Agilent GeneSpring Workgroup 5.2

Installation Guide

Agilent Technologies

Notices

Edition

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Software Revision

This guide is valid for the Agilent GeneSpring Workgroup 5.2 software, which includes Workgroup Server, Remote Server, Sample Loader, and GeneSpring Viewer.

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CAUTION

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In This Guide...

This guide contains information to install the GeneSpring Workgroup 5.2.

1 Workgroup Server Installation

In this chapter, you install and configure the Workgroup Server application.

2 Remote Server Installation

In this chapter, you install and configure the Remote Server application.

3 Sample Loader Configuration

In this chapter, you configure the Sample Loader application. Sample Loader is installed when you install the Workroup Server application.

4 GeneSpring Viewer Installation

In this chapter, you install and configure the GeneSpring Viewer application. You also create installation applications.

Contents

1

Workgroup Server Installation

This chapter contains instructions to install and configure Workgroup Server on a Windows or Linux/Solaris systems.

Installation

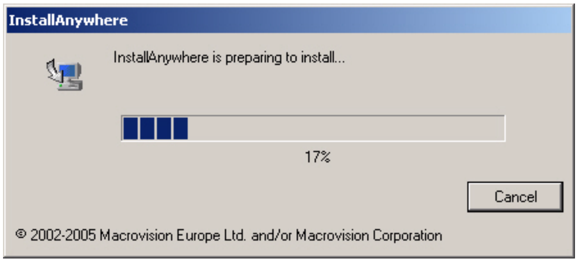
This section contains installation instructions for Windows and Sun.

To install and configure on Windows systems

The application is supplied by your Agilent customer service representative.

1. Copy the installer program to your server.
2. Double click the GeneSpringWG5_2Installer.exe icon to begin.

   In quick succession, the following dialog boxes appear ending with the Introduction dialog box.

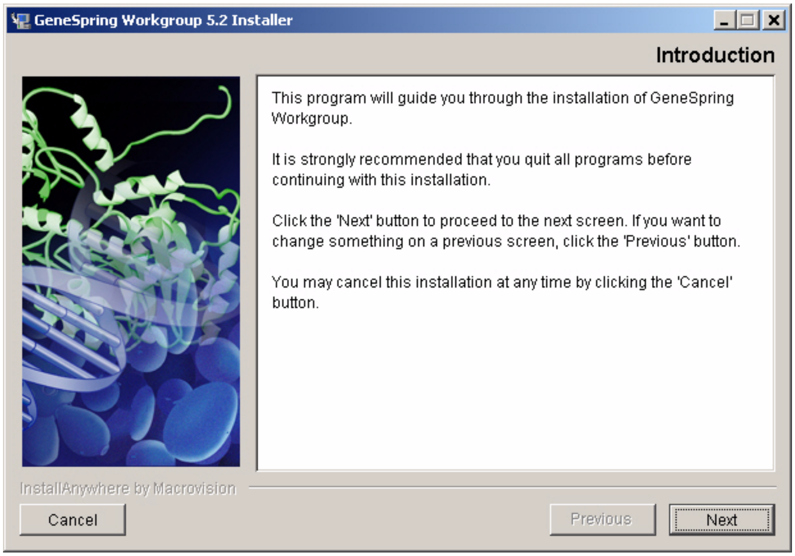


InstallAnywhere

InstallAnywhere is preparing to install...

17%

© 2002-2005 Macrovision Europe Ltd. and/or Macrovision Corporation

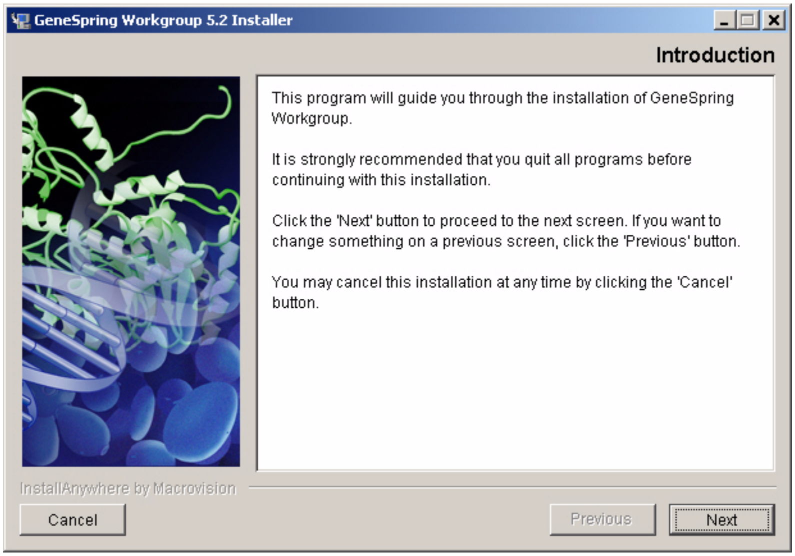


This program will guide you through the installation of GeneSpring Workgroup.

It is strongly recommended that you quit all programs before continuing with this installation.

Click the 'Next' button to proceed to the next screen. If you want to change something on a previous screen, click the 'Previous' button.

You may cancel this installation at any time by clicking the 'Cancel' button.



This program will guide you through the installation of GeneSpring Workgroup.

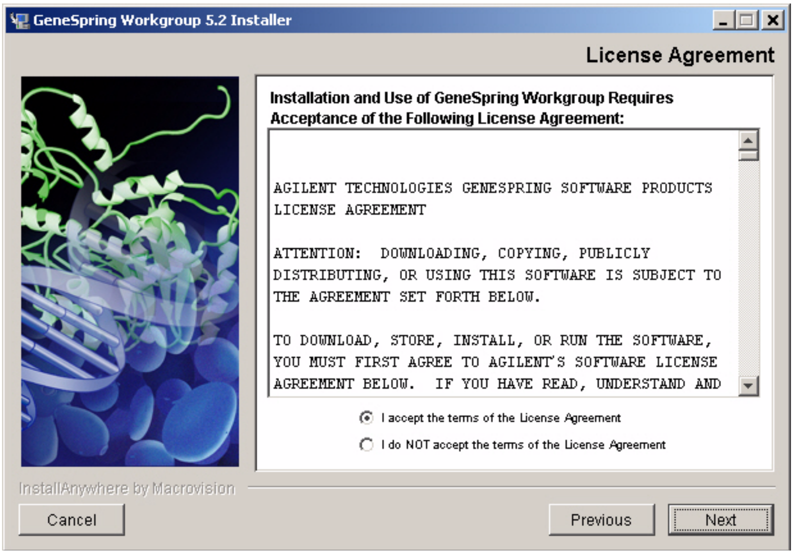
It is strongly recommended that you quit all programs before continuing with this installation.

Click the 'Next' button to proceed to the next screen. If you want to change something on a previous screen, click the 'Previous' button.

You may cancel this installation at any time by clicking the 'Cancel' button.

Figure 1 Introduction dialog box for Windows installation

3 Click **Next**. The License Agreement dialog box appears.



Installation and Use of GeneSpring Workgroup Requires Acceptance of the Following License Agreement:

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ATTENTION: DOWNLOADING, COPYING, PUBLICLY DISTRIBUTING, OR USING THIS SOFTWARE IS SUBJECT TO THE AGREEMENT SET FORTH BELOW.

TO DOWNLOAD, STORE, INSTALL, OR RUN THE SOFTWARE, YOU MUST FIRST AGREE TO AGILENT'S SOFTWARE LICENSE AGREEMENT BELOW. IF YOU HAVE READ, UNDERSTAND AND

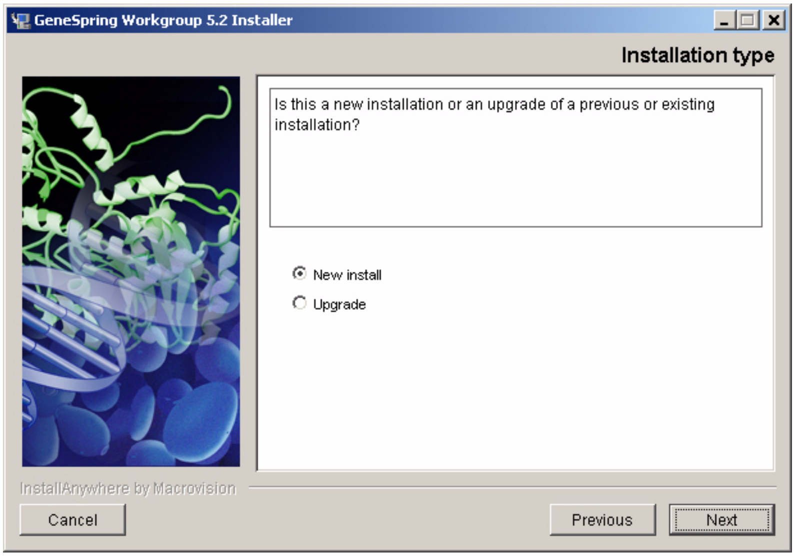
● I accept the terms of the License Agreement

○ I do NOT accept the terms of the License Agreement

Figure 2 License Agreement dialog box

4 Read and accept the terms of the license agreement.

5 Select the **I accept the terms of the License Agreement** radio button and click **Next**. (If you do not accept the license agreement installation cannot proceed.) The Installation type dialog box appears.



Is this a new installation or an upgrade of a previous or existing installation?

● New install
○ Upgrade

Figure 3 Installation Type

6 Indicate whether you are installing a new version of the Workgroup or an upgrade.

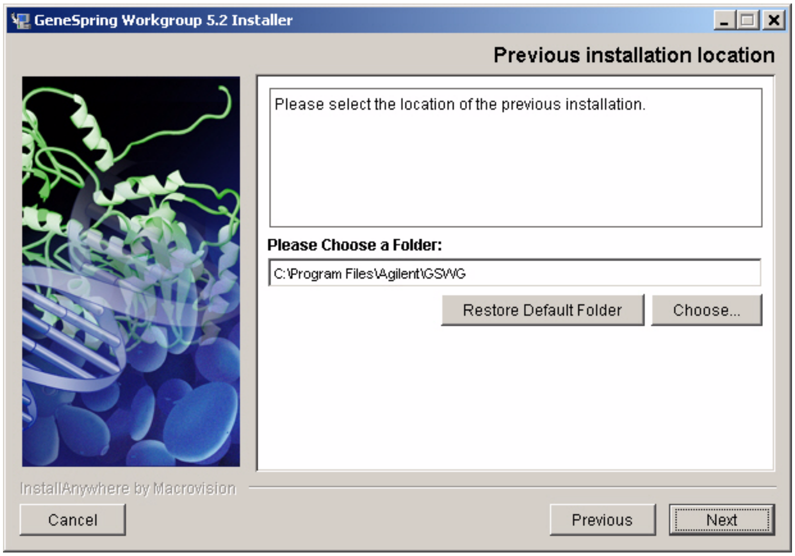
- If this is a new installation, select the **New Install** radio button and click **Next**. The Choose Install Folder dialog box appears. Proceed to Step 8.
- If you are upgrading, select the **Upgrade** radio button and click **Next**. The Please back up your existing installation dialog box appears.

NOTE If you have not already done so, back up your existing data now.

7 Click **Next**.

8 If this is a new installation, go to step 10 “Specify the GeneSpring Workgroup installation folder.” on page 17

The Previous installation location dialog box appears.



Please select the location of the previous installation.

Please Choose a Folder: C:\Program Files\Agilent\GSWG

Figure 4 Previous Installation Location

The previous installation folder displayed is **C:\Program Files\Agilent\GSWG**.

- If you would like to install into another directory, type the path name in the **Where Would You Like to Install** textbox.
- If you change your mind while entering a new path name, click **Restore Default Folder** to restore the default path.
- If you would like to browse for the installation folder, click **Choose** and make a choice in the File explorer window that appears. The default path for the previous installation location is **c:\Program Files\Silicon Genetics\ Signet**.

Specify the location of your previous installation or accept the default.

9 Go to step 11 "After choosing a folder, click Next. The Server Information for GeneSpring Workgroup dialog box appears." on page 17

The Choose Install Folder dialog box appears.

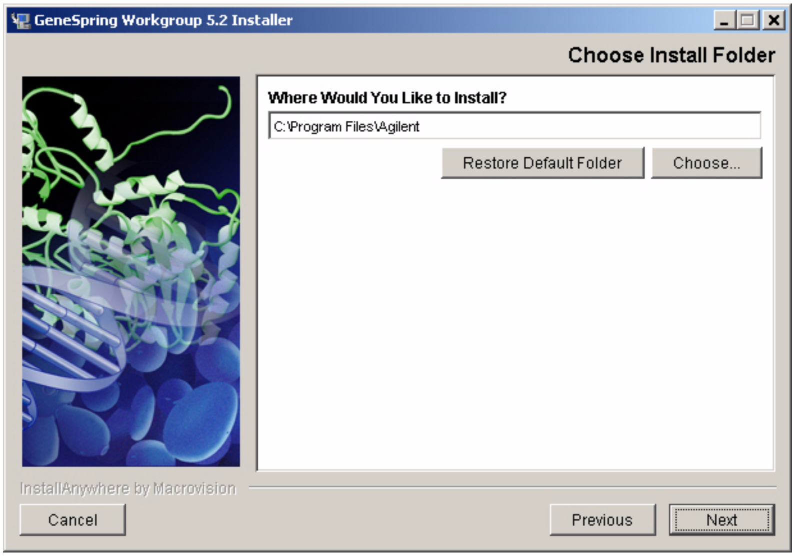


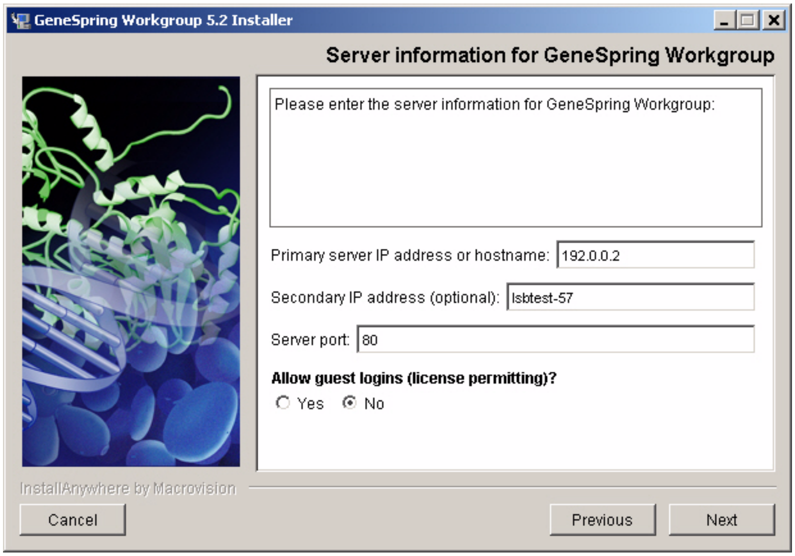
Figure 5 Installation Location

10 Specify the GeneSpring Workgroup installation folder.

The default installation folder displayed is **C:\Program Files\Agilent\GSWG**.

- If you would like to install into another directory, type the path name in the **Where Would You Like to Install** textbox.
- If you change your mind while entering a new path name, click **Restore Default Folder** to restore the default path.
- If you would like to browse for the installation folder, click **Choose** and make a choice in the File explorer window that appears.

11 After choosing a folder, click **Next**. The Server Information for GeneSpring Workgroup dialog box appears.



Server information for GeneSpring Workgroup

Please enter the server information for GeneSpring Workgroup:

Primary server IP address or hostname: 192.0.0.2

Secondary IP address (optional): lsbtest-57

Server port: 80

Allow guest logins (license permitting)?

○ Yes ● No

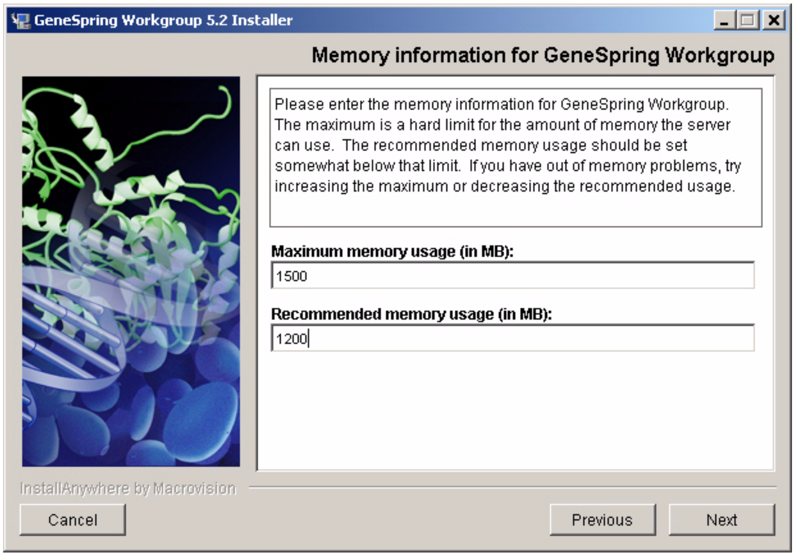
Figure 6 Server Information

Default selections appear for most choices. The IP address of your computer should appear in the first textbox. The default server port is **80** and **No** is selected for **Allow guest logins**. These defaults can be changed.

- **Secondary IP Address (optional)** – The host name of your computer can be entered here.
- **Server port** – The server port must be between **1** and **65535**.
- **Guest logins** – If you select **Yes** to allow guest logins, a **Guest** button will appear on the Workgroup login page. A user can then log in as **Guest**, but the available options are limited. See the *GeneSpring Workgroup User Guide* for more information on logging in as Guest.

12 Accept the defaults or make your selections, and click **Next**.

The “Command Prompt” screen appears and displays installation and status information. Then the Memory Information for GeneSpring Workgroup dialog box appears.



Please enter the memory information for GeneSpring Workgroup. The maximum is a hard limit for the amount of memory the server can use. The recommended memory usage should be set somewhat below that limit. If you have out of memory problems, try increasing the maximum or decreasing the recommended usage.

Maximum memory usage (in MB): 1500

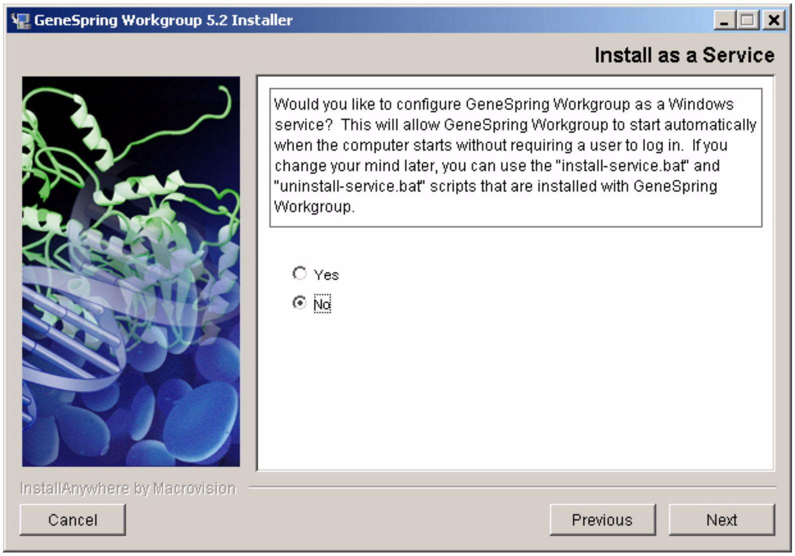
Recommended memory usage (in MB): 1200

Figure 7 Memory information for GeneSpring Workgroup

13 Set the Workgroup’s memory use.

The default for maximum memory is 1500 MB, and 1200 MB for recommended memory. Always set the recommended memory use *below* the maximum.

14 Click **Next**. The Install as a Service dialog box appears.



Would you like to configure GeneSpring Workgroup as a Windows service? This will allow GeneSpring Workgroup to start automatically when the computer starts without requiring a user to log in. If you change your mind later, you can use the "install-service.bat" and "uninstall-service.bat" scripts that are installed with GeneSpring Workgroup.

○ Yes
● No

Figure 8 Install as a service

15 Specify whether you want the Workgroup to run automatically as a Windows service. Select the **Yes** radio button if you would like the Workgroup to run automatically when the computer starts without requiring a user logon. Otherwise, select **No**.

If, after installation, you change your mind about running or not running the Workgroup as a Windows service, you have the following options:

- To start the GeneSpring Workgroup as a Windows service, run the following script:

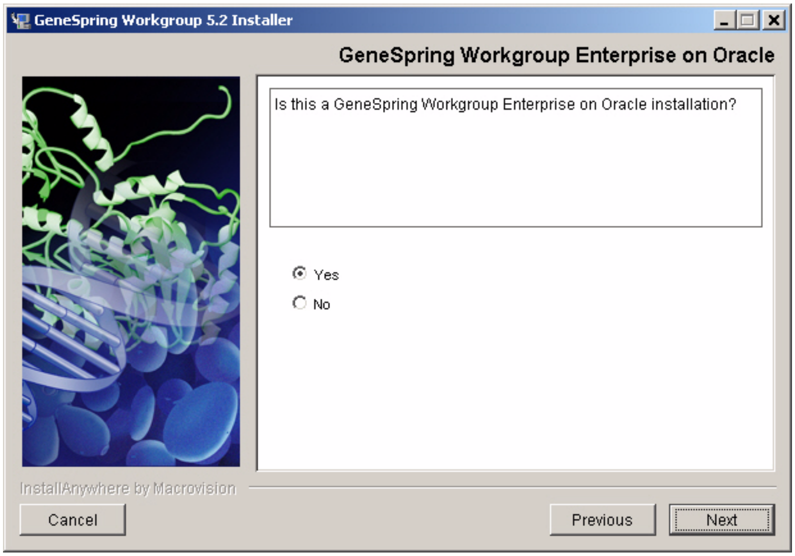
  ***Install directory*\Agilent\GSWG\install-service.bat**

This service appears in the Windows registry as “Agilent.”

- To change the behavior of the service, click **Start > Administrative Tools > Services > Agilent**.
- To remove the Workgroup as a Windows service, run the following script:

  ***Install Directory*\Agilent\GSWG\uninstall-service.bat**

16 Click **Next**. The GeneSpring Workgroup Enterprise on Oracle dialog box appears.



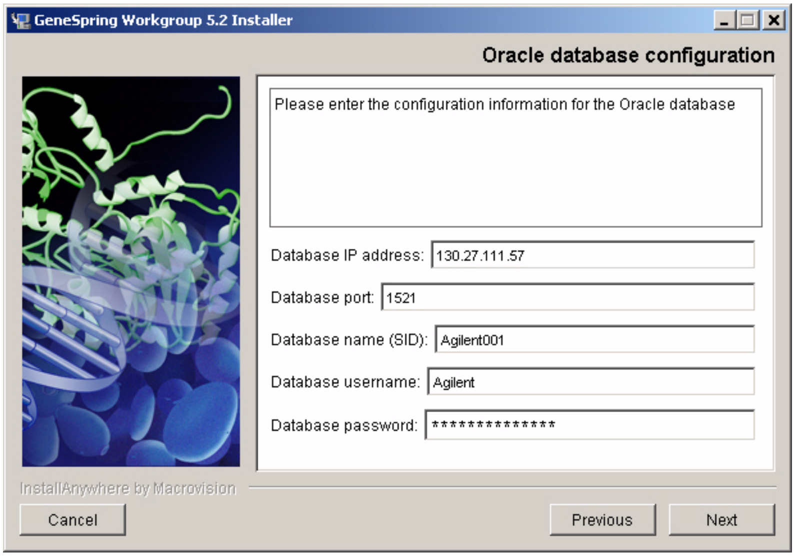
Is this a GeneSpring Workgroup Enterprise on Oracle installation?

● Yes
○ No

Figure 9 Oracle Usage

17 If you are not using Oracle, select the **No** radio button in the GeneSpring Enterprise on Oracle dialog box and click **Next**. The Configure Remote Server(s) dialog box appears. Go to step "The Configure Remote Server(s) dialog box appears." on page 24

18 If you are using an Oracle database, select the **Yes** radio button and click **Next**. The Oracle database configuration dialog box appears.



Please enter the configuration information for the Oracle database

Database IP address: 130.27.111.57

Database port: 1521

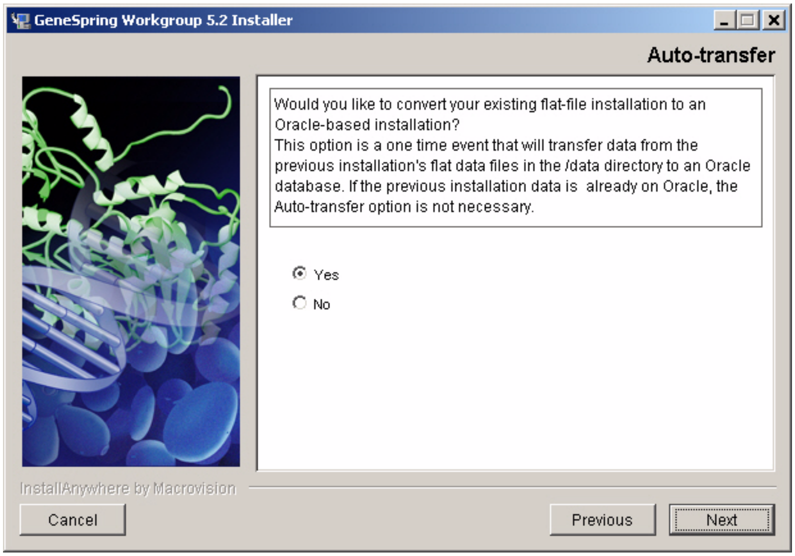
Database name (SID): Agilent001

Database username: Agilent

Database password: **************

19 Enter the configuration options for your Oracle database and click **Next**.

- If this is a new installation, the Configure Remote Server(s) dialog box appears. Proceed to step 20 “Indicate whether or not you want to convert your flat file.” on page 23.
- If this is an upgrade, the Auto Transfer dialog box appears.



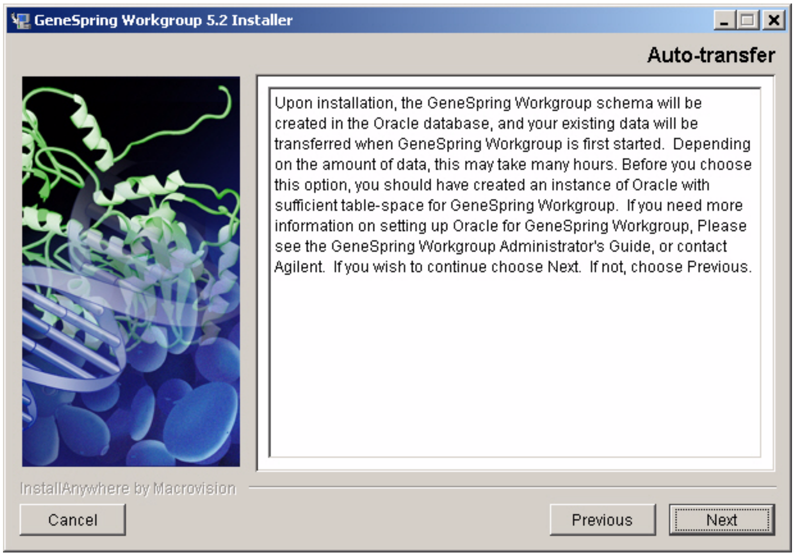
Would you like to convert your existing flat-file installation to an Oracle-based installation?
This option is a one time event that will transfer data from the previous installation's flat data files in the /data directory to an Oracle database. If the previous installation data is already on Oracle, the Auto-transfer option is not necessary.

● Yes
○ No

Figure 10 Auto-transfer dialog box

20 Indicate whether or not you want to convert your flat file.

- If you *do* ***not*** want to convert your existing flat-file installation to an Oracle-based installation, select the **No** radio button and click **Next**. The Configure Remote Server(s) dialog box appears.
- If you *do* ***not*** want to convert your existing flat-file installation to an Oracle-based installation, then proceed to step "The Configure Remote Server(s) dialog box appears." on page 24 .
- If you want to convert your existing flat-file installation to an Oracle-based installation, select the **Yes** radio button and click **Next**. The Auto-transfer dialog box displays the following message.



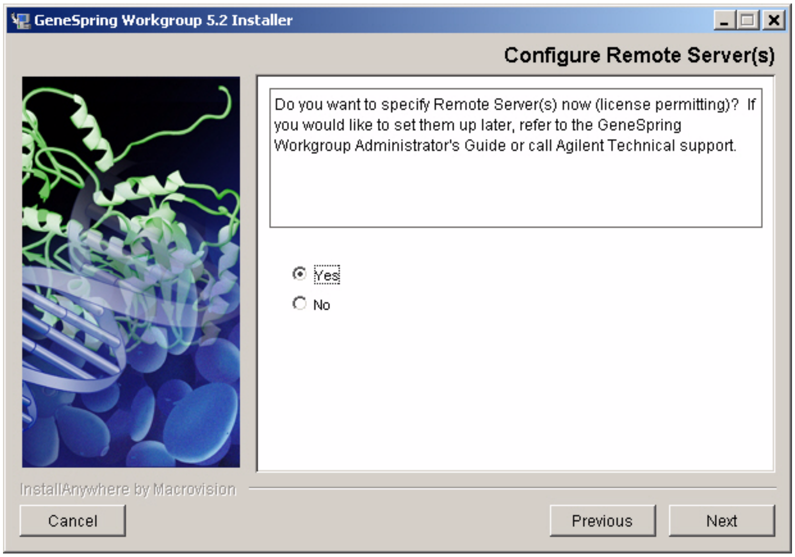
Auto-transfer

Upon installation, the GeneSpring Workgroup schema will be created in the Oracle database, and your existing data will be transferred when GeneSpring Workgroup is first started. Depending on the amount of data, this may take many hours. Before you choose this option, you should have created an instance of Oracle with sufficient table-space for GeneSpring Workgroup. If you need more information on setting up Oracle for GeneSpring Workgroup, Please see the GeneSpring Workgroup Administrator's Guide, or contact Agilent. If you wish to continue choose Next. If not, choose Previous.

Figure 11 Auto-transfer Informatioon

- If you want to continue, click **Next**.

The Configure Remote Server(s) dialog box appears.



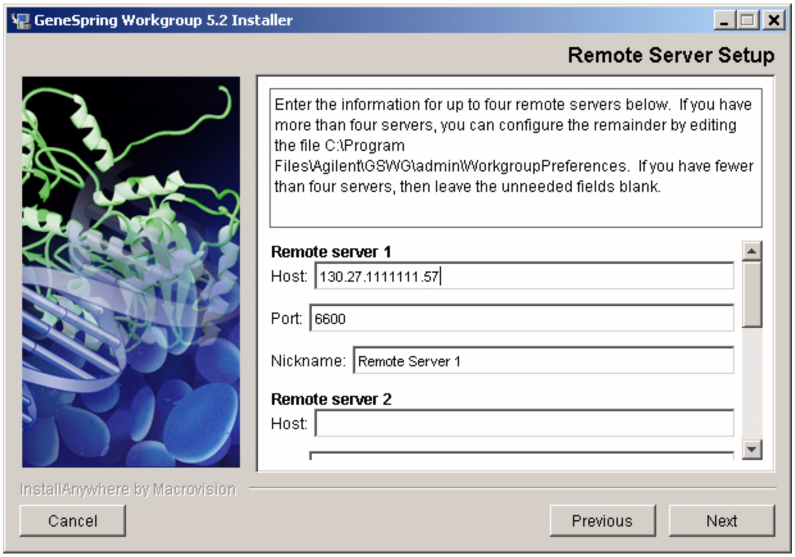
Configure Remote Server(s)

Do you want to specify Remote Server(s) now (license permitting)? If you would like to set them up later, refer to the GeneSpring Workgroup Administrator's Guide or call Agilent Technical support.

● Yes
○ No

21 On the Configure Remote Server(s) dialog box, if you are not configuring remote servers, select the **No** radio button and click **Next**. The Specify license file dialog box appears. Go to step 23 “Specify the location of the license file.” on page 26.

To configure remote servers at this time, select the **Yes** radio button and click **Next**. The Remote Server Setup dialog box appears.



Enter the information for up to four remote servers below. If you have more than four servers, you can configure the remainder by editing the file C:\Program Files\Agilent\GSWG\admin\WorkgroupPreferences. If you have fewer than four servers, then leave the unneeded fields blank.

Remote server 1
Host: 130.27.1111111.57
Port: 6600
Nickname: Remote Server 1

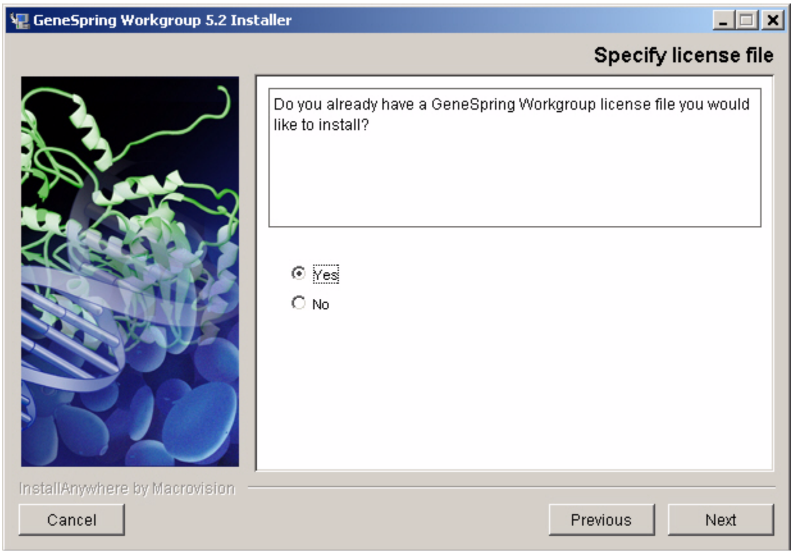
Remote server 2
Host:

Figure 12 Remote Servers Setup

You can configure up to four remote servers on this screen. If you need to configure more, you can edit the **ScriptServerAddress** preference under Remote Execution Preferences in the **<Install directory>\Agilent\GSWG\admin\Workgroup Preferences** file later using a text editor such as Notepad. See “Remote Server Preferences” in the *GeneSpring Workgroup User Guide* for more information.

22 Click **Next**. The Specify license file dialog box appears.

If this is not a new installation, the Pre-Installation Summary dialog box appears. Proceed to step 31 on page 31.



Do you already have a GeneSpring Workgroup license file you would like to install?

● Yes

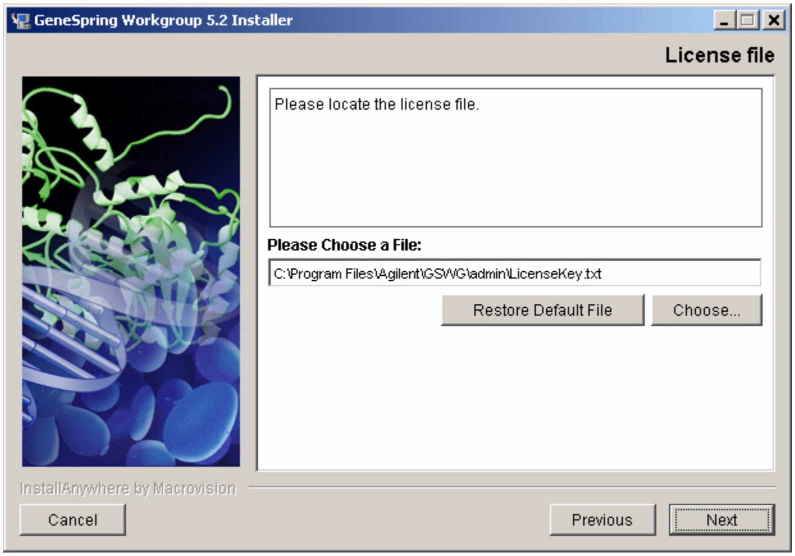
○ No

Figure 13 Specify License

23 Specify the location of the license file.

The license file (**LicenseKey.txt**) is sent to you separately from the installation program. If you do not have a license file, you must obtain one from Agilent support.

- If you select **No** and do not specify the location of the license file, you will get an error message when you try to access the GeneSpring Workgroup application with your browser.
- If you already have a license file, select the **Yes** radio button and click **Next**. The License file dialog box appears.



Please locate the license file.

Please Choose a File: C:\Program Files\Agilent\GSWG\admin\LicenseKey.txt

Figure 14 Locate License dialog box

24 Type in the name and path of the license key file in the textbox provided. If necessary, click **Choose** to browse for it.

25 Click **Next**. If this is not a new GeneSpring Workgroup Enterprise on Oracle installation, the Pre-Installation Summary dialog box appears. Proceed to step 31 on page 31. Otherwise, the Specify Oracle JDBC driver dialog box appears.

NOTE

You may encounter a problem working with certain Yeast genomes if the JDBC driver on your system is earlier than 9.2.0.1. Agilent highly recommends that you download the latest JDBC driver from Oracle at: http://www.oracle.com/technology/software/tech/java/sqlj_jdbc/ index.html

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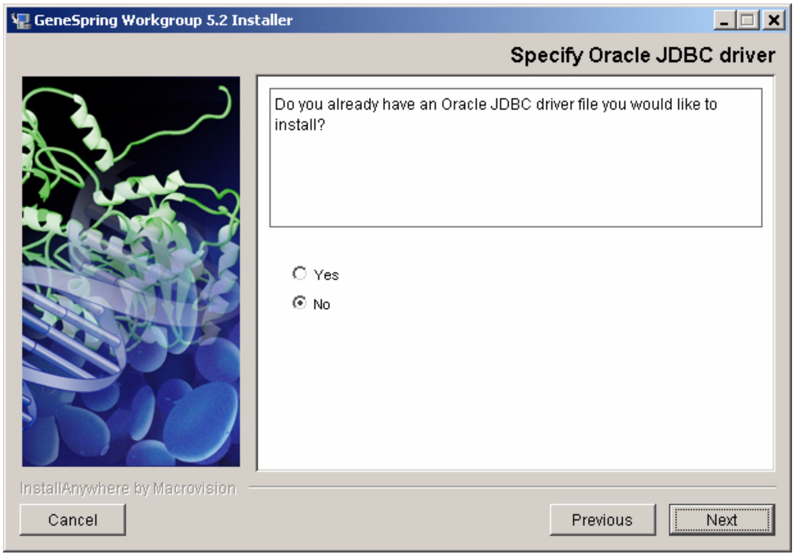
26 The Specify Oracle JDBC Driver dialog box appears.



Specify Oracle JDBC driver

Do you already have an Oracle JDBC driver file you would like to install?

○ Yes

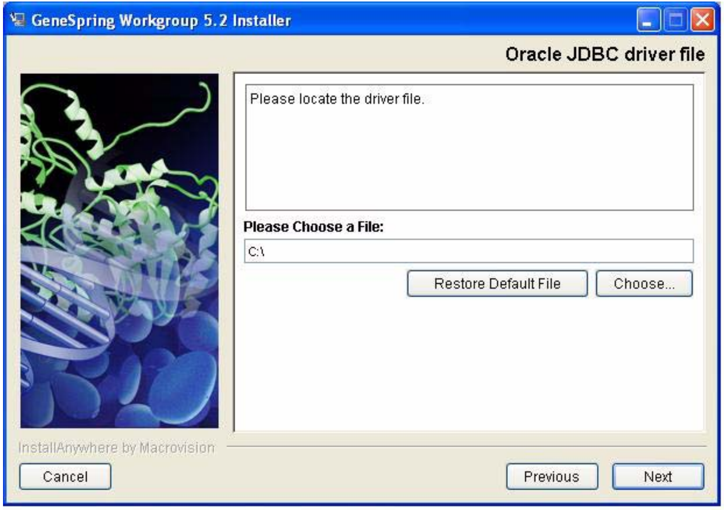
● No

Figure 15 Specify Oracle JDBC driver (only for new GeneSpring Workgroup Oracle installations)

27 Indicate whether or not you want to specify an Oracle JDBC Driver file by choosing the appropriate radio button.

- If you know the location of your Oracle JDBC driver file, select the **Yes** radio button and click **Next** The Oracle JDBC driver file dialog box appears.
- If you do not know the location of your Oracle JDBC driver file, select the **No** radio button and click **Next**. The Pre-Installation Summary dialog box appears. Proceed to step 31 on page 31

  After installing, we recommend you go to the Oracle Web site, download the appropriate JDBC driver and place it in the: ***Install directory*****/Agilent/GSWG/tomcat/GSWG/WEB-INF/ lib/** folder.



GeneSpring Workgroup 5.2 Installer

Oracle JDBC driver file

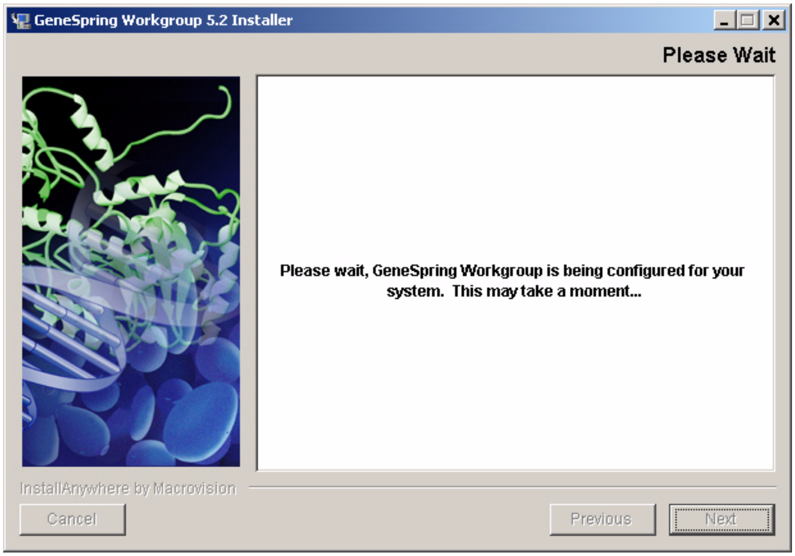
Please locate the driver file.

Please Choose a File: C:\

Figure 16 Oracle JDBC driver file dialog box

28 Type in the name and path of the driver file in the textbox provided. If necessary, click **Choose** to browse for it.

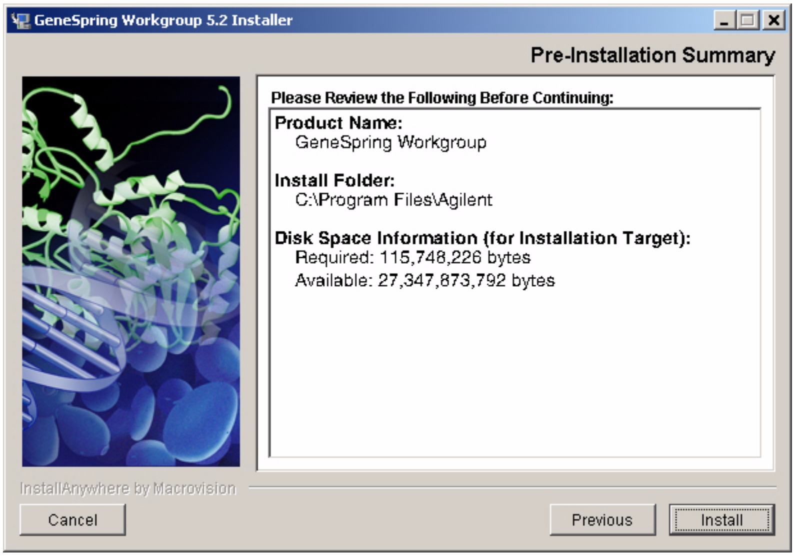
29 Click **Next**. A “please wait” message appears.



Please wait, GeneSpring Workgroup is being configured for your system. This may take a moment...

Figure 17 Please Wait message

30 The Pre-Installation Summary dialog box appears.



Please Review the Following Before Continuing:

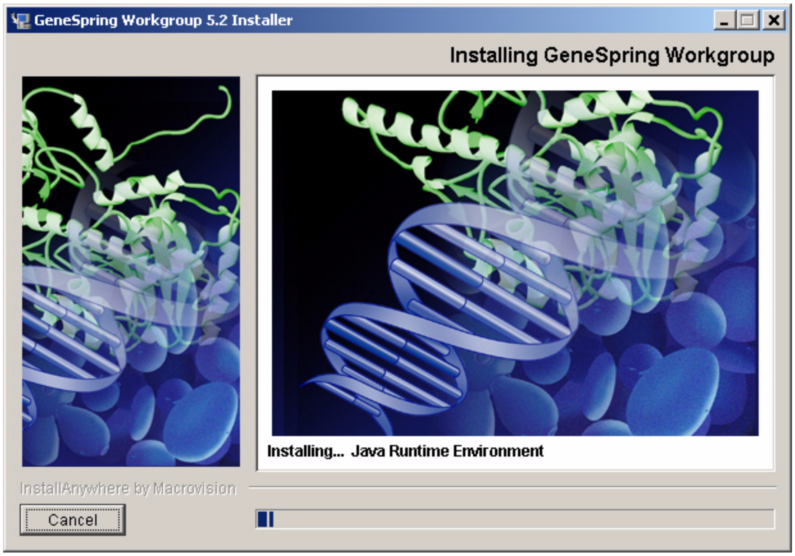
Product Name:
GeneSpring Workgroup

Install Folder:
C:\Program Files\Agilent

Disk Space Information (for Installation Target):
Required: 115,748,226 bytes
Available: 27,347,873,792 bytes

Figure 18 Pre-Installation Summary

31 Review and approve the parameters listed in the Pre-Installation Summary dialog box. Then click **Install** to begin installation. A dialog box appears informing you of the installation's progress.

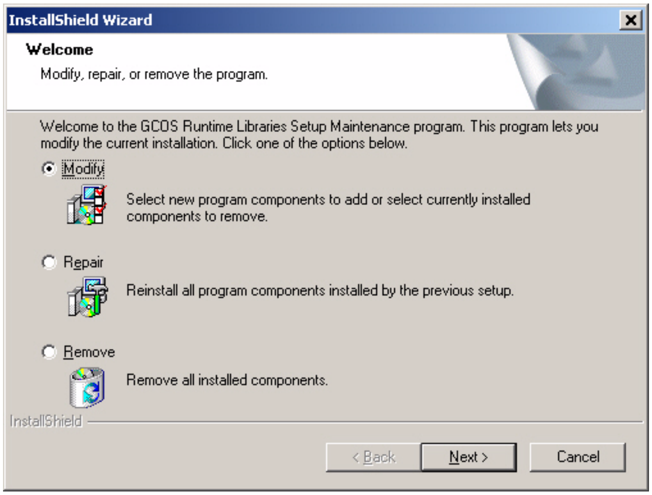


Installing... Java Runtime Environment

Figure 19 Progress - Installing GeneSpring Workgroup Server

If you specified the Oracle Database Server, then go to step 20 "GCOS Installation Welcome" on page 32.

32 If an Oracle database is not specified, then the following dialog box appears.


InstallShield Wizard

Welcome

Modify, repair, or remove the program.

Welcome to the GCOS Runtime Libraries Setup Maintenance program. This program lets you modify the current installation. Click one of the options below.

● Modify

Select new program components to add or select currently installed components to remove.

○ Repair

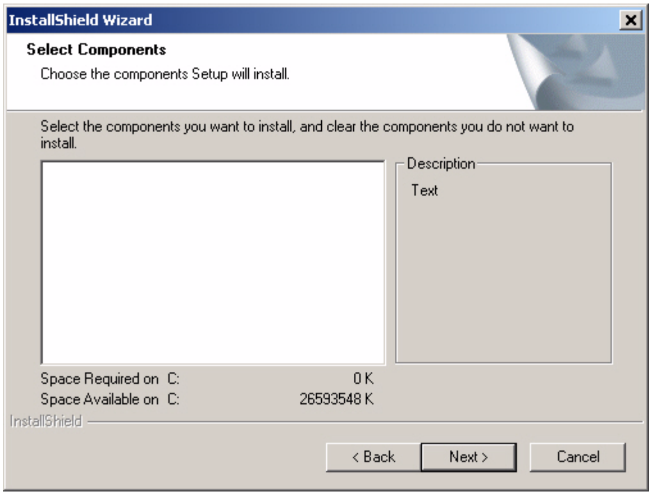
Reinstall all program components installed by the previous setup.

○ Remove

Remove all installed components.

Figure 20 GCOS Installation Welcome

a Select the Modify radio button. The following dialog box appears.


InstallShield Wizard

Select Components

Choose the components Setup will install.

Select the components you want to install, and clear the components you do not want to install.

Description

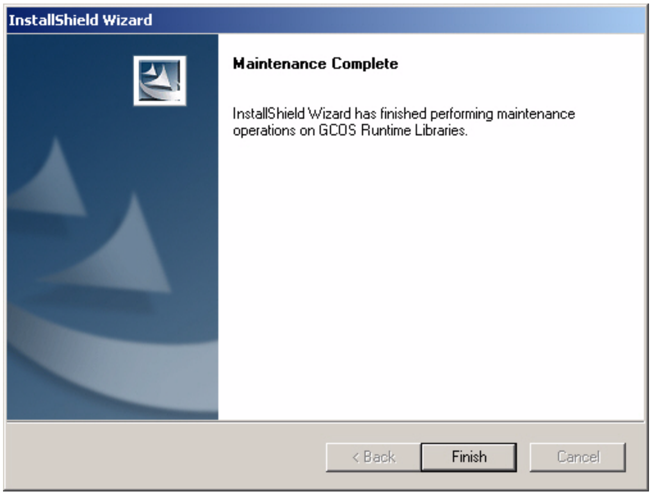
Text

Space Required on C: 0 K

Space Available on C: 26593548 K

Figure 21 GCOS Select Components

b Click **Next**. The following dialog box appears.



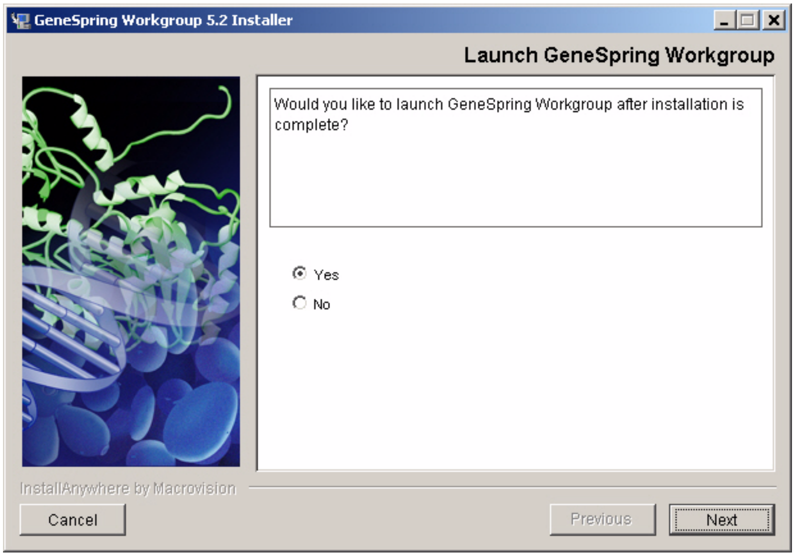
InstallShield Wizard

Maintenance Complete

InstallShield Wizard has finished performing maintenance operations on GCOS Runtime Libraries.

Figure 22 GCOS Installation Complete

33 After a brief interval, the Launch GeneSpring Workgroup dialog box appears.



GeneSpring Workgroup 5.2 Installer

Launch GeneSpring Workgroup

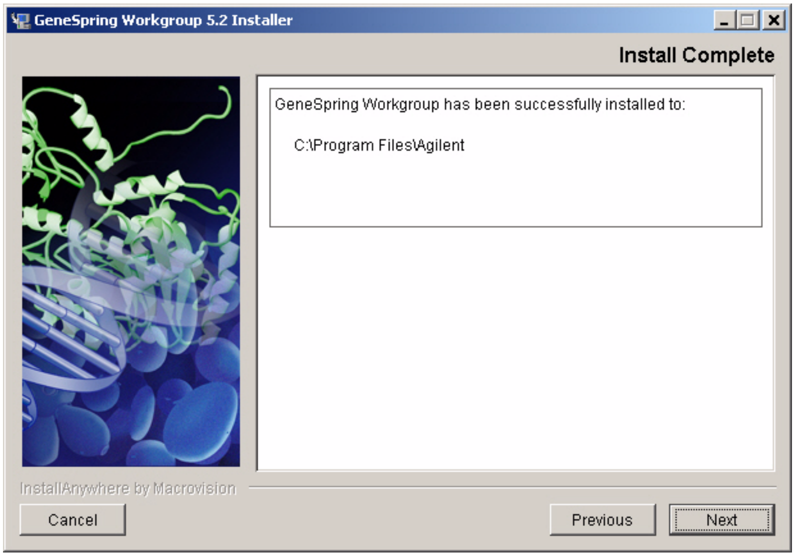
Would you like to launch GeneSpring Workgroup after installation is complete?

● Yes
○ No

Figure 23 Launch GeneSpring Workgroup

34 Decide whether you want to start the Workgroup after installation.

- Select the **Yes** radio button if you want to launch the Workgroup application.
- Select **No** if you do not want to launch the Workgroup application.



GeneSpring Workgroup has been successfully installed to:

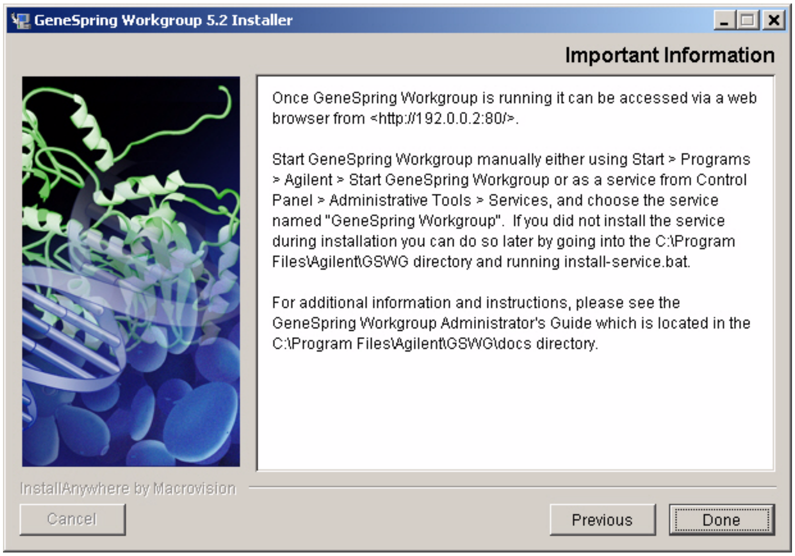
C:\Program Files\Agilent

Figure 24 Install Complete dialog box

- If you receive a warning or error message, you can review the file: <Install directory>\Agilent\GeneSpring_Workgroup_InstallLog.xml.
- If you are using the default installation directory, this would be C:\Program Files\Agilent\GeneSpring_Workgroup_InstallLog.xml.

The XML file can be viewed in a web browser. If, after reviewing this file, you have questions or concerns, contact Agilent support.

35 Click **Next**. The Important Information dialog box appears.



Important Information

Once GeneSpring Workgroup is running it can be accessed via a web browser from <http://192.0.0.2:80/>.

Start GeneSpring Workgroup manually either using Start > Programs > Agilent > Start GeneSpring Workgroup or as a service from Control Panel > Administrative Tools > Services, and choose the service named "GeneSpring Workgroup". If you did not install the service during installation you can do so later by going into the C:\Program Files\Agilent\GSWG directory and running install-service.bat.

For additional information and instructions, please see the GeneSpring Workgroup Administrator's Guide which is located in the C:\Program Files\Agilent\GSWG\docs directory.

Figure 25 Important Information

Read what is displayed on this screen and take notes for future reference, if necessary. The dialog box displays the Web-browser address you created during installation.

36 Click **Done**.

You have finished installing the GeneSpring Workgroup.

To install and configure on Linux/Solaris systems (GUI)

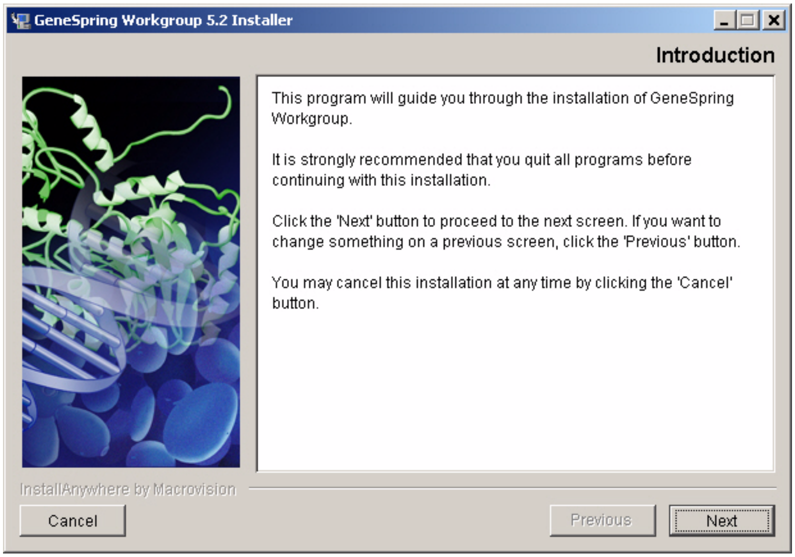
You must log in as **root** to install the GeneSpring Workgroup application. You must also be logged in as **root** the first time you start the application. After the initial startup, you can change the application's ownership. See "To change GeneSpring Workgroup Ownership in Linux or Solaris" on page 58 for more information.

The application is supplied by your Agilent customer service representative.

1 To run the GUI installation, open a terminal window, go to the directory where you copied the installation program, and type the following command:

```
. /Agilent5_2/Installer.bin -i console
```

Within a few minutes, the following console window appears.



This program will guide you through the installation of GeneSpring Workgroup.

It is strongly recommended that you quit all programs before continuing with this installation.

Click the 'Next' button to proceed to the next screen. If you want to change something on a previous screen, click the 'Previous' button.

You may cancel this installation at any time by clicking the 'Cancel' button.

2 Click **Next**.

3 The remainder of the installation including the screens, is the same as for a Windows installation. Go to step 3 on page 14.

To install and configure on Linux/Solaris systems (non-GUI)

You must log in as **root** to install the GeneSpring Workgroup application. You must also be logged in as **root** the first time you start the application, but after the initial startup, you can change the application’s ownership. See “To change GeneSpring Workgroup Ownership in Linux or Solaris” on page 58 for more information.

The application may be supplied via the Internet, CD, or other media. From the resource provided,

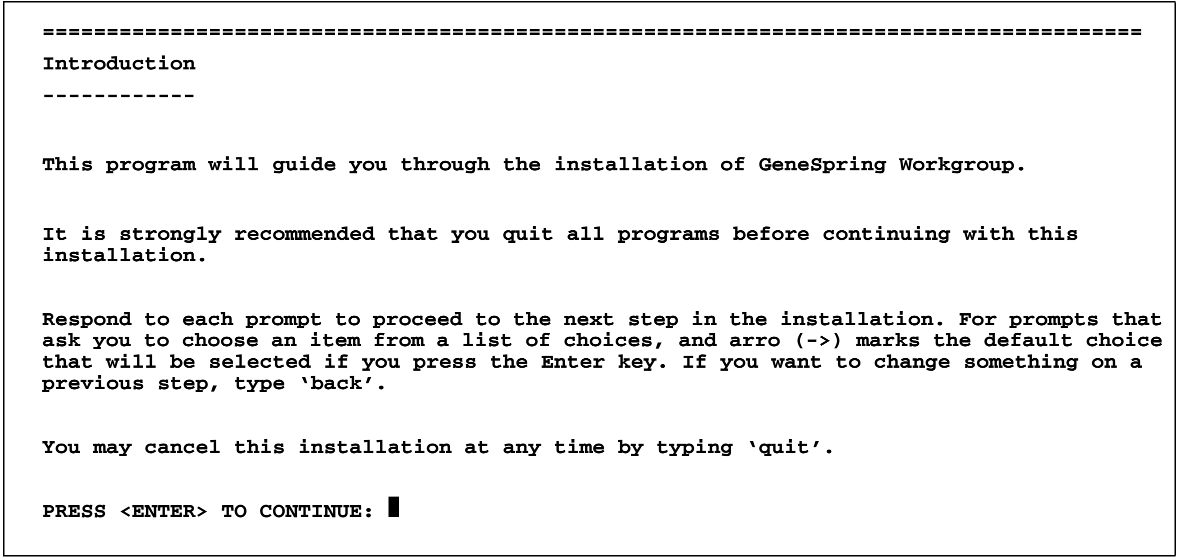
1 To run the non-GUI installation, open a terminal window, go to the directory where you copied the installation program, and type the following command:

```
. /GeneSpringWorkgroupInstaller.bin -i console
```

If you do not have execute privileges, use the command:

```
chmod +x GeneSpringWorkgroupInstaller.bin
```

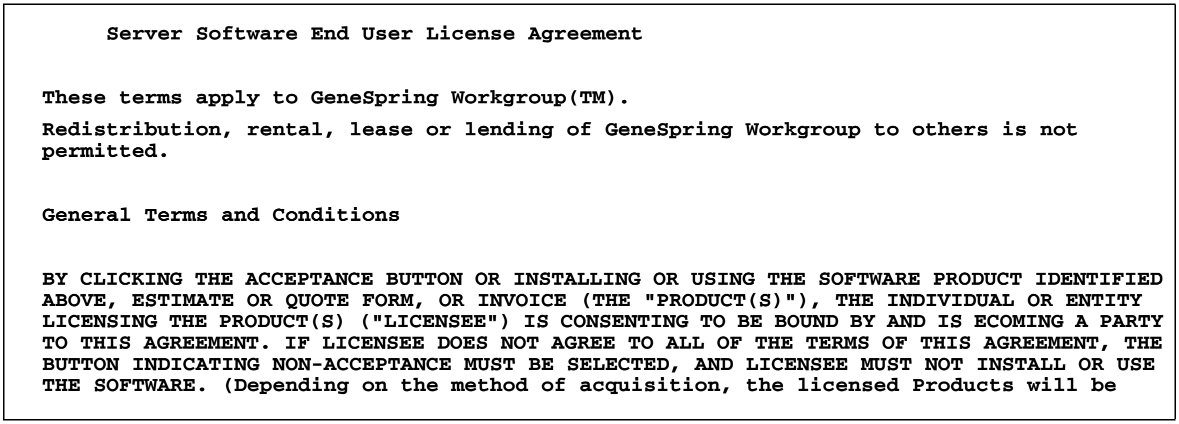
Within a few minutes, the following console window appears.



```
=====================================================================================
Introduction
------------


This program will guide you through the installation of GeneSpring Workgroup.


It is strongly recommended that you quit all programs before continuing with this
installation.


Respond to each prompt to proceed to the next step in the installation. For prompts that
ask you to choose an item from a list of choices, and arro (->) marks the default choice
that will be selected if you press the Enter key. If you want to change something on a
previous step, type ‘back’.


You may cancel this installation at any time by typing ‘quit’.


PRESS <ENTER> TO CONTINUE: █
```

Figure 26 Introduction prompt

2 Press **Enter**. The first License Agreement text prompts of several appears.



```
     Server Software End User License Agreement


These terms apply to GeneSpring Workgroup(TM).
Redistribution, rental, lease or lending of GeneSpring Workgroup to others is not
permitted.


General Terms and Conditions


BY CLICKING THE ACCEPTANCE BUTTON OR INSTALLING OR USING THE SOFTWARE PRODUCT IDENTIFIED
ABOVE, ESTIMATE OR QUOTE FORM, OR INVOICE (THE "PRODUCT(S)"), THE INDIVIDUAL OR ENTITY
LICENSING THE PRODUCT(S) ("LICENSEE") IS CONSENTING TO BE BOUND BY AND IS ECOMING A PARTY
TO THIS AGREEMENT. IF LICENSEE DOES NOT AGREE TO ALL OF THE TERMS OF THIS AGREEMENT, THE
BUTTON INDICATING NON-ACCEPTANCE MUST BE SELECTED, AND LICENSEE MUST NOT INSTALL OR USE
THE SOFTWARE. (Depending on the method of acquisition, the licensed Products will be
```

Figure 27 License Screen text (one of many)

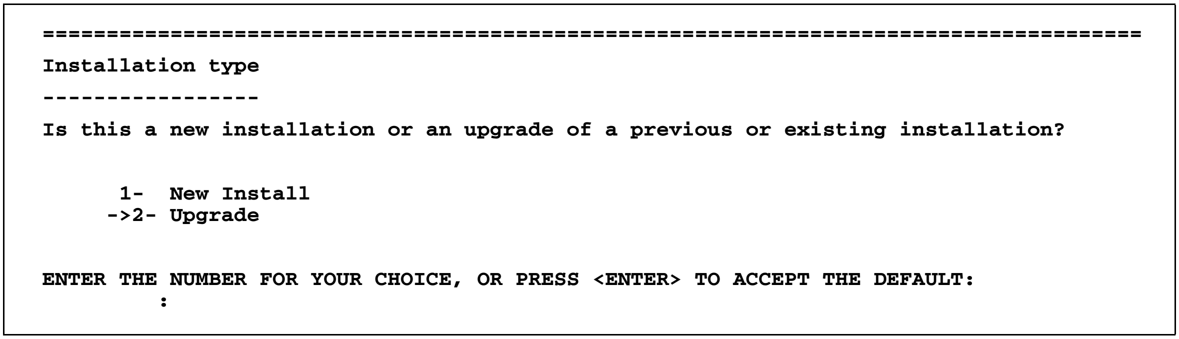
3 Read the text. You will need to press **Enter** several times to reach the end of the agreement.

```
XXXXX
XXXXX
XXXXX
```

Figure 28 License acceptance prompt

4 Accept the terms of the license agreement.

Type **Y**, and press **Enter** to accept the license agreement. (If you do not accept the license agreement, installation cannot proceed.) The Installation type prompt appears:

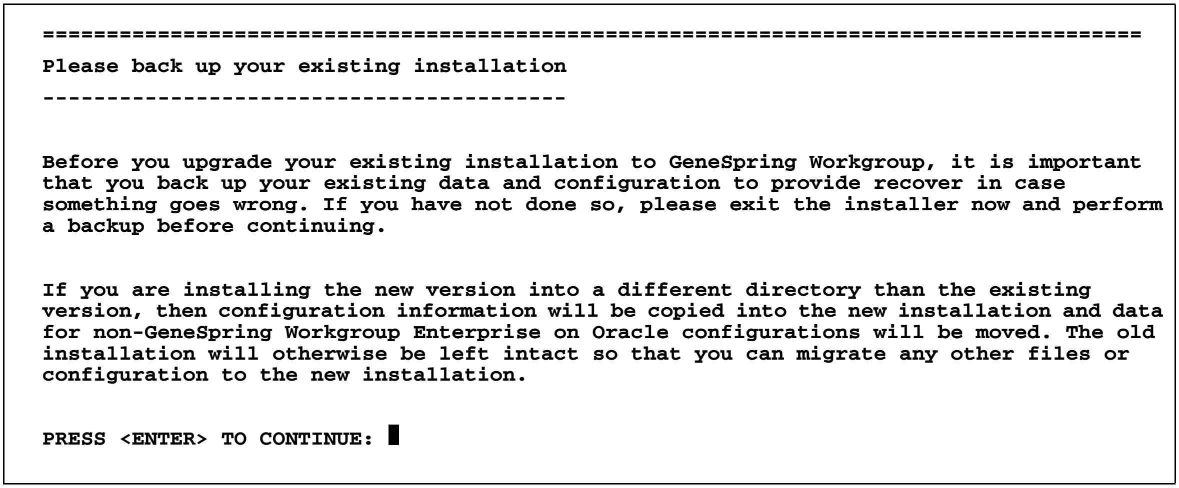


```
======================================================================================
Installation type
-----------------
Is this a new installation or an upgrade of a previous or existing installation?


      1-  New Install
     ->2- Upgrade


ENTER THE NUMBER FOR YOUR CHOICE, OR PRESS <ENTER> TO ACCEPT THE DEFAULT:
         :
```

Figure 29 Installation type prompt

5 Select whether this is a new installation or an upgrade.

- If this is a new installation, type **1** for **New Install** and press **Enter**. The Choose Install Folder prompt appears. Proceed to Step 4.
- If this is an upgrade, type **2** for **Upgrade** and press **Enter**. The Please back up your existing installation prompt appears:



```
======================================================================================
Please back up your existing installation
-----------------------------------------


Before you upgrade your existing installation to GeneSpring Workgroup, it is important
that you back up your existing data and configuration to provide recover in case
something goes wrong. If you have not done so, please exit the installer now and perform
a backup before continuing.


If you are installing the new version into a different directory than the existing
version, then configuration information will be copied into the new installation and data
for non-GeneSpring Workgroup Enterprise on Oracle configurations will be moved. The old
installation will otherwise be left intact so that you can migrate any other files or
configuration to the new installation.


PRESS <ENTER> TO CONTINUE: █
```

Figure 30 Please back up your existing installation prompt (upgrade only)

NOTE If you have not already done so, back up your system now.

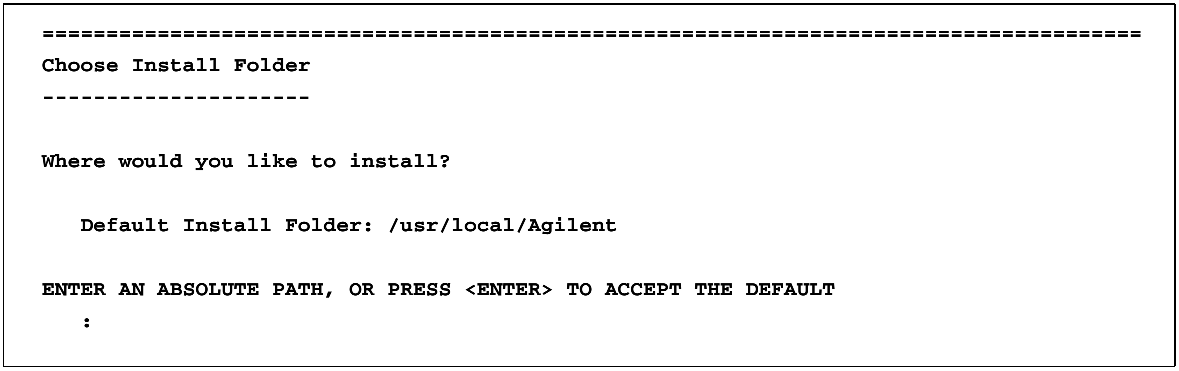
6 Press **Enter**. The Previous installation location prompt appears:

```
======================================================================================
Previous installation location
------------------------------

Please enter the location of the previous installaton.

Location: (DEFAULT: /usr/local/Agilent/GSWG):
```

Figure 31 Previous installation location prompt (upgrade only)

7 Specify the location of your previous installation or accept the default and press **Enter**. The Choose Install folder prompt appears.

8 Specify your GeneSpring Workgroup installation folder.



```
======================================================================================
Choose Install Folder
---------------------

Where would you like to install?

   Default Install Folder: /usr/local/Agilent

ENTER AN ABSOLUTE PATH, OR PRESS <ENTER> TO ACCEPT THE DEFAULT
   :
```

Figure 32 Choose Install Folder prompt

9 The default installation folder is **/usr/local/Agilent**. If you would like to install the application in another directory, type the path name, and press **Enter**. The Primary hostname prompt appears.

```
======================================================================================
Primary hostname
----------------

Please enter the server’s primary hostname or IP address

Hostname: (DEFAULT: 127.0.0.1):
```

Figure 33 Primary hostname prompt

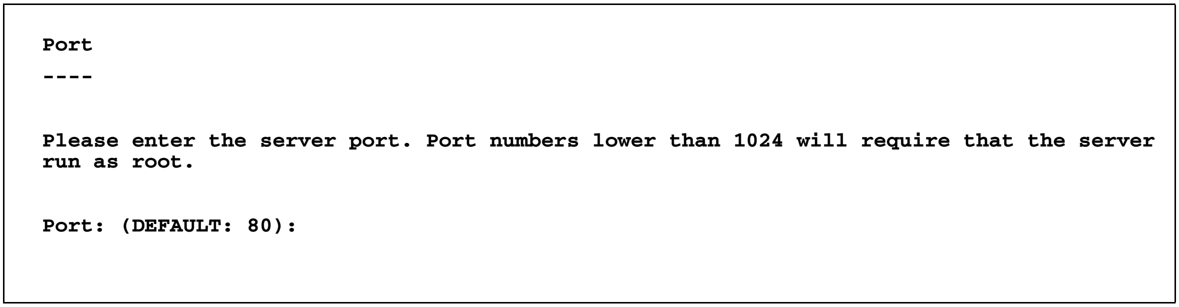
NOTE The default hostname or IP address that appears is different for each computer.

10 Type the primary hostname or IP address, or accept the default and press **Enter**. The Secondary hostname prompt appears.

```
======================================================================================
Secondary hostname
------------------

Please enter the server’s secondary hostname or IP address (optional)

Hostname: (DEFAULT: laureltemp):
```

Figure 34 Secondary hostname prompt

11 Type in the secondary hostname or IP Address, or accept the default and press **Enter**. The Port prompt appears.



```
Port
----

Please enter the server port. Port numbers lower than 1024 will require that the server
run as root.

Port: (DEFAULT: 80):
```

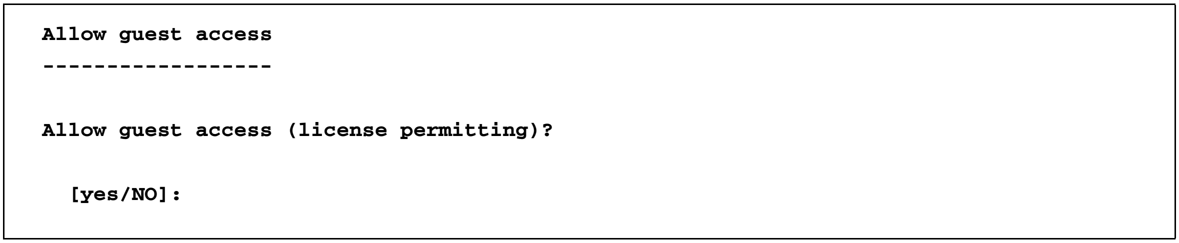
Figure 35 Port prompt

12 Type a port number or accept the default of 80 and press **Enter**.

The server port must be between 1 and 65535.

NOTE If you enter a port number below 1024, the Workgroup application must run as root. For information on running the Workgroup as a user other than root, see "To change GeneSpring Workgroup Ownership in Linux or Solaris" on page 58

The Allow guest access prompt appears.



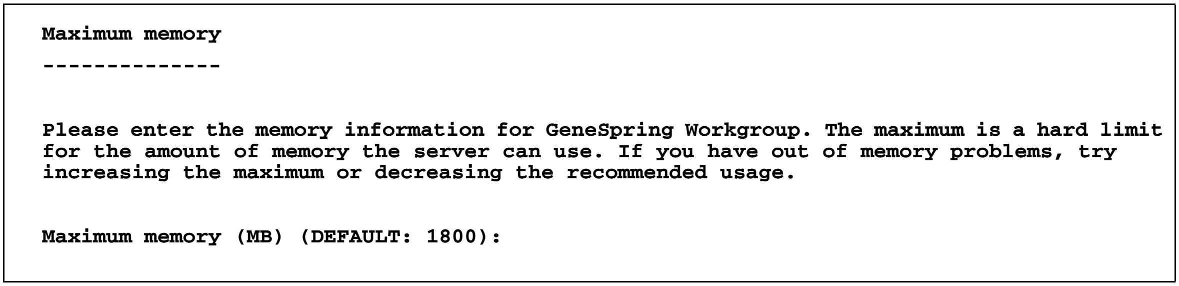
```
Allow guest access
------------------

Allow guest access (license permitting)?

  [yes/NO]:
```

Figure 36 Allow guest access prompt

13 Decide whether to allow guest logins.

- If you type **yes** to allow guest logins, a Guest button appears on the GeneSpring Workgroup login page. A user can then log in as "Guest," but the available options are limited. See the *GeneSpring Workgroup User Guide* for more information on logging in as Guest.

14 Type **yes** or accept the defaults, and press **Enter**. The Maximum memory prompt appears.

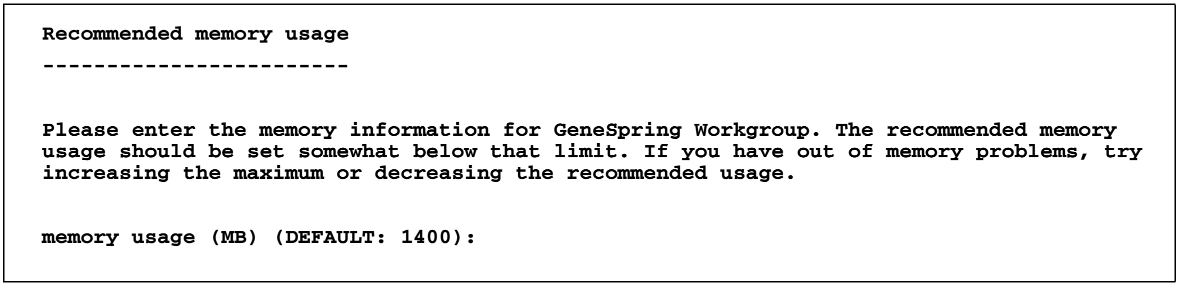


```
Maximum memory
--------------


Please enter the memory information for GeneSpring Workgroup. The maximum is a hard limit
for the amount of memory the server can use. If you have out of memory problems, try
increasing the maximum or decreasing the recommended usage.


Maximum memory (MB) (DEFAULT: 1800):
```

Figure 37 Maximum memory prompt

The default maximum memory is 1800 MB. The recommended memory use is always set below the maximum.

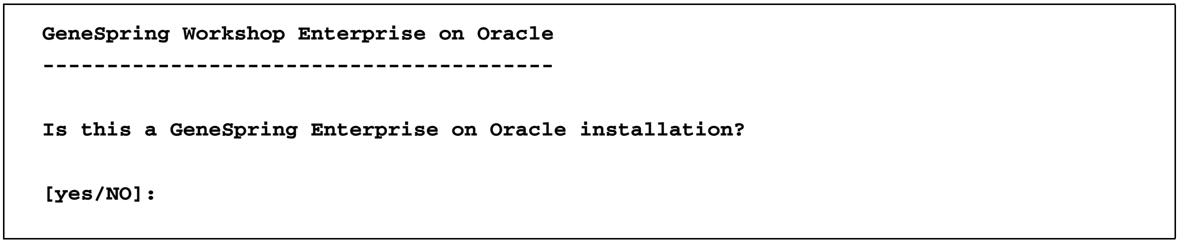
15 Type a maximum amount of memory or accept the default, and press **Enter**. The Recommended memory usage prompt appears.



```
Recommended memory usage
------------------------


Please enter the memory information for GeneSpring Workgroup. The recommended memory
usage should be set somewhat below that limit. If you have out of memory problems, try
increasing the maximum or decreasing the recommended usage.


memory usage (MB) (DEFAULT: 1400):
```

Figure 38 Recommended memory usage prompt

The default recommended memory is 1400 MB. Type a different number or accept the default, and press **Enter**. The GeneSpring Workgroup Enterprise on Oracle Installation prompt appears.

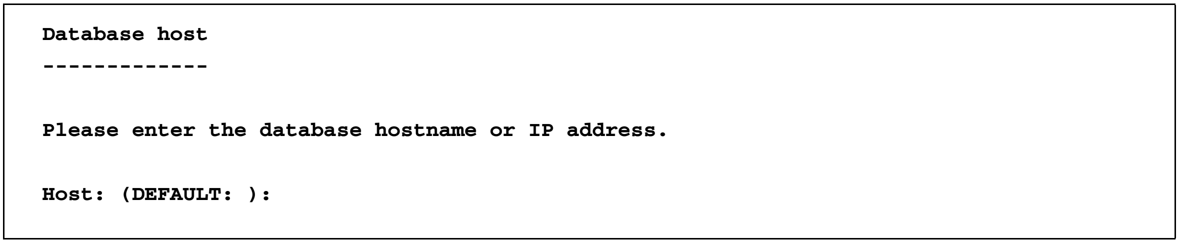


```
GeneSpring Workshop Enterprise on Oracle
----------------------------------------

Is this a GeneSpring Enterprise on Oracle installation?

[yes/NO]:
```

Figure 39 GeneSpring Workgroup Enterprise on Oracle installation prompt

16 Indicate the type of database you are using.

- If you *are not* using Oracle, type **No** and press **Enter**. The Configure Remote Server(s) prompt appears. Proceed to step 22 “Indicate whether or not you want to configure remote servers.”.
- If you are using an Oracle database, type **yes** and click **Enter**. The Database host prompt appears.



```
Database host
-------------

Please enter the database hostname or IP address.

Host: (DEFAULT: ):
```

Figure 40 Database host prompt

17 Enter the database hostname or IP address for your Oracle database, and press **Enter**. The Database name (SID) prompt appears.

```
Database name (SID)
-------------------

Please enter the database name.

Name: (DEFAULT: ):
```

Figure 41 Database name (SID) prompt

18 Type the Database name or accept the default, and press **Enter**. The Database port prompt appears.

```
Database port
-------------

Please enter the database port.

Port: (DEFAULT; 1521):
```

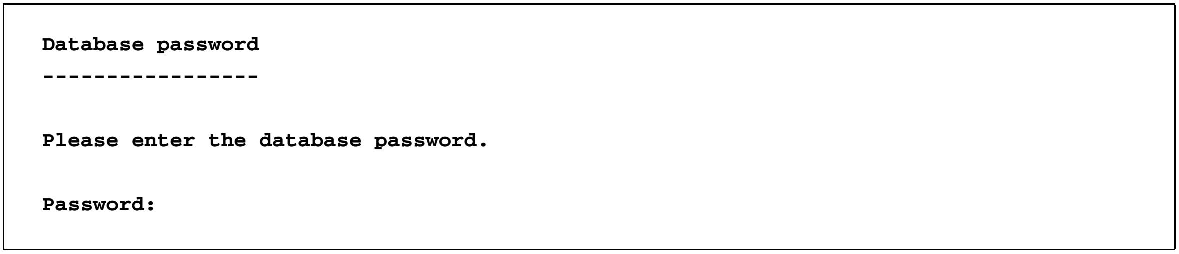
Figure 42 Database port prompt

Type the Database port or accept the default, and press **Enter**. The Database username prompt appears.

```
Database username
-----------------

Please enter the database username.

Username:
```

Figure 43 Database username prompt

19 Type the Database username and press **Enter**. The Database password prompt appears.

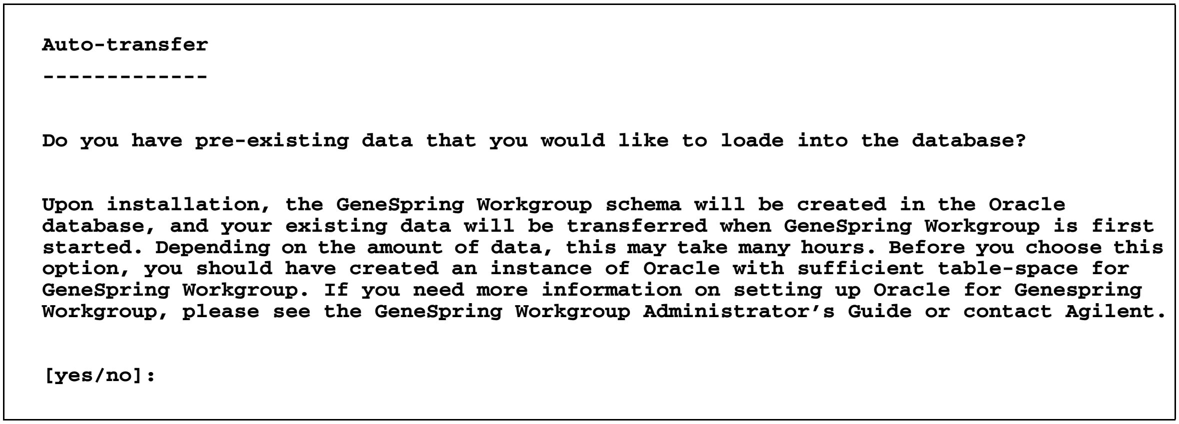


```
Database password
-----------------

Please enter the database password.

Password:
```

Figure 44 Database pasword prompt

20 Type the Database password and press **Enter**.

- If this *is not* an upgrade, the Configure Remote Server(s) prompt appears. Proceed to step 22 “Indicate whether or not you want to configure remote servers.” on page 47.
- If this *is* an upgrade, the Auto-transfer prompt appears.



```
Auto-transfer
-------------

Do you have pre-existing data that you would like to loade into the database?

Upon installation, the GeneSpring Workgroup schema will be created in the Oracle
database, and your existing data will be transferred when GeneSpring Workgroup is first
started. Depending on the amount of data, this may take many hours. Before you choose this
option, you should have created an instance of Oracle with sufficient table-space for
GeneSpring Workgroup. If you need more information on setting up Oracle for Genespring
Workgroup, please see the GeneSpring Workgroup Administrator’s Guide or contact Agilent.

[yes/no]:
```

Figure 45 Auto-transfer prompt (Oracle upgrade installations only)

Read the text and take notes for future reference. Be aware of the time involved in loading pre-existing data.

If you need help setting up Oracle, see “Using Oracle with GeneSpring” in the *GeneSpring Workgroup User Guide*.

21 Type **yes** or **no,** and press **Enter**. The Configure Remote Server(s) prompt appears.

```
Configure Remote Server(s)
--------------------------


Do you want to specify Remote Server(s) now (license permitting)? If you wuld like to set
them up later, refer to the Administrator's Guide or call Agilent technical support at
(XXX) XXX-XXXX.
```

Figure 46 Configure Remote Server(s) prompt

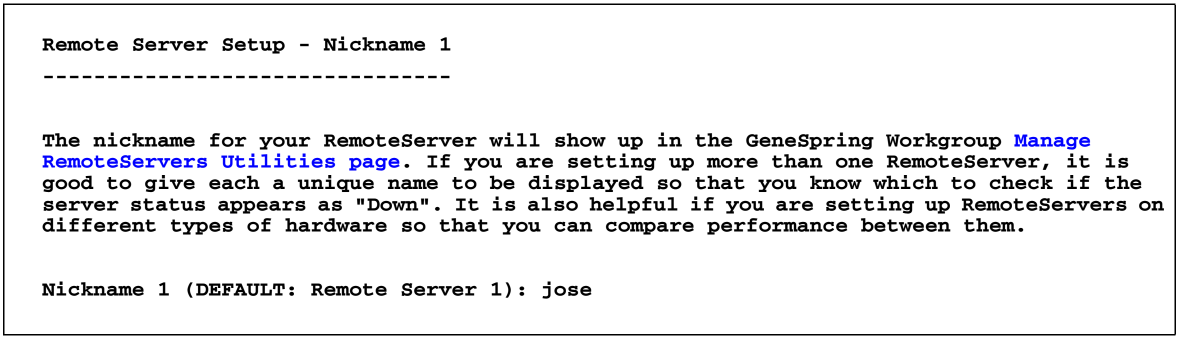
22 Indicate whether or not you want to configure remote servers.

- If you *do not want* to configure remote servers, type **no** and press **Enter**. The Specify license file prompt appears. Proceed to Specify the location of your license file.
- If you *want* to configure remote servers at this time, type **yes** and press **Enter**. The Remote Server Setup - Host 1 prompt appears.

```
Remote Server Setup - Host 1
----------------------------


Enter the information for up to four remote srvrs. If you have more than four servers, you
can configure the remainder by editing the file
/usr/local/Agilent/GSWG/admin/GeNetPreferences. If you have fewer than four srvers, then
leave the unneded fields blank.


Please enter the IP address or hostname of the remote server machine.


Host 1 (DEFAULT: ): 129.32.45.12
```

Figure 47 Remote Server Setup - Host 1 prompt

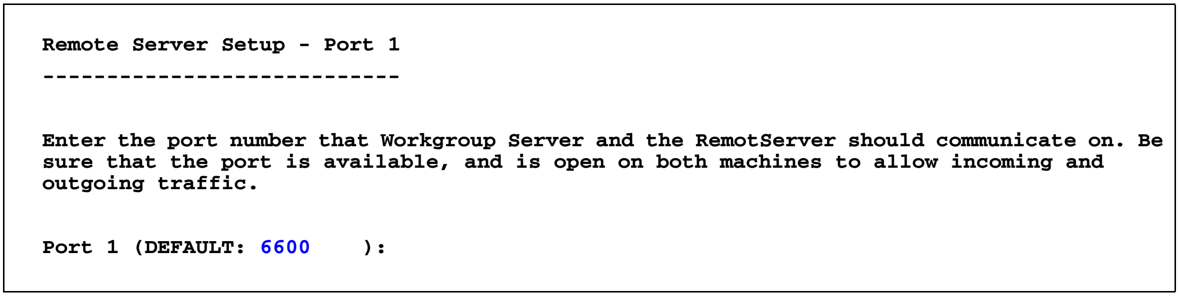
23 Type the hostname or IP address of your first remote server or accept the default, and press **Enter**. The Remote Server Setup - Nickname 1 prompt appears.



```
Remote Server Setup - Nickname 1
--------------------------------


The nickname for your RemoteServer will show up in the GeneSpring Workgroup Manage
RemoteServers Utilities page. If you are setting up more than one RemoteServer, it is
good to give each a unique name to be displayed so that you know which to check if the
server status appears as "Down". It is also helpful if you are setting up RemoteServers on
different types of hardware so that you can compare performance between them.


Nickname 1 (DEFAULT: Remote Server 1): jose
```

Figure 48 Remote Server Setup - Nickname 1 prompt

24 Type the nickname of your first remote server, or accept the default and press **Enter**. The Remote Server Setup - Port 1 prompt appears.



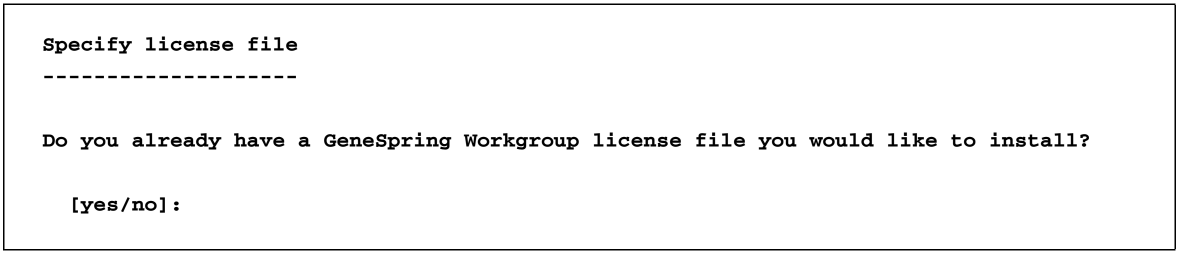
```
Remote Server Setup - Port 1
----------------------------


Enter the port number that Workgroup Server and the RemotServer should communicate on. Be
sure that the port is available, and is open on both machines to allow incoming and
outgoing traffic.


Port 1 (DEFAULT: 6600    ):
```

Figure 49 Remote Server Setup - Port 1 prompt

25 Type the port number of your first remote server or accept the default, and press **Enter**.

You can continue to configure up to four remote servers in this way or press **Enter** at any of the Remote Server Setup - Host Name prompts to exit.

- If this is not a new installation, the Pre-Installation Summary prompt appears. Proceed to Begin the installation.
- If this is a new installation, the Specify license file prompt appears.



```
Specify license file
--------------------

Do you already have a GeneSpring Workgroup license file you would like to install?

  [yes/no]:
```

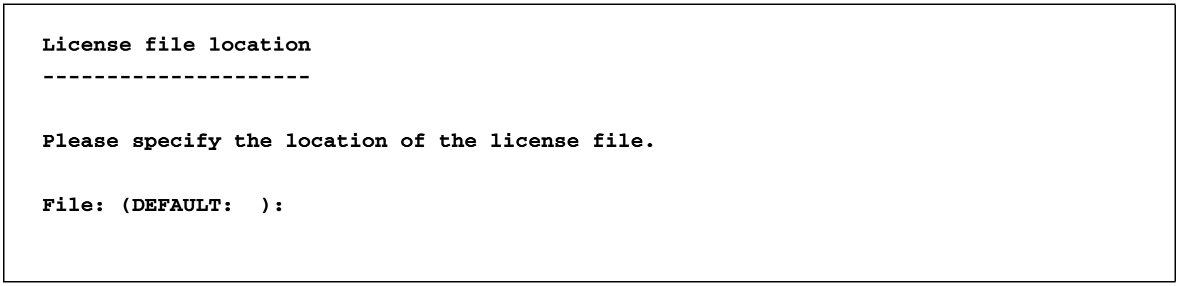
Figure 50 Specify license file prompt

26 Specify the location of the license file.

The license file (LicenseKey.txt) was sent to you separately from the installation program. If you do not have a license file, you will need to obtain one from Agilent support.

If you type **no** and do not specify the location of the license file, you will get an error message when you try to access the GeneSpring Workgroup with your browser.

27 If you already have a license, type **yes** and press **Enter**. The License file location prompt appears.

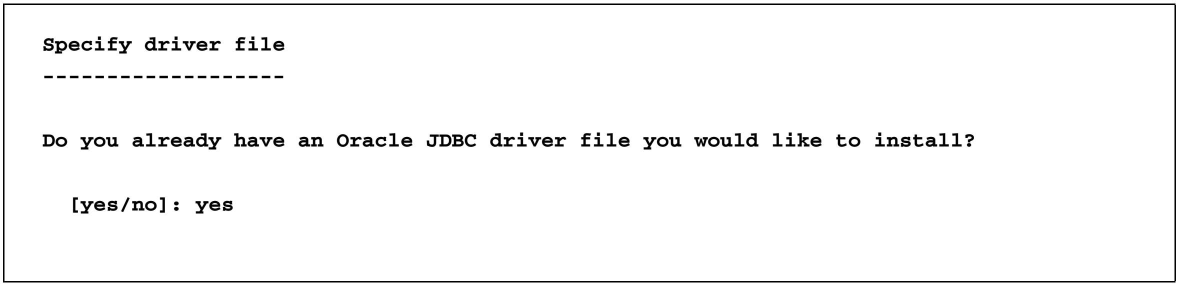


```
License file location
---------------------

Please specify the location of the license file.

File: (DEFAULT:  ):
```

Figure 51 License file location prompt (new installation only)

28 Type the name and path of the license file and press **Enter**.

If this is not a GeneSpring Workgroup Enterprise on Oracle installation proceed to Begin the installation. Otherwise, the Specify driver file prompt appears.



```
Specify driver file
-------------------

Do you already have an Oracle JDBC driver file you would like to install?

  [yes/no]: yes
```

Figure 52 Specify driver file prompt (Oracle new installation only)

29 Indicate whether or not you have an Oracle JDBC driver file.

- If you do not have an Oracle JDBC driver file, type **no** and press **Enter**. Proceed to Begin the installation.

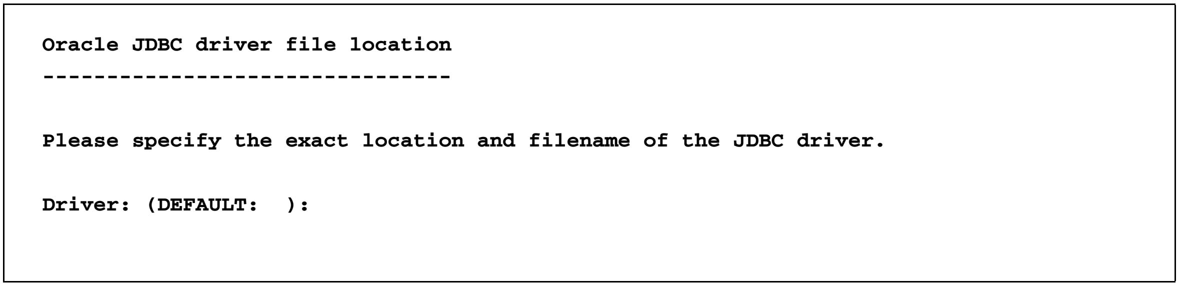
NOTE

After installation, you will need to go to Oracle's Web site, download the appropriate JDBC driver, and place it in the ***Install directory*****/GSWG/tomcat/GSWG/WEB-INF/lib/** directory.

- If you have an Oracle JDBC driver file and know the location, type **yes** and press **Enter**. The Oracle JDBC driver file location prompt appears.

NOTE

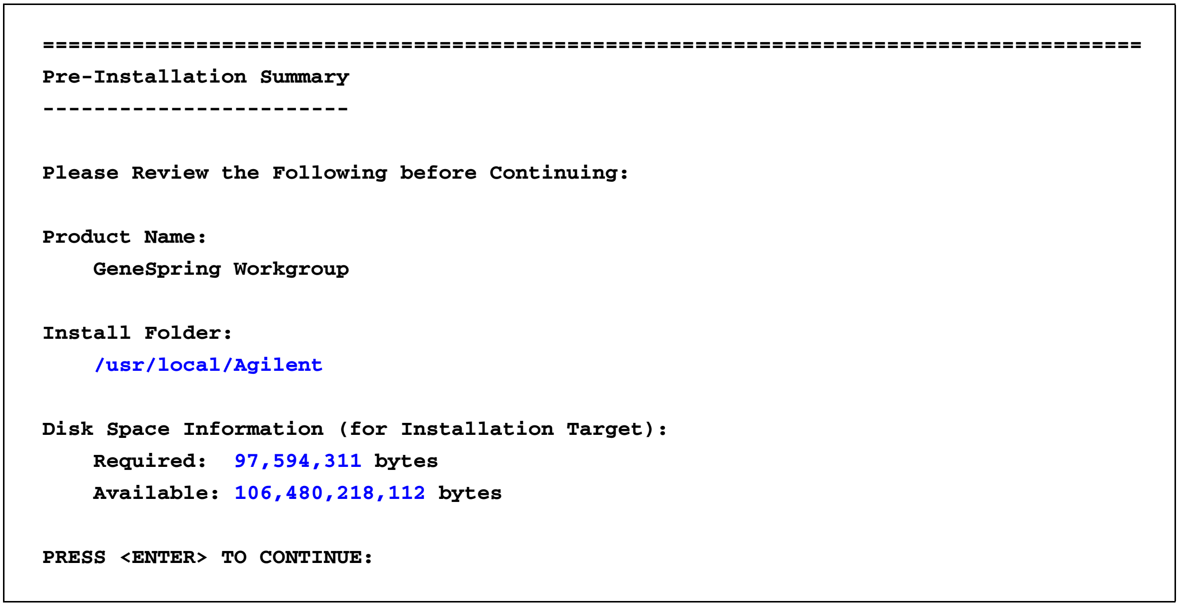
You may encounter a problem working with certain Yeast genomes if the JDBC driver on your system is earlier than 9.2.0.1. Agilent highly recommends that you download the latest JDBC driver from Oracle at:
http://www.oracle.com/technology/software/tech/java/sqlj_jdbc/index.html



```
Oracle JDBC driver file location
--------------------------------

Please specify the exact location and filename of the JDBC driver.

Driver: (DEFAULT:  ):
```

Figure 53 Oracle JDBC driver file location prompt (Oracle new installation only)

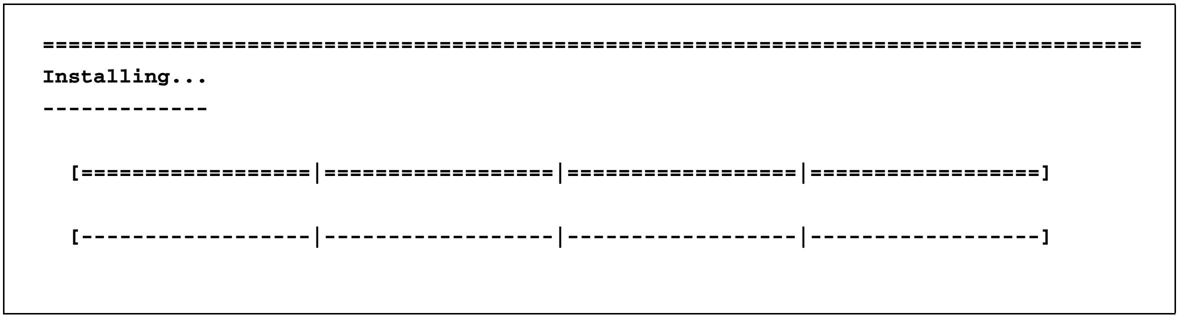
30 Type the name and path of the driver file and click **Next**. The Pre-Installation Summary dialog box appears.



```
=======================================================================================
Pre-Installation Summary
------------------------

Please Review the Following before Continuing:

Product Name:
    GeneSpring Workgroup

Install Folder:
    /usr/local/Agilent

Disk Space Information (for Installation Target):
    Required:  97,594,311 bytes
    Available: 106,480,218,112 bytes

PRESS <ENTER> TO CONTINUE:
```

Figure 54 Pre-Installation Summary dialog box

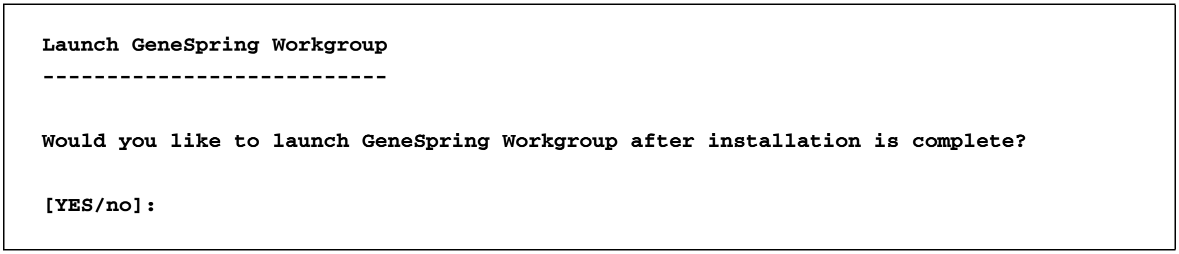
31 After you review the parameters listed in the dialog box, press **Enter**. Installation begins and the Installing... message box appears.



```
=======================================================================================
Installing...
-------------

  [==================|==================|==================|==================]

  [------------------|------------------|------------------|------------------]
```

Figure 55 Installing... message

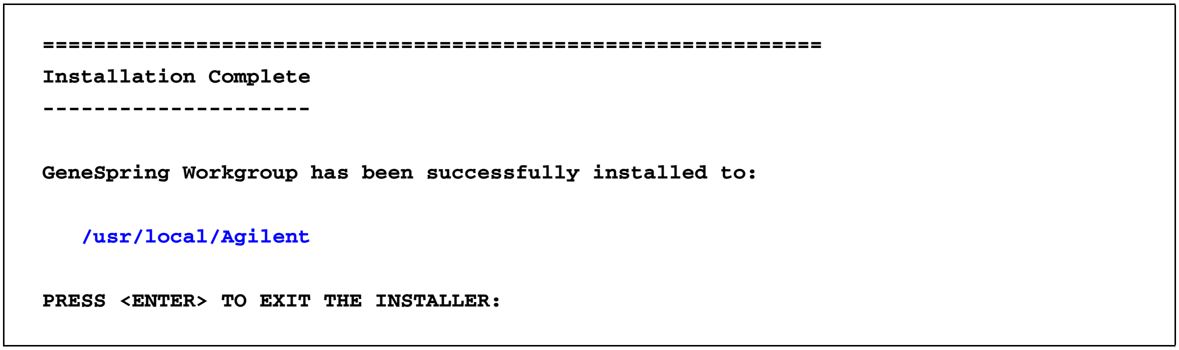
Dashes (“- - -”) are displayed as the GeneSpring Workgroup installs. After a few moments, the Launch GeneSpring Workgroup prompt appears:



```
Launch GeneSpring Workgroup
---------------------------

Would you like to launch GeneSpring Workgroup after installation is complete?

[YES/no]:
```

Figure 56 Launch GeneSpring Workgroup prompt

32 Decide whether you want to start the Workgroup after installation. Type **no** or accept the default and press **Enter**. After a brief interval, the Installation Complete prompt appears.



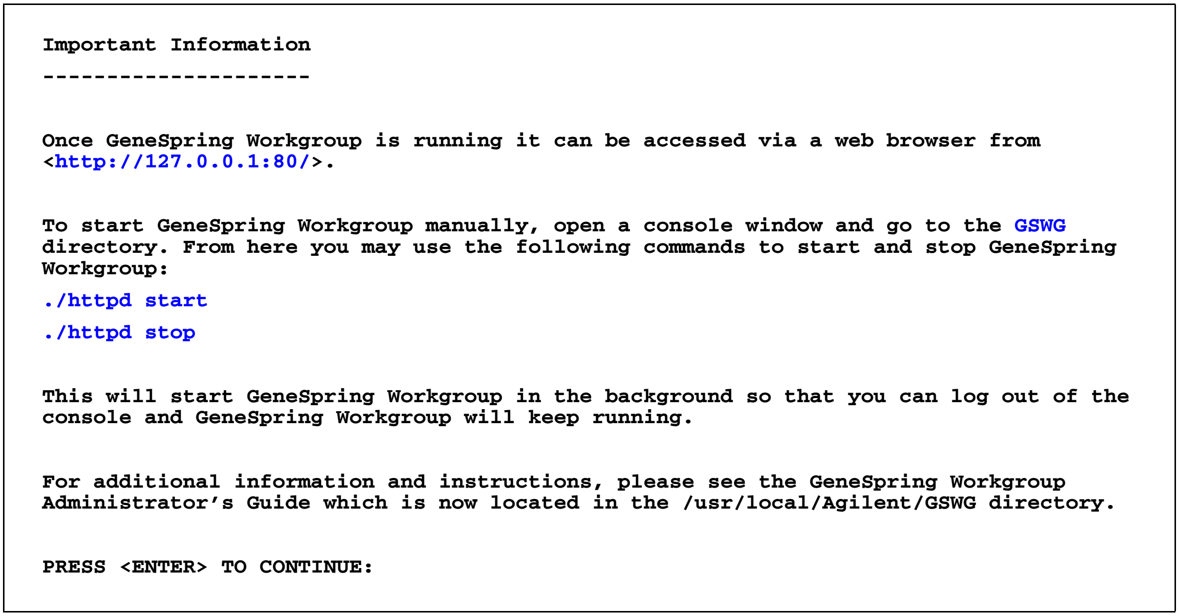
```
==============================================================
Installation Complete
---------------------

GeneSpring Workgroup has been successfully installed to:

   /usr/local/Agilent

PRESS <ENTER> TO EXIT THE INSTALLER:
```

Figure 57 Installation Complete prompt

If a warning or error message appears, you can review the file <Install directory>\ GSWG5_2_InstallLog. xml. You can view this XML file in a web browser.

If, after reviewing this file, you have questions or concerns, contact Agilent support.

33 Press **Enter**. The Important Information prompt appears.



```
Important Information
---------------------


Once GeneSpring Workgroup is running it can be accessed via a web browser from
<http://127.0.0.1:80/>.


To start GeneSpring Workgroup manually, open a console window and go to the GSWG
directory. From here you may use the following commands to start and stop GeneSpring
Workgroup:
./httpd start
./httpd stop


This will start GeneSpring Workgroup in the background so that you can log out of the
console and GeneSpring Workgroup will keep running.


For additional information and instructions, please see the GeneSpring Workgroup
Administrator's Guide which is now located in the /usr/local/Agilent/GSWG directory.


PRESS <ENTER> TO CONTINUE:
```

Figure 58 Important Information prompt

Read what is displayed on this screen and, if necessary, take notes for future reference.

34 Press **Enter**.

You have finished installing GeneSpring Workgroup.

GeneSpring Workgroup Address URLs and Aliases Configuration

You can configure your Genespring Workgroup to allow users to access it using the machine name, the IP address, or both. You can also add multiple aliases. For example, you could set up the web server so that all of the following addresses point to the same Workgroup:

- 192.168.123.153
- genomes.example.com
- Agilent.example.com

By default, the web server uses the DNS name or IP address that you specified during installation.

NOTE If you are using SSL (Secure Sockets Layer), you must configure the web server with a hostname, not an IP address. See "To configure GeneSpring Workgroup for Secure Sockets Layer (SSL)" on page 59 for more information on SSL configuration.

To configure GeneSpring Workgroup to use an IP address only

1. Open the configuration file *<Install directory>/Agilent/tomcat/conf/server.xml* in a text editor.
2. In the **<Host>** tag, enter the IP address of the GeneSpring Workgroup. The tag should look like the following: **<Host name="192.168.123.153" debug="0" appBase= "webapps" unpackWARs="true" autoDeploy="true">**

NOTE The address you enter here, whether it is an IP address or a DNS name, must match the one you entered for the Workgroup preference in the **WorkgroupPreferences** file. See "Agilent Server and Remote Server Preferences" in the *GeneSpring Workgroup User Guide* for more information on setting preferences in WorkgroupPreferences.

3. Save your changes and restart the Workgroup.

In Windows, you can either restart the GeneSpring Workgroup service or select *Start > All Programs > Agilent > Stop Workgroup Server*. On Linux, navigate to the main GeneSpring Workgroup directory and issue the following command: `% ./httpd restart`

To configure GeneSpring Workgroup to use multiple IP or DNS names

To enable users to access the GeneSpring Workgroup using either the IP address or hostname, add another line to the **server. xml** file to allow for both, as follows:

1 Open *<Install directory>/Agilent/tomcat/conf/server.xml* in a text editor.

2 Immediately after the **<Host>** tag, add one or more additional lines to specify the desired aliases. These lines should include beginning **<Alias>** and ending **</Alias>** tags. The following is an example of this type of configuration:

```
<Host name="192.168.123.153" debug="0" appBase="webapps"
unpackWARs="true" autoDeploy="true">

<Alias> genomes . example. com</Alias>

<Alias>Agilent . example. com</Alias>

...

</Host>
```

The GeneSpring Workgroup in the example above could be reached using http://192.168.123.153, http://genomes.example.com, or http://Agilent.example.com.

3 Save your changes and restart the GeneSpring Workgroup.

In Windows, you can either restart the GeneSpring Workgroup service or click **Start > All Programs > Agilent > Stop Agilent**. On Linux, navigate to the main GeneSpring Workgroup directory and issue the command:

```
% ./httpd restart
```

To configure GeneSpring Workgroup memory settings

If GeneSpring Workgroup does not start (in Windows) or its performance is sub-optimal (in Linux), check the memory settings. Usually, the memory should be set slightly lower than the total amount of physical memory available on the GeneSpring Workgroup.

NOTE

Note that the memory reserved for GeneSpring Workgroup must be greater than the memory setting in the **WorkgroupPreferences** file (for more information, see the *Agilent Workgroup Server Administration Guide*). For Windows systems, the GeneSpring Workgroup memory setting must be set to less than 2 GB, regardless of the physical amount of memory available.

To change the memory settings in Windows

1. Open **agilent.bat** in Notepad or another text editor. This file is located in ***Install directory/*****Agilent**. On Windows, this is typically **C:\ Program Files\ Agilent\Agilent.**
2. The variable *CATALINA_OPTS* controls the allocation of memory for use by the GeneSpring Workgroup. Reset this value according to your system's configuration.

To change the memory settings in Linux

1. Open *httpd* in vi or another text editor. This file is located in ***Install directory/*****Agilent/**. On Linux, this is typically **/usr/local/Agilent/**.
2. The variable *CATALINA_OPTS* controls the allocation of memory for use by the GeneSpring Workgroup. Reset this value according to your system configuration

To change the Default Port Number

If you are running a web server on your system and port 80 is already in use, the default port number used by the GeneSpring Workgroup must be changed in two locations. Use the following procedure for all systems.

1. Open the **WorkroupPreferences** file located in ***Install Directory*/Agilent/admin** using a text editor.
2. Locate the following line:

   PortNumber : 80
3. Change **80** to the desired port number. For example, to use port **8888**, change the line to read:

   PortNumber : 8888
4. Save your changes.
5. Open the *server.xml* file located in *<Install Directory>\Agilent\tomcat\conf.*
6. Search for the string **80**. Under the "Connectors" section you will find the following:

   <Connector className="org.apache.coyote.tomcat4 . CoyoteConnector" port="80" minProcessors="5" maxProcessors="50">

   Change **80** to the same number you used to change preferences file. For example, if you used port **8888**, change the line to read:

   <Connector className="org.apache.coyote.tomcat4 . CoyoteConnector" port="8888" minProcessors="5" maxProcessors="50">
7. Save your changes and restart your GeneSpring Workgroup.

   In Windows, you can either restart the GeneSpring Workgroup service or click **Start > All Programs -> Agilent > Start Agilent**. On Linux, navigate to the main GeneSpring Workgroup directory and issue the command:

   ```
   % ./httpd restart
   ```

To change GeneSpring Workgroup Ownership in Linux or Solaris

You can change the ownership of GeneSpring Workgroup files to allow the program to be run as a user other than root.

NOTE Before you make this change, you must have started GeneSpring Workgroup as root at least once.

After running once as root, you will need to change GeneSpring Workgroup's default port to one higher than 1024. To change the port, see “To change the Default Port Number” on page 58.

After you change the default port, take the following steps to change GeneSpring Workgroup ownership:

1. If you have not done so already, create the user and group that you want to own and run GeneSpring Workgroup. For details on creating users and groups, see "Managing Users and Groups" in the *GeneSpring User Guide*. For our example, we will use *joe* as the user and *GeneSpring Workgroup* as the group.
2. As root, stop GeneSpring Workgroup.
3. In the top-level directory, above the Agilent directory, run the following command:

```
chown -R joe:agilent
```

NOTE Take the above step only if GeneSpring Workgroup is the only program running under the Agilent directory.

---

4. Log out as root and log in again, but as the user to whom you assigned ownership. You should now be able to stop and start GeneSpring Workgroup as this user. In the future,this user should also be able to upgrade the GeneSpring Workgroup.

To configure GeneSpring Workgroup for Secure Sockets Layer (SSL)

GeneSpring Workgroup supports Secure Sockets Layer (SSL) authentication to ensure that data that passes between GeneSpring Workgroup and the client remains private. SSL uses public key cryptography, which is based on key pairs. Key pairs contain one public key and one private key. If data is encrypted with one key, it can be decrypted only with the other key of the pair.

This property is fundamental to establishing trust and privacy in transactions. For example, using SSL, the server computes a value and encrypts the value using its private key. The encrypted value is called a digital signature. The client decrypts the encrypted value using the server's public key and compares the value to its own computed value. If the two values match, the client can trust that the signature is authentic because only the private key could have been used to produce such a signature.

Digital certificates are used with the HTTPS protocol to authenticate Web clients. The HTTPS service of most Web servers will not run unless a digital certificate has been installed. Use the procedure outlined here to set up a digital certificate that your Web server can use to enable SSL.

Keytool can be used to set up a digital certificate. It is a key and certificate management utility that ships with most Java SDKs. It enables users to administer their own public/private key pairs and associated certificates for use in self-authentication, or data integrity and authentication services using digital signatures. Self-authentication is a process where the user authenticates himself or herself to other users or services. Keytool also allows users to cache the public keys of their communicating peers in the form of certificates.

To configure GeneSpring Workgroup to take advantage of SSL, take the following steps. Note that you need to set and use the following variables:

<*Hostname*> – the machine hostname for GeneSpring Workgroup server.

To find the hostname in Windows go to *Start > Control Panel > System > Computer Name > Full Computer Name*. If GeneSpring Workgroup is going to be accessed outside of a firewall, include the domain as part of the hostname.

<*JavaPath*> – the path to your Java runtime environment.

<*KeystorePath*> – the path and filename of your keystore file. In the example below, it is defined as *C:\ Program Files\ Agilent\ Agilent\admin\mykeystore*

<*CertificatePath*> – the path and filename of your generated certificate file.

JAVA_HOME – This variable is typically set to *< Install directory>\ Agilent\ Sig-net\ jre*

1. Set up SSL in your GeneSpring Workgroup preferences file.

   Open the GeneSpring Workgroup preferences file (***Install directory*>/Agilent/admin/WorkgroupPreferences**) in a text editor and set the following values:

   ```
   UseHostName : true
   Address: <hostname>
   UseSSL : true
   PortNumber: 8443
   ```

   If any of these lines don't exist, simply add them anywhere in the file.

   Using SSL requires the use of a hostname, not an IP address. The Java security code checks your computer's hostname against the name in the certificate and they must match. The port number, 8443, was chosen because 443 is the normal port for SSL but to run GeneSpring Workgroup as a user other than root on a Linux computer the port number must be higher than 1024.

2. Create or uncomment the SSL connector element in *server.xml*. Open ***Install Directory*\Agilent\tomcat\conf\ server.xml** in a text editor and make sure the following entries appear and are uncommented. (Items in XML are commented with "<!--" and "-->" delimiters.)

   The first connector tag sets up a non-SSL (HTTP) port. The second connector tag sets up an SSL (HTTPS) port. The comments in parentheses should not appear in the actual XML entries.

```
<!-- Define a non-SSL Coyote HTTP/1.1 Connector on port 80 -->
<Connector
     className="org.apache.coyote.tomcat4 .CoyoteConnector"
     port="80"
     minProcessors="5"
     maxProcessors="50"
     enableLookups="true"
     redirectPort="8443"
     acceptCount="100"
     debug=" 0"
     connectionTimeout="20000" (set to -1 to disable)
     useURIValidationHack=" false"
     disableUploadTimeout="true" />
```

```
<!-- Define a non-SSL Coyote HTTP/1.1 Connector on port 8443 -->
<Connector
     className="org.apache.coyote.tomcat4 .CoyoteConnector"
     port="8443" (SSL port)
     minProcessors="5"
     maxProcessors="75"
     enableLookups="true"
     acceptCount="100"
     debug=" 0"
     scheme="https"
     secure="true"
     useURIValidationHack=" false"
     disableUploadTimeout="true" />
     <Factory
        className="org.apache.coyote.tomcat4
.CoyoteServerSocket-Factory"
        keystoreFile="C:\Program Files\Agilent\Agilent\admin\
            mykeystore" (same as <KeystorePath> variable)
        keystorePass="changeit"
        clientAuth=" false"
        protocol="TLS" />

</Connector>
```

3 Create your own key in the <**KeystorePath**> file using the keytool utility.

```
<JavaPath>\bin\keytool -genkey -alias tomcat -keyalg RSA
-keystore <KeystorePath>
```

When prompted for a password, use *change it*. By default, this password is what the utility expects, but you are free to use a different one that you have set in server . xml (see Step 2).

When you run this command you are asked a number of questions regarding you and your organization.

4 When you are asked:

What is your first and last name?

You must enter your computer's hostname.

5 Self-certify your key for a desired number of days (optional).

Optionally, you can use the keytool utility to self-certify your key for a number of days, in this case, 720.

```
<JavaPath>\bin\keytool -selfcert -alias tomcat -validity
720 - keystore <KeystorePath>
```

When prompted for a password, use *"changeit"*.

6 Stop and restart GeneSpring Workgroup.

7 Connect to GeneSpring Workgroup server using a browser.

Launch your browser and connect using https://<hostname> : 8443.

8 In Windows, a Security Alert dialog box appears the first time you access the server. Click **View Certificate** and follow the directions for installing the certificate you created into a trusted store.

To see your certificate listed in Internet Explorer, click **Tools > Internet Options > Content > Certificates > Trusted Root Certificate Authorites**.

Reference

System Requirements

After you purchase an Agilent GeneSpring Workgroup license, an Agilent representative will contact you to discuss your site’s anticipated usage and future growth, and make a hardware recommendation that supports your site’s current and anticipated needs. When your hardware is in place, a representative will visit your site to install the application or talk-you-through the installation process over the telephone using this guide. Agilent recomends that you have an Information Technology (IT) professional perform this installation.

Supported Installations

Currently, there are three supported installations.

- Windows. To install Workgroup on Windows systems, see “To install and configure on Windows systems” on page 12.
- Linux/Solaris GUI. To install Workgroup on Solaris and Linux systems using a Graphical User Interface GUI), see “To install and configure on Linux/Solaris systems (GUI)” on page 36.
- Linux/Solaris (Non-GUI). To install Workbench on Solaris and Linux systems without using a GUI, see “To install and configure on Linux/Solaris systems (non-GUI)” on page 37.

The following are the ideal and minimum configurations required for installing the Workbench on GeneSpring and on Oracle servers:

GeneSpring Server - recommended configuration

- Quad processor system (1.6 GHz Xeon MP)
- 3-4 GB RAM
- 60 GB SCSI HDD
- Valid static IP address
- Modern video card (the more memory and power, the faster graphs will be drawn)
- 1 GB dedicated connection between GeneSpring and Oracle

GeneSpring Server - Minimum requirements

- Dual processor system (Pentium IV or better)
- 2-3 GB RAM
- 40 GB HDD
- Valid static IP address
- Modern video card (the more memory and power, the faster graphs will be drawn)
- 100 MB connection between GeneSpring and Oracle

Oracle Server

- Oracle version 8i or 9i
- Dual processor system (2.0 GHz or above Pentium IV)
- 2 GB RAM
- At least 200 GB RAID storage

NOTE

For performance reasons, Agilent recommends that you do not run GeneSpring and Oracle server on the same computer.

Remote Server - Hardware

- 1 GB RAM (2 recommended)
- Pentium III or comparable processor (The RemoteServer application will take advantage of multiple processors to improve performance.)
- 1 GB disk space
- Network connection
- Static IP address

Remote Server - Software

- Windows 2000, XP, Server 2003
- Red Hat Linux Enterprise Version 3.0, Solaris 8 or 9

The actual amount of memory, storage, and speed required for optimum performance is closely related to the type and complexity of the jobs you intend to execute remotely.

The optimal configuration is a rack of Linux machines each running Remote Server. Having your GeneSpring Workgroup in this rack may also improve results. For performance reasons, Agilent recommends that you not run Remote Server on the same computer that is also running the Workgroup or GeneSpring, or running two RemoteServer applications on the same computer.

About the Tomcat Web Server

The Tomcat web server is another components installed with GeneSpring Workgroup. Tomcat is a free, open-source implementation of Java Servlet and JavaServer Pages technologies developed under the Jakarta project at the Apache Software Foundation. The GeneSpring and Tomcat applications are bundled together as unified server application.

During installation, all files related to the Tomcat application are placed in their own folder: *<Install directory>/ Agilent/tomcat*. You need to be aware of this is because the */tomcat/conf/server.xml* file is also used to set various configurations such as IP addresses, DNS names, port numbers and more. See "GeneSpring Workgroup Address URLs and Aliases Configuration" on page 55 for information on using *server. xml.*

Configuration, Log, and Batch Files

During installation, several configuration, log, and batch files are placed in various directories. This is a list of these files, their significance, and where they are located.

Server.xml

This XML text file contains configurations for the Tomcat web server such as IP addresses, DNS names, and port numbers. See "GeneSpring Workgroup Address URLs and Aliases Configuration" on page 55 for information on using *server. xml.*

Location: *<Install directory>\GSWG\tomcat\conf\server.xml*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\tomcat\conf\server.xml*

On Linux, this is typically */usr/local/Agilent/tomcat/conf/ server.xml*

WorkgroupPreferences

This text file contains preferences for your GeneSpring Workgroup application in the following categories: General, Database, Appearance, Custom HTML, Proxy Server, Remote Server, and MetaMine.

Location: ***Install directory*\GSWG\admin\WorkgroupPreferences**

On Windows, this is typically **C:\Program Files\Agilent\admin\WorkgroupPreferences.**

On Linux, this is typically **/usr/local/Agilent/ admin/WorkgroupPreferences.**

LicenseKey.txt

This text file contains GeneSpring Workgroup license information and must be obtained directly from Agilent. It is supplied separately from the application installation program. During installation, you will be required to specify the location of this file. If you do not specify the location, you will get an error message when you try to access the GeneSpring Workgroup. ***Do not alter the contents of this file in any way.***

Location: You specify this during installation.

install-service.bat

During installation, you can choose whether you want the Workgroup to run as a Windows service. If you choose not to, but change your mind at a later time, you can run *install-service .bat*.

Location: *<Install directory>\Agilent\install-service.bat*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\ install-service .bat*

uninstall-service.bat

During installation, you can choose whether you want the Workgroup to run as a Windows service. If you choose to, but change your mind at a later time, you can run uninstall-service .bat.

Location: *<Install directory>\GSWG\uninstall-service.bat*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\uninstall-service .bat*

agilent.bat

You can use this file after installation to change the memory settings in Windows.

Location: *<Install directory>\Agilent\agilent.bat*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\ agilent .bat*

httpd

You can use this file after installation to change the memory settings in Linux or Solaris.

Location: *<Install directory>/Agilent/httpd*

On Linux, this is typically */usr/local/Agilent/httpd*

Agilent_5.2_InstallLog.xml

This is an XML file that contains GeneSpring Workgroup installation warning and error messages. The file can be viewed using a web browser. If you have trouble reading this file, or have concerns or questions, contact Agilent support.

Location: *<Install directory>\Agilent\Agilent_5.0_InstallLog.xml*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\ GeneSpring_Workgroup_InstallLog.xml*

On Linux, this is typically */usr/local/Agilent/logs/Agilent_5 . 0_InstallLog. xml*

AgilentLog.txt

This file tracks users who access the Workgroup — who, when, and what they did. The name and location of this file can be set in the **WorkgroupPreferences** file with the **WorkgroupLogFilename** preference. See the *GeneSpring Workgroup User Guide* for more information on configuring Workgroup preferences.

Location: ***Install directory*\Agilent\logs\GSWGLog.txt**

On Windows, this is typically **C:\Program Files\Agilent\GSWG\logs\ AgilentLog.txt.**

On Linux, this is typically **/usr/local/Agilent/ logs/GSWGLog.txt**.

AgilentDebug.txt

This file stores debugging information. The name and location of this file can be set in the **WorkgroupPreferences** file with the **WorkgroupDebugFilename** preference. See the *Agilent GeneSpring Workroup Server Administration Guide* for more information on Workgroup preferences.

Location: *Install directory*\Agilent\logs\GSWGDebug.txt

On Windows, this is typically **C:\Program Files\Agilent\GSWG\logs\GSWGDebug.txt.**

On Linux, this is typically **/usr/local/Agilent/ logs/ GSWDebug.txt.**

permission.txt

This file keeps track of which users and groups have access to certain directories. ***Please do not try to edit this file manually.*** Instead, log in as administrator and use the admin tool.

The name and location of this file can be set in the **WorkgroupPreferences** file with the **WorkgroupPermissionsFilename** preference. See the *Agilent GeneSpring Workroup Server Administration Guide* for more information on Workgroup preferences.

Location: *<Install directory>\Agilent\admin\permission.txt*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\admin\permission.txt*

On Linux, this is typically */usr/local/Agilent/admin/ permission.txt*

password .txt

This file stores usernames and passwords. GeneSpring Workgroup Oracle installations do not use this file but, instead, store password information in the database. ***Please do not try to edit this file manually.*** Instead, log in as the administrator and use the admin tool.

The name and location of this file can be set in the **WorkgroupPreferences** file with the **WorkgroupPasswordFilename** preference. See the *Agilent GeneSpring Workroup Server Administration Guide* for more information on Workgroup preferences.

Location: *<Install directory>\Agilent\admin\password.txt*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\admin\password.txt*

On Linux, this is typically */usr/local/Agilent/ admin/password.txt*

group.txt

This file keeps track of user groups. ***Please do not try to edit this file manually.*** Instead, log in as the administrator and use the admin tool.

The name and location of this file can be set in the **WorkgroupPreferences** file with the **WorkgroupPasswordFilename** preference. See the *Agilent GeneSpring Workroup Server Administration Guide* for more information on Workgroup preferences.

Location: *<Install directory>\Agilent\admin\group.txt*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\admin\group.txt*

On Linux, this is typically */usr/local/Agilent/admin/ group.txt*

GeNetTables.sql

You can customize the script that creates the Oracle tables for GeneSpring Workgroup to meet your specific needs. This script is called GeNetTables.sql and is located in the <Install directory>\Agilent\docs folder. The GeNetTables.sql script is run automatically when Agilent starts and discovers that there is no existing schema in the database for Agilent.

Location: *<Install directory>\Agilent\docs\GeNetTables.sql*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\docs\GeNetTables.sql*

On Linux, this is typically */usr/local/Agilent/ docs/GeNetTables.sql*

SVdownload.html

This HTML file holds the links for end-user downloads. It is accessible from the GeneSpring Workgroup login page. This file is principally used to hold a link for downloading GeneSpring Viewer and GeneSpring Viewer upgrades, but can also be used to hold other links.

Location: *<Install directory>\Agilent\docs\SVdownload.html*

On Windows, this is typically *C:\Program Files\Agilent\GSWG\docs\SVdownload.html*

On Linux, this is typically */usr/local/Agilent/ docs/SVdownload. html*

2

Remote Server Installation

GeneSpring Workgroup RemoteServer is a utility that lets you manage system resources for maximum efficiency. GeneSpring Workgroup users can use RemoteServer to send resource-intensive tasks to other machines. The results can be interpreted in GeneSpring, published to the Workgroup, or both.

GeneSpring Workgroup acts as a dispatcher that distributes jobs to available remote servers. To be available, a remote server must be running the RemoteServer application and have an entry in the Workgroup’s Preferences file (the Script-ServerAddress preference). Once a job has been sent, an administrator can view and manage its execution from either GeneSpring or the Workgroup. See the Workgroup Administrator's Guide for more information.

System requirements

This section lists RemoteServers system requirements on the supported platforms: Windows, Solaris, and Linux.

On Windows, Solaris, and non-IBM Linux, RemoteServer installation includes Sun JRE 1.4.2_09.

On IBM SuSE Linux Enterprise System 9.2, RemoteServer installation includes the IBM 1.4.2 64-bit JVM.

The following are *minimum* requirements for RemoteServer.

Windows systems

- Windows 2000, XP, or Server 2003
- 512 MB RAM (1 GB or more recommended)
- Pentium II processor (or equivalent)
- 1 GB disk space
- A JVM that supports JDK1.4 or later
- Access to a running GeneSpring Workgroup system
- The appropriate JDBC driver for each external database storing sample data, if using GeneSpring Workgroup Oracle or importing samples from an external SQL database

Unix-type systems

- Linux (Red Hat Enterprise Linux V3 or above), IBM Linux (Suse Linux Enterprise System 9.2 –SLES) or Solaris (versions 9 and 10 only)
- 512 MB RAM (1 GB or more recommended)
- 1 GB disk space
- A JVM that supports JDK1.4 or later
- Access to a running GeneSpring Workgroup system
- The appropriate JDBC driver for each external database storing sample data, if using GeneSpring Workgroup Oracle or importing samples from an external SQL database

NOTE

You can install multiple RemoteServers on the same machine, but each one has to be installed in a different directory and assigned a different port and assigned a different **Temp** directory.

The **WorkgroupPreferences** and **RemoteServer Preferences** files, which contain information about ports and other setup details, must be consistent. See "To edit the RemoteServer Preferences file" on page 86 for more information.

The RemoteServer installation installs the following items:

On Windows systems

- A **RemoteServer** icon on the desktop
- A **Stop RemoteServer** icon on the desktop
- The RemoteServer executable, **RemoteServer.jar**
- The **RemoteServer Preferences** file

On Unix and Linux systems

- **RemoteServer** script
- The RemoteServer executable, **RemoteServer.jar**
- The **RemoteServerPreferences** file

To upgrade the RemoteServer software

When you install a newer version of RemoteServer, you do not “upgrade” —you simply uninstall the previous version of RemoteServer, and then install the later version in the same directory.

The default paths for RemoteServer are as follows:

- Previous versions on Windows—**..\Program Files\Silicon Genetics\RemoteServer**
- 5.2 version on Windows—**..\Program Files\Agilent\RemoteServer**
- Previous versions on Unix-type system**s—/usr/local/Silicon Genetics/RemoteServer**
- 5.2 version on Unix-type systems—**/usr/local/Agilent/RemoteServer**

For information on uninstalling RemoteServer, see “To uninstall RemoteServer” on page 95.

1. Log in as a user with read/write privileges (such as **Administrator** on Windows systems).
2. Use **Add-Remove Programs** to remove the previous installation of RemoteServer software.
3. Contact your Agilent representative to acquire the latest RemoteServer installer.
4. Install RemoteServer in the same directory as the previous release. This might mean specifying a path different from the default (if the previous version was in a Silicon Genetics directory). See “To Install RemoteServer” on page 77.

To Install RemoteServer

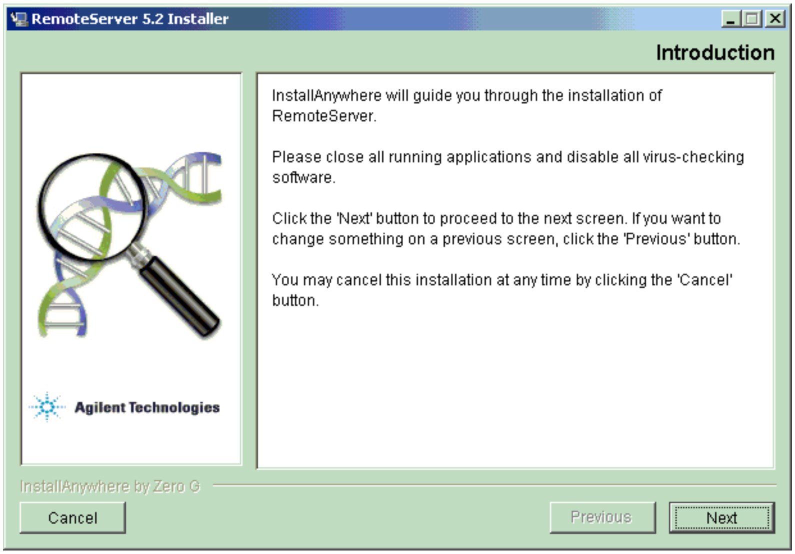
Contact your Agilent Application Engineer to obtain a RemoteServer installer.

The default destination directory is **Program Files\Agilent\RemoteServer** on Windows systems; **/usr/local/Agilent/RemoteServer** on Linux and Solaris.

Windows and Unix-type GUI installation

Follow the steps in this section *unless* you are installing on Unix-type systems from the command line.

1. Make sure you are logged on as a user with read/write privileges (such as **Administrator** on Windows systems).
2. Make sure your system meets the minimum requirements listed in "System requirements" on page 74.
3. Close all applications, and run the RemoteServer installer (for example, **RemoteServer5_2Installer**).
4. The installation program displays an introductory page. Click **Next**.



InstallAnywhere will guide you through the installation of RemoteServer.

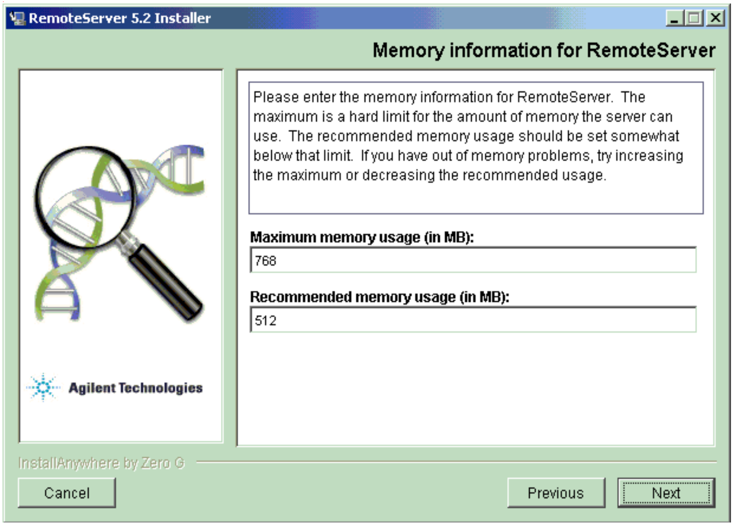
Please close all running applications and disable all virus-checking software.

Click the 'Next' button to proceed to the next screen. If you want to change something on a previous screen, click the 'Previous' button.

You may cancel this installation at any time by clicking the 'Cancel' button.

Figure 59 The introductory RemoteServer installation page.

5. Read the terms of the license agreement. Click **I accept...** or **I do not accept...** You must accept the terms of the license agreement in order to continue with installation.
6. Click **Next**.
7. Specify where the system should install the RemoteServer software on the Choose Install Folder page.
   - If this is a new installation (instead of an upgrade), Agilent recommends that you accept the default location (on Windows: **C:\Program Files\Agilent\RemoteServer.** On Solaris and Linux: **/usr/local/Agilent/RemoteServer**).
   - To specify a different location, click **Choose**.
   - If you are upgrading from a previous version of RemoteServer, click **Choose** and select the location where the previous version was installed.
   - To reinstate the default location, click **Restore Default Folder**.
8. Click **Next**.
9. In the Memory Information panel, make sure you have an appropriate amount of memory allocated for RemoteServer.



Please enter the memory information for RemoteServer. The maximum is a hard limit for the amount of memory the server can use. The recommended memory usage should be set somewhat below that limit. If you have out of memory problems, try increasing the maximum or decreasing the recommended usage.

Maximum memory usage (in MB): 768

Recommended memory usage (in MB): 512

Figure 60 The Memory Information page

- **a** Type the maximum amount of memory to allocate for this installation of RemoteServer in the **Maximum memory usage** field, and press **Enter**.

  This value should not exceed 2/3 of your machine's total memory, for all installations of RemoteServer on this machine.

- **b** Type the amount of memory to allocate for normal use of this installation of RemoteServer in the **Recommended memory usage** field, and press **Enter**.

  This value should not exceed 1/2 of your machine's total memory, for all installations of RemoteServer on this machine.

- **c** Click **Next**.

10 Specify the port on which RemoteServer listens for Workgroup Server requests.

Agilent recommends that you accept the default port, 6600, unless you have more than one installation of RemoteServer on the same machine.

If you have more than one installation of RemoteServer on the same Workgroup Server, you must specify a different port for each RemoteServer installation, and you must edit the WorkgroupPreferences file accordingly. See the *Workgroup Administration Guide*.

NOTE

It is the combination of IP address and port that needs to be unique.

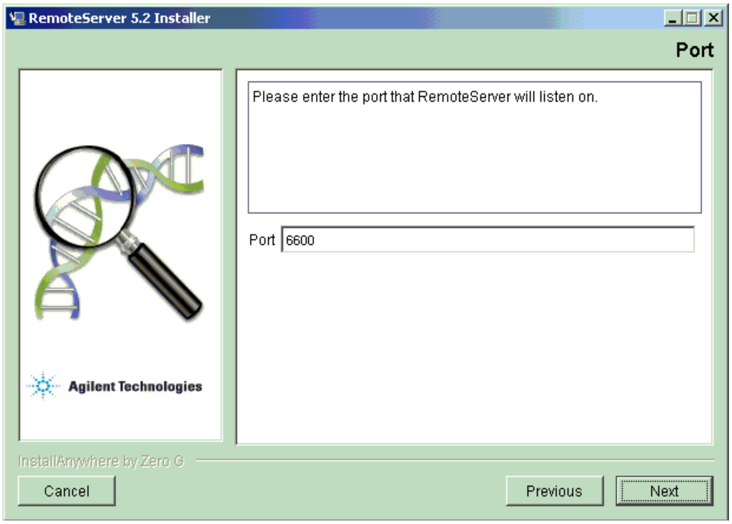
For example, if you install three copies of RemoteServer, each on a different server with a different IP address, they can all use the default port 6600.

In the WorkgroupPreferences file, it might look something like this:

192.6.7.64:6600

192.6.7.65:6600

192.6.7.66:6600



Please enter the port that RemoteServer will listen on.

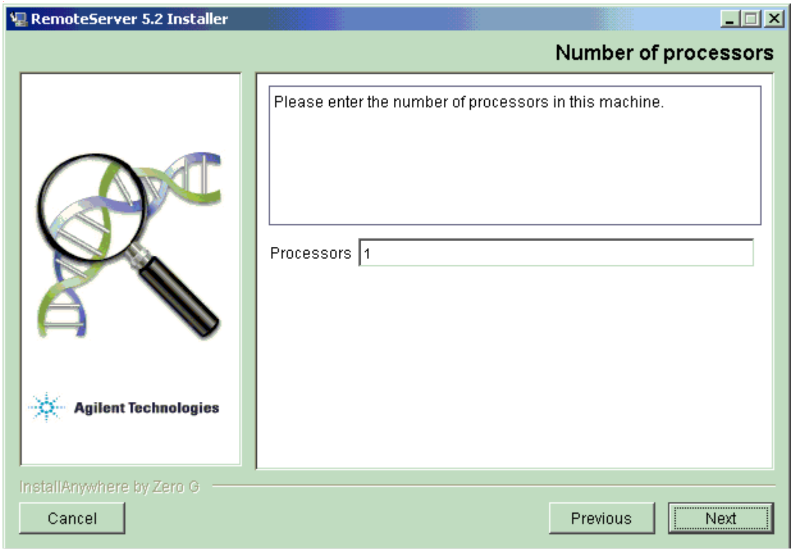
Port 6600

Figure 61 The Port page

Click **Next**.

11 Specify the number of processors on the machine where you are installing RemoteServer.

- Click **Next** to accept the default, **1.**
- If you are installing RemoteServer on a multi-processor machine, type the number of processors it has in the **Processors** text box, and click **Next**



Please enter the number of processors in this machine.

Processors 1

Figure 62 The Number of Processors page

12 Review the Pre-Installation Summary page.

Please Review the Following Before Continuing:

Product Name:
RemoteServer

Install Folder:
C:\Program Files\Agilent

Shortcut Folder:
C:\Documents and Settings\Administrator\Start Menu\Programs\Agilent

Java VM Installation Folder:
C:\Program Files\Agilent\rsjre

Disk Space Information (for Installation Target):
Required: 59,572,055 bytes

Figure 63 The Pre-Installation Summary page.

- If the information is correct, click **Install**.
- If the information is not correct, click **Previous** as many times as necessary and make the appropriate changes.

13. The installer displays the Launch RemoteServer 5.2 page.
    - To start RemoteServer as soon as the installation is complete, click **Yes**.
    - To complete installation without starting RemoteServer, click **No**.
14. After installing RemoteServer, the installer displays the Install Complete page. Click **Next**.
15. The Important Information page displays the Readme information. Read the page, and then click **Done.**

Unix-type command line installation

If you are installing RemoteServer on a Linux or Solaris system that does not support a GUI, or if you prefer not to use the GUI-based installer, follow the instructions below.

NOTE The installer names vary slightly between Solaris and Linux, so the installer is referred to in this section as <*installer_name*>.

---

1. Log on as **root.**
2. Check to make sure the installer file is executable. If not, then enter the following command:

   ```
   chmod +x RemoteServer<installer_name>
   ```

   for example:

   ```
   chmod +x RemoteServer5_2Installer.bin
   ```

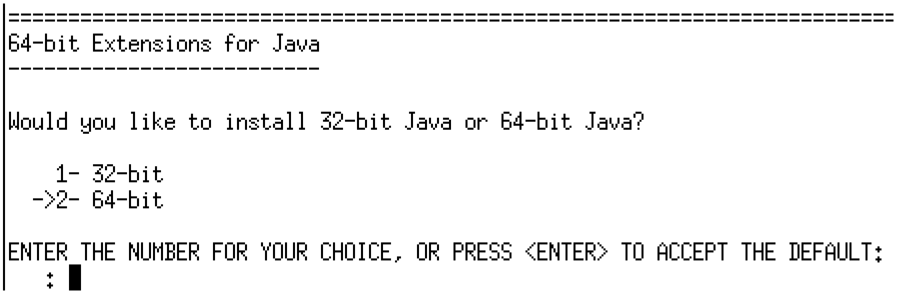
3. Enter the following command:

   ```
   ./RemoteServer<installer_name> -i console
   ```

   The system launches the installer.
4. When the installer displays the License Agreement, type **Y** to accept it or **N** to reject it, and press **Enter**. You must accept the license agreement in order to install RemoteServer.
5. The installer prompts you for an install directory location. Press **Enter** to accept the default location, or specify a different location.

6 On Solaris systems, the installer asks whether you want to use 64-bit Java or 32-bit Java.

Press **Enter** to accept the default (64-bit), or type **1** and press **Enter** to specify 32-bit Java.



```
===========================================================================
64-bit Extensions for Java
--------------------------

Would you like to install 32-bit Java or 64-bit Java?

    1- 32-bit
  ->2- 64-bit

ENTER THE NUMBER FOR YOUR CHOICE, OR PRESS <ENTER> TO ACCEPT THE DEFAULT:
   :
```

Figure 64 Java extensions prompt

7 The installer displays the **Max Memory** information. This value is the maximum amount of memory, in megabytes, that your machine will allocate for RemoteServer.

If you are running more than one installation of RemoteServer on the same machine, this value applies only to the installation you are currently installing. Set the **Max Memory** values for all RemoteServer installations on one server to approximately 2/3 of the server's total memory.

- Press **Enter** to accept the default, 768 MB.
- Type an integer value and press **Enter** to specify a different amount.

8 The installer displays the **Recommended Memory** information. This value is the amount of memory, in megabytes, that your machine will allocate for normal operation of RemoteServer.

If you are running more than one installation of RemoteServer on the same machine, this value applies only to the installation you are currently installing. Make sure the **Recommended Memory** values for all RemoteServer installations on one machine do not exceed 1/2 of the machine's total memory.

- Press **Enter** to accept the default, 512 MB.
- Type an integer value and press **Enter** to specify a different amount

9 The installer displays the port information.

This value identifies the port the RemoteServer application listens on for Workgroup Server requests.

Make sure this matches the port number configured for this remote server in the Workgroup Server's WorkgroupPreferences file (the ScriptServerAddress preference).

- Press **Enter** to accept the default, 6600.
- Type a valid port identifier to specify a different port.

NOTE

It is the combination of IP address and port that needs to be unique.

For example, if you install three copies of RemoteServer, each on a different server with a different IP address, they can all use the default port 6600.

In the Workgroup Preferences it might look something like this:

192.6.7.64:6600

192.6.7.65:6600

192.6.7.66:6600

---

10 The installer prompts for the number of processors your RemoteServer machine will use for RemoteServer.

- Press **Enter** to accept the default, **1.**
- If you are installing RemoteServer on a multi-processor machine, type the number of processors it has and press **Enter**.

11 The installer displays the pre-installation summary information.

- If all the information is correct, press **Enter** to install RemoteServer.
- If any information is incorrect, type `back` and press **Enter** until the installer displays the information you need to correct.

12 When installation is complete, the installer program displays a prompt, asking if you would like to start RemoteServer. Type **Y** or **N** and press **Enter**.

By default, the installer places:

- the RemoteServer program files in **usr/local/Agilent/RemoteServer**
- the **Uninstall** executable in **../RemoteServer/Uninstallerdata .**

13 When installation is complete, the installer displays the line:

PRESS <ENTER> TO EXIT THE INSTALLER

Press **Enter.**

The RemoteServer log

RemoteServer records its activity in a log file, with the default name **log.txt**.

On Windows systems, the default log file location is **Program Files\Agilent\RemoteServer\data\log.txt.**

On Unix-type systems, the default log file location is**/usr/local/Agilent/RemoteServer/data/log.txt.**

You can change the name and location of this file by editing the **RemoteServerPreferences** file. See "To edit the RemoteServer Preferences file" on page 86 for more information on configuring RemoteServer preferences.

To edit the RemoteServer Preferences file

If you have no more than one RemoteServer on your computer, and if you accepted all the defaults when you installed it, you do not have to edit the **RemoteServerPreferences** file.

The Workgroup Server and the RemoteServer application each have separate preferences files. When you edit the **RemoteServerPreferences** file, you must edit the corresponding fields in the **WorkgroupPreferences** file so that they are consistent. For information about the **WorkgroupPreferences** file, see “GeneSpring Workgroup Preferences" in the *GeneSpring Workgroup User Guide*.

These preferences apply if your GeneSpring Workgroup license supports at least one remote server. Settings for remote servers span two preferences files: **WorkgroupPreferences** and **RemoteServerPreferences**. The ScriptServerAddress entries in **WorkgroupPreferences** tell the Workgroup which remote servers are available (if it is running the RemoteServer application). See “GeneSpring Workgroup Preferences" in the *GeneSpring Workgroup User Guide* for more information on preferences. The remote server uses its own **RemoteServerPreferences** file to configure its RemoteServer application. Settings for **RemoteServerPreferences** are also described in *User Guide*.

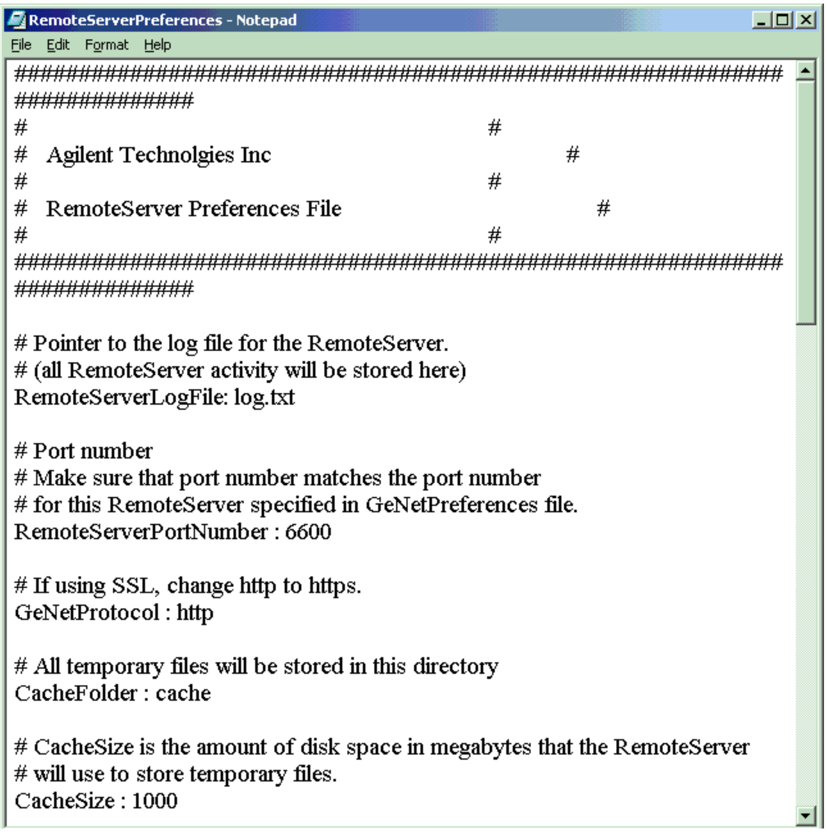
Do the following for each RemoteServer installation you have on any one machine. Each RemoteServer installation must have its own directory (including subdirectories).

NOTE

If there are multiple installations of remote server on a single machine:

- Each RemoteServer should be installed in a different directory.
- Each RemoteServer should use a different port number

If it is a Windows machine, each subsequent installation will overwrite the desktop icons and the Windows service created by the previous installation. On RemoteServers where the desktop icon is not available, run **Agilent\RemoteServer\data\RemoteServer.exe** and **Agilent\RemoteServer\data\RemoteServerStop.exe** respectively for starting and stopping



```
################################################################
###############
#                                       #
#   Agilent Technolgies Inc                     #
#                                       #
#   RemoteServer Preferences File                   #
#                                       #
################################################################
###############

# Pointer to the log file for the RemoteServer.
# (all RemoteServer activity will be stored here)
RemoteServerLogFile: log.txt

# Port number
# Make sure that port number matches the port number
# for this RemoteServer specified in GeNetPreferences file.
RemoteServerPortNumber : 6600

# If using SSL, change http to https.
GeNetProtocol : http

# All temporary files will be stored in this directory
CacheFolder : cache

# CacheSize is the amount of disk space in megabytes that the RemoteServer
# will use to store temporary files.
CacheSize : 1000
```

Figure 65 The RemoteServerPreferences file

1. Log on as Administrator (on Windows) or Root (on Solaris or Linux).
2. Using a text editor, open **RemoteServerPreferences.txt**. If you have more than one RemoteServer installation on this machine, navigate to the directory and preferences file that you want to change.

   By default, this file is in **Programs\Agilent\RemoteServer\data** on Windows systems, and **usr/local/Agilent/RemoteServer/data** on Unix-type systems.
3. Assign a port that is unique to this RemoteServer installation.

   If you only have one RemoteServer installed on this machine, *and* if the corresponding value in the **WorkgroupPreferences** file is set to the default value, you do not need to complete this step; you may retain the default value.

Change the value in RemoteServerPortNumber from 6600 to the port number you have assigned to this RemoteServer installation.

Make sure you edit the **WorkgroupPreferences** file to include the same port number as you have just set for RemoteServer. In the **WorkgroupPreferences** file, the field to change is called **ScriptServerAddress.**

4 If you have multiple RemoteServers installed on the same server, assign a temporary directory that is unique to this RemoteServer installation.

Change the value in **TempDirectory** to the temporary directory you have assigned to this RemoteServer installation.

5 When you have finished editing the RemoteServer and Workgroup preferences files, restart the Workgroup Server and RemoteServer.

If the machine on which you are installing RemoteServer has a firewall, contact Agilent Technical Support (see “To contact Agilent Technical Support” on page 96).

The following table lists the options in the **RemoteServerPreferences** file.

Table 1 RemoteServerPreferences

Option	Description	Default setting
• RemoteServerLogFile	Name of the RemoteServers log file. The log file is stored in the <**Install directory>/RemoteServer/data** directory.	**log.txt**
• RemoteServerPortNumber	The port the RemoteServer application listens on for Workgroup Server requests. Make sure this matches the port number configured for this remote server in the Workgroup Server’s **WorkgroupPreferences** file (the ScriptServerAddress preference).	6600
• GeNetProtocol	The protocol used for accessing Workgroup Server. If your system uses the Secure Sockets Layer (SSL), set this value to **HTTPS**.	HTTP

Table 1 RemoteServerPreferences

Option	Description	Default setting
• CacheFolder	Location of the RemoteServer cache folder within the RemoteServer directory. For example, on Windows: Program Files\Agilent\RemoteServer\data\cache	cache
• CacheSize	Size of the cache folder in megabytes.	1000
• MemorySize	The target memory size, in megabytes, used by the RemoteServer. If the total memory use exceeds the target, the RemoteServer unloads old data to free memory.	512
• NumProcessors	The number of processors on the RemoteServer machine.	1
• GUI	Specifies whether to display a GUI (graphic user interface) console. The console displays all information sent to the log file. Agilent recommends that you use the console for troubleshooting only, as it consumes resources and slows down the server somewhat. If you decide to enable the console, you can close it later without affecting the RemoteServer and logging functionality.	false
• TempDirectory	Changes the RemoteServer temp directory. This setting is only necessary if more than one RemoteServer installation exists on the same computer. If you specify a value here, it overrides the installation default.	This directory is not usually specified in the Preferences file, so the Preferences file contains no default for this value.
Proxy settings	if your site uses a proxy or firewall, you may need help from your network administrator to set these values.	

Table 1 RemoteServerPreferences

Option	Description	Default setting
• UseProxyFirewall	Specifies whether to use a firewall on the RemoteServer's JVM. Configure proxy settings only if **UseProxyFirewall** is **true**.	false
• UseProxyMimicry	Emulates a Netscape browser. Agilent recommends you accept the default setting.	false
• UseProxyPassword	Specifies whether to use a proxy password.	true
• ProxyAddress	Specifies the host address of the computer on which the firewall exists. This can be either a fully-qualified host name (for example, **hostname.domainname.com**) or an IP number.	myproxy.mycompany.com
• ProxyPort	Specifies the port on which to connect to the firewall host.	85
• ProxyUserName	The username to access the proxy server. This value must be a valid username accepted by the proxy server. This setting is ignored if **UseProxyFirewall** is **false**.	username

Table 1 RemoteServerPreferences

Option	Description	Default setting
• ProxyPassword	Specifies the password (corresponding to the **ProxyUserName** value) used to connect to the firewall host (if required) This value must be a valid password for accessing the proxy server This setting is ignored if **UseProxyFirewall** or **UseProxyPassword** is **false**.	password
• ProxyProtocol	Specifies the protocol used to communicate with the proxy server. Acceptable values are HTTP, SOCKS4, and SOCKS5.	HTTP

To start and stop RemoteServer

Windows systems

By default, RemoteServer is installed as a service.

- To start RemoteServer, double-click the **RemoteServer** shortcut icon created during installation.
- To stop RemoteServer, double-click the **Stop RemoteServer** icon.

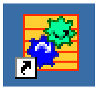


Figure 66 The **RemoteServer** icon (graphically similar to the **Stop RemoteServer** icon)

Unix-type systems

Invoke RemoteServer from the command line.

- To start RemoteServer: `./RemoteServer start`
- To stop RemoteServer: `./RemoteServer stop`
- To restart RemoteServer: `./RemoteServer restart`

When RemoteServer is running, you do not see any output to your monitor screen unless the GUI setting in the **RemoteServerPreferences** file is set to ***true***. If you need to check which computers are running RemoteServer, view the Workgroup’s Manage Remote Execution screen (**Utilities > Manage Remote Execution**), or see if the process is running on the actual remote server.

To use RemoteServer from GeneSpring Workgroup

The Workgroup’s Manage Remote Execution screen is similar to the GeneSpring RemoteServer Queue screen accessed from the GeneSpring **Tools** menu. In GeneSpring, you can create automatically executed scripts to distribute computationally intensive tasks to remote servers connected to the Workgroup. You can then monitor the progress of the scripts from GeneSpring or the Workgroup as they appear in the Remote Execution Queue screen.

- To access the Manage Remote Execution Queue in GeneSpring Workgroup, open the Utilities screen and click **Manage Remote Execution**. The Manage Remote Execution screen appears.
- To monitor the progress of a pending script, use the Remote Queue and click the **Refresh** button to update the queue.
- To modify the status of jobs that have been submitted to the queue, select the radio button to the left of the row that contains your job and choose one of the following options:
  - **Pause** – Temporarily halts a pending job
  - **Resume** – Restarts a paused job
  - **Delete** – Ends a job and removes it from the queue
  - **Refresh** – Updates the display to show the current status

To control and monitor RemoteServer jobs

GeneSpring Workgroup administrators can control how users use available remote servers. An administrator can view all jobs posted to a remote server, and pause or delete the jobs as desired. To shut down the RemoteServer application on a remote server, see "To start and stop RemoteServer" on page 92.

In addition to the buttons available to all users on the Manage Remote Execution screen, Workgroup administrators have access to two additional buttons:

Shutdown Remote Execution

- Click **Shutdown Remote Execution** to stop the RemoteServer from executing any new jobs, while allowing jobs currently running to continue to completion.
- Click **Start Remote Execution** to reverse this action. This button replaces the **Shutdown Remote Execution** button once its clicked. Clicking this button does not stop the RemoteServer application, but it does prevent the execution of any new jobs that a user sends.

Purge All Jobs

- Click **Purge All Jobs** to purge from the queue all jobs that have either finished or have not yet run. It does not cancel jobs that are currently-running. This action cannot be reversed.

To uninstall RemoteServer

To uninstall RemoteServer, do one of the following:

- On Windows: Double-click **UninstallerRemoteServer.exe,** located in the **..Agilent\RemoteServer\UninstallerData** directory.
- On Solaris and Linux: Run **Uninstall_RemoteServer,** located in the **../Agilent/RemoteServer/UninstallerData** directory.
- From the command line on Solaris and Linux, type the following command, and press **Enter**:

  ```
  ./ Uninstall_RemoteServer
  ```

NOTE The uninstall utility does not remove any files created after installation. You must manually delete any such files.

To contact Agilent Technical Support

Before calling Agilent Technical Support, refer to the RemoteServer section of the Workgroup Administrator's Guide.

If you need technical support, do any of the following:

- Contact Agilent at genespring_support@agilent.com.
- On your Web browser, go to www.agilent.com/chem/genespring and click **Submit a Support Request** at the bottom of the page.
- Call Agilent technical support at (866) SIG-SOFT (866-744-7638).

To expedite the support process, follow these steps:

Windows users

1. Start RemoteServer.
2. Take a screenshot of the splash screen, making sure to note:
    - the license serial number
    - the operating system
    - the current JVM that RemoteServer is using
3. Exit RemoteServer.
4. Check the log file (by default, **..\Program Files\RemoteServer\data\log.txt)** for any exceptions.

Solaris and Linux users

1. StartRemoteServer.
2. Take a screenshot of the splash screen, making sure to note:
    - the license serial number
    - the operating system
3. Exit RemoteServer.
4. Check the log file (by default, **/usr/local/Agilent/RemoteServer/data/log.txt)** for any exceptions.

3

Sample Loader Configuration

The Agilent GeneSpring Workgroup Sample Loader is an automated data importer for Workgroup Server, which is a genetic analysis software tool.

Sample Loader Requirements

Before you can run SampleLoader, Workgroup Server must already be installed, configured, and running. The following platforms are supported:

- Windows : 32 bit and JVM (All flavors of Windows are supported, but Windows XP is preferred.)
- Solaris: 32 or 64 bit and JVM)
- Linux Red Hat: 32 bit and JVM
- Linux Suze: IBM P Series: 64 bit and JVM
- Any of the above platforms (except IBM P Series): 32 bit and without JVM

The Java Virtual Machines (JVM) must support JDK1.4 or later.

All supported Linux or UNIX flavors can be installed either with a GUI, or remotely in "headless mode" (all text).

- Access to a running Workgroup Server is required,
- The appropriate JDBC driver for each external database storing sample data is required.

The SampleLoader distribution contains the following files, except for those that must be imported:

File	Description
Affy_GCOS_Publish.xml	Template to import data from GCOS database
GcdoAdminJava.dll	Necessary to import from GCOS database
GcdoAffyJava.dll	Necessary to import from GCOS database
GcdoAnalysisController.dll	Necessary to import from GCOS database
GcdoFSVCJava.dll	Necessary to import from GCOS database
GcdoImportJava.dll	Necessary to import from GCOS database
GcdoPublishJava.dll	Necessary to import from GCOS database
GcdoReportController.dll	Necessary to import from GCOS database
GCOS_RTL_Install-v1.3.exe	Intaller for GCOS runtime libraries for Windows
GCOSCELLoader.xml	Template to import CEL files from a GCOS database

File	Description
GCOSCHPLoader.xml	Template to import CHP files from a GCOS database
GCOSCoupling.jar	Necessary to import from GCOS database
GCOSSDK.jar	Necessary to import from GCOS database
load.sh	Run script for UNIX
SampleLoader.jar	Sample_Loader program file
SampleLoader.properties	Properties file for Sample_Loader
sl_affy_flatfile.xml	Template to import Affymetrix data from text files
sl_affy_gcos_oracle.xml	Template to import Affymetrix files from a GCOS database using Oracle queries
s1_affy_gcos_sqlserver.xml	Template to import Affymetrix from a GCOS database using SQL queries
sl_flatfile_db_attributes.xml	Template to import data and sample attributes from a database
sl_flatfile_imagene.xml	Template to import Imagene files
sl_flatfile_javaclass.xml	Template to import using a java class
sl_multi_db.xml	Template to import data from one database and sample attributes from a different database

To configure SampleLoader

1. Install GeneSpring Workgroup Server software. See "Workgroup Server Installation" on page 11.

   Sample Loader is automatically installed when you install the GeneSpring Workgroup server. SampleLoader cannot be installed in a separate operation but may be copied to another directory or computer if desired.

2. Log in as the user to run Sample Loader. You do not need to be the root user to run Sample Loader.
3. In the **SampleLoader** folder, open the Sample Loader .xml configuration file that best matches your data loading needs. See "Sample Loader Configuration Files" on page 103.
4. Edit the tags in this configuration file to match your needs.
5. Save and close the file.

To have SampleLoader output sent to an administrator, use the cron mailto command on Linux or UNIX systems.

For more information on configuring cron entries, enter man crontab at the Linux or UNIX command line.

To run Sample Loader

On UNIX systems, run SampleLoader from the shell script provided. On Windows systems, create a Desktop icon shortcut to simplify running SampleLoader.

1. In the shell script (**load.sh**) that invokes Sample Loader, check that the following command appears at the end of the script:

   ```
   $JAVA -classpath $CLASSPATH SampleLoader -config
   SampleLoader.xml
   ```

2. Append options as needed.
3. Type `./load.sh` and press **Enter** to run the shell script.

The following options are available:

Table 2 Command Line Options

Argument	Usage	Description
-config	-config *xmlConfigFilename*	Provides the filename of the XML configuration file for SampleLoader. This argument is required.
-login	-login *username*	Provides a login ID for Workgroup Server, overriding the login ID (if any) specified in the configuration file. This argument is optional.
-password	-password *password*	Provides a password for Workgroup Server, overriding the password (if any) specified in the configuration file. This argument is optional.
-owner	-owner *SampleOwnerName*	Provides a sample owner name for Workgroup Server, overriding the default sample owner name (if any) specified in the configuration file. This argument is optional.

Table 2 Command Line Options (continued)

Argument	Usage	Description
-sampleCount	-sampleCount n	Directs SampleLoader to load *n* (integer count) samples. If a sampleCount is not specified, Sample Loader loads all samples that meet the criteria defined in the configuration file. This argument is optional, and can be used to test connectivity by loading only one or a few samples. Using a count of 0 allows you to test connectivity without loading any data.
-version	-version	Displays the version of SampleLoader you are using (optional).

If you run SampleLoader with no arguments, a message appears similar to the following:

```
Thu Dec 19 18:26:03 PST 2002 SEVERE : SampleLoader: command line arguments:
-config xmlConfigFilename [-login loginName -password password] [-owner
sampleOwnerName] [-sampleCount n] [-version]
```

NOTE

Before running SampleLoader, verify that the XML configuration file is properly formatted. You can do this in most XML editors, or by opening the file in a web browser.

Sample Loader Configuration Files

This section describes the use of the SampleLoader configuration file. You must customize this file for your system before running SampleLoader. You can have any number of different configuration files.

Seven example XML files are included in the SampleLoader directory. Pick the one that most closely matches your data loading needs and modify the necessary tags. To edit any of these files, open them in a text editor and change settings as necessary.

The following sections describe the available configuration options and how to use them.

Tag References

This section contains a list of the tags used in the SampleLoader configuration file (*SampleLoader.xml*). The configuration file is in XML format and uses tags enclosed in angle brackets much like an HTML document.

In such a document, an element consists of a tag enclosed in angle brackets, and usually includes a closing tag. For example, the top-level element of this configuration file is the External Database Configuration element. This element consists of opening and closing tags, i.e.:

<ExternalDatabaseConfiguration>...</ExternalDatabaseConfiguration>.

An element's contents are tags or text nested between the current element's opening and closing tags. The following are examples of elements with contents:

<LoginInfo> <UserName>BioMan</UserName></LoginInfo>

In the above example, the <UserName> element (including its own contents and its closing tag) is the contents of the <LoginInfo> element. The username BioMan is the contents of the <UserName> element.

Attributes are values defined within the opening tag of the element itself. In the following example, name is an attribute, and “dbname” is the value of the <PhysicalDatabase> element:

<PhysicalDatabase name=”dbname”>

An element may have any number of attributes or contents. An empty element (an element that has attributes but no contents) can be closed within the opening tag by adding a slash at the end, i.e.,

<tag value="example" />.

Tag Reference Table

This table provides a list of all available tags for the SampleLoader configuration file. For more detailed information on the use of each tag, see "Element Details" on page 107.

The Element column lists each of the available tags. The Contents column lists the type of contents that tag can contain (i.e., plain text, or the names of the tags it can contain). The Attributes column lists the attributes that tag can contain.

Table 3 Tag reference table

Element	Contents	Attributes
<ExternalDatabaseConfiguration>	<GeneralConfiguration> <Database>	n/a
<GeneralConfiguration>	<LoadClass> <ProcessedDataListFile> <LoginInfo>	n/a
<Database>	<PhysicalDatabase> <TechnologyType> <Header> <GenomeNames> <GetSampleIDs> <GetSampleAttributes> <GetFile> <GetRawData> <GetSampleProjects>	name, icon
<LoadClass>	plain text	n/a
<ProcessedDataListFile>	plain text	n/a
<LoginInfo>	<UserName> <Password> <Address> <SampleOwner>	n/a

Table 3 Tag reference table (continued)

Element	Contents	Attributes
<PhysicalDatabase>	<UserName> <Password> <URL> <Prefetch>	name
<TechnologyType>	n/a	name
<Header>	<Author> <Research_Group> <Organization>	n/a
<GenomeNames>	<GenomeMappingSpec>	n/a
<UserName>	plain text	n/a
<Password>	plain text	n/a
<Address>	plain text	n/a
<SampleOwner>	plain text	n/a
<URL>	plain text	n/a
<Prefetch>	plain text	n/a
<Author>	plain text	n/a
<Research_Group>	plain text	n/a
<Organization>	plain text	n/a
<GetSampleIDs>	<DatabaseQuery> <DataDirectory> <FileNameMask> <IDFromFileName> <JavaQuery>	location
<GetSampleAttributes>	<DatabaseQuery> <JavaQuery>	cacheablenumeric
<GetFile>	<DatabaseQuery> <JavaQuery>	typelocationdeleteAfterwardsmimeType
<GetRawData>	<DatabaseQuery> <Format>	n/a

Table 3 Tag reference table (continued)

Element	Contents	Attributes
<GenomeMappingSpec>	n/a	targetNamesourceNamebaseDirectory
<DatabaseQuery>	SQL command	useGenomeName db
<DataDirectory>	plain text	n/a
<FileNameMask>	plain text	n/a
<IDFromFileName>	<RegexpMatch> <DatabaseQuery>	n/a
<RegexpMatch>	plain text	n/a>
<JavaQuery>	n/a	classextraArgs
<GetSampleProjects>	<FixedProject> <DatabaseQuery>	n/a
<FixedProject>	Project name	n/a
<DatabaseQuery>	SQL command	db

Element Details

<GetFile> Specifies parameters for retrieving associated files. This element has four attributes.

The “type” attribute specifies the type of file to be retrieved. This attribute is required, and is case-insensitive. There are seven possible values:

- Sample Image—a picture or pictures of the biological sample
- Array Image—a picture or pictures of the scanned array(s)
- CEL File—an Affymetrix CEL file (actually stored as a general attachment with MIME type application/x-AffyCELFile)
- Raw Data File—a raw data file or files
- Signal Raw Data File—a raw signal data file or files (Imagene only)
- Control Raw Data File—a raw control data file or files (Imagene only)
- Attachment—a general attachment

The “Signal Raw Data File” and “Control Raw Data File” attributes are provided for Imagene users. Use these tags to pair your files, using <MakeLocation> once for each file. For example:

```
<GetFile type="signal raw data file" location="file"> <MakeLocation
prefix="/raw data files/data_" suffix="_Cy3.txt"/></GetFile><GetFile
type="control raw data file" location="file"> <MakeLocation prefix="/raw
data files/data_" suffix="_Cy5*.txt"/></GetFile>
```

where the files are something like data_1001_Cy3_xxxx.txt and data_1001_Cy5_yyyy.txt.

The “location” attribute specifies the location of the files to be retrieved. This attribute is required, and is case-insensitive. There are four possible values:

- database—returns the contents of the file (typically a blob)
- file—returns a file pathname
- URL—returns a URL
- java—returns com.siGenetics.ext.database.getFile

The “deleteAfterwards” attribute specifies whether to delete the file once it has been uploaded to Workgroup Server. Accepted values are “true” and “false”. This attribute applies only if the “location” attribute is set to “file”. This attribute is optional. If not specified, its value defaults to “false”.

The “mimeType” attribute specifies the MIME type of the file or files being retrieved. Any valid MIME type is an acceptable value. This attribute is optional.

Contents: <DatabaseQuery>, **<JavaQuery> <Preprocessor>**

Attributes: type, location, deleteAfterwards, mimeType

Usage: <GetFile type=”Sample Image” location=”database” deleteAfterwards=”true” mimeType=”image/gif”>...</GetFile>

<GetFiletype=”Raw Data File” location=”Java”>

<JavaQuery>

class=”com.sigenetics.plugins.affy.GCOSRawCELFileLoader”

extraArgs=”myGCOSdbHost.mycompany.com” />

</GetFile>

Notes: Optional. Required if retrieving data from an Affymetrix GCOS process database, in which case the second form shown above must be used.

<MakeLocation> This option specifies the location of data not kept in a database, i.e., a file or a URL. This is done by building a path from a prefix, sample identifier, and suffix. For example:

<GetFile type = "Sample Image" location="file" mimeType="image/gif"> <MakeLocation prefix="/fred/chip" suffix="*.gif"/></GetFile>

If the location is a file, and the file pathnames obtained here do not start with an absolute path, the baseDirectory attribute of the <GenomeMappingSpec> section is prefixed (i.e., <GenomeMappingSpec baseDirectory=”filepathname”>). If the resulting pathname still does not start with an absolute path, it is assumed to be relative pathname to the current user directory (usually the one where program started).

Contents: n/a

Attributes: prefix, suffix

Usage:

<MakeLocation prefix=”directory_path” suffix=”.file_extension”>

Notes: Optional

<GetRawData> This option specifies how to retrieve the actual sample data. This may come from either a database or a raw file (or files). The raw file itself may have been a file downloaded from a database or extracted from a Java class.

If the data is located in a database, use <DatabaseQuery> to retrieve it. If it is in a file or directory of files, it is interpreted as a tab-delimited file, and you must specify the file format using the <Format> tag.

Contents: <DatabaseQuery>, **<Format> <Preprocessor>**

Attributes: n/a

Usage: <GetRawData>...**</GetRawData>**

Notes: Required

<Preprocessor> This option designates that all data retrieved from a database is to be passed through an external Java class before it is used to create Samples. If the database is an Affymetrix GCOS process database the use of this tag is mandatory, since neither GeneSpring GX nor SampleLoader can directly interpret the CEL and CHP format files such databases contain.

Contents: **<OriginalFileNameAtttribute>**

Attributes: class, jarfile

Usage: <Preprocessor class="com.sigenetics.plugins.affy.GCRMAFilePreprocessor"> <OriginalFileNameAttribute name ="CEL File" /> **</Preprocessor>**

Notes: Required with Affymetrix process databases or others offering only binary format data. Optional otherwise.

When used in SampleLoader XML configuration files, the fully qualified preprocessorclass name must be used as shown above. When used in a GeneSpring GX configuration file, the class attribute may be omitted, in which case GeneSpring GX will display a dialog allowing the user to select which preprocessor to use.

Preprocessors are not required to preserve a one-to-one relationship between their input and output files. Since the input files are those retrieved from the database any Sample Attributes retrieved with them will have been lost by the time the actual Samples are created. If it is desired that Sample Attributes loaded from the database be preserved, then the <OriginalFileNameAttribute> tag must be used to tell the Sample creation architecture which preprocessor output file corresponds to which input file originally retrieved from the database. The correct name of this tag is therefore specific to the preprocessor. In the case of the GC-RMA and RMA preprocessors used with Affymetrix GCOS process databases the correct name of this attribute is "CEL File".

<OriginalFileNameAtttribute> This option is used to preserve attributes retrieved from database when a preprocessor is used. See the entry for **<Preprocessor>** tag.

Contents: n/a

Attributes: name

Usage: <OriginalFileNameAttribute name="CEL File" />

Notes: Optional. Used to preserve attributes retrieved from databases in situations where preprocessors are used.

<GetSample-Projects> Defines project assigned to a sample, either using a fixed project name, or accessed from a database based on Sample ID:

Contents: <DatabaseQuery>, **<FixedProject>**

Attributes: n/a

Usage:

Notes: Optional

<FixedProject>

Specifies a project name to all samples loaded using XML file. Can be more than one set of <FixedProject> tags:

Contents: plain text

Attributes:

Usage:

Notes:

<DatabaseQuery>

This element allows you to enter an SQL query that produces a list of sample identifiers, attributes, or other data based on the provided genome name. If “useGenomeName” is true, the SQL query is passed the sourceName specified in the current <GenomeMappingSpec> tag. Use the “db” attribute to specify the database to query.

Accepted values for “useGenomeName” are “true” and “false”.

The data retrieved by this option varies depending on which tag contains it, as follows:

- **<GetSampleIDs>**—a list of sample identifiers
- **<GetSampleAttributes>**—three columns (or a multiple of three columns, in which case each set of three is considered independently).

These three columns are:

- sample attribute value
- sample attribute name
- sample attribute units

Each row represents one attribute. If there is more than one set of three columns, then for each set of three, each row represents an attribute.

- **<GetFile>**—if the “location” attribute is set to “database”, returns two or three columns:
  - •the data
  - •the filename
  - •the mime type (if present, this overrides the mimeType specified in **<GetFile>**)

Each row in the result represents a file to be loaded.

Contents: SQL command

Attributes: useGenomeName, db

Usage: <DatabaseQuery useGenomeName=”true” db=”dbname”>select ID from Experiments where Experiments.chipType=?</DatabaseQuery>

Notes: Required if the location attribute value in **<GetSampleIDs>** is “database”. For more usage examples, see the sample configuration files included with the SampleLoader distribution.

<DataDirectory>

If samples are contained in flat files rather than a database, this setting specifies the directory in which sample files are located. If a directory is not specified, or does not begin with an absolute path, then the baseDirectory attribute of the <GenomeMappingSpec> tag is used.

Contents: plain text

Attributes: n/a

Usage: <DataDirectory>*/usr/share/affy</DataDirectory>*

Notes: Optional

<FileNameMask>

FileNameMask is applied to all files in DataDirectory to filter the FileNames. If the DataDirectory is not specified or does not begin with an absolute path, the baseDirectory attribute of the current <GenomeMappingSpec> section is used. If baseDirectory does not begin with an absolute path, the current user directory is used.

Contents: plain text

Attributes: n/a

Usage: <FileNameMask>_*/AffyChipID*.chip</FileNameMask>_

Notes: Required for retrieving data from flat files in a directory

<IDFromFileName> This allows you to generate sample IDs directly from file names. If sample IDs are generated using <Regexpmatch>, only one genome should be specified in the <GenomeNames>/<GenomeMappingSpec> tags. The result of the <RegexpMatch> on the file names provides the sample IDs. If you are using <DatabaseQuery> instead, the file names are passed as arguments to the specified SQL query.

Contents: plain text

Attributes: n/a

Usage: <IDFromFileName>...</IDFromFileName>

Notes: Optional

<RegexpMatch> When using <IDFromFileName>, use either this tag or <DatabaseQuery>, but not both.

Contents: plain text

Attributes: n/a

Usage: <RegexpMatch>_AffyChipID(.*)\.chip_**</RegexpMatch>**

Notes: Optional

<JavaQuery> This allows you to use a Java class to return an array of identifiers. You specify a command such as:

```
<JavaQuery class="com.pharma.database.getParameters" extraArgs="Blah"/>
```

and it creates an instance of com.pharma.SampleLoader.getParameters using the default constructor. That class should implement com.sigenetics.ext.database.GetAttributes. Then for each attribute, a function is called with arguments of the database identifier, the database genome name, and the extra argument. The return value is an array of com.sigenetics.ext.database.Attribute objects, each with name, value, units and isNumeric fields.

Contents: n/a

Attributes: class, extraArgs (optional)

Usage: <JavaQuery class="com.pharma.SampleLoader.getIDs" extraArgs=""/>

Notes: Optional, applies only to <GetSampleIDs>, <GetSampleAttributes>, and <GetFile>. For additional usage examples, see the sample configuration files included with the SampleLoader distribution.

<Format> Specifies the format of raw data to be retrieved. If this data is in a known format, then you specify it using the “type” attribute. Currently supported types are:

- Incyte Internet Download
- Incyte
- Affymetrix
- Affymetrix Pivot Table
- AtlasImage
- GenePix Results
- Imagene
- ScanArray
- QuantArray
- CodeLink Export
- Amersham CodeLink (Mean)
- Amersham CodeLink (Median)
- Amersham Codelink Expression Report
- Agilent

NOTE Affymetrix Pivot files with more than one sample per file are not supported.

If you are retrieving data from a directory containing data in multiple formats, then any files that do not match the format you specify here will be ignored by SampleLoader.

NOTE SampleLoader cannot handle .csv files.

If you are retrieving data from a database as a set of columns using a SQL query, a known format type may not be used and must be explicitly defined using the format described below.

If your data are not in a standard format, you must define the format using the available tags. Columns can be specified either as a number (first column=1) or header. If columns are specified by the header, and data is retrieved from a database using a SQL query, make sure the headers retrieved in the SQL query exactly match the headers specified here. It is a good idea to write your SQL queries as follows:

- Select column1 as "column1" from table_name where ...
- If a column is not used, you can omit the line or enter -1 (" " for strings).

Contents: **<GeneColumn>, <Headlines>, <SignalColumn>, <NormalizedColumn>, <ReferenceColumn>, <SignalBackgroundColumn>, <ReferenceBackgroundColumn>, <ExperimentWorkedColumn>, <ExperimentWorkedDesignation>, <ExperimentAbsentDesignation>, <ExperimentMarginalDesignation>, <RegionColumn>, <TreatNoSignalAsInvalid>, <LowerBoundOnSignalColumn>, <UpperBoundOnSignalColumn>, <StandardDeviationSignalColumn>, <ColumnHeaderLine>**

Attributes: type

Usage: **<Format type="Affymetrix"/>** or **<Format>...</Format>**

Notes: Required

<GeneColumn> Specifies which column in the sample data contains the gene identifier. This tag is used only if your data are in a nonstandard format.

Contents: plain text

Attributes: n/a

Usage: **<GeneColumn>**1**</GeneColumn>**

Notes: Required if data type is not specified in the **<Format>** tag.

<Headlines> Number of header lines to skip at the top before further processing. This can usually be determined automatically if the columns are specified by header. This tag does not apply when sample data are retrieved from a database.

Contents: plain text

Attributes: n/a

Usage: **<Headlines>**0**</Headlines>**

Notes: Optional

<SignalColumn>	Specifies the column containing the raw signal data. **Contents:** plain text **Attributes:** n/a **Usage: <SignalColumn>**31**</SignalColumn>** **Notes:** Required if data type is not specified in the **<Format>** tag.
<NormalizedColumn>	Specifies the column containing normalized data. **Contents:** plain text **Attributes:** n/a **Usage: <NormalizedColumn>**30**</NormalizedColumn>** **Notes:** Optional, rarely used
<ReferenceColumn>	Specifies the column containing raw reference data. This is typically present in two-color experiments. **Contents:** plain text **Attributes:** n/a **Usage: <ReferenceColumn>**32**</ReferenceColumn>** **Notes:** Optional
<SignalBackgroundColumn>	Specifies the column containing the background signal to be subtracted from the main signal before further processing. **Contents:** plain text **Attributes:** n/a **Usage: <SignalBackgroundColumn>**-1**</SignalBackgroundColumn>** **Notes:** Optional, rarely used
<ReferenceBackgroundColumn>	Specifies the column containing the background signal to be subtracted from the reference signal before further processing. **Contents:** plain text **Attributes:** n/a **Usage: <ReferenceBackgroundColumn>**-1**</ReferenceBackgroundColumn>** **Notes:** Optional, rarely used
<ExperimentWorkedColumn>	Specifies the column containing a flag or flags indicating success of the measurement.

Contents: plain text

Attributes: n/a

Usage: <ExperimentWorkedColumn>33**</ExperimentWorkedColumn>**

Notes: Optional, see also <ExperimentWorkedDesignation>, <ExperimentAbsentDesignation>, <ExperimentMarginalDesignation>

<Experiment-Worked-Designation>

Specifies the flag in the column specified by <ExperimentWorkedColumn> that indicates that the measurement worked well.

Contents: plain text

Attributes: n/a

Usage:
<ExperimentWorkedDesignation>P**</ExperimentWorkedDesignation>**

Notes: Optional, see **<ExperimentWorkedColumn>**

<Experiment-Absent-Designation>

Specifies the flag in the column specified by <ExperimentWorkedColumn> that indicates that the measurement did not work well.

Contents: plain text

Attributes: n/a

Usage:
<ExperimentAbsentDesignation>A**</ExperimentAbsentDesignation>**

Notes: Optional, see **<ExperimentWorkedColumn>**

<Experiment-Marginal-Designation>

Specifies the flag in the column specified by <ExperimentWorkedColumn> that indicates that the measurement worked only marginally.

Contents: plain text

Attributes: n/a

Usage:
<ExperimentMarginalDesignation>M**</ExperimentMarginalDesignation>**

Notes: Optional, see **<ExperimentWorkedColumn>**

<RegionColumn>

Specifies the column that indicates regions to be normalized separately.

Contents: plain text

Attributes: n/a

Usage: <RegionColumn>-1**</RegionColumn>**

Notes: Optional, rarely used

<TreatNo-SignalAsInvalid> Specifies whether a signal of "0" should be treated as blank. If no value is specified for this tag, it defaults to "no". Accepted values are "no" and "yes".

Contents: plain text

Attributes: n/a

Usage: <TreatNoSignalAsInvalid>no**</TreatNoSignalAsInvalid>**

Notes: Optional, rarely used

<LowerBoundOnSignalColumn> When an error model is known, specifies a lower bound on the signal value.

Contents: plain text

Attributes: n/a

Usage:
<LowerBoundOnSignalColumn>-1**</LowerBoundOnSignalColumn>**

Notes: Optional, rarely used

<UpperBoundOnSignalColumn> When an error model is known, an upper bound on the signal value.

Contents: plain text

Attributes: n/a

Usage:
<UpperBoundOnSignalColumn>-1**</UpperBoundOnSignalColumn>**

Notes: Optional, rarely used

<StandardDeviationSignalColumn> When an error model is known, specifies the standard deviation of the signal value.

Contents: plain text

Attributes: n/a

Usage:
<StandardDeviationSignalColumn>-1**</StandardDeviationSignalColumn>**

Notes: Optional, rarely used

<ColumnHeaderLine> Specifies the row containing the header names. Usually this can be determined automatically.

Contents: plain text

Attributes: n/a

Usage: <ColumnHeaderLine>-1**</ColumnHeaderLine>**

Notes: Optional, rarely used

System requirements

PC Version Requirements

- Windows 2000/2003/XP
- Pentium III or later
- 512 MB RAM
- 250 MB of free disk space

Linux or UNIX Version Requirements

- Redhat Enterprise Linux or Sun Solaris
- A JVM installed that supports J2SE 1.4 or later
- 512 MB RAM
- 250 MB of free disk space

NOTE Large data sets may require significantly more RAM and storage for optimum performance.

4

GeneSpring Viewer Installation

GeneSpring Viewer is a powerful tool for inspecting the results of gene expression analysis experiments. It is specifically designed for users who need to examine, reformat, and redistribute data that is stored in GeneSpring Workgroup. GeneSpring Viewer is a standalone Java client that runs on Windows and Macintosh machines. All data created by GeneSpring Viewer is stored directly on the Workgroup.

GeneSpring Viewer includes the following:

- All of the viewing tools available in GeneSpring GX
- Search tools for samples, genes, and gene lists
- Simple tools to build gene lists from search results and hand-selected genes
- The ability to export charts, tables and graphs to generate reports
- Condition scatter plot to plot two or three experimental parameter values for conditions (in 2-D or 3-D scatter plots), giving you a better insight into the distribution of parameter values across your experiment. You can use GeneSpring Viewer to plot the results of the new Principal Component Analysis (PCA) on conditions functionality in GeneSpring.
- Improved Search GeneSpring Workgroup functionality that allows you to find any Workgroup analysis result regardless of its associated genome.

GeneSpring Viewer is only available on Windows XP, Windows Server 2003, Windows 2000, and Macintosh OSX 10.3.0 or later systems.

To distribute and install GeneSpring Viewer

To run GeneSpring Viewer, obtain a GeneSpring Viewer installer from your Agilent Field Application Specialist. The installer comes pre-configured with the correct license key and preferences file. As part of the Installation Services included with your GeneSpring Workgroup license, Agilent can provide you with one or both of the following installers:

- A Windows executable:
  GeneSpringViewer5_2Installer.exe
- A self-extracting Macintosh archive:
  GeneSpringViewer5_2Installer.zip

These installers include a license key that identifies their use in conjunction with the GeneSpring Workgroup application, and a preferences file that includes the Workgroup IP address and any necessary firewall information. The procedure for installing GeneSpring Viewer is easier than the procedure for installing and configuring GeneSpring GX. These installers provide almost instantaneous access to GeneSpring Workgroup data.

Summary of the Installation Procedure

1. Download the appropriate GeneSpring Viewer installer from the Agilent Web site or obtain a copy from your Agilent Field Application Specialist.
2. Run the installer on a client computer.

3 Run GeneSpring Viewer:
   - Select **Add New Workgroup Server**in the Workroup Server Login dialog box.
   - Type the Workgroup name (Nickname).
   - Configure the Workgroup address (the Workgroup's IP address)
   - Type the default user name.
   - Click **OK**.

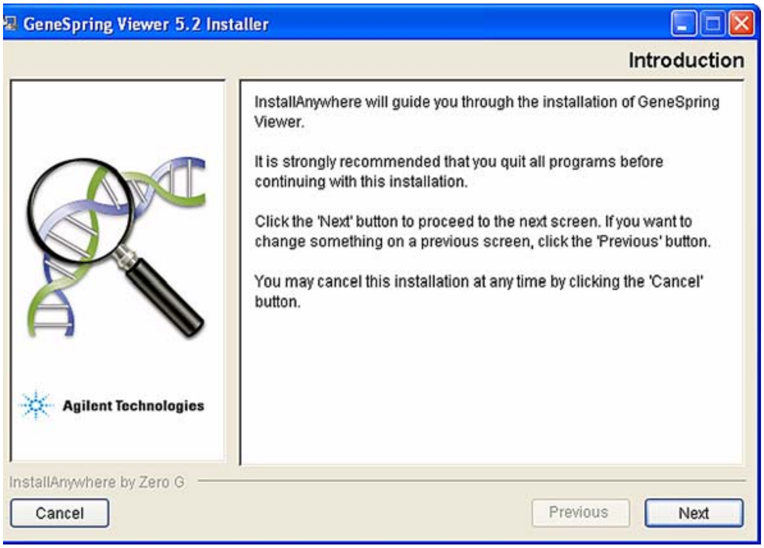
If a firewall is located between the Workgroup Server and the GeneSpring Viewer client, the Administrator should contact Agilent Technical Support for information on how to configure the preferences to pass the firewall.

Windows

1 Load the executable installer file, **GeneSpringViewer5_2Installer.exe**, on your system.

2 Click the file name, and a Preparing to Install message box appears to show the progress of the loading installer.

3 An Introduction dialog box appears when the installation is started. Click **Next**.



InstallAnywhere will guide you through the installation of GeneSpring Viewer.

It is strongly recommended that you quit all programs before continuing with this installation.

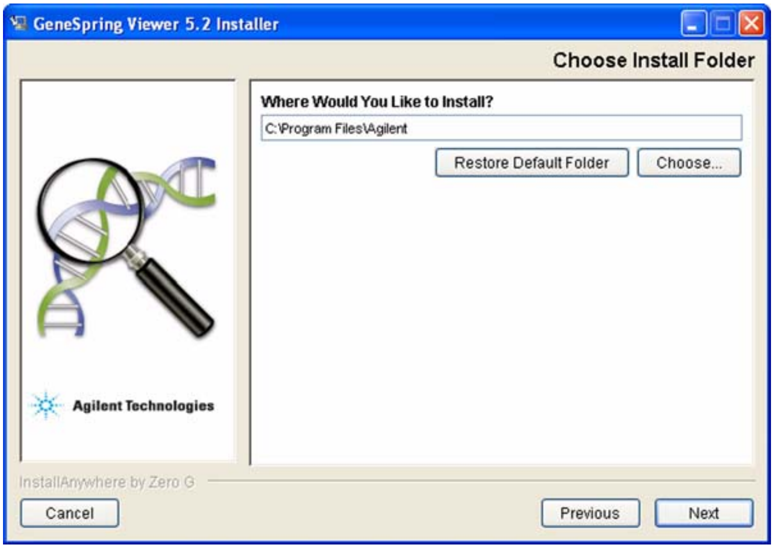
Click the 'Next' button to proceed to the next screen. If you want to change something on a previous screen, click the 'Previous' button.

You may cancel this installation at any time by clicking the 'Cancel' button.

Figure 67 Introduction dialog box

4 A License Agreement dialog box appears. Click the **I accept the terms of the License Agreement** radio button, then click **Next**.

5 The Choose Install Folder dialog box appears prompting you to select the folder in which you will install GeneSpring Viewer. The default folder is **C:\Program Files\Agilent**.



Where Would You Like to Install?
C:\Program Files\Agilent

Figure 68 Choose Install Folder dialog box

You also have the option of clicking **Choose** to install in a folder of your choice. (If you select another folder, then change your mind, click **Restore Default Folder** to return to the initial dialog box.)

Click **Next** to accept the selected Install Folder and continue.

6 The Choose Shortcut Folder dialog box appears. The default folder is displayed as in step 5. Click **Next** to continue.

Choose Shortcut Folder

Where would you like to create product icons?

○ In a new Program Group: GeneSpring Viewer

● In an existing Program Group: Agilent

○ In the Start Menu

○ On the Desktop

○ In the Quick Launch Bar

○ Other:

○ Don't create icons

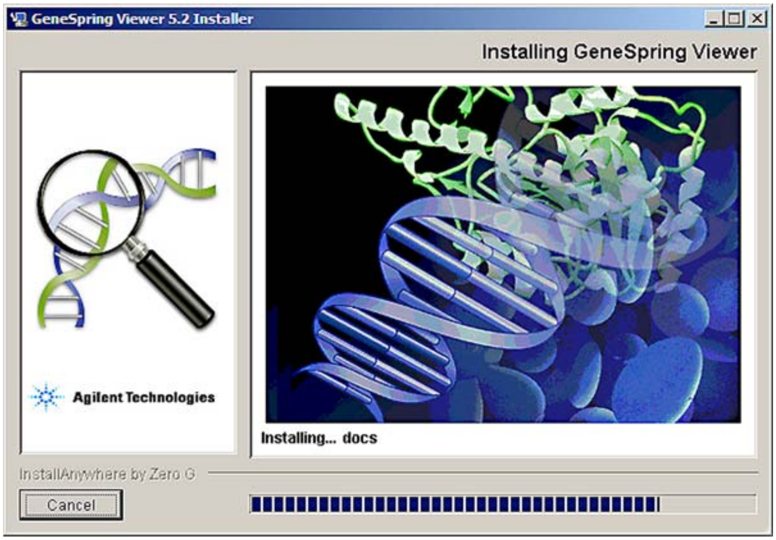
☐ Create Icons for All Users

Figure 69 Choose Shortcut Folder dialog box

7 A Pre-Installation Summary dialog box appears displaying a summary of all the choices you made in the previous steps. If any of the information is incorrect, click **Previous** one or more times until you are returned to the dialog box that contains the erroneous information.

8 Correct the information then click **Next** repeatedly until you are returned to the Pre-Installation Summary dialog box. Click **Install** to continue.

9 During installation, the Installing GeneSpring Viewer dialog box appears showing the progress of the installation.



Installing... docs

Figure 70 Installing GeneSpring Viewer dialog box

10 When GeneSpring Viewer is installed, an Install Complete dialog box appears. Click **Done** to quit the installation.

Congratulations! GeneSpring Viewer has been successfully installed to:

C:\Program Files\Agilent

Press "Done" to quit the installer.

Figure 71 Install Complete dialog box

A shortcut icon is placed on your desktop from where you can launch the GeneSpring Viewer.

NOTE You must connect to a GeneSpring Workgroup Server before you can use GeneSpring Viewer.

11. Click the shortcut icon to launch GeneSpring Viewer.
12. The GeneSpring Viewer splash screen appears, quickly followed by a Workgroup Server Login dialog box. Enter your login and click **Next**.

Workgroup Server Login

Enter username and password for Workgroup Server

Workgroup Server: Add New Workgroup Server...

Username:

Password:

Figure 72 Workgroup Server Login dialog box

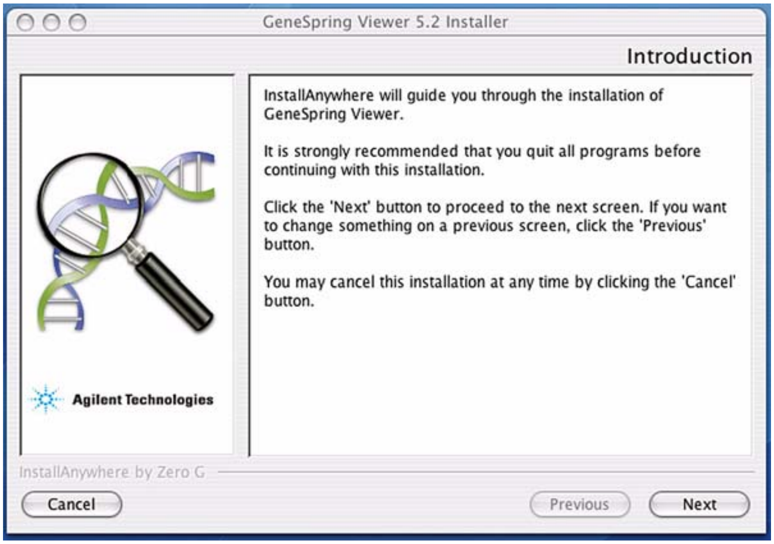
13. The Add Workgroup Server dialog box appears. If the server is not indicated by default, type your server information and click **OK**.
14. The application starts indicating that you have successfully installed and activated GeneSpring Viewer.

Macintosh OSX

The procedure for installing GeneSpring Viewer on a Macintosh system is almost identical to the installing in Windows.

1. Load the executable installer file, **GeneSpringViewer5_2Installer.zip** on your system.
2. Click the file name, and a Preparing to Install message box appears to show the progress of the loading installer.

3 An Introduction dialog box appears when the installation is started. Click **Next**.



InstallAnywhere will guide you through the installation of GeneSpring Viewer.

It is strongly recommended that you quit all programs before continuing with this installation.

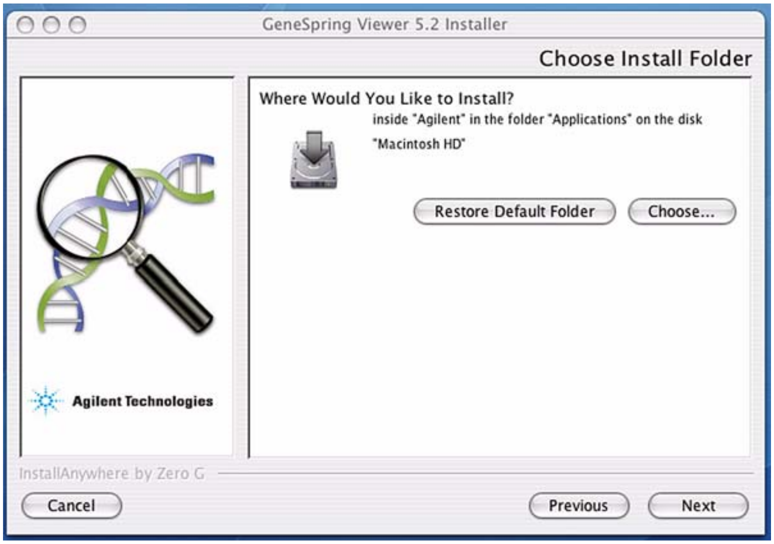
Click the 'Next' button to proceed to the next screen. If you want to change something on a previous screen, click the 'Previous' button.

You may cancel this installation at any time by clicking the 'Cancel' button.

Figure 73 Introduction dialog box

4 A License Agreement dialog box appears. Click the **I accept the terms of the License Agreement** radio button, then click **Next**.

5 The Choose Install Folder dialog box appears prompting you to select the folder in which you will install GeneSpring Viewer. The default folder is **Applications/Agilent**.



Where Would You Like to Install?

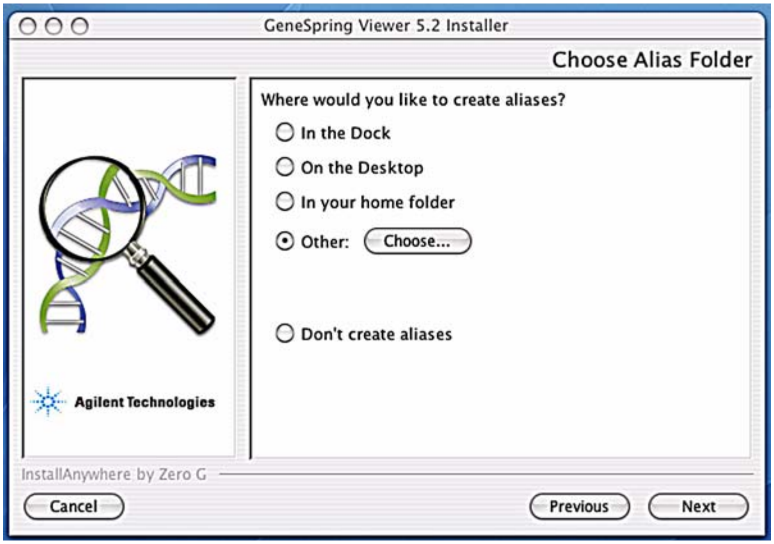
inside "Agilent" in the folder "Applications" on the disk "Macintosh HD"

Figure 74 Choose Install Folder dialog box

You also have the option of clicking **Choose** to install in a folder of your choice. (If you select another folder then change your mind, you can click **Restore Default Folder** to return to the initial dialog box.)

Click **Next** to accept the selected Install Folder and continue.

6 The Choose Alias Folder dialog box appears. The default folder is displayed is in step 5. Click **Next** to continue.



GeneSpring Viewer 5.2 Installer

Choose Alias Folder

Where would you like to create aliases?

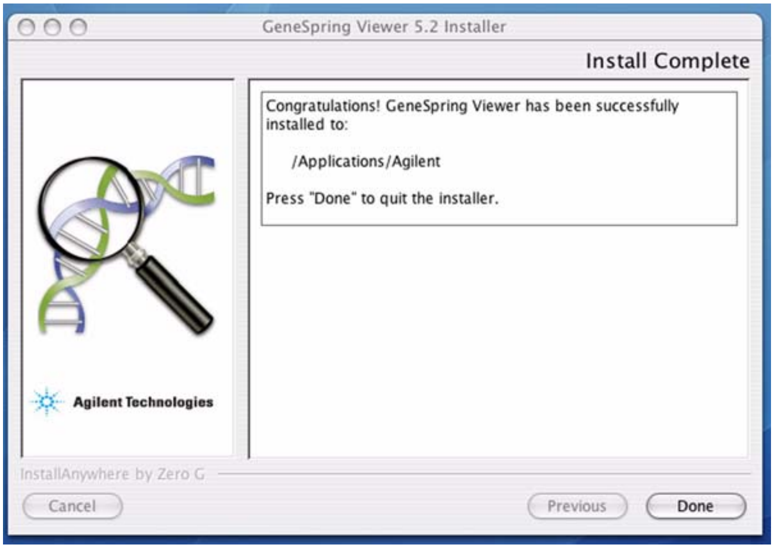
○ In the Dock
○ On the Desktop
○ In your home folder
● Other:
○ Don't create aliases

Figure 75 Choose Alias Folder dialog box

7 A Pre-Installation Summary dialog box appears displaying a summary of all the choices you made in the previous steps. If any of the information is incorrect, click **Previous** one or more times until you are returned to the dialog box containing the erroneous information.

8 Correct the information then click **Next** repeatedly until you are returned to the Pre-Installation Summary dialog box. Click **Install** to continue.

9 When GeneSpring Viewer is installed, an Install Complete dialog box appears. Click **Done** to quit the installation procedure.



Congratulations! GeneSpring Viewer has been successfully installed to:

/Applications/Agilent

Press "Done" to quit the installer.

Figure 76 Install Complete dialog box

A shortcut icon has been placed on your desktop from where you can launch the GeneSpring Viewer.

NOTE You must connect to a GeneSpring Workgroup Server before you can use GeneSpring Viewer.

10 Click the shortcut icon to launch GeneSpring Viewer.

11 The GeneSpring Viewer splash screen appears, quickly followed by the Workgroup Server Login dialog box. Enter your login and click **Next**.

12 The Add Workgroup Server dialog box appears. If the server is not indicated by default, type your server information and click **OK**.

Workgroup Server & GeneSpring Viewer on different sides of Firewall

Use Secure Connection No

Figure 77 Add Workgroup Server dialog box

13 The application starts indicating that you have successfully installed and activated GeneSpring Viewer.

To upgrade GeneSpring Viewer

To remain compatible when newer versions of GeneSpring Workgroup become available, you will need to upgrade your GeneSpring Viewer application.

- To upgrade, use the same installer that is used for a new installation. However, unlike a new (non-upgrade) installation of GeneSpring Viewer, you do not need to customize the installers for individual Workgroup servers.

NOTE Newer versions of GeneSpring Viewer can be installed over an earlier version.

To build GeneSpring Viewer Installers

Administrators can easily build their own GeneSpring Viewer installers and make them available to their users. To do this is a six-step procedure:

1 Download the upgrade installer from the Agilent Web site:

http://www.chem.agilent.com/Scripts/Generic.ASP?|Page=38605

2 Run the installer.

3 Add the appropriately configured GeneSpring Preferences file to the **<Install directory>\Agilent\GeneSpringViewer\data** folder in Windows or the comparable folder in Macintosh. See GeneSpring Viewer Preferences immediately following this procedure.

4 Use an archiving or installer-building program to bundle all of the files, folders, and subfolders in **<Install directory>\Agilent\GeneSpringViewer** in Windows, or Disc Image Application in Macintosh.

5 Make the bundled download available through a shortcut placed in the default program folder or a folder you define.

On Windows, the GeneSpring Viewer executable is named **GeneSpringViewer5_2Installer.exe.**

On Macintosh, it can be **GeneSpringViewer5_2Installer.zip** or **GeneSpringViewer5_2Installer.dmg**.

GeneSpring Viewer Preferences

GeneSpring Viewer preferences are very similar to GeneSpring GX preferences. If you have configured firewall preferences for GeneSpring GX, then you can use the same settings for GeneSpring Viewer.

Administrators or users only need to modify these settings if a firewall is situated between the user’s GeneSpring Viewer application and the GeneSpring Workgroup containing the data the user wishes to examine.

If you need to set these preferences manually, do the following:

1. Open a text editor.
2. Create a file containing all the fields that are needed for passing the firewall.
3. Save the file as GeneSpring Preferences in the data directory.

In such cases, you must verify the following fields and set them in the **GeneSpring Preferences** file.

- In Windows: **C:\Program Files\Agilent\GeneSpringViewer\data** directory.
- In Macintosh, this file can be found in the user’s home directory.
    - For an administrator, this would be **Applications/Agilent/GeneSpringViewer/data.**
    - For a non-administrator, it would be **Users/<user name>/Agilent/GeneSpringViewer/data**.

UseProxyFirewall

This field configure proxy preferences only if this field is *true*. The default is **false**.

Example: `UseProxyFirewall : false`

UseProxyPassword

This field determines whether to send the user name and password as part of the HTTP request. This field is only used if UseProxyFirewall is **true**. The default value is **false**.

Example: `UseProxyPassword : false`

ProxyPassword

This field contains the login password that is sent to the proxy server. Since it is an encrypted field, the easiest way to set it is by copying it from the GeneSpring application's GeneSpringPreferences file. This field is only used if UseProxyFirewall is **true**.

Example: `ProxyPassword : 0x3F54`

ProxyUserName

The field contains the login user name that is sent to the proxy server. This field is only used if UseProxyFirewall is **true**.

Example: `ProxyUserName : raoul`

ProxyProtocol

The field contains the protocol that is used to communicate with the proxy server. The default is HTTP, but, for example, it could also be Socks 4 or Socks 5. This field is only used if UseProxyFirewall is **true**.

Example: `ProxyProtocol : HTTP`

ProxyAddress

This field contains the proxy server's IP address or DNS name. The value must be a complete IP address or DNS name. This field is only used if UseProxyFirewall is **true**. There is no default value, since this setting is ignored if UseProxyFirewall is set to **false**.

Example: `ProxyAddress : myproxy.mycompany.com`

GenExAddress

This field contains the URL or IP address used to access the Workgroup in a web browser. This preference is composed of the four parts, separated by semicolons (;).

1. The Workgroup's user-defined, descriptive name
2. The Workgroup's URL or IP address
3. The default login name that GeneSpring Viewer should pre-populate in the login screen (optional)
4. Whether Workgroup is inside (local) or outside (remote) of the firewall

Example 1:

```
GenExAddress: localhost;156.123.10.08; ;remote
```

Example 2:

```
GenExAddress: my host;123.12.18. 13;ken;local
```

You can also set this field by starting GeneSpring Viewer, then selecting **Add New Workgroup** in the Workgroup login window.

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In This Book

This book describes how to install the GeneSpring Workgroup components: Workgroup Server, Remote Server, Sample Loader, and GeneSpring Viewer.

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