	MagneSil Yellow plus Wash	100	31	1000	1800
Greiner96Ubottom	MagneSil Yellow plus water	100	31	1000	1800

1/**Volume in µL** provides the number of µL of liquid added to each of the wells of the specified labware.
2/**Volume as %** provides the percent of each well filled by the value in **Volume in µL**.
3/**Shaking Speed (RPM)** is the recommended maximum speed the specified piece of labware should be shaken when the labware contains fluid. Exceeding this speed may spill or splash fluid out of the labware.
4/**Default Maximum Shaking Speed (Empty)** is the maximum shaking speed for the specified labware when it is empty. Exceeding this speed may compromise the ability of the clamping mechanism to securely hold the labware (Refer to the *Biomek 4000 ALPs and Accessories Manual*, for additional information on Maximum Shaking Speeds.)

Configuring the Device Action Step for Active ALPs

Instructions for configuring the **Device Action** step for active ALPs can be found in the *Biomek 4000 ALPs and Accessories Manual*.

CHAPTER 22

Using the Wash Tool Step Palette

Overview

The **Wash Tool** step palette incorporates the steps necessary for wash operations on the Biomek 4000 system. The steps include bulk dispense, purge, setup, vacuum, and wash. These steps are described in Table 22.1.

NOTE The Wash Tool must be installed and configured in **Hardware Setup**. Refer to the *Biomek 4000 Hardware Manual* for more information.

Table 22.1 Wash Tool Step Palette

Step	Icon	Description
Wash Tool Setup		Allows you to define the liquid type(s) currently available on the unit. For instruments with a six port valve installed, you will specify which valves contain liquid, as well as the type of liquid contained in each of those valves.
Wash Tool Bulk Dispense		Performs a bulk dispense operation from a wash liquid container using the selected wash tool.
Wash Tool Purge		Ensures that the lines are primed, purged, and ready for use. If the six port valve is installed on the instrument, this step can also be used to manually change the currently selected liquid.
Wash Tool Vacuum		Vacuums liquid to waste as specified within the step.
Wash Tool Wash		Performs wash operations by alternating between dispensing and vacuuming wash liquid within selected wells.

Displaying the Wash Tool Step Palette

In order to add wash tool steps into a method, first display the **Wash Tool** step palette by doing the following:

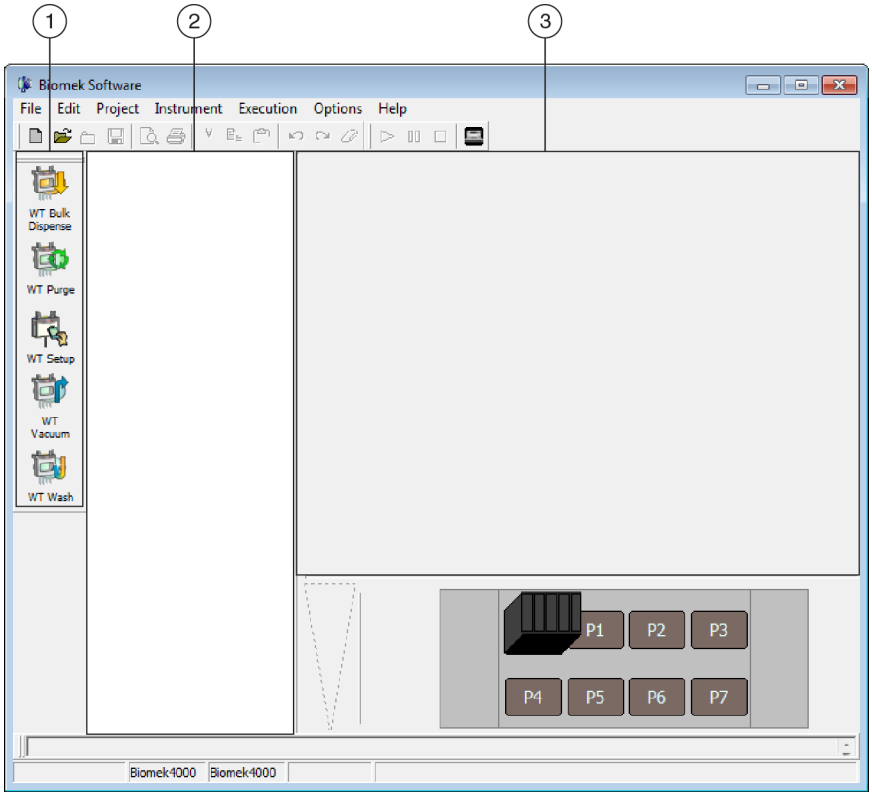
1 Right click any empty palette space, and the step palette menu appears. Select **Wash Tool**.

OR

From the toolbar, select **Options > Toolbars > Wash Tool**.

The **Wash Tool** step palette displays, as shown in (Figure 22.1).

Figure 22.1 Biomek Software Main Editor With Wash Tool Step Palette Displayed



1. **Wash Tool Step Palette**
2. **Method View**: The method is build step-by-step in the Method View.
3. **Step Configuration**: When a step is highlighted in the Method View, the corresponding configuration appears in this area.

Wash Tool Setup Step

The **Wash Tool Setup** step is normally the first wash operation step. This step allows you to configure which liquid(s) will be used by the wash tool. If your workstation has a six port valve installed, you can select which valves contain liquid and specify type of liquid contained those valves. Workstations without a six port valve installed can only use one wash liquid; therefore, you will designate the liquid currently on the wash system.

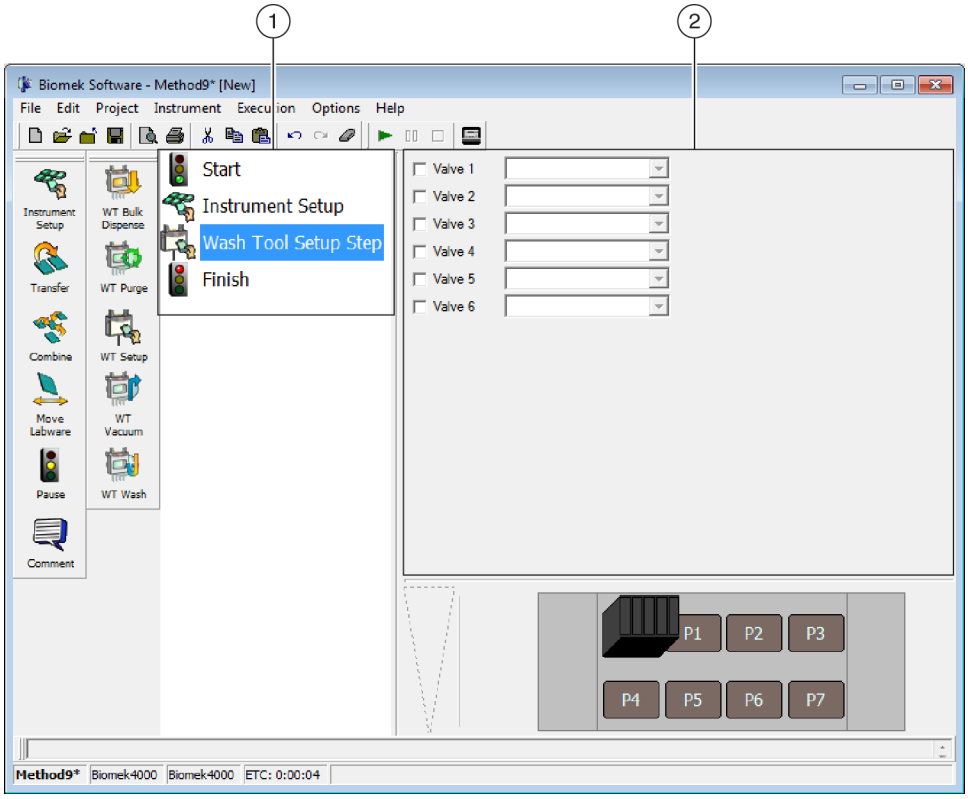
NOTE If the **Instrument Setup** step will be configured to start with a wash tool, the **Wash Tool Setup** step needs to be located prior to the **Instrument Setup** step in the Method View. This allows you to choose the appropriate liquid(s), supporting proper method execution and validation process.

To insert a **Wash Tool Setup** step into a method:

1 Drag and drop the 

icon into the method. The **Wash Tool Setup** step configuration appears (Figure 22.2).

Figure 22.2 Wash Tool Setup Step Configuration (With Six Port Valve Installed)



1. **Method View**: The method displayed contains a **Wash Tool Setup Step**.
2. **Wash Tool Setup Step configuration**:
   - For instruments with the six port valve installed (as shown above), this step configuration allows you to select the valves containing liquid, as well as the specific liquid located in each valve.
   - For instruments containing a single Wash Pump Valve, select the wash liquid located in the valve using this step configuration.

To configure the **Wash Tool Setup** step:

---

1 Select the liquid(s) currently available on the workstation. If your workstation:

- **does not have a six port valve installed:** from the drop-down list, select the wash liquid contained in the wash container.
- **has a six port valve installed:** select the check boxes next to each valve containing wash liquid, and then choose the specific liquid contained within the valve from the drop-down list.

NOTE Each liquid can only be specified once. Selecting the same liquid more than once will result in an error message.

Wash Tool Bulk Dispense Step

The **Wash Tool Bulk Dispense** step is used to dispense liquid using a single-channel or eight-channel wash tool. The wash tools have two needles for each channel: a long vacuum needle and a shorter dispense needle. Liquid is dispensed from the source wash liquid container through the dispense needles. The volume dispensed is limited only by the amount of liquid in the source container.

After dispensing, a **Backup Volume** is aspirated by the dispense needles to prevent droplets from forming on the dispense needles. The **Backup Volume** is set in Wash Tool Liquid Settings (see CHAPTER 8, *Creating New Liquid Types*) or the Pipetting Template Editor (see CHAPTER 10, *Using the Pipetting Template Editor*).

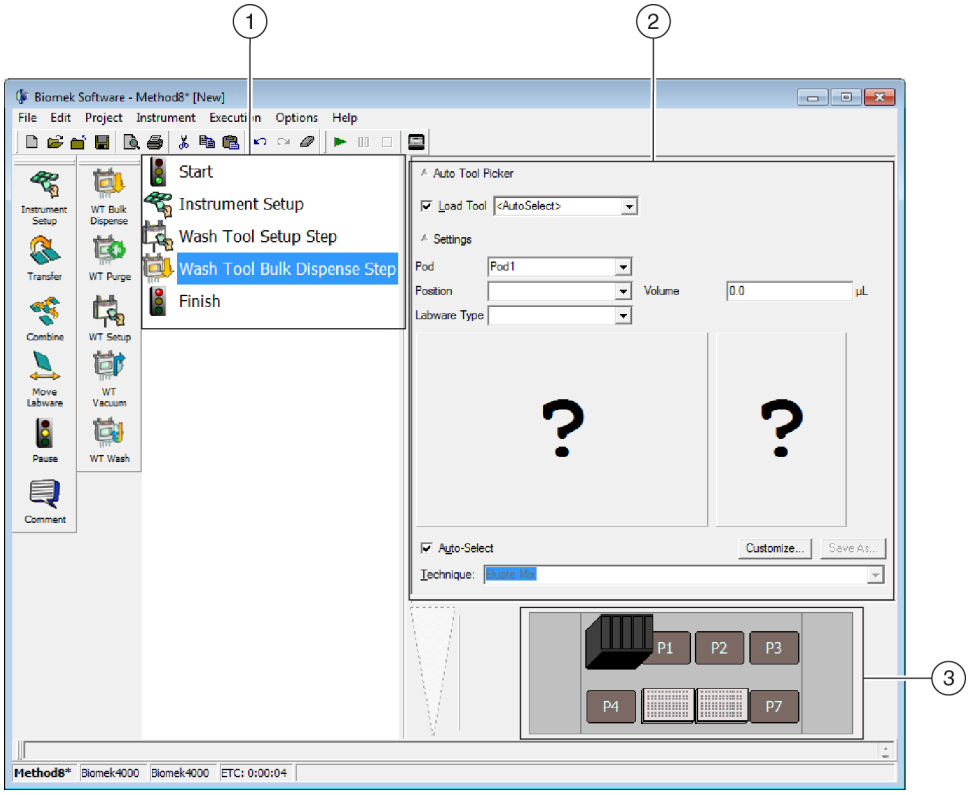
NOTE A Wash Unit must be installed on the Biomek 4000 Laboratory Automation Workstation to dispense liquid using the **Wash Tool Bulk Dispense** step.

To insert a **Wash Tool Bulk Dispense** step into a method:

1 Drag and drop the 

icon into the method. The **Wash Tool Bulk Dispense** step configuration appears (Figure 22.3).

Figure 22.3 Wash Tool Bulk Dispense Step Configuration



1. **Method View**: The Method View displayed contains a **Wash Tool Bulk Dispense Step**.
2. **Wash Tool Bulk Dispense Step configuration**
3. **Current Deck Display**: Select the labware to wash on the Current Deck Display.

To configure the **Wash Tool Bulk Dispense** step:

---

1 If the appropriate tool is not already loaded through a **Load Tool** or **Change Tool** step (from the **Biomek Instrument** step palette), either select the desired wash tool from the **Load Tool** drop-down list, or keep the default selection as **<Auto Select>**, which allows the software to choose the most appropriate tool for the operation.

NOTE Only wash tools are available for selection on the drop-down list.

2 Click the labware in the Current Deck Display that you wish to dispense into. The **Pod**, **Position**, and **Labware Type** for that piece of labware is entered automatically into the **Wash Tool Bulk Dispense** step configuration.

OR

Select a **Pod**, **Position** and **Labware Type** from the drop-down list.

3 On the plate map, select the wells to dispense into.

NOTE Hold (Shift) and click a well to select additional wells without deselecting any wells. Hold (Ctrl) and click a well to toggle the selection status of selected wells without affecting the status of other wells. If (Shift) or (Ctrl) is not held down when selecting wells, any previous selection is deleted.

4 Leave the tip height as is to use the settings specified in the pipetting technique.

OR

Set the dispense height manually using one of the following techniques:

a. Set the dispense height by positioning the cursor over the graphic of a tip inside a well. Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

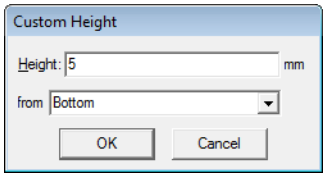
NOTE The cursor changes to a  when positioned over the graphic.

The phrase (**Overrides Technique**) appears below the graphic when the tip height is changed by manipulating the graphic or when the technique is changed with the **Customize** option. For more information on selecting and editing a technique for this method, refer to CHAPTER 9, *Understanding and Creating Techniques*.

b. Click in the graphic of a tip inside a well, and adjust the height using the (PgUp) and (PgDn) and the up and down arrow keys. (PgUp) and (PgDn) change the height by 1 mm at a time; the up and down arrow keys change the height by 0.1 mm at a time.

c. Right click on the graphic of a tip inside a well, and a menu appears. Select **Custom Height**, and the **Custom Height** prompt appears (Figure 22.4). Insert the **height** in millimeters and, in **from**, select a reference point from the drop-down list. Click **OK** to save the edits and return to the **Dispense** step configuration.

Figure 22.4 Custom Height Prompt



NOTE Changes made using the options listed above can be reset to the technique default height by right clicking on the graphic of the tip and selecting **Use Technique Settings**.

To change the point of reference from where aspirations are measured, right click on the graphic of the tip, and, from the pop-up menu, select the option you prefer. Options include the following:

- **Measure from Liquid**—If liquid is present, the surface of the liquid is the reference point.
- **Measure from Bottom**—The bottom of the destination labware is the reference point for the dispense height.
- **Measure from Top**—The top of the destination labware is the reference point for dispense height.

5 For instruments with a six port valve installed, select the liquid type to dispense in the **Wash Liquid** drop-down.

NOTE The liquid type must be one of the liquid types configured for the six port valve in the **Wash Tool Setup** step.

6 In **Volume**, enter the volume to dispense in microliters (µL).

7 The detailed operations of this step are controlled using a technique and template. The software automatically selects a pipetting technique based on the wash liquid type, labware type, tip type, and volume being transferred. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

OR

Choose **Customize** and configure the technique as desired in the **Technique Editor**.

NOTE For more information on customizing, configuring, and saving a technique, refer to CHAPTER 12, *Understanding Techniques*.

8 Select a step that occurs after the **Bulk Dispense** step or the **Finish** step to validate the step configuration.

Wash Tool Purge Step

The **Wash Tool Purge** step is used to rinse the tubing and needles of the tools before use. A purge is automatically performed when a wash tool is loaded or when liquids are switched using the six port valve. The **Wash Tool Purge** step enables another purge to occur at any time during a method. The **Wash Tool Purge** step is useful for rinsing the tubing and wash tool when changing wash liquids using a six port valve.

During a purge, a wash liquid is dispensed through the dispense tubing and dispense needles on the wash tool. At the same time, wash liquid is vacuumed using the vacuum needles on the wash tool and removed to waste through the aspirate tubing. The purge process effectively rinses the wash system tubing and wash tool, preparing it for use with the specified wash liquid.

After a purge operation, the dispense needles aspirate a **Backup Volume** to prevent droplets from forming on the dispense needles. The **Backup Volume** is set in Wash Tool Liquid Settings (see CHAPTER 8, *Creating New Liquid Types*) or the Pipetting Template Editor (see CHAPTER 10, *Using the Pipetting Template Editor*).

NOTE It is recommended to insert a **Wash Tool Purge** step using distilled or deionized water at the end of each method that uses the wash tool to maintain the wash system.

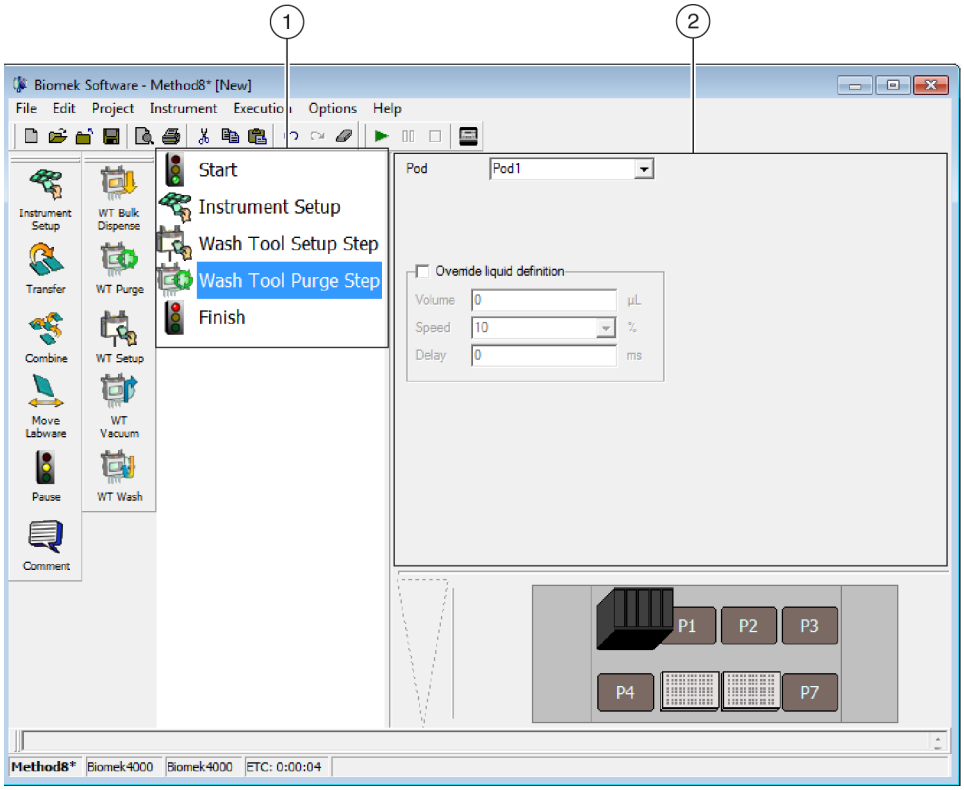
NOTE A Wash Unit must be installed on the instrument to purge using the **Wash Tool Purge** step.

To insert a **Wash Tool Purge** step into the method:

1 Drag and drop the 

icon into the method. The **Wash Tool Purge** step configuration appears (Figure 22.5).

Figure 22.5 Wash Tool Purge Step Configuration



1. **Method View**: The Method View displayed contains a **Wash Tool Purge Step**.
2. **Wash Tool Purge Step configuration**

To configure the **Wash Tool Purge** step:

NOTE A wash tool must be loaded onto the pod using either a **Load Tool** or **Change Tool** step prior to the **Wash Tool Purge** step.

1 If a six port valve is installed, in **Wash Liquid**, select the liquid type to use for the purge.

NOTE If using the **Wash Tool Purge** step with a six port valve, the liquid type must be one of the liquid types configured in the **Wash Tool Setup** step.

2 If a six port valve is installed on your workstation, select **Purge only if chosen liquid is different from the currently selected liquid** to specify that the purge is performed only if you choose a different wash liquid than the liquid currently in use.

NOTE Only one liquid can be primed at a time.

3 Select **Override Liquid Definition** if you wish to specify purge settings unique to this method. This allows you to override the definitions set up in the Wash Tool Liquid Settings window, which are defined when you introduce a new liquid onto the workstation. See CHAPTER 8, *Creating New Liquid Types*, for more information.

a. Enter the desired **Volume** in microliters (µL).

b. Enter the desired **Speed** as a percentage of the maximum speed.

c. Enter the desired **Delay** in milliseconds (ms). **Delay** specifies the amount of time after a purge operation before continuing.

Wash Tool Vacuum

The **Wash Tool Vacuum** step is used to vacuum liquid using a single-channel or eight-channel wash tool to an off-deck waste container. The wash tools have two needles for each channel: a long vacuum needle and a shorter dispense needle. Liquid is removed from the wells using the vacuum needles by applying a suction for a specified amount of time, and is then removed to an off-deck waste container.

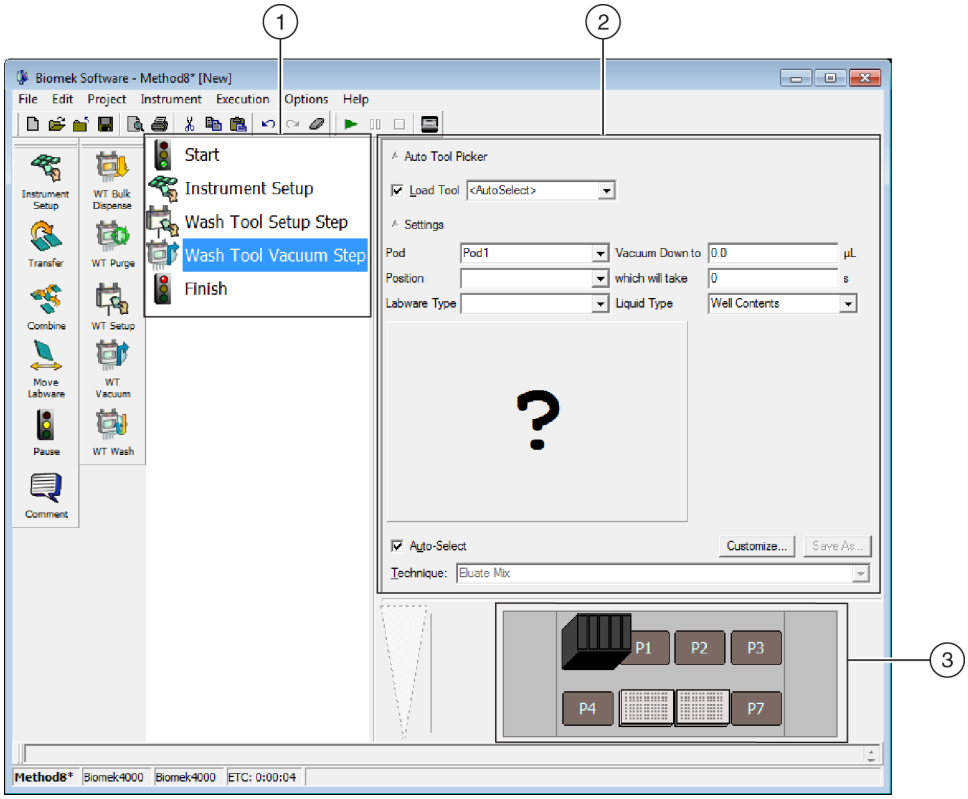
NOTE A Wash Unit must be installed on the instrument and connected to an external vacuum pump or vacuum source to remove liquid using the **Wash Tool Vacuum** step.

To insert a **Wash Tool Vacuum** step into a method:

1 Drag and drop the 

icon into the method. The **Wash Tool Vacuum** step configuration appears (Figure 22.6).

Figure 22.6 Wash Tool Vacuum Step Configuration



1. **Method View**: The Method View displayed contains a **Wash Tool Vacuum** step.
2. **Wash Tool Vacuum step configuration**
3. **Current Deck Display**: Select the labware to vacuum from on the Current Deck Display.

To configure the **Wash Tool Vacuum** step:

---

1 If the appropriate tool is not already loaded through a **Load Tool** or **Change Tool** step (from the **Biomek Instrument** step palette), either select the desired wash tool from the **Load Tool** drop-down list, or keep the default selection as **<Auto Select>**, which allows the software to choose the most appropriate tool for the operation.

NOTE Only wash tools are available for selection on the drop-down list.

---

2 Click the labware in the Current Deck Display from which you intend to vacuum. The **Pod**, **Position**, and **Labware Type** for that piece of labware is entered automatically into the **Wash Tool Vacuum** step configuration.

OR

Select a **Pod**, **Position** and **Labware Type** from the drop-down list.

---

3 In **Vacuum Down to**, enter the amount of liquid that you wish to leave behind in the well (**not** how much liquid to remove from the well).

4 In **which will take**, enter the amount of time it will take to vacuum to the desired level.

TIP The software is not capable of knowing when the volume has reached the desired level. Therefore, you must enter the amount of time that indicates the longest amount of time expected. After the set time elapses, the software assumes that the correct volume is left behind.

5 In **Liquid Type**, either keep the default selection of **Well Contents**, or choose a specific liquid type from the drop-down list.

6 On the plate map, select the wells to vacuum.

NOTE Hold (Shift) and click a well to select additional wells without deselecting any wells. Hold (Ctrl) and click a well to toggle the selection status of selected wells without affecting the status of other wells. If (Shift) or (Ctrl) is not held down when selecting wells, any previous selection is deleted.

7 The software automatically selects a pipetting technique based on the wash liquid type, labware type, tip type, and volume being vacuumed. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

OR

Choose **Customize** and configure the technique as desired in the **Technique Editor**.

NOTE For more information on customizing, configuring, and saving a technique, refer to CHAPTER 12, *Understanding Techniques*.

8 Select a step that occurs after the **Wash Tool Vacuum** step or the **Finish** step to validate the step configuration.

Wash Tool Wash Step

The **Wash Tool Wash** step is used to perform washing operations using a wash tool on the pod. Washing is performed as part of many assays to remove any unbound substrates before further processing.

A typical wash procedure performs the following actions:

1. Blow out any air gaps.
2. Vacuum liquid from wells using vacuum needles on the wash tool and remove it to waste.
3. Dispense desired wash liquid into well.
4. Repeat steps 2 and 3 for a specified number of times.

5. Aspirate the backup.

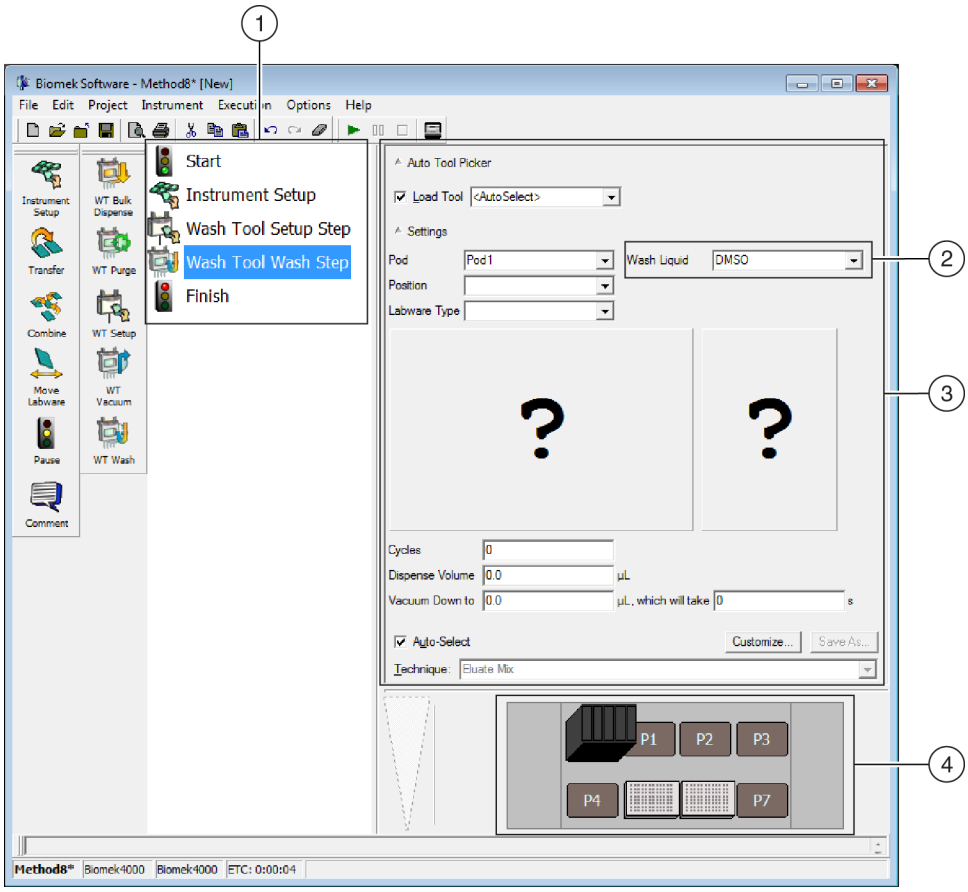
NOTE A Wash Unit must be installed.

To insert a **Wash Tool Wash** step into a method:

1 Drag and drop the 

icon into the method. The **Wash Tool Wash** step configuration appears (Figure 22.7).

Figure 22.7 Wash Tool Wash Step Configuration (With Six Port Valve Installed)



1. **Method View**: The Method View displayed contains a **Wash Tool Vacuum** step.
2. **Wash Liquid**: This field is only available if the six port valve is installed.
3. **Wash Tool Wash step configuration**
4. **Current Deck Display**: Select the labware to wash on the Current Deck Display.

To configure the **Wash Tool Wash** step:

1 If the appropriate tool is not already loaded through a **Load Tool** or **Change Tool** step (from the **Biomek Instrument** step palette), either select the desired wash tool from the **Load Tool** drop-down list, or keep the default selection as **<Auto Select>**, which allows Biomek Software to choose the most appropriate tool for the operation.

NOTE Only wash tools are available for selection on the drop-down list.

2 Click the labware in the Current Deck Display that you intend to wash. The **Pod**, **Position**, and **Labware Type** for that piece of labware is entered automatically into the **Wash Tool Wash** step configuration.

OR

Select a **Pod**, **Position** and **Labware Type** from the drop-down list.

3 For instruments with a six port valve installed, select the liquid type to dispense in the **Wash Liquid** drop-down.

NOTE This field does not appear if a six port valve in not installed on your workstation.

NOTE The liquid type must be one of the liquid types configured for the six port valve in the **Wash Tool Setup** step.

4 On the plate map, select the wells to wash.

NOTE Hold Shift and click a well to select additional wells without deselecting any wells. Hold Ctrl and click a well to toggle the selection status of selected wells without affecting the status of other wells. If Shift or Ctrl is not held down when selecting wells, any previous selection is deleted.

5 Leave the height as is to use the settings specified in the pipetting technique.

OR

Set the height manually using one of the following techniques:

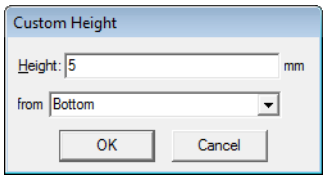
a. Set the height by positioning the cursor over the graphic of a tip inside a well. Click and drag the graphic up or down. The tip moves with the cursor, and the height displayed below the graphic is adjusted as the graphic is manipulated.

NOTE The cursor changes to a  when positioned over the graphic.

(**Overrides Technique**) appears below the graphic when the tip height is changed by manipulating the graphic or when the technique is changed with the **Customize** option. For more information on selecting and editing a technique for this method, refer to CHAPTER 9, *Understanding and Creating Techniques*.

b. Right click on the graphic of a tip inside a well, and a menu displays. Select **Custom Height**, and the **Custom Height** prompt displays (Figure 22.8). Insert the **height** in millimeters and, in **from**, select a reference point from the drop-down list. Click **OK** to save the edits and return to the **Aspirate** step configuration.

Figure 22.8 Custom Height Prompt



c. Click in the graphic of a tip inside a well, and adjust the height using the PgUp and PgDn and the up and down arrow keys. PgUp and PgDn change the height by 1 mm at a time; the up and down arrow keys change the height by 0.1 mm at a time.

NOTE Changes made using the options listed above can be reset to the technique default height by right clicking on the graphic of the tip and selecting **Use Technique Settings**.

To change the point of reference from where aspirations are measured, right click on the graphic of the tip, and, from the pop-up menu, select the option you prefer. Options include the following:

- **Measure from Liquid**—The surface of the liquid is the reference point. The value should be negative, as this indicates that the aspiration occurs below the surface of the liquid.
- **Measure from Bottom**—The bottom of the source labware is the reference point for the aspiration height.
- **Measure from Top**—The top of the source labware is the reference point for aspiration height. The value should be a negative number, as this indicates that the liquid is aspirated from below the top of the well.

6 In **Cycles**, enter the number wash cycles to perform (dispense/vacuum steps) within each well.

7 In **Dispense Volume**, enter the volume of wash liquid microliters (µL) to dispense for each cycle.

8 In **Vacuum Down to**, enter the amount microliters (µL) of wash liquid to leave in the well after the vacuum step. In **which will take**, enter the amount of time to complete the **Vacuum Down to** operation for each cycle.

TIP Biomek Software is not capable of knowing when the volume has reached the desired level. Therefore, you must enter the amount of time that indicates the longest expected time. After the set time elapses, the software assumes that the correct volume is left behind.

9 The detailed operations of this step are controlled using a technique and template. The software automatically selects a pipetting technique based on the wash liquid type, labware type, tip type, and volume being dispensed. To override this selection, deselect **Auto-Select** and choose the desired **Technique**.

OR

Choose **Customize** and configure the technique as desired in the **Technique Editor**.

NOTE For more information on customizing, configuring, and saving a technique, refer to CHAPTER 12, *Understanding Techniques*.

CHAPTER 23

Using the DataSets Step Palette

Overview

Steps on the **DataSets** step palette allow data sets to be created, managed, used, and reported in Biomek methods. Data sets allow sample tracking which means the contents of the plate or tube are known at any time in the method and decisions may be made during transfer or pipetting operations based on the contents of the plate or tube.

NOTE Refer to CHAPTER 14, *Using Sample Tracking and Data Sets in a Method*, for more information on using sample tracking and data sets in a method.

The steps available on the **DataSets** step palette are in Table 23.1:

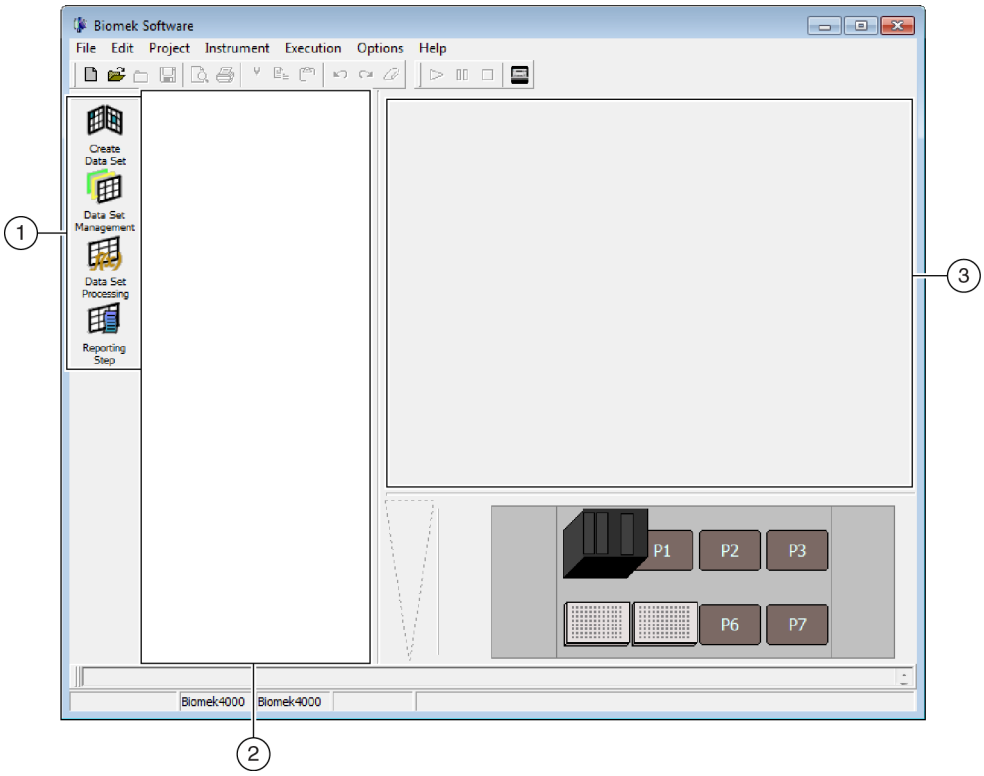
Table 23.1 DataSets Step Palette

Step	Icon	Description
Create Data Set		Specifies data in a data set.
Data Set Management		Renames, removes, copies, or modifies the properties of a data set.
Data Set Processing		Applies a transformation expression to an existing data set to create a new data set.
Reporting		Generates a report on data sets at any point during a method.

Displaying the DataSets Step Palette

In order to add data set steps to a method, display the **DataSets** step palette (Figure 23.1).

Figure 23.1 Biomek Software Main Editor with DataSets Step Palette Displayed



1. **DataSets Step Palette**: Displays the steps available for insertion into a method. Additional step palettes are available.
2. **Method View**: The method is built step by step in this area.
3. **Step Configuration**: When a step is highlighted in a Method View set the corresponding configuration in this area.

To display the **DataSets** step palette:

1 Right click any empty palette space, and select **DataSets** from the menu.

OR

From the toolbar, select **Options > Toolbars > DataSets.**

Configuring the Create Data Set Step

The **Create Data Set** step is used to create data sets from a text file or a database table. The specified file or database table is read and compared to either the plate bar code and well number of the plate or a data set specifying the sample ID. Data sets are created from the specified columns of the file or database table using the rows that matched the plate bar code and well number or data set specifying the sample ID.

NOTE The text file must reside on the local computer.

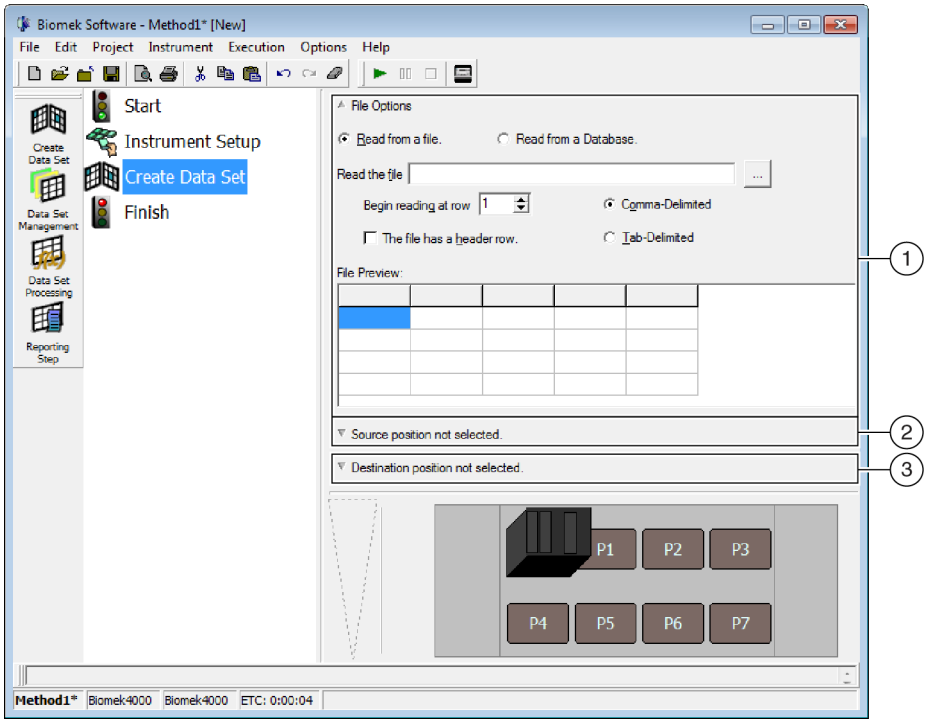
NOTE SQL Server 2005 is the version requirement to import the database table.

To insert a **Create Data Set** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 23.2).

Figure 23.2 Create Data Set Step Configuration



1. **File Options**
2. **Input Options**
3. **Output Options**

The **Create Data Set** step consists of three collapsible configuration areas. Each area can be collapsed or expanded independently from each other to display the configuration options for the section (Figure 23.2). To collapse or expand any of the configuration areas, click on the sentence summary.

Configuring the **Create Data Set** step includes configuring:

- the file or database to read (refer to *Configuring File Options*)
- the columns of the file or database table to compare (refer to *Configuring Input Options*)
- the columns of the file or database table used to create data sets (refer to *Configuring Output Options*)

Configuring File Options

File Options is used to select a comma- or tab-delimited text file (refer to *Reading from a Text File*) or a database table (refer to *Reading from a Database Table*) to use to create data sets for a piece of labware.

Reading from a Text File

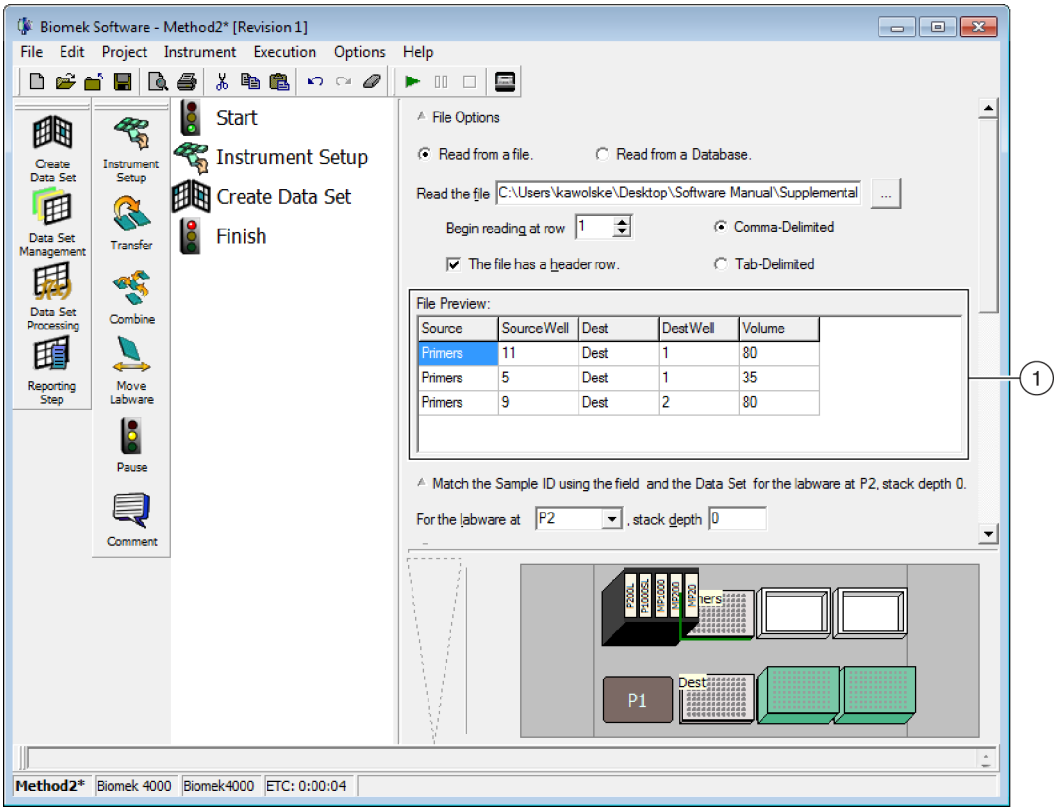
To configure **File Options** to read from a file:

---

1 If not expanded, select the sentence summary to display **File Options** (Figure 23.3).

NOTE By default, **File Options** is expanded when a **Create Data Set** step is inserted.

Figure 23.3 Create Data Set Step—File Options Displayed



1. **File Preview**

2 Under **File Options**, select **Read from a file.**

3 In **Read the file**, enter the full directory path and file name of the text file to read and press **Enter**. The first four rows of the selected data file are displayed in **File Preview**.

OR

Use the ... button to locate and select the file.

NOTE The text file must reside on the local computer.

4 In **Begin reading at row**, select the first row of the data file that should be read. **File Preview** updates.

5 Select **The file has a header row** if a header row is included in the data file. The first row that is read is used for column headings in the **File Preview** (Figure 23.3). For example, if **Begin reading at row** is set to 5 and **The file has a header row** is selected, the contents of row 5 are used as the column headings.

NOTE If **The file has a header row** is not selected, column headings are given a generic label **Column#**.

6 Select the appropriate file type option: **Comma-Delimited** or **Tab-Delimited. File Preview** updates accordingly.

Reading from a Database Table

File Options can be configured to read data from a database table stored in the SQL Server database.

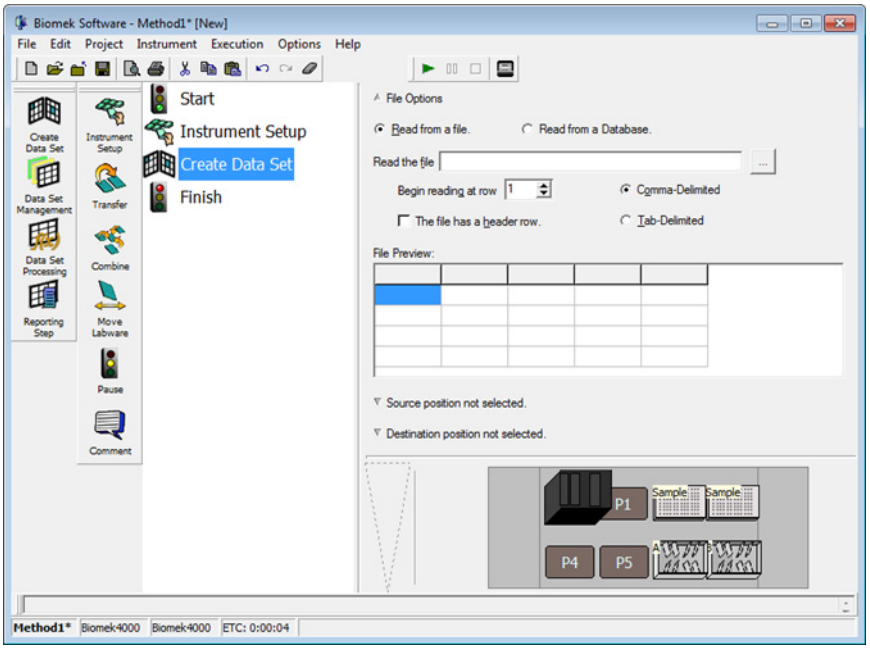
NOTE SQL Server is a Microsoft product that allows queries and provides analysis, and is required to run Biomek Software. The installation of this product is the responsibility of the user and is not supported by Beckman Coulter Representatives. SQL Server 2005 is the version requirement.

To configure **File Options** to read from a database:

1 If necessary, select the sentence summary to display **File Options** (Figure 23.4).

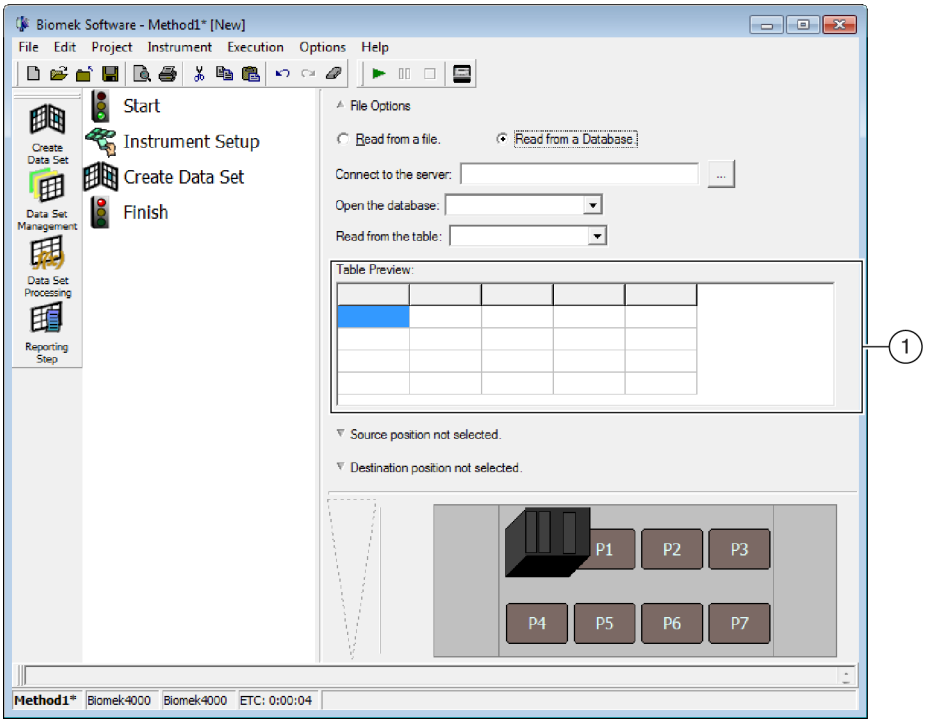
NOTE **File Options** is expanded when a **Create Data Set** step is inserted.

Figure 23.4 Create Data Set Step—File Options Displayed



2 Under **File Options**, select **Read from a Database. File Options** changes to display the database options (Figure 23.5).

Figure 23.5 Reading From a Database

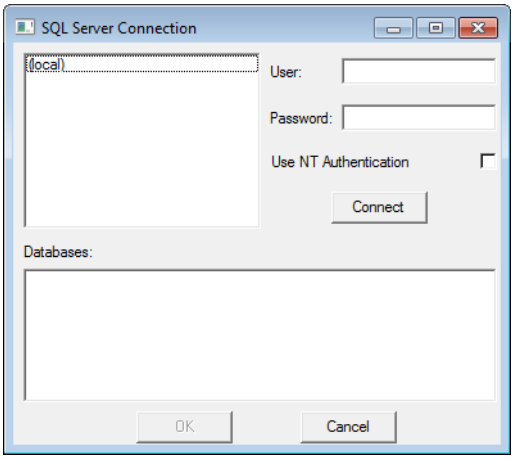


1. **Table Preview**: Displays the first four rows of the database table.

3 Browse to find the location of the desired database on that server. **SQL Server Connection** (Figure 23.6) appears on top of the **Create Data Set** step configuration.

NOTE SQL Server is a Microsoft product that allows queries and provides analysis. Installing this product is the responsibility of the user and is not supported by Beckman Coulter Representatives. SQL Server 2005 is the version requirement.

Figure 23.6 SQL Server Connection



4 Select the desired server from the list of servers on the left.

5 Enter the **User** name and **Password** to log in to the selected server.

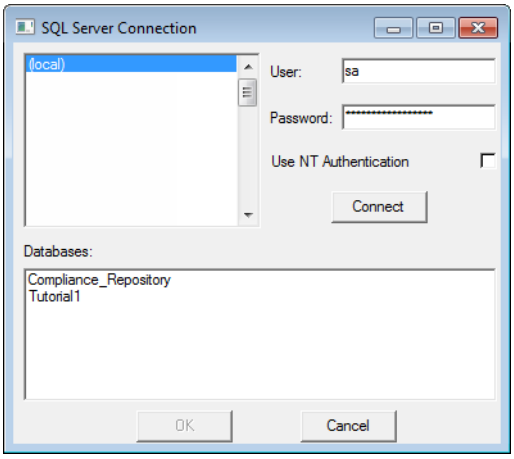
OR

Select **Use NT Authentication**.

NOTE The administrator of the **SQL Server Connection** sets the logging protocol for the user and password or NT authentication.

6 Choose **Connect**. A list of the available databases appear in **Databases** (Figure 23.7).

Figure 23.7 Connected to SQL Server



7 In **Databases**, select the desired database found on the server to use to create data sets.

OR

Repeat steps 3-6 to connect to a different server, if desired.

8 Choose **OK** to accept the server and close **SQL Server Connection**.

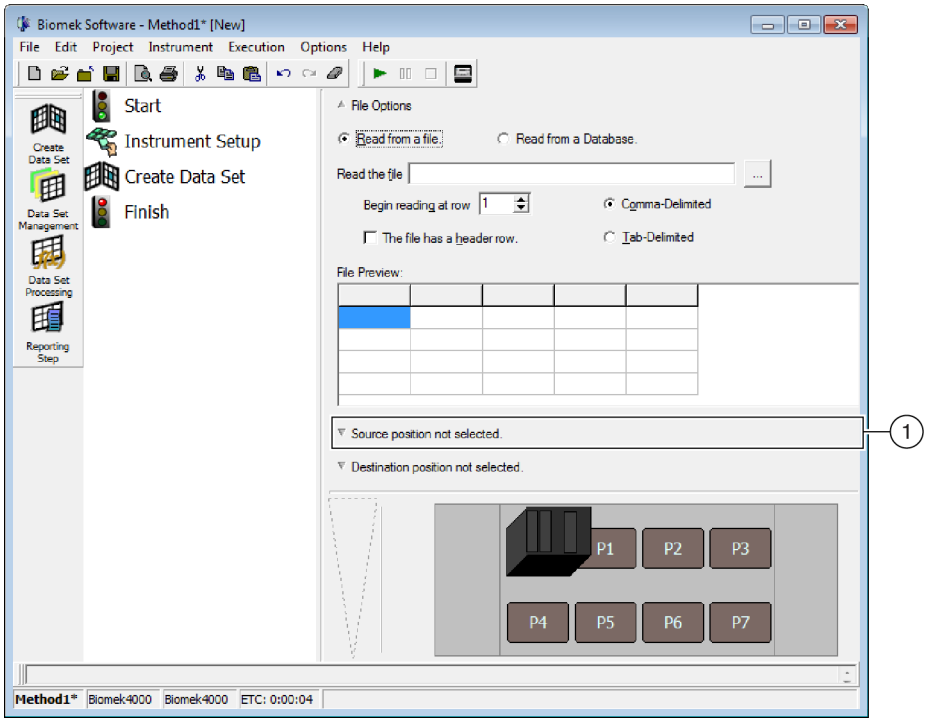
9 In **Read from the table** (Figure 23.5), select the database table to read. The first four rows of the selected database table are displayed in **Table Preview** (Figure 23.5).

Configuring Input Options

Input Options (Figure 23.9) is used to configure the columns of the file or database table to compare to the plate bar code and well number or data set specifying the sample ID of the specified plate. Rows that match the plate bar code and well number or data set specifying the sample ID are used to create the data set(s).

By default, **Input Options** is collapsed when a **Create Data Set** is inserted into a method (Figure 23.8).

Figure 23.8 Create Data Set Step—Expanding Input Options

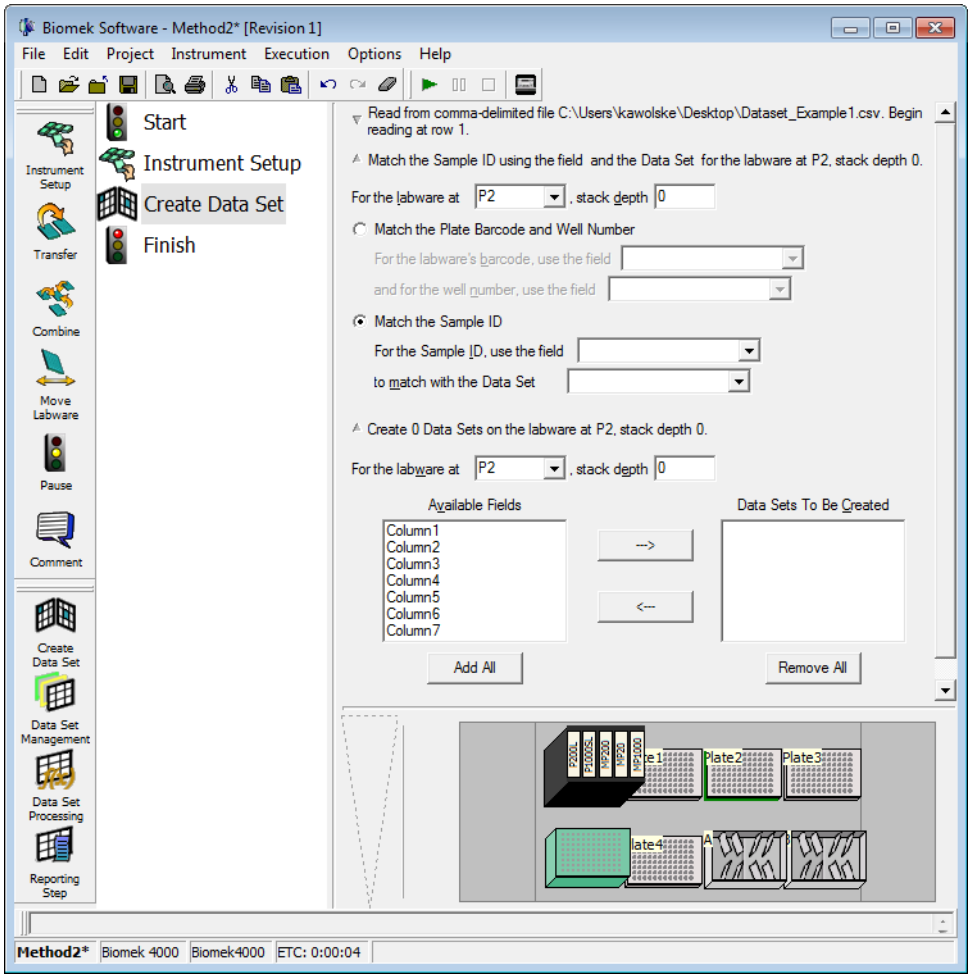


1. **Collapsed Input Options**

To expand **Input Options:**

1 Click on the sentence summary (Figure 23.9).

Figure 23.9 Create Data Set Step—Input Options Displayed



Matching Plate Bar Code and Well Number

The specified file or database table is compared to the plate bar code and well number to determine which rows of the file or database table to use to create the data set. Only the rows of the file or database table that match the plate bar code are used. The column for well number is used to assign the correct value of the data set to each well.

To configure **Input Options** to match the plate bar code and well number:

---

1 In **For the labware at**, select the deck position of the labware to compare the plate bar code and well number or data set specifying the sample ID to the file or database table (Figure 23.9).

OR

Click on the desired labware in the Current Deck Display.

2 If the labware is in a stack, enter the **stack depth**.

NOTE Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to CHAPTER 7, *Biomek Stacking Rules*, for information on using stacks.

3 Select **Match the Plate Barcode and Well Number** to compare the plate bar code and well number of the selected plate to the file or database table (Figure 23.9).

4 In **For the labware's barcode, use the field**, select the column of the file or database table to compare to the plate bar code.

NOTE **For the labware's barcode, use the field** is optional. If no field is specified, all rows of the file or database table are assumed to apply to that plate. If a well number is repeated, the last row of the file or database table to use that well number is used.

5 In **and for the well number, use the field**, select the column of the file or database table to compare to the well number.

Matching Sample IDs

The specified file or database table is compared to a data set that specifies the sample IDs for the selected plate to determine which rows of the file or database table to use to create the data set. Only the rows of the file or database table that match one of the sample IDs on the plate are used to create data sets.

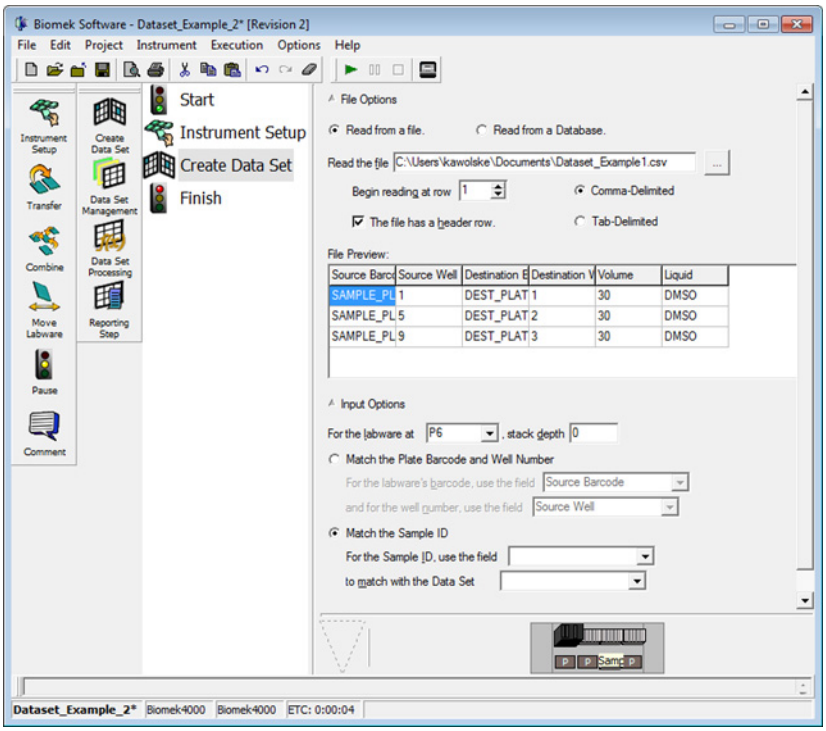
To configure **Input Options** to match the Sample ID:

1 In **For the labware** at, select the deck position of the labware to compare the data set specifying the sample ID to the file or database table (Figure 23.10).

OR

Click on the desired labware in the Current Deck Display.

Figure 23.10 Create Data Set Step—Input Options Displayed



2 If the labware is in a stack, enter the **stack depth**.

NOTE Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to CHAPTER 7, *Biomek Stacking Rules*, for information on using stacks.

3 Select **Match the Sample ID** to compare a data set specifying the sample IDs for the selected plate to the file or database table (Figure 23.10).

4 In **For the Sample ID, use the field**, select the column of the file or database table to compare to the data set specifying sample IDs for the plate.

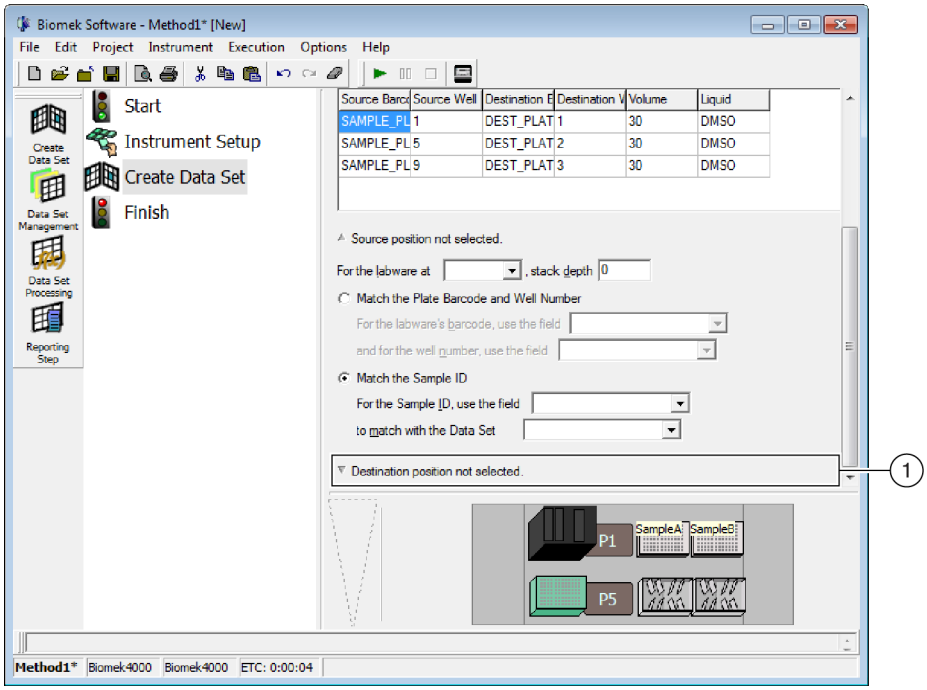
5 In **to match with the Data Set**, select the data set that specifies the sample IDs for the plate.

Configuring Output Options

Output Options is used to configure the plate for which data sets are created and to specify the columns of the file or database table to use to create data sets.

By default, **Output Options** is collapsed when a **Create Data Set** is inserted into the Method View.

Figure 23.11 Create Data Set Step—Exapnding Output Options

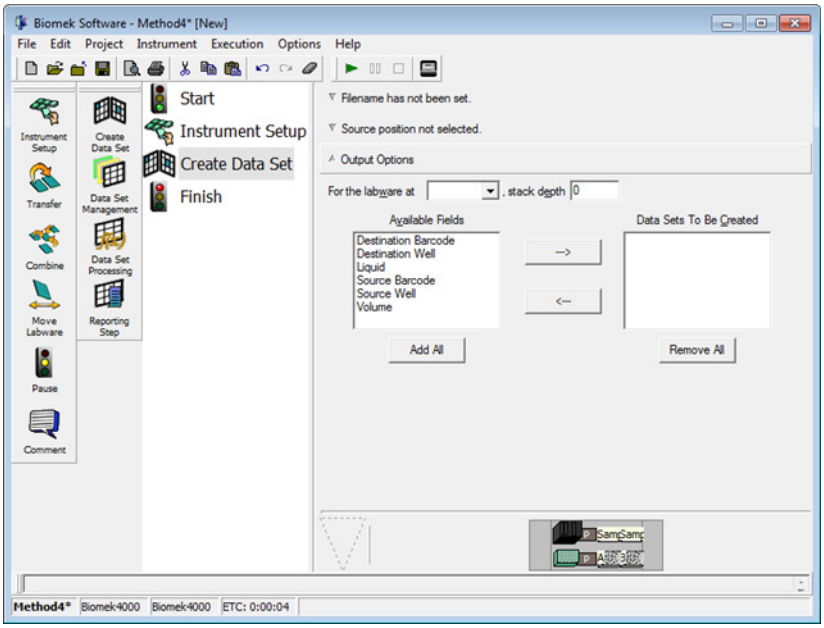


1. **Collapsed Output Options**: Click on the sentence summary to expand **Output Options**.

To configure **Output Options:**

1 Click on the sentence summary to expand the **Output Options** configurations (Figure 23.12).

Figure 23.12 Create Data Set Step—Output Options



2 In **For the labware at**, select the deck position of the labware for which data sets are created.

OR

Click on the desired labware in the Current Deck Display.

3 If the labware is in a stack, enter **stack depth**.

NOTE Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to CHAPTER 7, *Biomek Stacking Rules*, for information on using stacks.

4 Under **Available Fields**, select the desired columns from the file or database table from which to create data sets. The selected fields appear highlighted.

5 Select - - -> to move the selected fields to **Data Sets to be Created**.

NOTE To add all columns from **Available Fields** to **Data Sets to be Created** select **Add All**.

6 To remove an option from **Data Sets to be Created**, select the desired data set to remove and select <---. The selected field(s) are moved back to **Available Fields**.

NOTE To remove all columns from **Data Sets to be Created**, select **Remove All**.

Setting Data Set Properties

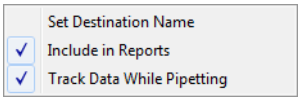
Properties for each data set can be modified in **Output Options** by right clicking on the data set name under **Data Sets to be Created**. Properties that can be modified are:

- data set name
- including the data set in reports
- tracking the data set during pipetting

To modify properties of a data set:

1 In **Data Sets to be Created**, right click the desired data set. The data set properties menu appears.

Figure 23.13 Changing Data Set Priorities



2 Select the desired option from the menu:

- Select **Set Destination Name** and enter a new name for the data set to rename the data set.
- Select **Include in Reports** to allow the data set to be included in the reports chosen in the **Reporting** (refer to *Configuring the Reporting Step*) or **Finish** steps (refer to CHAPTER 12, *Configuring the Finish Step*).
- Select **Track Data While Pipetting** to allow the system to track the data during pipetting operations.

NOTE When **Track Data While Pipetting** is selected, the data set is copied to the destination labware during pipetting.

3 Repeat steps 1 and 2 to select additional options, if desired.

Configuring the Data Set Management Step

The **Data Set Management** step is used to manage data sets that have been created automatically or created using the **Instrument Setup** step, the **Create Data Set** step, the **SILAS** step, or Visual Basic scripting.

NOTE Data sets are not created or processed in the **Data Set Management** step.

Managing data sets includes using the **Data Set Management** step for:

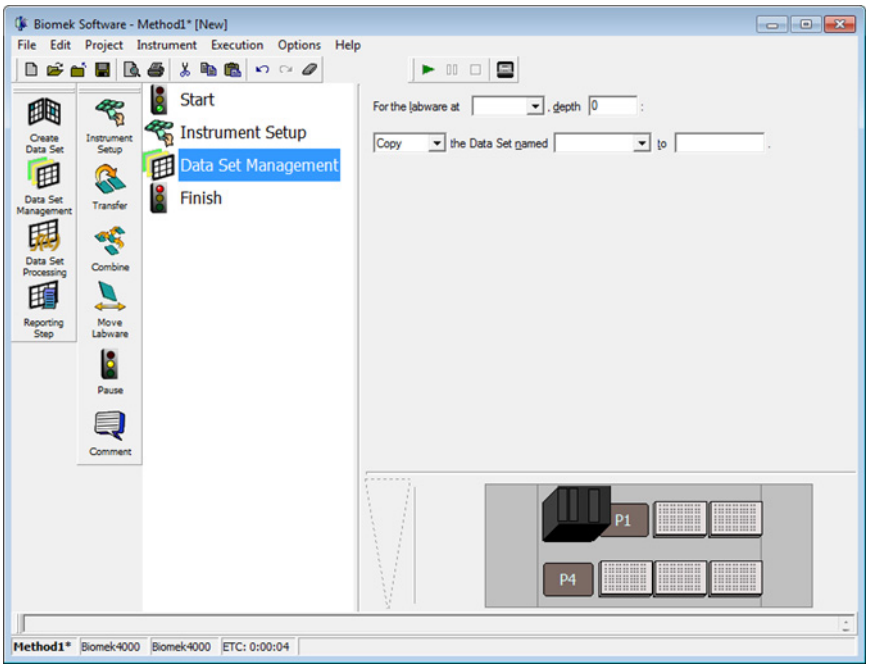
- *Copying a Data Set*.
- *Renaming a Data Set*.
- *Removing a Data Set*.
- *Changing the Properties of a Data Set*.

Copying a Data Set

To copy a data set:

1 Insert a **Data Set Management** step into the Method View. The **Data Set Management** step configuration appears (Figure 23.14).

Figure 23.14 Choosing Copy in Data Set Management Step



2 From **For the labware at**, choose the labware where the data set is copied.

3 If in a stack, enter the **depth** of the labware.

NOTE Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to CHAPTER 7, *Biomek Stacking Rules*, for information on using stacks.

4 From the drop-down menu, choose **Copy**.

5 From **the Data Set named**, choose the data set to copy.

NOTE Each data set must have a unique name. The method displays an error during validation if two data sets have the same name.

6 At **to**, enter the name of the coped data set. A copy of the data set is created with the entered name.

Renaming a Data Set

Rename renames a data set. Renaming data sets is an important function for sample tracking because only one data set named **Sample ID** can exist on a single piece of labware. When another data set is created from the **Instrument Setup** step using sample IDs, it overwrites the previous data set.

Rename a data set when sample IDs from the **Instrument Setup** are necessary for a transfer operation and then another set of sample IDs is necessary for a second transfer operation. For example, the name of the first **Sample ID** data set can be used to maintain a record of the first transfer operation and then the second **Sample ID** data set may be renamed before the second transfer operation.

NOTE Each data set must have a unique name. The method displays an error during validation if two data sets have the same name.

NOTE Refer to CHAPTER 15, *Creating the SampleID Data Set Using the Instrument Setup Step*, for more information on creating the **Sample ID** data set using the **Instrument Setup** step.

To rename a data set:

1 Insert a **Data Set Management** step into the Method View. The **Data Set Management** step configuration appears (Figure 23.14).

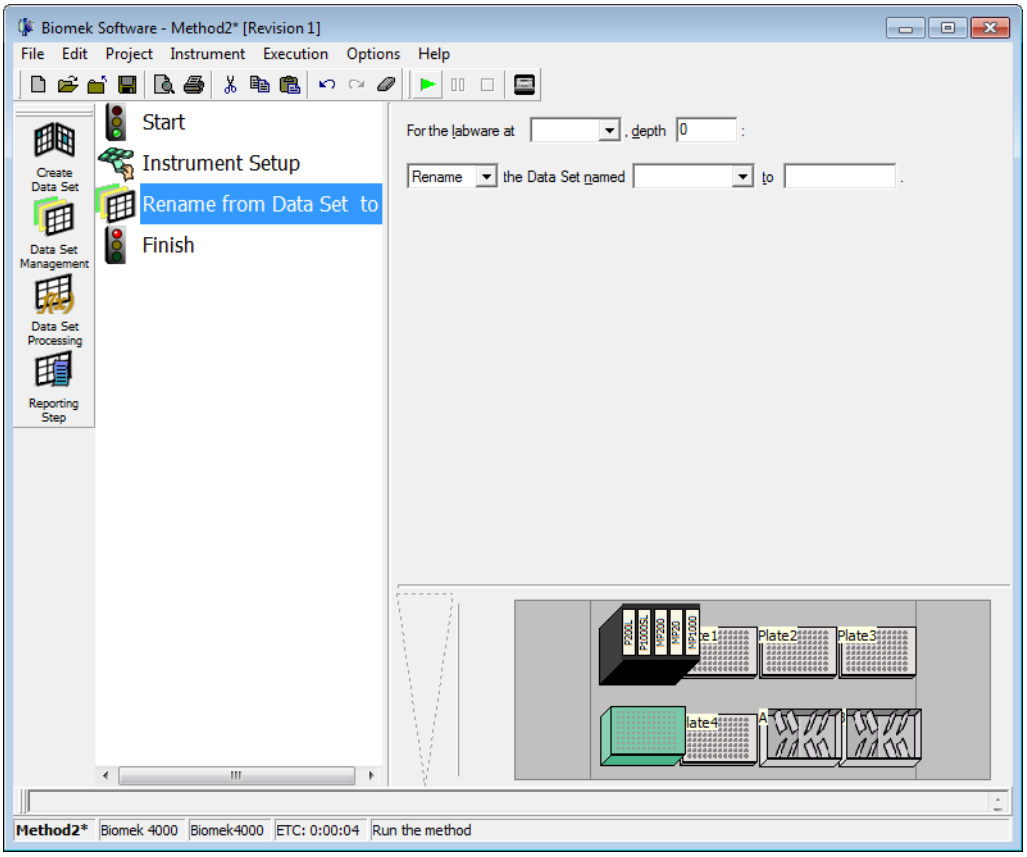
2 From **For the labware at**, choose the labware where the data set is renamed.

3 If in a stack, enter the **depth** of the labware.

NOTE Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to CHAPTER 7, *Biomek Stacking Rules*, for information on using stacks.

4 From the drop-down menu, choose **Rename.** Figure 23.15 appears.

Figure 23.15 Choosing Rename in Data Set Management Step



5 From **the Data Set named**, choose the data set to rename.

NOTE Each data set must have a unique name. The method displays an error during validation if two data sets have the same name.

6 At **to**, enter the new name of the data set. The data set is renamed.

Removing a Data Set

When a data set is no longer needed, it my be removed.

To remove a data set:

1 Insert a **Data Set Management** step into the Method View. The **Data Set Management** step configuration appears (Figure 23.14).

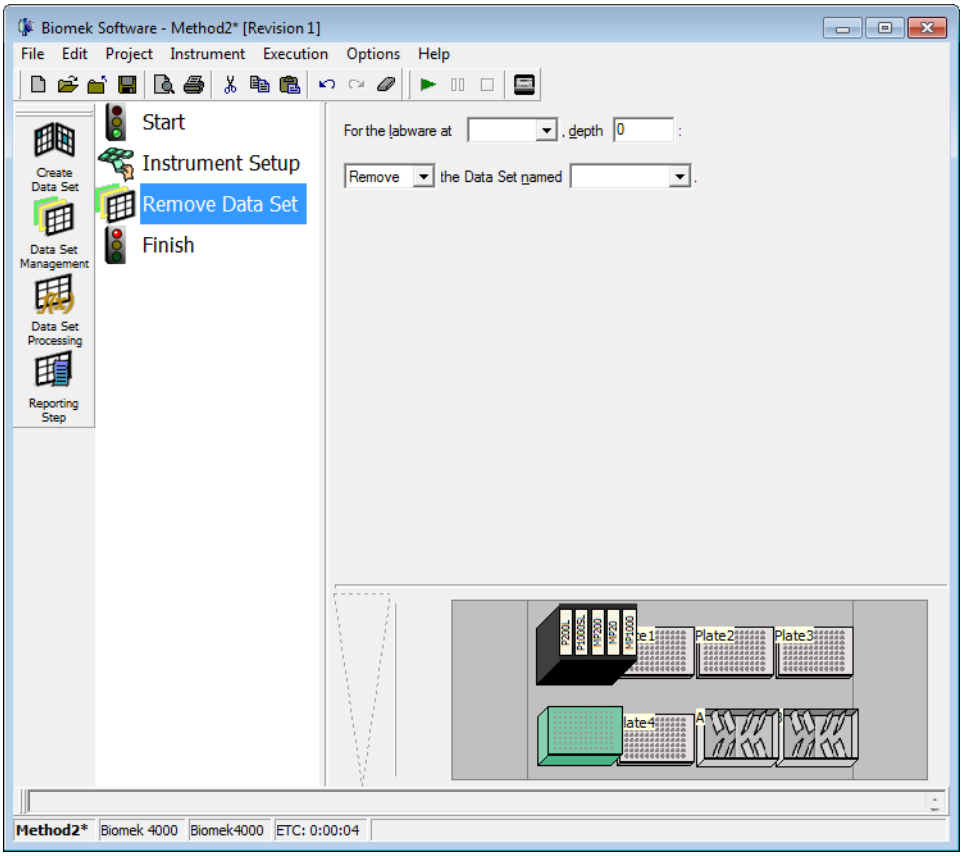
2 From **For the labware at**, choose the labware where the data set is removed.

3 If in a stack, enter the **depth** of the labware.

NOTE Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**:, to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to CHAPTER 7, *Biomek Stacking Rules*, for information on using stacks.

4 From the drop-down menu, choose **Remove.** Figure 23.16 appears.

Figure 23.16 Choosing Remove in Data Set Management Step



5 From **the Data Set named**, choose the data set to remove. The data set is removed.

Changing the Properties of a Data Set

When **Change** is chosen in the **Data Set Management** step, two options are available:

- Including or not including the data set in reports.
- Tracking or not tracking the data in the data sets during pipetting

To change the reporting properties of the data set:

1 Insert a **Data Set Management** step into the Method View. The **Data Set Management** step configuration appears (Figure 23.14).

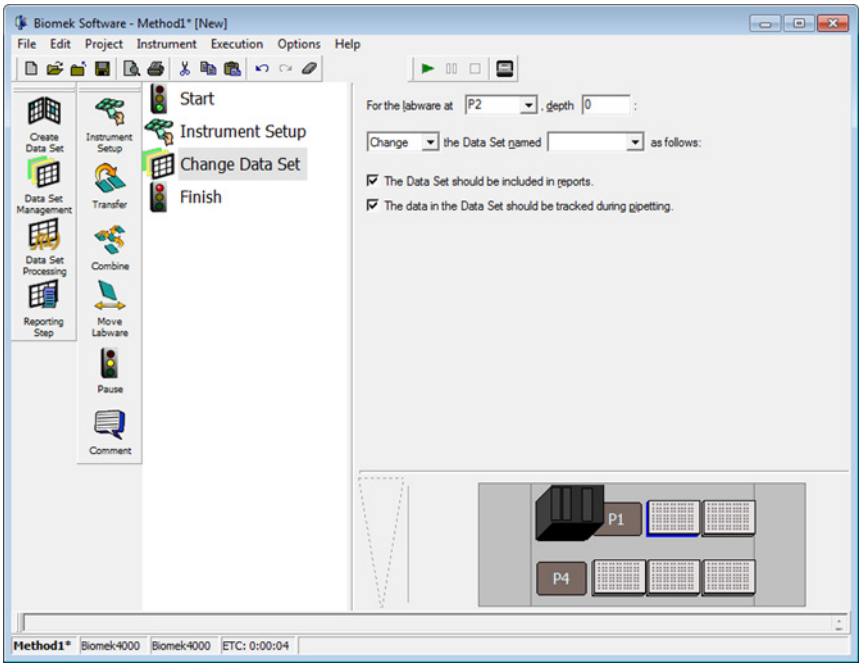
2 From **For the labware at**, choose the labware where the data set properties are changed.

3 If in a stack, enter the depth of the labware.

NOTE Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter 0; to use the second from the top piece of labware, enter 1; to use the third from the top piece of labware, enter 2; and so on. Refer to CHAPTER 7, *Biomek Stacking Rules*, for information on using stacks.

4 From the drop-down menu, choose **Change**. Figure 23.17 appears.

Figure 23.17 Change Chosen on Data Set Management Step Configuration



5 From **the Data Set named**, choose the data set to be changed.

6 Ensure **The Data Set should be included in reports** is checked to allow the data set to be included in the reports chosen in the **Reporting** or **Finish** steps.

7 Ensure **The data in the Data Set should be tracked during pipetting** is checked to allow the system to track the data during pipetting operations.

NOTE If the data set applies only to the source labware and should not be tracked, do not check **The data in the new Data Set should be tracked during pipetting**. Not checking this option may be useful for complex methods that use data sets, but may not require the data set to be transferred to the destination labware.

Configuring the Data Set Processing Step

The **Data Set Processing** step allows a transformation expression to be applied to an existing data set to create a new data set. The expression is applied to each well or tube in the existing (source)

data set and the result is stored in the corresponding well or tube of the newly created (destination) data set.

NOTE A transformation expression is an operation stated in symbolic form (refer to *Understanding Expressions*).

NOTE The destination data set is the result of the transformation expression applied to the existing data set.

The applied expression may result in numeric or Boolean values for the new data set (Table 23.3). These values are presented in a report on data sets that is configured in the **Reporting** (refer to *Configuring the Reporting Step*) or **Finish** steps (refer to CHAPTER 12, *Configuring the Finish Step*).

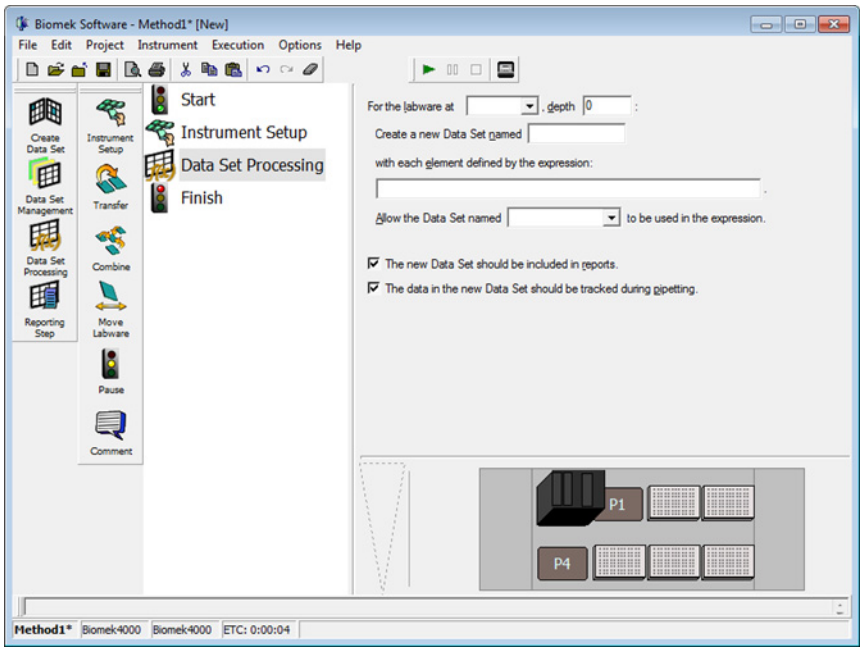
NOTE Boolean values are expressed at True or False in the reports configured in the **Reporting** or **Finish** steps.

To inset a **Data Set Processing** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 23.18).

Figure 23.18 Data Set Processing Step Configuration



To configure the **Data Set Processing** step:

1 From **For the labware at**, choose the labware where the new data set is located.

2 If in a stack, enter the **depth** of the labware.

NOTE Depth refers to a specific piece of labware in a stack. To use the top piece of labware, enter **0**; to use the second from the top piece of labware, enter **1**; to use the third from the top piece of labware, enter **2**; and so on. Refer to CHAPTER 7, *Biomek Stacking Rules*, for information on using stacks.

3 In **Create a new Data Set named**, enter the named of the new data set.

NOTE Each data set must have a unique name. The method displays an error during validation if two data sets have the same name.

4 In **with each element defined by the expression:**, enter the expression.

NOTE Refer to *Understanding Expressions*, for information on common symbols used in expressions.

NOTE An equal (=) sign must precede the expression entered in the **Data Processing** step.

5 At **Allow the Data Set named...to be used in the expression**, choose the previously created data set to be used in the expression.

NOTE The previously created data sets are available for selection.

NOTE Leave **Allow the Data Set named...to be used in the expression** blank to not use an existing data set as the basis of the transformation.

6 Ensure **The new Data Set should be included in reports** is checked to allow the new data set to be included in reports chosen in the **Reporting** or **Finish** steps.

7 Ensure **The data in the new Data Set should be tracked during pipetting** is checked to allow the data from the new data set to be tracked during pipetting operations.

NOTE If the expression is applied only to the source labware and should not be tracked, do not check **The data in the new Data Set should be tracked during pipetting**. Not checking this option may be useful for complex methods that use data sets, but may not require the data set to be tracked.

Understanding Expressions

Expressions, using symbols, allow a customized operation to be performed in the **Data Set Processing** step.

Using expressions in the **Data Set Processing** step includes understanding:

- some common symbols necessary to create an expression (Table 23.2).

- results of expressions on data sets (Table 23.3).

NOTE An equal (=) sign must precede an expression entered in the **Data Set Processing** step.

NOTE Refer to CHAPTER 13, *Using Expressions*, for more information on using expressions.

Table 23.2 Some Common Symbols Used in Expressions

Symbol	Definition
+	addition
-	subtraction
*	multiplication
/	division; returns a rational number
\	integer division; returns an integer, no remainder; for example, 13\5 returns a value of 2
a MOD b	returns the remainder after a is divided by b; for example, 13 MOD 5 returns a value of 3
>	greater than
<	less than
=	equal to
<>	not equal to
^	exponentiation; for example, a^b=a^b

Table 23.3 Some Expressions and the Results

Expression	Result
=DataSetName>5	Creates a new data set where each element is True if the value in the existing data set is greater than 5 and False if the value is less than or equal to 5
=DataSetName* 1.05	Creates a new data set where each value is the product of the existing data set multiplied by 1.05

NOTE Element refers to the value associated with a well or tube.

Configuring the Reporting Step

The **Reporting** step (refer to *Configuring the Reporting Step*) allows a report to be generated on data sets at any point during a method. While specifying the data desired from the data sets may be accomplished in the **Create Data Set, Data Set Management, Data Set Processing**, and **Script** steps, the report style and saved location of the report are chosen in the **Reporting** step.

The report contains data from all data sets that are configured to be included in reports and the type may be selected from four styles (refer to *Report Styles*).

Since the **Volume** data set (refer to CHAPTER 14, *Understanding the Volume Data Set*) is reported in every report, the volume in each well in a microplate or tube in a rack can be tracked throughout a method if a **Reporting** step is inserted after every transfer or pipetting operation.

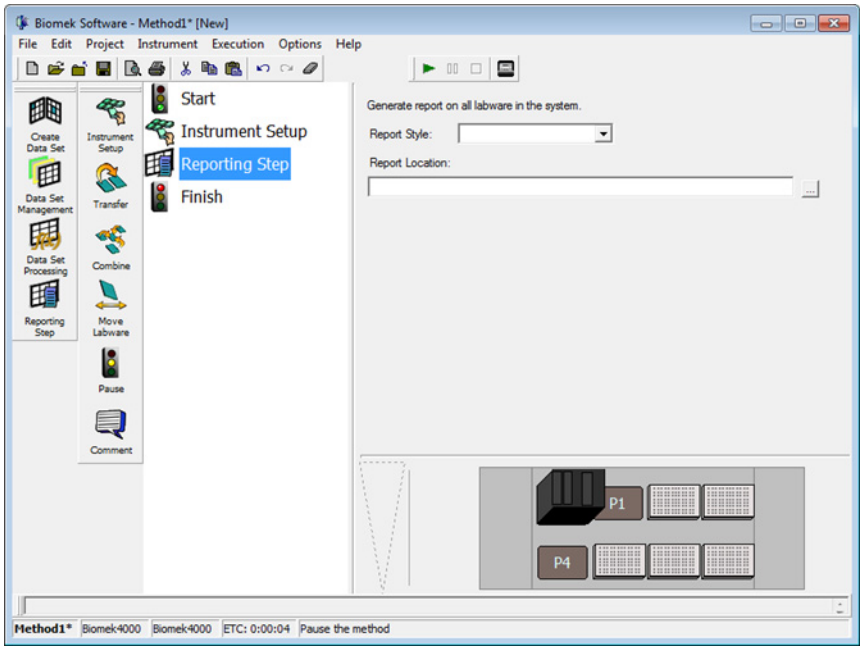
NOTE The report style and saved location of the report on data sets generated at the end of a method may also be chosen in the **Finish** step (refer to CHAPTER 12, *Configuring the Finish Step*).

To inset a **Reporting** step into a method:

1 Drag and drop the 

icon into the Method View (Figure 23.19).

Figure 23.19 Reporting Step Configuration



To choose the report style and location of the report:

1 From **Report Style**, choose one of the following:

- **Text File**
- **Per-Plate HTML Files**
- **Per-Plate Text Files**
- **SQL Server** (refer to *Configuring a SQL Server Report Style*)

NOTE Refer to *Report Styles*, for examples and information on the types of reports that may be generated.

2 In **Report Location**, browse to find the location where the file is to be saved, or configure the SQL Server settings (refer to *Configuring a SQL Server Report Style*). The **Reporting** step is configured.

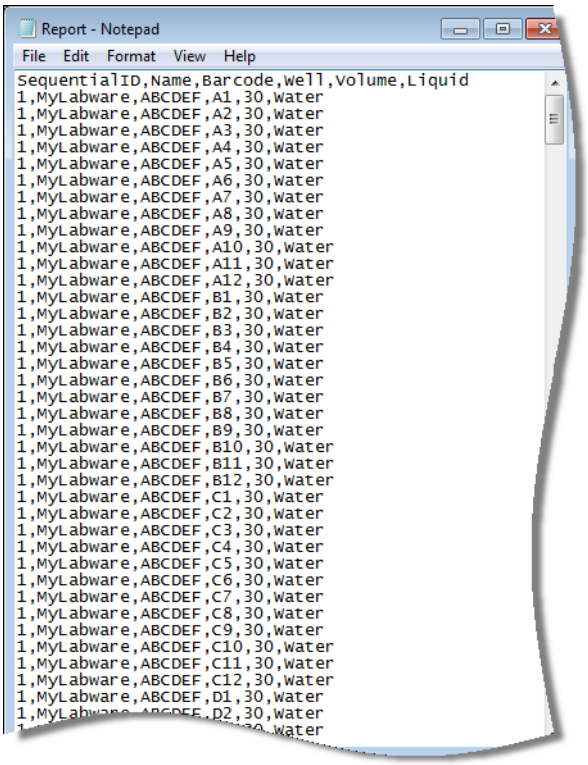
Report Styles

The report styles on data sets that may be generated are:

- **Text File** - a single text file listing all plates in the system. The columns in this file include the **SequentialID**, plate name, plate bar code, well number, sample ID (if the **SampleID** data set is created), and volume. A column for each data set that has reporting enabled is also included (Figure 23.20).

  NOTE The **SequentialID** is a number assigned to each plate. This number is the only way to identify a plate in a report if the plate name or bar code were not specified.

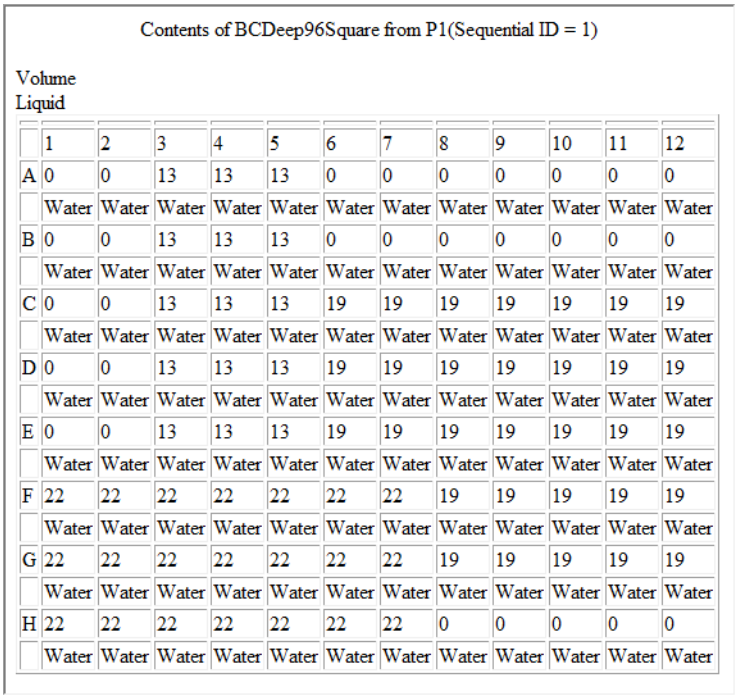
  Figure 23.20 Report Saved as Text File



- **Per-Plate HTML Files** - a folder containing an HTML file for each plate in the system. Each file contains the plate name, plate bar code, and an HTML table indexed by well number that includes the sample ID (if the **SampleID** data set is created) and volume. An entry for each data set that has reporting enabled is also included. The **SequentialID** is listed at the top of the file (Figure 23.21).

  NOTE The **SequentialID** is a number assigned to each plate. This number is the only way to identify a plate in a report if the plate name or bar code were not specified.

Figure 23.21 Report Saved as Per-Plate HTML Files



Contents of BCDeep96Square from P1(Sequential ID = 1)

Volume
Liquid

	1	2	3	4	5	6	7	8	9	10	11	12
A	0	0	13	13	13	0	0	0	0	0	0	0
	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water
B	0	0	13	13	13	0	0	0	0	0	0	0
	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water
C	0	0	13	13	13	19	19	19	19	19	19	19
	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water
D	0	0	13	13	13	19	19	19	19	19	19	19
	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water
E	0	0	13	13	13	19	19	19	19	19	19	19
	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water
F	22	22	22	22	22	22	22	19	19	19	19	19
	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water
G	22	22	22	22	22	22	22	19	19	19	19	19
	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water
H	22	22	22	22	22	22	22	0	0	0	0	0
	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water	Water

- **Per-Plate Text Files** - a folder containing a text file for each plate in the system. Each file contains the **SequentialID**, plate name, plate bar code, and columns that include the well number and sample ID (if the **SampleID** data set is created). A column for each data set that has reporting enabled is also included.

  NOTE The **SequentialID** is a number assigned to each plate. This number is the only way to identify a plate in a report if the plate name or bar code were not specified.

  NOTE The text files in the folder for each plate in the system look similar to Figure 23.20.

- **SQL Server** - a single database table listing all plates in the system. The columns of this table include the **SequentialID**, plate name, plate bar code, well number, and sample ID (if the **SampleID** data set is created). A column for each data set that has reporting enabled is also included. The table is created with a time-date stamp appended to the name (Figure 23.22).

  NOTE The **SequentialID** is a number assigned to each plate. This number is the only way to identify a plate in a report if the plate name or barcode were not specified.

  NOTE SQL Server is a Microsoft product that allows queries and provides analysis. The installation of this product is the responsibility of the user and is not supported by Beckman Coulter Representatives. SQL Server 2005 is the version requirement.

  NOTE Refer to CHAPTER 23, *Configuring a SQL Server Report Style*, for specific information on configuring a SQL Server report.

Figure 23.22 Report Saved as SQL Server

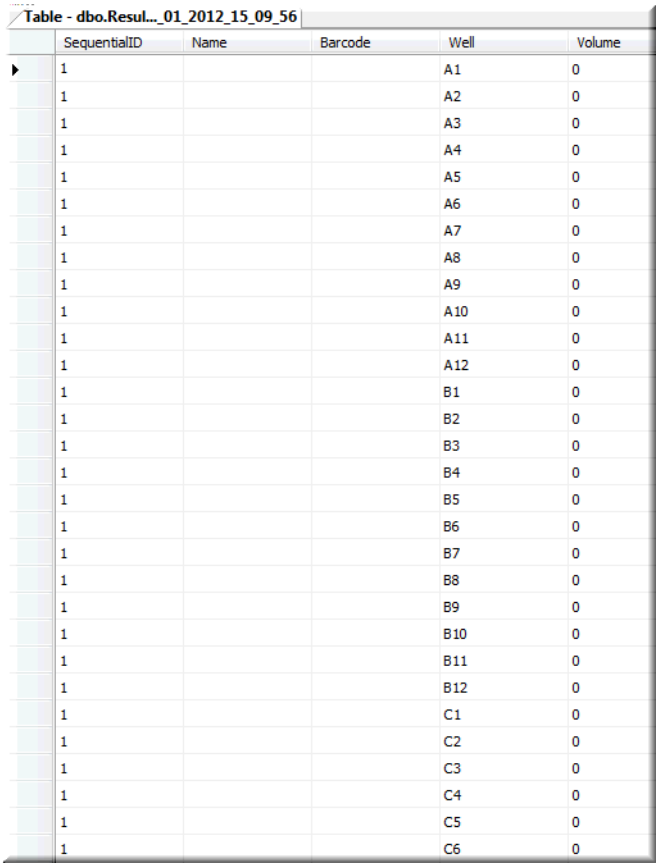


Table - dbo.Resul..._01_2012_15_09_56

SequentialID	Name	Barcode	Well	Volume
1			A1	0
1			A2	0
1			A3	0
1			A4	0
1			A5	0
1			A6	0
1			A7	0
1			A8	0
1			A9	0
1			A10	0
1			A11	0
1			A12	0
1			B1	0
1			B2	0
1			B3	0
1			B4	0
1			B5	0
1			B6	0
1			B7	0
1			B8	0
1			B9	0
1			B10	0
1			B11	0
1			B12	0
1			C1	0
1			C2	0
1			C3	0
1			C4	0
1			C5	0
1			C6	0

Configuring a SQL Server Report Style

When **SQL Server** is chosen as the report style, the server, database, and table name are configured.

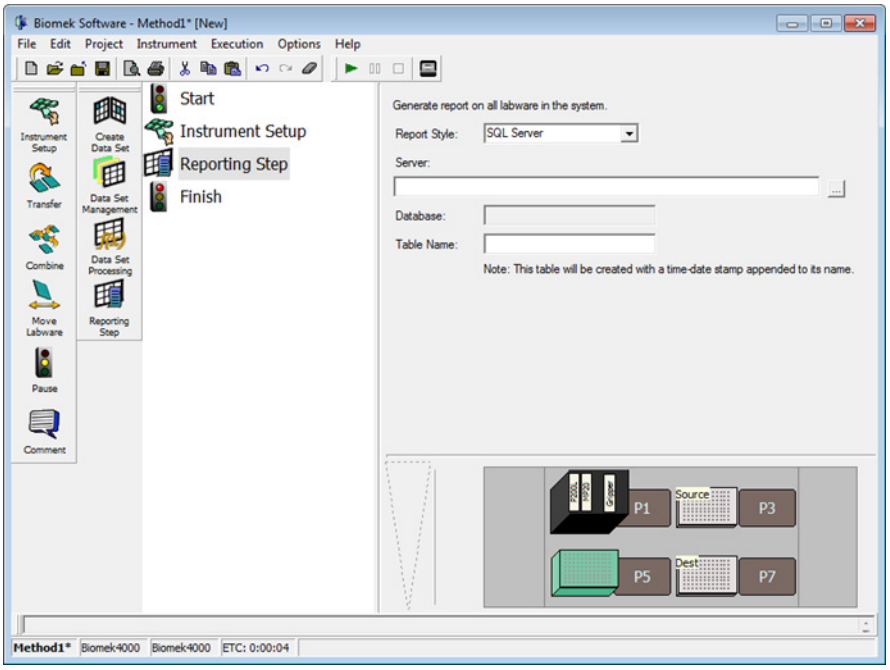
NOTE SQL Server is a Microsoft product that allows queries and provides analysis. The installation of this product is the responsibility of the user and is not supported by Beckman Coulter Representatives. SQL Server 2005 is the version requirement.

NOTE Refer to Figure 23.22 for an example of a **SQL Server** report style.

To configure a SQL server report style:

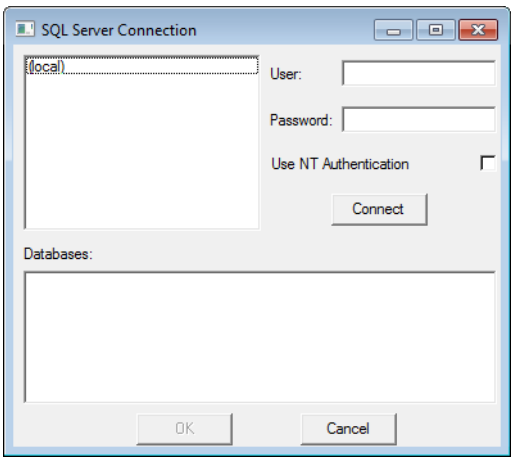
1 In **Report Style**, choose **SQL Server**. Figure 23.23 appears.

Figure 23.23 SQL Server Report Style Chosen



2 Select ... (browse) to choose and configure the SQL Server Connection. **SQL Server Connection** (Figure 23.24) appears on top of the **Reporting** step configuration.

Figure 23.24 SQL Server Connection



3 Highlight the desired server.

4 Enter the **User** and **Password**.

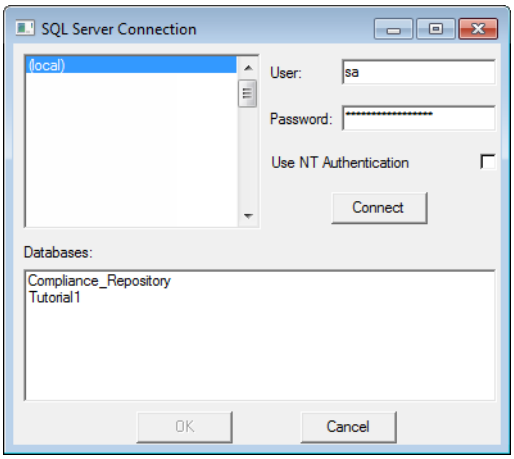
OR

Check **Use NT Authentication**.

NOTE The administrator of the **SQL Server Connection** sets the logging protocol for user and password or NT authentication.

5 Choose **Connect**. A list of available databases appears in **Databases** (Figure 23.25).

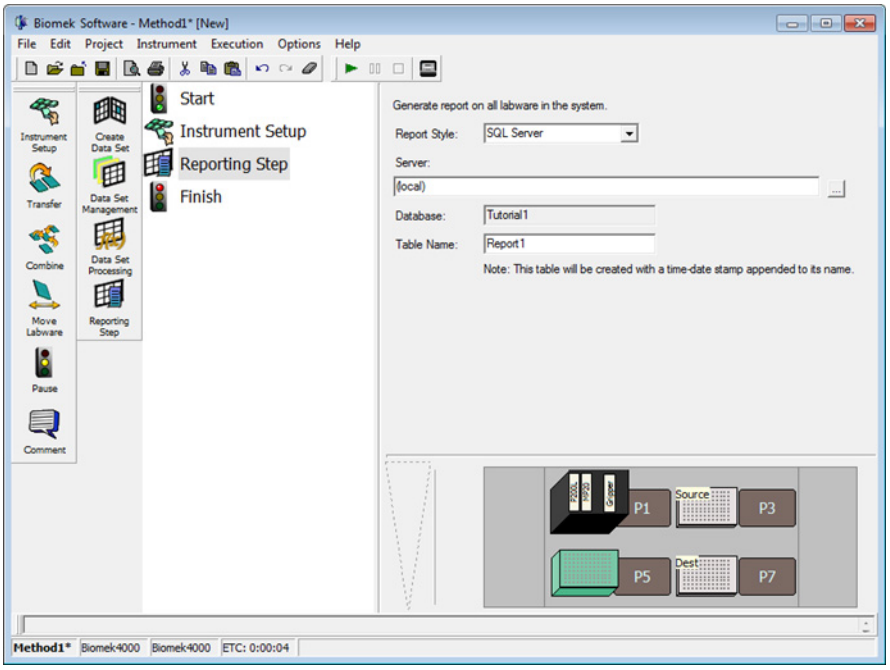
Figure 23.25 List of Databases in SQL Server Connection



6 From **Databases**, highlight the desired database.

7 Choose **OK**. **SQL Server Connection** closes and the chosen server and database are entered in the **Reporting** step configuration.

Figure 23.26 Server and Database Chosen



8 From the **Reporting** step configuration (Figure 23.26), enter the **Table Name.**

NOTE Table names must begin with a letter, and only letters, numbers and underscores (_) can be used.

NOTE The table is created with a time-date stamp appended to the name.

CHAPTER 24

Handling and Preventing Errors

Overview

Biomek Software provides extensive error handling and error prevention capabilities to help make sure the method being built, edited, set up, and run executes appropriately. Included in the Biomek Software error handling and prevention capabilities are:

- Error notification and cause messages.
- Error recovery options.
- Constant internal validation during method building and editing.
- Internal validation before running a method.

Error Message Overview

There are several types of error messages that may display while building and running methods using Biomek Software. The types of error messages generated depend on the type of error that has occurred. While errors may originate from more than one source, most errors fall into the general categories shown in Table 24.1.

Table 24.1 Common Error Types

Error Type	Description
Configuration Errors	Occurs when a device or step is not configured correctly during method development or instrument configuration.
Validation Errors	Occurs when a method or step is validating.
Manual Control Errors	Occurs when a manual control movement requested of the ALPs, bridge, pod, tool, or gripper is not compatible with the capabilities of the Biomek 4000 instrument.
Run-Time Errors	Occurs while a method is running.
Liquid Level Sensing Errors	Occurs while attempting to determine the liquid level in a piece of labware during a method run.
Multiple Error Messages	Numerous errors occurring during validation or method run.
Observed Errors	Errors observed by the operator as the method runs.

Error Recovery Overview

Error recovery is the process of making changes to ensure a method can be completed. When changes are made and no subsequent errors are detected, the method completes. Depending on the conditions causing the error, the error message displays the appropriate error recovery options available.

Error recovery options may include:

- Fixing the error and continuing the method from the point of interruption.
- Stopping the current method, making modifications, and running the entire method from the beginning.
- Ignoring the error and continuing with the method.

Error Prevention Overview

Errors may be prevented by validating a method during the method-building process. Validation detects a large class of common errors before they occur by internally simulating the method prior to execution. This internal simulation provides an opportunity to change the method before it is run.

Operations for validating a method include:

- Validating the method immediately before a run starts by selecting **Validate the current method before running it** in **Preferences** (see CHAPTER 28, *Configuring General Options* for details).
- Individually validating steps by highlighting subsequent steps or the **Finish** step in the Method View.
- Individually validating operations by using the **Single Step** tool, available from the **Execution** menu.

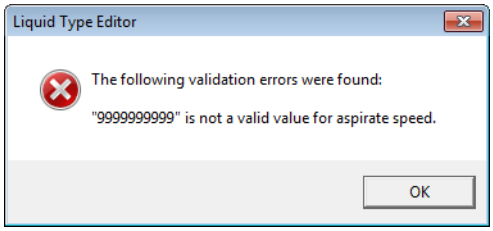
Configuration Errors

Configuration errors occur when steps, labware, or devices are not configured correctly during method development or system setup.

Configuration Error Messages

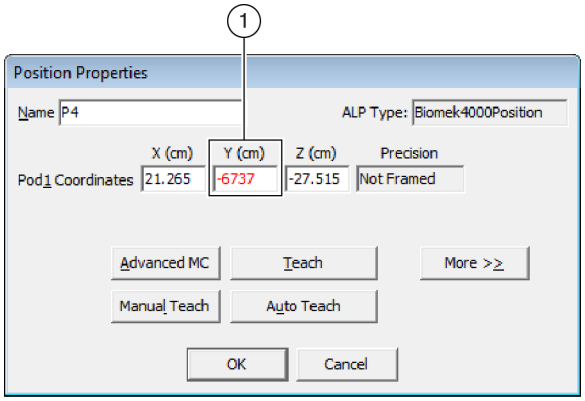
When a configuration error is encountered during system setup, an error message may be displayed immediately (Figure 24.1).

Figure 24.1 Example of a Configuration Error Generated Due to a Liquid Type Editor Configuration Problem



A configuration error notification can also be generated as soon as a device configuration entry is made; for example, an incorrect entry in the **Deck Editor** appears red rather than black (Figure 24.2).

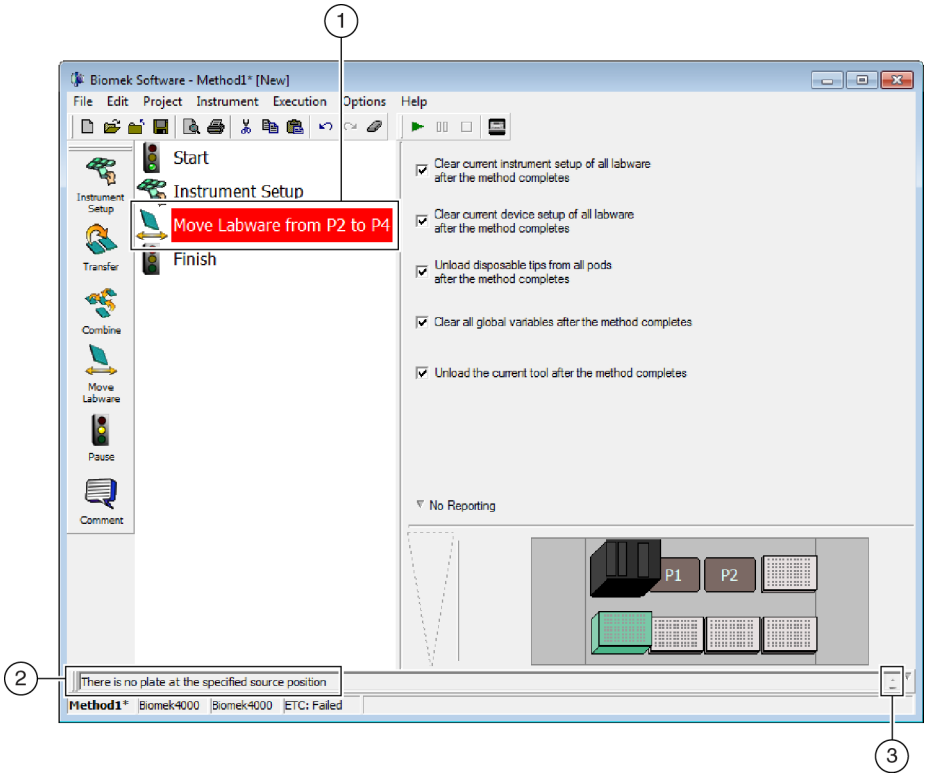
Figure 24.2 Example of a Configuration Error Generated from the Deck Editor



1. **Erroneous Entry in the Deck Editor**: The erroneous entry of "-6737" is highlighted in red.

When a step is not configured correctly, the step causing the error is highlighted in red in the Method View (Figure 24.3), and a message describing the error in detail is displayed at the bottom of the method editor and in a tool tip when the cursor is hovered over the step.

Figure 24.3 Example of an Error Generated During Method Validation Because a Step is Not Configured Correctly



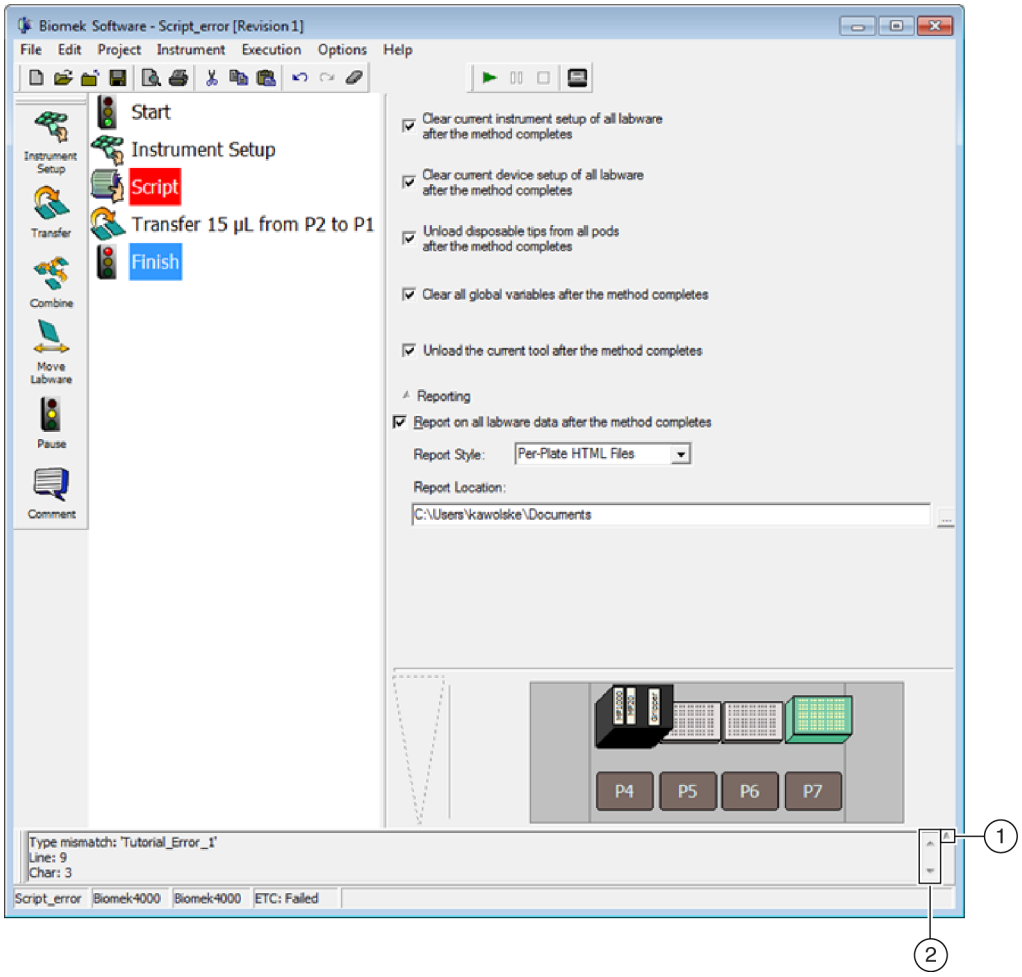
1. **Step Producing the Error**: The step producing the error is highlighted in red in the Method View.
2. **Error Message**: The error message is displayed in the status bar and as a tool tip.
3. **More/Less**: Expands and collapses status bar to view application error message content.

NOTE The Error Message status bar may be hidden by choosing **Options** > **Toolbars** and deselecting **Method Error**.

To view multiple lines for a long error message, click the **More** button (Figure 24.3) to expand the error display to show the entire message (Figure 24.4).

Click the **Less** button (Figure 24.4) to collapse the error display back to a single line (Figure 24.3).

Figure 24.4 Example of an Expanded Error Message



1. **Less**: Collapses status bar to display one line of error message.
2. **Expanded Error Message**: The error message is displayed in the status bar and as a tool tip.

Recovering from Configuration Errors

To recover from configuration errors, ensure that all of the facts pertaining to the step, labware, or device configuration have been supplied and are acceptable values. For example, make sure that volumes do not exceed the maximum capacity of the specified tips or labware.

Validation Errors

Validating a method prior to execution internally simulates the method to test for errors. If an error is detected during validation, an error message displays information about the error.

NOTE In this section, validation refers only to running methods in simulation mode to test for step or instrument configuration errors. It does not refer to validating a revision of a method using Beckman Coulter Accounts &Permissions. Refer to CHAPTER 12, *Validating a Method*, for more information about validating checked in revisions of methods.

NOTE Validation errors can occur due to step configuration or instrument configuration errors, as noted in *Configuration Errors*.

Validation Error Messages

Errors encountered during validation may display the following information in the error messages:

- Source
- Type
- Cause
- Location
- Error Code
- Recovery Option(s)
- Date and Time

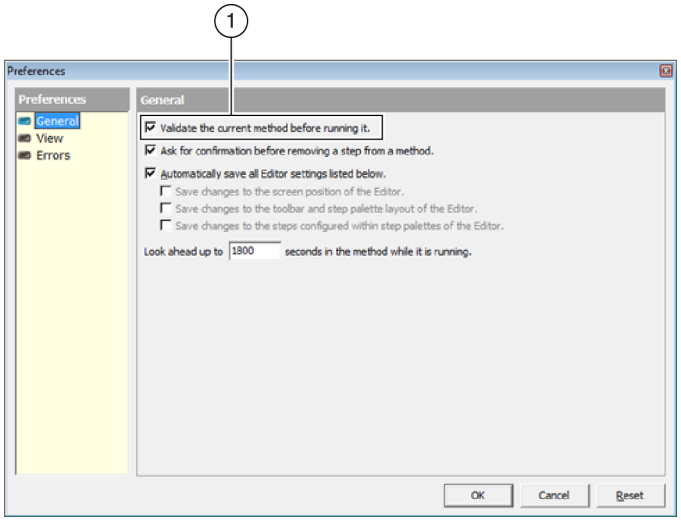
Validating a Method Before Run

When **Validate the current method before running it** is checked in **Preferences** (Figure 24.5), a method is internally simulated to test for errors when the method is run. If no errors are detected during this validation, the method is executed. If an error is encountered during this validation, the process stops and an error message displays information about the nature of the error.

When **Validate the current method before running it** is selected, the first step causing an error is highlighted in the Method View (Figure 24.6). **Validate the current method before running it** is enabled by default.

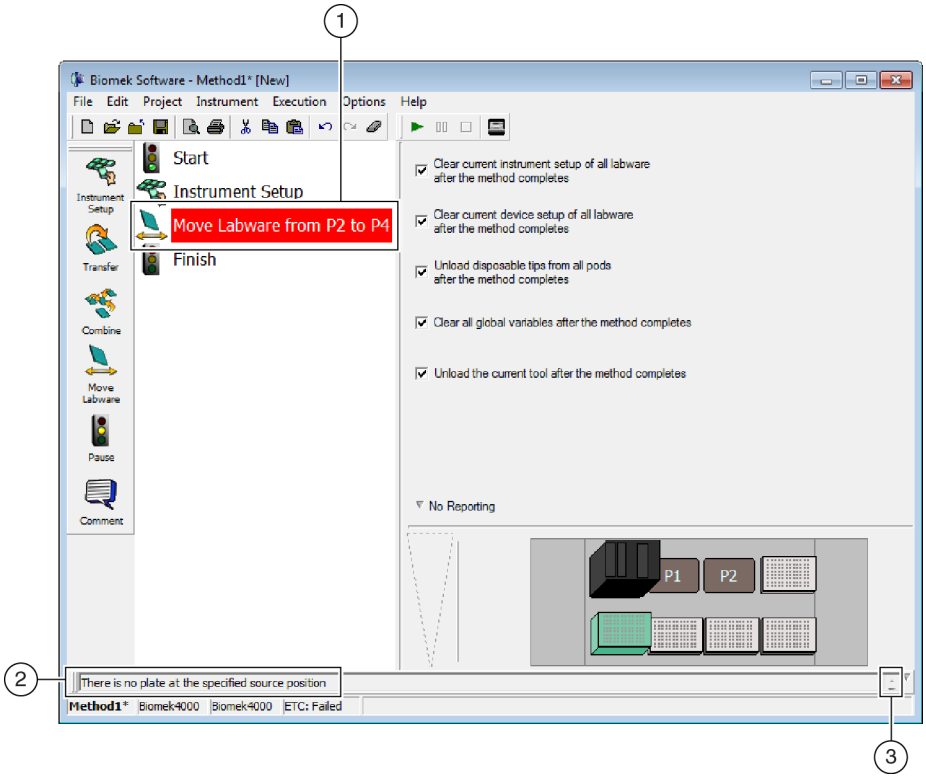
To prevent the system from slowing down due to unnecessary memory consumption, use **Look ahead up to ... seconds in the method while it is running** (refer to *Using Look ahead up to ... seconds in the method while it is running*).

Figure 24.5 Validate the Current Method Before Running It, Option in Preferences



1. **Method Validation**: Simulates methods internally to test for errors before the method is run.

Figure 24.6 Example of a Validation Error Message Generated During Method Development as a Result of Incomplete Step Configuration



1. **Step Producing the Error:** The step producing the error is highlighted in red in the Method View.
2. **Error Message**: The error message is displayed in the status bar and as a tool tip.
3. **More/Less**: Expands or collapses status bar to display more or less of the error message.

To use **Validate the current method before running it**:

1. From the toolbar, choose **Options > Preferences**. **Preferences** appears (Figure 24.5).
2. Make sure **Validate the current method before running it** is checked.
3. Choose **OK**.
4. Run the method.

NOTE Validating a complex or lengthy method could result in occupying system resources for a long period of time. **Validate the current method before running it** can be disabled prior to running a previously validated method, or a method not requiring validation, by using **Options** > **Preferences** and deselecting **Validate the current method before running it**.

Using Look ahead up to ... seconds in the method while it is running

When a method is run, the software translates the steps of the method into "to do" lists of actions to be performed on each device. This translation process occurs while the method is running. Since methods can be arbitrarily long, the lists of actions can consume large amounts of computer memory, possibly slowing the system.

To prevent unnecessary slowing of the system due to memory consumption, the **Look ahead up to ... seconds in the method while it is running** option in **Preferences** (Figure 24.5) designates a time-based governor for suspending the translation process. The time in seconds entered into **Look ahead up to ... seconds in the method while it is running** is a threshold at which the translation process may be suspended so that the "to do" lists do not become too large. If each currently active device requires more than the time-designated threshold to complete its "to do" lists, the suspension may occur. (The translation process is never suspended during a **Just In Time** step.) Once the system determines that some device may finish its list earlier than this threshold, it automatically resumes the translation process.

NOTE To prevent problems with executing actions that should occur simultaneously, it is important to enter a high enough **Look ahead up to ... seconds in the method while it is running** time.

Validation Error Messages Detected During Method Development

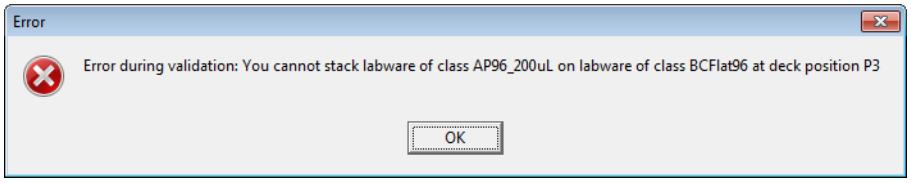
During method building, Biomek Software validates constantly. Errors that are detected during this process are displayed when a subsequent step in a method is highlighted. When the **Finish** step is highlighted, the entire method is validated. The first step causing an error is highlighted in red in the Method View, and a message describing the error in detail is displayed in the status bar at the bottom of the method editor as well as in a tool tip when the mouse pointer is hovered over the step.

Validation Error Messages Detected During Method Run

Validation errors may also be detected during method execution. The display of the error message depends on whether **Validate the current method before running it** is selected or not (refer to *Validating a Method Before Run*).

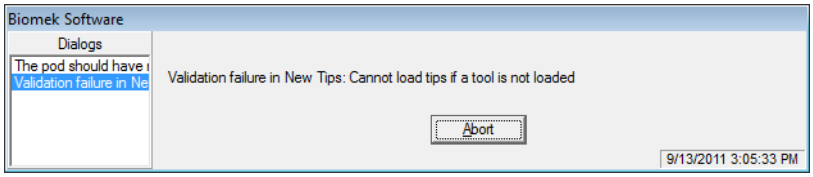
If **Validate the current method before running it** is selected, the method is validated before it starts. If an error is found, it displays an error message similar to Figure 24.7.

Figure 24.7 Example of a Validation Error Message Detected Before Method Run



If a method has not been previously validated and the **Validate the current method before running it** option is not selected, it displays an error message similar to Figure 24.8.

Figure 24.8 Example of a Validation Error Message Detected During Method Run



Recovering from Validation Errors

To recover from Validation errors encountered during method execution, choose one of the options provided on the error message. Validation error messages have either the **OK** recovery option or an **Abort** option.

Validation error message recovery options include:

- **Abort** - stops the method after Biomek instrument completes the move in progress.
- If the method is in the process of performing a move, such as aspirating or dispensing, the instrument completes the move; however, the instrument may not complete the entire step. For example, if the instrument is in the process of performing a dispense portion of the **Transfer** step and an error occurs while it is aspirating, selecting **Abort** results in completing the aspiration but not the dispense portion of the **Transfer** step.
- **OK** - stops the method, allowing changes.

  NOTE **OK** is presented only as an option for a validation error detected before the run has started if **Validate the current method before running it** is turned on (refer to *Validating a Method Before Run*).

Choosing Abort

Choose **Abort** to stop a method after completing the move in progress and leave the method open for editing.

To use **Abort**:

1 Read the error message to determine the cause of the problem.

2 Choose **Abort** to make the necessary changes in the original method file.

Manual Control Errors

Manual Control errors occur when a manual control movement requested of the bridge, pod, tool, or gripper is not compatible with the capabilities of the Biomek 4000 instrument.

Manual Control Error Messages and Recovery

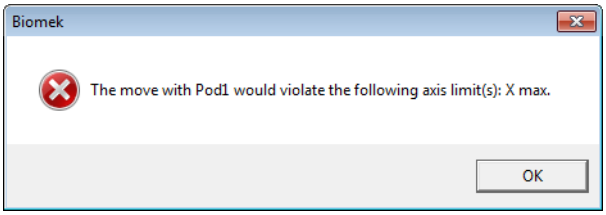
Manual Control errors have only one recovery option, and that is to choose **OK** on the error message (Figure 24.9). Manual Control error messages should be carefully read to determine whether the problem lies in the hardware or software. Once that determination has been made, appropriate changes can be made to recover from the error.

To recover from Manual Control errors:

1 Read the error message to determine the problem.

2 Choose **OK**, then make the necessary changes.

Figure 24.9 Example of a Manual Control Error Because the Instrument Tried to Move the Pod Too Far on the X Axis



Run-Time Errors

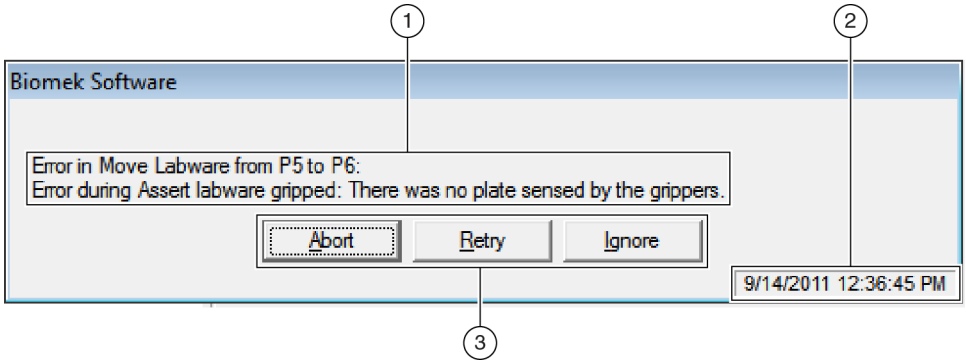
Run-Time errors result from problems that occur while a method is executing; for example, a tip failed to load properly. Run-Time error recovery options are presented on each error message.

Run-Time Error Messages

Run-Time error messages (Figure 24.10 and Figure 24.12) display the:

- Source
- Device
- Error Message
- Error Number
- Recovery Option(s)
- Date and Time

Figure 24.10 An Example of a Run-Time Error Due to Failing to Detect a Plate



1. **Error Message**: This error message indicates that the gripper did not detect a plate when trying to move labware.
2. **Date/Time**: Provides the date and time the error occurred.
3. **Recovery Options**: Refer to *Recovering from Run-Time Errors*, for more information on recovery options.

Recovering from Run-Time Errors

To recover from errors, choose one of the Recovery Options and correct the problem that caused the error.

The options available for recovering are:

- **Abort** - stops the method after Biomek instrument completes the move in progress.

  NOTE If the method is in the process of performing a move, such as aspirating or dispensing, the instrument completes the move; however, the instrument may not complete the entire step. For example, if the instrument is in the process of performing a **Transfer** step and an error occurs while it is aspirating, selecting **Abort** results in completing the aspiration but not the remainder of the **Transfer** step.

- **Retry** - attempts to complete the move in progress when the error was encountered and complete the method (refer to *Choosing Retry*).

⚠ WARNING

The "Ignore" error recovery option in Biomek Software is potentially dangerous since almost every action depends upon the successful completion of previous actions. Choosing "Ignore" can lead to mishandled labware and reagents or collisions and instrument damage. Choose "Ignore" only when the error cause is known and corrected, and instrument actions following "Ignore" are fully understood.

- **Ignore** - skips the move in progress and proceeds with the rest of the method, if possible (refer to *Choosing Ignore*).

After the errors are corrected, the method can be rerun or continued from where the error occured.

Choosing Abort

Choose **Abort** to stop a method after completing the move in progress and leave the method open for editing.

To recover from errors using **Abort**:

1. Read the error message to determine the cause of the problem.
2. Choose **Abort** to make the necessary changes in the original method file.

Choosing Retry

Choose **Retry** to attempt to complete the step that is in progress when the error was encountered. If the step is completed successfully, the method continues.

⚠ CAUTION

Resuming a method in Biomek Software assumes that the instrument is in the same state as when the error occurred. The pod may be moved to deal with a problem and changes can be made to labware contents, but no changes can be made to the instrument deck or devices in Biomek Software. Doing so can lead to instrument damage.

To recover from errors using **Retry**:

1. Read the error message to determine the cause of the problem.
2. Take any necessary steps to correct the problem.

3 Examine the instrument to verify it is safe to restart the method.

4 Choose **Retry**. The instrument attempts to perform the move in progress when the error occurred, and if successful, the method continues. If the method cannot continue after choosing **Retry**, another error message appears.

Choosing Ignore

⚠ WARNING

The "Ignore" error recovery option in Biomek Software is potentially dangerous since almost every action depends upon the successful completion of previous actions. Choosing "Ignore" can lead to mishandled labware and reagents or collisions and instrument damage. Choose "Ignore" only when the error cause is known and corrected, and instrument actions following "Ignore" are fully understood.

Choose **Ignore** to bypass the error and proceed with the method. The move in progress when the hardware error is detected does not complete, but the method attempts to continue the run.

To recover from errors using **Ignore**:

1 Read the error message to determine the cause of the problem.

2 Correct the problem and ensure that the instrument, labware, and reagents are in an acceptable state to continue the method.

3 Choose **Ignore**. The error is ignored, and the method continues to run, if possible. If the method cannot continue after choosing **Ignore**, another error message appears.

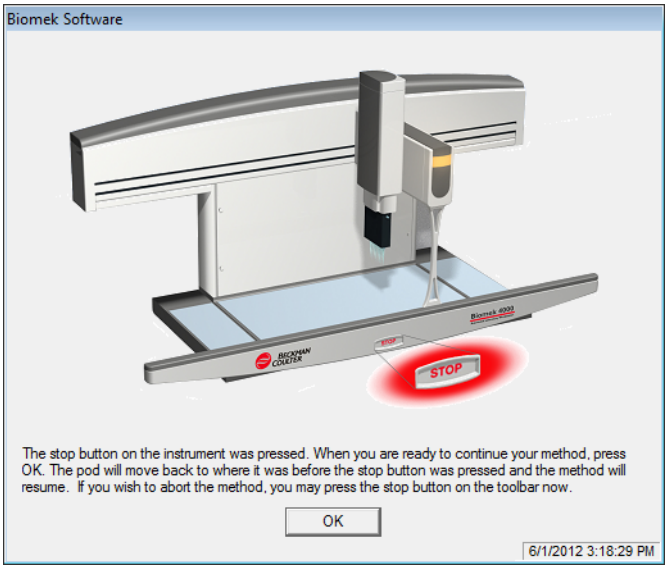
NOTE Ignore may be useful for failed **SILAS** steps such as failed bar code reads or device time-out errors that do actually complete.

Using the Stop Button

Pressing the emergency STOP button on the front rail of the Biomek 4000 instrument stops movement of the bridge, pod, and tools.

When the STOP button is pressed, Figure 24.11 appears.

Figure 24.11 Pressing STOP on the Front Rail of the Biomek 4000 Instrument



Two options are possible after pressing the emergency STOP:

NOTE ALPs stop running when the emergency STOP button is pressed.

- Choose **OK** to resume the method.

  NOTE If the STOP button is pressed while a tool is being loaded, the instrument must be homed before the method is resumed.

- From the toolbar, choose **Execution > Stop** to abort the method.

Liquid Level Sensing Errors

The P200L and P1000SL Single-Tip Pipette Tools include patented technology that sonically detects the liquid level. Liquid level sensing is performed using an acoustic process involving a transmitter and receiver within a single-channel tool. The transmitter emits a sound wave through the tip that bounces back when it contacts liquid. The receiver detects the wave as it bounces back past the end of the tip.

Recovering from Liquid Level Sensing Errors

Liquid level sensing error messages appear when no liquid is sensed or when the amount of liquid sensed is incompatible with the operation performed. Liquid level sensing error messages display one of the following error messages:

"There is insufficient volume in well ## for this operation. Check probe # before continuing."

"There is too much volume in well ## for this operation. Check probe # before continuing."

"Validation failure in Move to #. Consecutive senses did not provide a stable value. This can be caused by bubbles in the well or by the meniscus of the liquid."

Liquid level sensing errors display a variety of recovery options in the error message, based on the instrument and type of liquid level sensing error encountered.

Liquid Level is Incompatible with the Operation

When the liquid level detected is incompatible with the pipetting operation (refer to *Incompatible Pipetting Operation*), the error message provides recovery options.

Incompatible Pipetting Operation

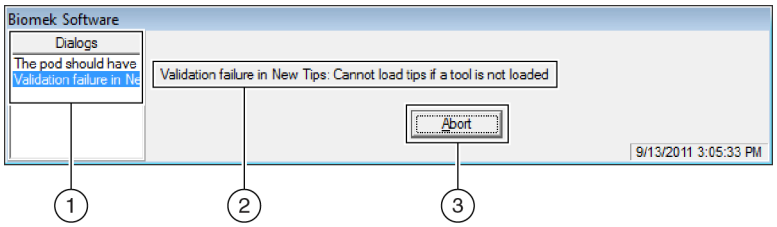
The following recovery options are available:

- **Adjust Manually Then Seek Liquid Again** - Allows for making adjustments before trying again.
- **Seek Again** - Prompts the software to seek liquid again.
- **Pipette Air** - Pipettes air when liquid is not available.
- **Pipette From Bottom** - Moves tip to bottom of well and continues pipetting operation.
- **Abort** - Stops the method after the instrument completes the move in progress.

Multiple Error Messages

When multiple error messages are generated during method validation, a dialog appears in the **Instrument Setup** prompt that contains a list of the errors (Figure 24.12) Specific information about each error in the list is displayed in the message area by highlighting the message in the error list. Recovery options for each message are also displayed.

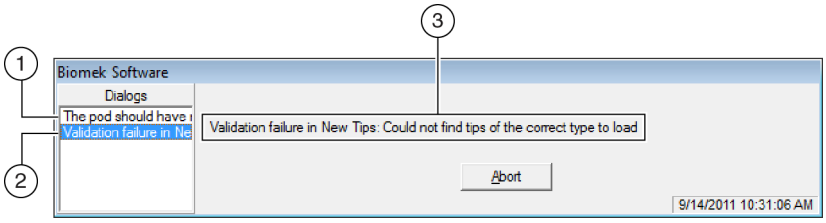
Figure 24.12 Error Message Dialog with Multiple Errors



1. **Error List**
2. **Message area**
3. **Recovery option**

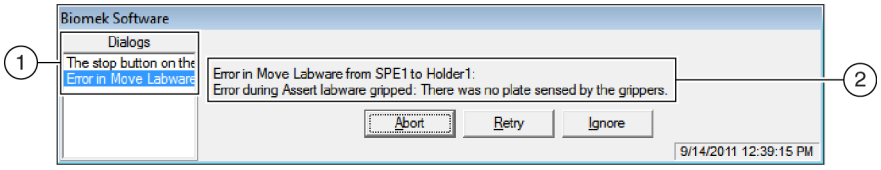
When multiple errors are encountered, the error messages appear in prompts similar to the examples displayed in Figure 24.13 and Figure 24.14.

Figure 24.13 An Example of Multiple Error Messages



1. **Instrument Setup Message**
2. **Validation Error Message**
3. **Message Area**

Figure 24.14 An Example of Multiple Error Messages Generated During Run-Time



1. **Error List**
2. **Message Area**

Recovering from Multiple Errors

Multiple error messages should be read carefully to determine where the problem lies: in the hardware, software, or in the method. Once that determination has been made, appropriate changes can be made to recover from the errors. Errors can be resolved in any order. Refer to *Recovering from Run-Time Errors*, for more information on error recovery options.

Observed Errors

Occasionally, errors are observed while watching the instrument execute a run. For example, the instrument may attempt to aspirate from an empty or missing microplate.

Observed errors may result from setup, hardware, or software issues.

Recovering from Observed Errors

Biomek Software provides three options for recovering from observed errors while the method is running:

- **Pause** — Halts a method.
- **Stop** — Halts a method when there is no intent to resume the method from the point where it was stopped.
- **E Stop** — Similar to a **Pause** step.

Pausing a Method

Use **Pause** to halt a method. **Pause** causes the method to halt after the instrument has completed the move in progress. For example, if the instrument is in the process of loading tips when **Pause** is selected, it finishes loading the tips before the system halts. When the method is resumed, it continues as though it were never halted.

NOTE A method cannot be edited during a pause.

Use one of the following procedures to pause a method:

⚠ CAUTION

To avoid equipment damage and/or hazardous waste spills, no changes to the Biomek 4000 state are permitted while a method is paused. Changes can be made to the labware contents, but not the deck or the devices.

1 Choose **Execution > Pause**.

OR

Choose  (**Pause**) on the toolbar. The instrument completes the move in progress and then stops.

2 Make the necessary changes to correct the observed error.

3 To resume the method run, choose **Pause** again. The method resumes from the point where it was paused.

Stopping a Method

⚠ WARNING

The emergency STOP button is a safety device. Use it to stop a method only in an emergency. Restarting a method can change how pipetting occurs, potentially leading to decreased instrument performance.

Use **Stop** to halt a method during its run when there is no intent to resume method execution. If the pod is in the process of a move, the operation is not completed. Since the method is halted, this option allows edits to the method or changes to the hardware and deck.

NOTE **Stop** may not halt operations already in progress on external devices.

Use one of the following procedures to stop a method during a run:

1 Choose **Execution > Stop**.

OR

Choose  (**Stop**) on the toolbar.

OR

Press the **STOP** button on the front of the instrument (refer to *Using the Stop Button*) and choose **Stop** from the toolbar.

NOTE Use standard procedures to rerun the method.

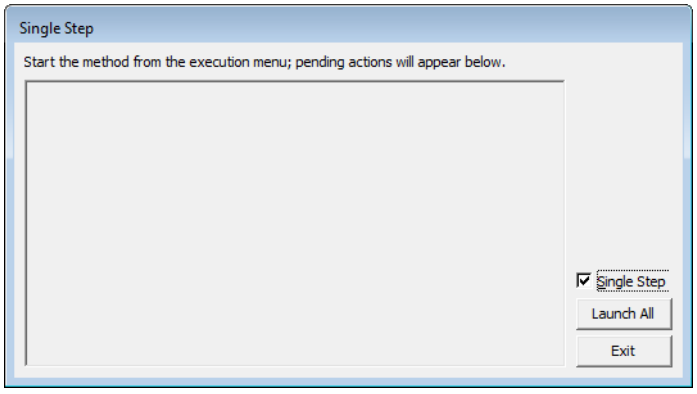
Performing Single Operations Within Steps

The **Single Step** option performs single operations within steps, such as **Aspirate** or **New Tips. Single Step** pauses the instrument between each operation in a step, allowing visual verification that the operation is correct. Performing single operations can help when fine tuning a method.

To open **Single Step**:

1 Choose **Execution** > **Single Step**. **Single Step** appears (Figure 24.15):

Figure 24.15 Single Step Prompt



Single Step allows a method to be executed, one operation at a time. For example, to visually verify that tips are loading properly, use **Single Step** to walk through the **New Tips** step operation by operation. It is important to move slowly when using **Single Step**. Moving too quickly through the method may bypass steps that need verification.

When visually verifying steps using **Single Step**, there are multiple operations that occur. For example, the **New Tips** step may walk through operations that include:

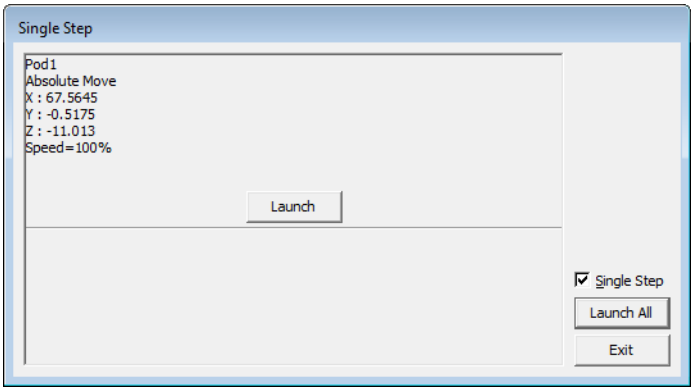
- Moving to a tip box.
- Preparing to load tips.
- Loading Tips.

To run a methods using **Single Step**:

1 Open the **Single Step** prompt. This can be done before or during a method run.

2 Start the method using the **Start** button on the toolbar. The method will stop for the first movement of a pod or bridge and the prompt will display the operation to perform (Figure 24.16).

Figure 24.16 First Move of Method Using Single Step



3 To perform the next move, choose **Launch**.

4 To perform all steps in the method after verifying the desired steps, uncheck **Single Step**.

NOTE Choose **Launch All** to launch all operations listed in the **Single Step** prompt. When there is more than one **Launch** button available, **Launch All** simultaneously presses all the Launch buttons.

5 Choose **Exit** to leave **Single Step** at any time.

CHAPTER 25

Generating and Using Log Data

Overview

Logs provide text records of a method run. The contents of the text record, or log file, are based upon the type of log requested. Logs include information on liquid transfer operations, errors, and gripper movements, as well as information contained in data sets. Log types are listed in Table 25.1:

Table 25.1 Log Types

Log Type	Description
Details	Captures every operation that occurs during a method run, including **Instrument Setup**, absolute moves, pod movements, and gripper movements.
Errors	Captures any errors that occur during a method run.
Pipetting	Captures pipetting operations completed during a method run, deck location, and labware name or type. This is available with all pipetting tools.
UnifiedPipetting	Captures pipetting operations, along with Sample IDs for wells, including information on the where the aspirate or dispense operation occurs.
UnifiedTransfer	Captures transfer operations, along with Sample IDs for wells, including information on the source and destination labware.

Log files are used to generate reports and capture the history of a method run. Log files can be printed using a standard text editor or by inserting them into a spreadsheet program, such as Microsoft Excel.

Types of Logs

The five types of logs available capture either a complete account of a method or specific operations that occur during a method run. The type of log captured is indicated by the file name in the **Logs** subdirectory. **Logs** is a subdirectory of the **Biomek** directory.

To access **Logs**:

1 Browse to **C:\Users\Public\Public Documents\Documents\Biomek\Logs.**

OR

Choose **Start** > **Beckman Coulter > Tools** > **Biomek Files** to open the **Biomek** directory and access **Logs.**

Examples of the naming procedures for log files are:

Type	Example Name
Details	Details03-09-2012 17.11.20.log
Errors	Errors03-27-2012 10.27.41.log
Pipetting	Pipetting03-09-2012 17.11.20.log
UnifiedPipetting	UnifiedPipetting09-27-2011 12.11.41.log
UnifiedTransfer	UnifiedTransfer09-27-2011 12.11.41.log

Details Log

The **Details log** provides comprehensive information about each move made by the instrument. It is used when trying to identify and correct movement problems.

Refer to *Details Log Contents*, for specific information about the **Details Log** contents.

NOTE The default setting for the **Details** log is **Off**.

NOTE The **Details** log is most useful to Beckman Coulter Representatives when troubleshooting an instrument.

Errors Log

The **Errors** log lists any errors or interruptions that occur during a method run. It is used to get the exact error message to include in a report or a discussion with Technical Support.

Refer to *Errors Log Contents*, for specific information about the **Errors** log contents.

NOTE The default setting for the **Errors** log is **On**.

Pipetting Log

The Pipetting log lists aspirate and dispense operations that are executed during a method run. It is used when validating a method or generating a comprehensive report about the pipetting operations used during a method. The Pipetting Log can be used with all pipetting tools.

Refer to *Pipetting Log Contents*, for specific information about the **Pipetting** log contents.

NOTE The default setting for the Pipetting log is **Off**.

UnifiedPipetting Log

The **UnifiedPipetting** log lists aspirate and dispense operations, along with Sample IDs for wells. It includes information on the labware where the aspirate or dispense operation occurs and is used when validating a method or generating a comprehensive report about pipetting operations used during a method.

Refer to *UnifiedPipetting Log Contents*, for specific information about the **UnifiedPipetting** log contents.

NOTE The default setting for the **UnifiedPipetting** log is **Off**.

UnifiedTransfer Log

The **UnifiedTransfer** log lists transfer operations, along with Sample IDs for wells. It includes information on the source and destination labware and is used when validating a method or generating a comprehensive report about liquid transfer operations used during a method.

Refer to *Unified Transfer Log Contents*, for specific information about the **UnifiedTransfer** log contents.

NOTE The default setting for the **UnifiedTransfer** log is **Off**.

Log Contents

Each of the logs provide specific types of information; however, all log files provide the following information in their header:

- Method name and file path.
- User.
- Method start date and time.
- Unit serial number.
- Pod serial number.
- Last date the pod was validated (by a Beckman Coulter Representative).
- A blank line (used as a separation between the header and the information captured during the method run).

Each line below the header can contain the following information:

- Date the information was captured.
- Time the information was captured.
- Information captured during the method run that is specific to the type of log requested.

  NOTE The information captured during the method run is based on the type of log generated. More specifically, when a **Pipetting Log** is generated, pipetting information such as the pod performing the operation, the type of pipetting operation performed, and the labware position and name are captured, along with other pipetting specific information.

The last line of a log file contains the date and time the method run ended.

Details Log Contents

Each line below the header of a **Details** log contains the following information:

- **Date/Time** — When the action occurred.
- **Action Completed** — Action performed by the instrument.
- **Device Completing the Action** — The device performing the action (if applicable).

Errors Log Contents

Each line below the header of an **Errors** log contains the following information:

- **Date/Time** — When the error occurred.
- **Error Description** — Provides the exact error message.

Pipetting Log Contents

Each line below the header of a **Pipetting** log contains the following information:

- **Date/Time** — When the error occurred.
- **Pod Name** — Which pod performed the operation (Pod1).
- **Position** — The location on the deck (P1, P2...).
- **Labware Name** — Name assigned to the labware in **Labware Properties**.
- **Labware Barcode** — Barcode assigned to the labware in **Labware Properties**.
- **Labware Section** — The labware well (the number of the first well accessed); i.e., for single-tip pipetting tools, the log lists every well accessed, but for multi-tip pipetting tools, the log lists the well accessed with the first tip of the tool only.
- **Amount** — The amount of fluid pipetted.

NOTE If no information was supplied for a particular field, the field is blank in the **Pipetting** log.

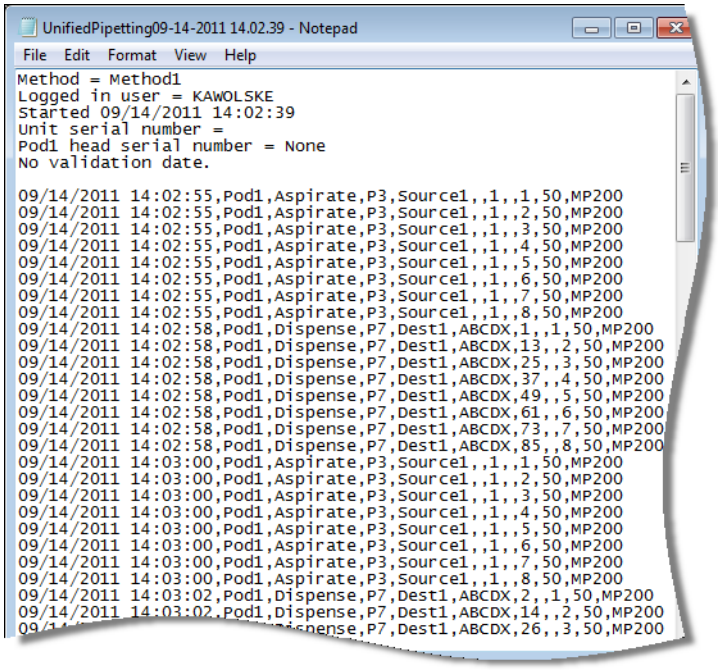
UnifiedPipetting Log Contents

Each line below the header of a **UnifiedPipetting** log (Figure 25.1) contains the following information:

Field	Description
Date/Time	When the pipetting operation occurred.
Pod Name	Which pod performed the pipetting operation (the Biomek 4000 instrument is equipped with one pod only; therefore, this will always be designated as **Pod1**).
Type of Pipetting Operation	Aspirate or dispense.
Source Position	Location of the source labware for the pipetting operation.
Labware Name	Name assigned to the labware in **Labware Properties**.
Labware Bar Code	Bar code assigned to the labware in **Labware Properties**.
Labware Well Number	Number of the well pipetted from in the labware. **NOTE** Wells are numbered left to right, top to bottom for all types of labware (Figure 25.1).
Labware Sample ID for Well	Sample ID assigned in **Instrument Setup** step for well for labware.
Tip Number	Tip used for the pipetting operation. Tips for the Multi-Tip Pipette Tools are numbered 1 through 8, from the back of the instrument to the front.
Volume	Amount of fluid pipetted.
Technique	The name of the technique used to govern the pipetting operation, or **Custom** if a customized technique was used.

NOTE If no information was supplied for a particular field, the field is blank in the **UnifiedPipetting** log.

Figure 25.1 UnifiedPipetting Log



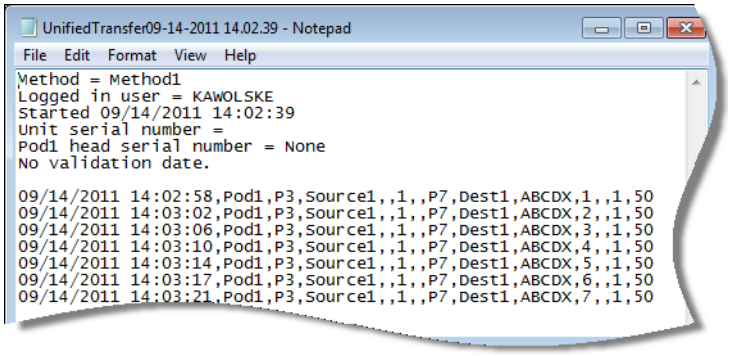
Unified Transfer Log Contents

Each line below the head of a **UnifiedTransfer** log (Figure 25.2) contains the following information:

Field	Description
Date/Time	When the transfer occurred.
Pod Name	Which pod performed the transfer (the Biomek 4000 instrument is equipped with one pod only, and, therefore, this will always be designated as **Pod1**).
Source Position	Location of the source labware for the transfer operation
Source Labware Name	Name assigned to the source labware in **Labware Properties**.
Source Labware Bar Code	Bar code assigned to the source labware in **Labware Properties**.
Source Labware Well	Number of the well pipetted from in the source labware. **NOTE** Wells are numbered left to right, top to bottom for all types of labware (Figure 25.1).
Source Labware Sample ID for Well	Sample ID assigned in **Instrument Setup** step for well for source labware.
Destination Position	Location of the destination labware for the transfer operation.
Destination Labware Name	Name assigned to the destination labware in **Labware Properties**.
Destination Labware Barcode	Barcode assigned to the destination labware in **Labware Properties**.
Destination Labware Well	The number of the well transferred to in the destination labware.
Destination Labware Sample ID for Well	Sample ID assigned in **Instrument Setup** step for well for destination labware.
Tip number	Tip used for the transfer operation. Tips for the Multi-Tip Pipette Tools are numbered 1 through 8, from the back of the instrument to the front.
Volume	Amount of fluid transferred.

NOTE If no information was supplied for a particular field, the field is blank in the **UnifiedTransfer** log.

Figure 25.2 UnifiedTransfer Log



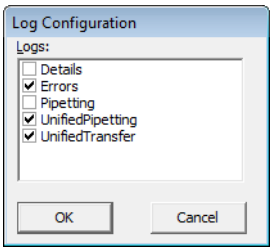
Selecting Log Types

To generate log(s) during a method run, the only information required is a selection of the type of log(s) desired.

To select log(s):

1 Choose **Options > Log Configuration**. **Log Configuration** displays (Figure 25.3).

Figure 25.3 Log Configuration Window



NOTE The default setting for **Errors** is **On**. The default settings for **Details**, **Pipetting**, **UnifiedPipetting**, and **UnifiedTransfer** logs are **Off**.

2 Select the desired logs.

3 Select **OK** when completed.

Viewing Log Files

View log files when creating reports or obtaining detailed information about a method. Log files are viewed in a standard text processor, such as Notepad (Figure 25.4), or in a spreadsheet, such as Microsoft Excel (Figure 25.5).

Figure 25.4 Pipetting Log Viewed in Notepad

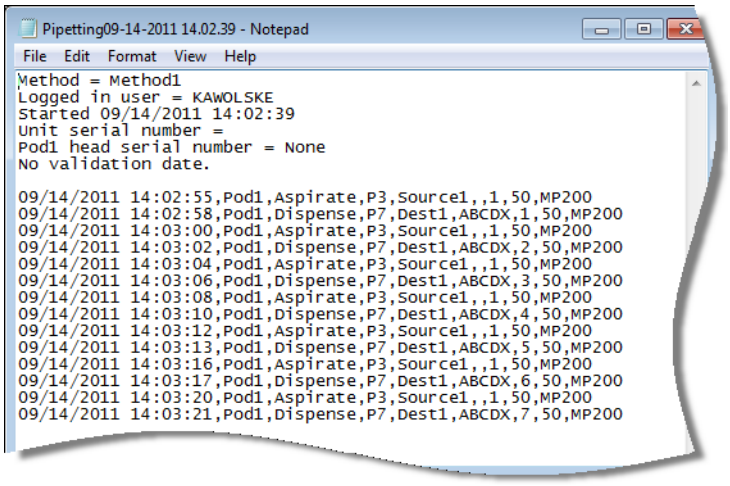
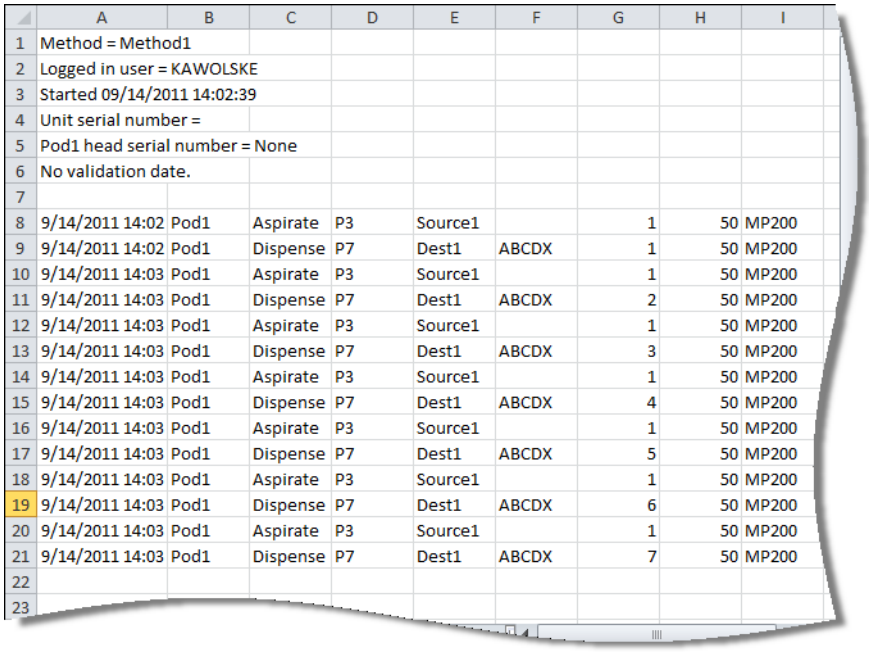


Figure 25.5 Span8Transfer Log Viewed in Microsoft Excel



	A	B	C	D	E	F	G	H	I
1	Method = Method1								
2	Logged in user = KAWOLSKE								
3	Started 09/14/2011 14:02:39								
4	Unit serial number =								
5	Pod1 head serial number = None								
6	No validation date.								
7									
8	9/14/2011 14:02	Pod1	Aspirate	P3	Source1		1	50	MP200
9	9/14/2011 14:02	Pod1	Dispense	P7	Dest1	ABCDX	1	50	MP200
10	9/14/2011 14:03	Pod1	Aspirate	P3	Source1		1	50	MP200
11	9/14/2011 14:03	Pod1	Dispense	P7	Dest1	ABCDX	2	50	MP200
12	9/14/2011 14:03	Pod1	Aspirate	P3	Source1		1	50	MP200
13	9/14/2011 14:03	Pod1	Dispense	P7	Dest1	ABCDX	3	50	MP200
14	9/14/2011 14:03	Pod1	Aspirate	P3	Source1		1	50	MP200
15	9/14/2011 14:03	Pod1	Dispense	P7	Dest1	ABCDX	4	50	MP200
16	9/14/2011 14:03	Pod1	Aspirate	P3	Source1		1	50	MP200
17	9/14/2011 14:03	Pod1	Dispense	P7	Dest1	ABCDX	5	50	MP200
18	9/14/2011 14:03	Pod1	Aspirate	P3	Source1		1	50	MP200
19	9/14/2011 14:03	Pod1	Dispense	P7	Dest1	ABCDX	6	50	MP200
20	9/14/2011 14:03	Pod1	Aspirate	P3	Source1		1	50	MP200
21	9/14/2011 14:03	Pod1	Dispense	P7	Dest1	ABCDX	7	50	MP200
22									
23									

CHAPTER 26

Using Manual Control

Overview

Manual Control and **Advanced Manual Control** are used to control:

- Movement of the bridge, tool, and gripper independently of a method.
- Pod when framing the deck or gripper and recovering from errors.
- Device Controllers and ALPs on a Biomek 4000 instrument manually.

For information on manually controlling the instrument, ALPs, or other devices through **Manual Control**, refer to the *Biomek 4000 Hardware Manual*. Refer to the *Biomek 4000 ALPs and Accessories Manual* or the appropriate integration manual for information on using **Manual Control** with specific ALPs or devices.

Accessing Manual Control

To open **Manual Control**:

1 Choose **Instrument > Manual Control**. An **Information** dialog (Figure 26.1) displays briefly as the connection is made with the instrument, immediately followed by **Manual Control** (Figure 26.2).

NOTE **Manual Control** is available only when a method is not being executed. If a need for manual control is realized during a method run, stop the method using the **Stop** button on the toolbar before accessing **Manual Control**.

Figure 26.1 Confirms Manual Control is Connecting

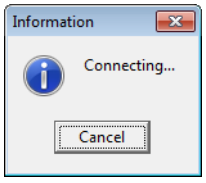
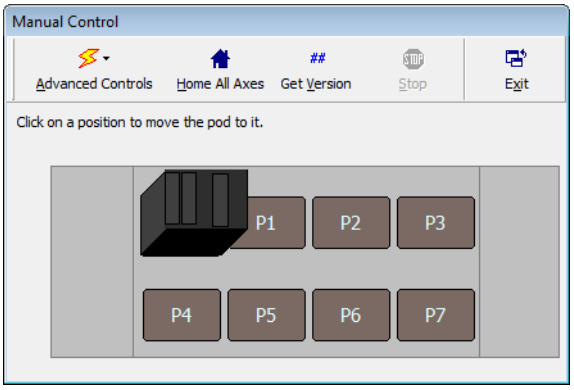


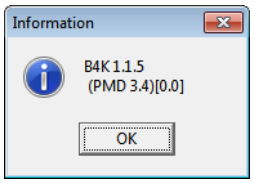
Figure 26.2 Manual Control



Understanding the Options in Manual Control

Table 26.1 lists and describes the options in **Manual Control:**

Table 26.1 Manual Control Options

Option	Description
Advanced Controls	Accesses **Advanced Manual Control** which allows a pod, ALP, or device to be selected. Refer to the specific hardware manual for details on using **Advanced Manual Control** for a device.
Home All Axes	Gives the instrument a point of reference from which to make subsequent moves. On Biomek 4000 instruments, the home position is left, back. **NOTE** The pod should be homed each time the instrument is powered on. Choose **OK** in the warning that displays after confirming that the actions have been addressed properly.
Get Version	Shows the current firmware version for installed devices and pod (Figure 26.3). **Figure 26.3** Information Displaying Firmware Version 
Stop	Stops a pod once movement has started after selecting the desired pod from **Click on a position to move**.
Exit	Closes **Manual Control**.

CHAPTER 27

Scripting

Overview

The scripting feature is based on Visual Basic Scripting, a subset of the Microsoft Visual Basic programming language. Any Visual Basic Scripting code can be interpreted by Biomek Software and may be included in a method.

The **Advanced** step palette provides a **Script** step and a **Scripted Let** step, which provide a configuration area in which code can be entered. These steps invoke a Visual Basic Scripting Engine that evaluates the code.

The **Script** step and **Scripted Let** step expose objects that are used internally by Biomek Software. This is accomplished through the use of the Microsoft Component Object Model (COM).

Data from a reader or LIMS file in a .csv file format may be translated into a data set using scripting. The data sets created from scripting behave like any other data set created in the **Create Data Set** step, from sample IDs in the **Instrument Setup** step, or in the **SILAS** step.

The sections in this chapter include:

- *Using the Script Step*
- *Scripting Data Sets*

Using the Script Step

A **Script** step, available from the **Advanced** step palette, provides a configuration area in which a description of the script step may be entered, and lines of code may be written.

NOTE Refer to CHAPTER 17, *Script Step*, for information on configuring a **Script** step.

A **Scripted Let** step is also available from the **Advanced** step palette and provides a configuration area in which a description of the script step may be entered, and lines of code may be written. However, two additional commands may be entered in the **Scripted Let** step that allow for variables

created in the script to be extended outside of the script and used in configuring other steps in the method. These two new commands are:

- **Extend:** Sets the variable name to the specified value for all steps contained within the **Scripted Let.** The proper syntax for **Extend** is **Extend "Variable Name", Value.**
- **WeakExtend**: Sets the variable name to the specified value for all steps contained within the **Scripted Let** step if the specified variable does not already have a value. This is similar to a **Let** variable with **Overridable** selected. The proper syntax for **WeakExtend** is: **WeakExtend "Variable Name", Value.**

  NOTE Refer to CHAPTER 17, *Scripted Let Step*, for information on configuring a **Scripted Let** step.

Scripting Data Sets

NOTE The information in this section requires an advanced skill level; it is not intended to offer instructions on learning VBScript. Scripting data sets is not supported by Beckman Coulter Representatives; however, information is available in VBScript in a Nutshell: A Desktop Quick Reference, 2nd Edition, Matt Childs, Paul Lomax, and Ron Petrusha 2003, O'Reilly & Associates, Inc.

Data from a reader or LIMS file in a .csv file format may be translated into a data set using scripting. The data sets created from scripting behave like any other data set created in the **Create Data Set** step, from sample IDs in the **Instrument Setup** step, or in the **SILAS** step.

The procedure (refer to *Procedure to Script Data Sets*) to script data sets includes:

- Creating a new data set to hold imported data.
- Opening a .csv file.
- Translating data from a .csv file to a new data set called **Sample ID**.
- Placing the translated data (the new data set called **Sample ID**) into the new data set to hold imported data.

Procedure to Script Data Sets

Execute the following script code:

```
' Create a new Data Set to hold our imported data.

Set DestinationDataSet = Labware("P5").DataSets.Add("SampleID")

' Create the Windows file system object. This object will allow us

' to find our data file on the disk.

Set FileSystemObject = CreateObject("Scripting.FileSystemObject")

' Check to see if the file is on the disk.

If Not FileSystemObject.FileExists("c:\demodata.csv") Then

  ' Call the system's error creator. This will cause a sensible

  ' error message to be shown to the person running the method.
```

```
  ' The first parameter is an error code number. 500 was chosen
  ' because it is not already in use by Windows.
  ' The second parameter is the source of the error.
  ' The third parameter is the description of the error.
  Err.Raise 500, "My Import Script", "File does not exist."
End If
' Open the data file.
Set FileStream = FileSystemObject.OpenTextFile("c:\demodata.csv")
For i = 0 To 7
  ' Read a line out of the file.
 RowLine = File.Stream.ReadLine
  ' Split the values in the line into an array of values, using
  ' the comma as a delimiter.
  ' Note that the array contains values 0, 1, ..., 11.
  RowDataArray = Split(Rowline, ",")
  ' Loop over the columns in the row.
  For j = 0 To 11
    ' Put the data from the array into our new Data Set.
    ' The expression "(i*12) + (j+1)" converts from the 0-based
    ' loop variables to well identifiers.
    DestinationDataSet((i*12) + (j+1)) = RowDataArray(j)
  Next ' end the column loop
Next ' end the row loop
' Close the file when we're done.
FileStream.Close
```

CHAPTER 28

Changing Window Appearance

Overview

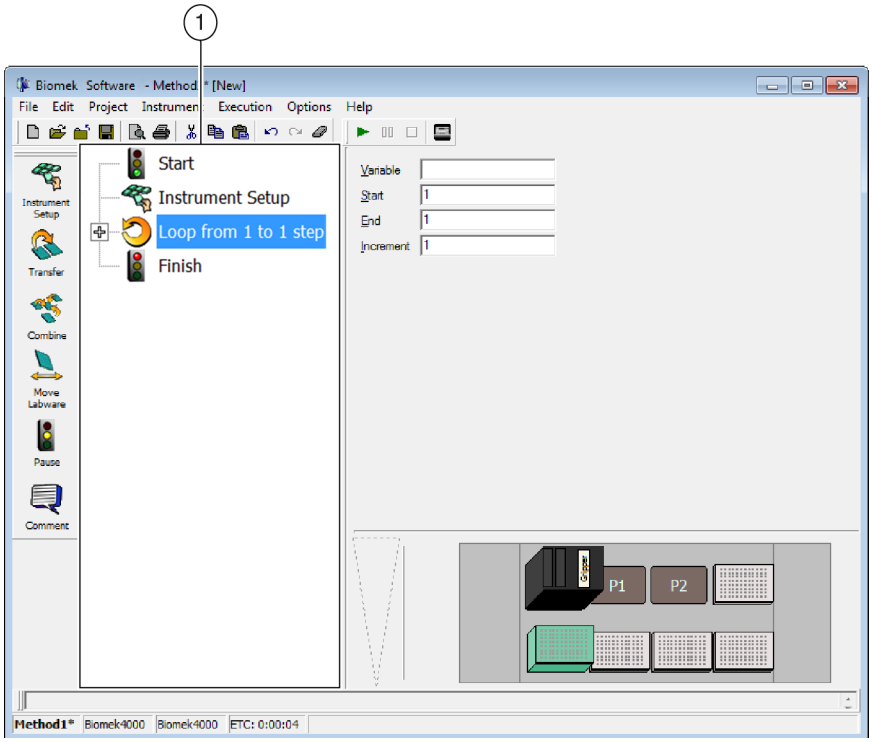
The Biomek Software main editor (Figure 28.1) contains the basic tools necessary to create and run methods; however, there may be times when additional tools are needed. To address this situation, steps and step palettes may be added to the main editor as necessary. These additional steps and step palettes provide more functionality when creating and running methods. By using **Preferences** (Figure 28.12) and **Step Palette Builder** (Figure 28.2), the look of the main editor can be changed to fit the needs of the laboratory.

Preferences is used to alter the Method View and change the size of the steps (or step buttons) in a step palette. For example, graph lines and + and - buttons may be added to the Method View (Figure 28.1), and toolbar and step palette positions may be saved automatically when the appropriate settings are checked in **Preferences**.

The **Step Palette Builder** allows the addition, removal, and manipulation of steps on the step palettes. Steps may be added to any step palette or combined into a new step palette. Individual devices, such as an incubator, operating with a SILAS module must be added to a step palette after the **SILAS** module has been installed so the device can be used in a method and controlled by Biomek Software.

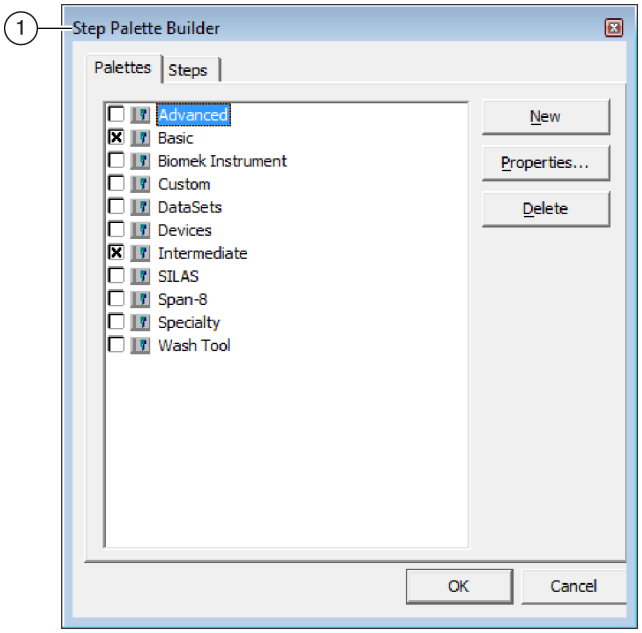
NOTE When the Biomek Software user interface size is decreased, the **Current Deck Display** size is also decreased accordingly to allow more room for method configuration.

Figure 28.1 Main Editor



1. **Method View**: Preferences allows the Method View to be altered. Two options selected in **Preferences** are displayed in this Method View:
   - Display graph lines between steps of a method in the Method View.
   - Display + and - buttons in the Method View when expanded or collapsed substeps are present in a method.

Figure 28.2 Step Palette Builder



1. **Step Palette Builder**: Allows the addition, removal, and manipulation of steps on the step palettes.
   A custom step palette may be created to display frequently used steps on a single palette.

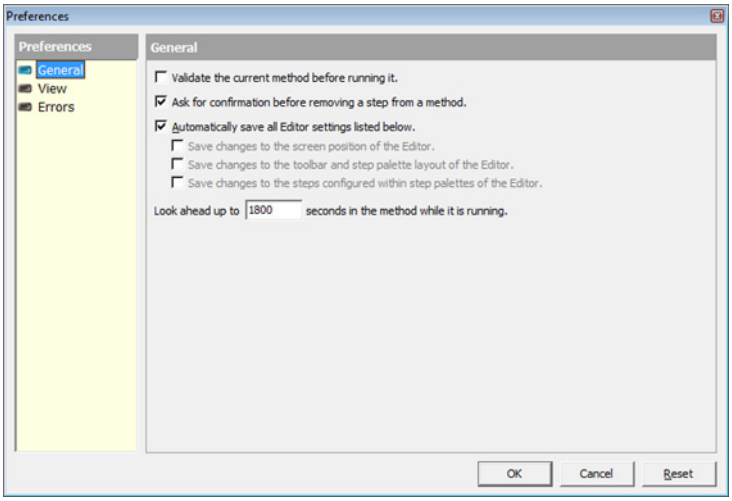
Changing Display Preferences

Preferences allows the main editor appearance to be customized. **Preferences** allows the customization of the main editor using options organized under **General**, **View**, and **Errors**.

To customize the appearance of the main editor:

1 Choose **Options > Preferences**. **Preferences** displays (Figure 28.3).

Figure 28.3 Preferences



2 Choose **General** to configure options concerning validating methods, confirmation on deleting steps, saving Editor settings, and Look Ahead (refer to *Configuring General Options*).

OR

Choose **View** to configure options concerning the appearance of the Method View, Step Palettes, and Toolbars (refer to *Configuring View Options*).

OR

Choose **Errors** to configure options concerning the notifications of errors (refer to *Configuring Errors Options*).

Configuring General Options

To update general options concerning validating methods, confirmation on deleting steps, saving Editor settings, and Look Ahead:

1 From **Preferences**, highlight **General** (Figure 28.3).

2 Check the desired options using Table 28.1.

3 Choose **OK** to save the checked options.

OR

Choose **Cancel** to cancel the checked options.

OR

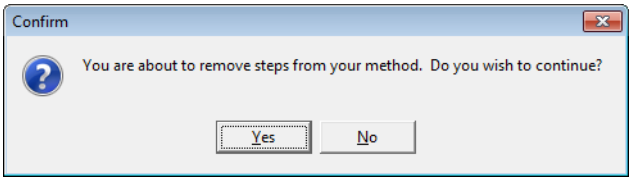
Choose **Reset** to reset all customizations, including custom labware, toolbar/palette organization, options chosen in **Preferences**, and position of the main editor.

Table 28.1 General Options

Option	Description
Validate the current method before running it.	Simulates methods internally to test for errors before the method is run. If no errors are detected, the method is executed. If an error is detected, the process stops and an error message displays information about the error.
Ask for confirmation before removing a step from a method.	Displays a confirmation prompt when deleting a step from a method (Figure 28.4).
Automatically save all Editor settings listed below.	Automatically saves the following three settings. (Enabled by default.)
Save changes to the screen position of the Editor.	When checked, automatically saves the size and position of the editor on the screen. (Available when **Automatically save all Editor settings listed below** is not selected.)
Save changes to the toolbar and step palette layout of the Editor.	When checked, automatically saves toolbar and step palette size, arrangement, and location. (Available when **Automatically save all Editor settings listed below** is not selected.)
Save changes to the steps configured within step palettes of the Editor	When checked, automatically saves steps on step palette (modified by Palette Builder). (Available when **Automatically save all Editor settings listed below** is not selected.)
Look ahead up to ... seconds in the method while it is running.	To prevent the system from slowing down due to unnecessary memory consumption, the software translate the steps of the method into "to do" lists of actions. This option prevents the software from slowing down by designating a length of time for suspending the translation process (refer to CHAPTER 24, *Using Look ahead up to ... seconds in the method while it is running*).

NOTE When **Automatically save all Editor settings listed below** is not selected, and when **Save changes to the screen position of the Editor**, **Save changes to the toolbar and step palette layout of the Editor**, and **Save changes to the steps configured within step palettes of the Editor** are also not selected, the main editor opens at default size with the last saved configuration for the editor, toolbars, and palettes.

Figure 28.4 Confirm to Delete Steps From a Method



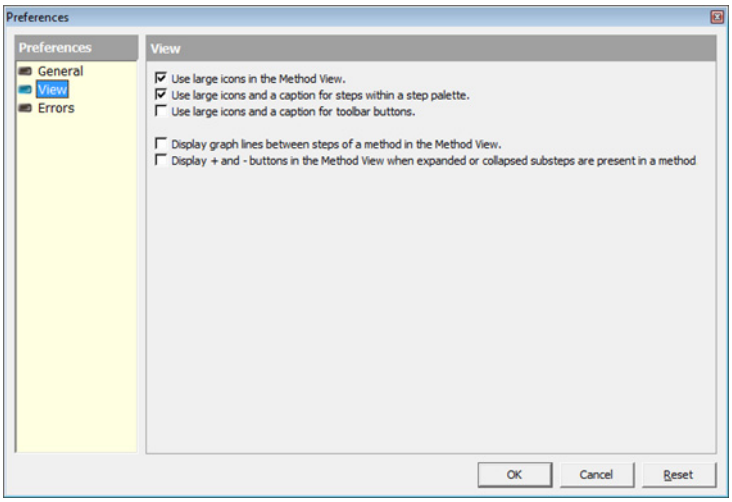
Configuring View Options

View options concern the appearance of the Method View, step palettes, and toolbar buttons.

To configure **View** options:

1 From **Preferences**, highlight **View** (Figure 28.5).

Figure 28.5 Preferences—View



2 Check the desired options using Table 28.2.

3 Choose **OK** to save the checked options.

OR

Choose **Cancel** to cancel the checked options.

OR

Choose **Reset** to reset all customizations, including custom labware, toolbar/palette organization, options chosen in **Preferences**, and position of the main editor

Table 28.2 View Options

Option	Description
Use large icons in the Method View.	Displays text and icons in the Method View in a larger size. (Enabled by default.)
Use large icons and a caption for steps within a step palette.	Displays large icons with labels (descriptive text) under the steps on the step palettes. (Enabled by default.)
Use large icons and a caption for toolbar buttons.	Displays large toolbars with labels (descriptive text) when checked.
Display graph lines between steps of a method in the Method View.	Displays lines which connect steps in the Method View when checked.
Display + and - buttons in the Method View when expanded or collapsed substeps are present in a method.	Displays + and - in front of steps, such as **Loop**, that contain nested steps. Click the + or - to expand or collapse the main step.

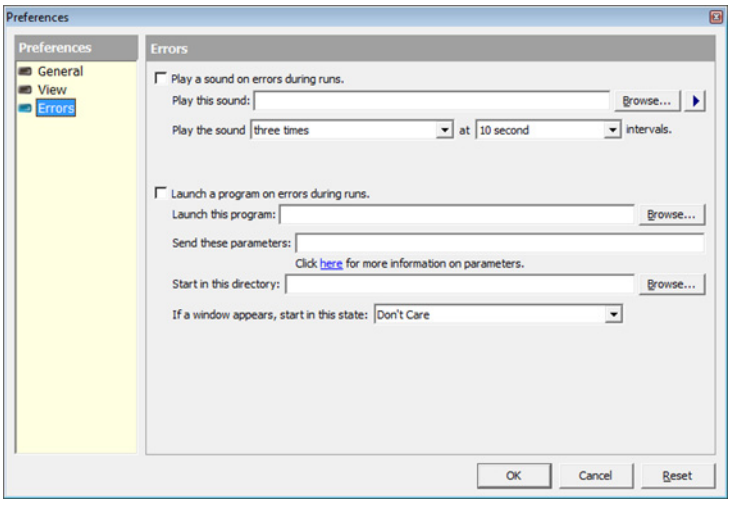
Configuring Errors Options

Error options concern the notifications of errors. An option to play a .wav file when an error occurs is available while another option allows a program, such as an .exe file, to be run when an error occurs

To configure **Errors** options:

1 From **Preferences**, highlight **Errors** (Figure 28.6).

Figure 28.6 Preferences - Errors



2 Choose **Play a sound on errors during runs** to run a .wav file when an error message displays.

3 In **Play this sound**, use **Browse** to find the desired .wav file.

4 Choose the desired .wav file. The desired file appears in **Play this sound**.

5 Select ▶ to play the sound.

6 From **Play the sound**, choose one of the following options from the drop-down menu to play the sound the desired number of times when an error message appears:

- once
- twice
- three times
- repeatedly until dismissed

7 From **intervals**, choose one of the following options from the drop-down menu to play the sound at the desired intervals when an error message displays:

- 1 second
- 5 second
- 10 second
- 30 second
- 1 minute
- 5 minute

8 Choose **Launch a program on errors during runs** to run an .exe file when an error message displays.

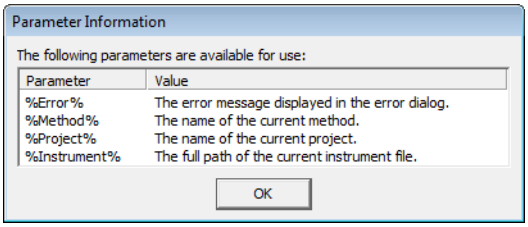
9 In **Launch this program**, use **Browse** to find the desired .exe file.

10 Choose the desired file. The desired file displays in **Launch this program**.

11 In **Send these parameters**, enter the desired parameters using the information displayed in Figure 28.7.

NOTE Choose **click here** to display **Parameter Information** (Figure 28.7). Choose **OK** to close **Parameter Information**. Highlighting the **Parameter** and **Value** and choosing **OK** does not enter the desired parameter; the desired parameters must be manually entered in **Send these parameters**.

Figure 28.7 Parameter Information



12 In **Start in this directory**, use **Browse** to start browsing in the desired directory.

13 From **If a window appears, start in this state**, choose one of the following options from the drop-down menu to display the style of the program:

- **Don't care** — The message appears in the default style of the program.
- **Maximize** — The message appears in the maximized state of the program.
- **Minimize** — The message appears in the minimized state of the program.

14 Choose **OK** to save the checked options.

OR

Choose **Cancel** to cancel the checked options.

OR

Choose **Reset** to reset all customizations, including custom labware, toolbar organization, options chosen in **Preferences**, and position of the main editor.

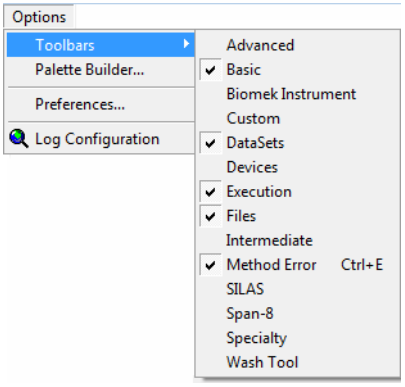
Toggling Toolbars and Step Palettes

The Biomek Software main editor provides toolbars and step palettes to allow quick access to method-building tools. Descriptions of the options in **Toolbars** are shown in Table 28.3.

To toggle toolbars and step palettes on and off:

1 Choose **Options > Toolbars.** A submenu displays listing the toolbars and step palettes (Figure 28.8).

Figure 28.8 Options for Step Palettes and Toolbars

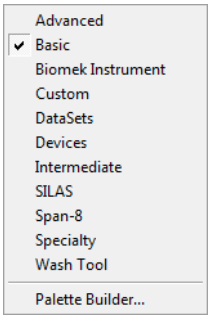


NOTE Any custom step palettes created with the **Step Palette Builder** also display in the submenu (refer to *Creating a New Step Palette*).

OR

Right click in a gray area around the toolbars or step palettes. A menu listing only the step palettes display (Figure 28.9).

Figure 28.9 Step Palette Menu



NOTE Any custom step palettes created with the **Step Palette Builder** also appear in the submenu (refer to *Creating a New Step Palette*).

2 Choose the desired toolbar or step palette to toggle it on or off. The corresponding toolbar or step palette appears or is hidden from view.

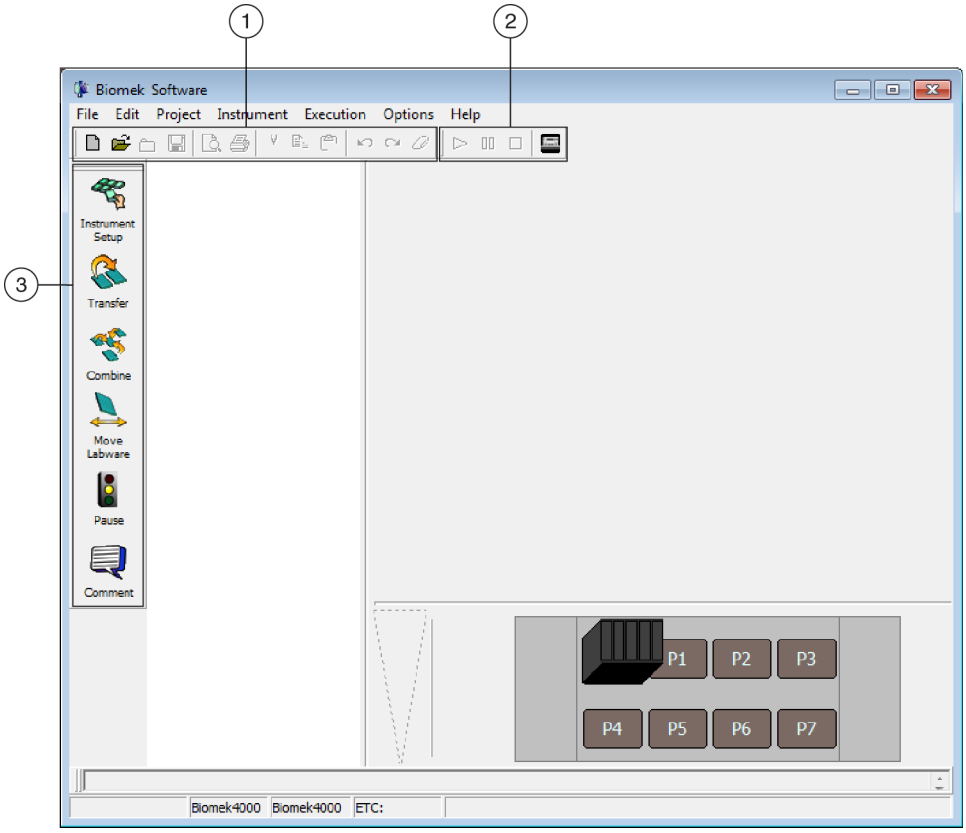
NOTE A check to the left of a toolbar or step palette in **Options** > **Toolbars** indicates that it is currently displayed.

NOTE Use the **Step Palette Builder** as an alternative method for displaying and hiding step palettes (refer to *Displaying and Hiding Step Palettes*)

Table 28.3 Toolbar Options

Option	Description
Advanced	Toggles on or off the Advanced Step Palette.
Basic	Toggles on or off the Basic Step Palette (Figure 28.10).
Biomek Instrument	Toggles on or off the Biomek Instrument Step Palette.
Custom	Toggles on or off the Custom Step Palette.
Devices	Toggles on or off the Devices Step Palette.
Execution	Toggles on or off the part of the toolbar that is associated with the running of methods (Figure 28.10).
Files	Toggles on or off the part of the toolbar that is associated with the building of methods (Figure 28.10).
Intermediate	Toggles on or off the Intermediate Step Palette.
Method Error	Toggles on or off the description of errors.
SILAS	Toggles on or off the SILAS Step Palette.
Span-8	Toggles on or off the Span-8 Step Palette.
Specialty	Toggles on or off the Specialty Step Palette.
Wash Tool	Toggles on or off the Wash Tool Step Palette.

Figure 28.10 Main Editor with Default Toolbar Options Displayed



1. **Files**: Not displayed when deselected from **Options** > **Toolbars**.
2. **Execution**: Not displayed when deselected from **Options** > **Toolbars**.
3. **Basic**: Not displayed when deselected from **Options** > **Toolbars**.

Customizing Step Palettes

Customize a step palette to add custom steps, change the view of the step palettes, or modify tool tips and labels of any step.

Displaying Large Step Palette and Toolbar Views

Captions for toolbars and step palettes can be displayed using **Preferences**. The large icon step palette view and the large icon toolbar view display labels for the steps and tools. A comparison of the large step palette view with captions and the step palette view without captions is shown in Figure 28.11.

Figure 28.11 Step Palette Views With and Without Captions



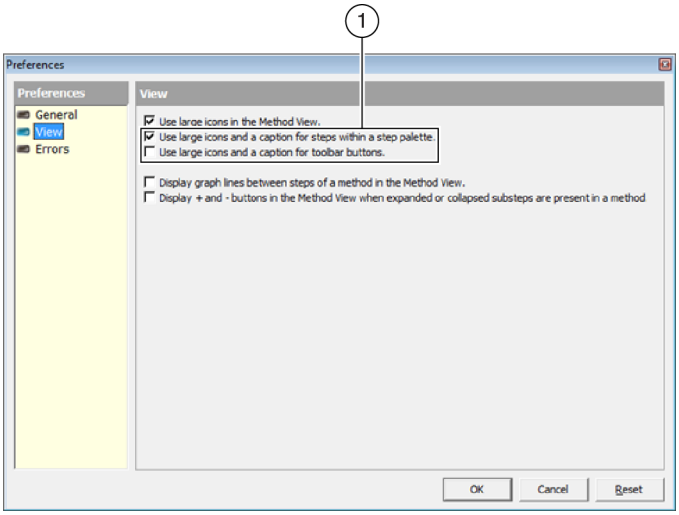
1. **Step palette view without captions.**
2. **Large step palette view with captions.**

To toggle the step palette view:

---

1 Choose **Options > Preferences > View**. Figure 28.12 appears.

Figure 28.12 Preferences - Main Editor Setting Options



1. **Large icon options.**

---

2 Choose **Use large icons and a caption for steps within a step palette** to toggle the step labels (Figure 28.12).

NOTE The default for **Use large icons and a caption for steps within a step palette** is **On**.

3 Choose **Use large icons and a caption for toolbar buttons** to toggle the toolbar labels.

NOTE The default for **Use large icons and a caption for toolbar buttons** is **Off**.

4 Choose **OK**.

Changing Step Properties

Change the properties associated with each step to make the step purpose easier to identify, or to distinguish custom, configured steps from standard steps. Each step has three properties:

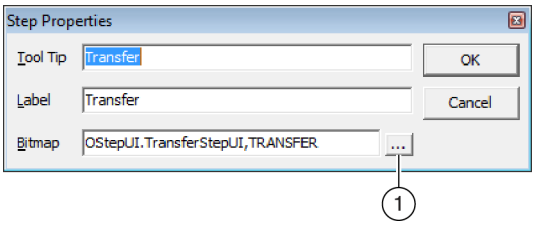
- **Tool Tip** — Brief tip on the step's usage that displays when the mouse pointer hovers over the step.
- **Label** — Text describing operations of a step.
- **Bitmap** — Graphic displayed on the step button.

To change step properties:

1 On the step palette, right click on the desired step.

2 Choose **Properties**. **Step Properties** displays (Figure 28.13).

Figure 28.13 Step Properties



1. **Browse**

3 In **Tool Tip**, enter a new **Tool Tip**.

4 In **Label**, enter a new **Label**.

5 In **Bitmap**, choose a different graphic for the step button by clicking on **Browse**, and selecting the desired bitmap.

6 Choose **Open** to accept the new bitmap and return to **Step Properties.**

7 Choose **OK** to save changes to the **Step Properties** and return to the main editor.

Modifying a Step Caption in Method View

A step caption may be modified in the Method View. This allows differentiation of the steps by their captions.

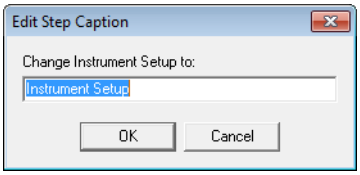
To change a step caption in the Method View:

1 Highlight the desired step in the Method View.

2 Right click on the step to open a menu.

3 Select **Change Caption**. **Edit Step Caption** displays (Figure 28.14).

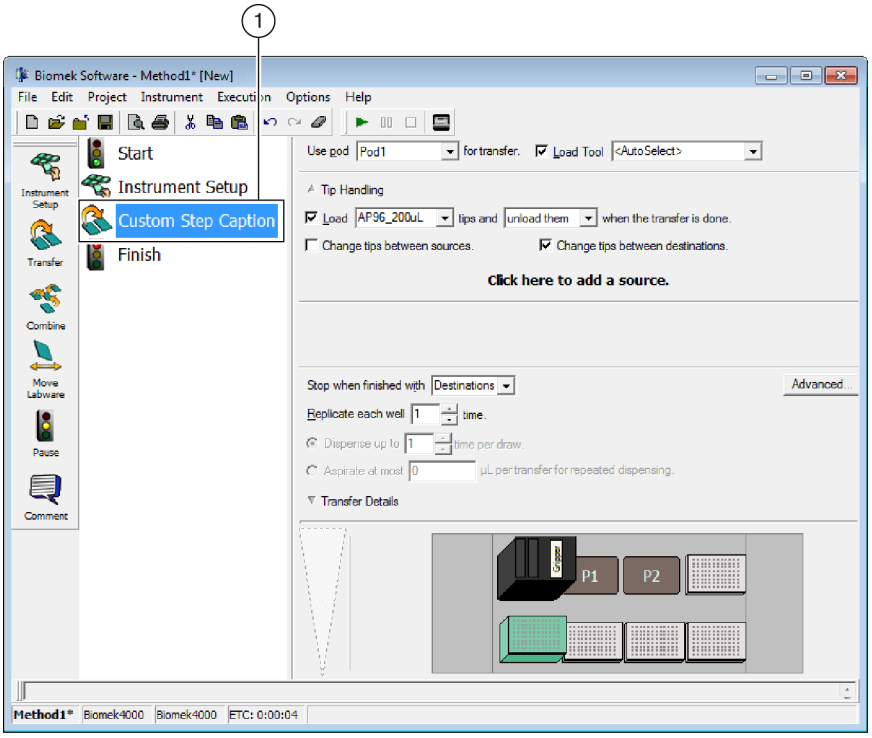
Figure 28.14 Change the Step Caption in Edit Step Caption



4 Enter the new step caption for the step.

5 Choose **OK**. The new caption appears at the appropriate spot in the Method View.

Figure 28.15 Modified Step Caption in Method View



1. **Step caption entered into Edit Step Caption is now shown in Method View.**

Using the Step Palette Builder

The **Step Palette Builder** is used to create, delete, and modify step palettes. If a step is no longer needed on a step palette, it can be removed easily with the **Step Palette Builder**.

Use the **Step Palette Builder** to:

- Display a step palette.
- Hide a step palette.
- Add steps.
- Remove steps.
- Rearrange steps.
- Create a step palette.
- Modify step palette properties.
- Delete a step palette.

Accessing the Step Palette Builder

To access the **Step Palette Builder**:

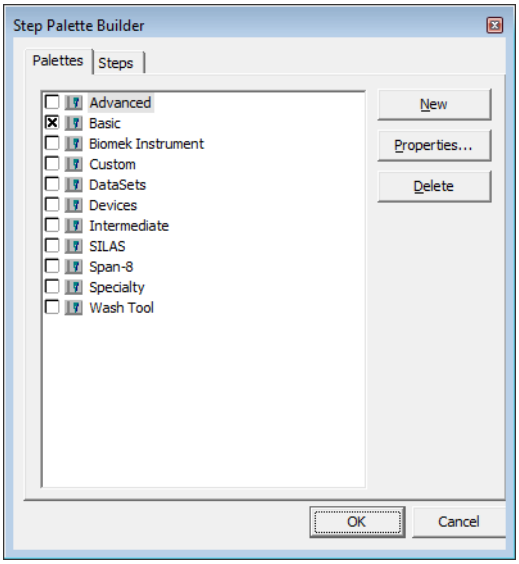
1 Choose **Options** > **Palette Builder....** **Step Palette Builder** displays (Figure 28.16).

OR

a. Right click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 28.9).

b. Choose **Palette Builder....** **Step Palette Builder** displays (Figure 28.16).

Figure 28.16 Step Palette Builder



Displaying and Hiding Step Palettes

Display and hide step palettes using the **Step Palette Builder.**

To display or hide a step palette:

1 In the **Step Palette Builder**, click on the check box to the left of the desired palette to toggle the display on and off.

2 Choose **OK**. The selected step palettes display or hidden from the Biomek Software main editor.

NOTE As an alternative method for toggling a step palette on or off, use the **Options** > **Toolbars** menu (refer to *Toggling Toolbars and Step Palettes*). This alternative method is available only when the **Step Palette Builder** is not open.

Customizing Step Palettes

There are two main sources for steps added to step palettes:

- With **Step Palette Builder** not open, steps can be moved from the Method View onto a step palette.
- With **Step Palette Builder** open, steps can be moved from the **Step Palette Builder** to a step palette or moved between palettes.

NOTE In order to use a SILAS module, such as the barcode reader, it must be placed on a step palette.

Adding Non-Configured Steps to a Step Palette

To add steps to a step palette:

---

1 Choose **Options > Palette Builder.... Step Palette Builder** displays (Figure 28.16).

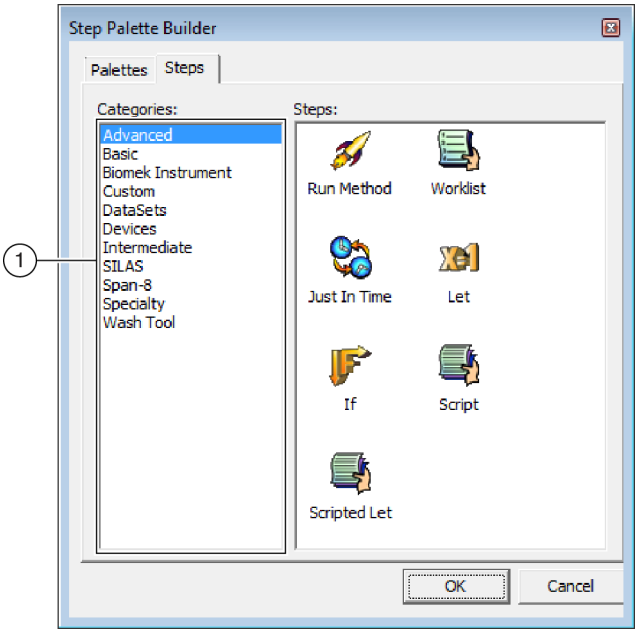
OR

Right click in a gray area around the toolbars or step palettes. A menu listing available step palettes displays (Figure 28.9). Choose **Palette Builder.... Step Palette Builder** displays (Figure 28.16).

---

2 Choose the **Steps** tab (Figure 28.17).

Figure 28.17 Step Palette - Steps Tab



1. **Categories**: Each category available for placement on step palettes consists of steps from predefined groups and installed SILAS modules.

3 In **Categories**, choose the desired category of steps. Steps from the selected category appear on the right side of the **Step Palette Builder**.

NOTE Multiple selections can be highlighted at once in the **Steps** tab by holding down Ctrl or Shift.

4 Drag the desired step from **Steps** to a step palette on the main editor. The step is added to the step palette.

OR

Drag the desired step from one palette to another on the main editor.

5 From the **Step Palette Builder**, choose **OK**.

Adding Configured Steps to a Step Palette

If a step configuration used in a method is to be used several times in various methods, add it to a step palette to save time during the method building process. By adding a configured step, any subsequent uses of the same configuration are added to a method easily.

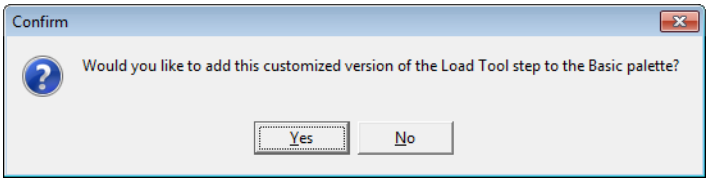
To add configured steps to a step palette:

1 Configure the step in the Method View.

2 Highlight the step to add to the step palette.

3 Drag the step to the desired step palette. The addition of the step must be confirmed before it is added to the palette (Figure 28.18).

Figure 28.18 Confirmation for Adding a Step to a Step Palette



Rearranging Steps on a Step Palette

To rearrange steps on a step palette:

1. Choose **Options > Palette Builder.... Step Palette Builder** displays (Figure 28.16).

   OR

   Right click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 28.9). Choose **Palette Builder.... Step Palette Builder** displays (Figure 28.16).

2. Drag and drop the desired step on the step below the desired location on the palette. The step inserts itself above the step on which it was dropped.

3. From the **Step Palette Builder,** choose **OK.**

Removing Steps From a Step Palette

Remove steps no longer needed to keep step palettes manageable.

To remove steps from a step palette:

1. Choose **Options > Palette Builder.... Step Palette Builder** displays (Figure 28.16).

   OR

   Right click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 28.9). Choose **Palette Builder... . Step Palette Builder** displays (Figure 28.16).

2. Drag and drop the desired step to a location where a step palette is not present.

3. From the **Step Palette Builder**, choose **OK.**

Creating a New Step Palette

Create custom step palettes to display frequently used or commonly used configured steps on a single palette.

To create a step palette:

1. Choose **Options > Palette Builder.... Step Palette Builder** displays (Figure 28.16).

   OR

   Right click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 28.9). Choose **Palette Builder.... Step Palette Builder** displays (Figure 28.16).

2. Choose **New**. A new step palette appears in the upper left corner of the main editor (Figure 28.19).

   Figure 28.19 New Step Palette

3. Change the new palettes properties (refer to *Modifying Step Palette Properties*).

4. Add steps to the step palette (refer to *Adding Non-Configured Steps to a Step Palette*).

5. From the Step Palette Builder, choose **OK**.

Modifying Step Palette Properties

Step palette names can be changed though the Step Palette Builder.

To change a step palette's properties:

1 Choose **Options > Palette Builder.... Step Palette Builder** displays (Figure 28.16).

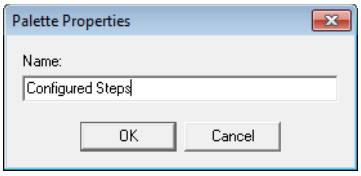
OR

Right click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 28.9). Choose **Palette Builder.... Step Palette Builder** displays (Figure 28.16).

2 Select the desired palette.

3 Choose **Properties.... Palette Properties** displays (Figure 28.20).

Figure 28.20 Palette Properties



4 Type a descriptive name for the step palette.

NOTE All alphanumeric and non-alphanumeric characters are allowed in palette names.

5 From **Palette Properties**, choose **OK** to save the name.

6 From **Step Palette Builder**, choose **OK**.

Deleting a Step Palette

Delete any step palettes that are no longer needed.

To delete a step palette:

1. Choose **Options > Palette Builder.... Step Palette Builder** displays (Figure 28.16).

   OR

   Right click in a gray area around the toolbars or step palettes. A menu listing available step palettes appears (Figure 28.9). Choose **Palette Builder.... Step Palette Builder** displays (Figure 28.16).

2. Select the desired palette.

3. Choose **Delete**. The step palette is removed from the main editor.

   NOTE Deleting a step palette cannot be undone. There is no confirmation for deleting a step palette. If a step palette is accidentally deleted, choose **Cancel** in **Step Palette Builder**.

4. Choose **OK**.

Abbreviations

.bat — batch file

.bif — Biomek instrument file

.bmf — Biomek method file

.csv — comma separated value file

.exe — executable file

.imp — Biomek import file

.txt — text file

µL — microliter

ALP — active labware positioner

CD — compact disk

CFR — Code of Federal Regulations

COM — communication port

COM — Component Object Model (Microsoft)

cm — centimeters

DMSO — dimethyl sulfoxide

DNA — deoxyribonucleic acid

ETC — estimated time to completion

ID — identification

in. — inch

JIT — just in time

LLS — liquid level sensing

Max — maximum

Min — minimum

mm — millimeter

ms — millisecond

mW — milliwatt

nm — nanometer

RGB — red, green, blue

s — second

sec — second

SPE — Solid Phase Extraction

SQL — Structured Query Language

USPTO — United States Patent and Trademark Office

VB — Visual Basic

WEEE — Waste Electrical and Electronic Equipment

Glossary

21 CFR Part 11 — Outlines the technical and procedural FDA requirements to implement electronic records and/or electronic signatures for computer systems.

Absolute Moves — Low level, position-to-position moves along one or more axes.

AccuFrame — A device that automates the process of teaching Biomek Software the location of the labware positioners and devices positioned on the deck.

Address Switch — Address switches allow Biomek Software to identify the device being used with hexidecimal numbering. Address switches are manually set on active ALPs.

Axis — Line along which motion occurs. The Biomek 4000 instrument has four axes (X-, Y-, Z-, and D- [T-]).

Barcode Reader ALP — Active ALP that scans barcode labels applied to labware.

Beckman Coulter Accounts & Permissions — An integrated set of features built into Beckman Coulter software that assists users in complying with 21 CFR Part 11 requirements for closed systems. With Biomek Software, support is extended only for the instrument; devices integrated with the instrument are not supported unless specified in separate documentation.

Biomek 4000 Laboratory Automation Workstation — Liquid handler designed for benchtop use and to fit in a laminar flow or fume hood for sterile or hazardous operations. The open architecture design, along with the extensible operating software, provides a foundation for integrating current and future specific-use components. The Biomek 4000 instrument uses a single pod with a series of interchangeable tools. Different tools provide options for performing a variety of functions, including liquid transfer and plate washing operations and moving labware around the deck.

Blowout — Process in which extra air is aspirated into tips before aspirating liquid and then dispensed after dispensing liquid to ensure all liquid has been dispensed from the tips.

Bridge — The Biomek 4000 bridge is the structure that moves along the rear support and front rails. The bridge holds the pod and enables movement of the pod in the Y- (front to back) and Z-axes (up and down). Built into the bridge is an indicator light that displays the current operational status of Biomek 4000 workstation. The Biomek 4000 instrument supports only one bridge.

Called Method — Method opened and run from a **Run Method** step.

Called Procedure — Procedure opened and run from a **Run Procedure** step.

CAN (Controller Area Network) — Controller Area Network communicates with multiple microprocessors.

Circulating Reservoir — Continually cycles a reagent between off-deck reagent bottles and wells of a four-well reservoir positioned on the Biomek 4000 deck.

Collar (SPE Vacuum Manifold ALP) — Device that supports the source microplate and encloses the receiver filter microplate during filtration operations using the SPE Vacuum Manifold ALP.

Combine Step — Biomek Software step that aspirates from multiple sources and dispenses to a single destination.

Communications Cable — Cable used to link the instrument or other devices to the host computer.

Configuration View — Part of Biomek Software main editor where the configuration for each step appears. The view changes to correspond to the highlighted step in the Method View.

Conic Length — Lowest triangular section of a tip.

Connections — Located on each side of the rear support panel. Connection include power and communications.

Coordinate — Any set of numbers used to specify the location of a point in space. The Biomek 4000 instrument has four axes (X-, Y-, Z-, and D [T-]).

Current Deck Display — Display located at bottom of the main editor showing the location of labware on the deck during a method run. Also shown in the **Deck Editor**.

D- [T-] axis — Axis that allows for aspirate, dispense, tip shucking, and gripping operations. Movement along axis is vertical.

Data Set — Stores specific information about wells or tubes. Using data sets, information about a sample in an individual well or tube is tracked along with the sample when it is moved to another well or tube.

Deck — Workspace on the software. Physical deck of the instrument. The Biomek 4000 deck is the worksurface of the instrument and provides eight standard positions for tool racks and labware positioners. The deck contains predrilled locating holes used to place labware positioners and tool racks precisely.

Deck Layout — Current configuration of the deck.

Deck Position — Specific place on the instrument deck. Positions may be named automatically or may be given custom names.

Define Procedure — Step used to create a series of steps that may be used multiple times in a method. A procedure is created by adding and configuring steps within a **Define Procedure** step.

Delta — Used for **Manual Control**. Change value for manual movement of pods.

Diluent — Inert substance used to dilute a sample during serial dilution.

Disposal Accessory — Provides a waste receptacle for disposing of tips and labware from the Biomek 4000 deck using the gripper tool. Tip boxes or other labware may be deposited directly to the disposal accessory, eliminating the need to manually dispose of waste.

DMSO — Reagent used to solubilize compounds. Irritating to eyes, skin, and the respiratory system.

Encoder — Tracks the absolute position of an axis.

Enqueue — Used internally by software and firmware to establish the order of operations of the instrument.

Expression — One-line combination of alphanumeric characters and/or variables combined using mathematical operations. May be used anywhere a variable can be used.

Filter Microplate — Labware through which fluids are separated from solids in the SPE Vacuum Manifold ALP.

Filtration System — Includes a vacuum valve unit that is connected to the instrument via RS-485 communication, and a manifold system with interchangeable collars to allow collection of filtrates to microplates or waste. The filtration system is used to run screening assays which require filtration, such as receptor binding and cell-based assays, and plasmid DNA purification applications on the Biomek 4000 workstation.

Follow Liquid — When chosen, the tips will follow the liquid level during aspirate or dispense. If no liquid levels are defined in the labware when **Follow Liquid** is active, an error will occur. The error will read **"Cannot move relative to liquid level if liquid amounts are not defined for specified labware."**

Framing — Process of providing exact coordinates of positions on the deck or exact offsets for the gripper. Also called teaching.

Framing Plate — Used to frame the gripper tool on the Biomek 4000 workstation. The gripper tool is framed visually using the gripper tool to pick up the framing plate.

Framing Tools — Tools used in the process of framing the deck or grippers.

Gripper — On the Biomek 4000 workstation, the gripper is usually referred to as the gripper tool. The gripper tool has gripper fingers (two in front and one in back) that grasp labware along the long side and move the labware from one location on the deck to another.

Hardware Error — Error resulting from problems with the hardware.

Home Position — Origin of an axis or coordinate system. This position is where the pod goes when it is homed. The home position is located toward the upper back left corner of the instrument. Also known as the Zero (0) point.

Homing — Process of locating the home position. This process must be done every time the instrument is powered up. Instrument homes Z-, Y-, X- and D- [T-] axes.

If Step — Step controlling actions in a method based upon a condition, such as liquid volume in labware or aspirate amount.

Import File — File that contains settings from a project file.

Import/Export Utility — Utility that allows settings from an instrument file to be recovered or shared.

Initialization — Process of setting or verifying a starting position when the instrument is powered up. This process sets the instrument to its starting configuration.

Instrument File — Stores information about the hardware configuration and deck layout of the instrument. Instrument files can represent different Biomek instruments, or different hardware configurations for the same instrument.

Instrument Setup — Step which specifies the configuration of the instrument deck and pod. Includes labware and labware contents for items on the deck.

Just in Time (JIT) — Step which synchronizes the execution of its substeps. Steps within the **Just In Time** block are enqueued in the order in which they appear in the Method View, but it may be possible to execute two or more steps simultaneously.

Labware Class Type — Groups of labware, such as microplates, available for use with the instrument. Labware class types may be added, modified, or deleted as needed.

Labware Positioners — Used to hold microplates, tube racks, reservoirs, or tip racks on the deck. The gripper tool can move labware to and from these labware positioners to other labware positioners or devices integrated on the left or right side of the instrument.

Labware Properties — Characteristics of labware for use in a method. Accessed from either **Device Setup** or **Instrument Setup** steps.

Liquid Level Sensing — On the Biomek 4000 workstation, P200L and P1000SL tools include patented technology that sonically detects the liquid level. Liquid level sensing is performed using an acoustic process involving a transmitter and receiver within the single-channel tools. The transmitter emits a sound wave through the tip that bounces back when it contacts liquid. The receiver detects the wave as it bounces back past the end of the tip.

Liquid Type — Liquid characteristics and properties. Edited in the Liquid **Type Editor**.

Locating Holes — Predrilled holes in the deck that are used to position ALPs, Labware Positioners, or devices on a Biomek deck or an off-deck position.

Logs — Files that provide text record of a method run. Biomek Software offers five types of logs: **Details**, **Errors**, **Pipetting**, **UnifiedPipetting**, and **UnifiedTransfer.**

Loop — Step that repeats a sequence of steps a number of times during a method.

Main Editor — Main window in Biomek Software for building liquid-handling methods for a Biomek instrument. Includes the Step Palettes, Method View, Configuration View, Current Deck Display, menu bar, toolbar, and status bar.

Mandrel — Part of a tool that holds a disposable tip and is used during aspirating and dispensing functions.

Manual Control — Allows pod to be moved manually via a software interface.

Marks — When labware is accessed, the software keeps track of which wells have been used. If **Set marks** is enabled, the wells accessed for any operation are marked and future operations may continue from the marked wells by either selecting the **At first selected well** or **At first unmarked well** option.

Method — Sequentially ordered list of steps comprising a liquid-handling procedure.

Method View — Pane in the main editor displaying the steps in a method.

Microplate — Labware used in liquid-handling procedures. Also referred to as a microtiter or titer plate.

Microtiter Plate — Labware used in liquid-handling procedures. Also referred to as a microplate or titer plate.

Nested Steps — Steps residing within another step, such as **Loop**, **If**, or **Let**.

Observed Error — Error observed during a method run not resulting in an error message.

Orbital Shaker ALP — Active ALP that shakes labware using an orbital shaking motion. Thumbscrews attach the ALP to the integration deck and a clamping mechanism anchors and positions labware for shaking and pipetting operations.

Off-Deck Tool Rack — Special off-deck tool rack, which is used to hold up to two interchangeable pipetting tools or one gripper in a single deck position attached directly to the left or right side of the deck or attached to the left side of the left-side module.

Offset — Distance from one point to another point.

Open Architecture — Philosophy used when designing the various Biomek platforms. Expansible and open to many uses. Users may pick the equipment that will be most beneficial to their liquid handling needs. The system is expandable in use and configuration so that as users' needs change, the unit can be changed to facilitate those needs.

Parameters — Configuration values that are part of a method or step.

Pipetting Template — Controls the pipetting actions and movements of a pod within the wells of labware.

Pipetting Tools — Single-channel and eight-channel tools used on the pod to aspirate and dispense liquid.

Plasmids — Circular double-stranded DNA molecules that exist independently from the bacterial chromosome. They are used extensively in DNA cloning procedures.

Pod — The pod is referred to as Pod1 in Biomek Software. The Biomek 4000 pod is supported and positioned by the bridge and moves in the Y- and Z-axes. The pod may hold various interchangeable tools, such as the P200L Single-Tip Pipette Tool or MP200 Multi-Tip Pipette Tool, that perform liquid-handling and labware manipulation.

Preferences — Dialog allowing for changes in the look of the main editor and sets method viewing options.

Prewet — Aspirates and dispenses a specific amount of liquid before performing actual pipetting procedures.

Project File — Stores information about liquid types, labware and tip types, and pipetting techniques as revisions that are used by a method file to configure the actions of the instrument. Project files store a history of all changes, additions, and deletions of items from the project file.

Properties — Characteristics of objects and operations used within Biomek Software. For example, labware has properties for well volume and liquid type, and a pod has properties for speed limit and axes limit.

PSI — Pounds per square inch. Measurement used when setting air pressure for pneumatic lines.

Record — Any item stored in a project file that has been saved. Examples include labware types, method revisions, and deleted items.

Relative Moves — Moves made relative to the current pod location. These are used in the **Advanced Manual Control** dialog to move a pod.

Reservoir — Labware receptacle holding liquid to be used in a method.

RS-232 Communication — Serial communication standard used for PC to Biomek 4000 instrument.

Run Method Step — Step that executes a method within the current method.

Run Procedure Step — Step that executes a procedure within the current method.

Run Time — Any period when a method is executing.

Sample — Substance of interest contained in labware.

Sample Tracking — Capabilities built into the functionality of Biomek Software that allow per-well and per-tube sample information to move with the transport (labware) during the method run. Information is attached to the transport and travels from the source labware to the destination well/tube. The desired data output is defined and set before the method run begins, and is reported as desired at the completion of the run.

Serial Dilution — Laboratory process that serially dilutes a sample to determine the lowest concentration of the sample required to achieve the desired result. Serial dilution is often used to achieve desired concentrations prior to conducting an assay.

Shaking Peltier ALP — A labware positioner with microplate shaking and heating and cooling capabilities from a connected controller.

Shucking — Removal of tips from mandrels.

SILAS — Open-standard protocol for inter-process messaging. Allows independent development and modification of software modules used to control devices such as a barcode reader.

SILAS Module — Software module used to control the operation of a device.

Single Step — Allows the performance of single operations within Biomek steps, such as **Aspirate** or **New Tips**. **Single Step** pauses the Biomek instrument between each operation in a step, allowing visual verification that the operation is correct.

Software Error — Error resulting from inconsistencies between the software and instrument or between configuration items.

SPE Stack — SPE Vacuum Manifold components that are stacked during a method to create the SPE Vacuum Manifold ALP.

SPE Vacuum Manifold ALP — Active ALP that filters fluid from samples by pulling the fluid through a filter microplate.

Speed Limit — Percentage of maximum speed at which an instrument move should occur.

Static Peltier ALP — A labware positioner with heating and cooling capabilities from a connected controller.

Status Bar — Bar located along the bottom of the main editor that shows the current method, project file, instrument file, estimated method time, and error messages.

Step Configuration — Pane in the main editor allowing for configuration of a highlighted step.

Step Palette — Panes in the main editor showing steps available for insertion in a method.

Steps (in Biomek Software) — User-configurable actions that may be included in a method and executed during a method run.

String — Series of contiguous characters used as the value of a variable or step parameter.

Substep — Nested step in another step, such as **Loop** or **If**.

Teaching — Process of providing exact coordinates of positions on the Biomek deck or exact offsets for grippers. Also called framing.

Technique — Pre-programmed and automatically selected ways to pipette based upon properties and values.

Technique Properties — Specific items, such as labware type and liquid type, associated with a technique. The number of properties that match a method determine the technique that is selected.

Thermal Exchange Unit — Heats or cools a reservoir or microplate on the Biomek 4000 deck. The temperature is controlled by a user-supplied circulating bath.

Timed Resource — Allows a method to be paused at the desired deck position for a specified period of time.

Tip Touch — Touching of the tip against the side of the well to remove residual drops of liquid before the tip leaves the well.

TiterPlate — Labware used in liquid-handling procedures. Also referred to as microplate, microtiter plate, or plate.

Tool Rack — Special labware positioner on the Biomek 4000 instrument used to hold up to five interchangeable tools in a single deck position during a method.

Tool Rack With Gripper — Labware positioner used to hold up to two interchangeable pipetting tools and one gripper in a single deck position during a method.

Trailing Air Gap — Aspirates air into tips after aspirating fluid to help prevent liquid leaks during liquid transfer.

Transfer Step — Biomek Software step that aspirates from a single source and dispenses to single or multiple destinations.

Validate (the current method before running it) — Option which signals the software to simulate the method prior to a run in order to allow errors to be detected before a method starts.

Validated Method — Revision of a method that is saved, approved with an electronic signature, and protected from further modification. Revisions of project items required to run the validated method are also saved and protected from further modification. This ensures that validated method runs are reproducible. When Beckman Coulter Accounts & Permissions is enabled, methods may be validated. Only users with Validate Methods permission can validate methods.

Vector — Quantity specified by direction and magnitude.

Wash System — Includes single-channel and eight-channel wash tools used to perform plate washing and bulk dispense operations on the Biomek 4000 workstation.

Well Depth — Distance in centimeters from the top of the well to the most bottom point of the well.

Worklist — External file containing names and related values. The names are symbolic identifiers used to represent the values.

Wrist ground strap — Device worn about the wrist and attached to the instrument deck to disperse electro-static discharge.

X-axis — Pod horizontal axis oriented along the front rail and rear support. Smaller X coordinates are to the left and larger ones are to the right.

Y-axis — Pod horizontal axis oriented along bridge. Smaller Y coordinates are to the back and larger ones are to the front.

Yoke Adapter Plate — The interconnect between the pod and the bridge.

Z-axis — Pod vertical axis. Smaller Z coordinates are downward and larger ones are upward.

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- Setting Up the Worksurface
- Pipetting Tools
- Gripper Tool
- Hardware Setup
- Framing
- Controlling the Workstation

Biomek 4000 Preinstallation Manual
PN A99499
- Preinstallation Requirements

Biomek 4000 ALPs and Accessories Manual
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- Understanding and Creating Liquid Types
- Understanding and Creating Techniques
- Using the Pipetting Template Editor
- Creating Well Patterns
- Creating and Using Methods
- Using Variables and Expressions in a Method
- Using Sample Tracking and Data Sets in a Method
- Using the Basic Step Palette
- Using the Intermediate Step Palette
- Using the Advanced Step Palette
- Using the Span-8 Step Palette
- Using the Biomek Instrument Step Palette
- Using the Specialty Step Palette
- Using the Devices Step Palette
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- Using the DataSets Step Palette
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- Biomek 4000 System Updates
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- Hardware Installation
- Software Installation
- Software Setup
- Framing Using AccuFrame
- Installing Adapter Plates and Creating Labware Offsets
- Operations

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