Software Tutorial

Biomek 4000

Laboratory Automation Workstation

PN A99502AA
October 2012

Beckman Coulter, Inc.
250 S. Kraemer Blvd.
Brea, CA 92821

BECKMAN COULTER

Biomek 4000 Software Tutorial
PN A99502AA (October 2012)

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Revision History

This document applies to the latest software listed and higher versions. When a subsequent software version changes the information in this document, a new issue will be released.

Initial Issue, 10/12
Software version 4.0

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.

Contents

Illustrations

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Introduction

Biomek Software

Welcome to Biomek Software and the Biomek 4000 Laboratory Automation Workstation.

Biomek Software controls the instrument and is designed to:

- do a substantial amount of method-building work for you.
- allow you to take as much direct and precise control over the method-building process as you want.

The flexibility that results from this combination gives the instrument its power.

Using This Tutorial

This tutorial is designed to help you become comfortable using Biomek Software with your instrument. The chapters in this tutorial can be completed consecutively or, depending on the learning required, may be completed in any order. This format will allow advanced users to complete only the chapters that include the topics they need to learn.

TIP For effective learning, **print** this tutorial before use, leaving your computer screen free for viewing Biomek Software.

IMPORTANT For the tutorials to work correctly, complete all tutorials in this manual using the default Biomek 4000 Project File, and ensure that the **Default** technique is used for all aspiration and dispense activities.

IMPORTANT This tutorial provides instructions requiring you to enter text into specific fields. The text to be entered is indicated by **bold** font. If the bolded phrase is followed by a period, do not enter the period into the text field.

In addition to the step-by-step instructions in this tutorial, you will also see helpful information in the following two forms:

Biomek Concept	
	These boxes contain information to help you understand important features and capabilities of Biomek Software or the Biomek 4000 Laboratory Automation Workstation. While the step-by-step instructions may be completed without reading the information in these boxes, the information will enhance your knowledge and give you a fuller picture of what Biomek Software and your instrument can do.

TIP The information in these **Tips** offer suggestions on how to use your instrument and software to enhance the activities you want to do in your laboratory.

CHAPTER 1

Getting Started

What You'll Learn In This Chapter

In this chapter, you will learn how to:

- Launch Biomek Software and see what the method-building process looks like.
- Set up the deck for a liquid transfer.
- Build a liquid-transfer method.
- Run a method.
- Save and check in a method.

Launching Biomek Software

To launch Biomek Software:

1 From the **Start** menu, select **All Programs > Beckman Coulter > Biomek Software.**

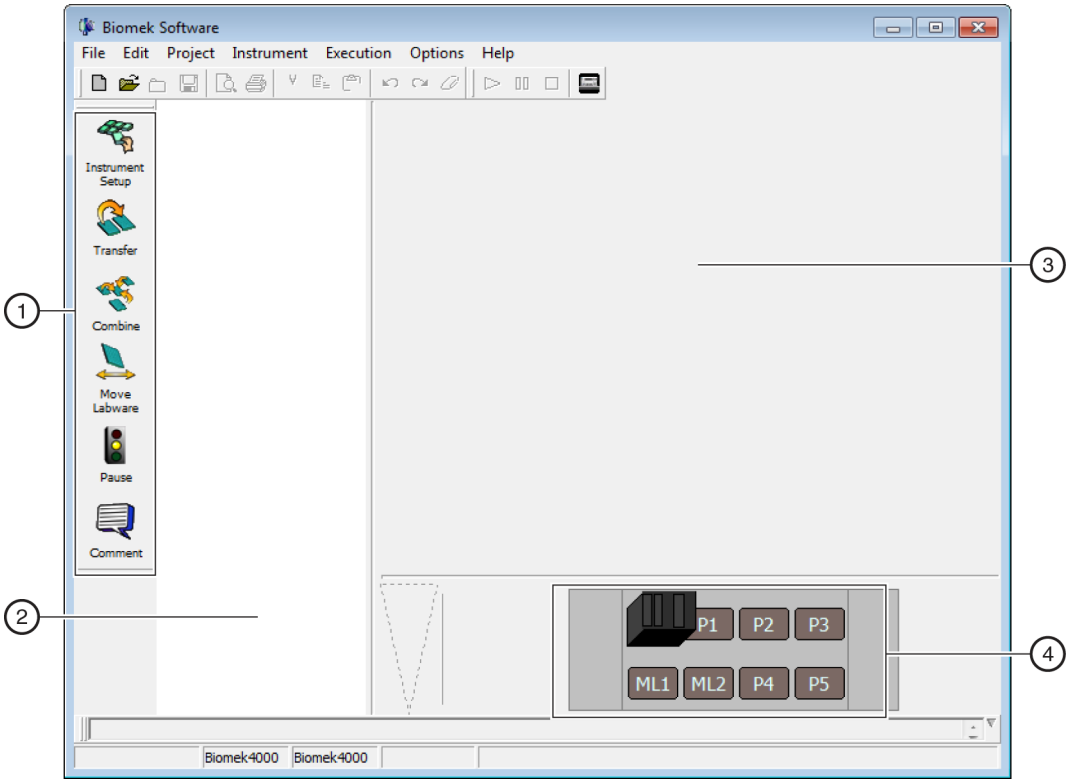
If Beckman Coulter Accounts & Permissions is enabled on your system, you must have an account established and log in using that account name and password in order to fully complete this tutorial. For more information, contact your system administrator.

Biomek Concept: Accounts & Permissions	
	Beckman Coulter Accounts & Permissions is an integrated set of features built into Biomek Software that assists users in complying with 21 CFR Part 11 requirements for closed systems. Permissions provide the ability to control user access to specific program operations. Refer to the *Biomek 4000 Software Manual* for additional details.

Viewing the Main Editor

The main editor (Figure 1.1) is your starting point for building liquid-handling methods for the Biomek 4000 Laboratory Automation Workstation. You will choose method steps from a step palette and place them into the Method View in a linear fashion. The configuration for each of these steps appears in the Configuration View.

Figure 1.1 Biomek Main Editor



1. **Step Palettes**: Icons representing predefined steps for building methods are displayed in this area.
2. **Method View**: Place in this area the steps you want your method to complete.
3. **Configuration View**: The configuration for each step appears in this area. The view changes to correspond to the step highlighted in the Method View.
4. **Current Deck Display**: This display changes dynamically to reflect the status of the deck upon completion of the previous step.

Beginning a Method

To begin a method, you have the option of creating a new method or opening an existing method you've completed, named, and saved. In this tutorial, you'll create a new method.

But before you create a new method, get into the habit of ensuring you are using the correct Project File.

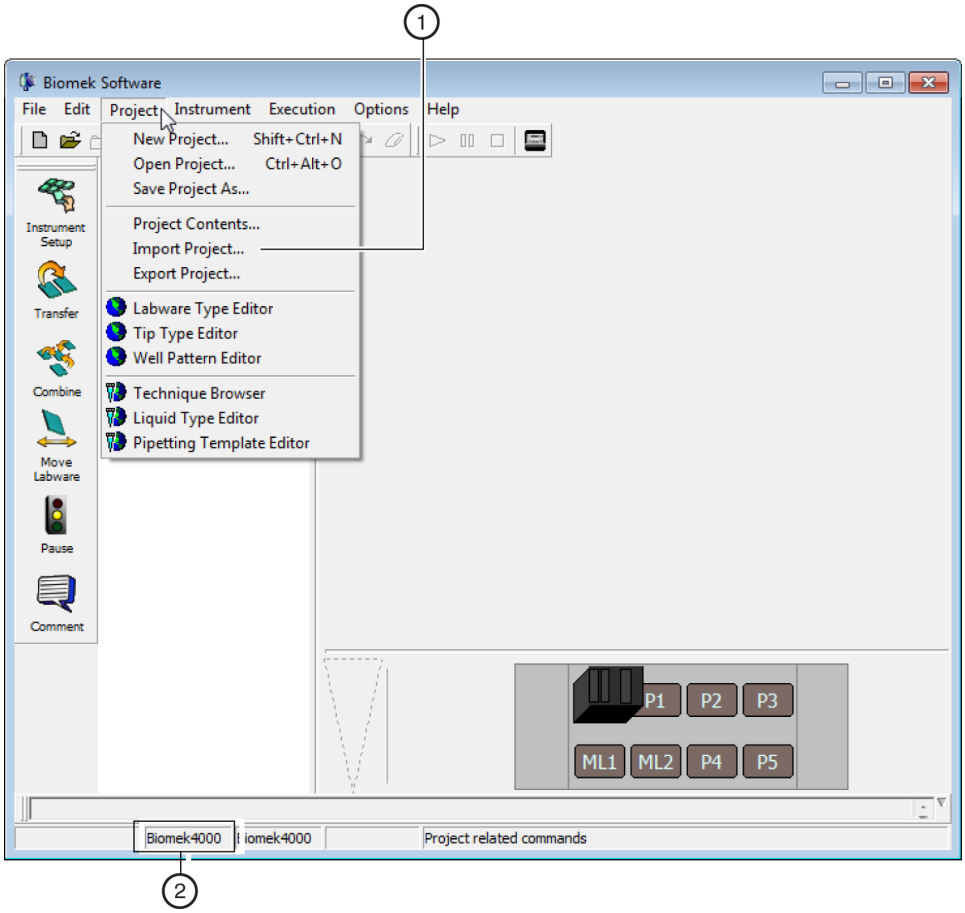
Introducing Project Files

While Project Files may be created, revised, deleted, imported, or exported, in this tutorial you will use the Project File on your system that was created or imported when your instrument and Biomek Software were installed.

Biomek Concept: Project File	
	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. Methods are associated with projects and contain all of the items required to perform the method.

View Figure 1.2 to learn where Project File information is accessed or viewed from the main editor.

Figure 1.2 Project File



1. The actions and editors associated with Project Files are displayed in the drop-down menu under **Project** on the toolbar.
2. **Project File**: The currently opened Project File is displayed here. The Project File displayed here is the default for the Biomek 4000 instrument.

Adding Tools to Biomek Software

To make tools available for use in Biomek Software:

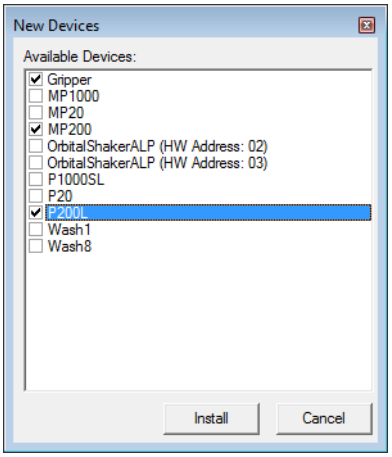
1 In Biomek Software, select **Instrument > Hardware Setup. Biomek Hardware Setup** appears.

2 In **Biomek Hardware Setup**, select Add Device.

3 In **New Devices**, select the devices to add (Figure 1.3) to Biomek Software, and then select **Install**.

NOTE For this tutorial, you will need to add the **P200L**, **MP200**, and, if available, the **Gripper**.

Figure 1.3 New Devices



4 In **Biomek Hardware Setup**, select Accept to complete the process.

Creating a New Method

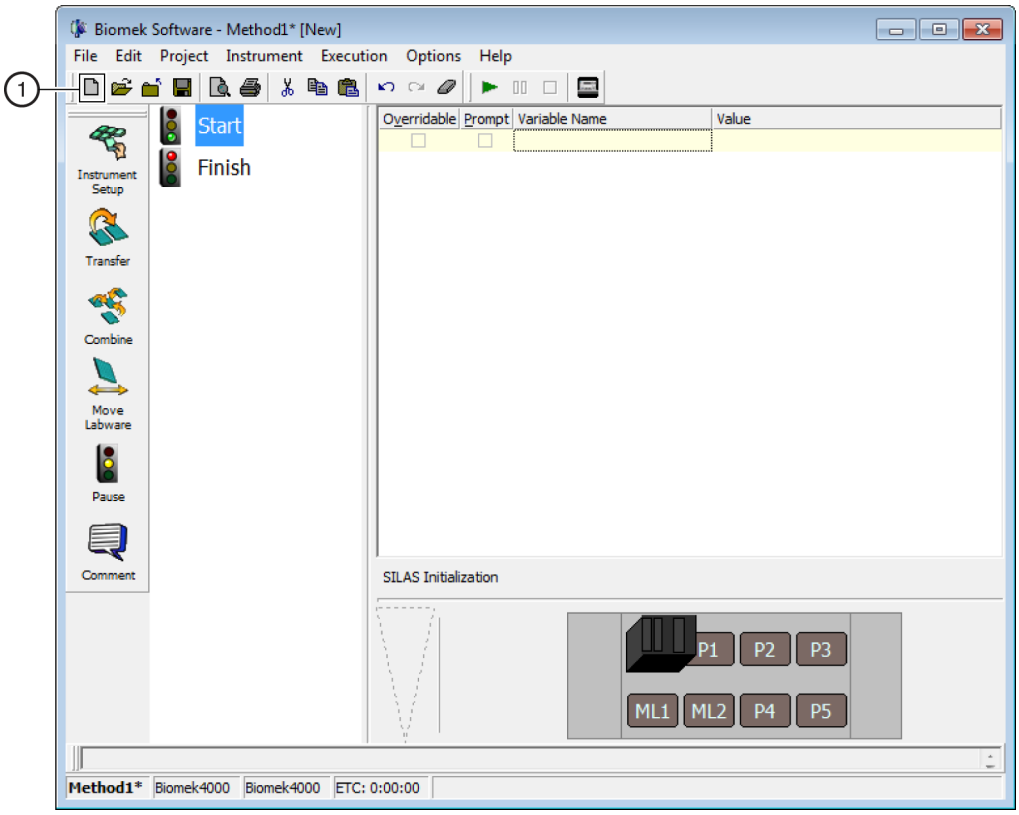
Biomek Concept: Method	
	A method is a series of steps that control the operation of the instrument. The step palettes in the main editor present a group of icons representing the steps available for a method. To build a method, you simply select the step icon you want, and move it into the method-building space (Method View) in the main editor. Place and configure each step to perform the operations as desired.

To create a new method:

1 Select the **New Method** icon located on the toolbar (Figure 1.4).

This creates the beginning for your new method. It's a good idea to expand the Biomek editor to fill the entire screen.

Figure 1.4 Main Editor When a New Method is Created



1. **New Method**

Understanding the Start and Finish Steps

As you can see (Figure 1.4), the Method View of the main editor now contains the **Start** and **Finish** steps that appear automatically when you create a method. These two steps are always there and indicate the beginning and end of your method. You'll insert all the rest of the steps you want the instrument to complete between **Start** and **Finish**.

When the **Start** step is highlighted in the Method View, you are presented with the opportunity to create some variables in the Configuration View. Ignore this configuration for our first chapter in this tutorial.

If you want to know more in-depth information on the **Start** configuration right now, refer to the *Biomek 4000 Software Manual*.

You'll learn more about using the **Finish** step in *Determining the Estimated Time of Completion (ETC) of the Method*.

Setting Up the Deck

Biomek Concept: Deck Editor	
	The **Deck Editor** is used to define and change the deck configurations stored in the current instrument file. A deck is a software visual representation of the deck 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. Refer to the *Biomek 4000 Software Manual* for details.

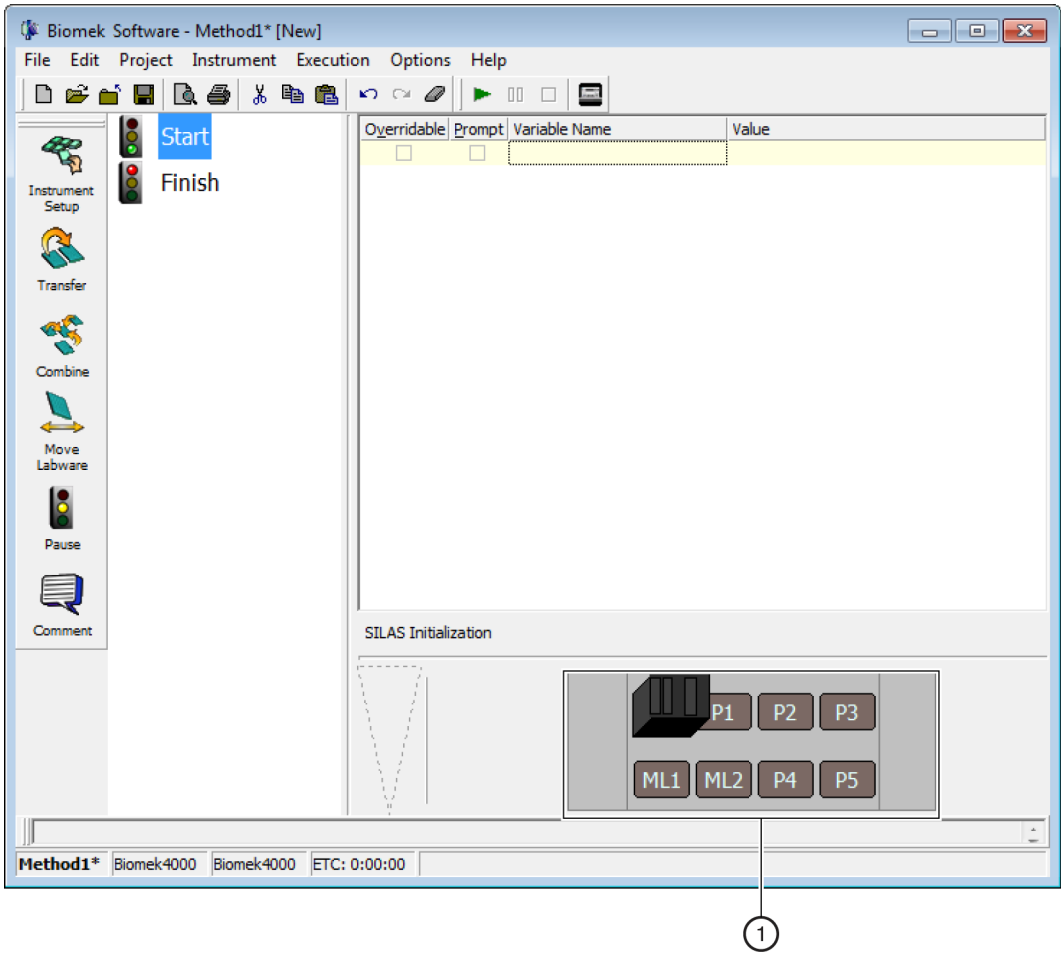
Setting up the deck includes:

- Ensuring the current deck used in Biomek Software via the **Deck Editor** matches the physical deck of the instrument.
- Configuring the **Instrument Setup** step to tell the software what labware and what deck position each labware piece occupies on the deck.

Ensuring the Deck in Biomek Software is Correct

To avoid hardware crashes, it is important that the deck in Biomek Software matches the physical deck of your instrument and is properly framed (refer to the *Biomek 4000 Hardware Manual*). If you wish to run these tutorial methods on hardware rather than in simulation mode and your deck varies from what is shown (Figure 1.5), you need to either create a deck both physically and in Biomek Software to match the setup within this tutorial or modify the methods contained in this manual to work with your hardware. For instructions on setting up your deck to match this tutorial, see *Creating a New Deck*.

Figure 1.5 Current Deck for This Tutorial



1. **Current Deck**

Creating a New Deck

To create a deck to match the deck used in all tutorials in this manual:

1 From the **Instrument** menu, select **Deck Editor**. **Deck Editor** appears, showing the Default Deck setup.

2 Select **New Deck**.

3 Enter a name for the new deck and select **OK**.

The Default Deck setup remains as a template, allowing you to make minor modifications if needed. For this tutorial, you are going to create the deck from scratch.

4 Select **Clear Deck** to remove all positioners associated with the Default Deck.

5 From the ALPs Type List, select and drag one of the following into the upper left on-deck position:

- **ToolRack**

  OR

- **ToolRackGripper**, if your instrument is equipped with the optional **Gripper** tool

The tool rack appears on the deck as **Rack1** when you finish placing the position.

6 Place a **Biomek4000Position** positioner directly to the right of **Rack1** using the same method described in the step above. Continue placing two more Biomek 4000 positions on the same row, each to the right of the previous positioner. These positions appear as **P1**, **P2**, and **P3**.

7 Place two additional **Biomek4000Position** positioners on the deck, the first directly under position **P2**, and the second directly under position **P3**. These positions appear as **P4** and **P5.**

8 Place two **ManualLatch** positioners on the deck, placing the first one directly under **Rack1**, and the second one under position **P1.** These positions appear as **ML1** and **ML2**.

NOTE Manual Latch positioners enable the placement of tip boxes.

9 Your new deck should match Figure 1.6. Select **Save** to save your new deck and exit from the **Deck Editor**.

Figure 1.6 Tutorial Deck Setup

Configuring the Instrument Setup Step

The next activity of this tutorial is to configure the **Instrument Setup** step for your liquid-transfer procedure. You will place on the deck:

- **P200L** tool
- Tips
- Source reservoir
- Destination microplate

TIP If the **Instrument Setup** step, or any step, is inserted into the wrong location in the Method View, you can drag and drop it to the proper location.

To insert the **Instrument Setup** step:

---

1 Choose (highlight) **Start** in the Method View.

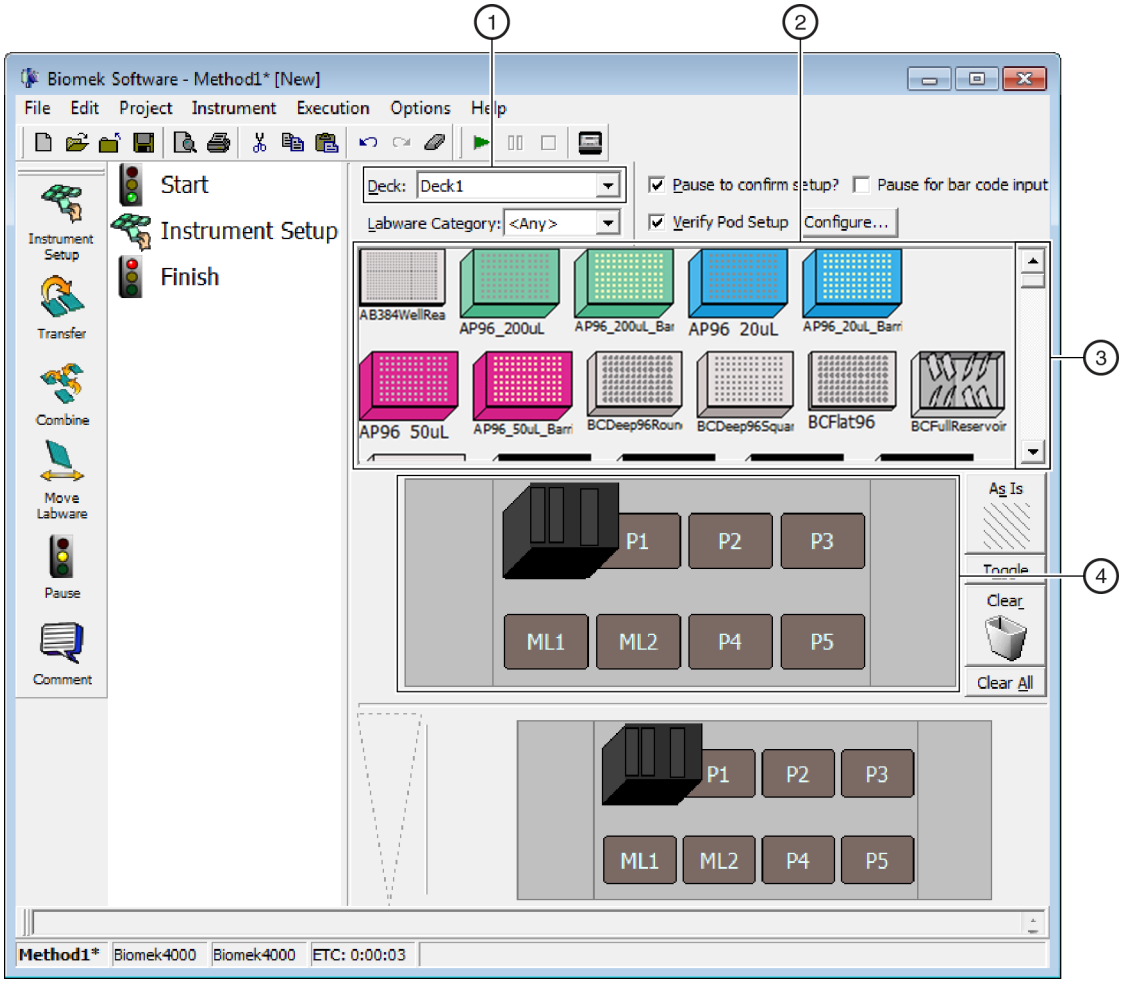
---

2 Hover the cursor over the **Instrument Setup** icon in the step palette. As you hover, look at the Method View and you'll see a black bar appear just below **> Start**. This black bar indicates the insertion point where your next step will appear. In this case, it's where the **Instrument Setup** step will be inserted.

---

3 Click the **Instrument Setup** icon to insert the step. The **Instrument Setup** configuration appears (Figure 1.7).

Figure 1.7 Instrument Setup Step Configuration



1. **Deck Selection**: Change the current deck setup by selecting another deck previously created using the **Deck Editor**.
2. **Labware Available**: Represents the labware choices for your method. Move your selections onto the Deck Layout display.
3. Move this scrollbar down to display all the labware choices.
4. **Deck Layout**: Represents the layout of your deck. Place your labware selections onto the desired deck layout positions.

Using the **Instrument Setup** step you just inserted, you'll learn how to select and place:

- **P200L** tool at **Rack1**
- **AP96_200µL** tips onto **ML1** deck position

  NOTE Tip boxes must be placed on ManualLatch (MLx) or AutoLatch (ALx) positions.

- **BCUpsideDownTipBoxLid** reservoir onto **P5** deck position
- **BCFlat96** microplate onto **P4** deck position

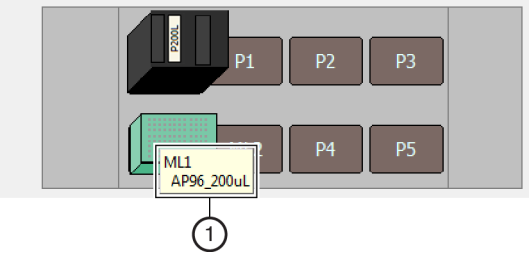
To select and place your tool and labware:

1 Verify that your deck matches the deck setup shown in Figure 1.7. If your current deck does not match, select the appropriate deck from the **Deck** drop-down.

2 On the Deck Layout, double click the tool rack and drag a **P200L** tool into one of the slots. Click **OK** and you will see that the tool rack graphic in the **Instrument Setup** step now lists a **P200L** tool as occupying the space where it was dropped.

3 Click the **AP96_200µL** tips icon, and then click on the **ML1** deck position. Notice that when you hover the cursor over the tip box on the Deck Layout, an InfoTip (Figure 1.8) identifies the deck position and labware. This technique applies to all the labware you place on the deck.

Figure 1.8 InfoTip



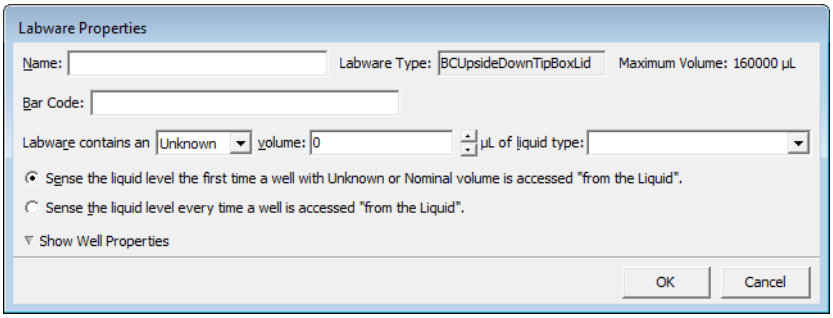
1. **InfoTip**: Identifies the deck position and labware type.

4 Using the above procedure, place a **BCUpsideDownTipBoxLid** reservoir onto the **P5** deck position.

5 After you have positioned the reservoir on the deck, either double click it or right click and select **Properties**. This opens **Labware Properties** (Figure 1.9). Each piece of labware added to the Deck Layout is configured using **Labware Properties**. The information provided in **Labware Properties** is used when a pipetting technique is selected or when tips are loaded and unloaded.

NOTE A technique instructs the Biomek instrument in performing pipetting operations, such as aspirate, dispense, and mix.

Figure 1.9 Labware Properties for Reservoir



6 In **Labware Properties**, you can give the reservoir a name. You'll name this one "**Rsvr**," but in general you can assign labware any name you want. Type **Rsvr** in the **Name** field. After configuration is complete, the name will appear over the reservoir in the Current Deck display (Figure 1.10).

TIP It is helpful to name your labware on the deck. You can assign a name that identifies the contents of the labware, or a descriptive name that fits the work being done in your laboratory. This can reduce confusion considerably.

7 Leave **Bar Code** blank for this tutorial, but it can be used to identify a specific plate in certain methods.

8 In **Labware contains an**, select **Known**.

9 In the **Volume** field, type **100000**. This means you know you have 100,000 microliters of liquid in the source reservoir.

10 Choose **Water** from the **Liquid Type** drop-down menu, or type **Water** into this field.

11 Ignore the two options to **Sense the liquid level**. Since we have known volumes in the labware, we won't use liquid level sensing in this chapter, but you'll use liquid level sensing in later chapters.

12 Choose **OK**.

13 Place a **BCFlat96** microplate onto the deck in position **P4**.

14 Double click on the **P4** microplate, or right click and select **Properties**.

15 Type **Dest** in the **Name** field.

16 In **Labware contains an**, select **Known**.

17 In the **Volume** field, leave this value at **0**.

18 Do not specify a **Liquid Type** for this destination plate since it is presently empty. The software defaults to **Water** as the **Liquid Type**. To remove the default liquid type, delete **Water** from the **Liquid Type** field.

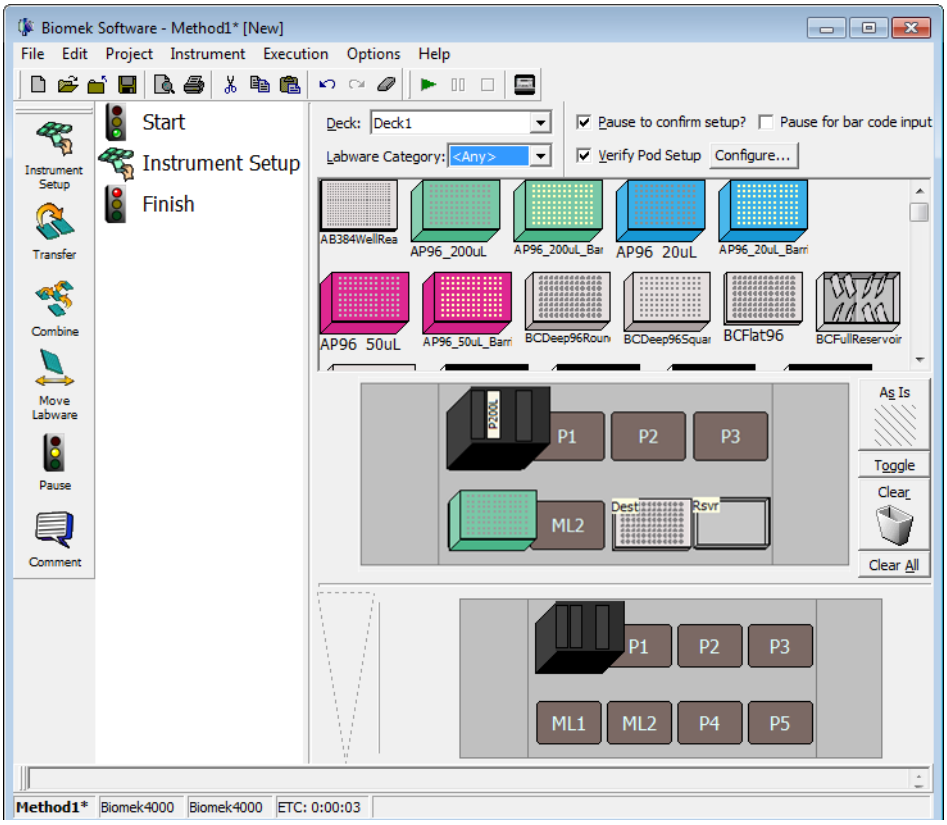
NOTE All liquids specified in Biomek Software are tracked and will be listed in the **Liquid Type** drop-down once a new type is added.

19 Choose **OK**.

That's it. Your deck is now set up for transferring liquid, and the main editor should look like Figure 1.10.

TIP You can set the properties (name, volume, and liquid type) as you've just done in these steps, then drag the labware back up, and drop it into the Labware Available display once you've selected the **Custom** labware category. This labware will retain the properties you set and be available to use in other methods when you access **Instrument Setup**.

Figure 1.10 Instrument Setup Step Completed



Transferring Liquid

Now you are ready to insert and configure your procedure to transfer liquid. Biomek Software provides a **Transfer** step on the Basic Step Palette that makes it easy to accomplish this task.

Configuring the **Transfer** step includes configuring:

- Tool handling
- Tip handling
- Source labware
- Destination labware

Biomek Concept: Transfer Step	
	The **Transfer** step transfers liquid from one source to one or more destinations. The **Transfer** step will by default complete the following: load tool, load tips, aspirate liquid, dispense liquid, and unload tips. This concept eliminates the need to insert five separate steps, although occasionally a method may require these steps be performed individually. These individual steps will be covered in CHAPTER 2, *Using More Steps in a Method*, of this tutorial.

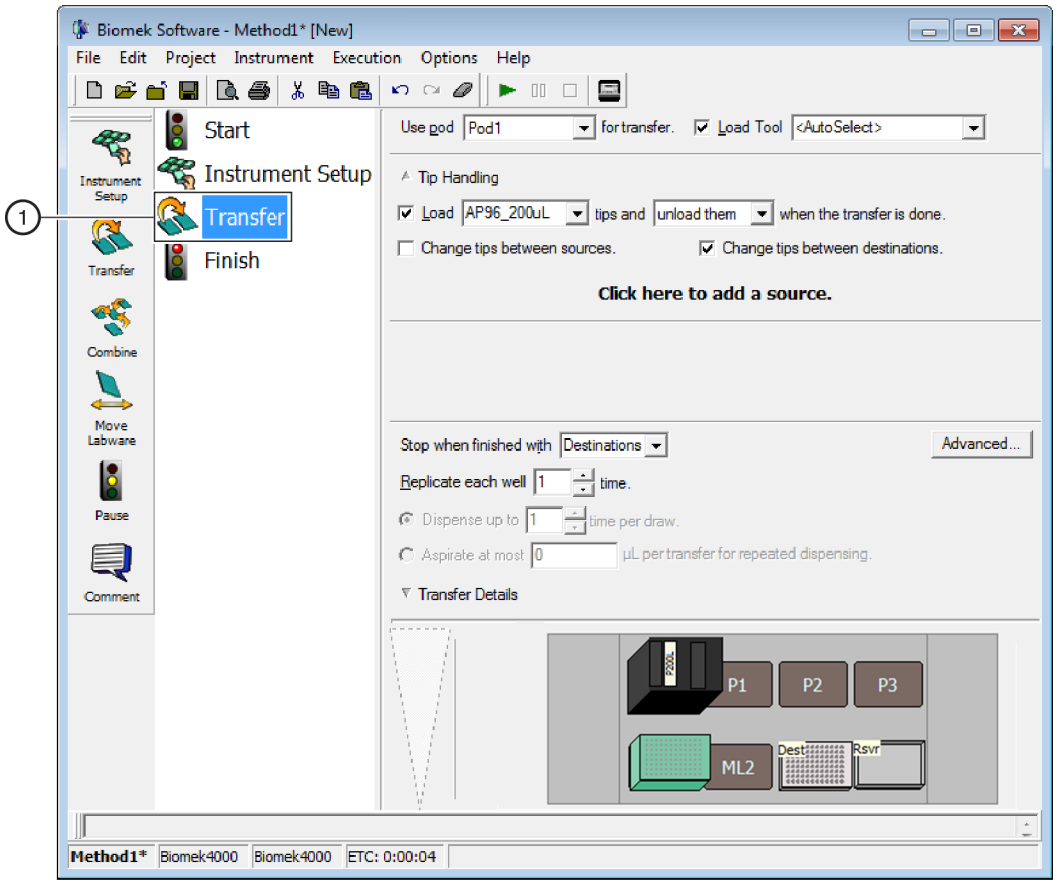
Configuring Tip Handling

To set up a liquid transfer, insert the **Transfer** step into the Method View in the main editor, and configure **Tip Handling** by completing the following:

1 Highlight the **Instrument Setup** step.

2 Choose the **Transfer** icon from the step palette, and insert it into the method by dragging and dropping it after the **Instrument Setup** step. The **Transfer** step configuration appears (Figure 1.11). Notice the Current Deck Display at the bottom of the editor is now populated to illustrate your deck setup since it changes dynamically to match the state of the deck at the start of the current step.

Figure 1.11 Transfer Step Inserted



1. **Transfer** step icon

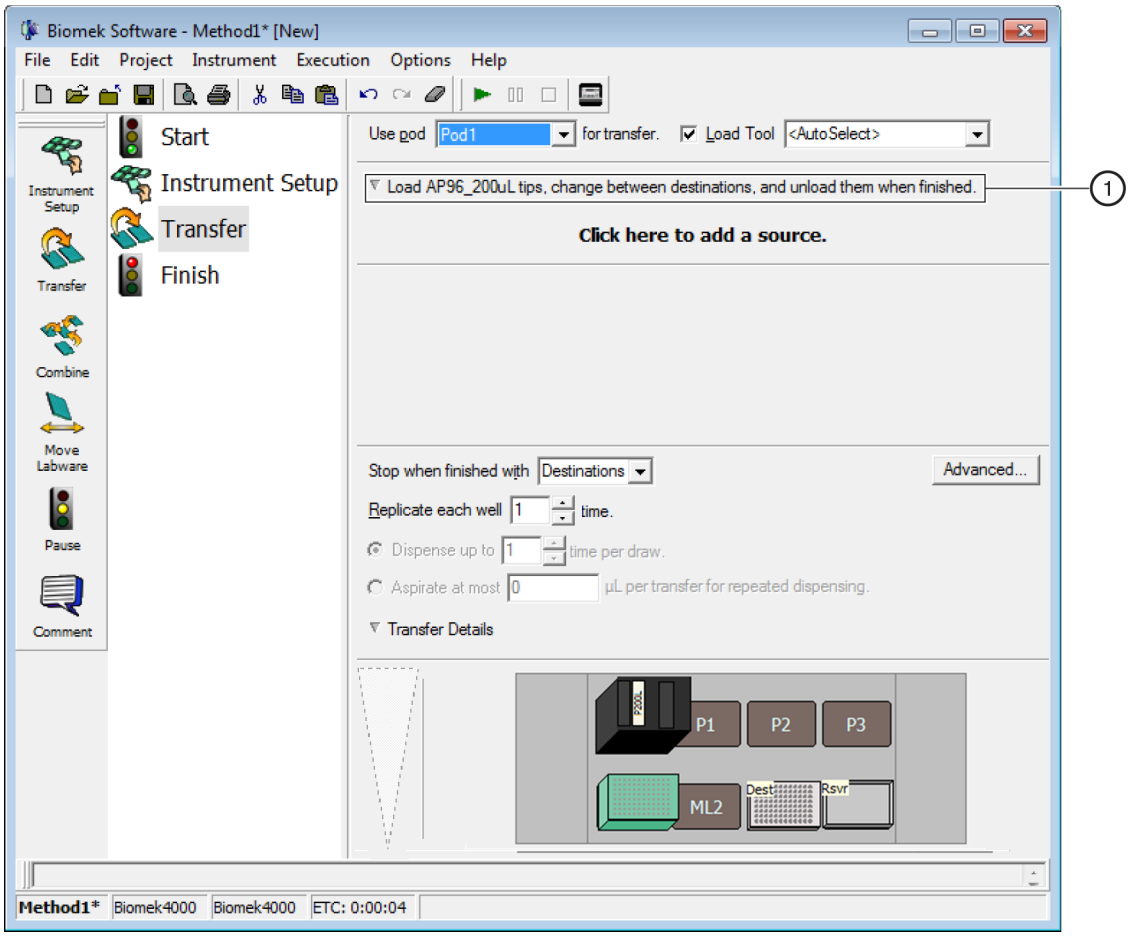
3 Make sure the type of tips displayed is **AP96_200µL**, the type of tips you configured in the **Instrument Setup** step.

4 Make sure **unload them** is selected in the next field.

5 Allow the default **Change tips between destinations** to be checked.

6 Your tips are configured for your liquid transfer, so click the **up arrow** next to **Tip Handling** (Figure 1.11). This collapses the **Tip Handling** configuration to allow more room for labware configuration. A simple text description of the way tips will be handled is displayed in place of the expanded **Tip Handling** configuration. The editor now looks like (Figure 1.12).

Figure 1.12 Tip Handling Configured and Collapsed



1. **Tip Handling** collapsed

Configuring Source Labware

Now you will configure the source labware. Here you will specify from which labware liquid will be aspirated and the height to which the tip descends into the labware before aspirating.

To configure the reservoir named **Rsvr** as the source labware:

1 Click on **Click here to add a source**.

2 Click on **Rsvr** labware on the **P5** position in the Current Deck display. As you can see, the information you supplied in the **Instrument Setup** step is displayed in the source labware configuration.

3 Right click on the large tip illustration next to the reservoir graphic in the configuration and choose **Measure from Bottom**.

TIP After you click on the tip, you can adjust the height more precisely by using the up or down arrow keys on your keyboard to change the height by 0.10 mm, or you can use the **Page Up** and **Page Down** keys to change the height by 1.0 mm with each press of the key. You can also right click on the graphic, then select **Custom Height** from the menu that appears.

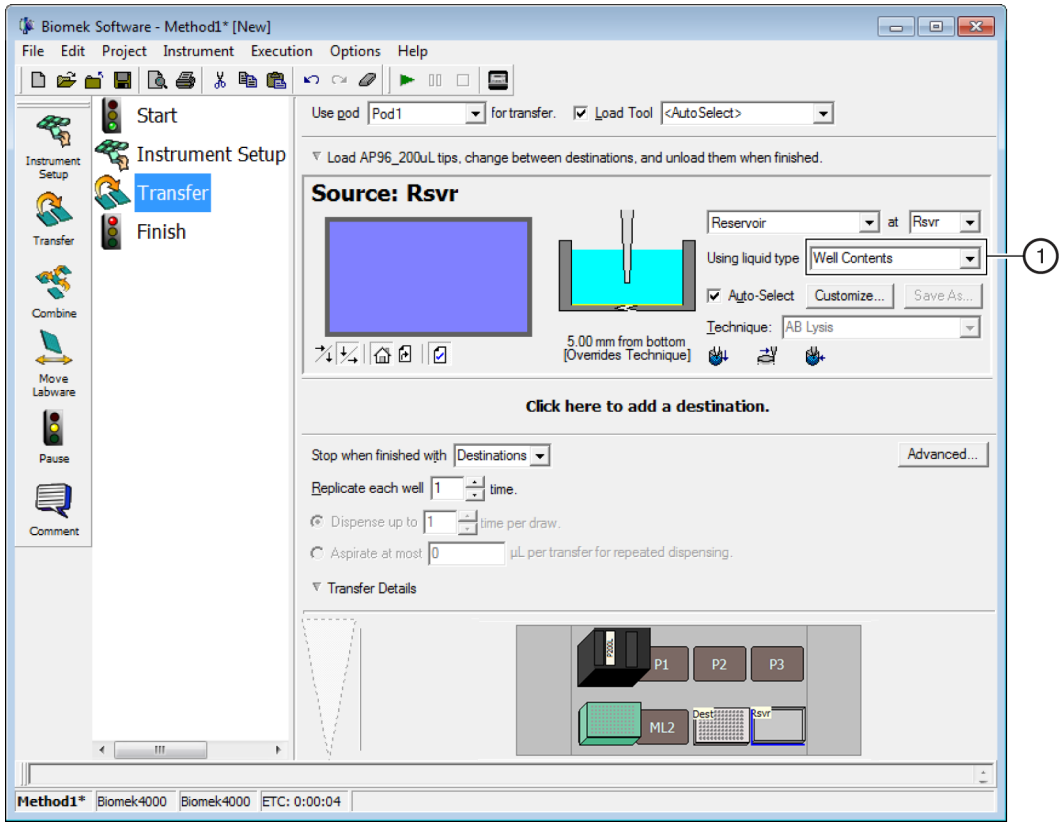
4 To adjust and set the aspirate height to which the tip descends into the reservoir, place the mouse cursor over the tip illustration. When the cursor turns into a hand, hold the left mouse button down to move the hand up and down until the depth is as close to **5.00 mm from bottom** as you can get. Then, adjust the height precisely to 5.00 mm using the **Tip** described above. There is a slight break in the bottom of the source reservoir graphic with the large tip that indicates that the reservoir is wider than the graphic can display.

OR

To select a custom height, right click on the illustration and select **Custom Height**, and then select **Bottom** from the drop-down menu. Type **5.00** in the text box, and then click **OK**.

The source labware is complete, and the editor now looks like Figure 1.13.

Figure 1.13 Configured Source Labware



1. The software defaults to **Well Contents** for the **Liquid Type** for Source labware. The **Liquid Type** is not specified, as Source labware could contain multiple liquid types.

Configuring Destination Labware

Here you will configure where you want the water from the source reservoir to be dispensed. In this case, you want to dispense water into the **BCFlat96** microplate on deck position **P4**. To do this:

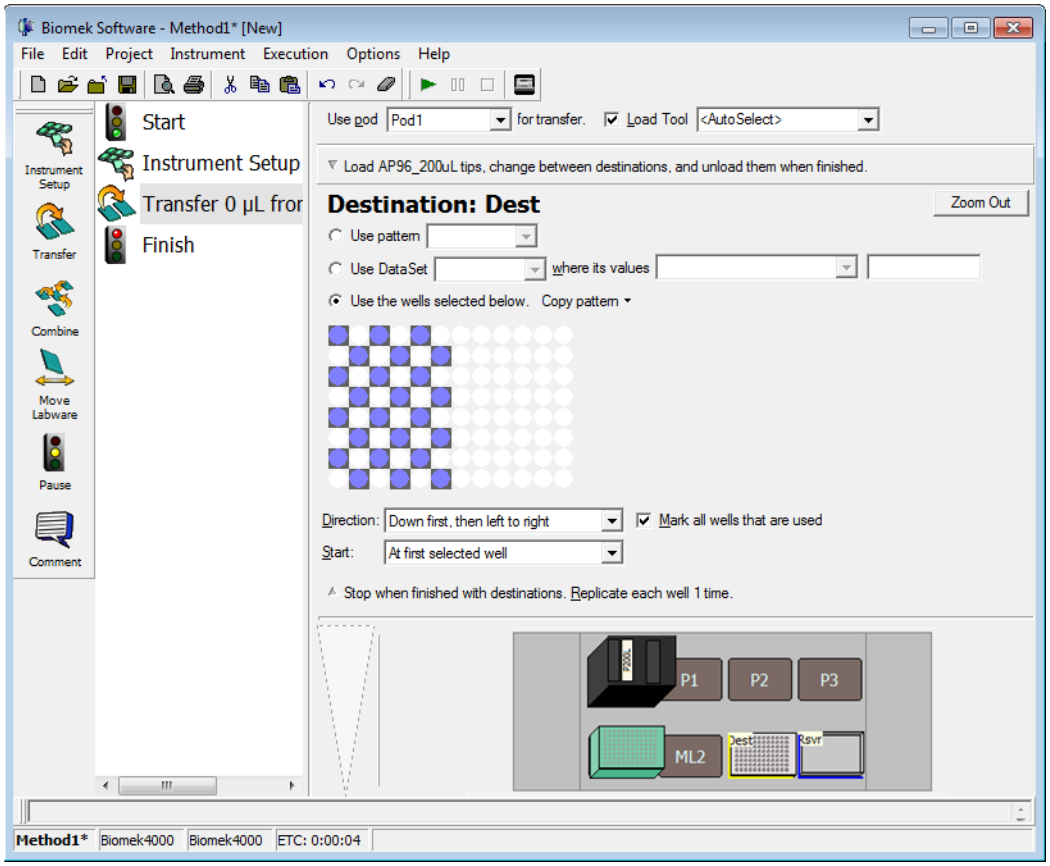
1 Click on **Click here to add a destination** and the click the **Dest** microplate in the current deck display. This one operation accomplishes the same tasks as steps 1 and 2 of *Configuring Source Labware*. Notice that the source labware configuration fields are now replaced with a brief sentence summary of the setup. If you want to reopen this source configuration for any reason, click anywhere in the collapsed configuration area.

TIP If you accidentally open too many destination configurations, just right click on the title in the configuration. Click **Delete** from the popup menu and the entire configuration goes away.

2 Double click the **Destination Labware** in the step configuration to zoom in on the labware. All of the wells are selected by default.

3 Since all of the wells are selected by default, select the first well of the first column by clicking on the well. Now the only well that is selected is that first well that you just clicked; all the other wells are deselected. Then, select every other well of the first six columns by holding down Ctrl key and clicking the wells. Your pattern should look like Figure 1.14. You have just configured which wells will be filled with water from the source reservoir **Rsvr**.

Figure 1.14 Destination Labware Zoomed In



4 Allow the default selections in **Direction**, **Start**, and **Mark last well that is used** to remain.

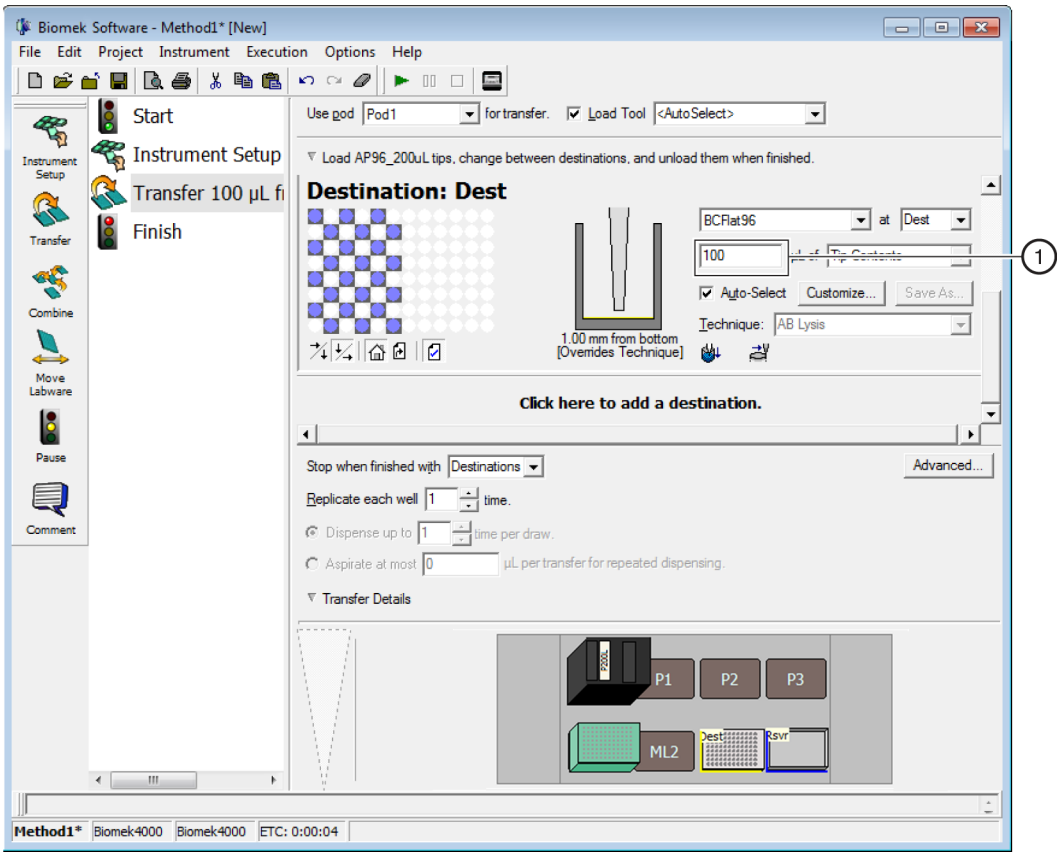
5 Choose **Zoom Out**.

6 Select the volume field, which allows you to designate the amount of liquid to be dispensed. For this tutorial, you're transferring 100 µL; so type **100** into the **Volume** field. This means you will be dispensing 100 µL into each of the wells you selected.

7 Right click on the large tip illustration and choose **Measure from Bottom** or **Custom Height** and set the dispense height to **1.00 mm from the bottom** using whichever technique you prefer.

The destination labware is now configured and the editor looks like Figure 1.15.

Figure 1.15 Configured Destination Labware



1. **Volume** field

Determining the Estimated Time of Completion (ETC) of the Method

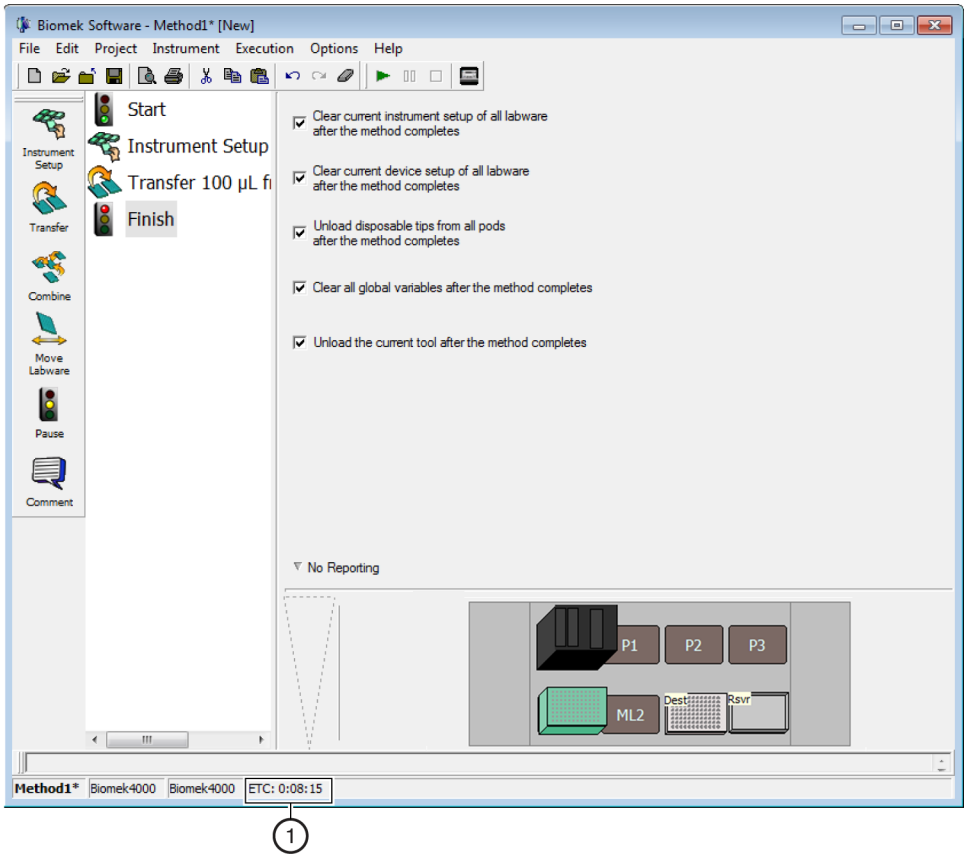
Your liquid transfer is set up, so let's see how long it will take to run the entire method by using the **Finish** step.

To do this:

1 Click on the **Finish** step in the Method View.

2 Check the status bar at the bottom of the editor for a display of the **ETC**. For this method, the **ETC** is approximately 8:15 (Figure 1.16). It's all right if your **ETC** varies slightly.

Figure 1.16 Finish Step Displaying the ETC



1. **ETC**: The Estimated Time of Completion for the method in the **Method View**.

Congratulations! You've just built a liquid transfer method using Biomek Software that:

- Prepared the main editor for a new method.
- Set up the deck and configured the labware you wanted to use using an **Instrument Setup** step.
- Added and configured a liquid transfer using a **Transfer** step.

Running the Method

Now that you've built a method, let's run it.

IMPORTANT If you have not already configured the physical deck and you are planning to run the method on hardware rather than in Simulation Mode (see *Viewing the Method in the Biomek Simulator*), add the labware and tools as specified in the **Instrument Setup** step (see *Configuring the Instrument Setup Step*). Verifying that the correct labware and tools are used ensures proper pipetting and labware handling.

Validating the Method and Confirming the Deck Setup

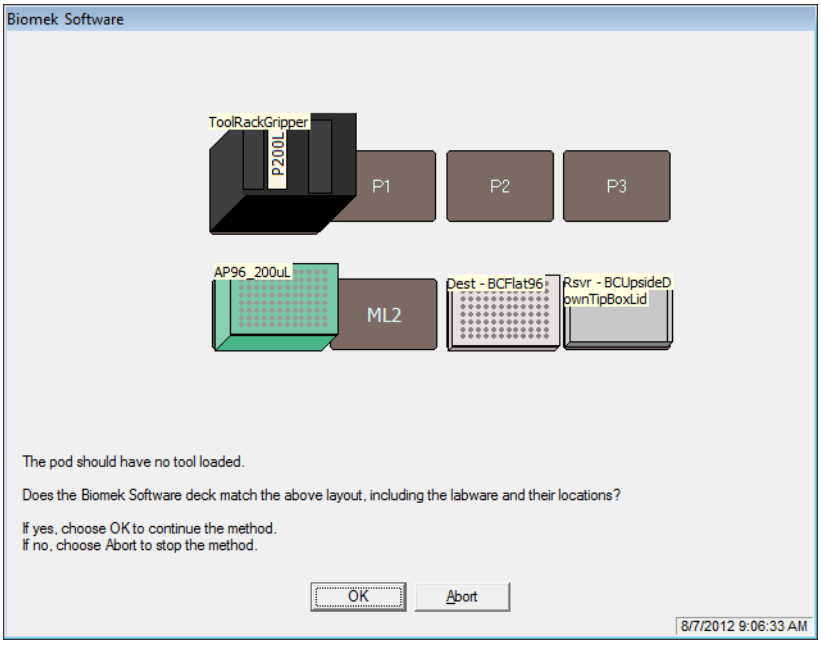
When you select **Run**, the method will be validated internally to check for errors. After this validation is complete, a deck confirmation prompt will appear over the main editor (Figure 1.17). This prompt displays the deck setup as interpreted by the software.

If you wish, you can also view the method in the Biomek Simulator. Refer to *Viewing the Method in the Biomek Simulator*.

To confirm the deck setup:

1 Click on the **green arrow** button on the toolbar, or from the **Execution** menu, choose **Run**. A deck confirmation appears (Figure 1.17).

Figure 1.17 Deck Confirmation Prompt



2 Visually confirm the physical deck setup matches the deck confirmation.

3 Choose **OK** if the deck confirmation matches the physical deck setup or choose **Abort** and then change the **Instrument Setup** step to match the physical deck setup. The method runs as soon as you choose **OK**. You can visually follow the run in the Method View; steps are highlighted as the step is executed.

Viewing the Method in the Biomek Simulator

⚠ CAUTION

Make sure the proper port is selected in the "Hardware Setup" window within Biomek Software. "Simulate" is used only when running methods on the Biomek Simulator, and will not initiate the physical instrument to run. To run methods on the instrument, choose the COM port to which the instrument is connected.

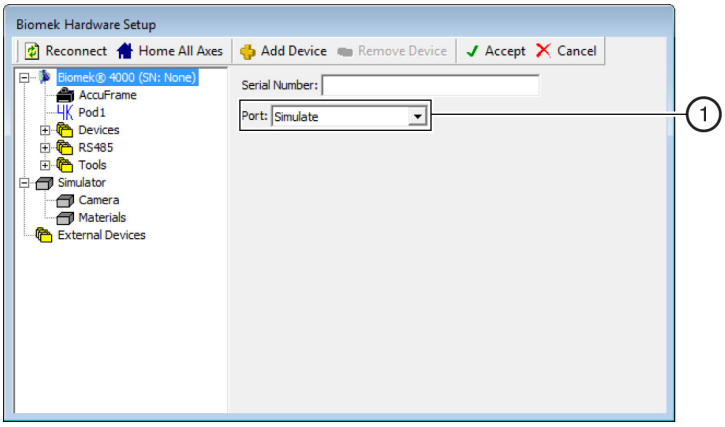
When a method is run in simulation, the Biomek Simulator appears, showing an animated 3-D model of the instrument performing the method. Setting the simulation mode is configured in **Hardware Setup** (Figure 1.18).

Biomek Concept: Hardware Setup	
	**Hardware Setup** is used to configure Biomek Software with the appropriate Biomek instrument information, including the Biomek Simulator. 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**. Refer to the *Biomek 4000 Software Manual*.

If you wish to view the method in simulation:

1 From the toolbar, choose **Instrument > Hardware Setup**. **Hardware Setup** appears (Figure 1.18).

Figure 1.18 Hardware Setup



1. Choose **Simulate** here to allow methods to be run in the Biomek Simulator.

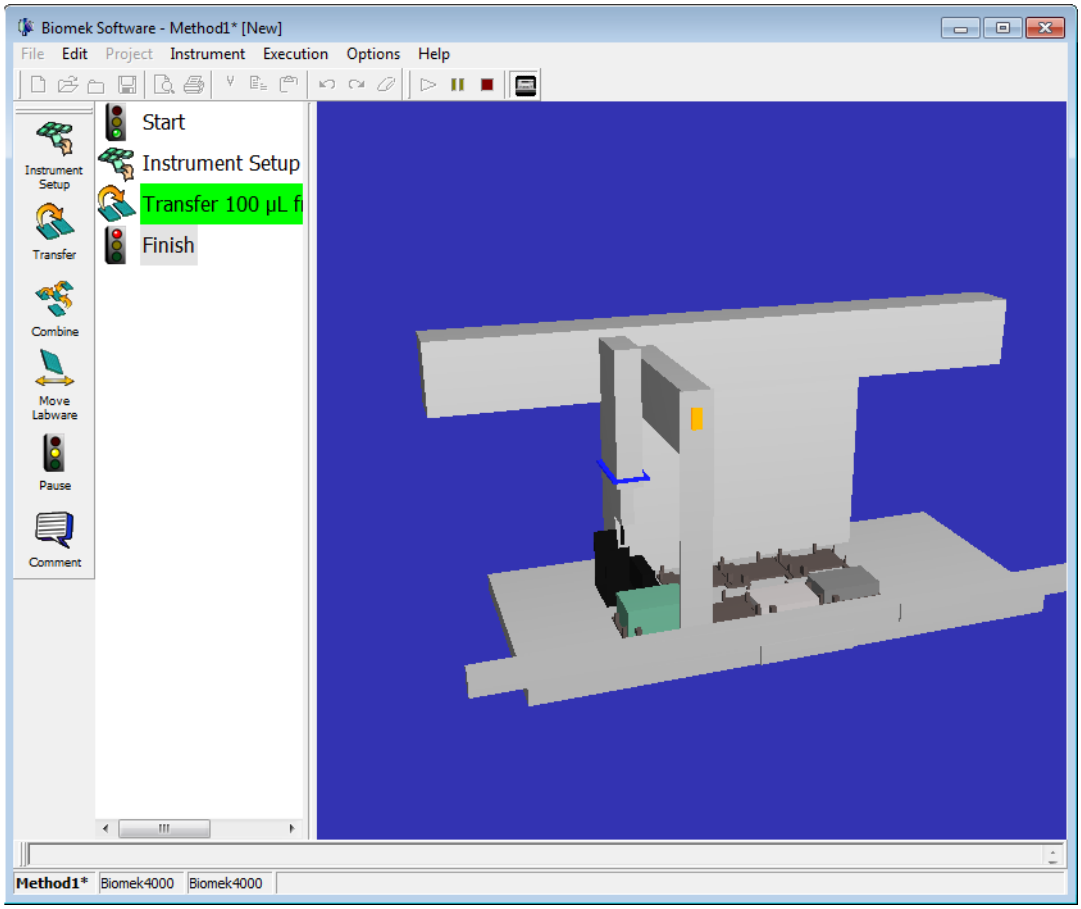
2 From **Port**, choose **Simulate**.

3 Choose **Accept**. Now, when a method is run, an animated 3-D model of the Biomek instrument is displayed (Figure 1.19). You can now watch a simulation of the Biomek instrument perform the steps in the method.

If you wish to run the method on hardware, you must go back to **Hardware Setup** and change the **Port** from **Simulate** to the appropriate **COM** port to connect your instrument to your PC.

TIP The simulator can be a useful tool to test methods to ensure that they are performing as expected without using up valuable reagents or tips, and can also save time not only in set up, but also by running at an accelerated speed. Refer to the *Biomek 4000 Software Manual* for more information on the simulator.

Figure 1.19 Running a Method in Simulation



Saving a Method

You will save the method you've just created.

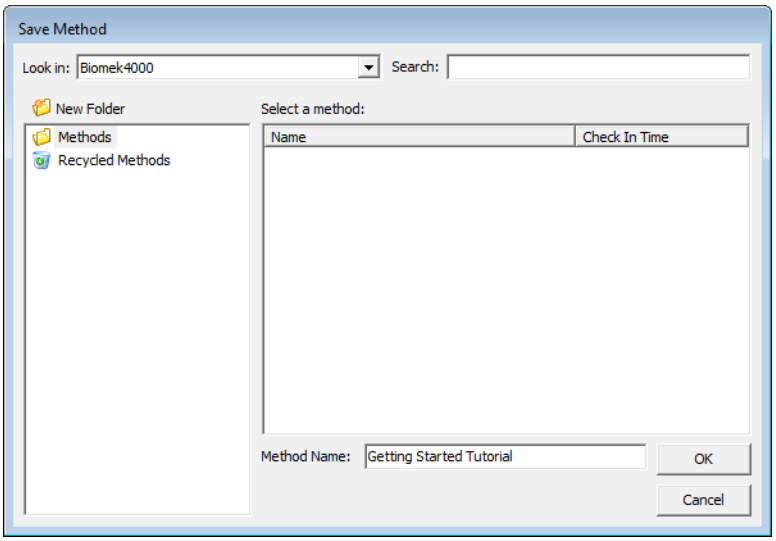
Biomek Concept: Saving Methods	
	Methods can be saved at any time during their development. Saving a method automatically creates a record of the revision that preserves the method configuration at the time it was saved. Revisions may be accessed from the revision history at a later time. If any project items, such as labware definitions or techniques, change after the method is saved, when the method is opened next, the latest definitions are used. Refer to the *Biomek 4000 Software Manual* for additional details.

To save your method:

1 Choose (**Save Method**) on the toolbar.

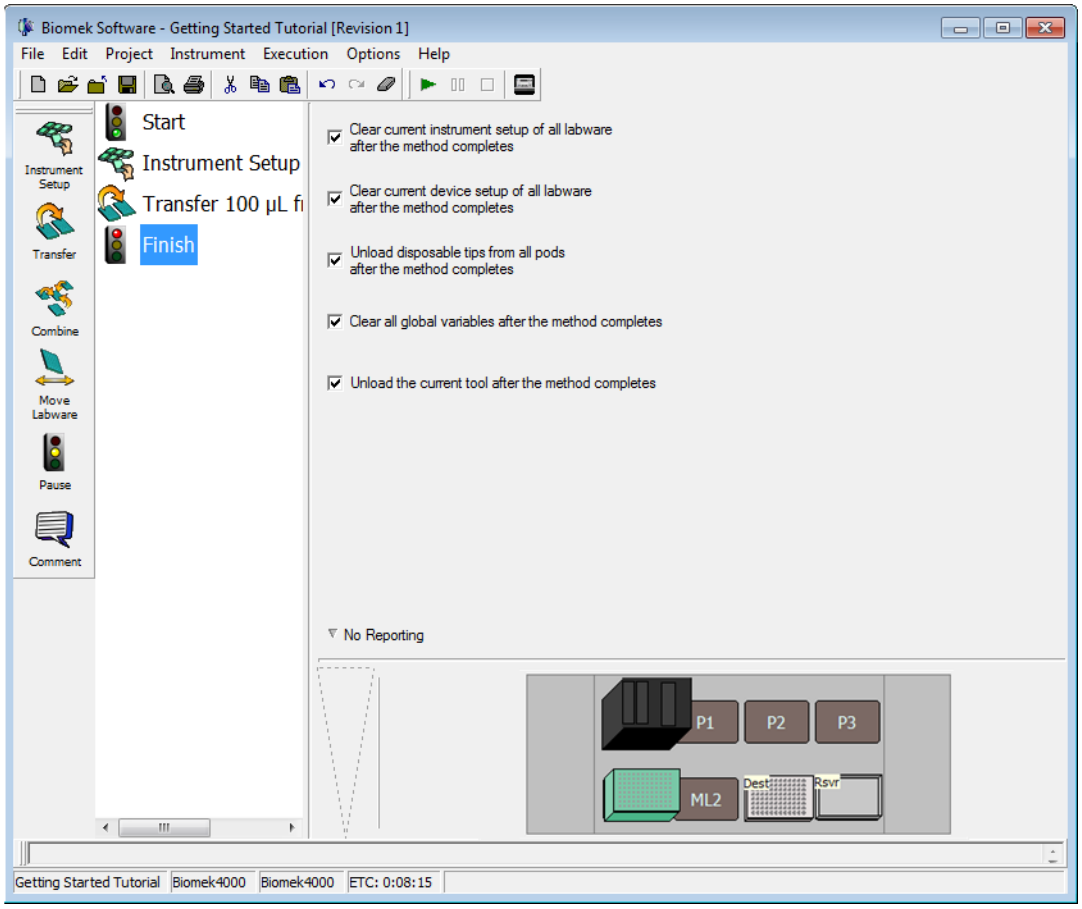
2 In **Method Name**, type the file name under which your method will be saved. For this chapter, type **Getting Started Tutorial** (Figure 1.20).

Figure 1.20 Save Method



3 Choose **OK**. Now notice how the method name in the Biomek main editor has changed to **Getting Started Tutorial [Revision 1]** (Figure 1.21).

Figure 1.21 Method Name Has Changed



Now go to the next chapter to learn how to use more steps in a method.

CHAPTER 2

Using More Steps in a Method

Introduction to Using More Steps in a Method

In the previous chapter of this tutorial (refer to CHAPTER 1, *Getting Started*), you learned how to:

- Launch Biomek Software.
- Set up the deck for a liquid transfer.
- Build a liquid-transfer method.
- Save and run a method.

If you already know how to complete these tasks, you can start with this chapter or subsequent chapters.

What You'll Learn in This Chapter

This chapter will help you develop the skills to create methods for tasks such as transferring liquid from tubes to plates, liquid level sensing, and serial dilution. You will also learn how to pause the system to add more labware to the deck and handle errors. Using **Single Step** to perform single operations to improve method development will also be described.

In this chapter, you will learn how to:

- Transfer liquid from two sources to a single destination.
- Mix contents in labware.
- Move labware on the deck using the optional **Gripper** tool.

  NOTE Your Biomek 4000 instrument must be equipped with the optional **Gripper** tool to move labware.

- Remove and add labware to the deck once a method has started to run.
- Group steps logically in the Method View.
- Use the automatic serial dilution feature.
- Respond to errors.
- Perform single operations.

Setting Up Your Deck for This Chapter

Using what you learned in CHAPTER 1, *Getting Started*, launch Biomek Software and configure an **Instrument Setup** step with the following:

1. Place a **P200L** tool in the tool rack by double clicking the tool rack displayed in the Configuration View and selecting the **P200L** icon and dragging into one of the slot positions. Repeat this procedure for the **MP200** tool, using one of the other open slots, and the **Gripper**, if your instrument is equipped with an optional **Gripper** tool.

   NOTE To place the optional **Gripper** on your tool rack, you must have a **ToolRackGripper** on your deck, rather the 5-slot **ToolRack**. For the purposes of this tutorial, the **ToolRackGripper** is installed on the deck. The **Gripper** can only be placed in the **Gripper** slot, which is custom-sized to fit the **Gripper** tool.

2. Place an **AP96_200µL** tip box on **ML1**.

3. Place **SmallTuberack_Microfuge** tube racks on **P4** and **P5** and name them **Tubes1** and **Tubes2**. Give these a **Nominal** volume of **1000 µL** of **Water** and choose **Sense the liquid every time a well is accessed "from the Liquid."** Sensing the liquid level **from the Liquid** helps pipetting performance since air will not be likely to be aspirated along with the liquid. Refer to the Biomek Concept below.

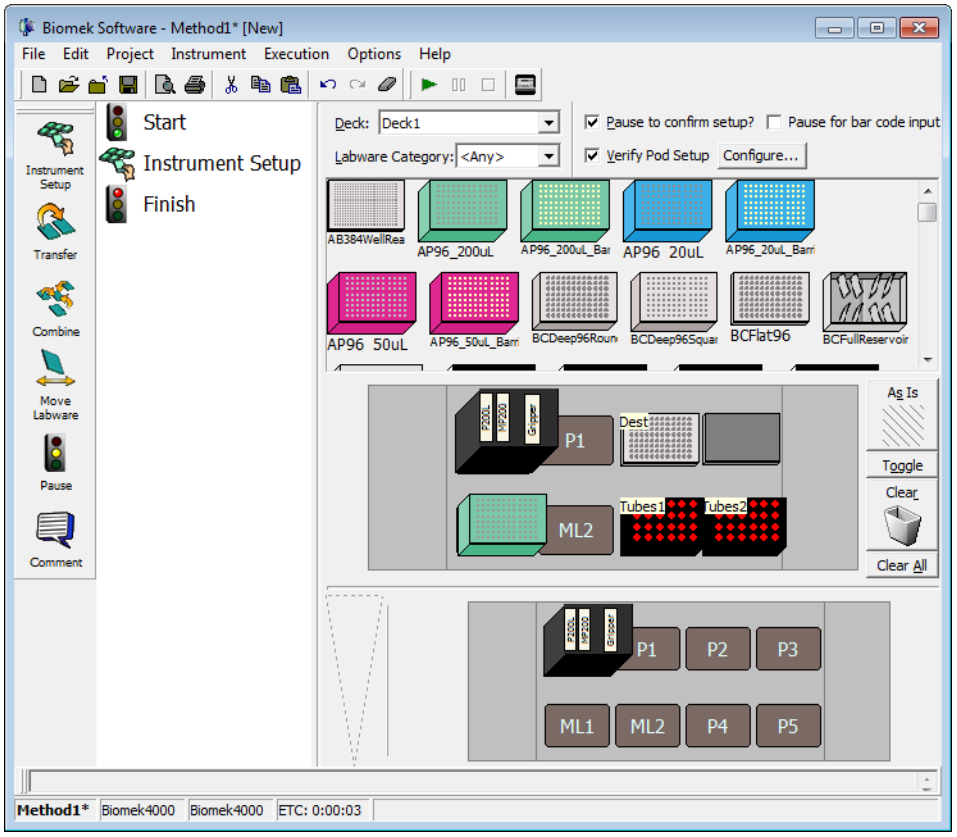
Biomek Concept: Liquid Level Sensing	
	Liquid level sensing is used to determine the liquid level within a piece of labware using specially-designed LLS tools. Refer to the *Biomek 4000 Hardware Manual* for details.

4. Place a **BCFlat96** on **P2** and name it **Dest**. Give this microplate a **Known** volume of **0 µL**.

5. If your instrument is equipped with the **Gripper** tool, place a **TiterPlateLid** onto the deck at **P3**.

Your deck should look like Figure 2.1. Now go to the next activity to learn how to use other steps in your methods.

Figure 2.1 Completed Instrument Setup Step



Transferring Liquid from Multiple Sources to a Single Destination

To transfer liquid from one or more sources to a single destination, a **Combine** step is used. It is similar to a **Transfer** step which uses a single source and one or more destinations.

Like the **Transfer** step, the **Combine** step will by default complete the following:

- Load tool
- Load tips
- Aspirate liquid
- Dispense liquid
- Unload tips

For this activity, you will use the default tip handling, configure the two sources, configure the destination, and configure transfer details to perform a tube-to-plate transfer and pool samples into the first column of 96-well plate.

Configuring Tip Handling

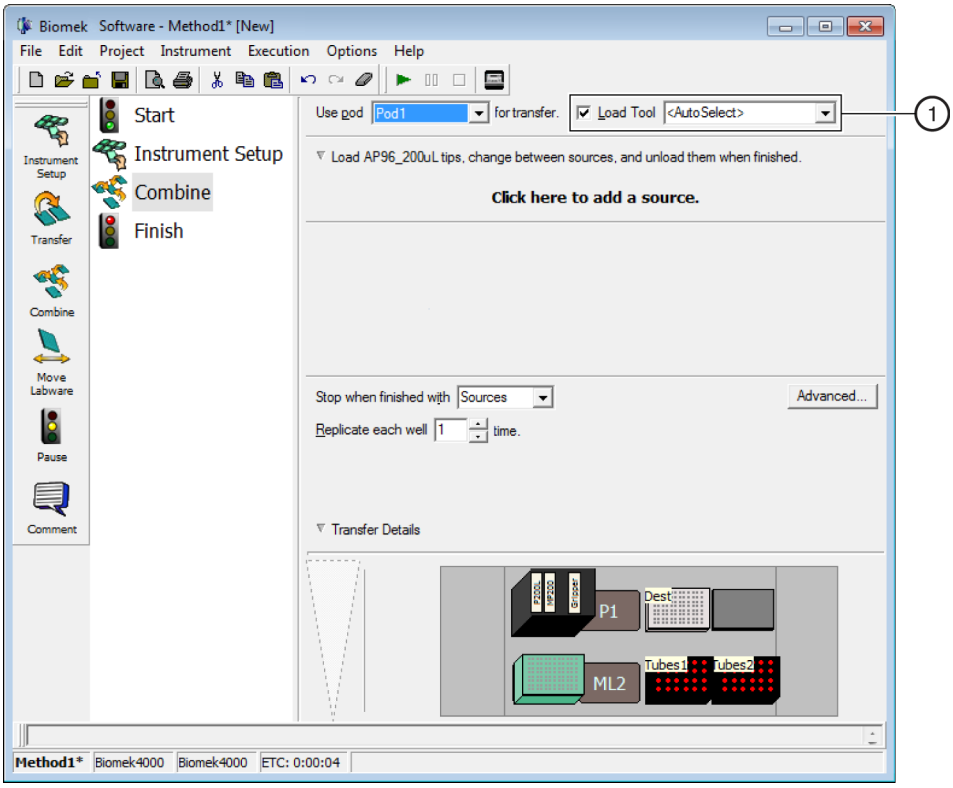
To set up the **Combine** step, you will insert the **Combine** step in the Method View and configure the step. To do this:

1 Ensure your deck is configured according to the instructions in *Setting Up Your Deck for This Chapter*.

2 Add a **Combine** step after the **Instrument Setup** step.

3 Collapse **Tip Handling** since you will use the default settings for your liquid transfer. Make sure **Load AP96_200µL tips, change between sources, and unload them when finished** is displayed. Your main editor should look like Figure 2.2.

Figure 2.2 Combine Step Inserted and Tip Handling Collapsed



1. **Load Tool** field: This field is available for **Transfer** or **Combine** steps. You can either specify a tool using the drop-down, or you can leave the default as **<AutoSelect>**, where the software selects the appropriate tool based upon the tips you have selected for the step. Each tip type has a set of compatible tools, and these tools are prioritized based on the degree of compatibility with that tip. Compatible tools associated with each tip type can be viewed and changed using the **Tip Type Editor**.

Configuring Source Labware

To configure the two small tube racks from which you're going to aspirate:

1. Click on **Click here to add a source**.

2. Click on **Tubes1** sitting on **P4**.

3. In the **Volume** field, designate the amount of liquid to be aspirated. For this method, you're aspirating 25 µL, so type **25** into the **Volume** field and select **Water** from the drop-down to specify the liquid type.

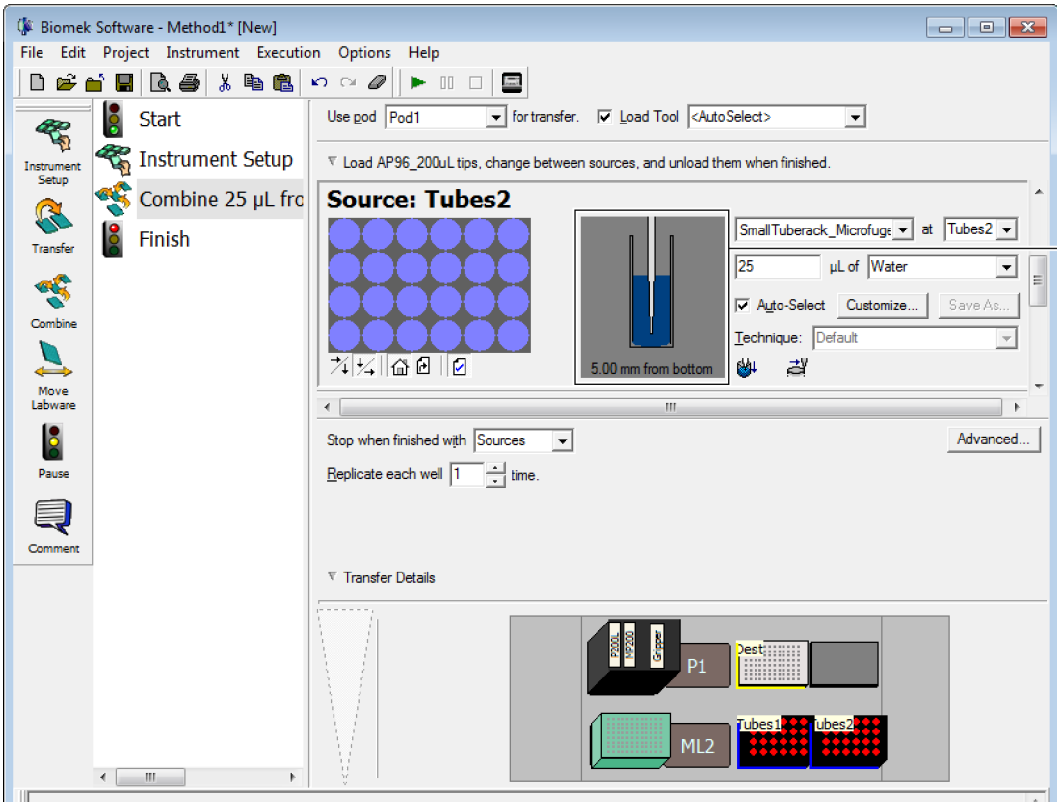
4. Click on the **Dest** plate in the Current Deck Display to add a destination. You will configure the destination in the next section, but must choose it here to activate another source option.

5. Click on the next **Click here to add a source**.

6. Click on **Tubes2** sitting on **P5** and type **25** into the **Volume** field.

   The sources are now configured, and the editor should now look like Figure 2.3.

Figure 2.3 Source Labware for Combine Step Configured



1. Well Volume Display

TIP The well volume display shows how much liquid is in the well. If the liquid is not visible in the display, you may be accidentally trying to aspirate from an empty destination rather than a source.

Configuring Destination Labware

The next task is to designate where you want to dispense the aspirated liquid. For this method, you want to dispense into the first column of the 96-well plate on deck position **P2.** To accomplish this:

1 If necessary, scroll down until you see **Destination: Dest.** Click anywhere in the **Destination: Dest** configuration.

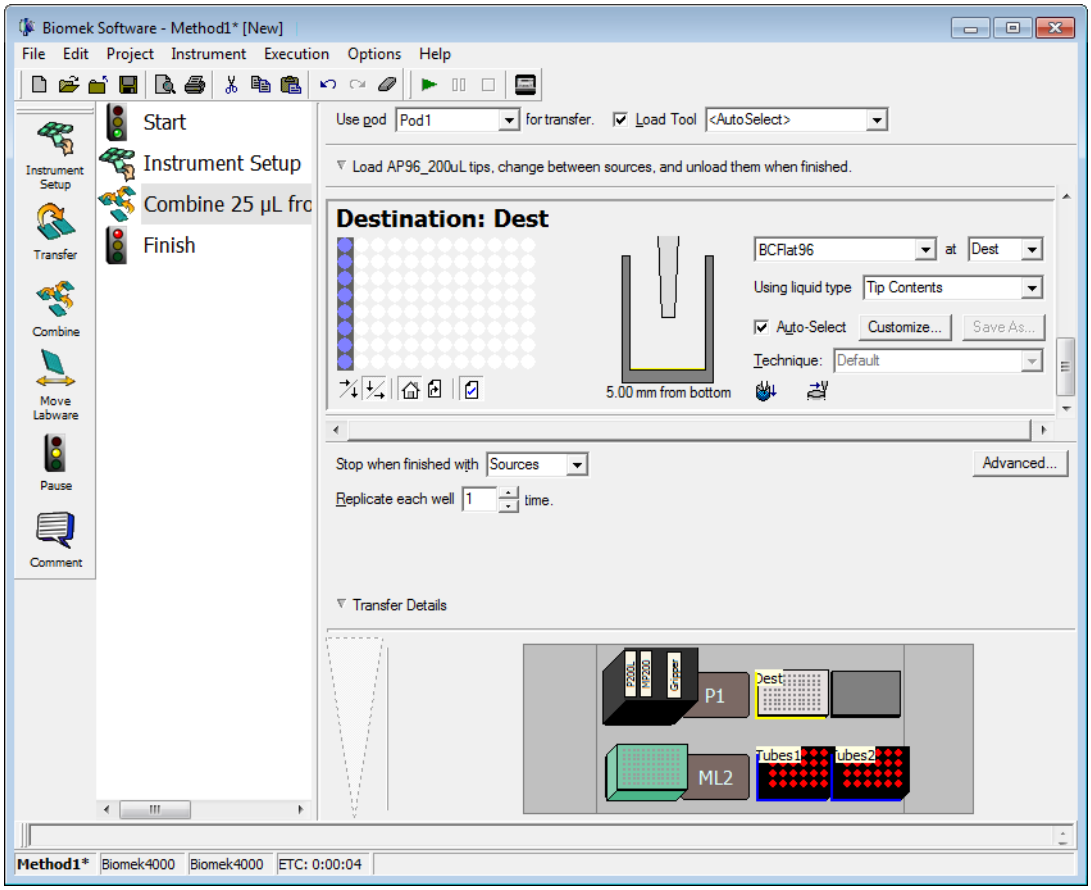
2 Double click the **Destination** labware graphic in the Step Configuration.

3 Select only the wells in the first column.

4 Choose **Zoom Out.**

5 In **Stop when finished with**, make sure **Sources** is chosen (Figure 2.4).

Figure 2.4 Stop When Finished with Sources Chosen



That's it. You've just configured a **Combine** step to aspirate liquid from two sources in order to dispense it to a single destination. Go to the next activity to learn how to mix the liquid in the destination plate after dispensing.

Mixing Contents in Labware

In the **Transfer** and **Combine** steps, you can alter liquid-handling functions that extend beyond simple aspirating and dispensing. For example, you can turn off the tip touch feature, activate the pre-wet function, or configure mixing operations. These modifications are accomplished through customizing the technique and are used to control the pipetting process.

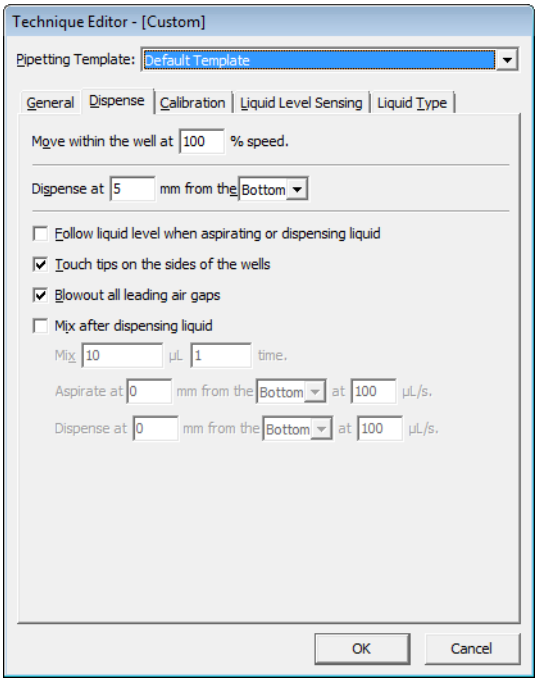
Let's suppose you wish to mix the contents of the destination plate once liquid from the two sources has been dispensed.

To complete this task:

1 Select the **Destination: Dest** labware configuration in the **Combine** step, if it is not already selected.

2 In the **Destination** configuration fields, select **Customize.** The **Technique Editor** opens to the **Dispense** tab (Figure 2.5).

Figure 2.5 Dispense Tab of the Technique Editor



Biomek Concept: Techniques	
	Techniques are sets of predefined and stored values, including aspirate and dispense height, tip touch and other properties that affect pipetting. Based upon these stored sets of values and properties, the appropriate pipetting technique is selected automatically. If you want control over this otherwise automatic function, you can choose **Customize** for each source and destination in a liquid transfer. This customizing option is also available via the **Technique Editor**. Refer to the *Biomek 4000 Software Manual*.

Configuring “Mix after dispensing liquid”

Now, you will configure the options to mix the contents in the destination after dispensing.

To mix after dispensing:

1 From the **Dispense** tab (Figure 2.5), check **Mix after dispensing liquid.** The fields for this option are enabled. We'll allow some of the defaults to remain except for the amount and number of times to mix.

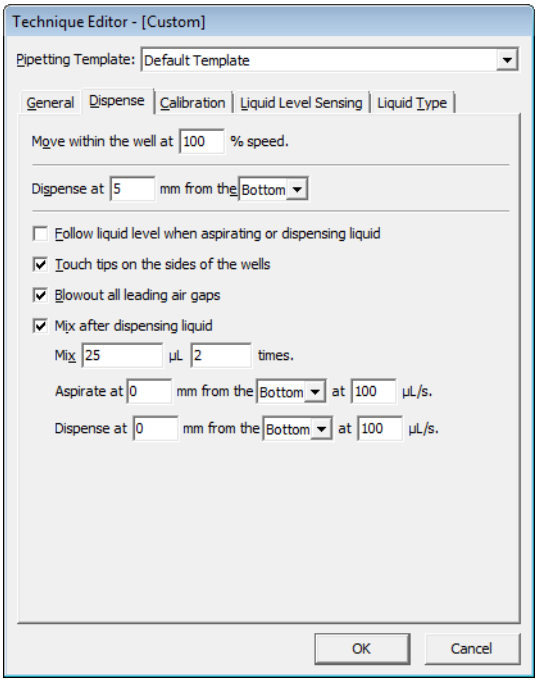
2 In **Mix**, enter **25.** This specifies the volume in microliters (µL) that will be aspirated and dispensed during mixing.

3 In **time**, enter **2.** This specifies the number of times you want to mix the liquid after dispensing.

You're finished configuring the mix after dispensing process. The **Technique Editor** should now look like Figure 2.6.

TIP Pipetting from the **Bottom** can sometimes cause wells to overflow, or it can contaminate the tips. Aspirating and dispensing from the liquid would be a good choice in these cases. This is not a concern for this tutorial, so you are leaving the default.

Figure 2.6 Configured Mix in a Custom Technique



4 Choose **OK**.

After you configure the mix operation and return to the **Combine** step configuration, you see a  icon, indicating that the technique now includes mixing. This is one of several icons that indicate different procedures in the pipetting technique. You will also notice that the **Auto-Select** option is turned off when the technique has been customized.

Moving Labware Around the Deck

IMPORTANT If your instrument is not equipped with the optional **Gripper** tool, skip this section and go to *Adding Labware During a Method Run*.

If the instrument is equipped with an optional **Gripper** tool, you can move labware around the deck during a method. On the step palette, you can see the **Move Labware** icon. When you insert and configure this step in your method, the instrument behaves as follows:

- The **Gripper** tool moves over the selected labware and moves down.
- The **Gripper** tool squeezes and grips the labware.
- The **Gripper** tool moves up and carries the labware to the designated position.
- The **Gripper** tool moves down, and releases the labware at the new position.

Moving Labware Using the Gripper Tool

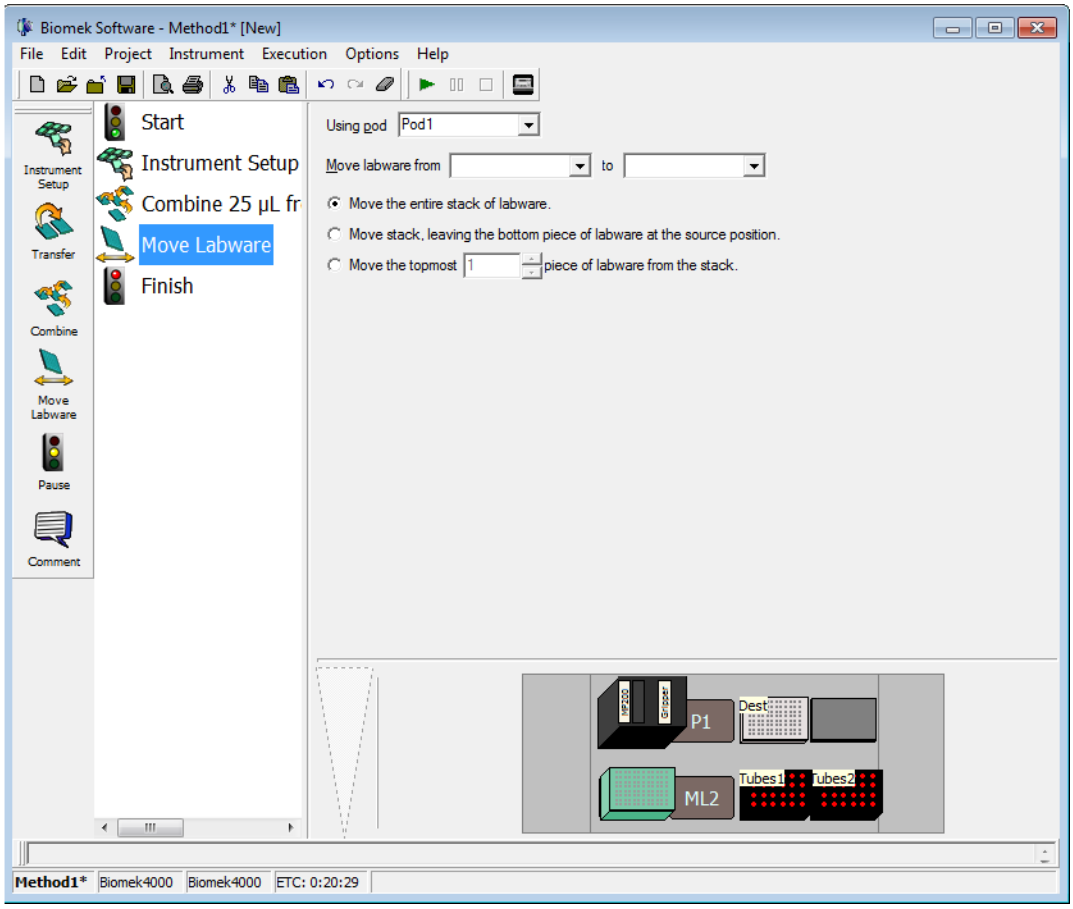
For this part of the tutorial, let's suppose that the contents of the destination plate are sensitive to light and need a lid to keep them from decomposing. Let's suppose further that you have a titer plate lid on the deck. Using a similar deck setup to the one that you created in *Setting Up Your Deck for This Chapter*, you will use the **Gripper** tool to move the titer plate lid to the position with the light sensitive compound.

To move labware on the deck:

1 Highlight the **Combine** step in the Method View.

2 Insert the **Move Labware** step from the step palette after the **Combine** step. The **Move Labware** configuration appears (Figure 2.7).

Figure 2.7 Move Labware Step Configuration



3 Choose **P3** in the **Move labware from** field.

4 Choose **P2** in the **to** field.

5 Keep **Move the entire stack of labware** selected.

6 Now, click on the **Finish** step in the Method View following the **Move Labware** step to validate the method. The Current Deck Display shows the **TiterPlateLid** now at its new position, **P2**.

In order to complete the procedures in the following sections, the well plate on **P2** needs to be available for a serial dilution procedure, and therefore, the lid must be removed to make that possible.

To remove the lid:

1. Insert a **Move Labware** step into the Method View directly under the current **Move Labware** step.
2. Choose **P2** in the **Move labware from** field.
3. Choose **P3** in the **to** field.
4. Select **Move the topmost 1 piece of labware from the stack**.
5. Select the **Finish** step to validate the method. The lid is now back on its original position, **P3**.

Adding Labware During a Method Run

Now you are ready to add labware to the deck for another liquid transfer process. Suppose that you want to add another reagent to the destination plate, but you don't want to place the second reagent on the deck until after the first Transfer is complete (perhaps it can only be exposed to light or open air for a very short time). This means that you will add a second **Instrument Setup** step to your method to indicate to the software that there is more labware now on the deck.

Before you add a second **Instrument Setup** step, you will:

- Move the pod to a new location by configuring a **Move Pod** step to make sure the pod is moved to a part of the deck where it won't prevent you from physically adding more labware.
- Pause the instrument by configuring a **Pause** step to give you enough time to physically add more labware.

Moving the Pod to a New Location

The **Move Pod** step is used to reposition the pod away from the positions on the deck you want to reach manually. Since you are going to be adding more labware to the deck to prepare for another liquid transfer, you will need to move the pod away from the deck locations affected before pausing the system and adding more labware.

Displaying the Intermediate Step Palette

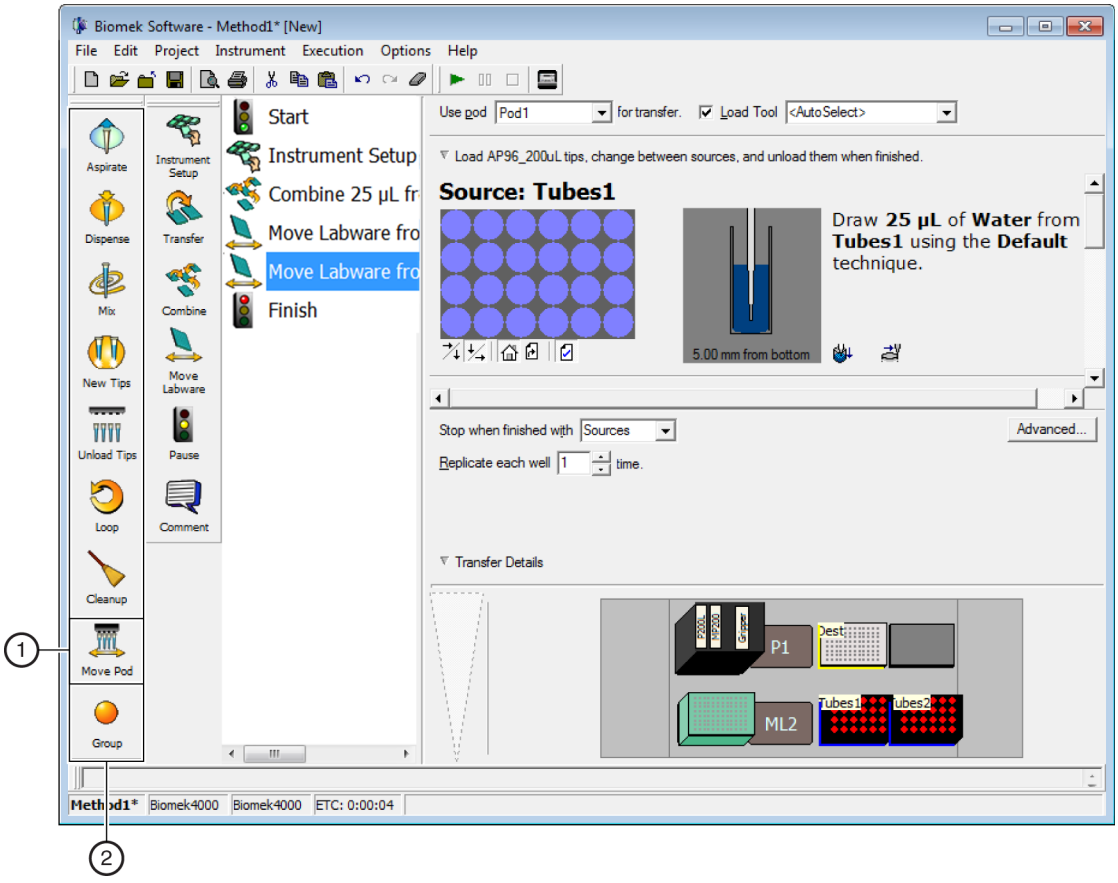
Biomek Concept: Step Palettes	
	Steps are grouped on step palettes based upon the complexity of the operations they control and the depth of knowledge required to configure them, although some steps are grouped on step palettes according to the specific pod or instrument they control.

The **Move Pod** step is located on the Intermediate Step Palette. You will need to add the Intermediate Step Palette to the main editor:

1 Right click anywhere in the space below the Basic Step Palette.

2 Choose **Intermediate.** The Intermediate Step Palette appears on the main editor (Figure 2.8).

Figure 2.8 Intermediate Step Palette Displayed



1. **Move Pod** Step
2. Intermediate Step Palette

Configuring the Move Pod Step

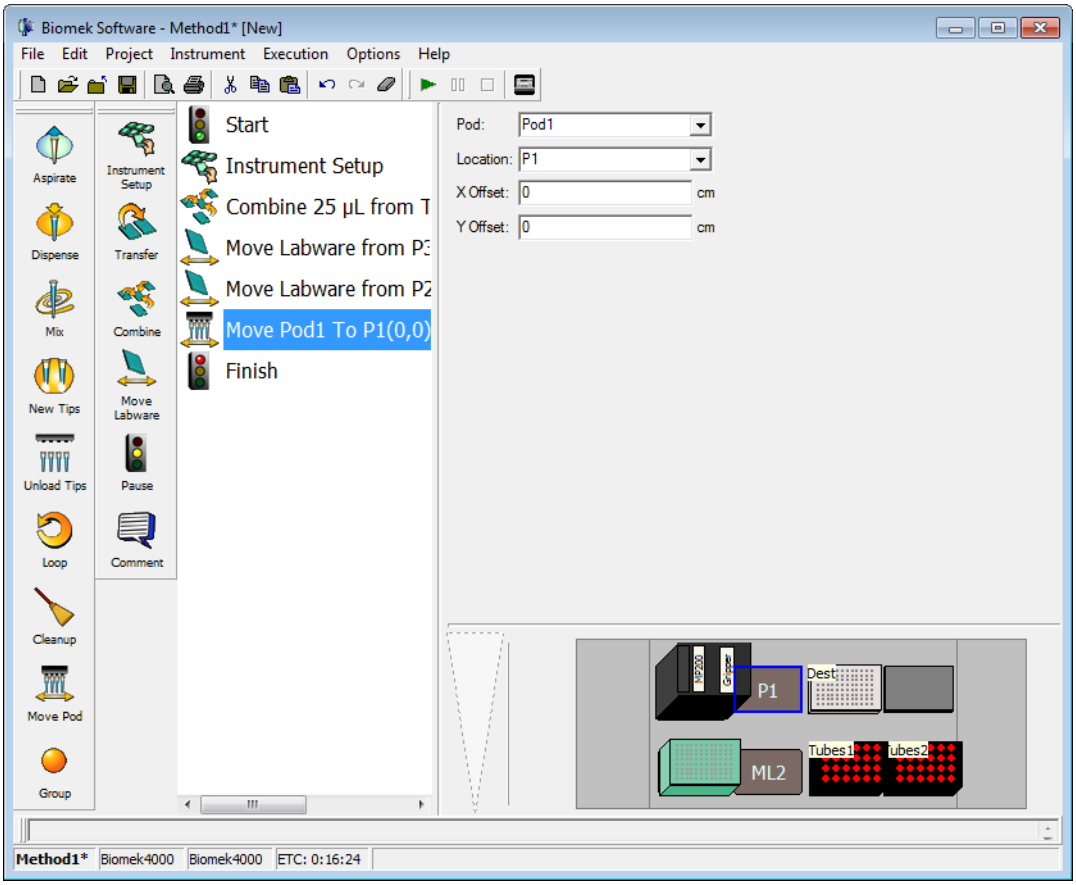
To configure the **Move Pod** step:

1 Insert the **Move Pod** step in the Method View in one of the following locations:

- If your instrument is equipped with a **Gripper**, and you completed the instructions in *Moving Labware Around the Deck*, insert the **Move Pod** step after the second **Move Labware** step.
- If your instrument is not equipped with a **Gripper**, insert it after the **Combine** step.

2 From the **Location** drop-down menu, choose **P1**. This instructs the pod to move and stop over the **P1** position (Figure 2.9).

Figure 2.9 Configured Move Pod Step



3 Click **Finish** to validate the method.

Pausing the Instrument

The instrument may be paused during a method run for either a specified amount of time or for an indefinite period of time by adding and configuring a **Pause** step. Depending on the purpose of the pause, you configure the step in one of the following ways:

- If you want to incubate a piece of labware in a specific position for a specific amount of time, you configure the desired time in seconds that you want that position to be idle and unavailable for interaction with the instrument.
- If you want to move labware manually during a method (either move it around on the deck, or remove it from the deck to take it to a device, such as a reader), you configure the step to pause the instrument for an indefinite period of time.

When the **Pause** step occurs during a run, the pod remains in the position of the last operation.

Configuring the Pause Step

You will configure the **Pause** step for indefinite amount of time to add more labware to the deck manually. The software will display a message on top of the main editor until you complete your manual operations, at which time it will resume the method run.

To configure the **Pause** step for an indefinite amount of time:

1 Insert a **Pause** step into the Method View below the **Move Pod** step.

2 Choose **Pause the whole system and display this message**:

3 Replace **Paused** in the message box by typing in the message:
Remove and store the tube racks located at P4 and P5.

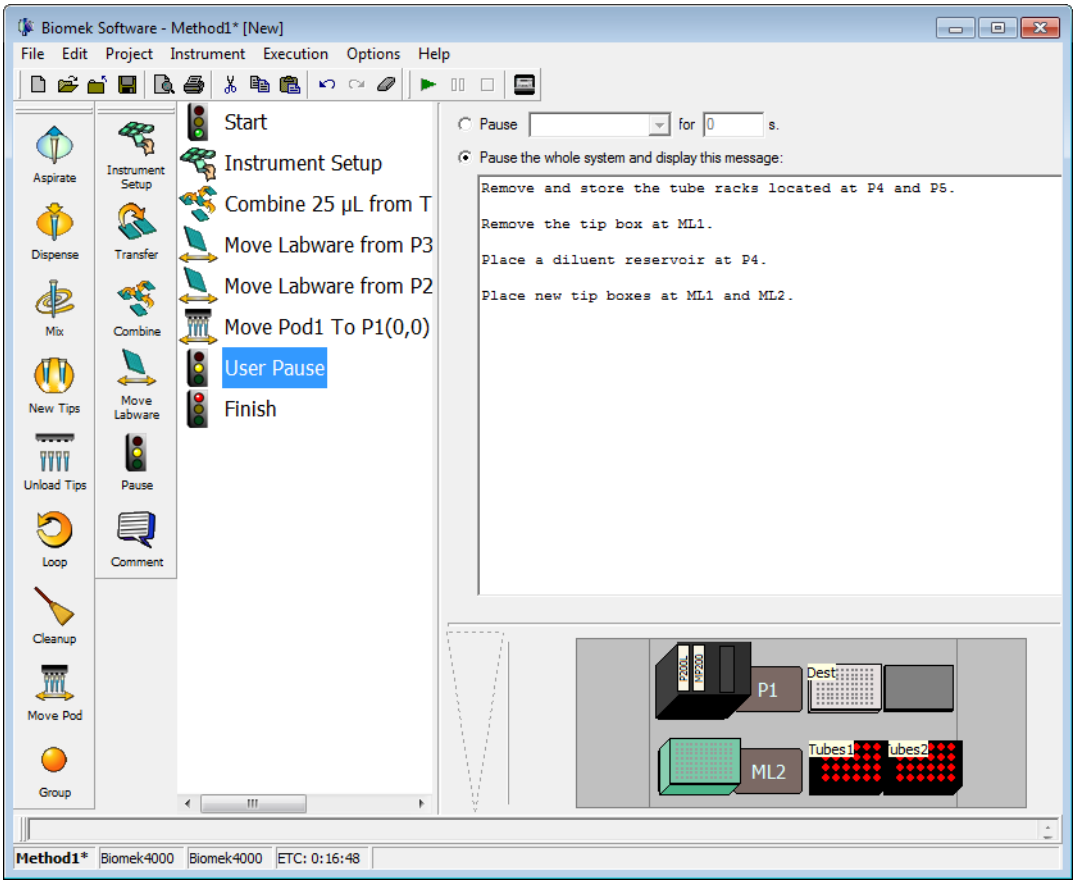
Remove the tip box at ML1.

Place a diluent reservoir at P4.

Place new tip boxes at ML1 and ML2.

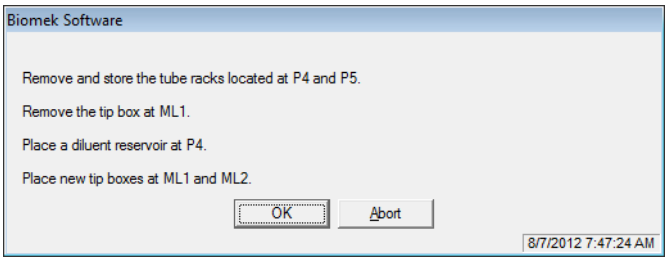
The main editor should now look like Figure 2.10.

Figure 2.10 Pause Configuration With Message Inserted



When the method is run, you will see a prompt similar to Figure 2.11 that will remain displayed until you choose **OK**.

Figure 2.11 Pause Prompt Displaying the Configured Message



Adding a Second Instrument Setup Step

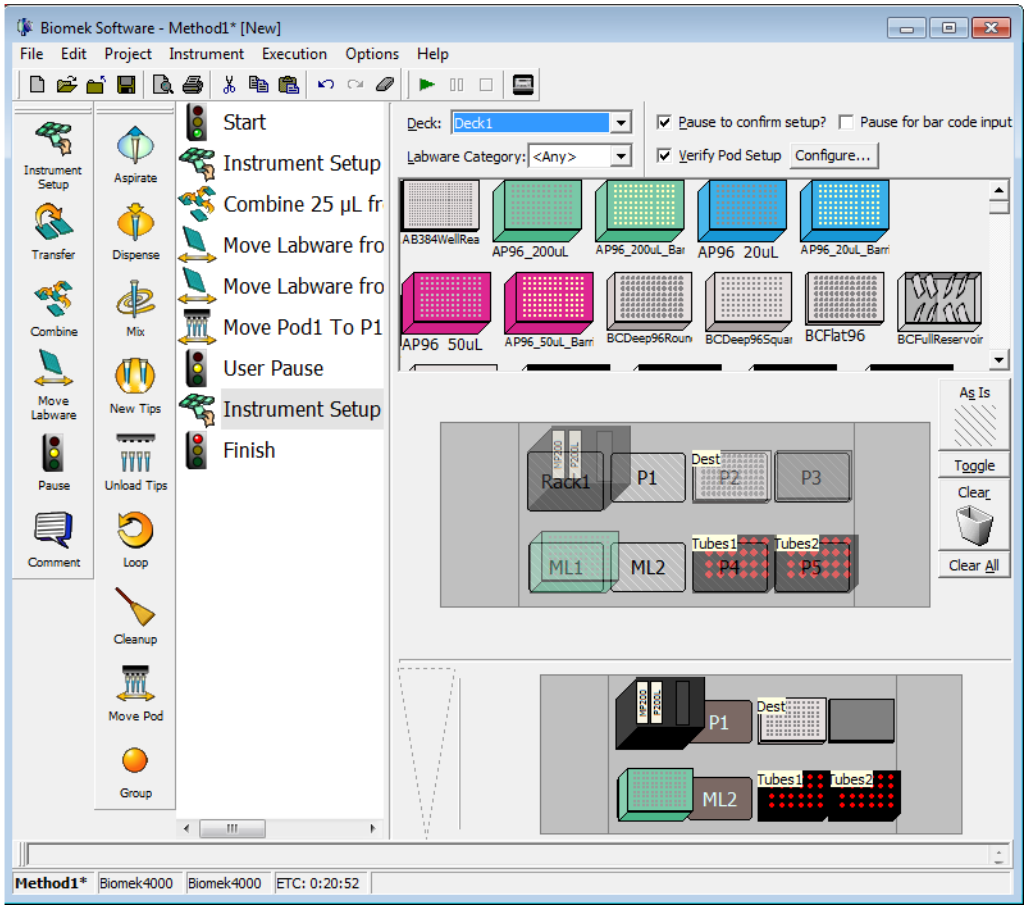
Now that you have prepared to add more labware to the deck during a method, you are ready to configure a second **Instrument Setup** step. You will insert a second **Instrument Setup** step after the **Pause** step. The second **Instrument Setup** step not only indicates the current state of the deck, but it also allows you to add more labware. But before you will add more labware to the deck, you will remove some labware.

To configure the second **Instrument Setup** step:

1 Insert an **Instrument Setup** step into the Method View below the **User Pause** step. This opens a second **Instrument Setup** step configuration.

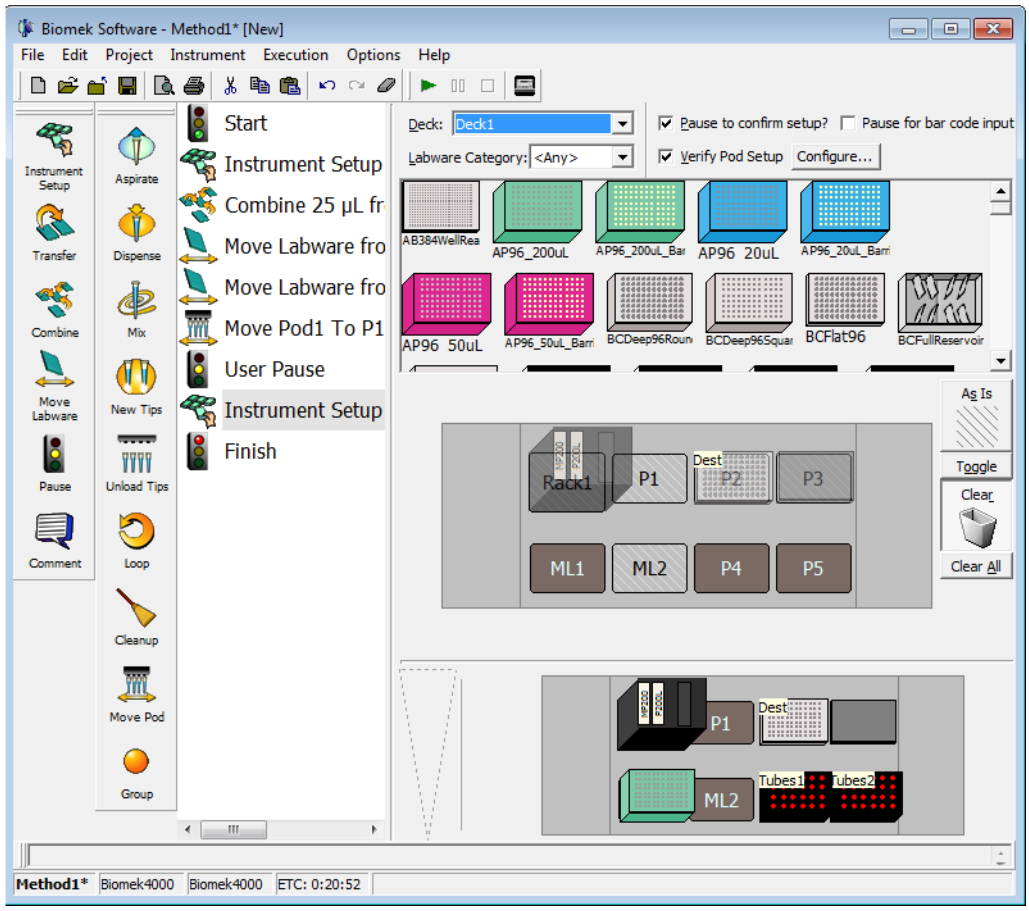
2 Choose **Toggle** under the **As Is** square. This lets the software know that all deck positions are to remain as they are. The main editor should now look like Figure 2.12.

Figure 2.12 Adding an Instrument Setup Step and Toggling All Deck Positions As Is



3 Select **Clear** and then click on **ML1**, **P4**, and **P5**. This removes the tube racks and used tip box. Now the main editor should look like Figure 2.13.

Figure 2.13 Using Clear to Remove Labware



Adding Labware to the Deck

Now you will add the labware to prepare for the next liquid-handing process, which is a Serial Dilution. For this next liquid-handling process, you will need to add two more tip boxes and an additional source reservoir. This new labware was what you configured to display when the instrument paused for manual placement.

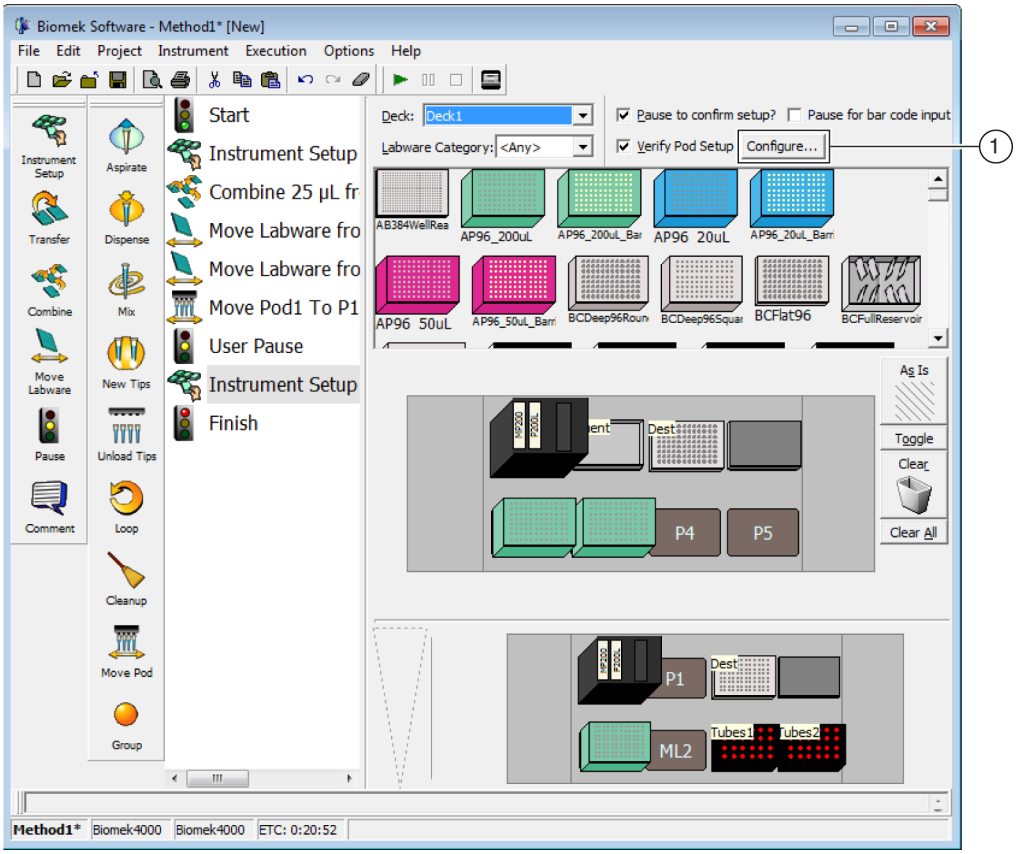
TIP Even though the software finds tips automatically, you have to ensure there are enough tips on deck to do the job. If you don't, you will get an error message.

1 Place a **BCUpsideDownTipBoxLid** reservoir on **P1** and name it **Diluent**. Configure the reservoir to have an **Unknown** volume of **Water**. Make sure **Sense the liquid level the first time a well with Unknown or Nominal volume is accessed "from the Liquid"** is selected.

2 Place **AP96_200uL** tip boxes on positions **ML1** and **ML2**.

3 Select Configure... to inform the software that a tool is currently loaded on the pod (see Figure 2.14).

Figure 2.14 Configure Pod Setup

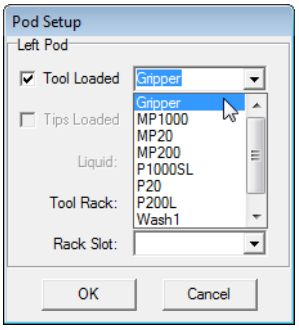


1. **Configure**: Select to configure the current pod setup.

4 In **Pod Setup**, select the **Tool Loaded** check box.

5 In the **Tool Loaded** drop-down (Figure 2.15), select the tool currently loaded on the pod.

Figure 2.15 Pod Setup Configuration



6 In the **Tool Rack** drop-down, select the rack where the loaded tool is stored when not in use.

7 In the **Rack Slot** drop-down, select the rack slot where the tool is stored, and then select **OK**.

You may think that all the steps in the Method View make your method look complex. Go to the next section to learn what you can do about that.

Using a Group Step

To prevent your method from appearing too complex, you can group steps together logically under one unique heading by inserting the **Group** step into the Method View. This group of steps is hidden in the Method View under the name that you've given it during configuration of the **Group** step.

Biomek Concept: Group Step	
	The **Group** step allows you to "nest" a series of connected steps together, and gives the group a logical name that appears in your Method View. When you open your method, the **Group** step appears collapsed with the connected steps hidden. This makes the method appear shorter, and it allows you to see more of the method without scrolling the Method View up or down. You simply double click on the **Group** step in the Method View to expand it and expose the nested steps.

Configuring the Group Step

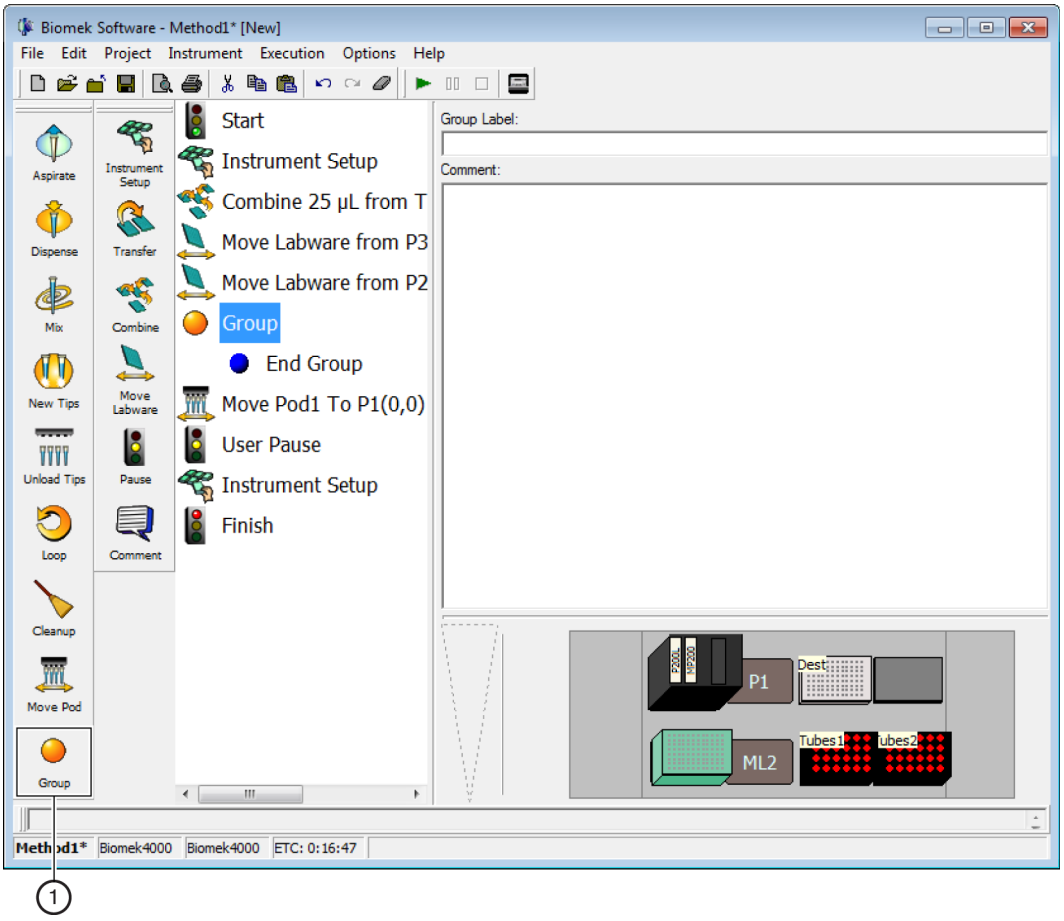
For this activity, you will group under one heading the **Move Pod**, **Pause**, and **Instrument Setup** steps you already have in your method. These steps are all associated with the preparation for the serial dilution.

To group these steps:

1 Insert the **Group** step from the Intermediate Step Palette in the Method View before the **Move Pod** step.

2 Double click on the **Group** step to reveal the **End Group** step. Scroll the Method View to the left if necessary (Figure 2.16).

Figure 2.16 Expanded Group Step



1. **Group** step

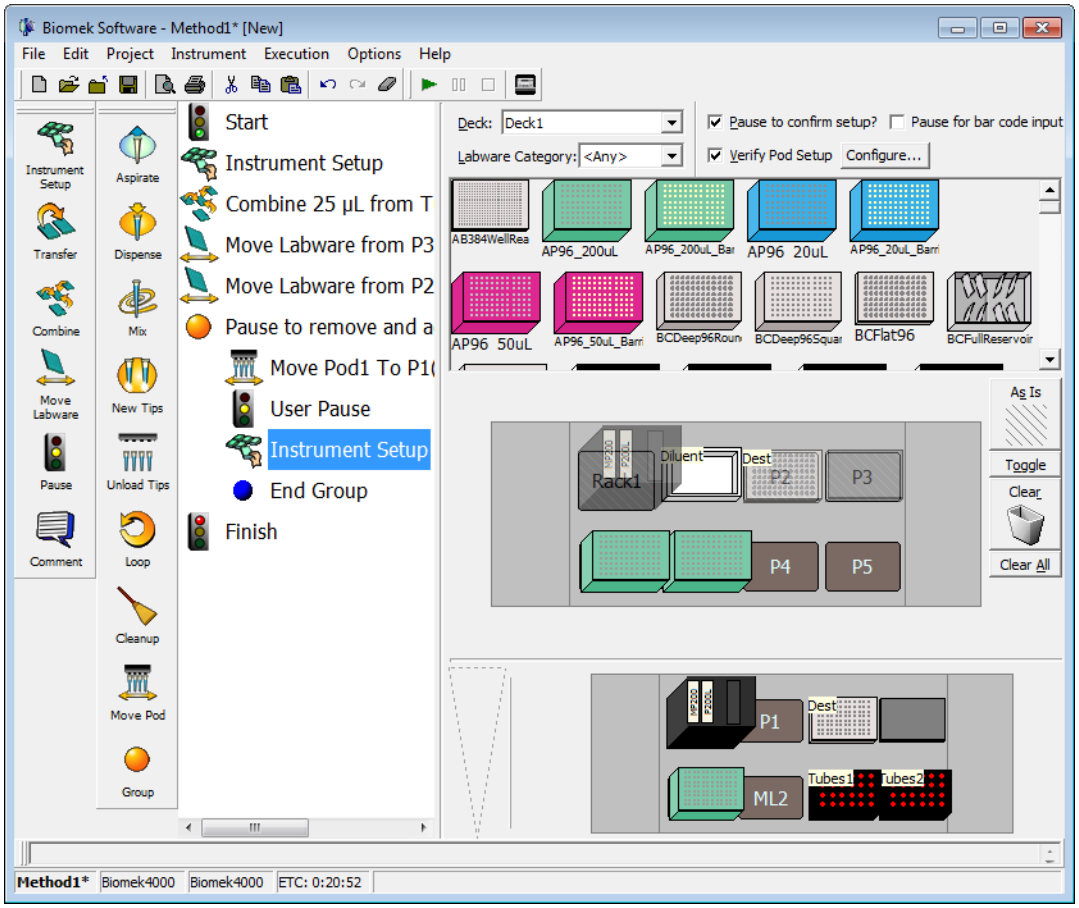
3 In **Group Label** of the step configuration, enter **Pause to remove and add labware**.

4 Highlight the **Move Pod** step, then drag and drop it into the **Group** step above **End Group**.

5 Repeat step 4 above for the **User Pause** and the second **Instrument Setup** step.

Now the **Move Pod**, **User Pause**, and second **Instrument Setup** steps are nested logically within a **Group** step (Figure 2.17). You can expand and collapse this step as desired by double clicking on the **Group** step title.

Figure 2.17 Configured Group Step With Nested Steps Expanded



Go to the next section to learn how to perform multiple dilutions of a sample on a single microplate.

Performing Multiple Dilutions of a Sample

The **Serial Dilution** step is used to perform multiple dilutions of a sample on a single microplate. This step transfers liquid from wells on a microplate to other wells on the same microplate and may also add diluent to those wells.

Biomek Concept: Serial Dilution Step	
	The **Serial Dilution** step completes multiple dilutions by performing the following actions in sequence: • Transfer a volume of diluent to all selected wells (optional). • Transfer a volume of sample from the first selected well to the next selected well. • Mix the solution via the **Technique Editor**. • Transfer a volume of solution to the next selected well. • Mix the solution via the **Technique Editor**. • Repeat transfer and mix operations until all selected wells are used. • Discard extra volume from last column or last wells.

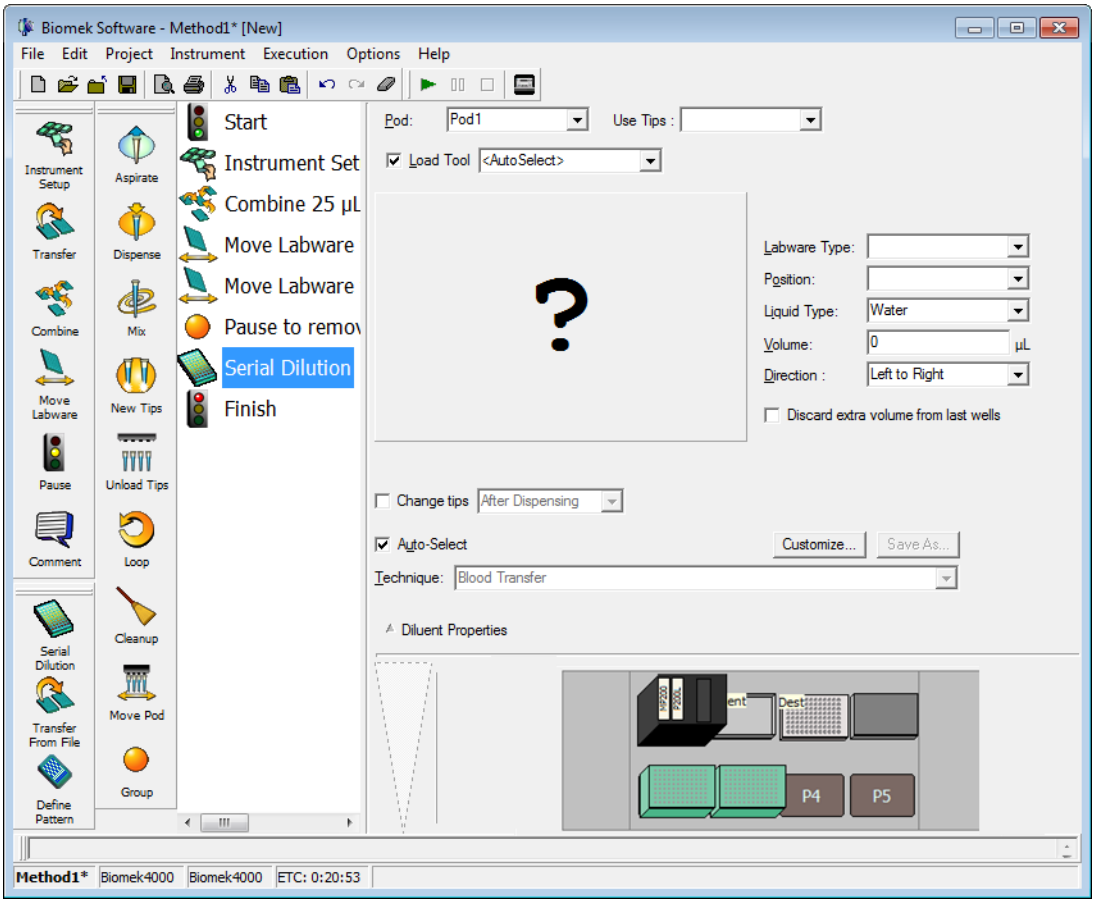
For this next activity, we will use the sample in the first column in the microplate on **P2**.

1 Right click anywhere in the space below the Basic Step Palette.

2 Choose **Span-8.** The Span-8 Step Palette appears on the main editor.

3 Insert a **Serial Dilution** step after the collapsed **Group** step (Figure 2.18).

Figure 2.18 Serial Dilution Step Inserted



4 In **Use Tips**, choose **AP96_20uL**.

5 Click on the **Dest** plate on **P2**.

6 In **Liquid Type**, choose **Water**.

7 In **Volume**, enter **50**. This is how much liquid is transferred from one well to the next.

8 In **Direction**, make sure **Left to Right** is selected since you will be diluting across the rows of the plate.

TIP With the **Serial Dilution** step, contiguous wells must be used. In **Direction**, **Left to Right** is faster.

NOTE **Top to Bottom** dilutions were not possible using Biomek 3000 instruments, as serial dilutions could only be completed using multi-tip pipetting tools. Biomek 4000 serial dilutions allow use of multi-tip **or** single-tip pipetting tools, thus allowing for dilutions to be performed one well at a time, in a **Top to Bottom** or **Left to Right** direction.

9 Check **Discard extra volume from last wells** and **Change tips After Every Sample**.

10 Select **Diluent Properties** to expand.

11 Check **Add diluent before transfer**.

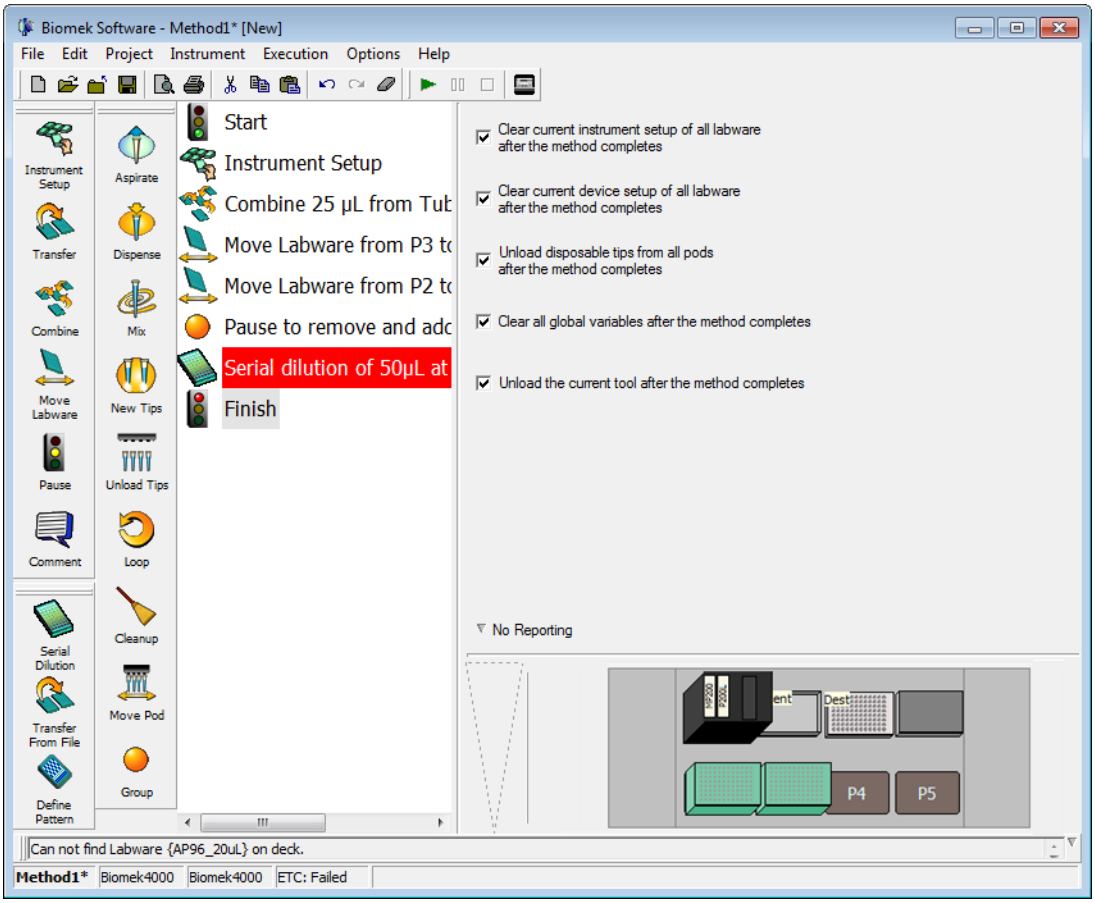
12 Select the **Diluent** reservoir at **P1**. This means the diluent is added to all wells before the sample transfers.

13 Configure the **Dilution Ratio** to 1:2 by entering **2** in the field. The dilution ratio is a ratio of volume of sample to total solution, so a dilution ration of 1:2 means that for every µL of sample there is 1 µL of diluent added, or a 50% dilution.

14 Make sure **Change tips between diluent transfers** is not checked.

15 Highlight the **Finish** step to validate the method. OOPS! The red indicates an error (Figure 2.19). Go to the next section to learn how to correct this error.

Figure 2.19 Error Displayed



Responding to an Error Message

For this activity, you'll learn how to locate and respond to the error message you just received.

Locating the Error

Biomek Software alerts you to errors in several ways, including:

- The step with the error appears in red in the Method View when any step following the error is highlighted.
- A tool tip describes the error when you hover the cursor over the step causing the error.
- An associated red error message is displayed in the status bar at the bottom of the editor.
- The error is displayed in an error bar just above the status bar.

There are other errors that are displayed in error message boxes. These errors state the problem and display appropriate recovery options. Refer to the *Biomek 4000 Software Manual*.

Correcting the Error

In this tutorial, the error message is **Can not find labware {AP96_20µL} on deck**. If you recall, you selected **AP96_20µL** tips in the **Serial Dilution** step rather than the **AP96_200µL** tips you used in the last **Instrument Setup** step. Since you have configured the **Serial Dilution** step to transfer 50 µL using **AP96_20µL** tips, but the tips you placed on your deck are actually **AP96_200µL** tips, an error is produced. To correct the error:

1 Highlight the **Serial Dilution** step in the Method View.

2 In the **Use Tips**, change the tip type to **AP96_200µL**.

3 Click the **Finish** step again in the Method View. The error has been corrected.

Biomek Software continually validates the steps as you progress through building your methods. When you highlight any step, the steps above that point in the method will be validated. If an error is encountered, the step causing the error will be highlighted in red.

Now go to the next section to learn how to use **Single Step** to view each operation of this method.

IMPORTANT If you have not already configured the physical deck and you are planning to run the method on hardware rather than in Simulation Mode (see CHAPTER 1, *Viewing the Method in the Biomek Simulator*), add the labware and tools as specified in the **Instrument Setup** step (see *Setting Up Your Deck for This Chapter*). Verifying that the correct labware and tools are used ensures proper pipetting and labware handling.

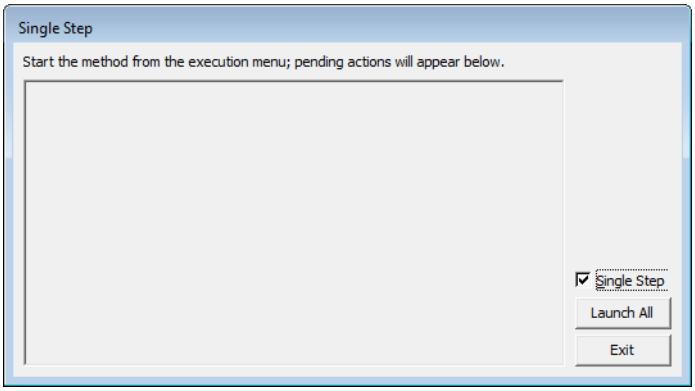
Performing Single Operations With the Biomek 4000 Laboratory Automation Workstation

Biomek Concept: Single Step	
	**Single Step** pauses the Biomek 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.

In this activity, you will use **Single Step** to view each operation of the method you just created:

1 Choose **Execution** > **Single Step**. **Single Step** appears (Figure 2.20).

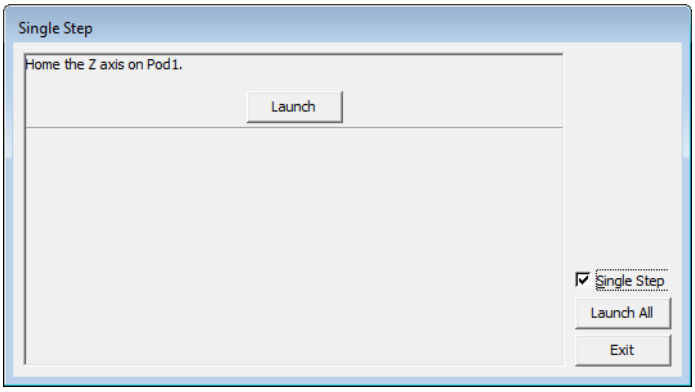
Figure 2.20 Single Step



2 While **Single Step** is still open, choose **Execution > Run** from the grayed-out toolbar. **Single Step** with specific operations displayed appears (Figure 2.21). If you have other ALPs configured on your deck, the initialization process for them appears in **Single Step**.

TIP Go slowly when using **Single Step**. It is possible to move too quickly through the method and bypass the steps that need verification.

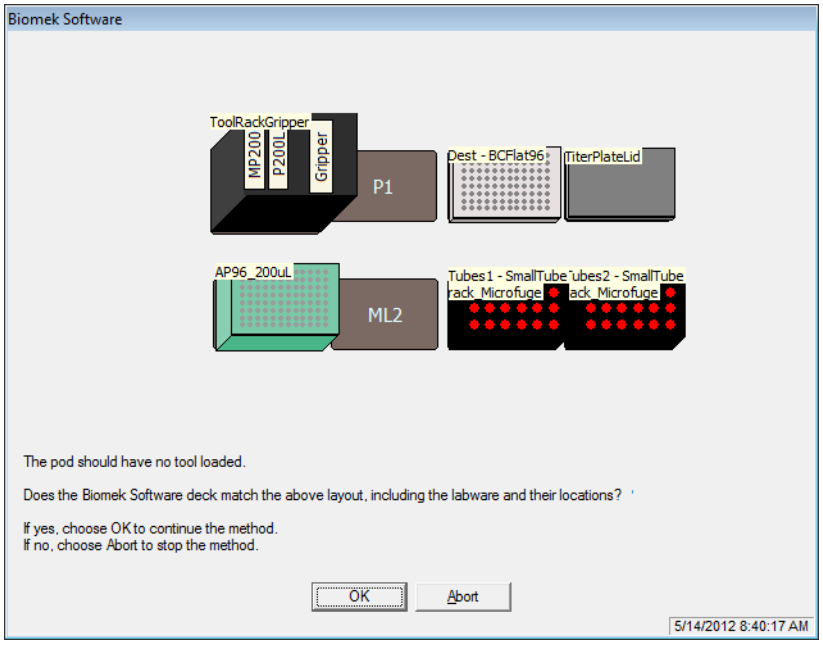
Figure 2.21 Single Step With Specific Operations Displayed



3 Under **Home the Z axis on Pod1**, choose **Launch**. The next operation is launched.

4 Keep choosing **Launch** until the Biomek Software prompt appears (Figure 2.22). If the physical deck matches the software prompt, choose **OK**. **Single Step** continues displaying each operation, along with the option to **Launch** and execute that operation.

Figure 2.22 Biomek Software Prompt



5 Continue to view each operation by choosing **Launch** or to stop **Single Step**, choose **Exit** to allow the method to run without the option to view each operation.

6 Clicking the **Launch All** button launches all of the steps currently displayed inside the **Single Step** window.

Go to the next chapter to learn how to use individual steps to more precisely control a liquid transfer.

CHAPTER 3

Using Individual Steps to Transfer Liquid

Introduction to Using Individual Steps to Transfer Liquid

In the previous chapters of this tutorial (CHAPTER 1, *Getting Started* and CHAPTER 2, *Using More Steps in a Method*) you learned how to:

- Launch Biomek Software and build, run, and save a simple transfer method.
- Transfer liquid from two sources to a single destination.
- Mix contents in labware.
- Remove and add more labware to the deck once a method has started to run.
- Group steps logically in the Method View.
- Use the automatic serial dilution feature.
- Perform single operations.

If you already know how to complete these tasks, you can start with this chapter or subsequent chapters.

What You'll Learn in This Chapter

This chapter will help you enhance your method-building skills to create more advanced methods using variables, expressions, and "loops" to repeat tasks. You will also learn how to conserve tips and view a log file.

More specifically, the step-by-step instructions in this chapter will teach you how to:

- Aspirate and dispense liquid independently using individual steps.
- Use variables and expressions.
- Use a **Loop** step to repeat actions.
- Load and unload tips independently using individual steps.
- Handle lids in a method.

  NOTE Your instrument must be equipped with the optional **Gripper** tool to handle lids in a method.

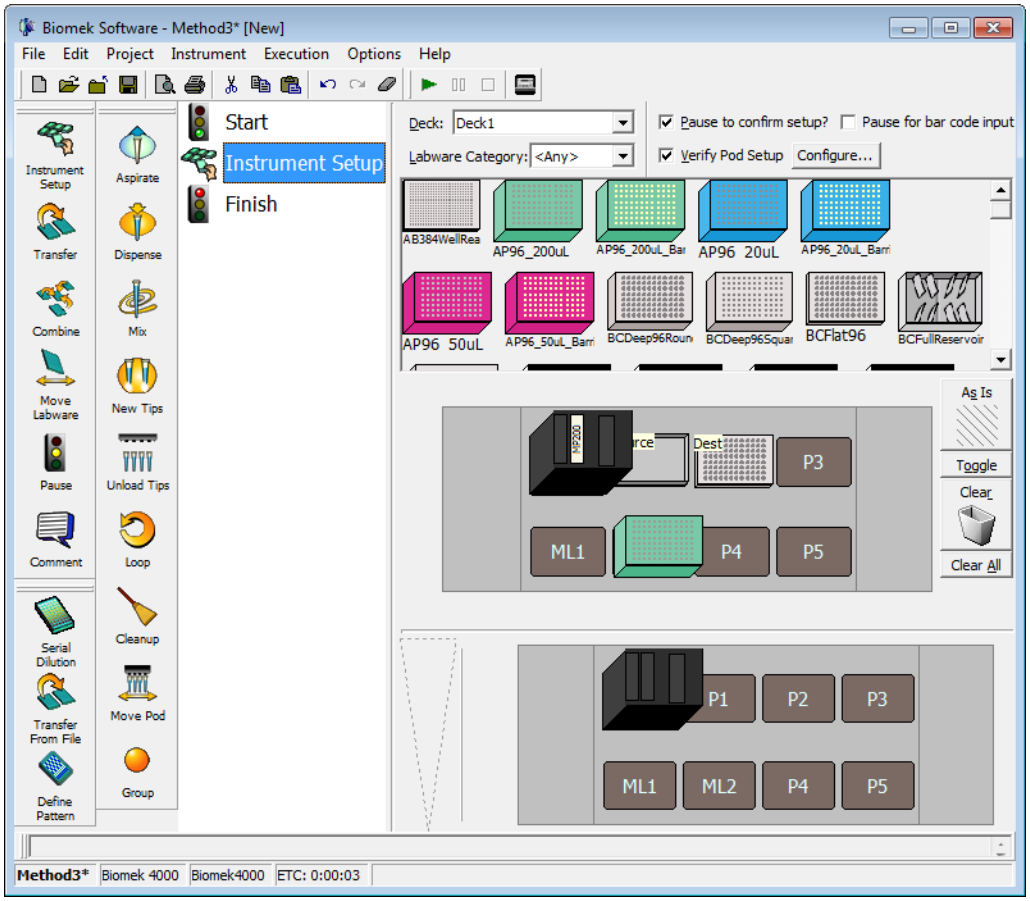
- View a log file associated with a method.

Setting Up Your Deck for This Chapter

1. Launch Biomek Software, start a new method, and using an **Instrument Setup** step, configure the deck by following the steps below.
2. Place an **MP200** tool in the tool rack.
3. Place an **AP96_200µL** tip box on **ML2**.
4. Place a **BCUpsideDownTipBoxLid** reservoir on **P1**. Name it **Source** and configure it to contain an **Unknown** volume.
5. Place a **BCFlat96** microplate on **P2**. Name it **Dest** and configure it to contain an **Unknown** volume.

Your deck should look like Figure 3.1. Now go to the next activity to learn how to use individual steps to transfer liquid in a method.

Figure 3.1 Initial Instrument Setup for Using Individual Steps



Using Individual Steps to Transfer Liquid

In previous chapters, when you wanted to transfer liquid from one plate to another, you used the **Transfer** and **Combine** steps to perform all the necessary actions - loading tips, aspirating and dispensing liquid, and unloading tips. Sometimes, however, you want precise control over the order in which samples are transferred or when tips are loaded and unloaded.

When you need more control over the liquid transfer operation than the **Transfer** and **Combine** steps provide, you can configure liquid transfers using individual steps. Unlike the **Transfer** and **Combine** steps, these individual steps each perform only one task (e.g., aspirate, dispense, load tips, or unload tips).

In this section, you will use the **Aspirate** and **Dispense** steps to transfer liquid from the **BCUpsideDownTipBoxLid** reservoir source to the **BCFlat96** destination plate.

Load Tool Step

Before any aspirating can occur, you must first load the proper tool.

To select a tool for this operation:

1 From the Biomek Instrument Step Palette, drag and drop a **Load Tool** step under the **Instrument Setup** step in the Method View.

2 From the **Load Tool** drop-down, select **MP200**.

This completes the Load Tool process.

Aspirating Liquid Using the Aspirate Step

You can use the **Aspirate** step to aspirate liquid from a microplate or reservoir.

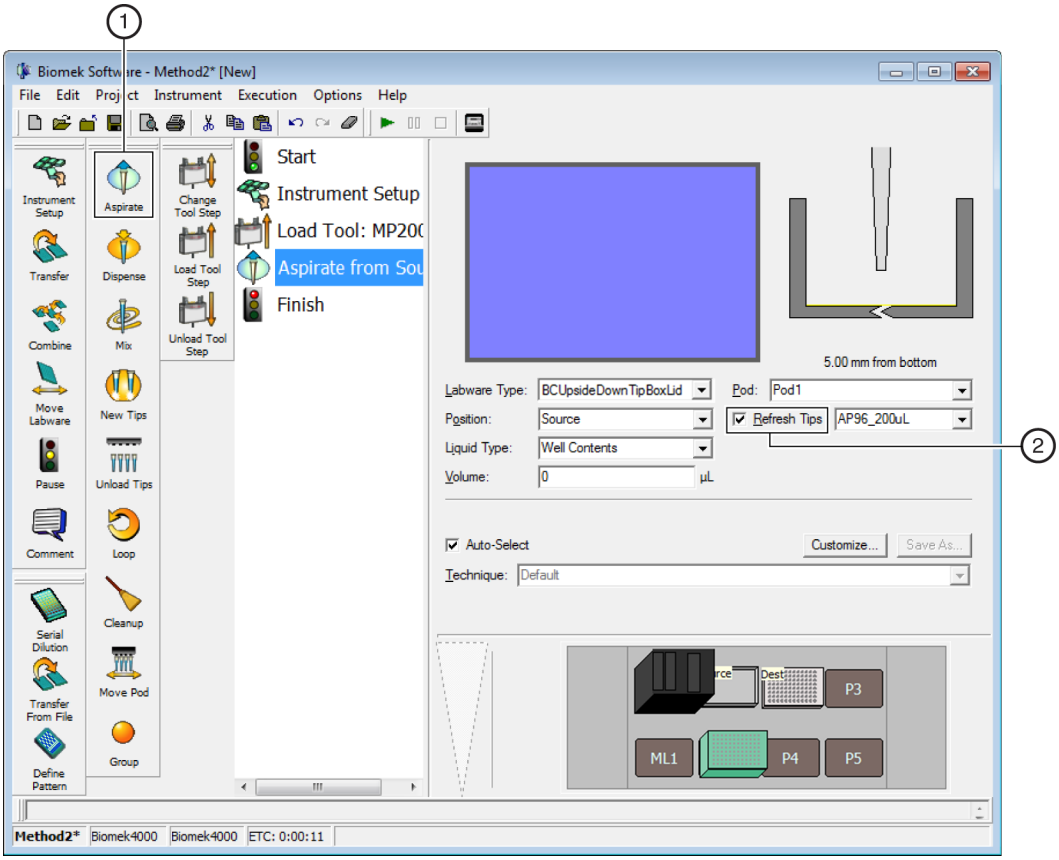
To aspirate liquid from the reservoir using the **Aspirate** step:

1 Ensure you configured the deck according to the instructions in *Setting Up Your Deck for This Chapter*.

2 Drag an **Aspirate** step from the Intermediate Step Palette to the Method View and drop it after the **Load Tool** step.

3 In the current deck display, click on **Source** to select it as the labware from which to aspirate. Figure 3.2 appears.

Figure 3.2 Source Chosen for Aspirate Step

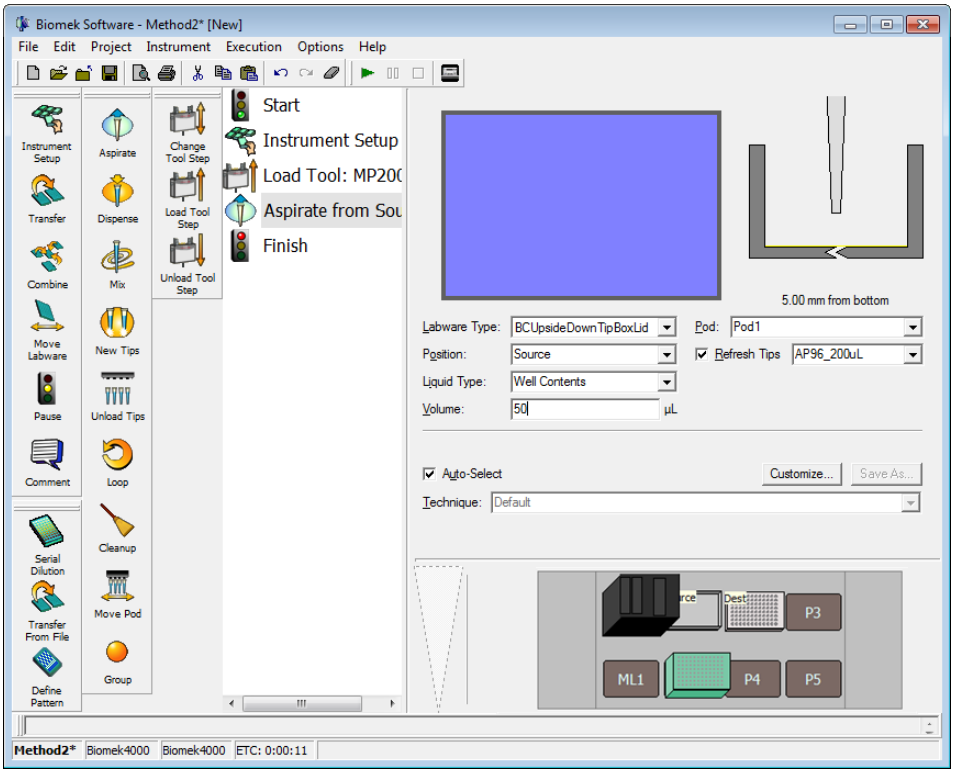


1. **Aspirate** step
2. **Refresh Tips**

4 In **Volume**, enter **50** µL.

5 From the **Aspirate** step configuration, keep the default selection of **Refresh Tips** (Figure 3.2). This loads new tips before the pod aspirates. Make sure **AP96_200µL** is selected. Your **Aspirate** step is configured and the main editor should look like Figure 3.3.

Figure 3.3 Aspirate Step Configured



TIP If tips are already loaded, **Refresh Tips** unloads those tips (along with any liquid in those tips if they are not empty) and loads new tips prior to aspirating. This option should be used only when there are either no tips loaded or the tips are empty.

Dispensing Liquid Using the Dispense Step

Now that you have aspirated some liquid, you need to dispense it into another piece of labware. In this tutorial, you will dispense the aspirated liquid into some wells of the **Dest** plate. To dispense previously aspirated liquid:

1. Drag a **Dispense** step from the Intermediate Step Palette to the Method View and drop it after the **Aspirate** step.

2. In the current deck display, click on the **Dest** plate on position **P2** to select it as the destination.

3. Make sure the first column of the microplate is selected.

4. Since you are going to be transferring 50 µL, verify **Volume** field specifies **50** µL.

You have now configured a simple method that aspirates from a reservoir source plate and dispenses into one column of a destination plate using individual steps. If you like, you can run this method on your instrument or in the simulator (refer to CHAPTER 1, *Getting Started*, for more information on how to do this).

In the next section, you will reconfigure this simple method to use a variable for the volumes to aspirate and dispense.

Using Variables in a Method

Biomek Concept: Variables	
	Using a variable provides several advantages: • If you want to change a value that is used in several places within a method, you can change it in one place and it is automatically changed everywhere that variable is used. • The value of a variable can be set at run time and the method is automatically updated appropriately. • Decisions can be made at run time based on the value of a variable (you will do this in the next chapter).

Variables make it easier to modify a method. When configuring steps, you enter the name of the variable in the desired field; when the method is run, the actual value of the variable is substituted and the action executed.

You will now create a variable for the volumes to transfer and use it in the **Aspirate** and **Dispense** steps. This includes:

- *Creating a Variable in the Start Step*
- *Using a Variable with Expressions in Step Configurations*
- *Changing the Value of a Variable at Run Time*

Creating a Variable in the Start Step

The **Start** step, in addition to being the first step in the method, also can be used to create and name variables that can be used throughout the method. Variables named in a **Start** step may be used in configuring other steps in the method. Other steps in Biomek Software also allow you to create variables, but those variables are local and are particular to the steps in which they are created. You will work with local variables later in the chapter with the **Loop** step.

You will now create a variable for the volume to transfer using the **Start** step.

1 To create a variable in the **Start** step:

2 Select the **Start** step in the method view to display its configuration.

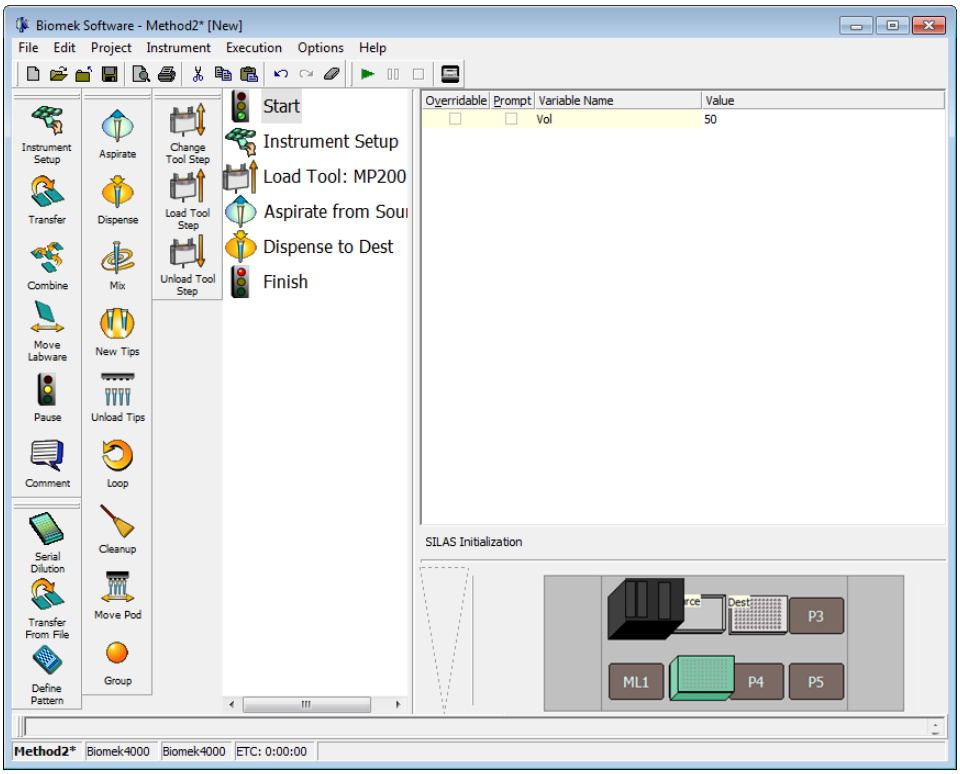
TIP Variable names are not case sensitive, so entering the name **VOL**, **vol**, **Vol**, or **VoL** are all evaluated the same.

3 In **Variable Name**, enter **Vol**.

TIP Do not use the variable **C__Volume**. This variable is built into Biomek Software and is associated with tracking volume.

4 In **Value**, enter **50**. Your **Start** configuration should look like Figure 3.4. You have created a variable named **Vol** that has a value of **50**.

Figure 3.4 Vol Variable Created in the Start Step



Using a Variable with Expressions in Step Configurations

Biomek Concept: Expressions	
	Expressions combine text, numerical constants, and variables using operators to modify a variable. These operators may perform a number of mathematical operations or combine text strings. Just like with variables, the expression is evaluated and the resulting value is substituted for the expression at run time.

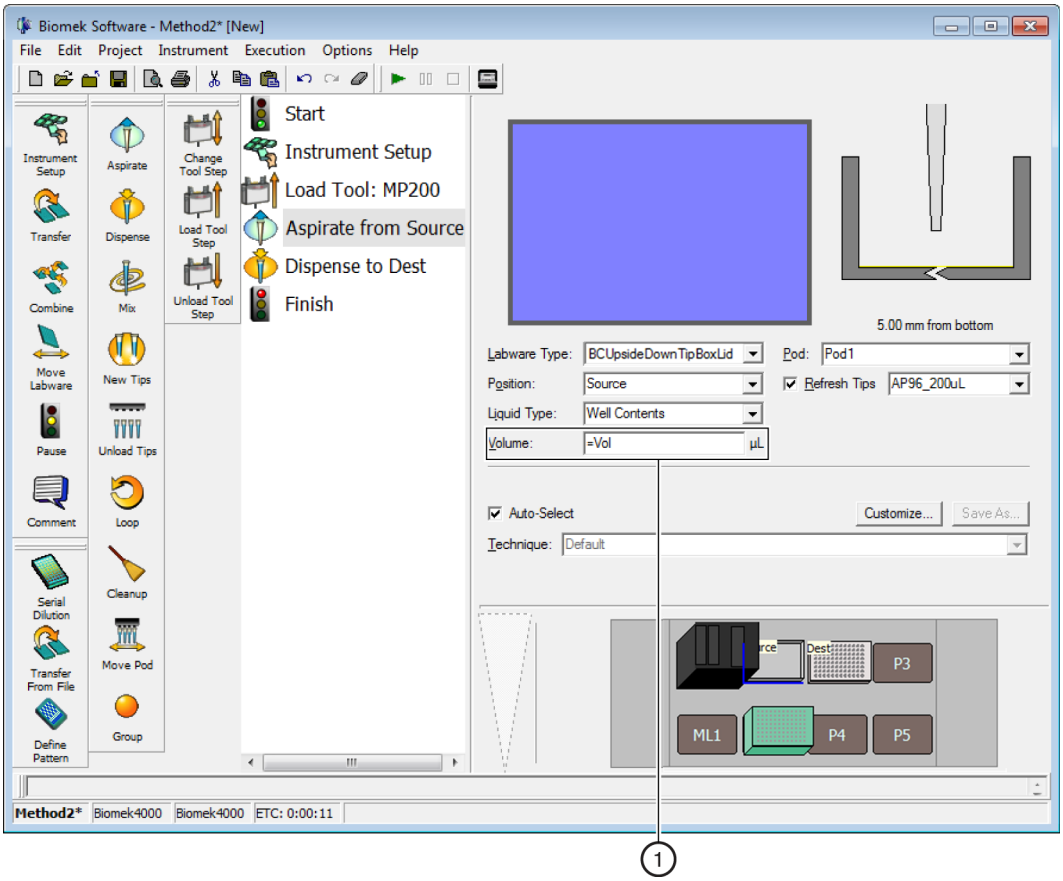
You will now use the **Vol** variable you created in the **Start** step with expressions to configure volumes to transfer in the **Aspirate** and **Dispense** steps.

To use a variable in a step configuration:

1 Select the **Aspirate from Source** step in the Method View.

2 In **Volume** enter **=Vol** (including the equal sign). Variables and expressions are always preceded by an equal sign when entering them into a step configuration field. When the method is run, **Vol** is replaced by the value of the variable and the expression is evaluated; in this case, **50 µL** (see Figure 3.5).

Figure 3.5 Volume Field



1. **Volume** field.

---

3 Select the **Dispense to Dest** step in the Method View and configure **Volume** using the same variable and volume as you did for the **Aspirate from Source** step. You will need to configure this as it won't automatically display the volume you configured in the **Aspirate from Source** step like it did in *Dispensing Liquid Using the Dispense Step* since it will only update the first time the volumes are configured for a step.

To change the volume you want to transfer, you would change the value of the variable **Vol** in the **Start** step. The amount specified in **Volume** for both the **Aspirate** and **Dispense** steps would then automatically be updated when the value of **Vol** is substituted at run time.

IMPORTANT If you have not already configured the physical deck and you are planning to run the method on hardware rather than in Simulation Mode (see CHAPTER 1, *Viewing the Method in the Biomek Simulator*), add the labware and tools as specified in the **Instrument Setup** step (see *Setting Up Your Deck for This Chapter*). Verifying that the correct labware and tools are used ensures proper pipetting and labware handling.

Changing the Value of a Variable at Run Time

Since the value of a variable can be changed throughout the method by changing the value of the variable in the **Start** step, it makes it easy to quickly reconfigure methods that are similar except for one or two items.

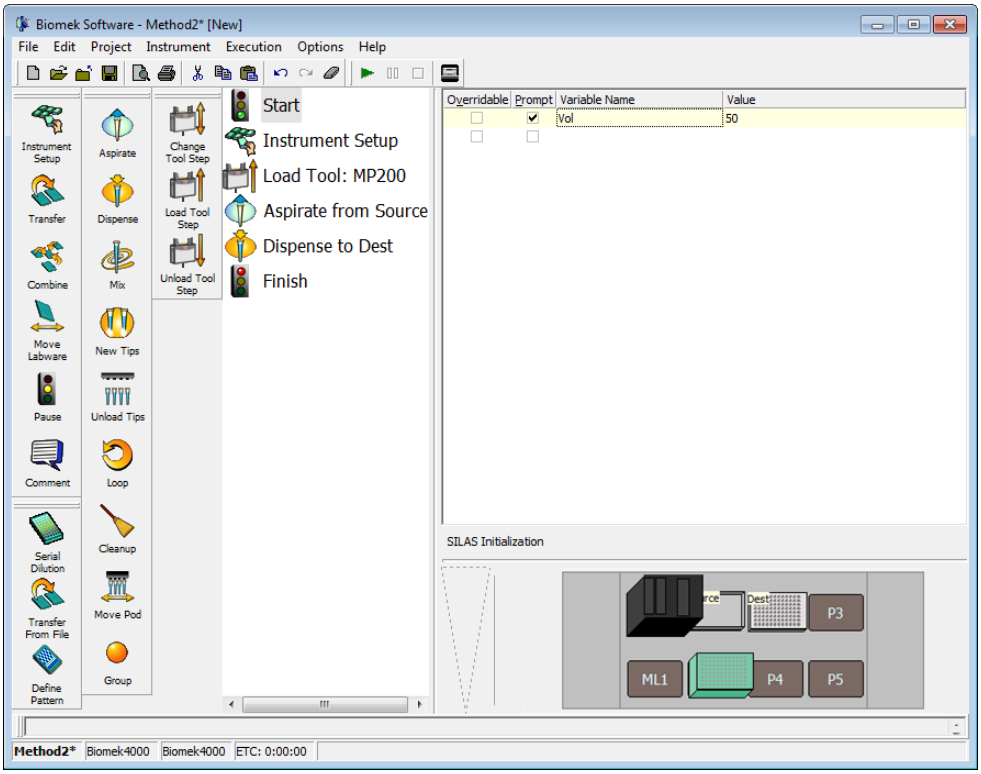
For variables that are created in the **Start** step, you can configure Biomek Software to prompt you to specify a value for the variable at run time. When configured to do this, a prompt appears for each variable when the method is run. The value that you entered for the variable in the **Start** step is now the default value for the variable. You can use that value by choosing **OK**, or enter a new value and choose **OK** to change the value of the variable. The method run then uses the specified value for the variable and updates the method accordingly.

To specify the value of a variable at run time:

1 Select the **Start** step.

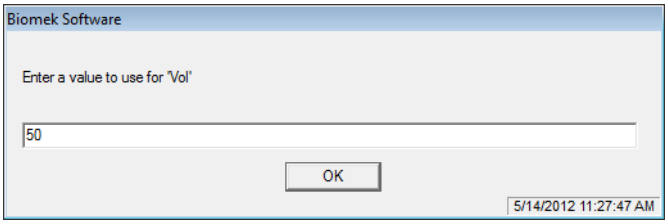
2 Select the **Prompt** check box for the variable **Vol**. Your **Start** configuration should now look like Figure 3.6.

Figure 3.6 Prompting for Value of a Variable



3 Run the method. A prompt appears allowing you to enter a value for the variable (Figure 3.7).

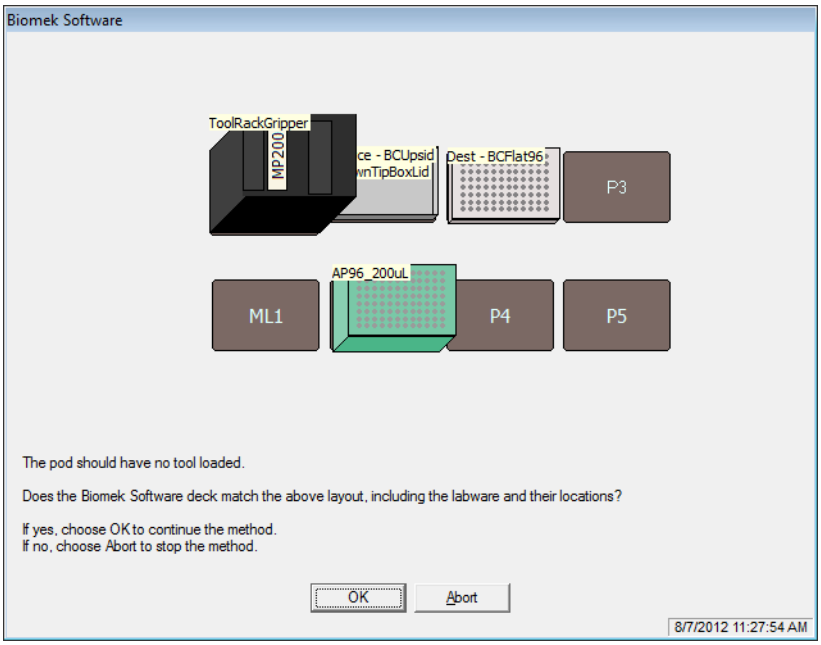
Figure 3.7 Prompt to Specify the Value of a Variable



4 Enter **50** and choose **OK**. If you run the method on your Biomek 4000 instrument, you should notice that 50 µL was transferred with the **MP200** tool.

5 The **Biomek Software** deck setup confirmation prompt appears (Figure 3.8). Respond appropriately.

Figure 3.8 Biomek Software Deck Setup Confirmation



In the next section, you will learn to use variables and a **Loop** step to perform repeated actions in order to dispense to the destination plate.

Repeating Liquid Transfer Steps Using a Loop

The **Loop** step enables you to repeat one or more steps for multiple cycles. Each cycle or iteration repeats the steps contained inside the **Loop** step. An optional variable may also be created in the **Loop** step. This variable is assigned a start value that is incrementally processed with each cycle of the loop until it reaches the end value.

In this section, you will modify the method to use a **Loop** step to aspirate and dispense to all 12 columns of a plate rather than just the first column. In completing this task, you will create a variable in the **Loop** step and use this variable to reconfigure the **Aspirate** and **Dispense** steps as the liquid transfer actions are repeated during method execution.

Repeating Actions Using the Loop Step

When you want to repeat actions several times during a method run, you use a **Loop** step. The **Loop** step allows you to repeat the actions of one or more steps without inserting and configuring those steps for each time they are to be repeated. Steps to repeat are placed, or nested, inside the **Loop** step.

Biomek Software internally tracks the value of the **Loop** for each cycle, and **Start**, **End**, and **Increment** values are specified (see Biomek Concept below). If desired, a name can be assigned to the **Loop** value to create a variable. This variable can then be used like any other variable to configure steps, but can only be used with steps contained within the **Loop** step.

Biomek Concept: Loop Step	
	The **Loop** step repeats the nested step or steps until its **End** value is exceeded. For the first cycle of a **Loop**, its value is the **Start** value. After completing all steps inside the loop, the value changes by the **Increment** and the steps are repeated again. This process repeats until the **Increment** changes the value to be greater than the **End** value.

To repeat the **Aspirate** and **Dispense** steps:

1. Insert a **Loop** step after the **Load Tool** step. The **Loop** and **End Loop** icons appear in the Method View, and the **Loop** step configuration is displayed.

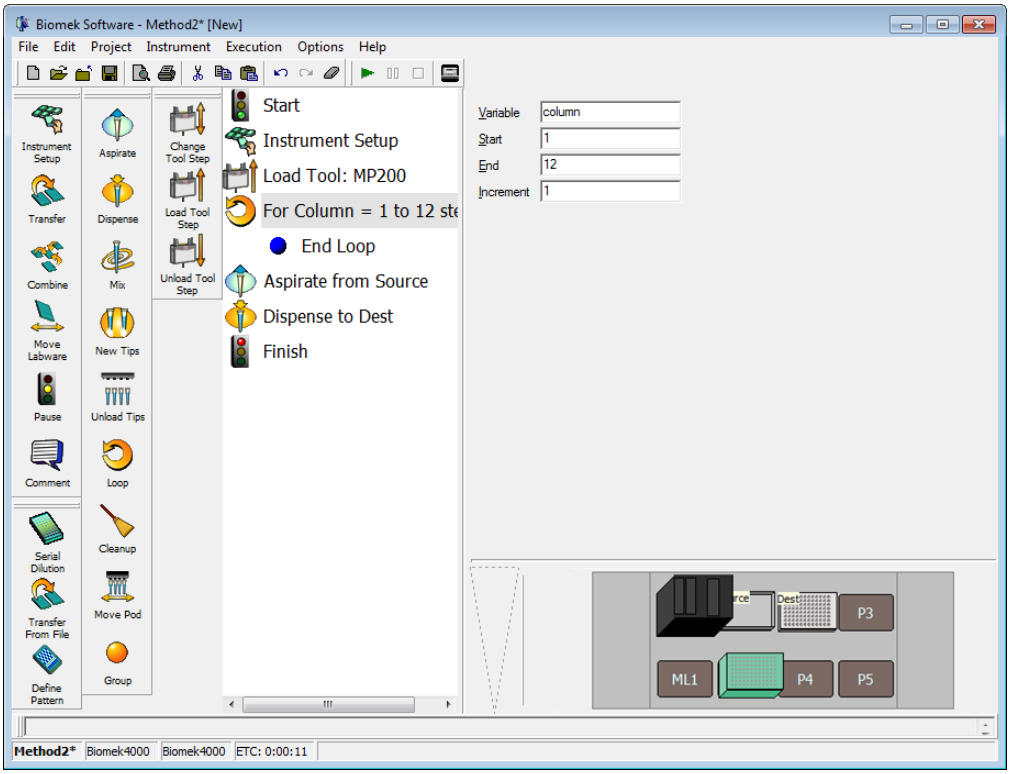
2. In **Variable**, enter **column**. This will create a variable named *column* that can be used to configure steps within the **Loop**.

3. In **Start**, enter **1**. This will be the initial value assigned to the variable *column* on the first iteration of the loop.

4. In **End**, enter **12**. This will be the final value for the variable *column*. When the value of *column* exceeds the **End** value, the **Loop** step ends and the remainder of the method continues.

5 In **Increment**, enter **1**. The **Increment** value is how much the value for the variable **column** changes with each iteration of the **Loop**. Your **Loop** step configuration should look like Figure 3.9.

Figure 3.9 Loop Step for Repeating Aspirate and Dispense



6 Drag the **Aspirate from Source** and **Dispense to Dest** steps between the **Loop** and **End Loop** icons.

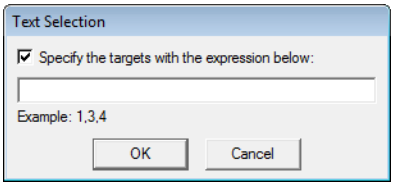
Specifying the Column to Dispense to in the Dispense Step

Now that you have configured the **Loop** step to create the variable *column* and placed the **Aspirate** and **Dispense** steps inside the **Loop**, you can use the variable *column* to reconfigure the **Dispense** step so all 12 columns on the **Dest** microplate are dispensed to rather than just the first column you originally configured.

1 Highlight the **Dispense to Dest** step configuration.

2 Right click anywhere in the labware graphic and choose **Specify Selection as Text. Text Selection** appears (Figure 3.10).

Figure 3.10 Text Selection

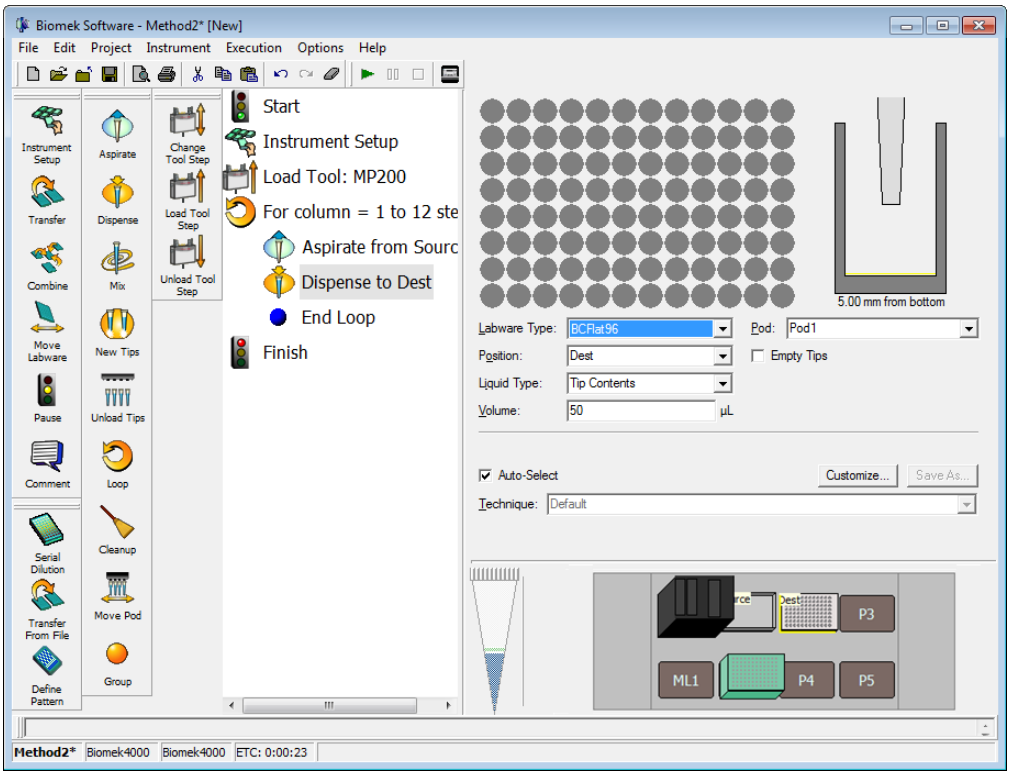


3 Enter **=column**. This means that the dispense starts with the well number equal to the value of the **Loop** variable. Since the wells in the first row are numbered 1 through 12, it will dispense to the column that starts with value of *column*.

4 Choose **OK**.

5 The **Dispense** step configuration looks like Figure 3.11. The graphical representation of the labware is grayed out to indicate that the target wells to dispense into are specified by text.

Figure 3.11 Dispense Step Inside the Loop



Conserving Tips Using Individual Steps

As the method is currently configured, an entire box of tips will be used. This is because the **Aspirate** step loads tips for each iteration of the **Loop**. Since the source is a reservoir and cross contamination is not a concern, you could reuse tips for all 12 iterations of the **Loop** step. To accomplish this, you will use a **New Tips** step before the loop and an **Unload Tips** step after the loop.

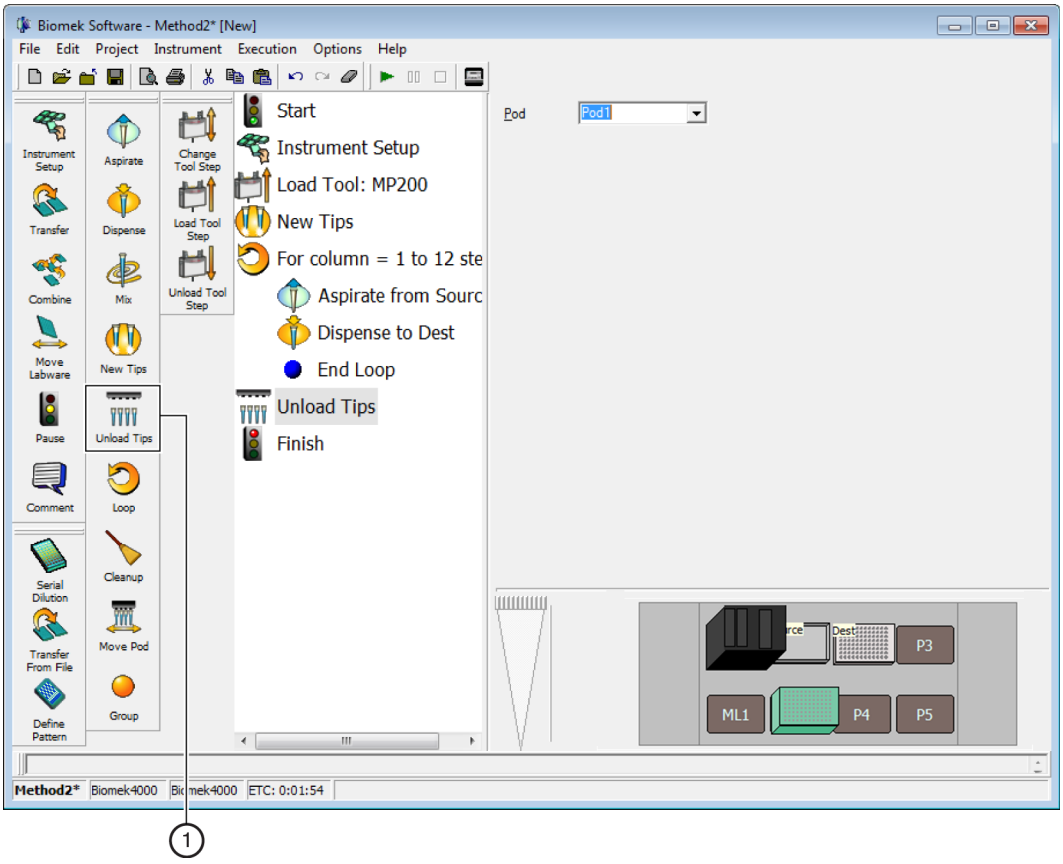
Loading and Unloading Tips Outside the Loop

To load and unload tips outside of the loop:

1. Insert a **New Tips** step between the **Load Tool** and **Loop** steps.
2. Make sure **AP96_200µL** is displayed in the **Tips** drop-down.
3. Select the **Aspirate** step inside the loop.
4. Deselect the **Refresh Tips** check box. This tells Biomek to use whatever tips are already loaded to perform the aspirate instead of loading new tips at the start of the **Aspirate** step.
5. Insert an **Unload Tips** step after the **End Loop** icon in the Method View.

   Your method should now look like Figure 3.12.

Figure 3.12 Loading and Unloading Tips Outside the Loop



1. **Unload Tips** step

This method loads new tips, uses those same tips to perform all 12 iterations of the **Loop**, and unloads the tips after the last iteration of the **Loop**.

Using Lids in the Method

NOTE If your instrument is not equipped with the optional **Gripper** tool, you cannot place or remove lids. Skip this section and go to *Viewing Log Data*.

In CHAPTER 2, *Using More Steps in a Method*, you learned about using the **Move Labware** step to move labware on the deck. Another use of the **Move Labware** step is to remove lids from lidded microplates or tip boxes. In this section, you will modify the method to use a lidded 96-well plate for the destination.

To use lids in a method:

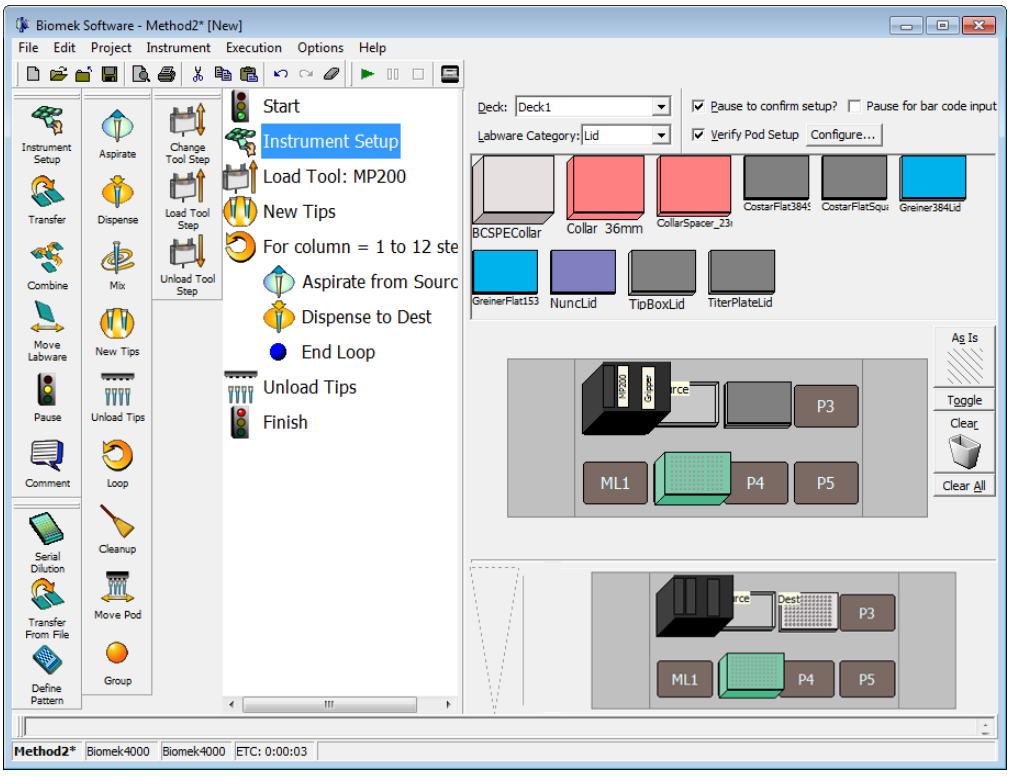
1 In the Method View, select the **Instrument Setup** step.

2 Place a **Gripper** tool in the **Gripper** tool rack by double clicking the tool rack displayed in the Configuration View and selecting the **Gripper** icon and dragging into the **Gripper** slot.

3 In **Labware Category**, select **Lid** to display only the lids.

4 Drag a **TiterPlateLid** on top of the **BCFlat96** plate located on position **P2**. Your **Instrument Setup** step should now look like Figure 3.13.

Figure 3.13 Modifying Instrument Setup Step to Add a Lid

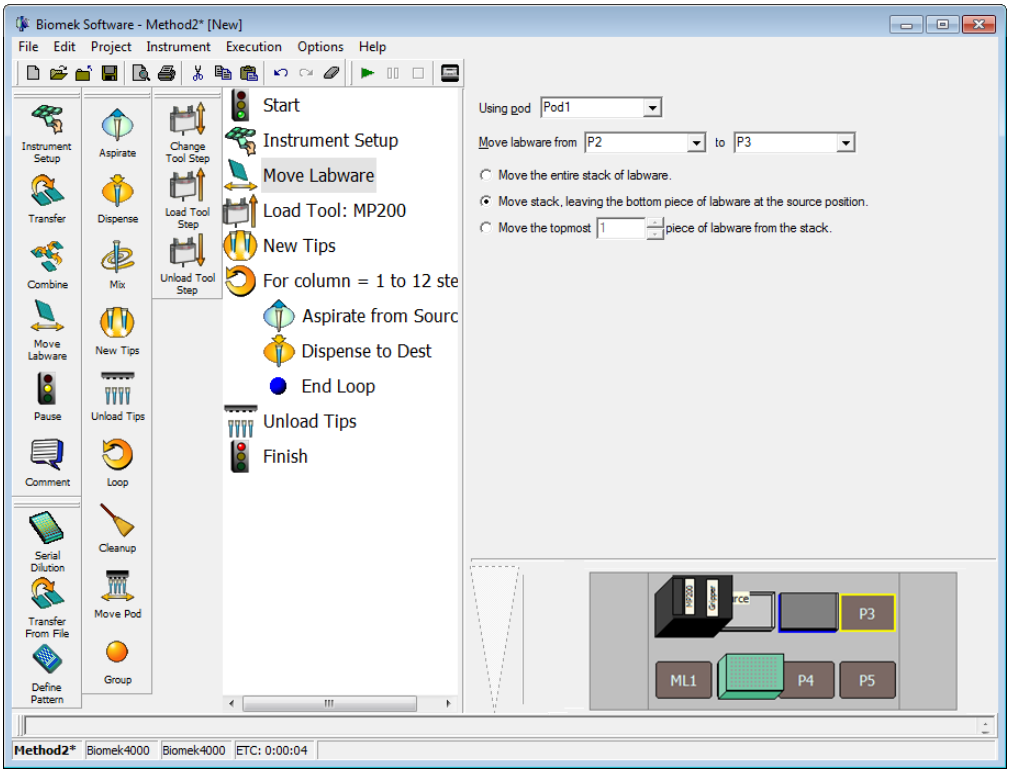


5 To remove the lid as part of the method, insert a **Move Labware** step immediately after the **Instrument Setup** step.

6 Configure the **Move Labware** step to move labware from **P2** to **P3**.

7 Select the second option to **Move stack, leaving the bottom piece of labware at the source position**. This tells Biomek to pick up only the lid and leave the plate at its current position. Your **Move Labware** step configuration should look like Figure 3.14.

Figure 3.14 Using Move Labware to Remove a Lid



8 Select **Finish** to validate the method. The lid appears on position **P3** in the Current Deck Display.

Go to the next section to learn how to view the log data associated with the method.

Viewing Log Data

Biomek Concept: Log Files	
	The following log files are available for the Biomek 4000 Latoratory Automation Workstation: • **Details**—captures every operation that occurs during a method run. • **Errors**—captures any errors that occur during a method run. • **Pipetting**—captures pipetting operations, including location and labware name or type. • **Transfer**—captures transfer operations, including location and labware name or type. • **UnifiedPipetting**—captures pipetting operations, along with sample IDs for wells. • **UnifiedTransfer**—captures transfer operations, along with sample IDs for wells. Refer to the *Biomek 4000 Software Manual* for more information.

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. For example, the logs **Errors**, **Pipetting**, and **Transfer** are, by default, available for the method you just ran, although other logs may be generated. See Biomek Concept above.

To run the method and view log data for the method you just ran:

1. Highlight **Finish** to validate the method.

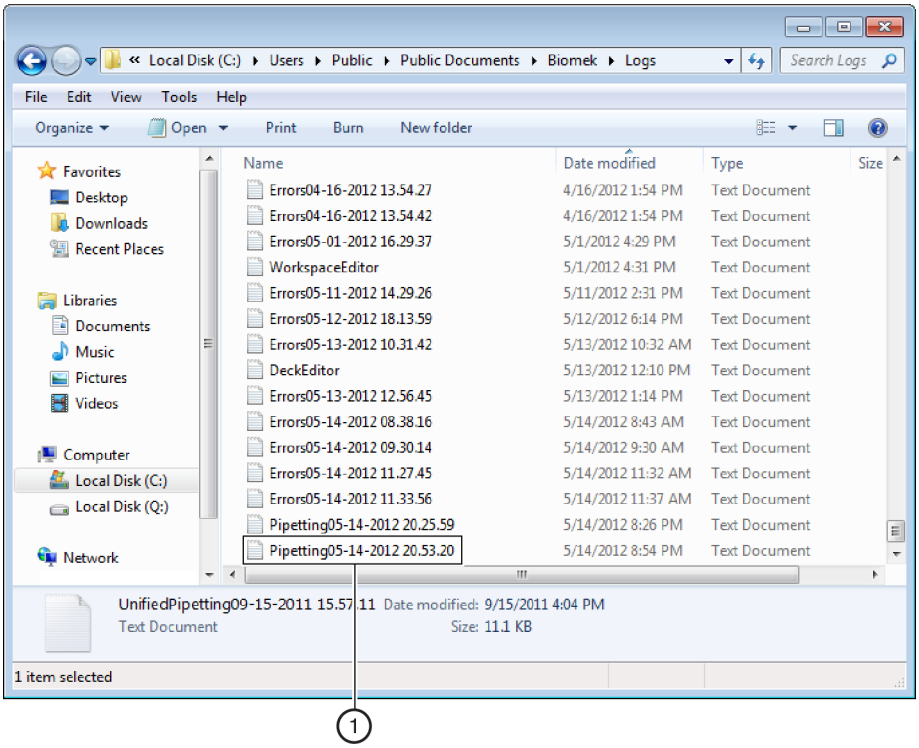
2. Choose **Options > Log Configuration**. **Log Configuration** appears.

3. In **Log Configuration**, deselect the default selection, and select **Pipetting**, and then choose **OK**. This allows you to save and view the Pipetting log file after you run the method.

4. Save and run the method.

5. Browse to **C:\Users\Public\Public Documents\Biomek\Logs** (Figure 3.15).

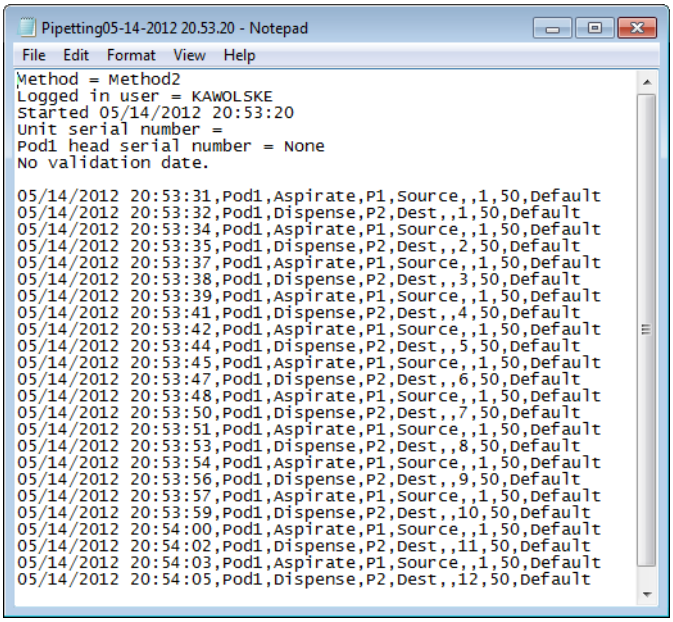
Figure 3.15 Browse to Logs



1. Pipetting log.

6 Double click the latest **Pipetting** log. Figure 3.16 appears.

Figure 3.16 Pipetting Log



7 From Figure 3.16, note the following specifics about the log for the method you just created and ran. The specifics (listed in the order following) are displayed from left to right on each line of the log.

- Date and time of the pipetting action.
- Pod that performed the operation.
- Operation (aspirate or dispense).
- Location where the operation took place.
- Name assigned to labware in **Labware Properties**.
- Blank field.

  NOTE This field is intentionally blank to retain backwards compatibility and compatibility with other Biomek instruments.

- Well number pipetted to or from.
- Amount of liquid.
- Technique name.

8 Close the file.

Go to the next chapter to learn how to use worklists and conditions.

CHAPTER 4

Using Worklists and Conditions

Introduction to Using Worklists and Conditions

To successfully complete the activities in this chapter, you will need to know how to:

- Configure an **Instrument Setup** step and **Labware Properties** to reflect the physical deck you will set up for the method in this chapter (refer to CHAPTER 1, *Configuring the Instrument Setup Step*).
- Configure a **Transfer** step (refer to CHAPTER 1, *Transferring Liquid*).
- Use variables and expressions in Biomek Software (refer to CHAPTER 3, *Creating a Variable in the Start Step*).
- Display step palettes.

If you already know how to complete these tasks, you can start with this chapter or subsequent chapters.

What You'll Learn in This Chapter

In this chapter, you will develop the advanced skills to use external data sources, such as a worklist, with a Biomek 4000 method. Using a worklist will allow you to create a method using transfer amounts and destinations defined in a text file. You will learn how to use procedures to run the same set of configured steps several times in a method to eliminate having to configure each step several times. You will also learn how to configure a conditional statement that will allow a step or steps to be executed based on real-time conditions that occur during the method.

More specifically, the step-by-step instructions in this chapter will teach you how to:

- Create a worklist file that defines variables and values.
- Use the worklist file in a **Worklist** step for executing a sequence of liquid transfers without configuring individual **Transfer** steps.
- Use an **If** step to transfer liquid from specific reservoirs using specific tips based on conditional decisions.
- Define a procedure using the **Define Procedure** step that will run based on the conditional decisions within an **If** step.
- Run the defined procedure based on the conditional decisions using the **Run Procedure** step.
- Stack plates in a method.

NOTE Your Biomek 4000 instrument must be equipped with the optional **Gripper** tool to stack plates in a method.

Setting Up Your Deck for This Chapter

Using what you learned earlier, launch Biomek Software, begin a new method, and configure an **Instrument Setup** step as follows:

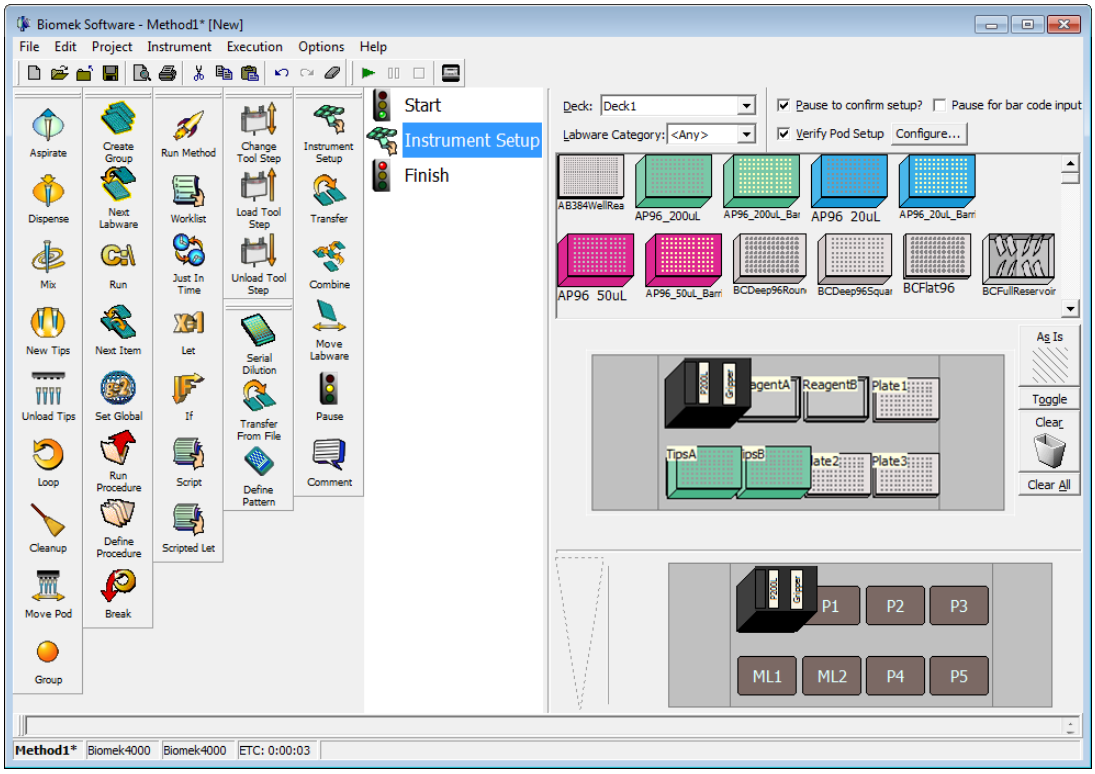
1. Place a **AP96_200µL** tip box on **ML1** and name it **TipsA**.
2. Place the same tip box type on **ML2** and name it **TipsB**.
3. Place a **BCUpsideDownTipBoxLid** reservoir on **P1** and name it: **ReagentA**
   Configure the liquid type as **Water** with an **Unknown** volume.
4. Place another **BCUpsideDownTipBoxLid** reservoir on **P2** and name it: **ReagentB**
   Configure the liquid type as **Water** with an **Unknown** volume.
5. Place **BCFlat96** plates on **P3**, **P4**, and **P5**. Name them **Plate1**, **Plate2**, and **Plate3**.
6. Place a **P200L** tool in the tool rack. Also, if you have a **Gripper** tool, place the **Gripper** into the tool rack (the **ToolRackGripper** must be used instead of the **ToolRack**).

Make sure you have the following step palettes displayed on the main editor:

- Basic
- Intermediate
- Advanced
- Specialty
- Span-8
- Biomek Instrument

Your deck should look like Figure 4.1. Now go to the next activity to learn how to use worklists and conditions in your methods.

Figure 4.1 Instrument Setup Step Configured



Creating a Worklist Text File

A worklist is a text file that contains multiple values for one or more variables. The **Worklist** step in Biomek Software uses the variables and values defined in the worklist to configure a series of repetitive actions during the method run. This is different from the **Loop** step that you learned earlier in this tutorial in that a worklist can contain non-incremental values and multiple variables for use during repetitive actions.

Before you can use the **Worklist** step, you must create the worklist text file and define the variables and associated values. For the method in this chapter, you will create a worklist for a series of transfers using different amounts of liquid for each transfer.

Configuring a Worklist Text File

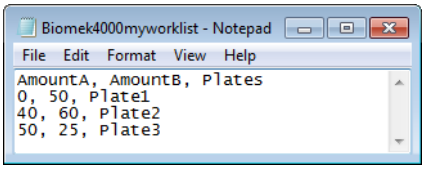
The first line of a worklist text file defines the variable names. The subsequent lines list the values to be assigned to those variables. The variable and names are separated by commas. If a value such as a plate name or bar code contains a comma, enclose the entire value in double quotes; for example, "**Dest1**, **4**".

TIP When creating a worklist text file, white space between values is not important; however, using a comma (,) between values and pressing the Enter key at the end of a line of text are important to create and use the file properly. Do not press the Enter key after the last line.

To configure the worklist text file for this tutorial:

1 Using Notepad, create a text file that looks like Figure 4.2.

Figure 4.2 Created Worklist



2 Save your text file as **Biomek4000myworklist.txt** to the desktop.

Now that you have configured the worklist, you will insert and configure a **Worklist** step to enable the software to use the worklist in the method. Go on to the next section to learn how to do this.

Configuring a Worklist Step to Use a Worklist

Biomek Concept: Worklist Step	
	The **Worklist** step offers several advantages: • 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 to the step without individually entering all the variables. • A dynamic link exists between the method and the text file. Any updates made to the text file are included in the next method run, although the text file must maintain the original file path to allow the method to find the file.

The **Worklist** step is located on the Advanced Step Palette and uses a text file to supply to the method multiple values for one or more variables. **Worklist** is useful when repetition of the same action is required, but one or more variables needs to change each time the step cycles through the worklist. When a step or group of steps using the variables defined in a text file are placed inside a **Worklist** step, **Worklist** automatically performs each step once for each line in the text file.

For this part of the tutorial, we will use a **Worklist** step to transfer specific amounts of liquid from two different sources to three destination plates. The text file you configured in *Creating a Worklist Text File*, contains all the needed details.

To configure the **Worklist** step:

1 Ensure your deck is configured according to the instructions in *Setting Up Your Deck for This Chapter*.

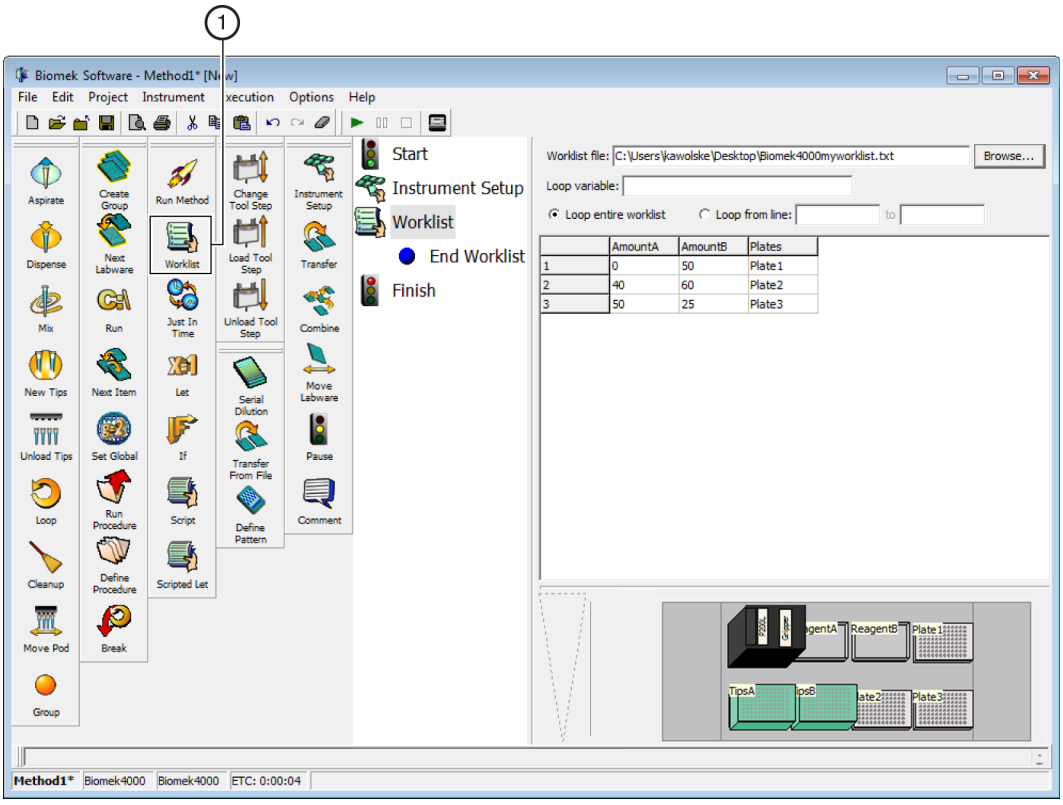
2 Drag and drop a **Worklist** step Figure 4.3 into the Method View below the **Instrument Setup** step.

3 From **Worklist file** in the configuration window, use the **Browse** button to find and choose **Biomek4000myworklist.txt**, the text file you configured in *Creating a Worklist Text File*.

4 Make sure **Loop entire worklist** is selected. This ensures that all the values contained in the worklist are used. The **Worklist** step configuration should look like Figure 4.3.

TIP You can use **Loop from line** to execute the loop for only some of the lines in the worklist.

Figure 4.3 Worklist Step With Text File Displayed



1. **Worklist** step

Now, you will define a procedure using a **Define Procedure** step and insert it before the **Worklist** step. This procedure will be run as the method cycles through the worklist. This procedure will be configured to load tips, transfer liquid, and unload tips.

Defining and Running Procedures

The **Define Procedure** step is used to configure and save a series of steps that may be used multiple times in a method without having to reconfigure each individual step within that procedure. The **Run Procedure** step is inserted into the method and is used to identify the defined procedure to be used in a method. The procedure defined in the **Define Procedure** step can be run only by inserting a **Run Procedure** step and choosing the desired procedure in the step configuration.

Biomek Concept: Procedures	
	Procedures offer advantages such as running the same steps multiple times within a method but configuring them only once. Procedures control the size of the current method in the Method View by listing only the **Run Procedure** step in the Method View and not all the steps accessed by the procedure.

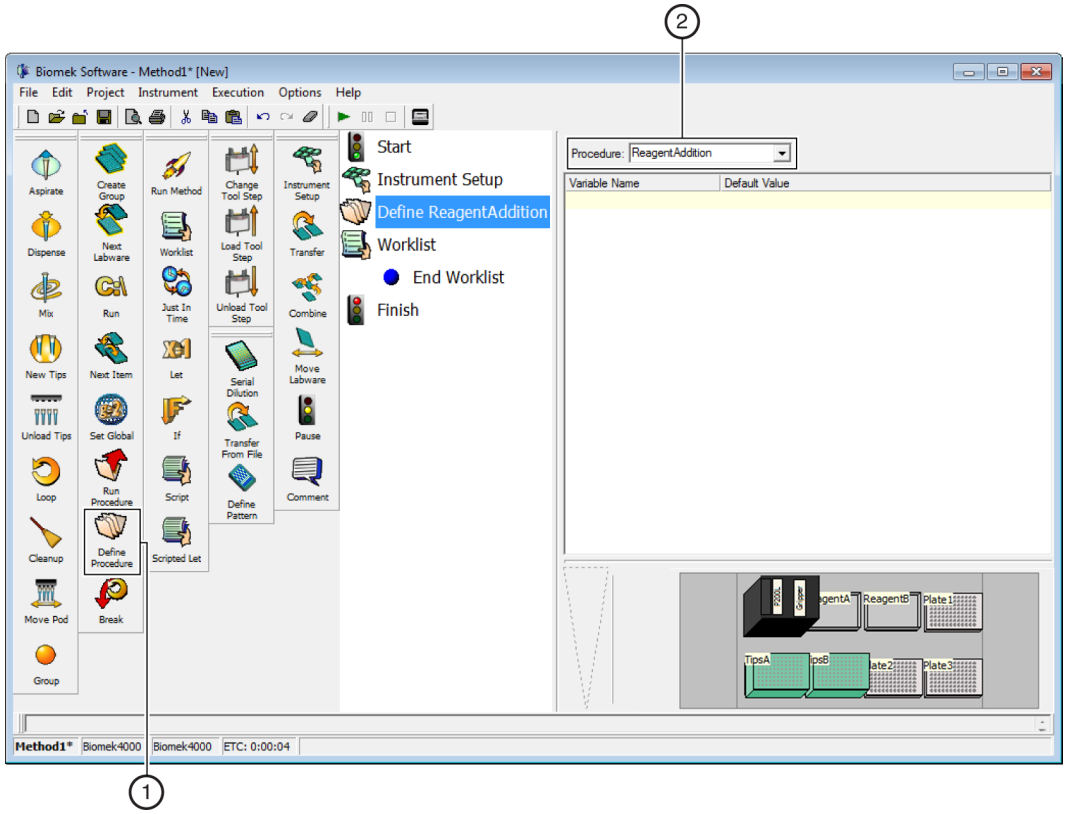
Defining a Procedure Using the Define Procedure Step

For this part of the tutorial, you will insert and configure a **Define Procedure** to load specific tips, transfer volumes based on the worklist you configured earlier, and unload tips. The defined procedure will then be run as part of the **If** step that you will configure later. You will also create variables in this procedure whose values will be specified in the **Run Procedure** step. This lets you run the steps in the procedure with different values associated with the defined variables.

1 From the Specialty Step Palette (Figure 4.4), insert a **Define Procedure** step below the **Instrument Setup** step.

2 In **Procedure**, enter **ReagentAddition** (Figure 4.4). This becomes the name of your procedure and will appear as **Define ReagentAddition** in the method view once you select any other step in the Method View.

Figure 4.4 Procedure Named



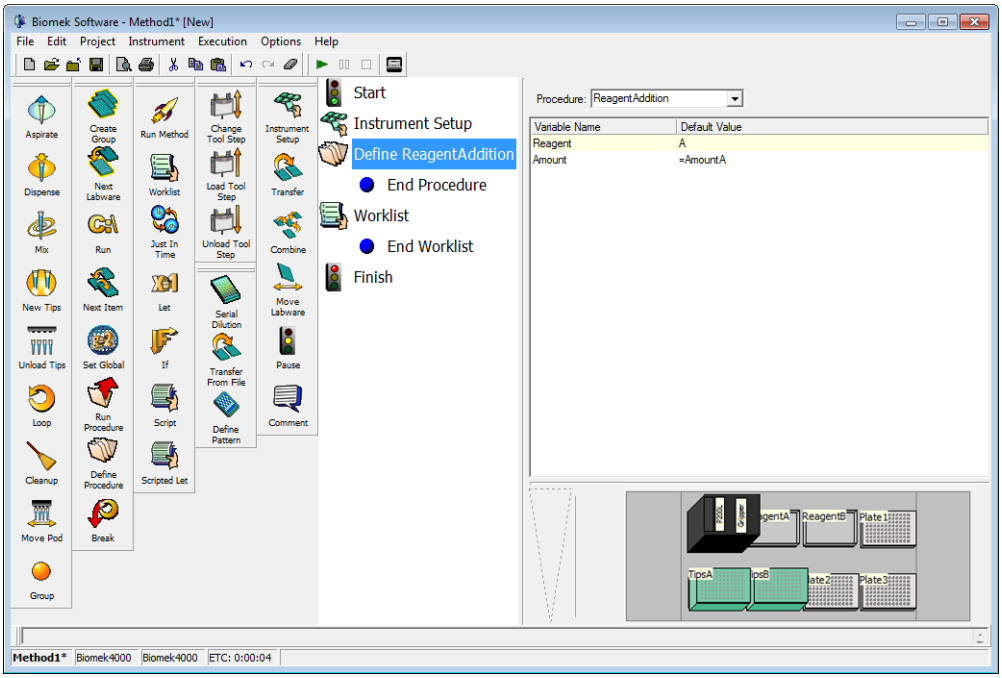
1. **Define Procedure** step
2. Enter name of **Procedure** here.

3 Under **Variable Name**, enter **Reagent** and tab over to **Default Value** and enter: **A**
The **Reagent** variable is the part of the expressions that dictate which tips and reagent reservoir to use for a transfer (for example, **TipsA** and **ReagentA**).

4 Press Enter on the keyboard, then under **Variable Name**, enter **Amount** and tab over to **Default Value** and enter: **=AmountA**

5 Double click the **Define ReagentAddition** step in the Method View to expose **End Procedure** (Figure 4.5).

Figure 4.5 Variables Entered in Define Procedure Step



Configuring Steps Inside the Define Procedure Step

To configure the **Define Procedure** step to load a tool, load tips, transfer volumes based on the worklist you configured earlier, and unload tips, the following steps will be configured individually inside the **Define Procedure** step:

- **Load Tool** step (refer to *Loading a Tool for a Procedure*)
- **New Tips** step (refer to *Configuring Different Tips for Accessing Sources*)
- **Transfer** step (refer to *Transferring Liquid During a Procedure*)
- **Unload Tips** step (refer to *Unloading Tips During a Procedure*)

The **Define Procedure** will be run as part of the **If** step that you will configure later.

Loading a Tool for a Procedure

Before loading tips you must tell the instrument what tool to use to access the tips. To do this:

1 From the Biomek Instrument Step Palette, insert a **Load Tool** step into the Method View inside the **Define ReagentAddition** step.

2 From the **Load Tool** drop-down, choose **P200L**.

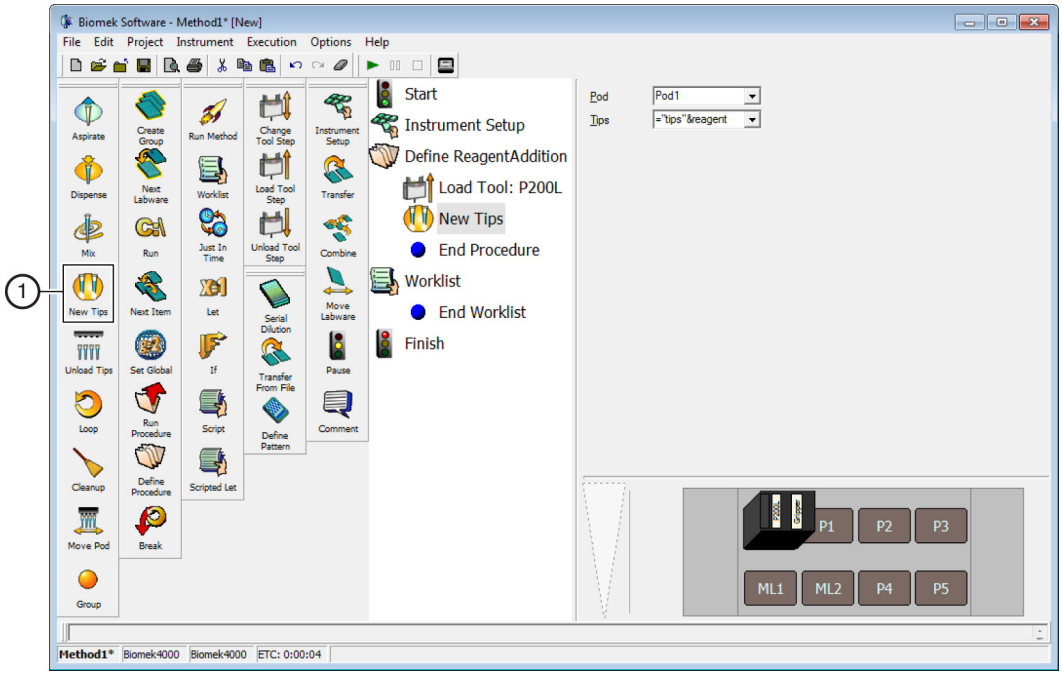
Configuring Different Tips for Accessing Sources

Since your reservoirs in this tutorial method contain different reagents, you will want different tips designated for each reservoir. You will configure the **New Tips** step as part of your procedure to ensure that the correct tips are loaded to access the correct source reservoir.

1 From the Intermediate Step Palette, insert a **New Tips** step into the Method View below the **Load Tool** step.

2 In **Tips** in the Configuration View, highlight the field and enter: **="tips"&reagent** (Figure 4.6) Remember that variable names are not case sensitive.

Figure 4.6 New Tips Configured



1. **New Tips** step

Transferring Liquid During a Procedure

To configure the actual liquid transfer that will be executed when the procedure is run, configure the transfer as follows:

1 Insert a **Transfer** step into the Method View below the **New Tips** step.

TIP The deck is inactive when configuring a **Transfer** step inside the **Define Procedure** step.

2 Deselect **Load Tool**.

3 Deselect **Load AP96_200µL** tips and **Change tips between destinations**.

4 Configure the **Source** in the **Transfer** step as: **BCUpsideDownTipBoxLid** at **="Reagent"&Reagent**

Configuring **="Reagent"&Reagent** means that the reservoir on the deck that has the same name as the value of the variable **Reagent** will be used. You'll configure this variable later in the **Define** and **Run Procedure** steps.

5 Configure the **Destination** as a **BCFlat96** at **=plates**. Configuring **=plates** means that the destination will be the destination labware configured in your worklist.

6 In the **Destination** configuration **µL** field, enter: **=Amount**

TIP If you want to reuse a procedure in other methods, drag the configured procedure and drop it onto any of the displayed step palettes. A prompt appears to ask if you would like to include the step on that specific palette. You could also create a custom step palette (refer to the *Biomek 4000 Software Manual*). Either way, the procedure may then be used in other methods by dragging and dropping it into the Method View.

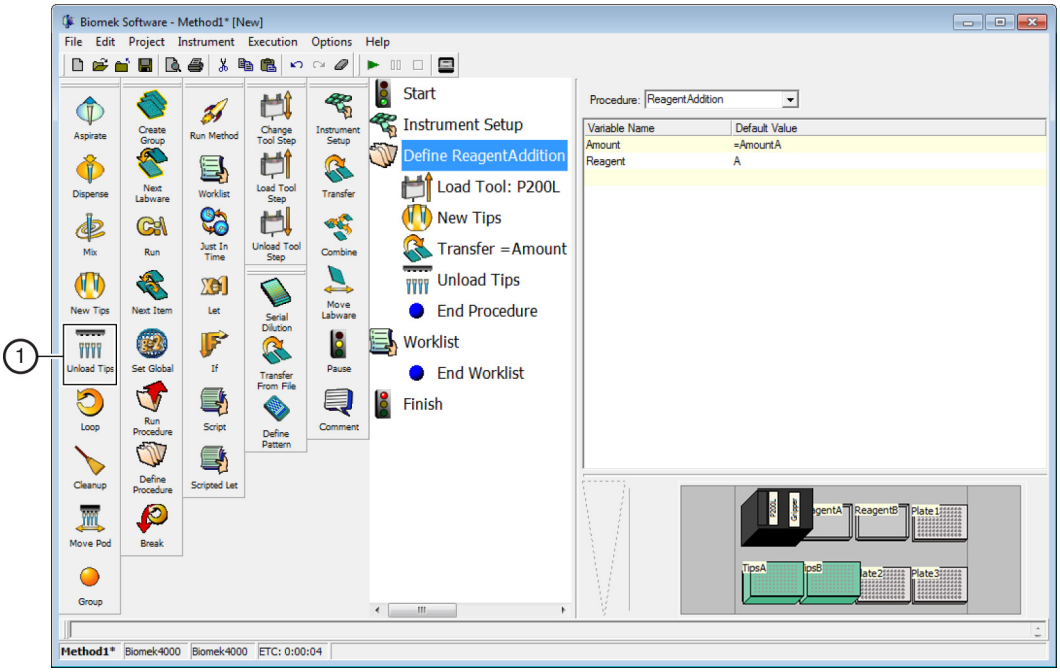
Unloading Tips During a Procedure

Here you will configure the procedure to unload the tips after the liquid transfer action. To unload the tips:

1 Insert an **Unload Tips** step below the **Transfer** step.

2 Click on the **Define ReagentAddition** step. Your main editor should look like Figure 4.7, and the variables in the named procedure you just created will be used to specify when new tips are used and which reservoir will be accessed when transferring liquid.

Figure 4.7 Define Procedure Step Configured



1. **Unload Tips** step

3 Double click the **Define ReagentAddition** step to collapse it.

4 Click on the **Finish** step to validate the method.

Go on to the next section where you will configure an **If** step to learn how to use conditions in a method.

Configuring the If Step to Use Conditions in a Method

Biomek Concept: If Step	
	The substeps of an **If** step are: • **Then** - if the condition is true, substeps following **Then** are processed. • **Else** - if the condition is false, substeps following **Else** are processed. • **End** - The **End** substep terminates each **If**, **Then**, and **Else** block of steps.

The **If** step controls the steps that are executed in a method based on conditional decisions. When **If** is run, Biomek Software tests the **If** condition as true or false, then processes the appropriate block of substeps based on the results of the test (see **Biomek Concept** above).

To configure the **If** steps to use conditions in this tutorial, you will:

- Insert an **If** step and enter the condition for a transfer from source **ReagentA**.
- Insert a **Run Procedure** step for the transfer from source **ReagentA** for the
- **Then** substep.
- Insert another **If** step and enter the condition for a transfer from source **ReagentB**.
- Insert a **Run Procedure** step for the transfer from source **ReagentB** for the **Then** substep.

Setting Conditions Using If Steps

For this section of the tutorial, you will configure two **If** steps that will specify the reagent reservoirs to access and the specific tip boxes for each transfer based on the sources you configured for the **Worklist** step. You will configure the **If** steps and insert them into the **Worklist** step. The transfers will then run the **ReagentAddition** procedure you configured earlier. The procedure locates the correct tips and transfers the appropriate volume from the correct reservoir.

To configure the **If** steps:

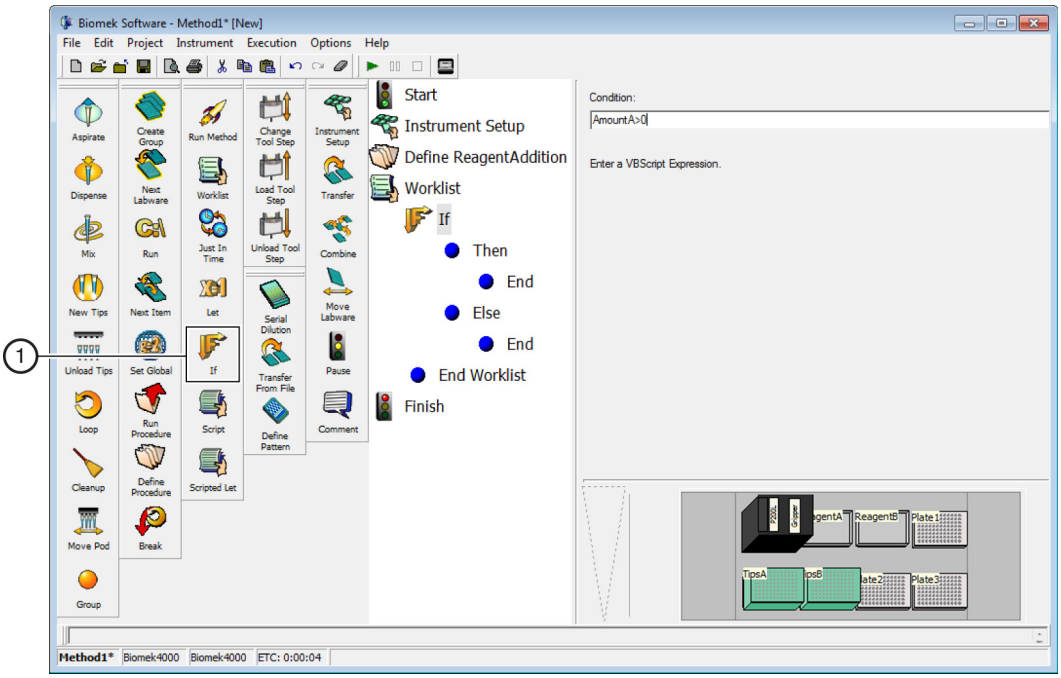
---

1 From the Advanced Step Palette, insert an **If** step into the Method View into the **Worklist** step.

---

2 In **Condition**, enter: **AmountA>0**
The main editor should look like Figure 4.8.

Figure 4.8 Condition Entered in If Step



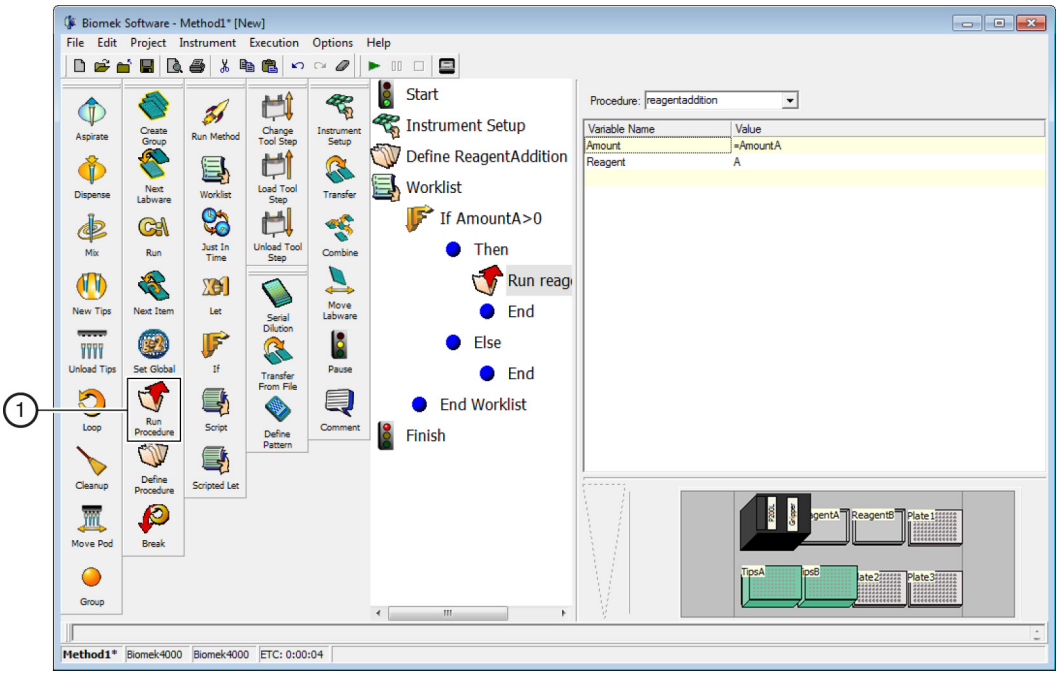
1. **If** step

3 From the Specialty Step Palette, insert a **Run Procedure** step into the Method View below the **Then** substep of the **If** step.

4 In **Procedure**, choose **reagentaddition**.

For this tutorial, you won't place steps in the **Else** substep. This means that if the evaluation of the **If** step is false, no further action occurs. The main editor should now look like Figure 4.9.

Figure 4.9 ReagentAddition Procedure Inserted as a Then Substep



1. **Run Procedure** step

5 Insert another **If** step into the Method View below the last **End** substep and above **End Worklist.**

6 In **Condition**, enter: **AmountB>0**

7 Insert a **Run Procedure** step into the Method View below the **Then** substep of the second **If** step.

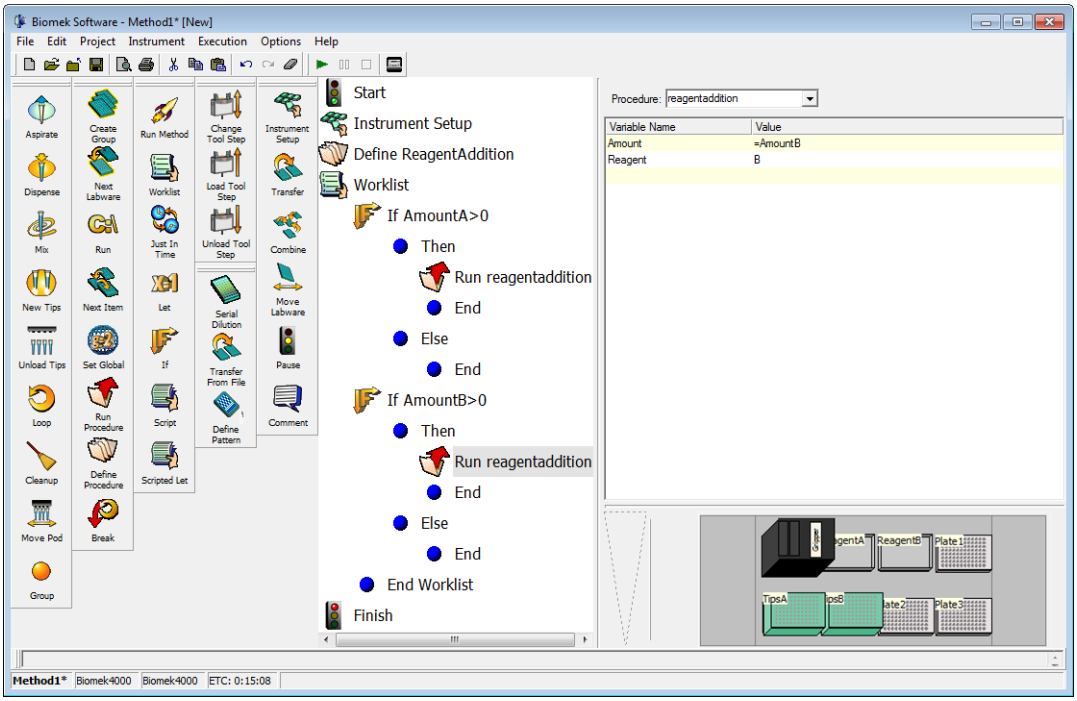
8 From **Procedure**, choose **reagentaddition.**

9 Change the **Value** for Amount to: **=AmountB**

10 Change the **Value for Reagent** to: **B**

You won't use an **Else** substep here either, so the main editor should look like Figure 4.10.

Figure 4.10 Variable Name and Value Changed



Congratulations! You have just created a method using a worklist and **If** steps with configured conditions. If you would like to see this method run in simulation mode, click the green run button on the toolbar.

IMPORTANT If you have not already configured the physical deck and you are planning to run the method on hardware rather than in Simulation Mode (see CHAPTER 1, *Viewing the Method in the Biomek Simulator*), add the labware and tools as specified in the **Instrument Setup** step (see *Setting Up Your Deck for This Chapter*). Verifying that the correct labware and tools are used ensures proper pipetting and labware handling.

If you have the optional **Gripper** tool installed on your instrument, continue to the next section to learn about stacking labware in a method; otherwise, continue to the next chapter to learn how to use some advanced features in Biomek Software.

Stacking Plates in a Method

NOTE If your instrument is not equipped with the optional **Gripper** tool, you cannot stack plates in a method. Skip this section and go ahead to the next chapter.

Biomek Concept: Using Stacks	
	When stacking or unstacking labware, Biomek Software works from the bottom up. If stacking four microplates on the deck, the top plate is placed on the second plate by the **Gripper**, then the top two plates are placed on the third plate, and finally the top three plates are placed on the bottom plate. They must be stacked in this way to follow the stacking rules for the Biomek 4000 **Gripper**. Refer to the *Biomek 4000 Software Manual* for more information on using stacks in a method. The maximum height of stacks of microplates allowed on the Biomek 4000 instrument is 5.5 cm (2.17 in.). A stack of four standard 96-well plates is approximately 5.2 cm (2.05 in.) tall.

The instrument can also handle stacks of labware, both stacking and unstacking labware stacks in a method using the **Gripper**. In this section, you will use what you have learned previously about the **Loop** step and the **Move Labware** step to stack the three destination plates.

To do this, you will use another **Loop** step with a variable that will be used to specify the deck positions from which to pick up labware and an expression to specify to which position to move labware. Once configured, the three cycles of the **Loop** will move labware as shown in Table 4.1

Table 4.1 Values of Variables and Expressions Used in Move Labware Step for Cycles

Cycle	Stack Value	From: =“Plate”&stack	To: =“Plate”&(stack-1)
1	3	Plate3	Plate2
2	2	Plate2	Plate1
3	1	Value of stack is below **End** value; breaks out of loop and continues with method.	

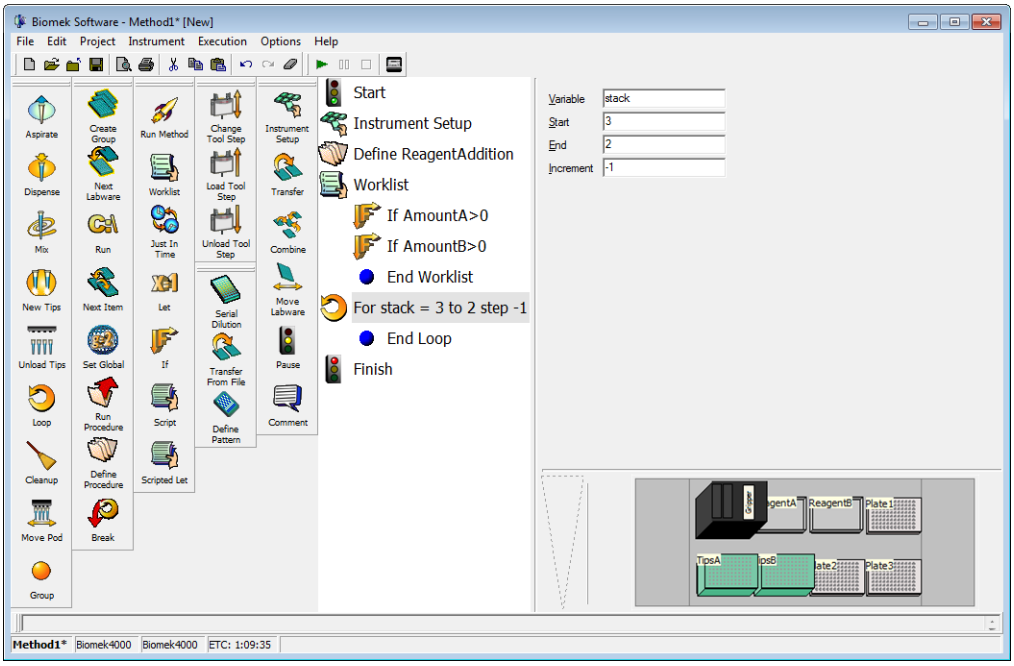
To stack the three destination plates:

TIP Double click the two **If** steps to collapse them, allowing more of the method to be displayed in the Method View.

1 Insert a **Loop** step after the **Worklist** step.

2 Configure the **Loop** step to create a **Variable** named **stack** with a **Start** value of **3**, an **End** value of **2**, and an **Increment** value of **-1**. Your **Loop** step should look like Figure 4.11.

Figure 4.11 Loop to Stack Plates



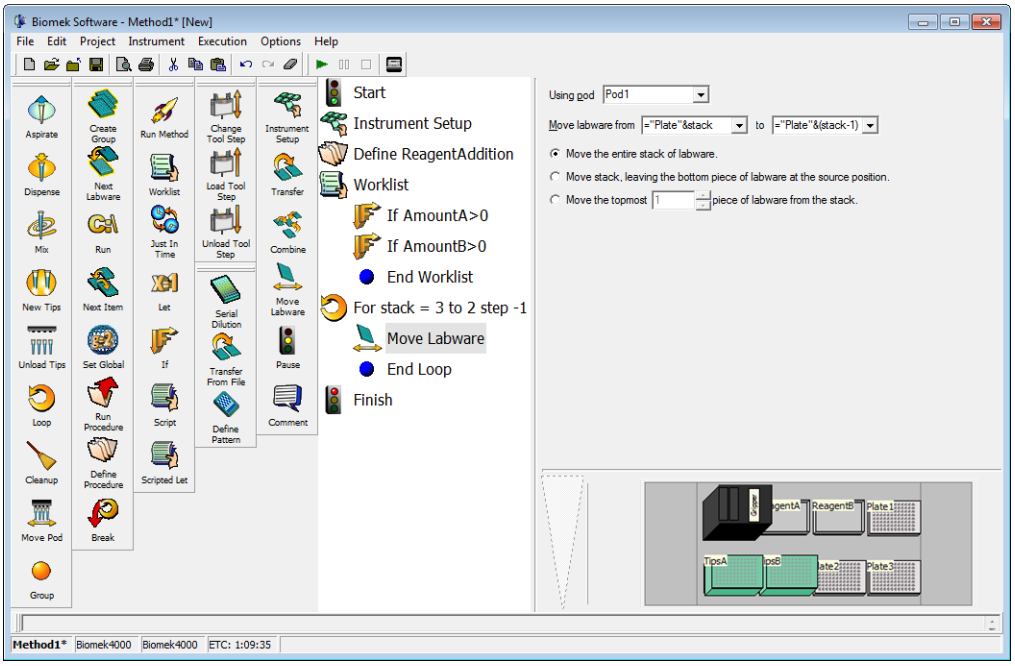
3 Insert a **Move Labware** step between the **Loop** and **End Loop** icons.

4 In **Move Labware from**, type: **="Plate"&stack**

5 In **to**, type: **="Plate"&(stack-1)**

6 Select the first option, **Move the entire stack of labware**. Your **Move Labware** configuration should look like Figure 4.12.

Figure 4.12 Use Variables to Stack Plates



7 Select **Finish** to validate the method. The three **BCFlat96** microplates are stacked on position **P3** in the Current Deck Display.

You have just configured plate-stacking in a method. If you would like to see this method run in simulation mode, click the green run button on the toolbar.

IMPORTANT If you have not already configured the physical deck and you are planning to run the method on hardware rather than in Simulation Mode (see CHAPTER 1, *Viewing the Method in the Biomek Simulator*), add the labware and tools as specified in the **Instrument Setup** step (see *Setting Up Your Deck for This Chapter*). Verifying that the correct labware and tools are used ensures proper pipetting and labware handling.

Now move on to the last chapter of this tutorial to learn how to use some advanced features in Biomek Software.

CHAPTER 5

Using Files to Direct Transfers

Introduction to Using Transfer From File

To successfully complete the activities in this chapter, you will need to know how to:

- Configure an **Instrument Setup** step to reflect the physical deck you will set up for the method in this chapter (refer to CHAPTER 1, *Configuring the Instrument Setup Step*).
- Configure **Labware Properties** for labware you will use in this chapter.
- Configure a **Transfer** step (refer to CHAPTER 1, *Transferring Liquid*).
- Use variables and expressions in Biomek Software (refer to CHAPTER 3, *Creating a Variable in the Start Step*).
- Display step palettes.

If you already know how to complete these tasks, you can start with this chapter.

What You'll Learn in This Chapter

In this chapter, you will use the advanced skills you've developed earlier to configure a **Transfer from File** step.

More specifically, the step-by-step instructions in this chapter will teach you how to:

- Configure a **Loop** step for hit picking.
- Insert a **Define Pattern** step inside the **Loop** step.
- Configure a **Transfer from File** step using two .csv files (file storage location is specified in *Copying .csv Files to the Desktop*).

Setting Up Your Deck for This Chapter

Using what you learned earlier, launch Biomek Software, create a new method, and configure an **Instrument Setup** step as follows:

1 Place a **P200L** tool in the tool rack. Also, if you have a **Gripper** tool, place the **Gripper** into the tool rack (the **ToolRackGripper** must be used instead of the **ToolRack**).

2 Place **AP96_200µL** tip boxes on **ML1** and **ML2**.

3 Place **BCDeep96Round** plates on **P1**, **P2**, and **P3**.

4 Name the three plates at **P1**, **P2**, and **P3**: **Samples1**, **Samples2**, and **Samples3**. Configure these to have an **Unknown** volume of **Water**.

5 Place a **BCFlat96** on **P4** and name it **Dest.** This plate starts out empty, so configure a **Known** volume of **0 µL**.

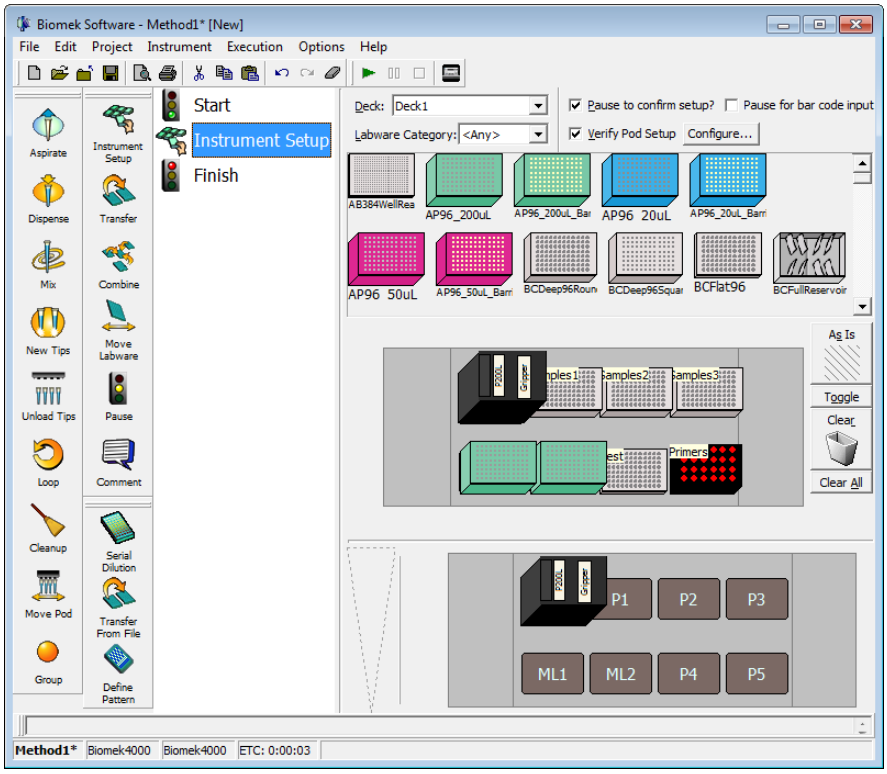
6 Place a **SmallTuberack_Microfuge** at **P5** and name it **Primers**. Configure it to have an **Unknown** volume of **Water**.

Make sure you have the following step palettes on the main editor:

- Basic
- Intermediate
- Span-8

Your deck should look like Figure 5.1.

Figure 5.1 Instrument Setup Step Configured



Copying .csv Files to the Desktop

Copy the two supplied .csv files (**hits.csv** and **transferfromfile.csv**) to your desktop. These files are stored in the following location:

- C:\Program Files (x86)\Common Files\Beckman Coulter\Manuals

Creating a Loop for Hit Picking

Since library compounds are used in drug discovery labs for high throughput screening on large numbers of microplates that produce "hits," the repeating process of a loop is useful. In this section, you will use the supplied **hits.csv** file and assume it has identified a number of hits on several microplates that will be processed further in your method. Before you create a loop to further process the hits, you will open the .csv file. Then you will use a **Define Pattern** step to specify the hits into which liquid will be transferred via a **Transfer** step.

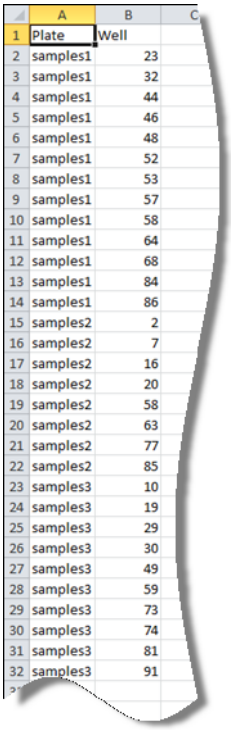
Viewing the hits.csv File

The hits.csv file is a simple, two-column file. Each row specifies one well that is a hit requiring further study or processing. The first column specifies on which plate the hit is located, and the second column specifies which well on that plate the hit is located.

To view the .csv file:

1 Double click **hits.csv** on your desktop. The **hits.csv** file opens (Figure 5.2).

Figure 5.2 Supplied hits.csv File



	A	B
1	Plate	Well
2	samples1	23
3	samples1	32
4	samples1	44
5	samples1	46
6	samples1	48
7	samples1	52
8	samples1	53
9	samples1	57
10	samples1	58
11	samples1	64
12	samples1	68
13	samples1	84
14	samples1	86
15	samples2	2
16	samples2	7
17	samples2	16
18	samples2	20
19	samples2	58
20	samples2	63
21	samples2	77
22	samples2	85
23	samples3	10
24	samples3	19
25	samples3	29
26	samples3	30
27	samples3	49
28	samples3	59
29	samples3	73
30	samples3	74
31	samples3	81
32	samples3	91

2 Notice how each row specifies one well that is a hit. Also notice that the first column specifies on which plate the hit is located, and the second column specifies in which well on the plate the hit is located.

NOTE Wells on a microplate are numbered from left to right across each row before continuing numbering across the next row down.

3 Close the **hits.csv** file since it must be closed to use it in the **Define Pattern** step.

Inserting a Loop Step

To insert the **Loop** step:

1. Insert a **Loop** step in the Method View after the **Instrument Setup** step.
2. In **Variable**, enter **plate**.
3. In **Start**, enter **1**.
4. In **End**, enter **3**.
5. In **Increment**, enter **1**.

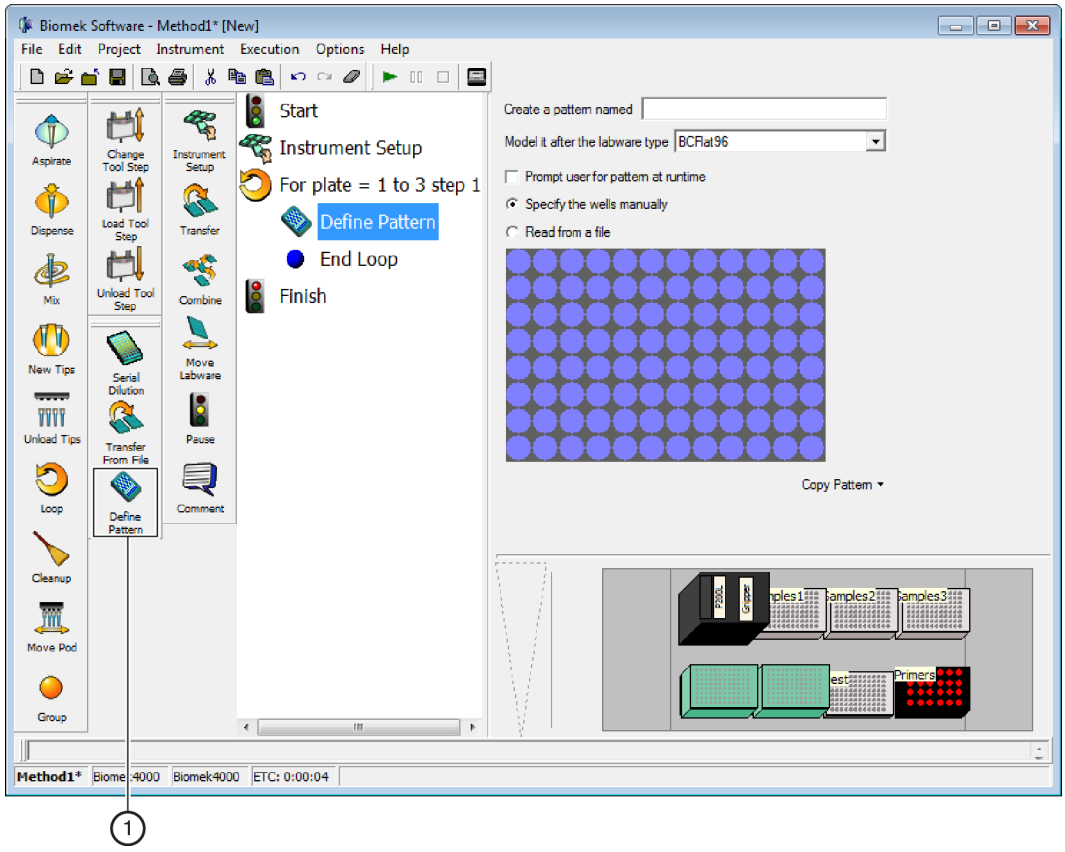
Inserting a Define Pattern Step

Biomek Concept: Define Pattern Step	
	The **Define Pattern** step 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, as compared to well patterns created in the **Well Pattern Editor** which are project specific and may be used across methods. Refer to the *Biomek 4000 Software Manual* for more information on using the **Well Pattern Editor**.

To insert the **Define Pattern** step:

1. If it is collapsed, double click the **Loop** step.
2. Insert a **Define Pattern** step inside the **Loop** step (Figure 5.3).

Figure 5.3 Define Pattern Inserted Inside Loop



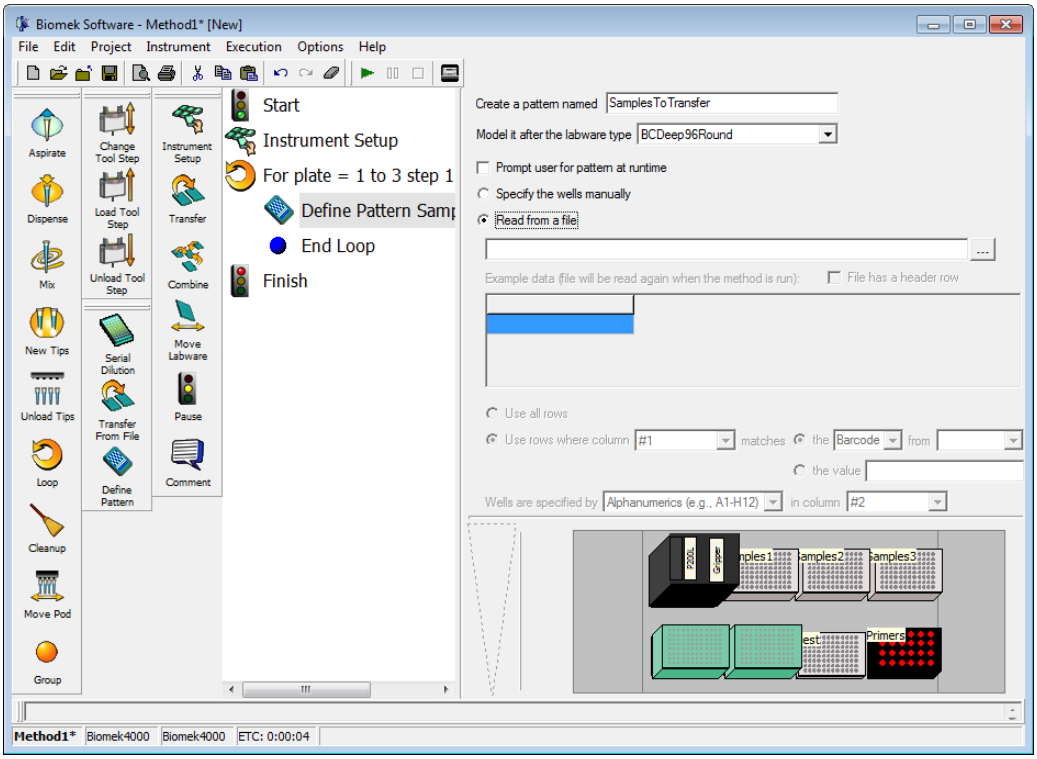
1. **Define Pattern** step

3 In **Create a pattern named**, enter: **SamplesToTransfer**

4 From **Model it after the labware type**, choose **BCDeep96Round**.

5 Click **Read from a file**. The configuration changes (Figure 5.4).

Figure 5.4 Read from File Chosen



6 From the **Browse** button, choose **hits.csv**. The first few rows display in **Example data**.

7 Check **File has a header row**.

8 Choose **Use rows where column** and select **Plate**.

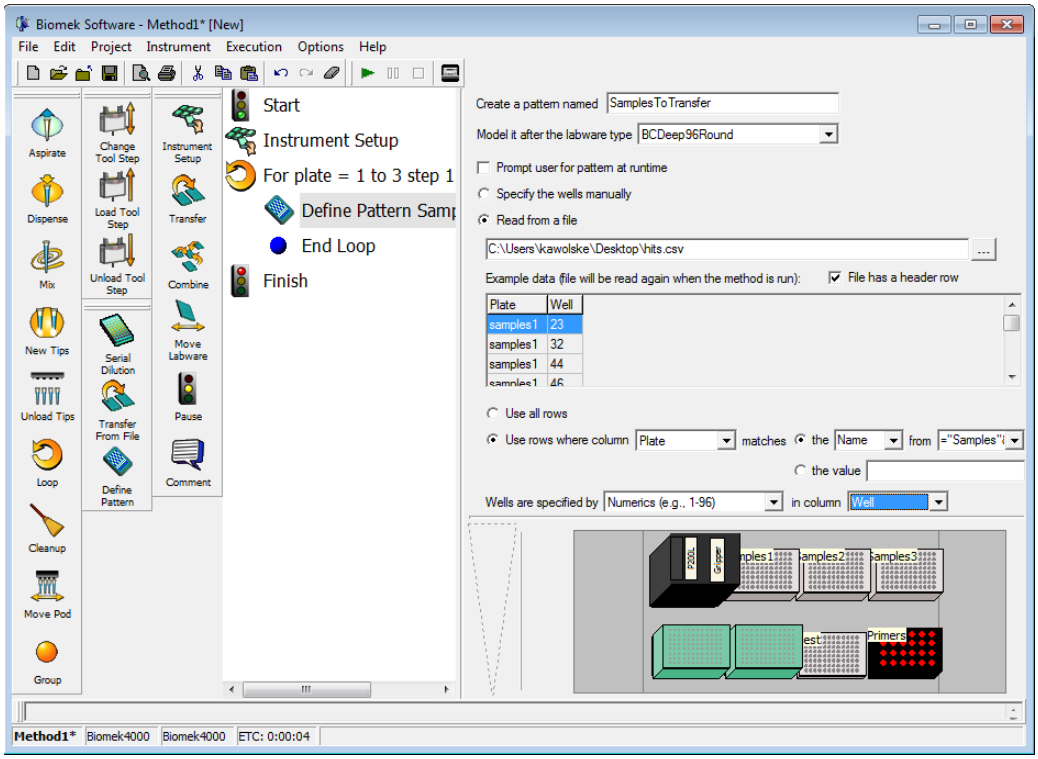
9 After **matches**, keep the next option selected and choose **Name** from the drop-down.

10 In **from**, enter: **="Samples"&plate**
This uses the variable created in the **Loop** step to specify which sample plate the pattern is for. In this way, each time through the **Loop**, the pattern will change to match the sample plate that is being processed for that iteration.

11 In **Wells are specified by**, select **Numerics (e.g., 1-96)**.

12 From **in column**, select **Well**. The step configuration should look similar to Figure 5.5.

Figure 5.5 Read From File Configured



Inserting and Configuring a Transfer Step

To insert and configure a **Transfer** step:

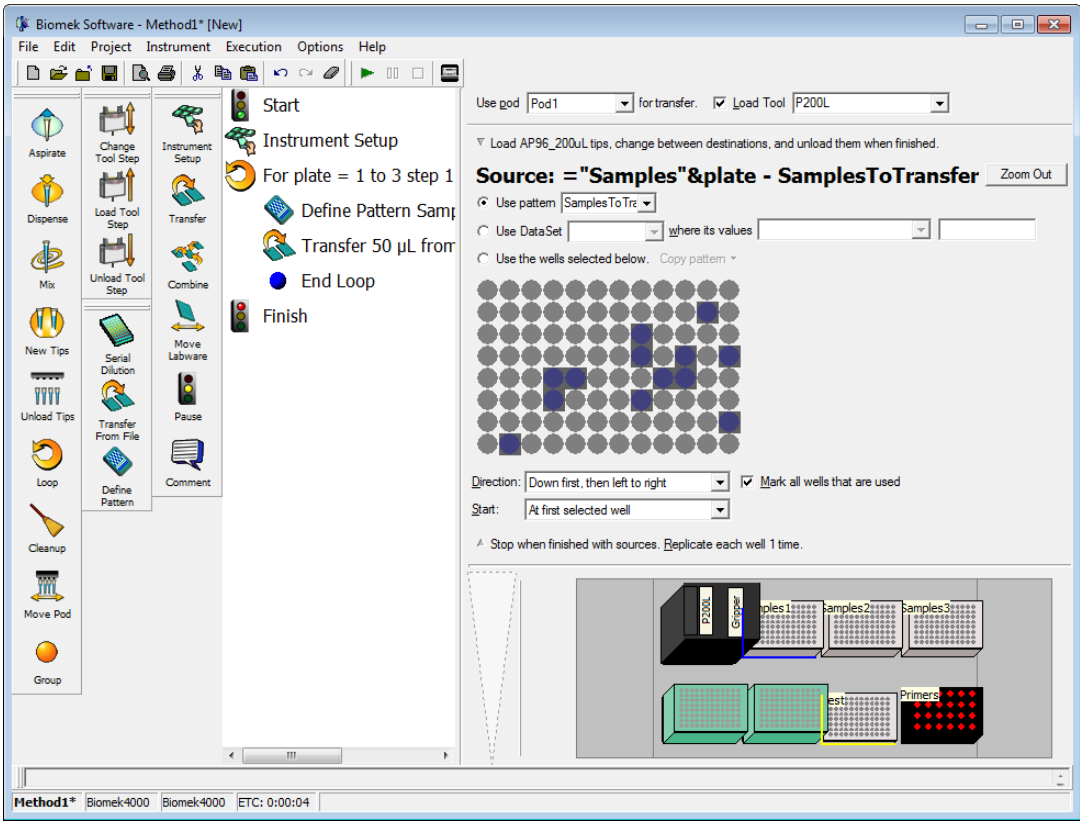
1. Insert a **Transfer** step below the **Define Pattern** step.
2. From the **Load Tool** drop-down, select **P200L**.
3. Allow the default **Tip Handling** to remain and collapse it.
4. Select **Click here to add a source**.
5. Select **BCDeep96Round** from the labware type drop-down in the **Source** configuration.
6. In **at**, enter: **="Samples"&plate**
7. In **Using liquid type**, choose **Well Contents** from the drop-down.

8 Choose **Customize**. In the **Aspirate** tab, deselect **Touch tips on the sides of the wells.** Select **OK**.

9 Double click the source plate to zoom in on it.

10 Select **Use Pattern** and choose the **SamplesToTransfer** pattern that was created earlier in the **Define Pattern** step. The main editor should look like Figure 5.6.

Figure 5.6 SamplestoTransfer Pattern Chosen



11 Choose **Zoom Out** to return to the main **Transfer** step configuration.

12 Select **Click here to add a destination**.

13 Click on the **Dest** labware on **P4** in the Current Deck Display to select it.

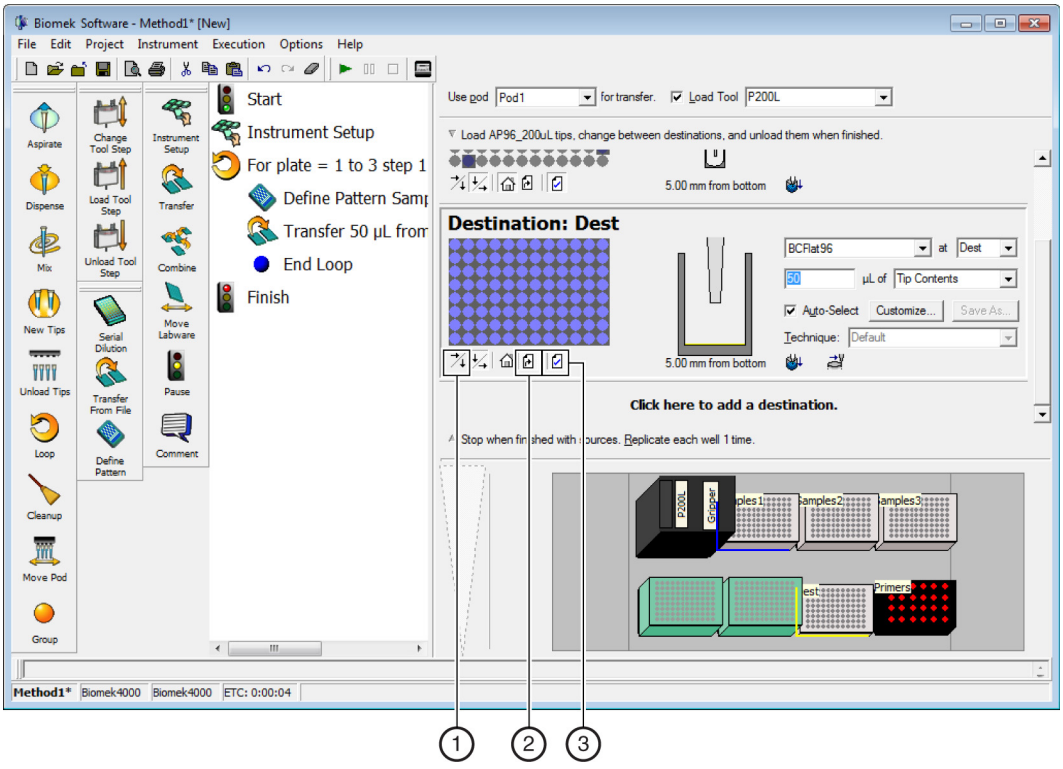
14 Enter a volume of **50** µL. You will be transferring the same volume for each of the hit wells. This is a key difference to using the **Transfer From File** step you will configure later in this chapter, as **Transfer From File** allows you to also configure a different volume for each well-to-well transfer.

15 Underneath the destination labware graphic, select **Right, then down**, which is the first button from the left. If this is not selected, transfers won't match.

16 Underneath the destination labware graphic, make sure that **Start at first unmarked well** and **Set mark** are selected. These are the last two from the right. If either of these is not selected, then with each iteration of the **Loop**, the **Transfer** will start with the first selected well (A1).

17 In **Transfer Details**, select **Stop when finished with Sources**. The main editor should look like Figure 5.7.

Figure 5.7 Configured Transfer Step for Inside Loop



1. **Right, then down**
2. **Start at first unmarked well**
3. **Set mark**

Inserting a Transfer From File Step for Reaction Setup

Biomek Concept: Transfer From File Step	
	The **Transfer From File** step 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.

In this section, you will insert a **Transfer From File** step to perform a reaction setup. Each of the hit wells that was transferred earlier will need to have two primers added from the **Primers** tube rack. Which primer is added and the volume of each is different for each sample. The transferfromfile.csv file that you copied to your desktop at the beginning of the chapter specifies which primers and the volumes to transfer for each of the destinations.

First you will view the transferfromfile.csv file.

Viewing the transferfromfile.csv File

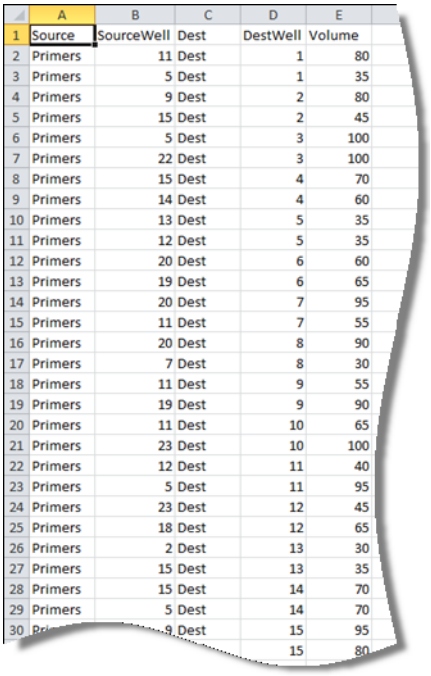
The transferfromfile.csv file is a five-column file with each row specifying one well-to-well transfer:

- The first column specifies the source labware.
- The second column specifies the well on the source labware from which to aspirate.
- The third column specifies the destination labware.
- The fourth column specifies the well on the destination labware to which to dispense.
- The fifth column specifies the volume to transfer.

To view the .csv file:

1 Double click **transferfromfile.csv** on your desktop. The **transferfromfile.csv** file opens (Figure 5.8).

Figure 5.8 Supplied transferfromfile.csv File



	A	B	C	D	E
1	Source	SourceWell	Dest	DestWell	Volume
2	Primers	11	Dest	1	80
3	Primers	5	Dest	1	35
4	Primers	9	Dest	2	80
5	Primers	15	Dest	2	45
6	Primers	5	Dest	3	100
7	Primers	22	Dest	3	100
8	Primers	15	Dest	4	70
9	Primers	14	Dest	4	60
10	Primers	13	Dest	5	35
11	Primers	12	Dest	5	35
12	Primers	20	Dest	6	60
13	Primers	19	Dest	6	65
14	Primers	20	Dest	7	95
15	Primers	11	Dest	7	55
16	Primers	20	Dest	8	90
17	Primers	7	Dest	8	30
18	Primers	11	Dest	9	55
19	Primers	19	Dest	9	90
20	Primers	11	Dest	10	65
21	Primers	23	Dest	10	100
22	Primers	12	Dest	11	40
23	Primers	5	Dest	11	95
24	Primers	23	Dest	12	45
25	Primers	18	Dest	12	65
26	Primers	2	Dest	13	30
27	Primers	15	Dest	13	35
28	Primers	15	Dest	14	70
29	Primers	5	Dest	14	70
30	Pri	9	Dest	15	95
				15	80

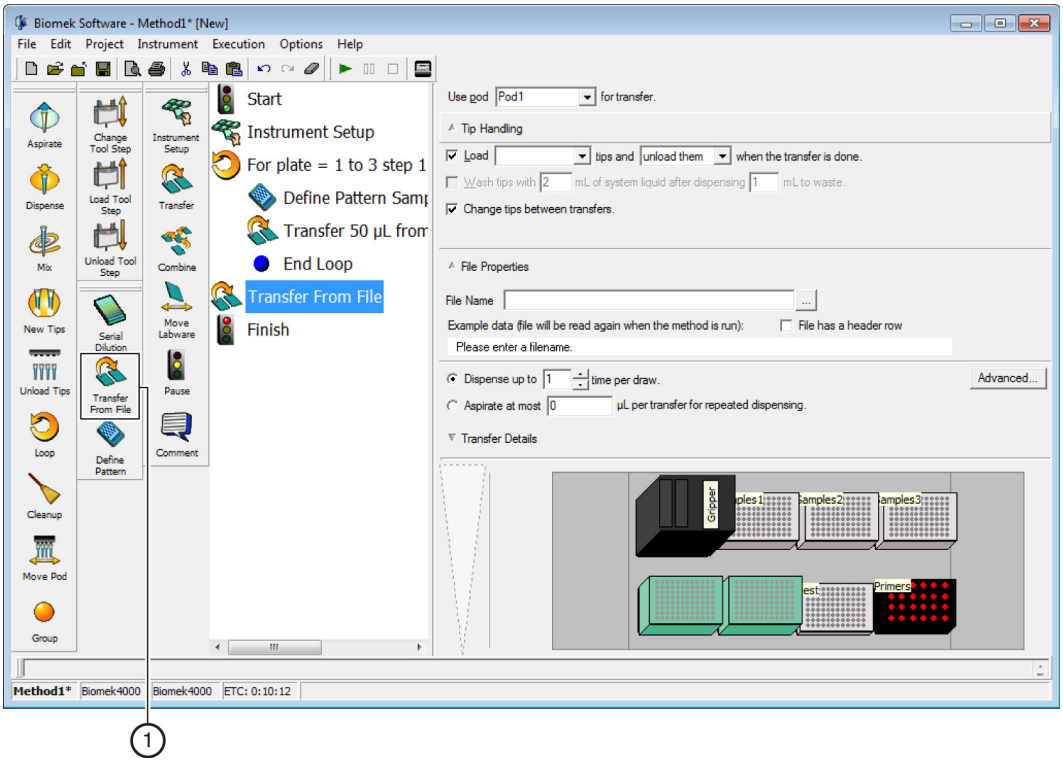
2 Notice the five columns.

3 Close the **transferfromfile.csv** file since it must be closed to use it in the **Transfer From File** step.

Inserting a Transfer From File Step

1 Insert a **Transfer From File** step after the end of the **Loop** step (Figure 5.9).

Figure 5.9 Transfer From File Inserted



1. **Transfer From File** step.

2 in **Load**, select **AP96_200uL** and then collapse **Tip Handling**.

3 If it is not displayed, expand the **File Properties** section. This option specifies which file to use and instructs Biomek Software how to use the data contained in the file.

4 From the **Browse** button, choose **transferfromfile.csv**. The first few rows display in **Example** data.

5 Check **File has a header row**.

6 Select all five check boxes beneath **Example** data.

7 In **File specifies source position in column**, select **Source**.

8 In **File contains source well information in column**, select **SourceWell**. This is the only item that is required to be included in the file; everything else can be configured as a regular **Transfer** step.

9 In **File specifies destination position in column**, select **Dest**.

10 In **File contains destination well information in column**, select **DestWell**.

11 In **File contains volume information in column**, select **Volume**. The final check box instructs the **Transfer From File** step to ignore any rows where the volume is 0. If this is not selected, it will go through the actions of loading tips for the 0 volume transfer without actually transferring any liquid.

12 Collapse **File Properties**. Even though the **Source** and **Destination** are specified by the file, the file does not contain any information about the labware and liquid types. This information is needed by the **Transfer From File** step, so it can select the correct techniques to use for the liquid transfers (refer to *Configuring Some Needed Source and Destination Information for the Transfer From File Step*).

Configuring Some Needed Source and Destination Information for the Transfer From File Step

1 Click on the **Source** configuration to open it.

2 In the first drop-down, select **SmallTuberack_Microfuge**.

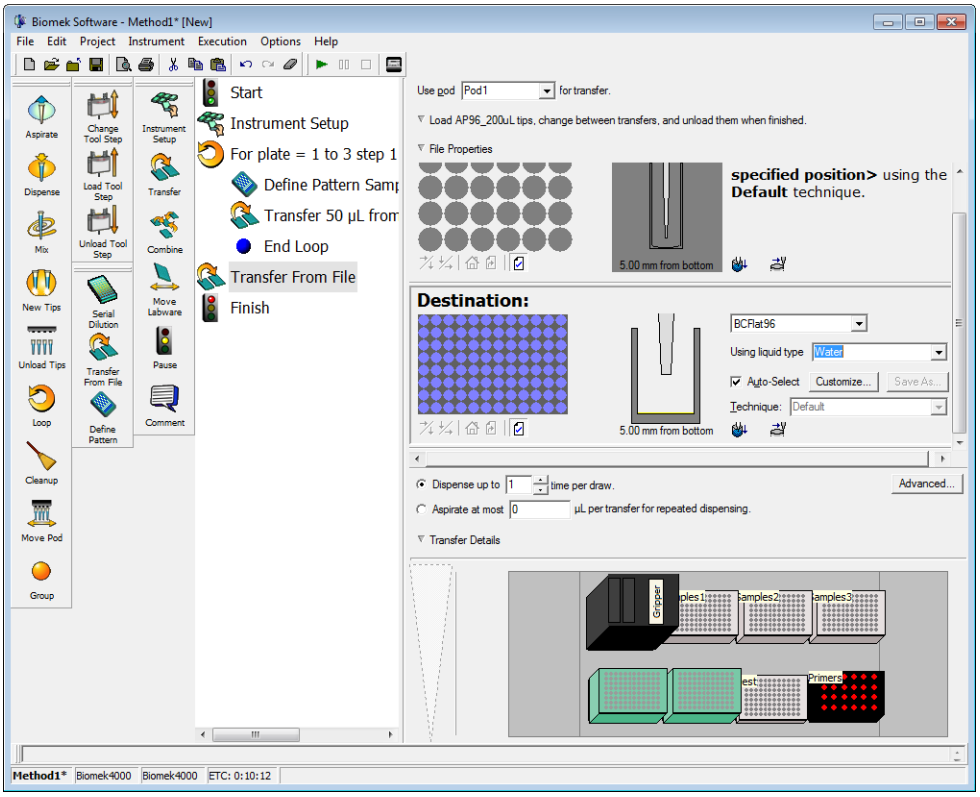
3 In **Using liquid type**, select **Water**.

4 Click on the **Destination** configuration to open it.

5 In the first drop-down menu, select **BCFlat96**.

6 In **Using liquid type**, select **Water**. The main editor should look like Figure 5.10.

Figure 5.10 Transfer From File Configured



You can run the method, but as you can see, it will take over 20 minutes.

IMPORTANT If you have not already configured the physical deck and you are planning to run the method on hardware rather than in Simulation Mode (see CHAPTER 1, *Viewing the Method in the Biomek Simulator*), add the labware and tools as specified in the **Instrument Setup** step (see *Setting Up Your Deck for This Chapter*). Verifying that the correct labware and tools are used ensures proper pipetting and labware handling.

Congratulations! You have completed the Biomek 4000 tutorial.

Abbreviations

µL — microliter

ANSI — American National Standards Institute

ALP — active labware positioner

COM — communication port

csv — comma separated values

ETC — estimated time of completion

MLx — a Manual Latch position on the Biomek 4000 deck

MSDS — material safety data sheets

mW — milliwatt

nm — nanometer

Px — a Biomek 4000 deck position

SDS — safety data sheets

USPTO — United States Patent and Trademark Office

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.

Axis — Biomek 4000 instrument has four axes (X-, Y-, Z-, and D- [T-]).

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 Biomek instrument; devices integrated with the Biomek 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 Laboratory Automation Workstation is a single pod instrument 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.

Combine Step — Biomek Software step that aspirates from multiple sources and dispenses to a single destination.

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.

Current Deck Display — Display located at bottom of the Biomek main editor showing the location of labware on the deck during a method run. Also shown in the **Deck Editor**.

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 Biomek instrument. The Biomek 4000 deck is the worksurface of the Biomek 4000 workstation 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 Biomek 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.

Diluent — Inert substance used to dilute a sample during serial dilution.

Expression — One-line combination of alphanumeric characters and/or variables combined using mathematical operations. May be used anywhere a variable can be used.

Gripper — 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 Biomek deck to another.

If Step — Step controlling actions in a method based upon a condition, such as liquid volume in labware or aspirate amount.

Instrument Setup — Step which specifies the configuration of the Biomek instrument deck and pods. Includes labware and labware contents for items on the deck.

Labware Positioners — Used to hold microplates, tube racks, reservoirs, or tip racks on the Biomek 4000 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.

Liquid Level Sensing — On the Biomek 4000 system, 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**.

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.

Method — Sequentially ordered list of steps comprising a liquid-handling procedure.

Method View — Pane in the Biomek main editor displaying the steps in a method.

Microplate — Labware used in liquid-handling procedures. Also referred toas a microtiter or titer plate.

Microtiter Plate — Labware used in liquid-handling procedures. Also referred to as a microplate or titer plate.

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 Biomek 4000 pod to aspirate and dispense liquid.

Pod — The pod is referred to as Pod1 in the Biomek Software. The 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, tool loading/unloading, and labware manipulation.

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.

Reservoir — One-well labware receptacle holding liquid to be used in a method.

Run Procedure Step — Step that executes a procedure within the current method.

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.

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.

Step Palette — Panes in the Biomek main editor showing steps available for insertion in a method. Located on the left of the Biomek main editor.

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.

Technique — Preprogrammed 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.

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 workstation 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.

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 checked in, approved with an electronic signature, and protected from further modification. Revisions of project items required to run the validated method are also checked in 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.

Worklist — External file containing names and related values. The names are symbolic identifiers used to represent the values.

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Beckman Coulter, Inc.
Warranty and Returned Goods Requirements

All standard Beckman Coulter, Inc. policies governing returned goods apply to this product. Subject to the exceptions and upon the conditions stated below, the Company warrants that the products sold under this sales agreement shall be free from defects in workmanship and materials for one year after delivery of the products to the original Purchaser by the Company, and if any such product should prove to be defective within such one year period, the Company agrees, at its option, either (1) to correct by repair or at the Company's election by replacement, any such defective product provided that investigation and factory inspection discloses that such defect developed under normal and proper use, or (2) to refund the purchase price. The exceptions and conditions mentioned above are as follows:

1. Components or accessories manufactured by the Company which by their nature are not intended to and will not function for one year are warranted only to reasonable service for a reasonable time. What constitutes a reasonable time and a reasonable service shall be determined solely by the Company. A complete list of such components and accessories is maintained at the factory.
2. The Company makes no warranty with respect to components or accessories not manufactured by it. In the event of defect in any such component or accessory, the Company will give reasonable assistance to Purchaser in obtaining the manufacturer's own warranty.
3. Any product claimed to be defective must, if required by the Company, be returned to the factory, properly decontaminated of any chemical, biological, or radioactive hazardous material, transportation charges prepaid, and will be returned to the Purchaser with transportation charges collect unless the product is found to be defective.
4. The Company shall be released from all obligations under all warranties, either expressed or implied, if any product covered hereby is repaired or modified by persons other than its own authorized service personnel, unless such repair by others is made with the written consent of the Company.
5. If the product is a reagent or the like, it is warranted only to conform to the quantity and content and for the period (but not in excess of one year) stated on the label at the time of delivery.

It is expressly agreed that the above warranty shall be in lieu of all warranties of fitness and of the warranty of merchantability, and that the company shall have no liability for special or consequential damages of any kind or from any cause whatsoever arising out of the manufacture, use, sale, handling, repair, maintenance, or replacement of any of the products sold under the sales agreement.

Representatives and warranties made by any person, including dealers and representatives of the Company, which are consistent or in conflict with the terms of this warranty, shall not be binding upon the Company unless reduced in writing and approved by an expressly authorized officer of the Company.

Parts replaced during the warranty period are warranted to the end of the instrument warranty.

NOTE
Performance characteristics and specifications are only warranted when Beckman Coulter replacement parts are used.

Except as provided in writing signed by an officer to Beckman Coulter, Inc., this system and any related documentation are provided “as is” without warranty of any kind, expressed or implied, including that the system is “error free.” This information is presented in good faith, but Beckman Coulter does not warrant, guarantee, or make any representations regarding the use or the results of the use of this system and related documentation in terms of correctness, accuracy, reliability, currentness, omissions, or otherwise. The entire risk as to the use, results, and performance of this system and related documentation is assumed by the user.

Related Documents

Biomek 4000 Hardware Manual
PN A99498
- Moving and Installing the Biomek 4000 Workstation
- 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
PN A99501
- 1x1 Standard ALP
- Auto-Latching Tip Rack Holders
- Bar Code Reader
- Bar Code Reader Hand-Held
- Circulating Reservoir
- Filtration System
- Liquid Waste Station
- Off-Deck Platform
- Orbital Shaker
- Test Tube Racks
- Thermal Exchange Unit
- Wash Unit

Biomek 4000 Software Tutorial
PN A99502
- Getting Started with Biomek Software
- Using More Steps in a Method
- Using Worklists and Conditions
- Using Files to Direct Transfers

Biomek 4000 Customer Start-Up Guide
PN A99598
- Biomek 4000 Laboratory Automation Workstation
- Preparing to Run
- Creating a Simple Method
- Advanced Features
- Best Practices

Biomek 4000 Software Manual
PN B08852
- Using Accounts and Permissions
- Using Password Protection
- Using Instrument Files and Settings
- Configuring Hardware Setup
- Preparing and Managing the Deck
- Understanding and Using Project Files
- Creating and Modifying Tip and Labware Types
- 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
- Using the Wash Tool Step Palette
- Using the DataSets Step Palette
- Handling and Preventing Errors
- Generating and Using Log Data
- Using Manual Control
- Scripting
- Changing Window Appearance

Biomek 4000 Migration Guide for Biomek 3000 Methods
PN B08853
- Migrating Methods
- Biomek 4000 System Updates
- Continued Features
- Discontinued Features

Shaking Peltier ALP Instruction Manual for Biomek 4000 Instruments
PN B20570
- Overview of Shaking Peltier ALP
- Hardware Installation
- Software Installation
- Software Setup
- Framing Using AccuFrame
- Installing Adapter Plates and Creating Labware Offsets
- Operations

Static Peltier ALP Instruction Manual for Biomek 4000 Instruments
PN B20569
- Overview of Static Peltier ALP
- Hardware Installation
- Software Installation
- Software Setup
- Framing Using AccuFrame
- Installing Adapter Plates and Creating Labware Offsets
- Operations

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