Agilent CytoGenomics 5.0

Product Overview and Installation Guide

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Agilent Technologies

Notices

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In This Guide...

This *Product Overview and Installation Guide* provides an overview of Agilent CytoGenomics 5.0 and instructions for installing and administering the software.

1 Product Overview

This chapter provides an overview of Agilent CytoGenomics. It explains the overall design of the program and how different users can work with it to fulfill their roles in the laboratory.

2 Installation Instructions for Windows

This chapter shows you how to install Agilent CytoGenomics 5.0 and migrate data from a previous version of CytoGenomics on computers running a compatible Microsoft Windows operating system.

3 Installation Instructions for Macintosh

This chapter shows you how to install Agilent CytoGenomics 5.0 and migrate data from a previous version of CytoGenomics on systems running a Macintosh OS.

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Contents

1

Product Overview

This chapter provides an overview of Agilent CytoGenomics. It explains the overall design of the program and how different users can work with it to fulfill their roles in the laboratory.

What is Agilent CytoGenomics?

Cytogenetic research labs are increasingly turning to array CGH to improve detection of copy number changes and increase sample throughput. Alongside Agilent’s gold standard CGH+SNP and CGH microarrays, Agilent CytoGenomics software completes Agilent’s array-based cytogenetic research solution. Agilent CytoGenomics provides a statistically and visually powerful tool to streamline the day-to-day cytogenetic sample analysis research workflow. It offers full support for efficient analysis of cytogenetic samples and easy report generation, based on information from both external databases and an internal database. Key automation features enable a seamless flow through the experimental process, starting with full automation of data upload and analysis, and ending with customized report generation.

With Agilent CytoGenomics, cytogenetic research labs can analyze data from a microarray image in 5–30 minutes. This increases efficiency and throughput, while enabling cytogenetic researchers to better detect copy number and copy-neutral aberrations across the genome.

Agilent CytoGenomics supports CGH analysis for both constitutional and tumor samples from either fresh or FFPE sample sources. The SNP-based LOH (Loss or Lack of Heterozygosity) and UPD (Uniparental Disomy) analysis is supported for both constitutional and liquid tumor samples from fresh sample sources only.

Agilent CytoGenomics provides cytogenetic laboratories security data access through three types of user roles: Technician, Scientist, and Administrator. Each of the three user roles has unique permissions to access a selected set of features and data in the software. (See Table 1.) In addition to these three default user roles, Administrators can create custom user roles with a defined set of user privileges.

An Agilent CytoGenomics workflow (Figure 1) automatically feature extracts images generated by a microarray scanner. The extracted data is then filtered and analyzed, and aberrant intervals are identified. You can edit, suppress, add, or classify identified aberration calls during sample triage. A set of reports is generated at the end of the workflow, and a Cyto report is generated upon sign-off of the record. Audit trails of changes are available for display or inclusion in the Cyto report.

* The exact time required to process a workflow job is dependent on the format of the microarray and the specifications of the computer running the software.

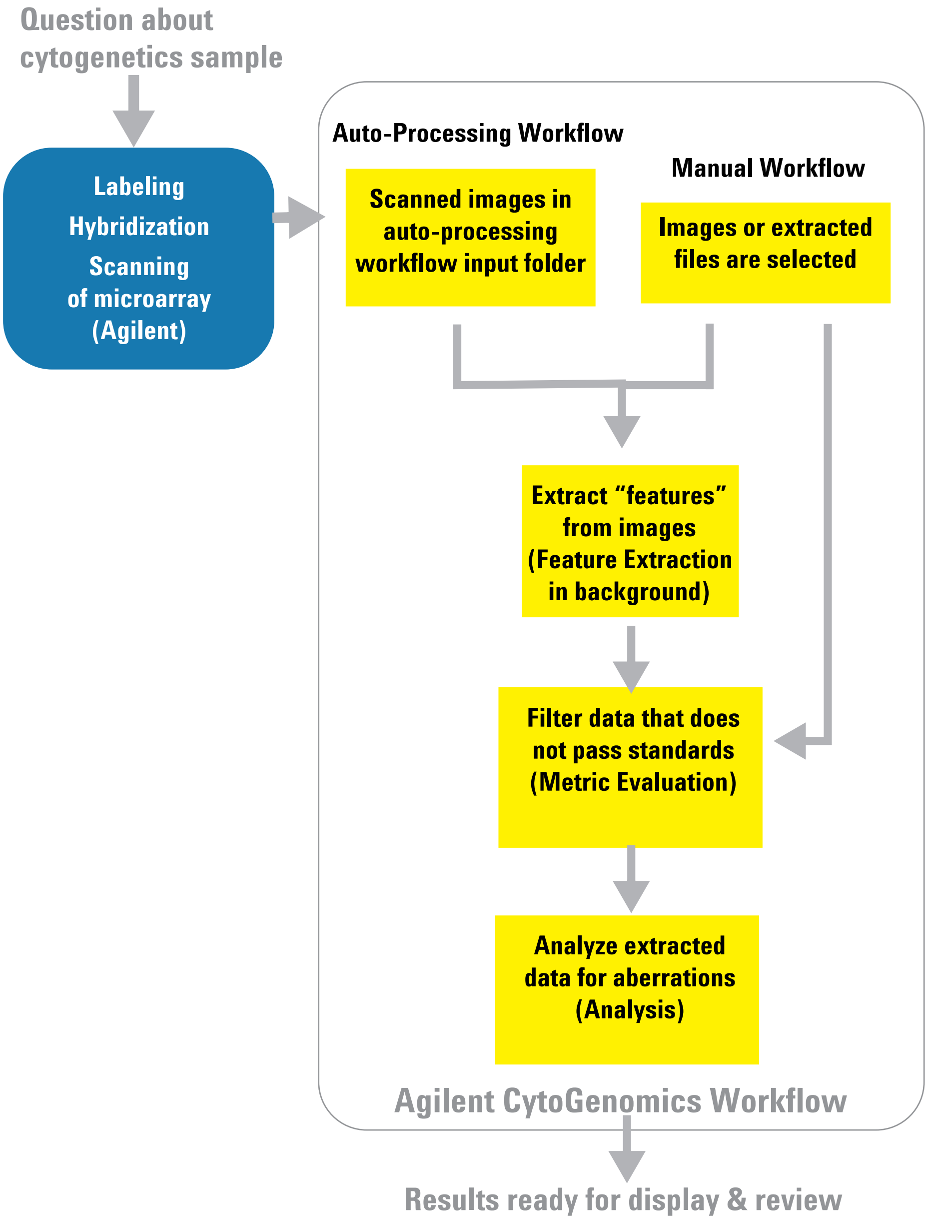

Figure 1 Agilent CytoGenomics Workflow — from image to result

To get help within Agilent CytoGenomics 5.0

Agilent CytoGenomics 5.0 has an online help system that provides detailed instructions on using the software and descriptions of the user interface. To open the help, click **Help** near the top right corner of the program window.

Help videos are also available from within the Agilent CytoGenomics program. These short videos give you instructions for doing basic tasks within the program. You can access the videos from the CytoGenomics Home screen.

To contact Agilent Technical Support

Technical support is available by phone and/or e-mail.

Resource	To find technical support contact information
Contact Agilent Technical Support by telephone or e-mail message (United States and Canada)	Telephone: 800-227-9770 (option 3, 4, 4) E-mail message: informatics_support@agilent.com
Contact Agilent Technical Support by telephone or e-mail message (for your country)	1 Go to www.agilent.com/en/contact-us/page. 2 Under **Worldwide** click to select a country or region. Complete e-mail message and telephone contact information for your country is displayed.

To learn about Agilent Genomics products and services

To view information about the Genomics products and services that are available from Agilent, go to www.agilent.com.

Key Features

This section provides an overview of the features and capabilities available in Agilent CytoGenomics 5.0. The “tabs” at the top of the program window provide access to related tasks and commands. Users see only the tabs for which they have access, according to their assigned user role. (See “User Roles and Capabilities” on page 16.)

The Home tab - getting started with CytoGenomics

Capabilities within the Home tab include:

- Entering your user license for the software
- Watching help videos for CytoGenomics
- Viewing news and updates from Agilent
- Opening links to other Agilent Genomics software programs
- Opening links to Agilent social media sites

The Analysis Workflow tab – selecting samples and running analyses

Capabilities within the Analysis Workflow tab include:

- Running manual workflows
- Adding sample information
- Importing design files
- Viewing array images by launching the Feature Extraction program

The Sample Review tab – reviewing analyses

Capabilities within the Sample Review tab include:

- Monitoring and searching for workflow jobs
- Displaying Cyto reports and aberration results
- Selecting sample results for triaging tasks:
    - Check in/out samples
    - Compare results from multiple samples
    - Add sample and interval notes
    - Modify, add, or suppress calls
    - Add/change interval classifications
    - Search database for similar classified intervals
    - Sign off samples and generate sign off reports
- Reanalyzing samples
- Reviewing QC metrics and SNP fit, and changing copy number peak assignments
- Transferring results to Cartagenia BENCH

The Configure Settings tab – setting up system defaults and analysis methods

Capabilities within the Configure Settings tab include:

- Setting up analysis method parameters
- Creating customized QC metric sets
- Creating customized Cyto report templates
- Viewing, creating, and updating dynamic and static tracks
- Configuring system preferences, including:
    - Default view preferences
    - Default input/output folders
    - Default genome build
    - Standard notes and classifications
    - Cartagenia BENCH data transfer settings
- Entering Cartagenia BENCH and Agilent SureDesign accounts

The Auto Processing tab – setting up Auto-Processing workflows

Capabilities within the Auto Processing tab include:

- Designating input folders and archive folders for tiff images and sample attribute files
- Setting up criteria for stopping or failing Auto-Processing
- Viewing Auto-Processing workflow logs

Note that Auto-Processing is not available in the Macintosh version of CytoGenomics.

The Supporting Files tab – managing samples, designs, gene lists, tracks, and other supporting files

Capabilities within the Supporting Files tab include:

- Viewing sample attributes and data
- Downloading new builds of a design from eArray
- Exporting sample attribute files
- Configuring spike-in identifiers
- Importing design files
- Importing genotype reference files
- Importing and exporting probe ID lists
- Importing and exporting tracks
- Opening the workflow log
- Displaying list of samples in the database, organized by design/build

The Admin tab – managing users and database

Capabilities within the Admin tab include:

- Adding new users and creating user roles
- Changing roles for existing users
- Enabling/disabling user access to the program
- Displaying or changing database connection parameters for the client computer
- Backing up the CytoGenomics database
- Clearing cached data

User Roles and Capabilities

The following table lists the capabilities allowed for the three different default user roles within Agilent CytoGenomics 5.0.

Table 1 User roles and capabilities

Role	Tasks and capabilities
Technician	• Run manual or auto-processing workflows • Add sample information • Monitor workflow jobs • Display reports and aberration results • View sample results in Triage View • Display auto-processing logs (Technicians cannot sign off samples.)

Scientist	Technician tasks, plus:
	• Configure system preferences, including
	  • Default input/output folders
	  • Auto-processing workflow settings
	  • Default view preferences
	  • Default genome build
	  • Standard notes, classifications, and queries
	  • Dynamic and static tracks
	  • Cartagenia BENCH data transfer settings
	• Set analysis and workflow settings
	• Create standard notes, classifications, and queries
	• Create customized Cyto report templates
	• Manage samples
	• Evaluate and chart QC trends
	• Sign off and unlock results

Administrator	Complete system access, including all Technician and Scientist tasks, plus • Add users and create user roles • Change database connection settings for client systems • Backup and restore database

2

Installation Instructions for Windows

This chapter shows you how to install Agilent CytoGenomics 5.0 and migrate data from a previous version of CytoGenomics on computers running a compatible Microsoft Windows operating system.

Installing Agilent CytoGenomics 5.0 – Windows

This section includes detailed instructions and important notes for installing Agilent CytoGenomics 5.0 on a Windows system that does not have a previous version of CytoGenomics installed.

Agilent CytoGenomics consists of two parts: a PostgreSQL database server and the client software. Once you have installed the database server and client software on one computer, you can install additional copies of the client software on client computers that have network access to the database computer.

For instructions on how to upgrade an existing Agilent CytoGenomics installation, see "Upgrading from CytoGenomics 3.0 or 4.0 to CytoGenomics 5.0 and Migrating Data – Windows" on page 44.

Step 1. Prepare for installation

a. Download the Windows version of the software and release notes

1. Go to the CytoGenomics download page on the Agilent website at: www.agilent.com/en/download-agilent-cytogenomics-software.
2. Click the **Download** link for the Windows version of the software.
3. Save the Installer on your computer. (Do not start the installation at this time.)
4. Click the **Release Notes** link to download the software release notes.
5. Save the release notes to your computer.

b. Check system requirements before you start

Check to make sure that your computer systems meet the following requirements. All client installations point to the computer on which the server software is installed. Requirements are listed in Table 2.

NOTE If an operating system is not listed in Table 2, it is not supported.

Table 2 Requirements for Agilent CytoGenomics computers – Windows

Operating system	64-bit Windows 7 Enterprise, or 64-bit Windows 10 Enterprise or Professional, or Windows Server 2012 Note: For all of these operating systems, the regional setting must be set to English
Programs	Any program that enables you to open PDF files (for example, Adobe Reader)
Processor	Minimum: > 2 GHz Recommended: > 3 GHz
Working memory (RAM)	Minimum: 4 GB Recommended: 8 GB
Hard disk space	500 GB
Display Resolution	1280 x 768 or higher

c. Set up permissions for Installer and users

- Make sure that the user account used to install the Agilent CytoGenomics 5.0 software has administrator permissions on the installation computer.
- Make sure that every user account running the Agilent CytoGenomics 5.0 software has read/write permissions in the computer where the client software is installed. In addition, users must have read/write permissions in the installation folder of the computer where the database server is installed.

The way you set permissions varies between operating systems. Contact your network administrator for help in checking or changing user account permissions. If the user account permissions are not set correctly, the software will fail to install or run properly.

d. Adjust User Account Control settings for Windows 7 and Windows 10

If you are using the Windows 7 or Windows 10 operating system, change the User Account Control settings from the default setting to “Never Notify.”

1 Go to Control Panel.

2 Click **System and Security**.

3. Click **Change User Account Control setting** (found under **Action Center** for Windows 7 and under **Security and Maintenance** for Windows 10).
4. Change the setting to “Never Notify” and click **OK**.
5. Restart the machine.

Step 2. Install the database server and client on a single Windows computer

NOTE

Whether you plan on having a centralized, shared database, or plan on having one standalone installation, you must first install both the CytoGenomics client and server software on a machine with adequate disk space. (Available and required disk space are provided during installation at the Pre-Installation Summary screen. See Figure 14 on page 32.)

The server is the program that hosts the CytoGenomics database. The client is the program you run when you want to use CytoGenomics. You can run the client program on the same computer as the server, or from any other computer with the client program installed. After installation, the database server software runs silently in the background and manages the shared database for all Agilent CytoGenomics 5.0 users. All client computers must have network access to the server computer and users must have read/write permissions.

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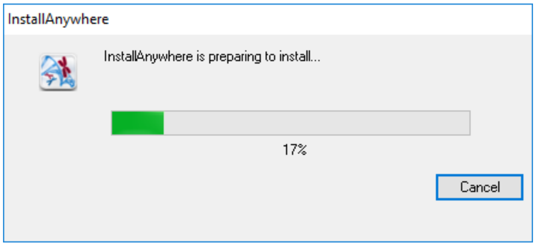
1. Log on to the Windows system where you want to install Agilent CytoGenomics 5.0 server. Use an account that has administrator permissions.
2. Locate the installation program that you downloaded in Step 1, “a. Download the Windows version of the software and release notes” on page 18. Double-click the Agilent CytoGenomics 5.0.X.X application file to start the installation wizard.

   The following message is displayed.

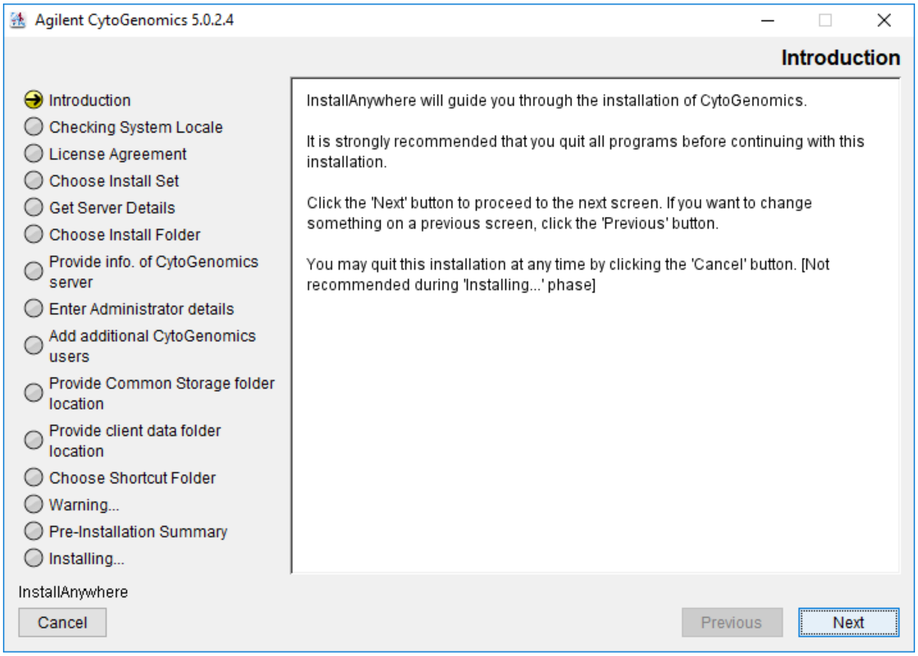


InstallAnywhere is preparing to install...

17%

Figure 2 InstallAnywhere dialog box - preparing to install

The installation wizard opens to the Introduction screen.



InstallAnywhere will guide you through the installation of CytoGenomics.

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.

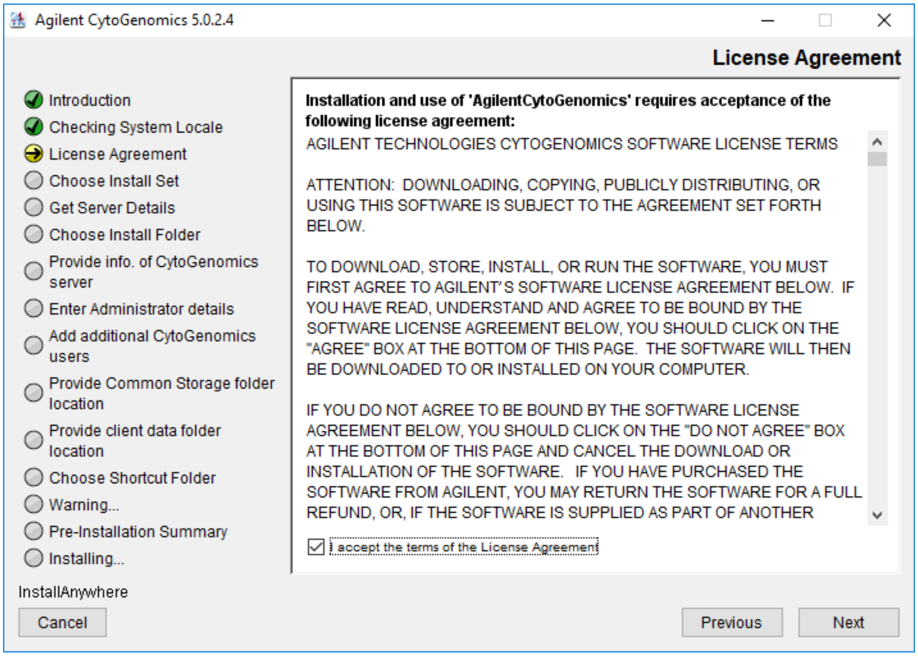
You may quit this installation at any time by clicking the 'Cancel' button. [Not recommended during 'Installing...' phase]

Figure 3 Introduction screen for the installation wizard – Windows

3 Read the introductory information.

4 Click **Next**.

The License Agreement screen opens.



Installation and use of 'AgilentCytoGenomics' requires acceptance of the following license agreement:

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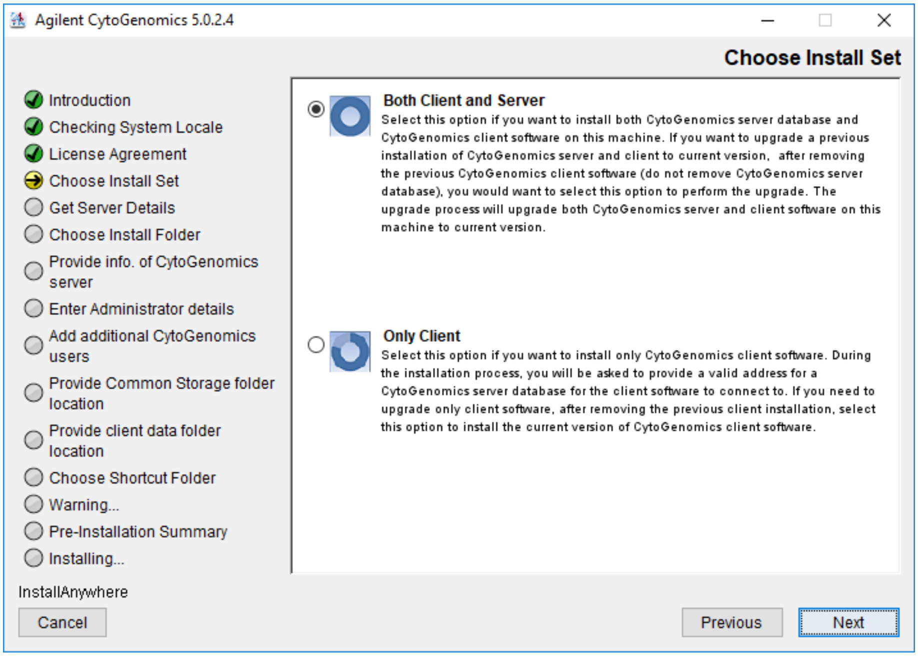
☑ I accept the terms of the License Agreement

Figure 4 License Agreement screen – Windows

5 Read the license agreement. Click **I accept the terms of the License Agreement** and then click **Next**. (Click **Previous** to review information in a previous section.)

The Choose Install Set screen opens.



● **Both Client and Server**

Select this option if you want to install both CytoGenomics server database and CytoGenomics client software on this machine. If you want to upgrade a previous installation of CytoGenomics server and client to current version, after removing the previous CytoGenomics client software (do not remove CytoGenomics server database), you would want to select this option to perform the upgrade. The upgrade process will upgrade both CytoGenomics server and client software on this machine to current version.

○ **Only Client**

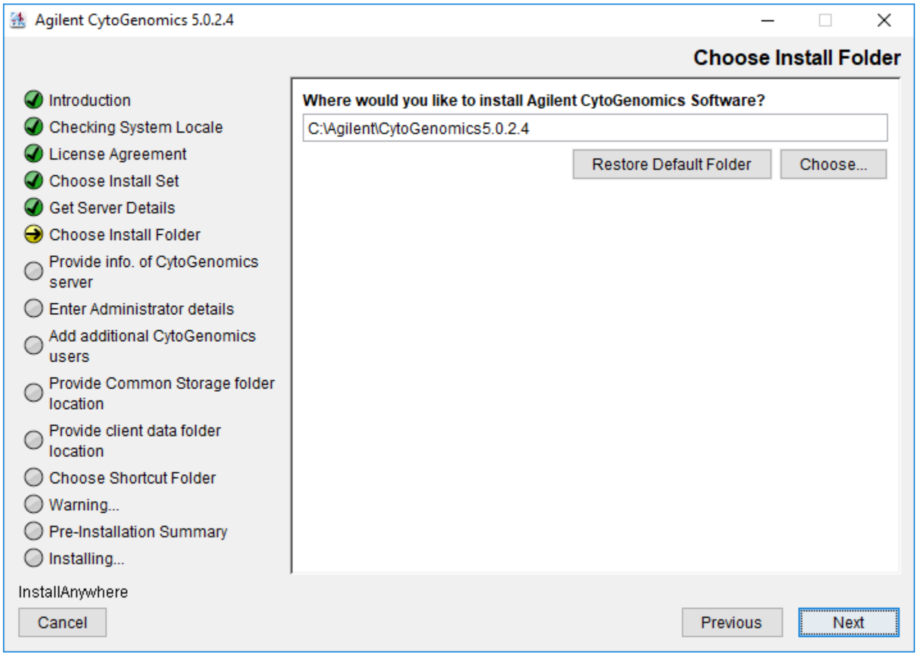
Select this option if you want to install only CytoGenomics client software. During the installation process, you will be asked to provide a valid address for a CytoGenomics server database for the client software to connect to. If you need to upgrade only client software, after removing the previous client installation, select this option to install the current version of CytoGenomics client software.

Figure 5 Choose Install Set screen – Windows

6 Click the icon next to **Both Client and Server** to install both the database server and client software on this computer.

7 Click **Next**.

An Information message opens. Click **OK** to continue. The Choose Install Folder screen opens.



Where would you like to install Agilent CytoGenomics Software?

C:\Agilent\CytoGenomics5.0.2.4

Figure 6 Choose Install Folder screen – Windows

8 By default, the program is installed in: C:\Agilent\AgilentCytoGenomics5.0.X.X (where X.X is the revision number). Leave this folder as-is, or type the location and name of the folder where you want to install Agilent CytoGenomics 5.0. Within this folder, one folder is created for the server software and one folder is created for the client software.

OR

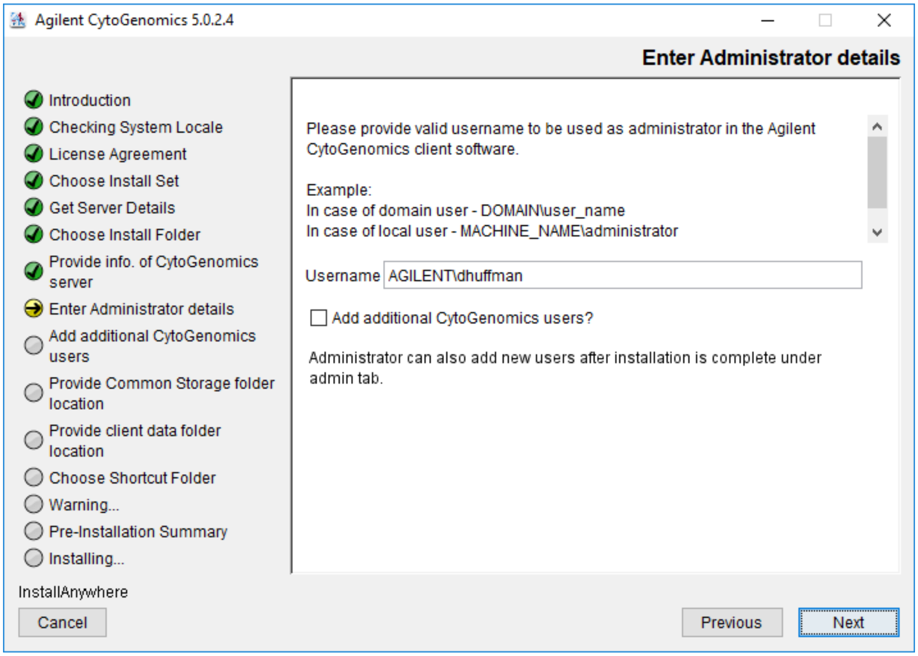
Click **Choose**, browse to a location where you want to install the program, and then click **Save.**

NOTE For installations on Windows 7, the installation program folder must not be in the C:\Program Files folder.

---

9 Click **Next**.

The Enter Administrator details screen opens.



Enter Administrator details

Please provide valid username to be used as administrator in the Agilent CytoGenomics client software.

Example:
In case of domain user - DOMAIN\user_name
In case of local user - MACHINE_NAME\administrator

Username AGILENT\dhuffman

☐ Add additional CytoGenomics users?

Administrator can also add new users after installation is complete under admin tab.

Figure 7 Enter Administrator details screen – Windows

10 The domain and user name of the person currently logged on to the computer appear in Username. If this Username is not the administrator for the Agilent CytoGenomics 5.0 software, type the correct user, using the format example shown.

For domain user: DOMAIN\username

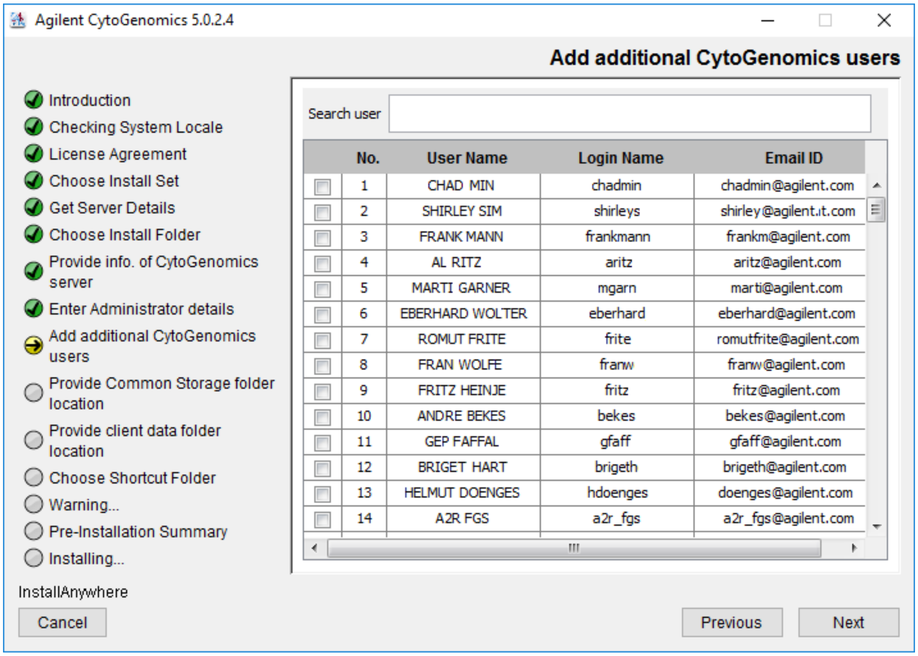
For local machine: MACHINENAME\username

11 To set up additional CytoGenomics users, mark the check box labeled **Add additional CytoGenomics users?**. In the Password field that appears, type the password for the administrator account.

If you do not want to set up new users at this time, proceed directly to step 16 on page 27. Note that the administrator can set up new users from within CytoGenomics once installation is complete (see “To manage users and roles” on page 110).

12 Click **Next**.

The Add additional CytoGenomics users screen opens.



Search user

	No.	User Name	Login Name	Email ID
☐	1	CHAD MIN	chadmin	chadmin@agilent.com
☐	2	SHIRLEY SIM	shirleys	shirley@agilent.it.com
☐	3	FRANK MANN	frankmann	frankm@agilent.com
☐	4	AL RITZ	aritz	aritz@agilent.com
☐	5	MARTI GARNER	mgarn	marti@agilent.com
☐	6	EBERHARD WOLTER	eberhard	eberhard@agilent.com
☐	7	ROMUT FRITE	frite	romutfrite@agilent.com
☐	8	FRAN WOLFE	franw	franw@agilent.com
☐	9	FRITZ HEINJE	fritz	fritz@agilent.com
☐	10	ANDRE BEKES	bekes	bekes@agilent.com
☐	11	GEP FAFFAL	gfaff	gfaff@agilent.com
☐	12	BRIGET HART	brigeth	brigeth@agilent.com
☐	13	HELMUT DOENGES	hdoenges	doenges@agilent.com
☐	14	A2R FGS	a2r_fgs	a2r_fgs@agilent.com

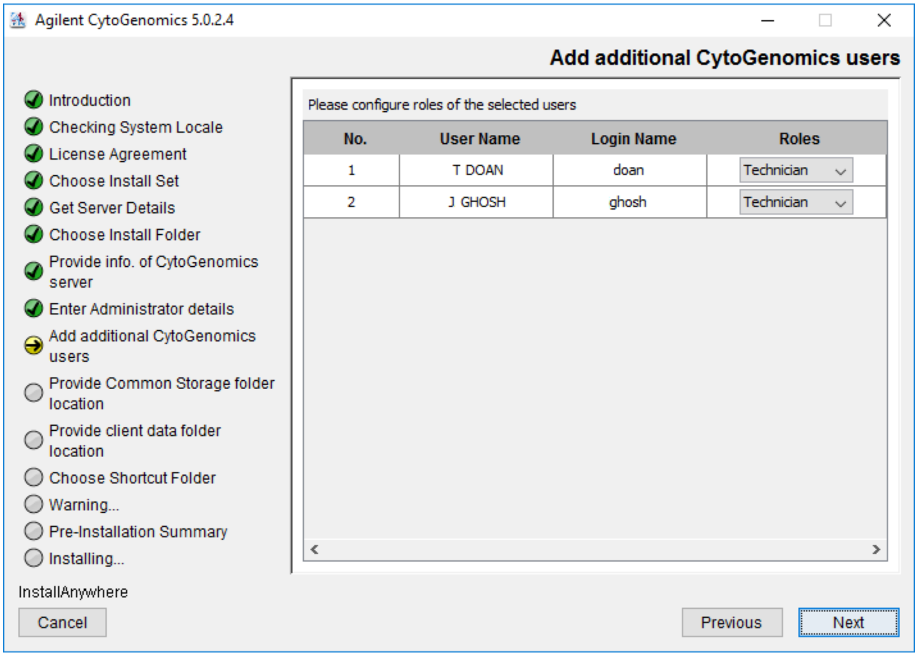
Figure 8 Add additional CytoGenomics users screen – Windows

13 The Add additional CytoGenomics users screen lists all of the users in the domain or on the local machine. Mark the check box next to the users that you want to add to the CytoGenomics database.

To search for a user, type the user name into the search box at the top of the screen.

14 Click **Next**.

The Add additional CytoGenomics users screen advances to the step for configuring user roles.



Please configure roles of the selected users

No.	User Name	Login Name	Roles
1	T DOAN	doan	Technician
2	J GHOSH	ghosh	Technician

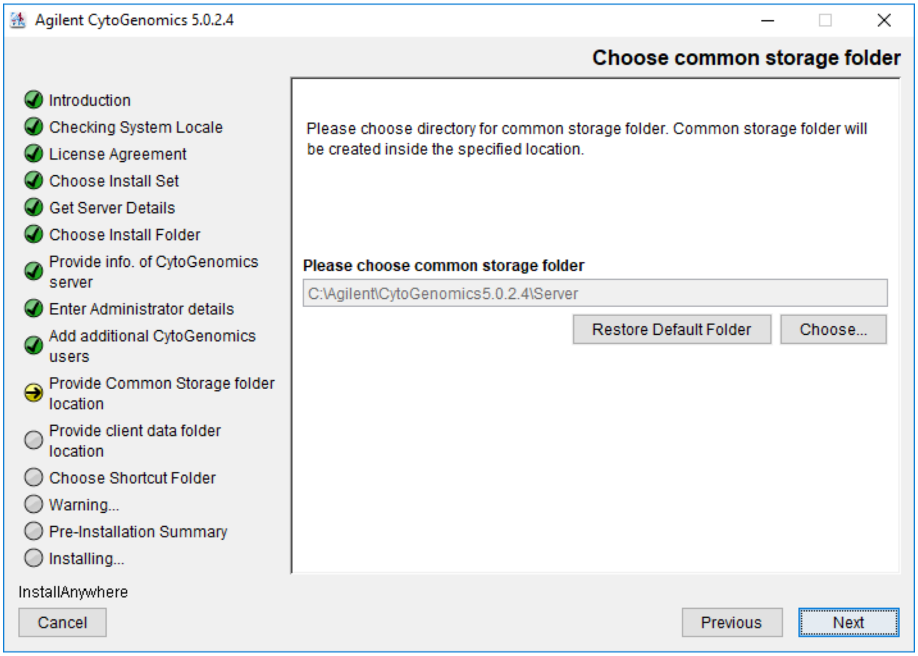
Figure 9 Add additional CytoGenomics users screen – Configure roles step – Windows

15 For each user listed on the screen, select a role in the Roles drop-down list. The default selection is *Technician*.

See “User Roles and Capabilities” on page 16 for a description of each role.

16 Click **Next**.

The Choose common storage folder screen opens.



Please choose directory for common storage folder. Common storage folder will be created inside the specified location.

Please choose common storage folder: C:\Agilent\CytoGenomics5.0.2.4\Server

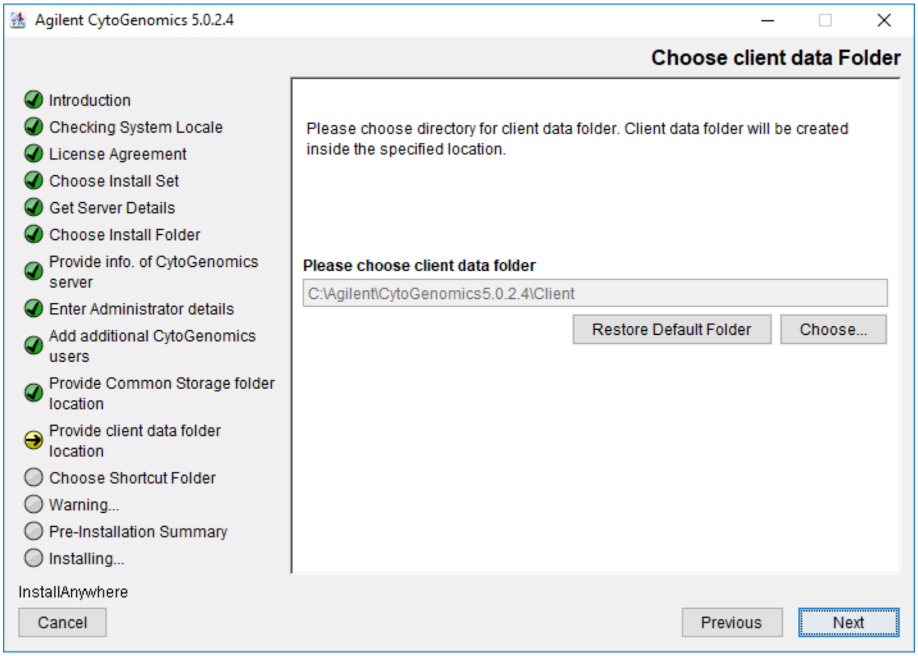
Figure 10 Choose common storage folder screen – Windows

17 By default, the common storage folder is created inside the folder C:\Agilent\AgilentCytoGenomics5.0.X.X\Server (where X.X is the revision number). Leave this folder as-is, or Click **Choose**, browse to the desired folder, and then click **Save.**

The common storage folder is where the program saves files that are used at the server level.

18 Click **Next**.

The Choose client data folder screen opens.



Please choose directory for client data folder. Client data folder will be created inside the specified location.

Please choose client data folder: C:\Agilent\CytoGenomics5.0.2.4\Client

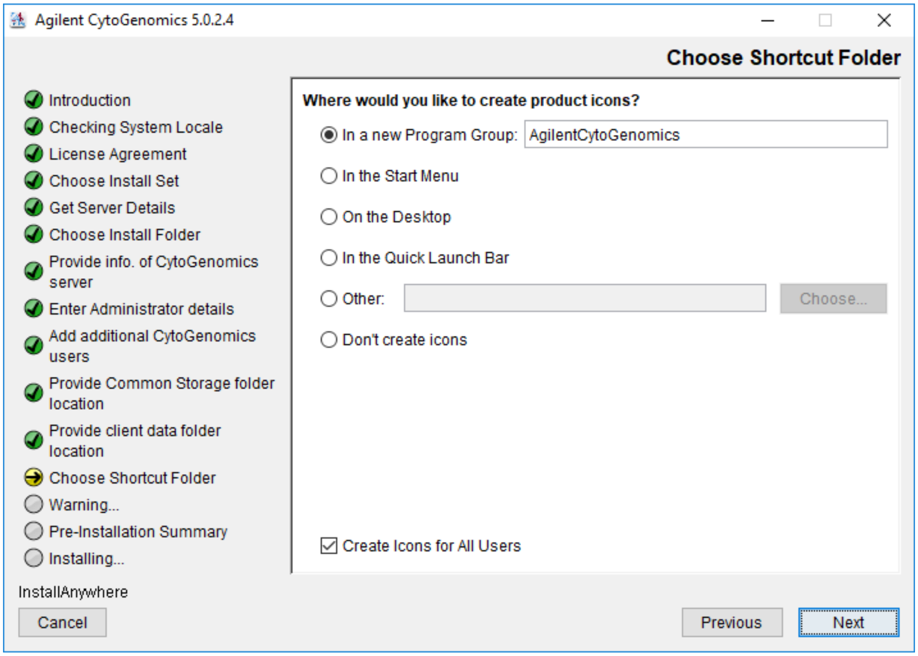
Figure 11 Choose client data folder screen – Windows

19 By default, the client data folder is created inside the folder C:\Agilent\AgilentCytoGenomics5.0.X.X\Client (where X.X is the revision number). Leave this folder as-is, or Click **Choose**, browse to the desired folder, and then click **Save.**

The client data folder is where the program installs the files for the genome build and reference genomes.

20 Click **Next**.

The Choose Shortcut Folder screen opens.



Choose Shortcut Folder

- ✓ Introduction
- ✓ Checking System Locale
- ✓ License Agreement
- ✓ Choose Install Set
- ✓ Get Server Details
- ✓ Choose Install Folder
- ✓ Provide info. of CytoGenomics server
- ✓ Enter Administrator details
- ✓ Add additional CytoGenomics users
- ✓ Provide Common Storage folder location
- ✓ Provide client data folder location
- ➔ Choose Shortcut Folder
- ○ Warning...
- ○ Pre-Installation Summary
- ○ Installing...

Where would you like to create product icons?

● In a new Program Group: AgilentCytoGenomics

○ In the Start Menu

○ On the Desktop

○ In the Quick Launch Bar

○ Other:

○ Don't create icons

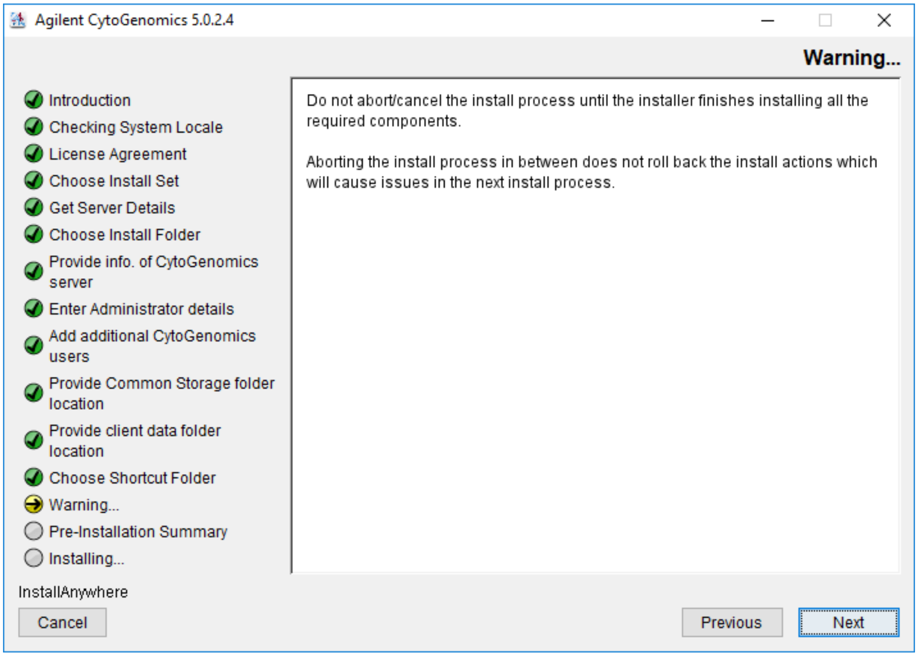
☑ Create Icons for All Users

Figure 12 Choose Shortcut Folder screen – Windows

21 By default, program icons are installed in the Agilent CytoGenomics 5.0.X.X program group on your computer (where X.X is the revision number). To select another location for the program icons, select the desired location (on the desktop, for example) and then click **Next**.

NOTE If more than one user plans to use Agilent CytoGenomics 5.0 on this computer, select **Create Icons for All Users**. Otherwise, other users do not see the program icons.

The Warning screen opens.



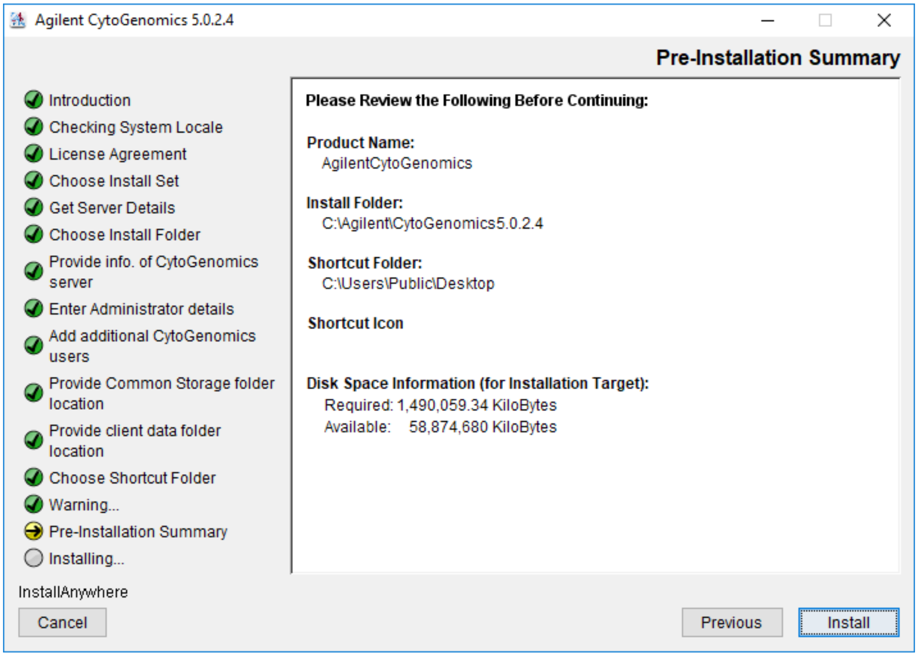
Do not abort/cancel the install process until the installer finishes installing all the required components.

Aborting the install process in between does not roll back the install actions which will cause issues in the next install process.

Figure 13 Warning screen – Windows

22 Read the message that cautions you not to stop the installation once it has started, and then click **Next**.

The Pre-Installation Summary screen opens.



Please Review the Following Before Continuing:

Product Name:
AgilentCytoGenomics

Install Folder:
C:\Agilent\CytoGenomics5.0.2.4

Shortcut Folder:
C:\Users\Public\Desktop

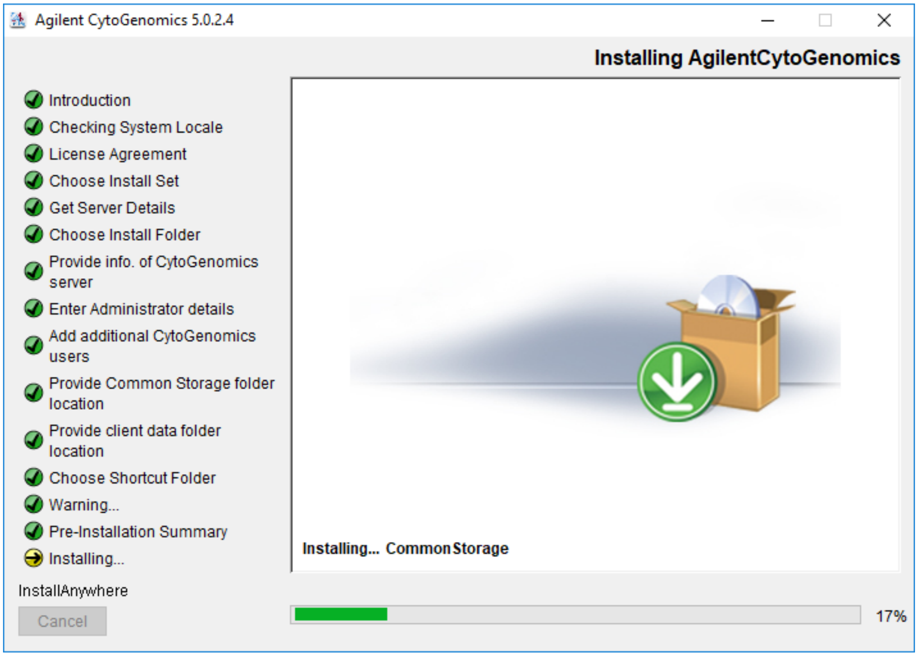
Shortcut Icon

Disk Space Information (for Installation Target):
Required: 1,490,059.34 KiloBytes
Available: 58,874,680 KiloBytes

Figure 14 Pre-Installation Summary screen – Windows

23 Review the installation setup information. If you want to change any of the settings, click **Previous** and go back and change the settings. To start the installation, click **Install**.

The Installing Agilent CytoGenomics screen opens and is displayed until the installation is complete.



Agilent CytoGenomics 5.0.2.4

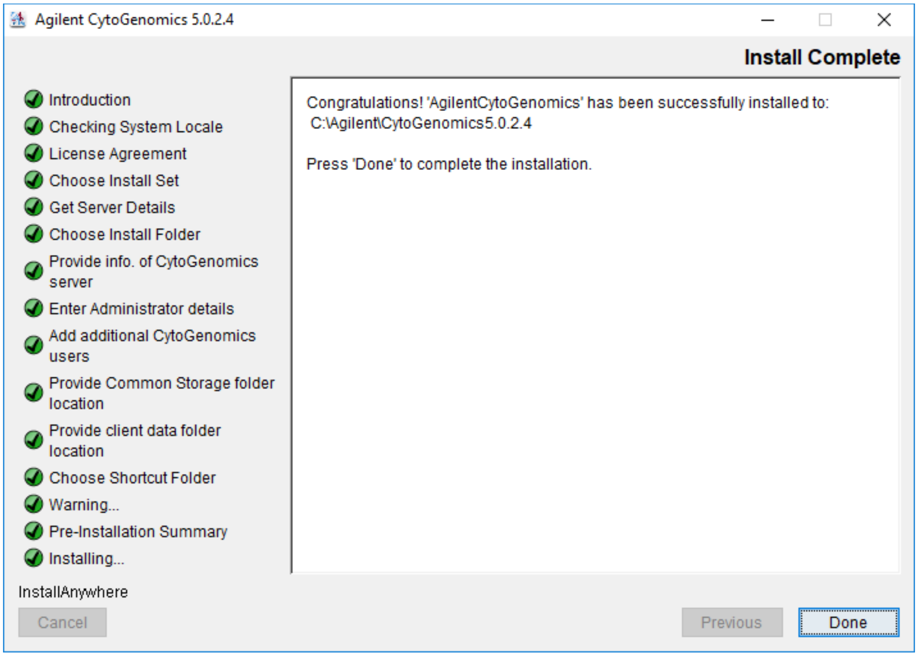
Installing AgilentCytoGenomics

Installing... CommonStorage

17%

Figure 15 Installing Agilent CytoGenomics screen – Windows

When the installation is complete, the Installation Complete screen opens.



Congratulations! 'AgilentCytoGenomics' has been successfully installed to:
C:\Agilent\CytoGenomics5.0.2.4

Press 'Done' to complete the installation.

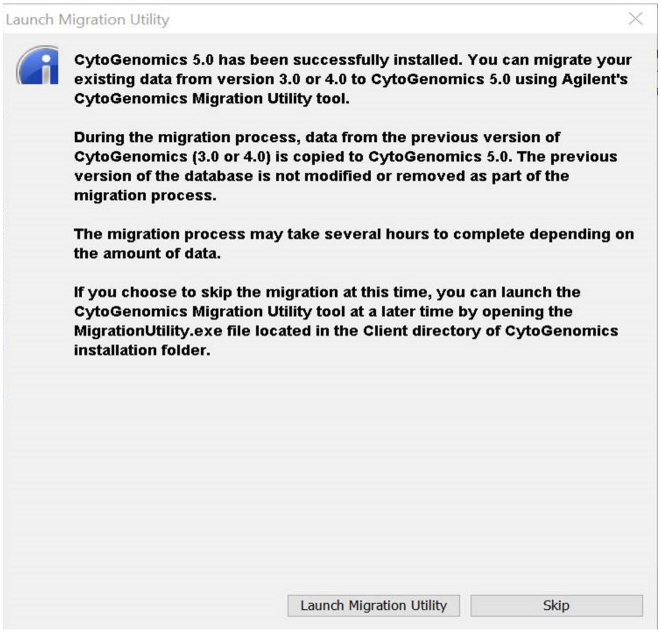
Figure 16 Installation Complete screen – Windows

24 Click **Done**.

The Launch Migration Utility dialog box opens asking if you want to launch Agilent's migration utility tool designed to transfer data from a previous version of CytoGenomics server to the CytoGenomics 5.0 server.

NOTE

If the installer was unable to complete installation of CytoGenomics, then the Install Complete screen will note the installation errors and provide instructions on how to proceed.



CytoGenomics 5.0 has been successfully installed. You can migrate your existing data from version 3.0 or 4.0 to CytoGenomics 5.0 using Agilent's CytoGenomics Migration Utility tool.

During the migration process, data from the previous version of CytoGenomics (3.0 or 4.0) is copied to CytoGenomics 5.0. The previous version of the database is not modified or removed as part of the migration process.

The migration process may take several hours to complete depending on the amount of data.

If you choose to skip the migration at this time, you can launch the CytoGenomics Migration Utility tool at a later time by opening the MigrationUtility.exe file located in the Client directory of CytoGenomics installation folder.

Figure 17 Launch Migration Utility dialog box – Windows

25 Click **Skip** to close the dialog box without launching the migration utility tool.

Because these instructions are for installing Agilent CytoGenomics 5.0 on a Windows system that does not have a previous version of CytoGenomics installed, there is no need to use the migration utility tool to transfer data.

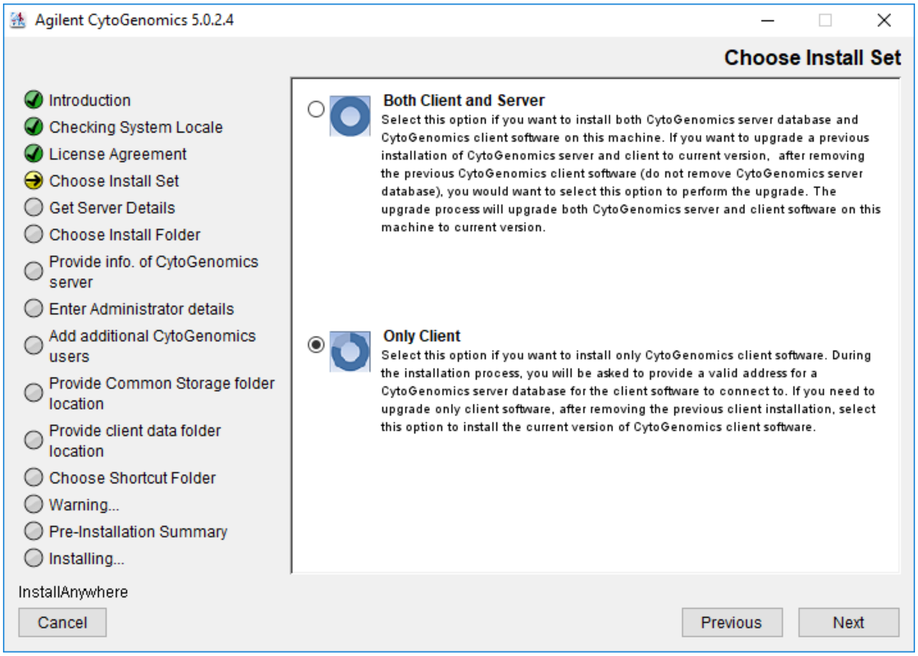
26 Make sure the folder where you installed the software is shared with read/write permission for all client computers and for all users who run Agilent CytoGenomics.

Step 3. Install the client software on additional Windows computers

To use other computers to run Agilent CytoGenomics 5.0 client software (with a shared database), install the client software on each of the computers.

1 On each computer you want to run the Agilent CytoGenomics 5.0 program, run the installation wizard, as described in "Step 2. Install the database server and client on a single Windows computer" on page 20.

2 When the Choose Install Set screen opens, select **Only Client**.



Choose Install Set

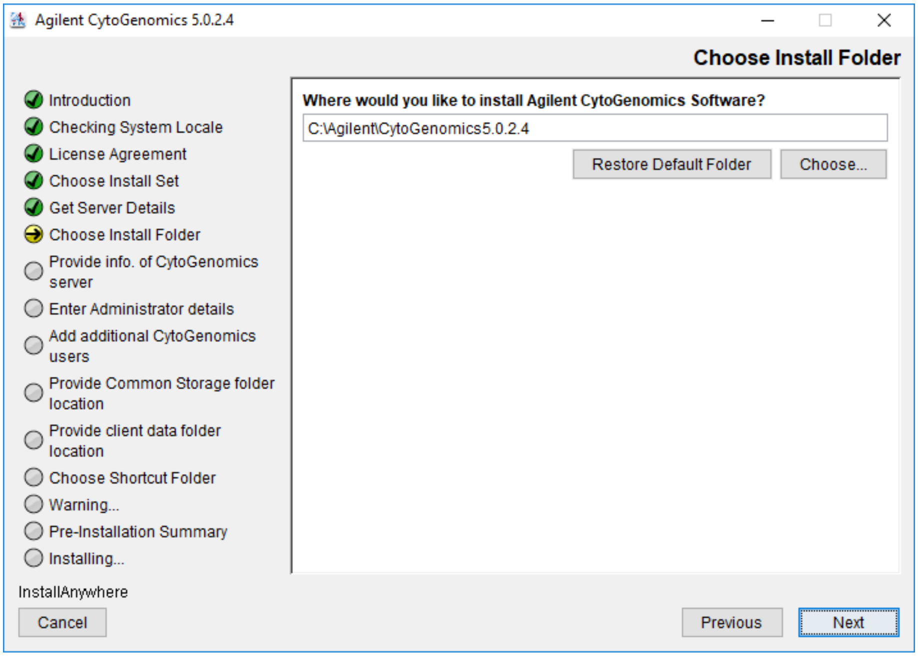
○ **Both Client and Server**
Select this option if you want to install both CytoGenomics server database and CytoGenomics client software on this machine. If you want to upgrade a previous installation of CytoGenomics server and client to current version, after removing the previous CytoGenomics client software (do not remove CytoGenomics server database), you would want to select this option to perform the upgrade. The upgrade process will upgrade both CytoGenomics server and client software on this machine to current version.

● **Only Client**
Select this option if you want to install only CytoGenomics client software. During the installation process, you will be asked to provide a valid address for a CytoGenomics server database for the client software to connect to. If you need to upgrade only client software, after removing the previous client installation, select this option to install the current version of CytoGenomics client software.

Figure 18 Choose Install Set screen – Windows – select **Only Client**

3 Click **Next**.

The Choose Install Folder screen opens.



Where would you like to install Agilent CytoGenomics Software?

C:\Agilent\CytoGenomics5.0.2.4

Figure 19 Choose Install Folder screen – Windows

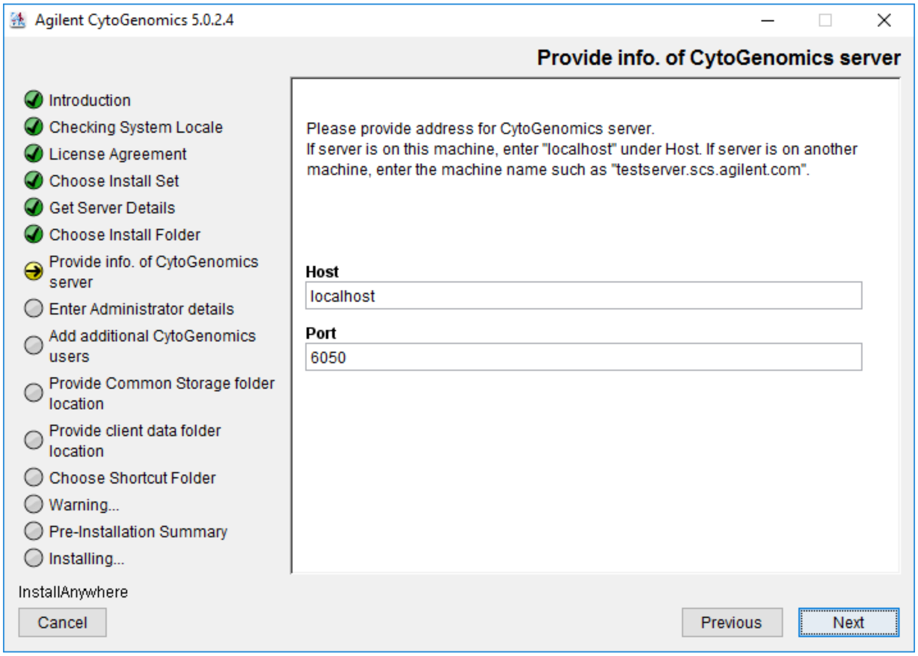
4 By default, the program is installed in C:\Agilent\AgilentCytoGenomics5.0.X.X (where X.X is the revision number). Leave this folder as-is, or type the location and name of the folder where you want to install Agilent CytoGenomics 5.0.

OR

Click **Choose** and browse to a location where you want to install the program, and then click **Save.**

5 Click **Next**.

The Provide Info. of CytoGenomics server screen opens.



Please provide address for CytoGenomics server.
If server is on this machine, enter "localhost" under Host. If server is on another machine, enter the machine name such as "testserver.scs.agilent.com".

Host: localhost

Port: 6050

Figure 20 Provide Info. of CytoGenomics server screen – Windows

6 Under **Host**, type the assigned computer name or IP address of the computer (from step 2) where you installed the Agilent CytoGenomics 5.0 database server. (To find the computer name of your current computer, click **Start** > **Control Panel** > **System**.)

7 Accept the default **Port**, unless your system administrator tells you otherwise.

8 Click **Next**.

Installer immediately tests the connection to the specified database. If incorrect database parameters are provided, or the PostgreSQL database service is not running, a message is displayed.

You can choose to complete the installation and change database connection parameters when launching the client software. However, Agilent recommends that you provide the correct database information during installation.

Continue the installation wizard. The next screen is the Choose client data folder screen. Follow the instructions for the installation wizard to enter the client data folder location, choose a shortcut location, and start the installation. For information, see step 19 through step 26 in the section "Step 2. Install the database server and client on a single Windows computer" on page 20.

Step 4. Start the Agilent CytoGenomics 5.0 client software

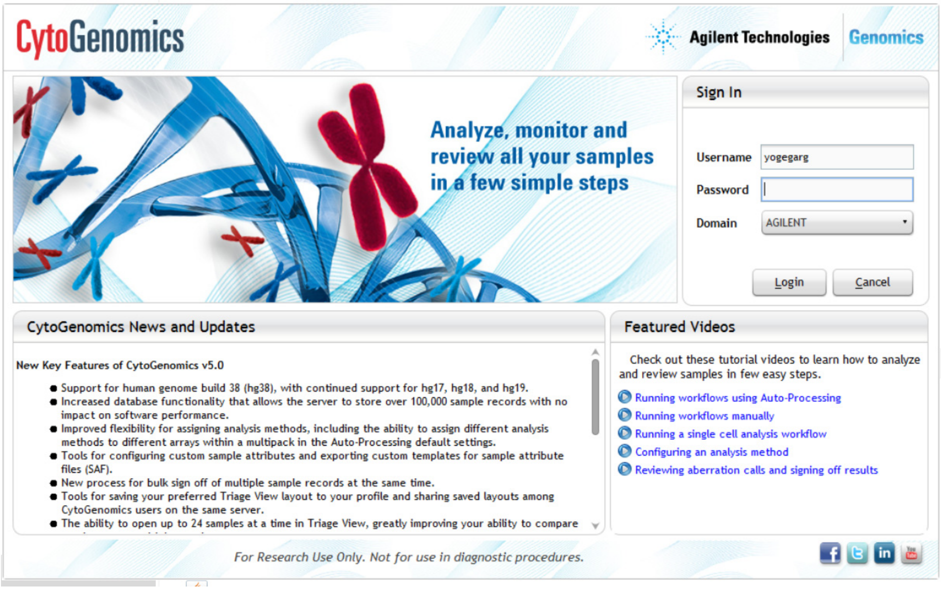
After you install the Agilent CytoGenomics database server and client programs as described in this manual, start the program.

- Double-click the Agilent CytoGenomics 5.0 icon, or select Agilent CytoGenomics 5.0 from the Windows Start menu.

NOTE How you start the program depends on the choice you made for Shortcut Folder during installation of the Agilent CytoGenomics client.

Step 5. Log in to Agilent CytoGenomics

After you start the program, the Login screen opens. The username and domain for the administrator set during installation appears in the Sign In area of the screen.



Username: yogegarg

Domain: AGILENT

New Key Features of CytoGenomics v5.0

- Support for human genome build 38 (hg38), with continued support for hg17, hg18, and hg19.
- Increased database functionality that allows the server to store over 100,000 sample records with no impact on software performance.
- Improved flexibility for assigning analysis methods, including the ability to assign different analysis methods to different arrays within a multipack in the Auto-Processing default settings.
- Tools for configuring custom sample attributes and exporting custom templates for sample attribute files (SAF).
- New process for bulk sign off of multiple sample records at the same time.
- Tools for saving your preferred Triage View layout to your profile and sharing saved layouts among CytoGenomics users on the same server.
- The ability to open up to 24 samples at a time in Triage View, greatly improving your ability to compare

Check out these tutorial videos to learn how to analyze and review samples in few easy steps.

- Running workflows using Auto-Processing
- Running workflows manually
- Running a single cell analysis workflow
- Configuring an analysis method
- Reviewing aberration calls and signing off results

For Research Use Only. Not for use in diagnostic procedures.

Figure 21 Login screen

1 Enter your username and password.

   To change the domain, click the arrow next to **Domain** and select the correct domain. Otherwise, leave it as-is.

2 Click **Login**.

   After the software is started, users with administrator privileges can add additional users and assign their roles.

NOTE

If you are using a local machine that is not part of a domain, you will see a message that the software cannot find the domain. Click **OK** to ignore this message.

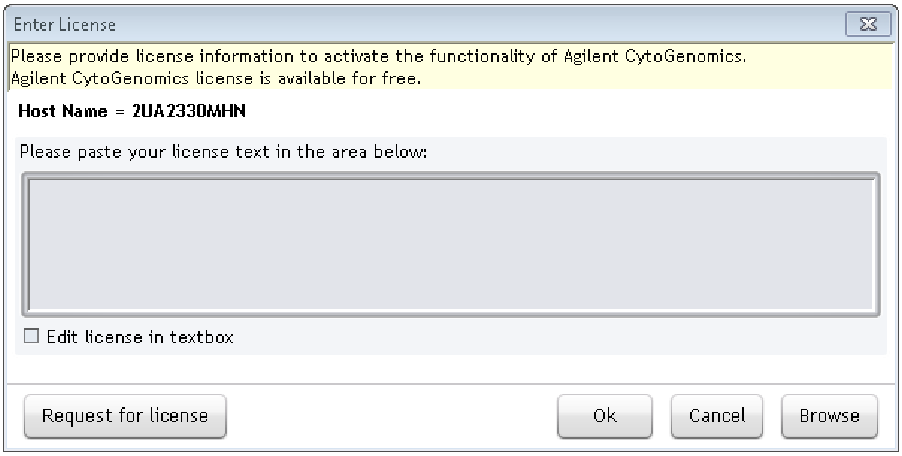
If the installer did not properly share the common storage folder during installation, then an Application Initialization Error message will open notifying you that you do not have access to the common storage folder. This error message provides instructions on how to share the folder with all users. Follow the steps in the error message, then click **OK** to close the message and restart the application.

Step 6. Add your software license

When you log in for the first time, the Enter License dialog box opens (Figure 22).

1. If you do not already have the license file saved to your computer, click **Request for license** to open the Agilent website to the CytoGenomics license request page. Complete the fields in the request form to obtain a CytoGenomics software license. The license is contained in a text file and sent by email.
2. At the bottom of the Enter License dialog box, click **Browse**.

   The Open dialog box opens.



Please provide license information to activate the functionality of Agilent CytoGenomics.
Agilent CytoGenomics license is available for free.

Host Name = 2UA2330MHN

Please paste your license text in the area below:

Figure 22 Enter License dialog box

3. Browse to the saved license text file. Select the file and click **Open**.

   The program loads the contents of the file into the text box on the Enter License dialog box.
4. Click **OK**.

   The Agilent CytoGenomics program opens to the Home screen (Figure 23).

   Upon opening the program, you may see a message notifying you that updates are available for the software.

- If you want to download the available updates at this time, mark the check box next to **Software update** then click **Download**. During the download process, you are blocked from using CytoGenomics. Download time is dependent on internet speed.
- If you do not want to download the available update at this time, click **Cancel**.
- To stop being automatically notified of available updates, clear the check box labeled ***Check for updates at application start up***. This check box is also accessible from Local Settings tab of the Configure Settings > Settings screen of CytoGenomics.

CytoGenomics is a workflow-based application that helps you analyze, review, and report on CGH and CGH+SNP microarray data in a few simple steps. You import your samples and run an analysis, then return to CytoGenomics to review the QC metrics, review and classify aberration calls in the triage view, and finally create reports.

You can use CytoGenomics as a standalone program, or you can share data by connecting to a central database.

CytoGenomics can run a background process to automatically feature extract and analyze data as microarrays are scanned, using preconfigured design files and analysis workflow settings. Use Settings on the **Auto-Processing** tab to set up the input and archive folders, then start automated processing using the controls. You can then exit from CytoGenomics and return when you wish to review your samples.

Figure 23 Agilent CytoGenomics program Home screen

Step 7. Add users and assign roles

Before other users can log in to Agilent CytoGenomics, a user with administrator privileges must add the users and assign user roles (if the users were not added during installation of the server). The user role determines what capabilities the user has within Agilent CytoGenomics. For information on what capabilities each user role has, see *"User Roles and Capabilities"* on page 16. For information on how to add users and assign roles, see "To manage users and roles" on page 110.

Upgrading from CytoGenomics 3.0 or 4.0 to CytoGenomics 5.0 and Migrating Data – Windows

These instructions are for users of CytoGenomics 3.0 or 4.0 who want to upgrade to CytoGenomics 5.0 and migrate all sample records from the previous database to the new CytoGenomics 5.0 database.

NOTE

CytoGenomics 5.0 is compatible with and can co-exist on the same machine as CytoGenomics 3.0 or 4.0. It is not necessary to uninstall the previous version of CytoGenomics (i.e., v3.0 or 4.0) in order to install v5.0.

Step 1. Install CytoGenomics 5.0 on the server computer

Follow these steps to install Agilent CytoGenomics 5.0 on the computer where the CytoGenomics server software is installed.

1 Download Agilent CytoGenomics 5.0.X.X from Agilent Technologies and check the system requirements.

   See “a. Download the Windows version of the software and release notes” on page 18 for detailed instructions on this step.

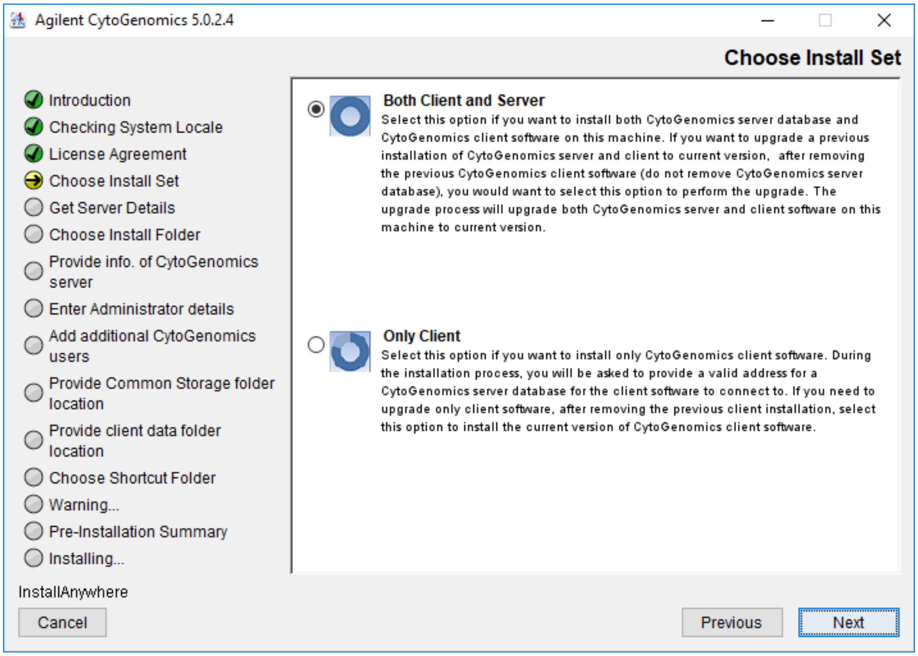
2 Double-click the Agilent CytoGenomics 5.0 application file that you downloaded from Agilent.

3 On the Introduction screen, read the introductory information and then click **Next**.

   The License Agreement screen opens.

4 Read the license agreement. Click **I accept the terms of the License Agreement** and then click **Next**.

   The Choose Install Set screen opens.



● **Both Client and Server**
Select this option if you want to install both CytoGenomics server database and CytoGenomics client software on this machine. If you want to upgrade a previous installation of CytoGenomics server and client to current version, after removing the previous CytoGenomics client software (do not remove CytoGenomics server database), you would want to select this option to perform the upgrade. The upgrade process will upgrade both CytoGenomics server and client software on this machine to current version.

○ **Only Client**
Select this option if you want to install only CytoGenomics client software. During the installation process, you will be asked to provide a valid address for a CytoGenomics server database for the client software to connect to. If you need to upgrade only client software, after removing the previous client installation, select this option to install the current version of CytoGenomics client software.

Figure 24 Choose Install Set screen – Windows – select **Both Client and Server**

5 On the Choose Install Set screen, select **Both Client and Server**. Click **Next**.

The following dialog box opens to inform you that you have selected to install the CytoGenomics server and client.

Agilent CytoGenomics software Installation.

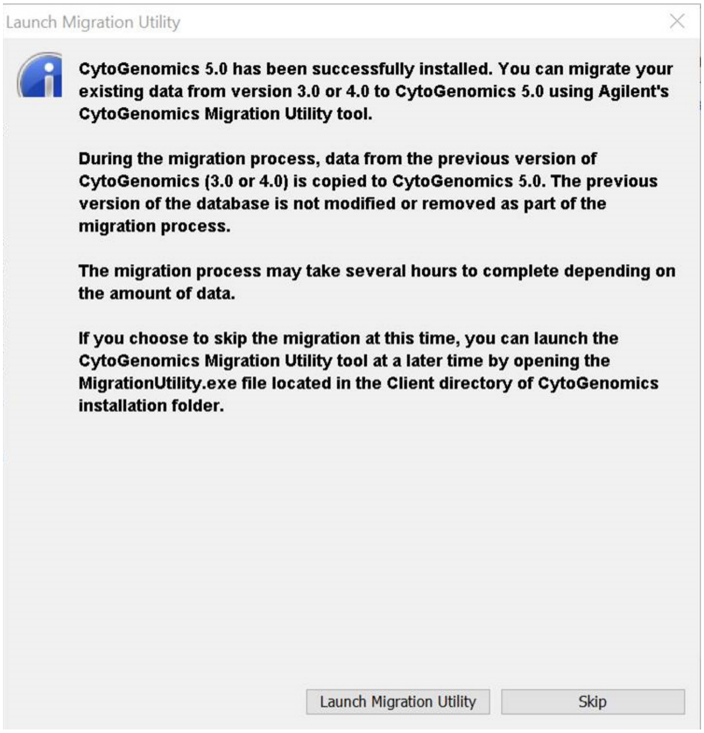
You have opted to install both Agilent CytoGenomics Server and Agilent CytoGenomics Client.

Figure 25 Dialog box – Agilent CytoGenomics software installation

6 Click **OK** in the dialog box to continue.

7 Continue the installation wizard. The next screen is the Choose Install Folder screen. Follow the instructions for the installation wizard to enter the client data folder location, choose a shortcut location, and start the installation. For information, see step 8 through step 24 in the section "Step 2. Install the database server and client on a single Windows computer" on page 20.

At the completion of installation, the Launch Migration Utility dialog box opens asking if you want to launch Agilent's migration utility tool designed to transfer data from a previous version of CytoGenomics server to the CytoGenomics 5.0. server.



CytoGenomics 5.0 has been successfully installed. You can migrate your existing data from version 3.0 or 4.0 to CytoGenomics 5.0 using Agilent's CytoGenomics Migration Utility tool.

During the migration process, data from the previous version of CytoGenomics (3.0 or 4.0) is copied to CytoGenomics 5.0. The previous version of the database is not modified or removed as part of the migration process.

The migration process may take several hours to complete depending on the amount of data.

If you choose to skip the migration at this time, you can launch the CytoGenomics Migration Utility tool at a later time by opening the MigrationUtility.exe file located in the Client directory of CytoGenomics installation folder.

Figure 26 Launch Migration Utility dialog box – Windows

8 Depending on your needs, click either **Launch Migration Utility** or **Skip**.

- Click **Launch Migration Utility** if you have data saved to the previous version of CytoGenomics server (e.g., sample results, track files, and other supporting files) and you want to transfer that data to the CytoGenomics 5.0 server. The migration utility tool launches on your PC. Proceed to "Step 2. Migrate data to CytoGenomics 5.0 server" on page 47.
- Click **Skip** if you do not want to transfer any data (e.g., sample results, track files, and other supporting files) from the previous version of CytoGenomics server to the CytoGenomics 5.0 server at this time. The dialog box will close and that data will remain on the previous version of the server. Proceed to "Step 3. Upgrade to CytoGenomics 5.0 on the client computers" on page 52.

NOTE

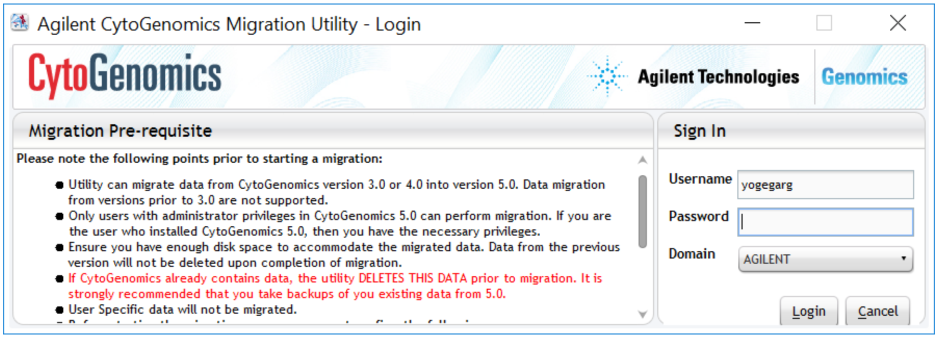
To protect against loss of data and ensure migration of all analyzed samples, Agilent strongly recommends migrating data immediately upon completion of the CytoGenomics 5.0 installation.

If you click **Skip** with the intention of migrating your data at a later time, be aware that if CytoGenomics 5.0 already contains data at the time of migration, the Migration Utility application will delete that data and overwrite it with data from the previous version of CytoGenomics.

Step 2. Migrate data to CytoGenomics 5.0 server

If you selected to launch the migration utility tool, follow these step to use the tool to transfer data from the previous version of CytoGenomics server to CytoGenomics server 5.0. If you do not want to transfer data, bypass this step and proceed to "Step 3. Upgrade to CytoGenomics 5.0 on the client computers" on page 52.

1 On the Sign In screen of the migration utility application (Figure 27), review the list of migration prerequisites and make sure they are all met before you continue.



Please note the following points prior to starting a migration:

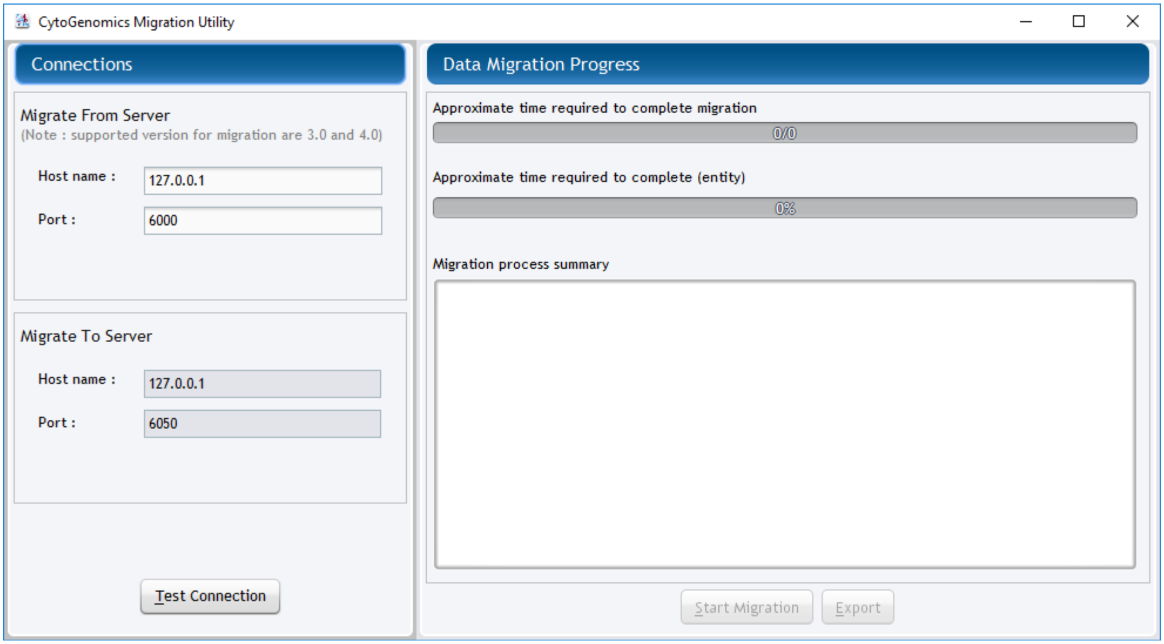
- Utility can migrate data from CytoGenomics version 3.0 or 4.0 into version 5.0. Data migration from versions prior to 3.0 are not supported.
- Only users with administrator privileges in CytoGenomics 5.0 can perform migration. If you are the user who installed CytoGenomics 5.0, then you have the necessary privileges.
- Ensure you have enough disk space to accommodate the migrated data. Data from the previous version will not be deleted upon completion of migration.
- If CytoGenomics already contains data, the utility DELETES THIS DATA prior to migration. It is strongly recommended that you take backups of you existing data from 5.0.
- User Specific data will not be migrated.

Username yogegarg
Password
Domain AGILENT

Figure 27 CytoGenomics Migration Utility application login screen

2 Log in with your username and password. The username and domain for the administrator set during installation appears in the Sign In area of the screen. (Only accounts with administrator privileges can migrate data.)

The CytoGenomics Migration Utility application opens.



(Note : supported version for migration are 3.0 and 4.0)

Migrate From Server
Host name : 127.0.0.1
Port : 6000

Migrate To Server
Host name : 127.0.0.1
Port : 6050

Figure 28 CytoGenomics Migration Utility application

3 Under **Migrate From Server**, enter the host name (i.e., IP address) and port number where the previous version of CytoGenomics server is installed.

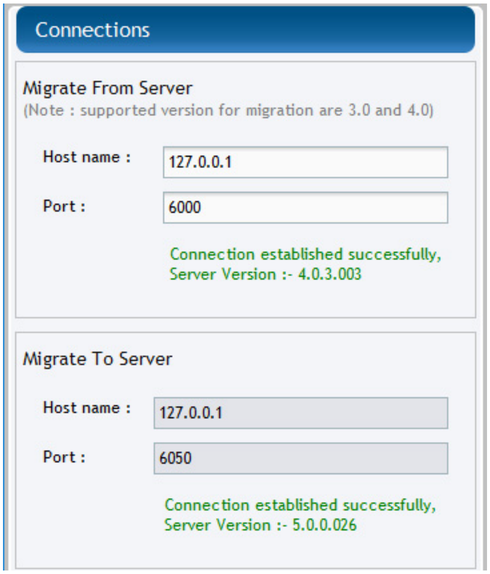
4 Under **Migrate To Server**, enter the host name (i.e., IP address) and port number where the CytoGenomics 5.0 server is installed. If CytoGenomics 5.0 server is installed on the same PC as the previous version of CytoGenomics server, then the host names are the same.

NOTE

If CytoGenomics 5.0 server is installed on the same PC as the previous version of CytoGenomics server, then the host names of the two servers are the same.

5 Click **Test Connection**.

The screen displays the results of connection test with each server.



Migrate From Server
(Note : supported version for migration are 3.0 and 4.0)

Host name : 127.0.0.1

Port : 6000

Connection established successfully,
Server Version :- 4.0.3.003

Migrate To Server

Host name : 127.0.0.1

Port : 6050

Connection established successfully,
Server Version :- 5.0.0.026

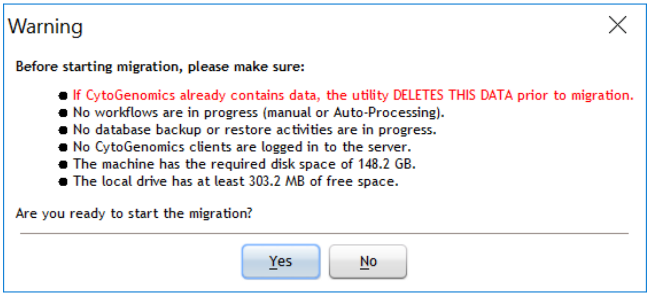
Figure 29 CytoGenomics Migration Utility application – Connections established

NOTE If the application was unable to successfully establish a connection to one or both servers, verify that the correct host name and port number are entered and test the connection again. You cannot proceed to data migration until the application connects to the servers.

---

6 Once the application has successfully connected to the servers, click **Start Migration**.

The Warning message box opens.



Before starting migration, please make sure:

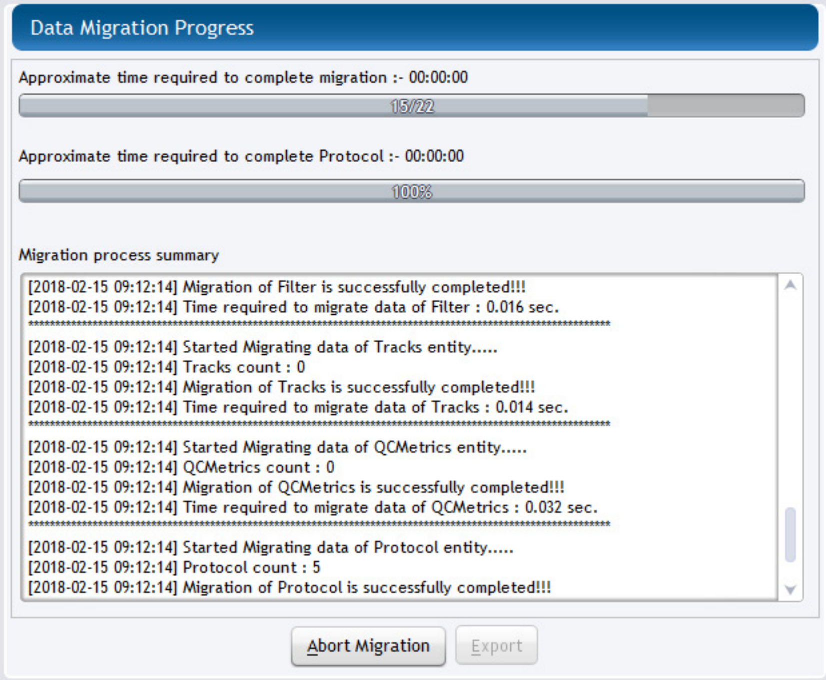
- If CytoGenomics already contains data, the utility DELETES THIS DATA prior to migration.
- No workflows are in progress (manual or Auto-Processing).
- No database backup or restore activities are in progress.
- No CytoGenomics clients are logged in to the server.
- The machine has the required disk space of 148.2 GB.
- The local drive has at least 303.2 MB of free space.

Are you ready to start the migration?

Figure 30 Warning message box

7 As instructed in the Warning message box, make sure that CytoGenomics is not actively running any workflows or performing any database backup or restore activities and that all clients are logged out. If your CytoGenomics 5.0 database already contains date, make sure that data has been backed up. Then, click **Yes** to continue with the migration.

The right side of the screen (under **Data Migration Process**) displays the progress of the migration and the migration process summary.



Approximate time required to complete migration :- 00:00:00

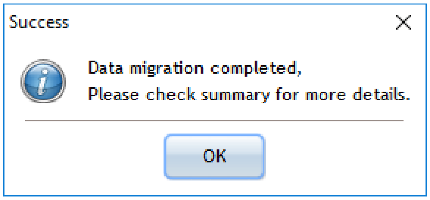
Approximate time required to complete Protocol :- 00:00:00

Migration process summary

```
[2018-02-15 09:12:14] Migration of Filter is successfully completed!!!
[2018-02-15 09:12:14] Time required to migrate data of Filter : 0.016 sec.
****************************************************************************************************
[2018-02-15 09:12:14] Started Migrating data of Tracks entity.....
[2018-02-15 09:12:14] Tracks count : 0
[2018-02-15 09:12:14] Migration of Tracks is successfully completed!!!
[2018-02-15 09:12:14] Time required to migrate data of Tracks : 0.014 sec.
****************************************************************************************************
[2018-02-15 09:12:14] Started Migrating data of QCMetrics entity.....
[2018-02-15 09:12:14] QCMetrics count : 0
[2018-02-15 09:12:14] Migration of QCMetrics is successfully completed!!!
[2018-02-15 09:12:14] Time required to migrate data of QCMetrics : 0.032 sec.
****************************************************************************************************
[2018-02-15 09:12:14] Started Migrating data of Protocol entity.....
[2018-02-15 09:12:14] Protocol count : 5
[2018-02-15 09:12:14] Migration of Protocol is successfully completed!!!
```

Figure 31 CytoGenomics Migration Utility application – Migration in progress

Upon completion of the migration process, the following message box opens.



Data migration completed,
Please check summary for more details.

Figure 32 CytoGenomics Migration Utility application – Data migration complete

8 Click **OK** to close the message box.

9 If desired, click **Export** to export a summary of the migration job.

10 Click the X in the top right corner of the Migration Utility application window to close the application.

Step 3. Upgrade to CytoGenomics 5.0 on the client computers

Follow these steps to install Agilent CytoGenomics 5.0 on each client computer.

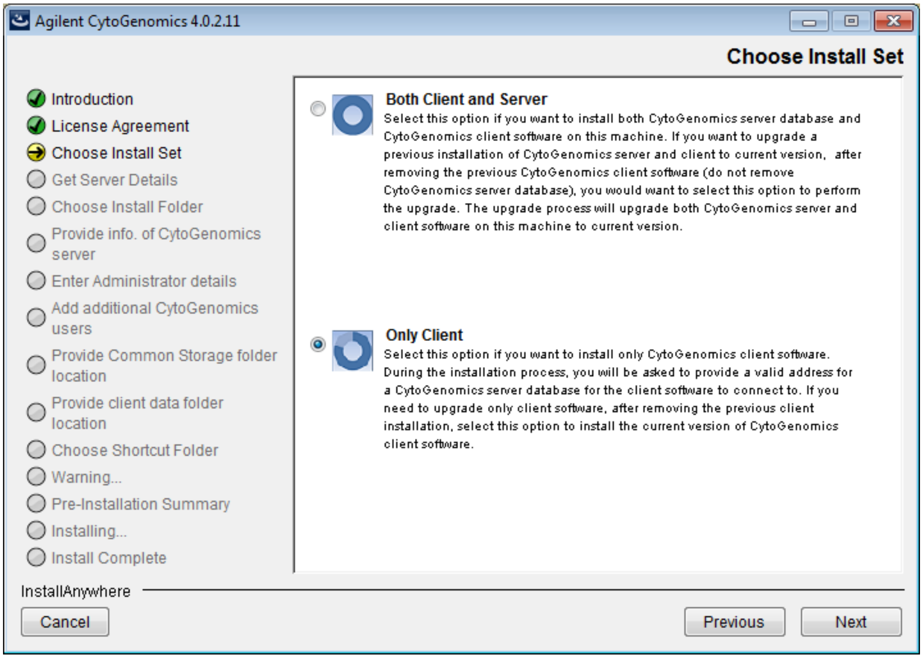
1 Double-click the Agilent CytoGenomics 5.0.X.X application file that you downloaded from Agilent.

2 On the Introduction screen, read the introductory information then click **Next**.

The License Agreement screen opens.

3 Read the license agreement. Click **I accept the terms of the License Agreement** and then click **Next**.

The Choose Install Set screen opens.



○ **Both Client and Server**

Select this option if you want to install both CytoGenomics server database and CytoGenomics client software on this machine. If you want to upgrade a previous installation of CytoGenomics server and client to current version, after removing the previous CytoGenomics client software (do not remove CytoGenomics server database), you would want to select this option to perform the upgrade. The upgrade process will upgrade both CytoGenomics server and client software on this machine to current version.

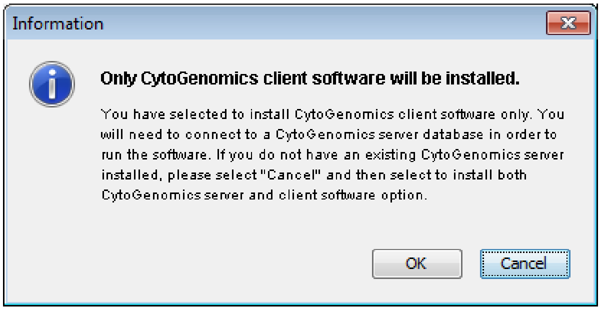
● **Only Client**

Select this option if you want to install only CytoGenomics client software. During the installation process, you will be asked to provide a valid address for a CytoGenomics server database for the client software to connect to. If you need to upgrade only client software, after removing the previous client installation, select this option to install the current version of CytoGenomics client software.

Figure 33 Choose Install Set screen – Windows – select **Only Client**

4 On the Choose Install Set screen, select **Only Client**. Click **Next**.

The following dialog box opens to inform you that you have selected to install only the Agilent CytoGenomics 5.0 client.



Only CytoGenomics client software will be installed.

You have selected to install CytoGenomics client software only. You will need to connect to a CytoGenomics server database in order to run the software. If you do not have an existing CytoGenomics server installed, please select "Cancel" and then select to install both CytoGenomics server and client software option.

Figure 34 Dialog box – Only CytoGenomics client software will be installed

5 Click **OK** in the dialog box to continue.

The Choose Install Folder screen opens.

6 At the Choose Install Folder screen, the default folder for installation of the program is C:\Agilent\AgilentCytoGenomics5.0.X.X (where X.X is the revision number). Leave this folder as-is, or click **Choose** and browse to a location where you want to install the program, and then click **Save.**

7 Click **Next**.

8 Continue the installation wizard. Follow the instructions to provide server information, choose a shortcut location, and start the installation. See step 6 through step 8 in the section “Step 3. Install the client software on additional Windows computers” on page 36.

Step 4. Start the Agilent CytoGenomics 5.0 client software, log in, and add new software license

1 On the server and client computers, start the Agilent CytoGenomics program.

   See “Step 4. Start the Agilent CytoGenomics 5.0 client software” on page 39.

2 Log in.

   See “Step 5. Log in to Agilent CytoGenomics” on page 39.

3 Enter your updated license information.

   See “Step 6. Add your software license” on page 41.

Upgrading from CytoGenomics 5.0.0 or 5.0.1 to CytoGenomics 5.0.2

If you are using CytoGenomics 5.0.0 or 5.0.1 and want to upgrade to CytoGenomics 5.0.2, you only need to upgrade the CytoGenomics client application. You do not need to upgrade to the CytoGenomics server application or migrate data from the previous version to the new version.

Step 1. Install CytoGenomics 5.0.2 client and uninstall CytoGenomics 5.0.0 or 5.0.1 client

1. Download Agilent CytoGenomics 5.0.2 from Agilent Technologies and check the system requirements.

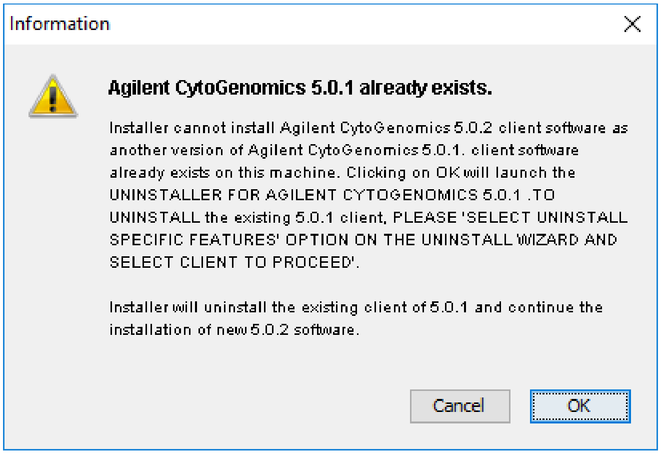
   See "a. Download the Windows version of the software and release notes" on page 18 for detailed instructions on this step.

2. Double-click the Agilent CytoGenomics 5.0.2 application file that you downloaded from Agilent.

   The InstallAnywhere dialog box is displayed. Then, the installation wizard opens to the Introduction screen.

3. Read the introductory information, then click **Next**.

   The following message box opens notifying you that the existing version of CytoGenomics client must be uninstalled before installing CytoGenomics 5.0.2 client.


Information

Agilent CytoGenomics 5.0.1 already exists.

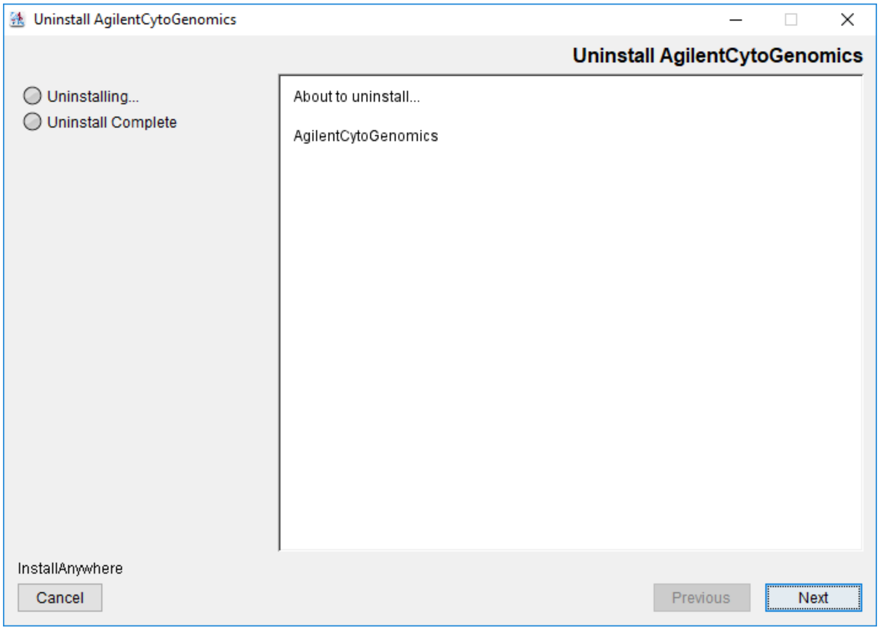
Installer cannot install Agilent CytoGenomics 5.0.2 client software as another version of Agilent CytoGenomics 5.0.1. client software already exists on this machine. Clicking on OK will launch the UNINSTALLER FOR AGILENT CYTOGENOMICS 5.0.1 .TO UNINSTALL the existing 5.0.1 client, PLEASE 'SELECT UNINSTALL SPECIFIC FEATURES' OPTION ON THE UNINSTALL WIZARD AND SELECT CLIENT TO PROCEED'.

Installer will uninstall the existing client of 5.0.1 and continue the installation of new 5.0.2 software.

Figure 35 “Agilent CytoGenomics 5.0.1 already exists” message box

4 Click **OK** in the message box.

The CytoGenomics uninstaller opens.



About to uninstall...

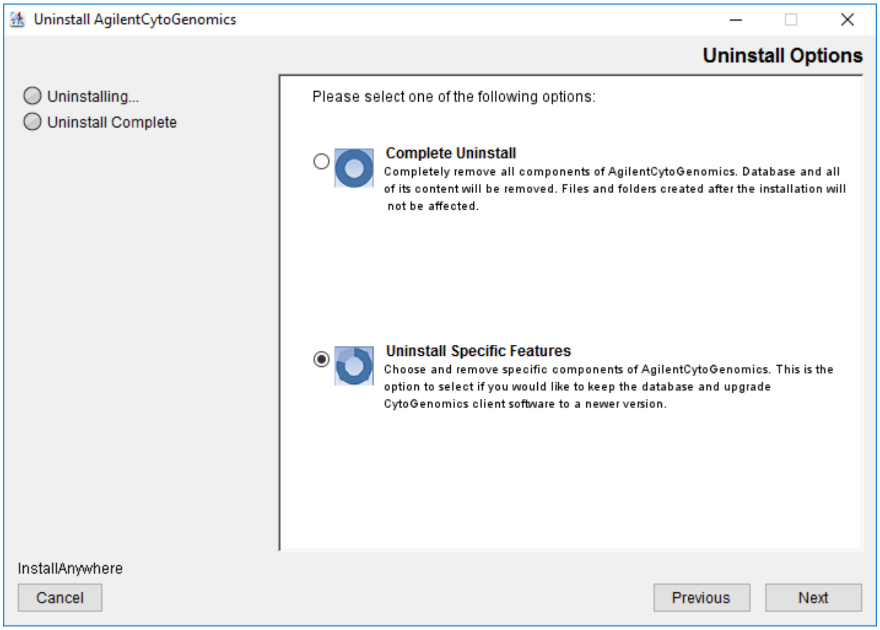
AgilentCytoGenomics

Figure 36 CytoGenomics Uninstaller – Windows

5 Click **Next**.

6 Read the warning information. You are cautioned not to stop the Uninstaller once it has started to remove the programs. Click **Next**.

The Uninstall Options screen opens.



Please select one of the following options:

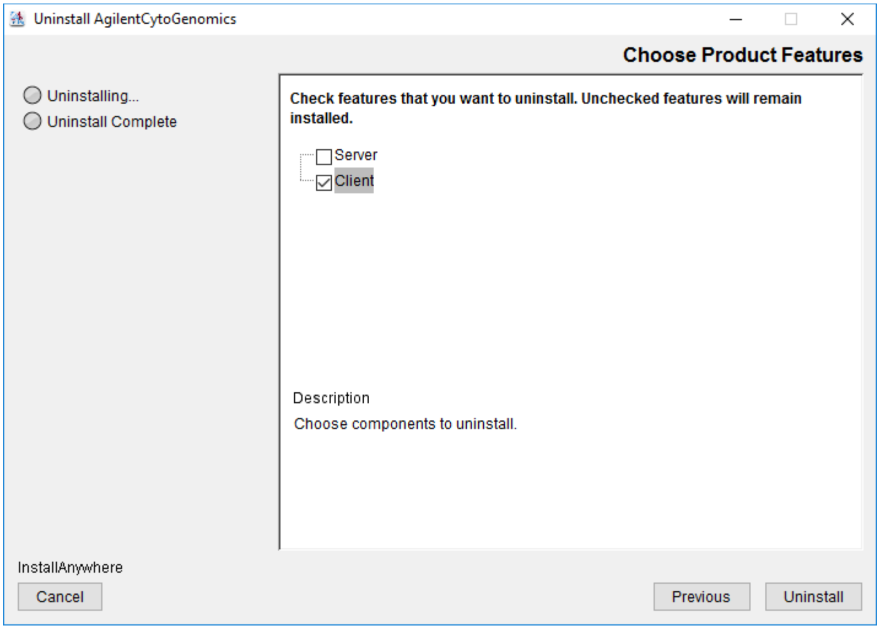
○ **Complete Uninstall**
Completely remove all components of AgilentCytoGenomics. Database and all of its content will be removed. Files and folders created after the installation will not be affected.

● **Uninstall Specific Features**
Choose and remove specific components of AgilentCytoGenomics. This is the option to select if you would like to keep the database and upgrade CytoGenomics client software to a newer version.

Figure 37 Uninstall Options screen – Windows – select **Uninstall Specific Features**

7 Select **Uninstall Specific Features**.

The Choose Product Features screen opens.



Check features that you want to uninstall. Unchecked features will remain installed.

☐ Server
☑ Client

Description
Choose components to uninstall.

Figure 38 Choose Product Features screen – Windows – select **Client**

8 Mark **Client**, then click **Uninstall**.

NOTE Do not mark **Server** on the Choose Product Features screen. Doing so will result in removal of all previously analyzed data from your existing CytoGenomics server.

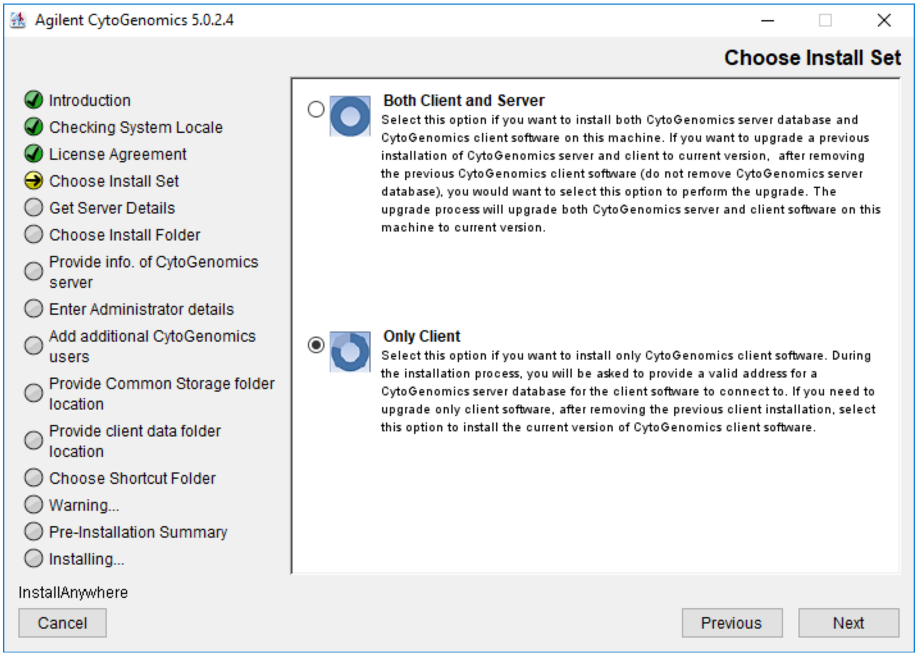
9 In the confirmation message box that opens, click **Yes** to continue uninstalling CytoGenomics client for version 5.0.0 or 5.0.1.

10 When the uninstallation is complete, a message opens. Click **Done**.

The uninstaller closes and you are directed to the License Agreement screen of the CytoGenomics 5.0.2 installer.

11 Continue the installation wizard, as described in “Step 2. Install the database server and client on a single Windows computer” on page 20.

12 When the Choose Install Set screen opens, select **Only Client**.



○ **Both Client and Server**

Select this option if you want to install both CytoGenomics server database and CytoGenomics client software on this machine. If you want to upgrade a previous installation of CytoGenomics server and client to current version, after removing the previous CytoGenomics client software (do not remove CytoGenomics server database), you would want to select this option to perform the upgrade. The upgrade process will upgrade both CytoGenomics server and client software on this machine to current version.

● **Only Client**

Select this option if you want to install only CytoGenomics client software. During the installation process, you will be asked to provide a valid address for a CytoGenomics server database for the client software to connect to. If you need to upgrade only client software, after removing the previous client installation, select this option to install the current version of CytoGenomics client software.

Figure 39 Choose Install Set screen – Windows – select **Only Client**

13 Click **Next**.

14 Continue the installation wizard. For information, refer to “Step 3. Install the client software on additional Windows computers” on page 36.

Step 2. Start the Agilent CytoGenomics 5.0.2 client software, log in, and add new software license

1 Start the Agilent CytoGenomics program.

See “Step 4. Start the Agilent CytoGenomics 5.0 client software” on page 39.

2 Log in.

See “Step 5. Log in to Agilent CytoGenomics” on page 39.

3 Enter your updated license information.

See “Step 6. Add your software license” on page 41.

Uninstalling Agilent CytoGenomics on Windows computers

The Uninstall program for Agilent CytoGenomics provides an easy way to remove the Agilent CytoGenomics client, server, and PostgreSQL programs from your computer.

NOTE

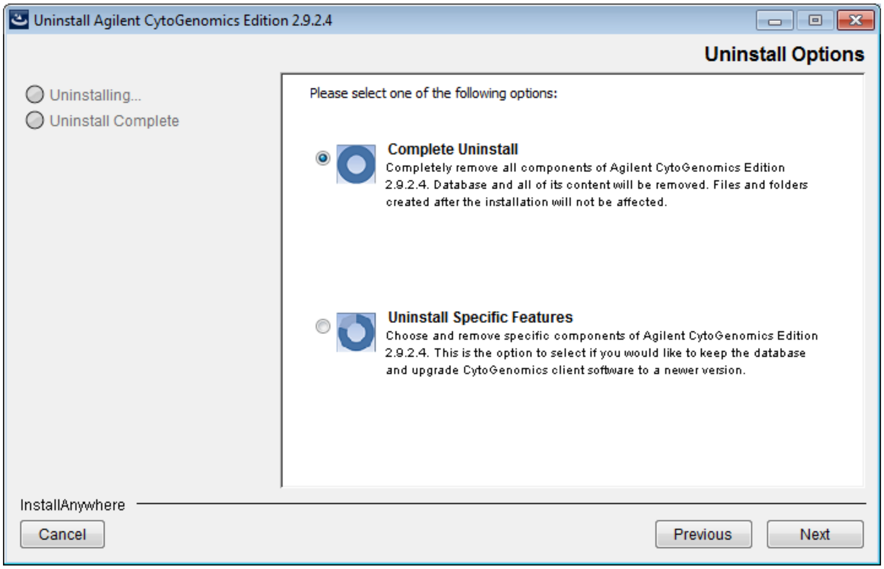
CytoGenomics 5.0 is compatible with and can co-exist on the same machine as CytoGenomics 3.0 or 4.0. It is not necessary to uninstall the previous version of CytoGenomics (i.e., v3.0 or 4.0) in order to install v5.0.

When you completely uninstall Agilent CytoGenomics, the database and the data contained in it are completely removed. Do not uninstall the entire program unless you have backed up your database or no longer wish to use it.

1. Start the **Uninstall AgilentCytoGenomics.exe** file, located in the \Uninstall_AgilentCytoGenomics folder of your program folder.

   The Uninstaller program starts.
2. Read the introductory information, and then click **Next**.
3. Read the warning information. You are cautioned not to stop the Uninstaller once it has started to remove the programs. Click **Next**.

   The Uninstall Options screen opens.



Please select one of the following options:

● **Complete Uninstall**
Completely remove all components of Agilent CytoGenomics Edition 2.9.2.4. Database and all of its content will be removed. Files and folders created after the installation will not be affected.

○ **Uninstall Specific Features**
Choose and remove specific components of Agilent CytoGenomics Edition 2.9.2.4. This is the option to select if you would like to keep the database and upgrade CytoGenomics client software to a newer version.

Figure 40 Uninstall Options screen – Windows – select **Complete Uninstall**

4 Select **Complete Uninstall**.
Depending on which version of CytoGenomics you are uninstalling, you may see a warning message advising you to backup the database before proceeding with the uninstall.

5 When the uninstallation is complete, a message opens. Click **Done**.

The Agilent CytoGenomics client program, server program and database, and PostgreSQL program were removed from your computer. Program folders and data folders (such as data output folders) created after installation were not removed.

Troubleshooting

If the Agilent CytoGenomics program does not open

✔ Try opening the program by running the *run_CytoGenomics.bat* file.

a Open the installation folder AgilentCytoGenomics5.0.X.X.

b Double-click *run_CytoGenomics.bat*.

Agilent CytoGenomics opens and you can operate the program normally.

If the program still does not open, try adjusting the amount of RAM allocated to the program using the approach provided below.

✔ Adjust the amount of RAM that is allocated to the program.

a Open the Client folder inside the AgilentCytoGenomics5.0.X.X installation folder.

b Open the file *Agilent CytoGenomics.lax* in Notepad.

c In this file, locate the following text.

```
lax.nl.java.option.additional=Xms1000m
```

d Change `Xms1000m` to `Xms900m`.

e Save and close the file.

f Open the Agilent CytoGenomics client program.

- Double-click the Agilent CytoGenomics 5.0 icon, or select Agilent CytoGenomics 5.0 from the Windows Start menu.

If Agilent CytoGenomics opens, you can operate the program normally.

If Agilent CytoGenomics still does not open, repeat step a through step f, and reduce the Xms value by 100 again. Continue to reduce this value in increments of 100 until the program opens successfully.

3

Installation Instructions for Macintosh

This chapter shows you how to install Agilent CytoGenomics 5.0 and migrate data from a previous version of CytoGenomics on systems running a Macintosh OS.

NOTE

The Macintosh version of CytoGenomics does not permit analysis of scanner image files. To run an analysis workflow, you must first extract the image file using the Agilent Feature Extraction program, then use the extracted FE file in the workflow.

Installing Agilent CytoGenomics 5.0 – Macintosh

This section includes detailed instructions and important notes for installing Agilent CytoGenomics 5.0 on a Macintosh system that does not have a previous version of CytoGenomics installed.

Agilent CytoGenomics consists of two parts: a PostgreSQL database server and the client software. Once you have installed the database server and client software on one computer, you can install additional copies of the client software on client computers that have network access to the database computer.

For instructions on how to upgrade an existing Agilent CytoGenomics installation, see "Upgrading from CytoGenomics 3.0 or 4.0 to CytoGenomics 5.0 and Migrating Data – Macintosh" on page 91.

Step 1. Prepare for installation

a. Download the Macintosh version of the software and release notes

1. Go to the CytoGenomics download page on the Agilent website at: www.agilent.com/en/download-agilent-cytogenomics-software.
2. Click the **Download** link for the Macintosh version of the software.
3. Save the Installer on your computer. (Do not start the installation at this time.)

   The Mac installer is downloaded as a compressed folder (Agilent_CytoGenomics_5_0_X_X_MAC.zip). Do not start the installation at this time.
4. Click the **Release Notes** link to download the software release notes.
5. Save the release notes to your computer.

b. Check Macintosh system requirements before you start

Check to make sure that your computer systems meet the following requirements. All client installations point to the computer on which the server software is installed. Requirements are listed in Table 3.

NOTE If an operating system is not listed in Table 3, it is not supported.

Table 3 Requirements for Agilent CytoGenomics on Macintosh computers

Operating System	Macintosh OS Sierra, or Macintosh OS X El Capitan
Programs	Java 1.8 Any program that enables you to open PDF files (for example, Adobe Reader)
Processor	3 GHz Intel Core 2 Duo CPU or better
Working memory (RAM)	Minimum: 4 GB Recommended: 8 GB
Hard disk space	40 GB (For analysis of large datasets, more space is required)
Display resolution	1280 x 768 or higher

c. Set up permissions for installer and users

- Make sure that the user account used to install the Agilent CytoGenomics 5.0 software has administrator permissions on the installation computer.
- Make sure that every user account running the Agilent CytoGenomics 5.0 software has read/write permissions in the computer where the client software is installed. In addition, users must have read/write permissions in the installation folder of the computer where the database server is installed.

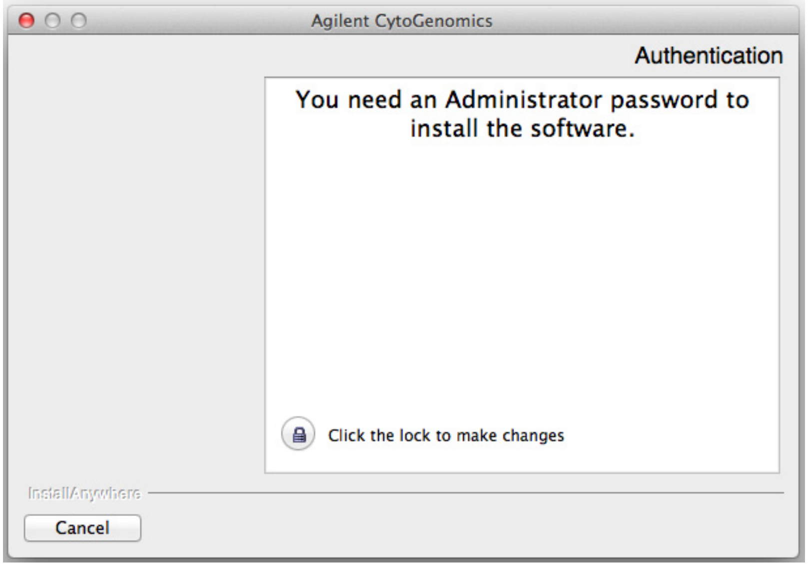
The way you set permissions varies between operating systems. Contact your network administrator for help in checking or changing user account permissions. If the user account permissions are not set correctly, the software will fail to install or run properly.

Step 2. Install the database server and client on a single Macintosh computer

NOTE Only one copy of the server software is installed. To run the client software, the database server must be installed. The client is the program you run when you want to use Agilent CytoGenomics. You can run the client program on the same computer as the server, or from any other computer with the client program installed. After installation, the database server software runs silently in the background and manages the shared database for all Agilent CytoGenomics 5.0 users. All client computers must have network access to the server computer and users must have read/write permissions.

1. Log on to the Macintosh system where you want to install Agilent CytoGenomics 5.0 server. Use an account that has administrator permissions.
2. Locate the compressed folder (Agilent_CytoGenomics_5_0_X_X_MAC.zip) that you downloaded in Step 1, "a. Download the Macintosh version of the software and release notes" on page 66. Double-click the folder to expand the contents of the folder and save the installer on your computer.
3. Double-click the Mac installer.

   The following window opens.



Agilent CytoGenomics

Authentication

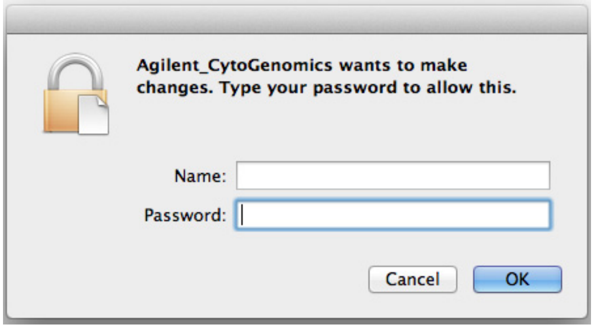
You need an Administrator password to install the software.

Click the lock to make changes

Figure 41 Authentication dialog box - preparing to install

4 Click directly on the lock icon near bottom of the dialog box.

The following dialog box opens.



Agilent_CytoGenomics wants to make changes. Type your password to allow this.

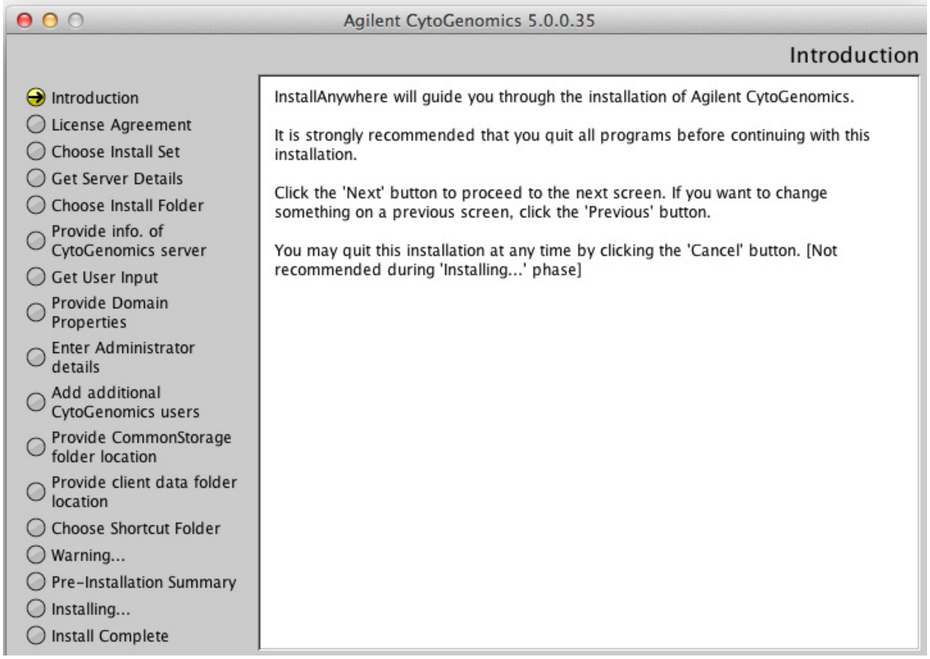
Name:

Password:

Figure 42 Administrator credentials dialog box - preparing to install

5 In this dialog box, enter the Name and Password for a user with administrator rights to the computer, then click **OK**.

The installation wizard starts.



InstallAnywhere will guide you through the installation of Agilent CytoGenomics.

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.

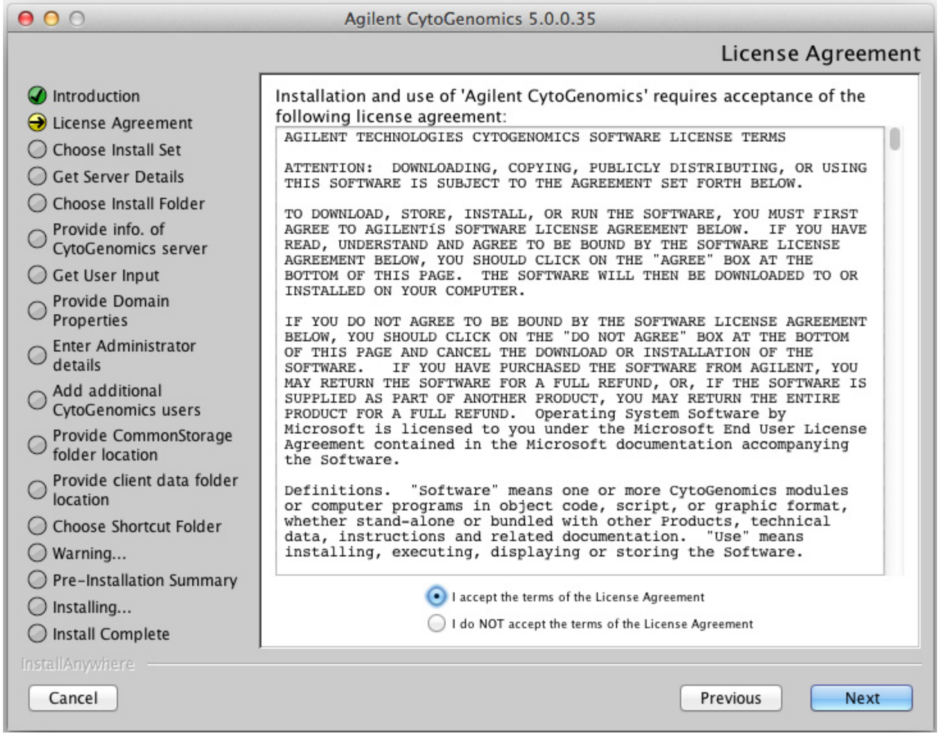
You may quit this installation at any time by clicking the 'Cancel' button. [Not recommended during 'Installing...' phase]

Figure 43 Introduction screen for the installation wizard – Macintosh

6 Read the introductory information.

7 Click **Next** to display the next section.

The License Agreement screen opens.



Installation and use of 'Agilent CytoGenomics' requires acceptance of the following license agreement:

AGILENT TECHNOLOGIES CYTOGENOMICS SOFTWARE LICENSE TERMS

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 AGILENTíS SOFTWARE LICENSE AGREEMENT BELOW. IF YOU HAVE READ, UNDERSTAND AND AGREE TO BE BOUND BY THE SOFTWARE LICENSE AGREEMENT BELOW, YOU SHOULD CLICK ON THE "AGREE" BOX AT THE BOTTOM OF THIS PAGE. THE SOFTWARE WILL THEN BE DOWNLOADED TO OR INSTALLED ON YOUR COMPUTER.

IF YOU DO NOT AGREE TO BE BOUND BY THE SOFTWARE LICENSE AGREEMENT BELOW, YOU SHOULD CLICK ON THE "DO NOT AGREE" BOX AT THE BOTTOM OF THIS PAGE AND CANCEL THE DOWNLOAD OR INSTALLATION OF THE SOFTWARE. IF YOU HAVE PURCHASED THE SOFTWARE FROM AGILENT, YOU MAY RETURN THE SOFTWARE FOR A FULL REFUND, OR, IF THE SOFTWARE IS SUPPLIED AS PART OF ANOTHER PRODUCT, YOU MAY RETURN THE ENTIRE PRODUCT FOR A FULL REFUND. Operating System Software by Microsoft is licensed to you under the Microsoft End User License Agreement contained in the Microsoft documentation accompanying the Software.

Definitions. "Software" means one or more CytoGenomics modules or computer programs in object code, script, or graphic format, whether stand-alone or bundled with other Products, technical data, instructions and related documentation. "Use" means installing, executing, displaying or storing the Software.

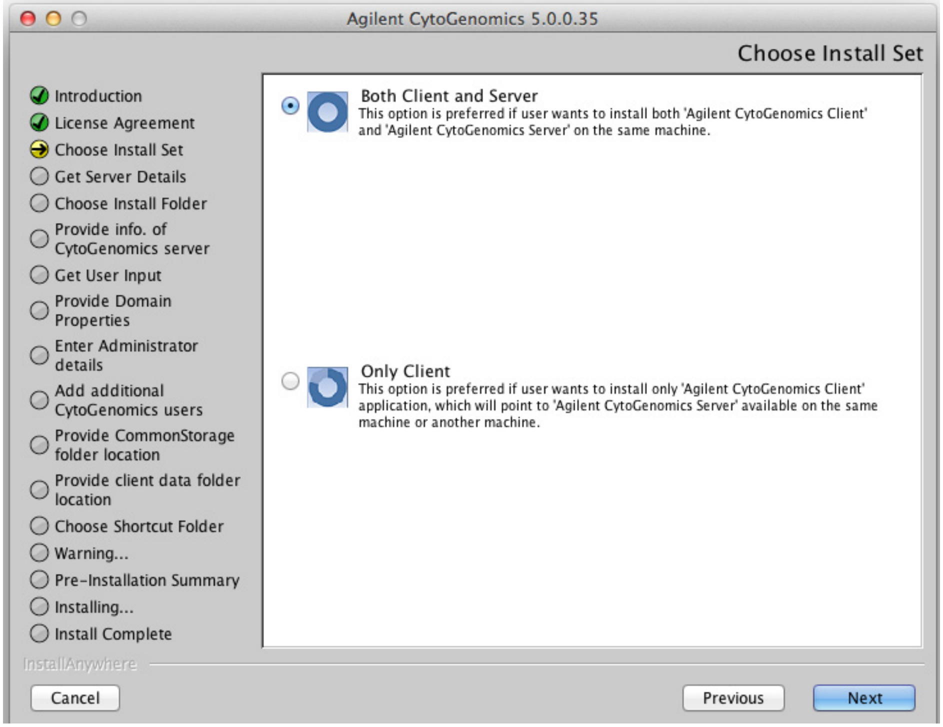
● I accept the terms of the License Agreement

○ I do NOT accept the terms of the License Agreement

Figure 44 License Agreement screen – Macintosh

8 Read the license agreement. Click **I accept the terms of the License Agreement** and then click **Next**. (Click **Previous** to review information in a previous section.)

The Choose Install Set screen opens.



Agilent CytoGenomics 5.0.0.35

Choose Install Set

● Both Client and Server
This option is preferred if user wants to install both 'Agilent CytoGenomics Client' and 'Agilent CytoGenomics Server' on the same machine.

○ Only Client
This option is preferred if user wants to install only 'Agilent CytoGenomics Client' application, which will point to 'Agilent CytoGenomics Server' available on the same machine or another machine.

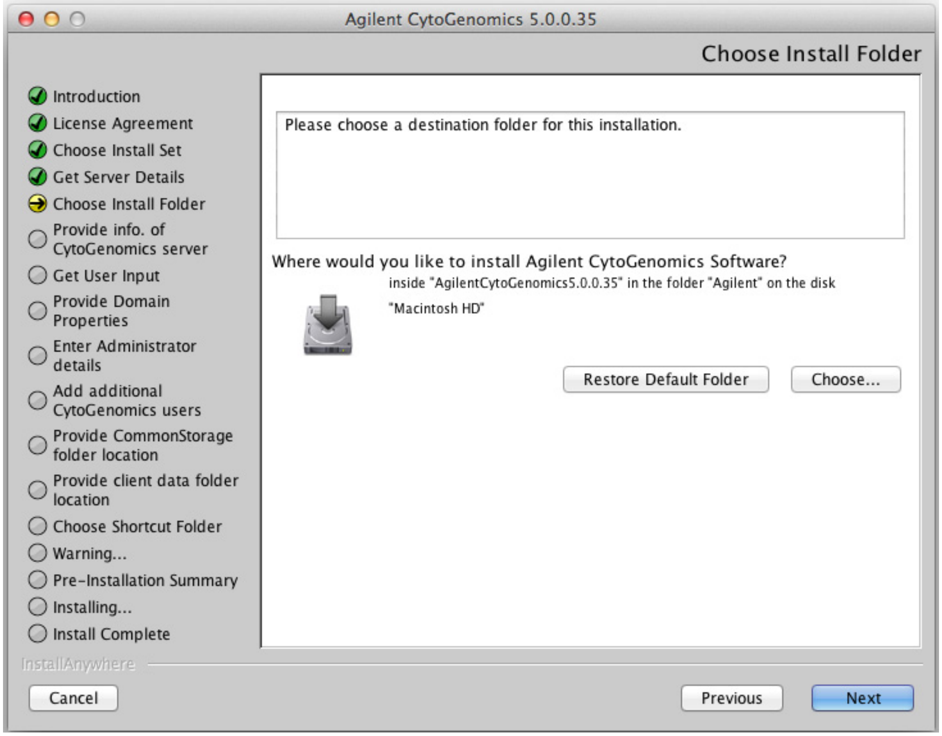
Figure 45 Choose Install Set screen – Macintosh

9 Click the icon next to **Both Client and Server** to install both the database server and client software on this computer.

10 Click **Next**.

11 An Information message opens.

Click **OK**. The Choose Install Folder screen opens.



Please choose a destination folder for this installation.

Where would you like to install Agilent CytoGenomics Software?

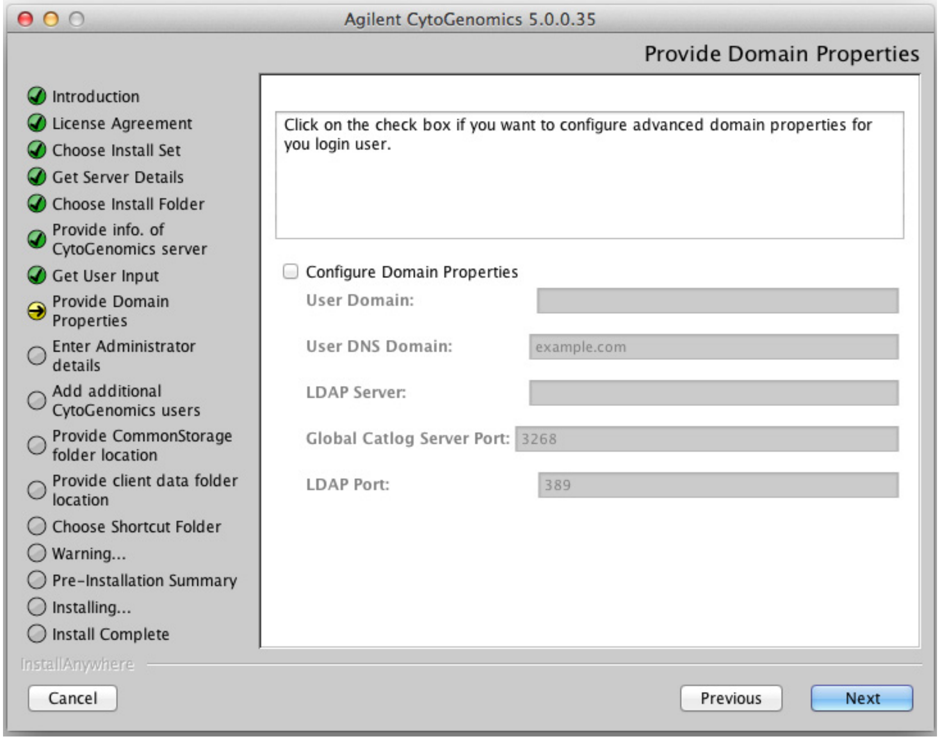
inside "AgilentCytoGenomics5.0.0.35" in the folder "Agilent" on the disk "Macintosh HD"

Figure 46 Choose Install Folder screen – Macintosh

12 By default, the program is installed in the AgilentCytoGenomics5.0.X.X folder (where X.X is the revision number) in the Agilent folder on the Macintosh HD disk. Leave this folder as-is, or click **Choose** to select a new location where you want to install Agilent CytoGenomics 5.0 folder. Within this folder, one folder is created for the server software and one folder is created for the client software.

13 Click **Next**.

The Provide Domain Properties screen opens.



Agilent CytoGenomics 5.0.0.35

Provide Domain Properties

Click on the check box if you want to configure advanced domain properties for you login user.

☐ Configure Domain Properties

User Domain:

User DNS Domain: example.com

LDAP Server:

Global Catlog Server Port: 3268

LDAP Port: 389

Figure 47 Provide Domain Properties screen – Macintosh

14 If only the administrator will be accessing Agilent CytoGenomics 5.0 from this computer, click **Next**. The Enter Administrator details screen opens, and you can proceed to step 26.

If more than one user plans to use Agilent CytoGenomics 5.0 on this computer, configure the domain properties using the instructions in the following substeps.

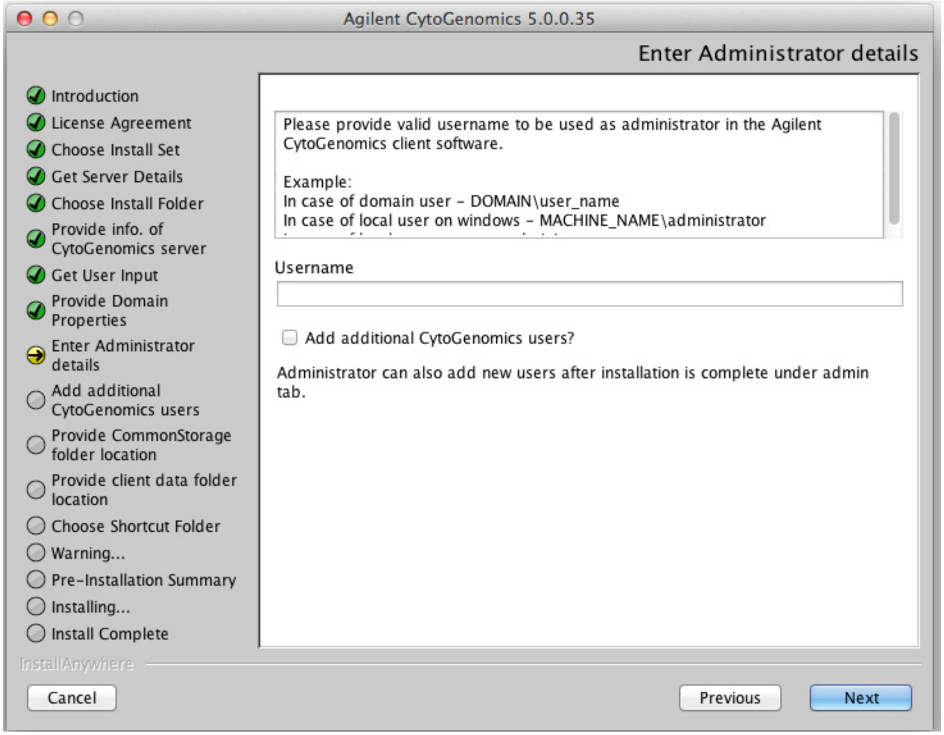
a Mark **Configure Domain Properties**.

b Using the domain properties for your system, complete the fields for User Domain, User DNS Domain, LDAP Server, Global Catalog Server Port, and LDAP Port.

c Click **Next**.

The Enter Administrator details screen opens.

NOTE If you see a warning message titled **Domain validation failed**, click **OK** in the message box, and then click **Previous** in the install window to return to the Provide Domain Properties screen. Repeat step b above with the correct domain properties. Do not proceed with the installation until you enter the domain properties and do not receive the **Domain validation failed** warning message.



Please provide valid username to be used as administrator in the Agilent CytoGenomics client software.

Example:
In case of domain user - DOMAIN\user_name
In case of local user on windows - MACHINE_NAME\administrator

Username

☐ Add additional CytoGenomics users?

Administrator can also add new users after installation is complete under admin tab.

Figure 48 Enter Administrator details screen – Macintosh

15 In the Username field, type the user name of the person who will be the administrator for the Agilent CytoGenomics 5.0 software, using the format example shown.

For domain user: DOMAIN\username

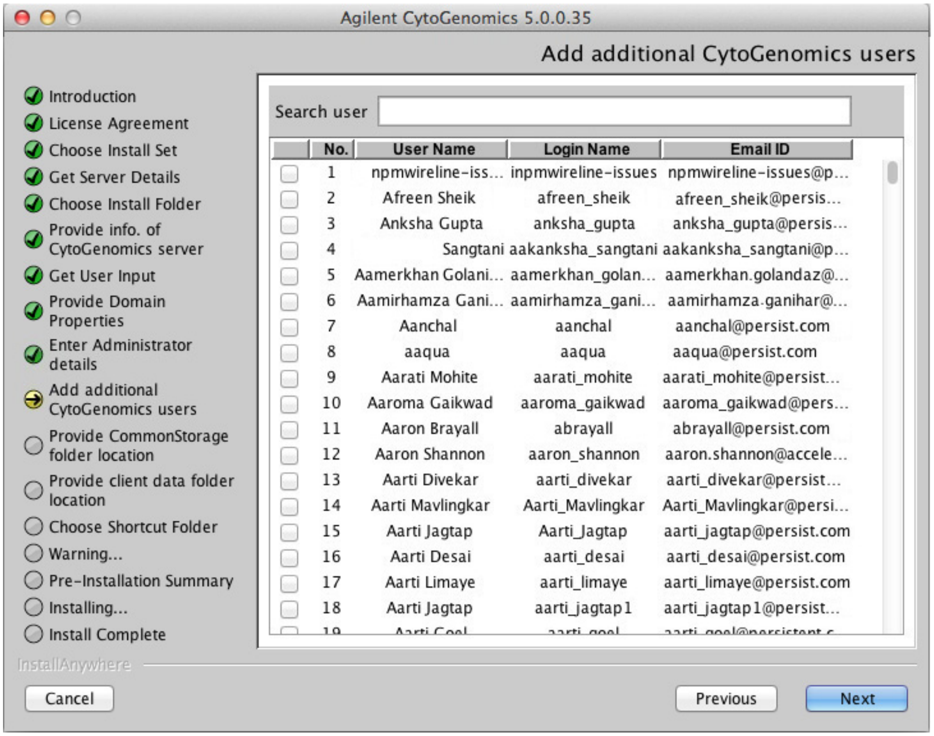
For local machine: \username

16 To set up additional CytoGenomics users, mark the check box labeled **Add CytoGenomics users?**. In the Password field that appears, type the password for the administrator account.

If you do not want to set up new users at this time, proceed directly to step 21 on page 77. Note that the administrator can set up new users from within CytoGenomics once installation is complete (see “To manage users and roles” on page 110).

17 Click **Next**.

The Add CytoGenomics Users screen opens.



Search user

	No.	User Name	Login Name	Email ID
☐	1	npmwireline-iss...	inpmwireline-issues	npmwireline-issues@p...
☐	2	Afreen Sheik	afreen_sheik	afreen_sheik@persis...
☐	3	Anksha Gupta	anksha_gupta	anksha_gupta@persis...
☐	4	Sangtani	aakanksha_sangtani	aakanksha_sangtani@p...
☐	5	Aamerkhan Golani...	aamerkhan_golan...	aamerkhan.golandaz@...
☐	6	Aamirhamza Gani...	aamirhamza_gani...	aamirhamza.ganihar@...
☐	7	Aanchal	aanchal	aanchal@persist.com
☐	8	aaqua	aaqua	aaqua@persist.com
☐	9	Aarati Mohite	aarati_mohite	aarati_mohite@persist...
☐	10	Aaroma Gaikwad	aaroma_gaikwad	aaroma_gaikwad@pers...
☐	11	Aaron Brayall	abrayall	abrayall@persist.com
☐	12	Aaron Shannon	aaron_shannon	aaron.shannon@accele...
☐	13	Aarti Divekar	aarti_divekar	aarti_divekar@persist...
☐	14	Aarti Mavlingkar	Aarti_Mavlingkar	Aarti_Mavlingkar@persi...
☐	15	Aarti Jagtap	Aarti_Jagtap	aarti_jagtap@persist.com
☐	16	Aarti Desai	aarti_desai	aarti_desai@persist.com
☐	17	Aarti Limaye	aarti_limaye	aarti_limaye@persist.com
☐	18	Aarti Jagtap	aarti_jagtap1	aarti_jagtap1@persist...

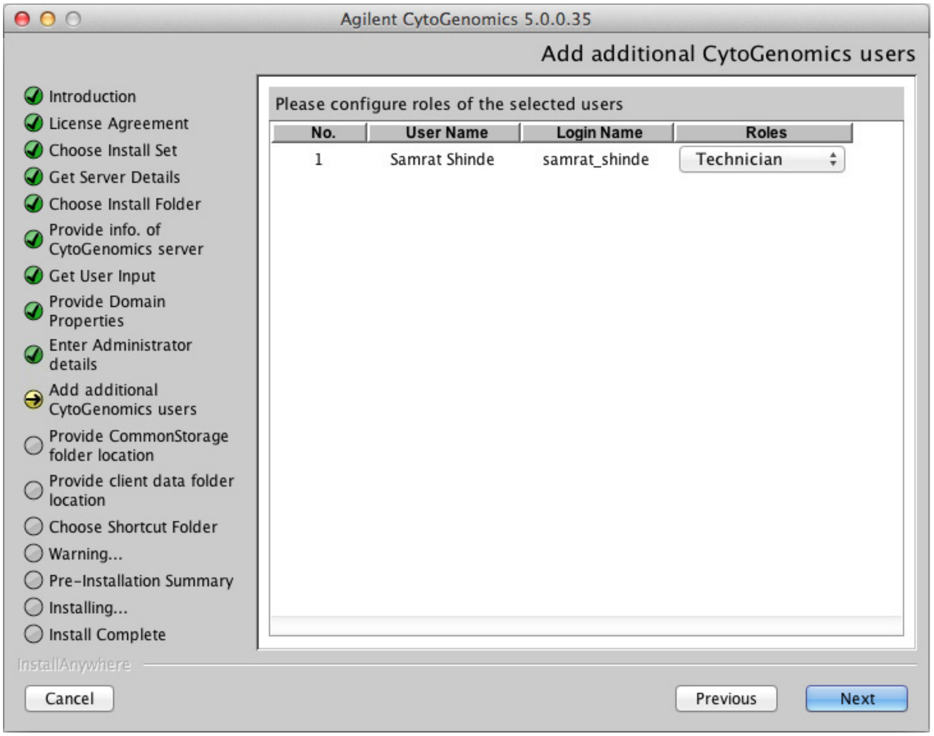
Figure 49 Add CytoGenomics Users screen – Macintosh

18 The Add CytoGenomics Users screen lists all of the users in the domain or on the local machine. Mark the check box next to the users that you want to add to the CytoGenomics database.

To search for a user, type the user name into the search box at the top of the screen.

19 Click **Next**.

The Add CytoGenomics Users screen advances to the step for configuring user roles.



Please configure roles of the selected users

No.	User Name	Login Name	Roles
1	Samrat Shinde	samrat_shinde	Technician

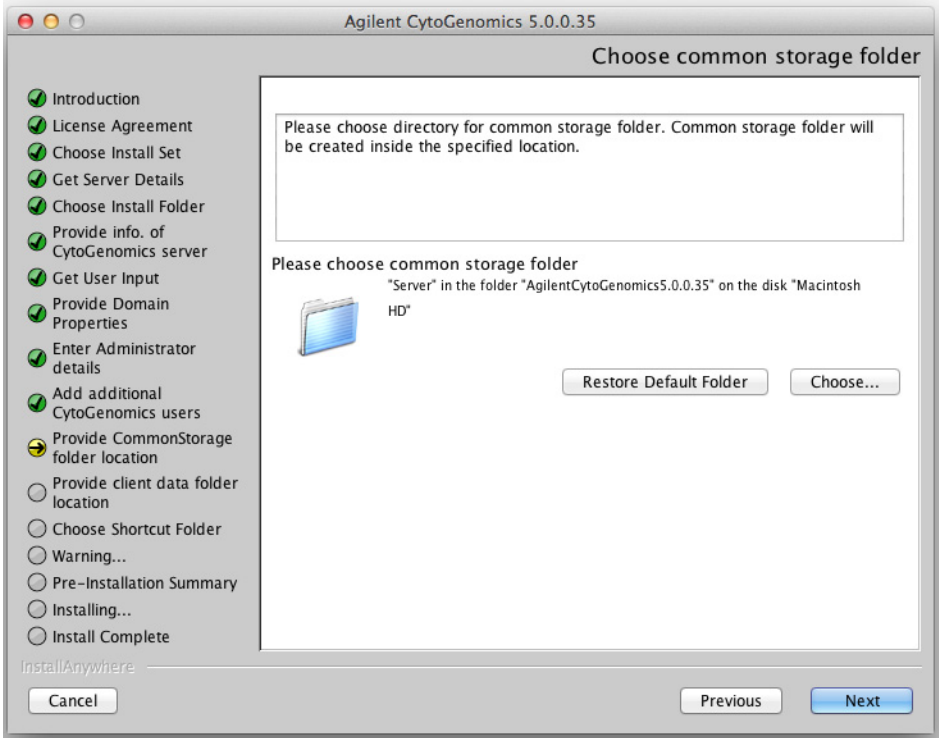
Figure 50 Add CytoGenomics Users screen – Configure roles step – Macintosh

20 For each user listed on the screen, select a role in the Roles drop-down list. The default selection is *Technician*.

See "User Roles and Capabilities" on page 16 for a description of each role.

21 Click **Next**.

The Choose common storage folder screen opens.



Please choose directory for common storage folder. Common storage folder will be created inside the specified location.

Please choose common storage folder

"Server" in the folder "AgilentCytoGenomics5.0.0.35" on the disk "Macintosh HD"

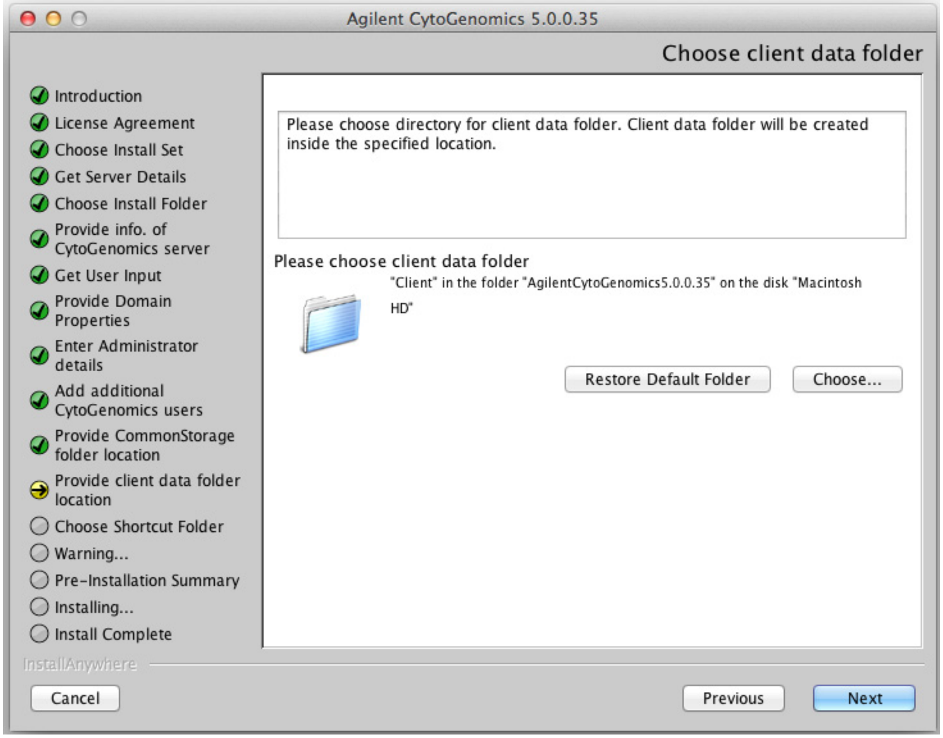
Figure 51 Choose common storage folder screen – Macintosh

22 By default, the common storage folder is created inside the Server folder in the AgilentCytoGenomics5.0.X.X folder (where X.X is the revision number) on the Macintosh HD disk. Leave this folder as-is, or Click **Choose**, browse to the desired folder, and then click **Save.**

The common storage folder is where the program saves files that are used at the server level.

23 Click **Next**.

The Choose client data folder screen opens.



Please choose directory for client data folder. Client data folder will be created inside the specified location.

Please choose client data folder

"Client" in the folder "AgilentCytoGenomics5.0.0.35" on the disk "Macintosh HD"

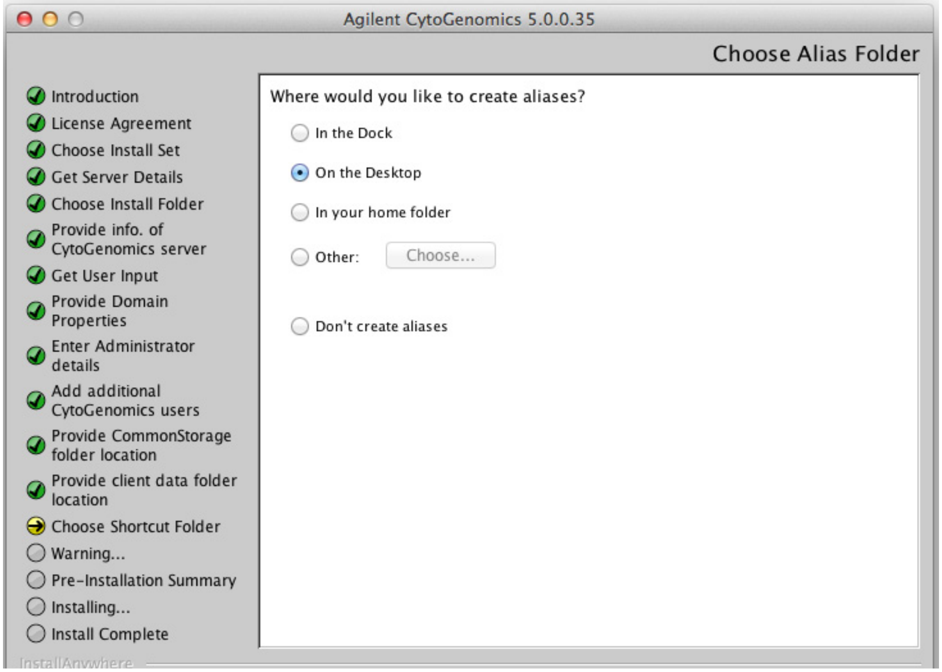
Figure 52 Choose client data folder screen – Macintosh

24 By default, the client data folder is created inside the Client folder in the AgilentCytoGenomics5.0.X.X folder (where X.X is the revision number) on the Macintosh HD disk. Leave this folder as-is, or Click **Choose**, browse to the desired folder, and then click **Save.**

The client data folder is where the program installs the files for the genome build and reference genomes.

25 Click **Next**.

The Choose Alias Folder screen opens.



Where would you like to create aliases?

○ In the Dock

● On the Desktop

○ In your home folder

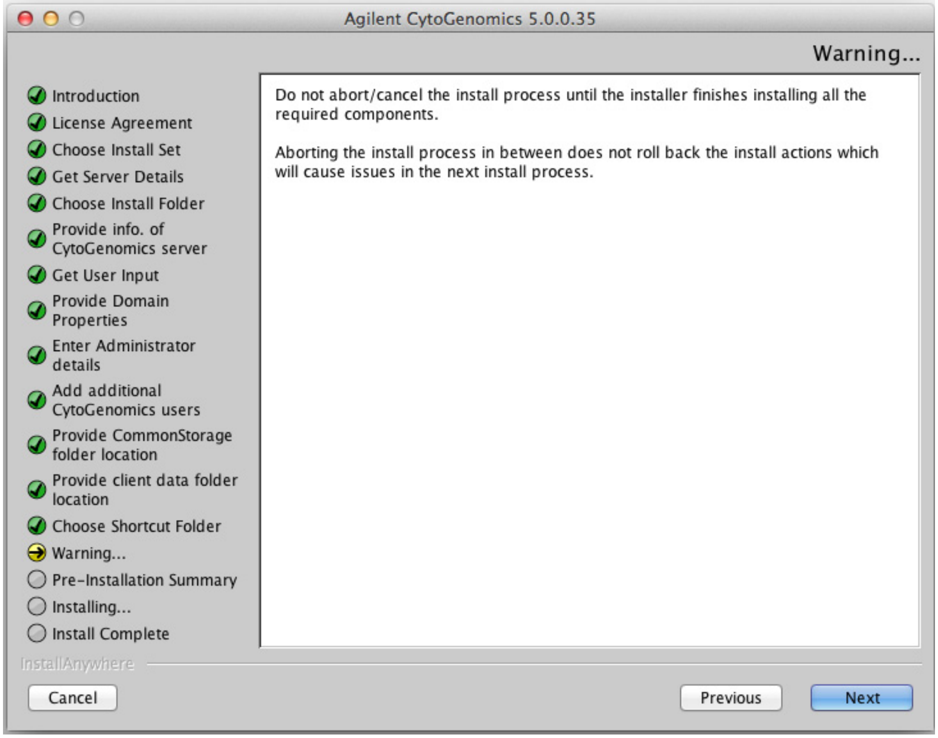
○ Other: Choose...

○ Don't create aliases

Figure 53 Choose Alias Folder screen – Macintosh

26 By default, program icons are installed on the Desktop of your computer. To select another location for the program icons, select the desired location (In the Dock, for example) and then click **Next**.

The Warning screen opens.



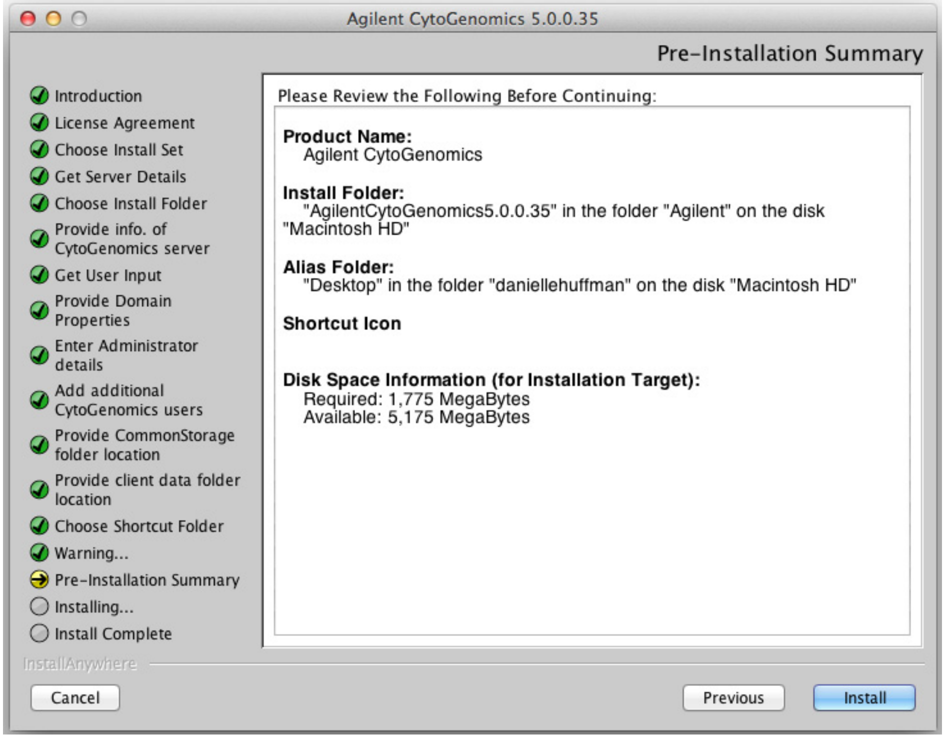
Do not abort/cancel the install process until the installer finishes installing all the required components.

Aborting the install process in between does not roll back the install actions which will cause issues in the next install process.

Figure 54 Warning screen – Macintosh

27 Read the message that cautions you not to stop the installation once it has started, and then click **Next**.

The Pre-Installation Summary screen opens.



Please Review the Following Before Continuing:

Product Name:
Agilent CytoGenomics

Install Folder:
"AgilentCytoGenomics5.0.0.35" in the folder "Agilent" on the disk "Macintosh HD"

Alias Folder:
"Desktop" in the folder "daniellehuffman" on the disk "Macintosh HD"

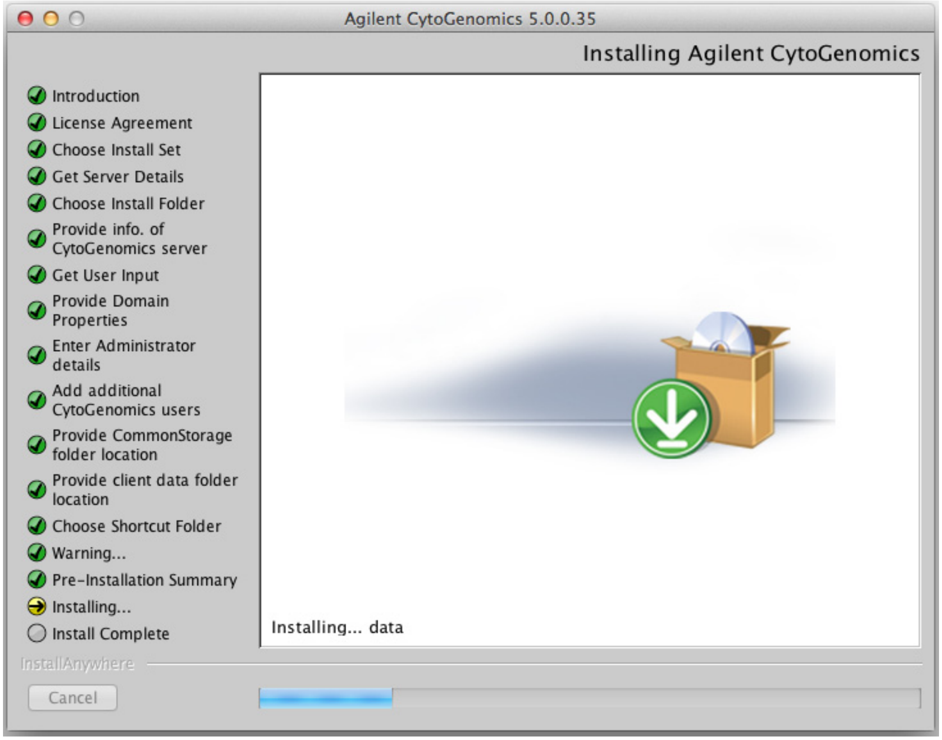
Shortcut Icon

Disk Space Information (for Installation Target):
Required: 1,775 MegaBytes
Available: 5,175 MegaBytes

Figure 55 Pre-Installation Summary screen – Macintosh

28 Review the installation setup information. If you want to change any of the settings, click **Previous** and go back and change the settings. To start the installation, click **Install**.

The Installing Agilent CytoGenomics 5.0.X.X screen opens and is displayed until the installation is complete.



Installing... data

Figure 56 Installing Agilent CytoGenomics 5.0.X.X screen – Macintosh

When the installation is complete, the Installation Complete screen is displayed.

29 Click **Done**.

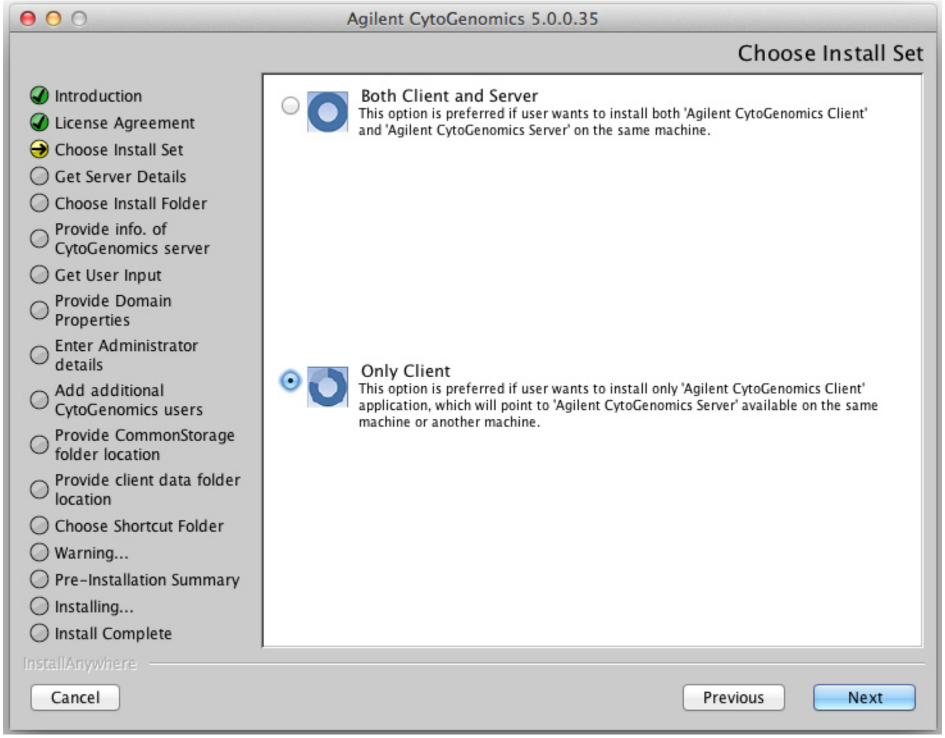
30 Make sure the folder where you installed the software is shared with read/write permission for all client computers and for all users who run Agilent CytoGenomics.

Step 3. Install the client software on additional Macintosh computers

To use other computers to run Agilent CytoGenomics 5.0 client software (with a shared database), install the client software on each of the computers.

1 On each computer you want to run the Agilent CytoGenomics 5.0 program, run the installation wizard, as described in "Step 2. Install the database server and client on a single Macintosh computer" on page 68.

2 When the Choose Install Set screen appears, select **Only Client**.



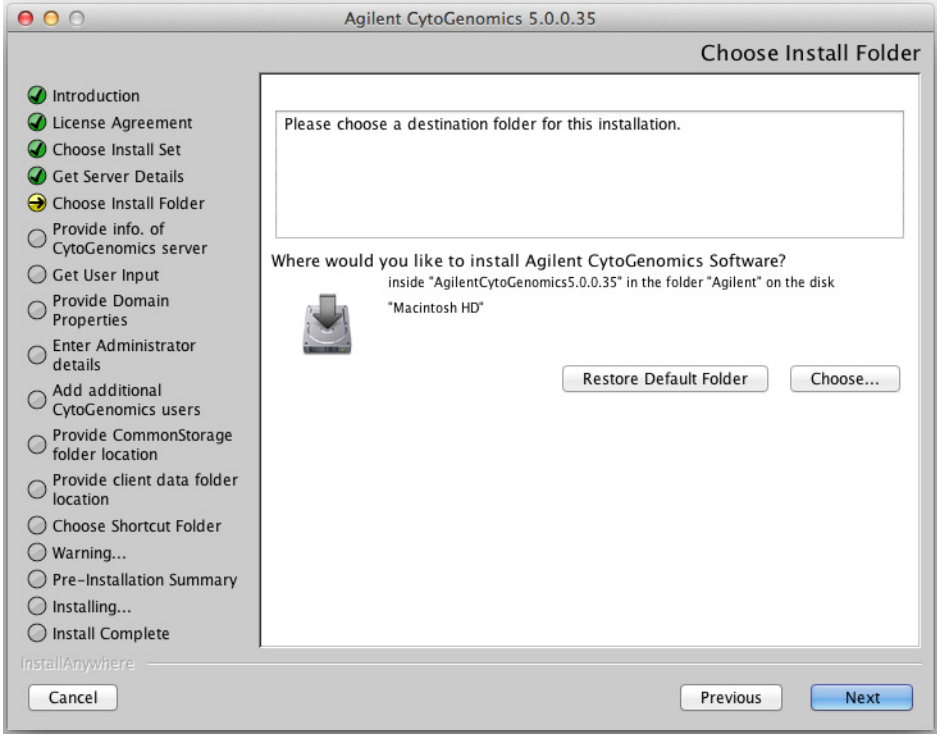
○ Both Client and Server
This option is preferred if user wants to install both 'Agilent CytoGenomics Client' and 'Agilent CytoGenomics Server' on the same machine.

● Only Client
This option is preferred if user wants to install only 'Agilent CytoGenomics Client' application, which will point to 'Agilent CytoGenomics Server' available on the same machine or another machine.

Figure 57 Choose Install Set screen – Macintosh

3 Click **Next**.

The Choose Installation Folder opens.



Please choose a destination folder for this installation.

Where would you like to install Agilent CytoGenomics Software?

inside "AgilentCytoGenomics5.0.0.35" in the folder "Agilent" on the disk "Macintosh HD"

Figure 58 Choose Install Folder screen – Macintosh

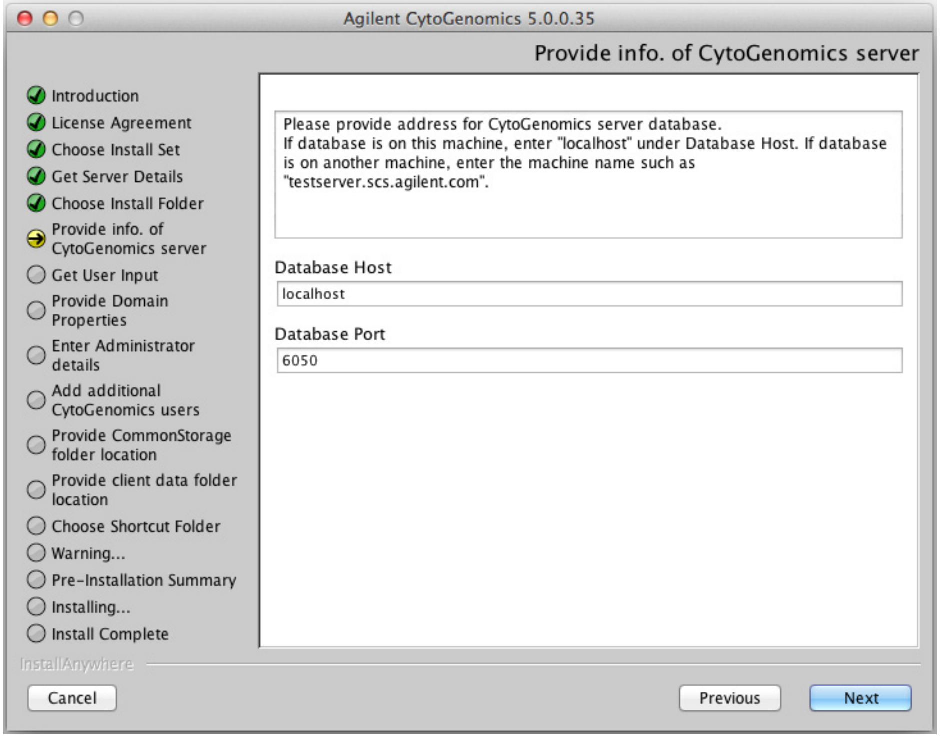
4 By default, the program is installed in the AgilentCytoGenomics5.0.X.X folder (where X.X is the revision number) in the Agilent folder on the Macintosh HD disk. Leave this folder as-is, or type the location and name of the folder where you want to install Agilent CytoGenomics 5.0.

OR

Click **Choose** and browse to a location where you want to install the program, and then click **Save.**

5 Click **Next**.

The Provide Information of CytoGenomics server screen opens.



Please provide address for CytoGenomics server database.
If database is on this machine, enter "localhost" under Database Host. If database is on another machine, enter the machine name such as "testserver.scs.agilent.com".

Database Host: localhost

Database Port: 6050

Figure 59 Provide information of CytoGenomics server screen – Macintosh

6 Under Database Host, type the assigned computer name or IP address of the computer (from step 2) where you installed the Agilent CytoGenomics 5.0 database server.

7 Accept the default **Database Port**, unless your system administrator tells you otherwise.

8 Click **Next**.

Installer immediately tests the connection to the specified database. If incorrect database parameters are provided, or the PostgreSQL database service is not running, a message is displayed.

You can choose to complete the installation and change database connection parameters when launching the client software. However, Agilent recommends that you provide the correct database information during installation.

Continue the installation wizard. Follow the instructions for the installation wizard to provide domain properties, enter administrator information, choose an alias location, and start the installation. For information, see step 15 through step 30 in the section "Step 2. Install the database server and client on a single Macintosh computer" on page 68.

Step 4. Start the Agilent CytoGenomics 5.0 client software

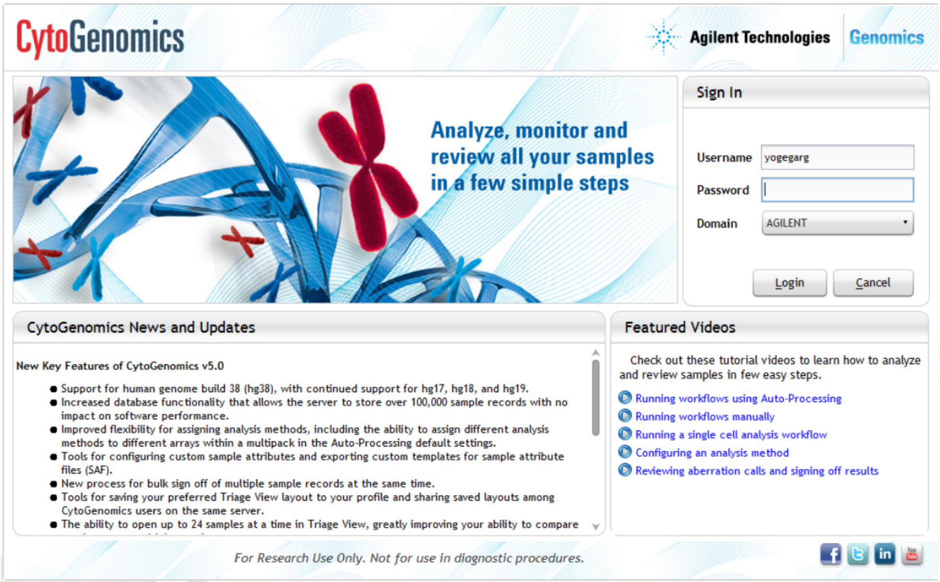
After you install the Agilent CytoGenomics database server and client programs as described in this manual, start the program.

- Double-click the Agilent CytoGenomics 5.0 icon to open the program.

NOTE How you start the program depends on the choice you made for the Alias or Install Folder during installation of the Agilent CytoGenomics client.

Step 5. Log in to Agilent CytoGenomics

After you start the program, the Login screen appears. The name and domain for the administrator set during installation appears in the dialog box.



Username yogegarg

Password

Domain AGILENT

New Key Features of CytoGenomics v5.0

- Support for human genome build 38 (hg38), with continued support for hg17, hg18, and hg19.
- Increased database functionality that allows the server to store over 100,000 sample records with no impact on software performance.
- Improved flexibility for assigning analysis methods, including the ability to assign different analysis methods to different arrays within a multipack in the Auto-Processing default settings.
- Tools for configuring custom sample attributes and exporting custom templates for sample attribute files (SAF).
- New process for bulk sign off of multiple sample records at the same time.
- Tools for saving your preferred Triage View layout to your profile and sharing saved layouts among CytoGenomics users on the same server.
- The ability to open up to 24 samples at a time in Triage View, greatly improving your ability to compare

Check out these tutorial videos to learn how to analyze and review samples in few easy steps.

- Running workflows using Auto-Processing
- Running workflows manually
- Running a single cell analysis workflow
- Configuring an analysis method
- Reviewing aberration calls and signing off results

For Research Use Only. Not for use in diagnostic procedures.

Figure 60 Login screen

1. Log in with your username and password. After the software is started, administrators can add additional users and assign their roles.
2. Next to **Password** type your password.
3. To change the domain, click the arrow next to **Domain** and select the correct domain. Otherwise, leave it as-is.
4. Click **Ok**.

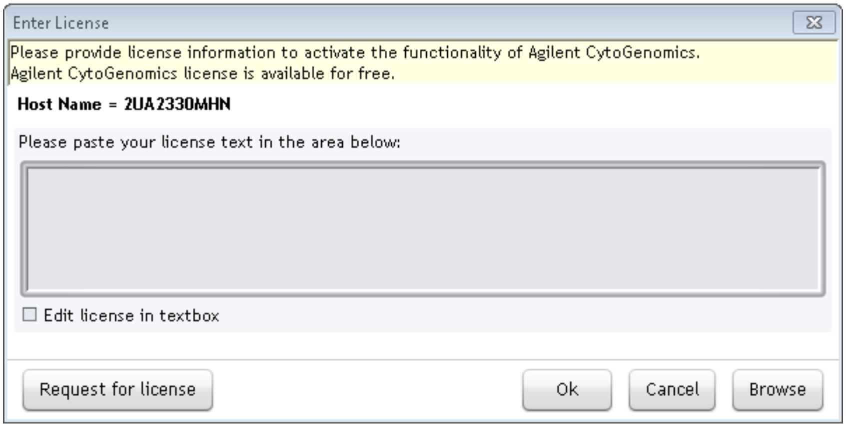
NOTE

If you are using a local machine that is not part of a domain, you see a message that the software cannot find the domain. Click **OK** to ignore this message.

If the installer did not properly share the common storage folder during installation, then an Application Initialization Error message will open notifying you that you do not have access to the common storage folder. This error message provides instructions on how to share the folder with all users. Follow the steps in the error message, then click **OK** to close the message and restart the application.

Step 6. Add your software license

After you log in for the first time, the following dialog box opens.



Enter License

Please provide license information to activate the functionality of Agilent CytoGenomics.
Agilent CytoGenomics license is available for free.

Host Name = 2UA2330MHN

Please paste your license text in the area below:

☐ Edit license in textbox

Figure 61 Enter License dialog box

1. If you do not already have the license file saved to your computer, click **Request for license** to open the Agilent website to the CytoGenomics license request page. Complete the fields in the request form to obtain a CytoGenomics software license. The license is contained in a text file and sent by email.
2. At the bottom of the Enter License dialog box, click **Browse**.

   The Open dialog box opens.
3. Browse to the saved license text file. Select the file and click **Open**.

   The program loads the contents of the file into the text box on the Enter License dialog box.
4. Click **OK**.

   The Agilent CytoGenomics program opens.

Introduction

CytoGenomics is a workflow-based application that helps you analyze, review, and report on CGH and CGH+SNP microarray data in a few simple steps. You import your samples and run an analysis, then return to CytoGenomics to review the QC metrics, review and classify aberration calls in the triage view, and finally create reports.

You can use CytoGenomics as a standalone program, or you can share data by connecting to a central database.

Setting up for analysis and review

Automated processing

CytoGenomics can run a background process to automatically feature extract and analyze data as microarrays are scanned, using preconfigured design files and analysis workflow settings. Use Settings on the **Auto-Processing** tab to set up the input and archive folders, then start automated processing using the controls. You can then exit from CytoGenomics and return when you wish to review your samples.

Figure 62 Agilent CytoGenomics program Home screen

Step 7. Add users and assign roles

Before other users can log in to Agilent CytoGenomics, the administrator must add the users and assign user roles. The user role determines what capabilities the user has within Agilent CytoGenomics. For information on what capabilities each user role has, see “User Roles and Capabilities” on page 16. For information on how to add users and assign roles, see “To manage users and roles” on page 110.

Upgrading from CytoGenomics 3.0 or 4.0 to CytoGenomics 5.0 and Migrating Data – Macintosh

These instructions are for users of a previous version of CytoGenomics (specifically, version 3.0 or 4.0) who want to upgrade to CytoGenomics 5.0 and migrate all sample records from the previous database to the new CytoGenomics 5.0 database.

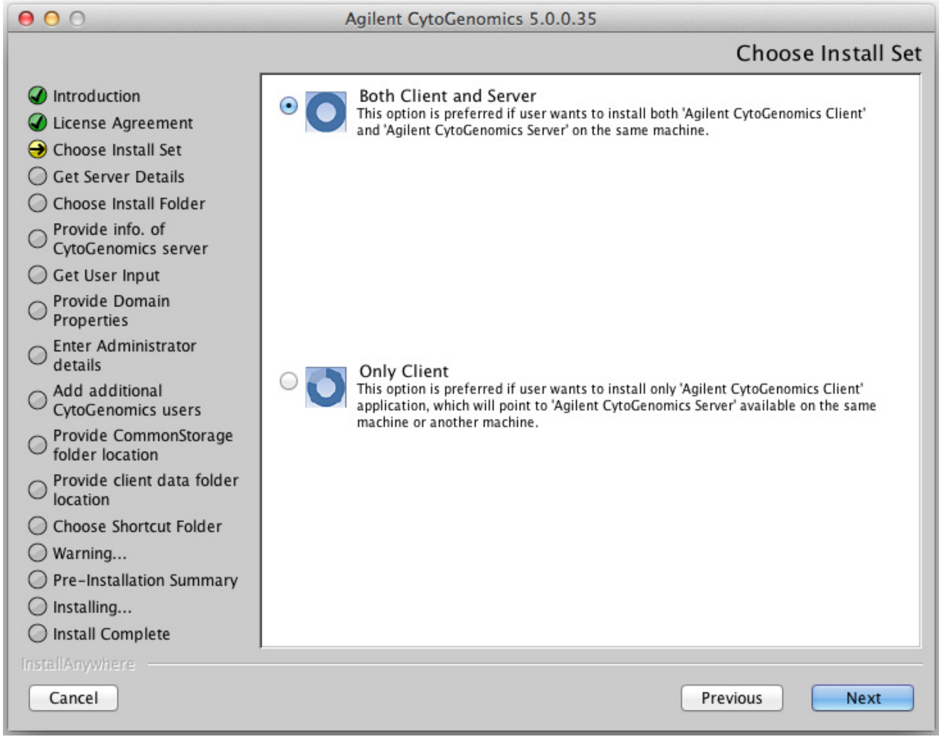
NOTE CytoGenomics 5.0 is compatible with and can co-exist on the same machine as CytoGenomics 3.0 or 4.0. It is not necessary to uninstall the previous version of CytoGenomics (i.e., v3.0 or 4.0) in order to install v5.0.

Step 1. Install CytoGenomics 5.0 on the server computer

Follow these steps to install the CytoGenomics 5.0 server and client software.

1. Download the new software revision from Agilent Technologies and check the system requirements.

   See “a. Download the Macintosh version of the software and release notes” on page 66 for detailed instructions on this step.
2. Start the installation program you downloaded from Agilent.
3. Read the Introduction and then click **Next**.
4. Click **Accept** and then click **Next** to accept the license agreement.
5. On the Choose Install Set screen, select **Both Client and Server**.



Choose Install Set

● Both Client and Server
This option is preferred if user wants to install both 'Agilent CytoGenomics Client' and 'Agilent CytoGenomics Server' on the same machine.

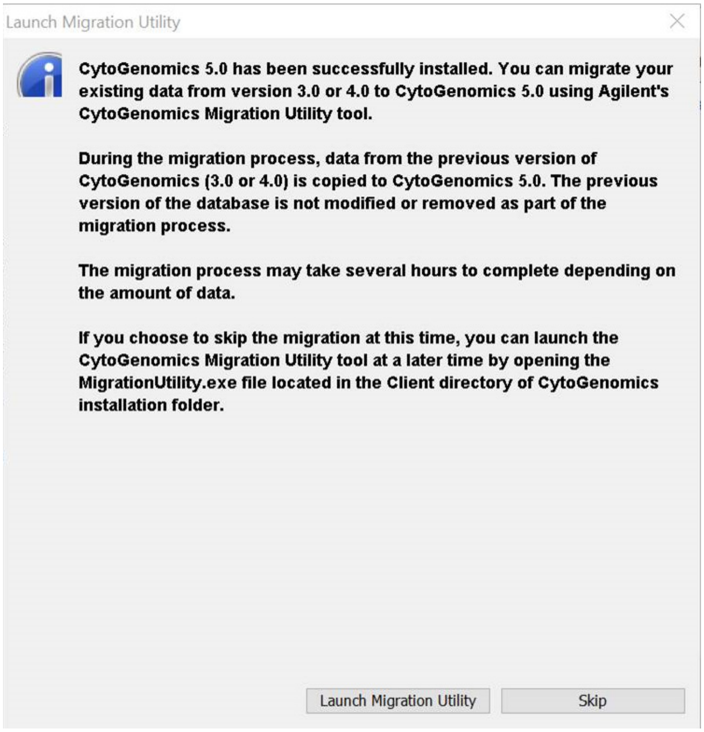
○ Only Client
This option is preferred if user wants to install only 'Agilent CytoGenomics Client' application, which will point to 'Agilent CytoGenomics Server' available on the same machine or another machine.

Figure 63 Choose Install Set screen – Macintosh - select **Both Client and Server**

6 Click **Next**.

7 Continue the installation wizard. Follow the instructions to enter administrator information, choose a shortcut location, and start the installation. For more information, see step 12 through step 29 in the section “Step 2. Install the database server and client on a single Macintosh computer” on page 68.

At the completion of installation, the Launch Migration Utility dialog box opens asking if you want to launch Agilent’s migration utility tool designed to transfer data from a previous version of CytoGenomics server to the CytoGenomics 5.0 server.



CytoGenomics 5.0 has been successfully installed. You can migrate your existing data from version 3.0 or 4.0 to CytoGenomics 5.0 using Agilent's CytoGenomics Migration Utility tool.

During the migration process, data from the previous version of CytoGenomics (3.0 or 4.0) is copied to CytoGenomics 5.0. The previous version of the database is not modified or removed as part of the migration process.

The migration process may take several hours to complete depending on the amount of data.

If you choose to skip the migration at this time, you can launch the CytoGenomics Migration Utility tool at a later time by opening the MigrationUtility.exe file located in the Client directory of CytoGenomics installation folder.

Figure 64 Launch Migration Utility dialog box – Macintosh

8 Depending on your needs, click either **Launch Migration Utility** or **Skip**.

- Click **Launch Migration Utility** if you have data saved to the previous version of CytoGenomics server (e.g., sample results, track files, and other supporting files) and you want to transfer that data to the CytoGenomics 5.0 server. The migration utility tool launches on your PC. Proceed to “Step 2. Migrate data to CytoGenomics 5.0 server” on page 94.
- Click **Skip** if you do not want to transfer any data (e.g., sample results, track files, and other supporting files) from the previous version of CytoGenomics server to the CytoGenomics 5.0 server at this time. The dialog box will close and that data will remain on the previous version of the server. Proceed to “Step 3. Upgrade to CytoGenomics 5.0 on the client computers” on page 98.

NOTE

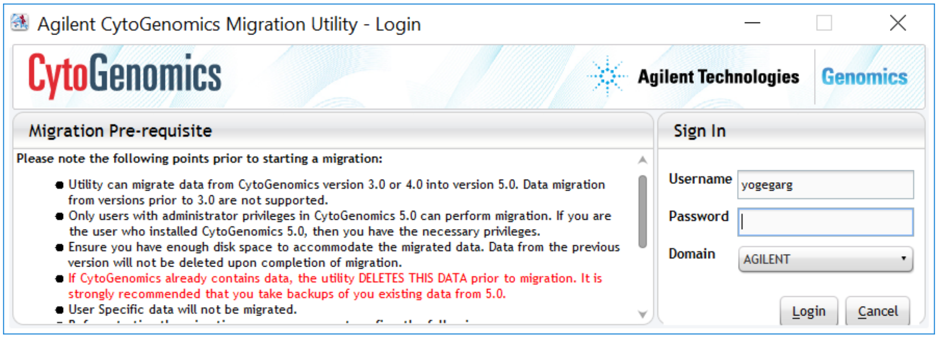
To protect against loss of data and ensure migration of all analyzed samples, Agilent strongly recommends migrating data immediately upon completion of the CytoGenomics 5.0 installation.

If you click **Skip** with the intention of migrating your data at a later time, be aware that if CytoGenomics 5.0 already contains data at the time of migration, the Migration Utility application will delete that data and overwrite it with data from the previous version of CytoGenomics.

Step 2. Migrate data to CytoGenomics 5.0 server

If you selected to launch the migration utility tool, follow these step to use the tool to transfer data from the previous version of CytoGenomics server to CytoGenomics server 5.0. If you do not want to transfer data, bypass this step and proceed to "Step 3. Upgrade to CytoGenomics 5.0 on the client computers" on page 98.

1 On the Sign In screen of the migration utility application (Figure 65), review the list of migration prerequisites and make sure they are all met before you continue.



Please note the following points prior to starting a migration:

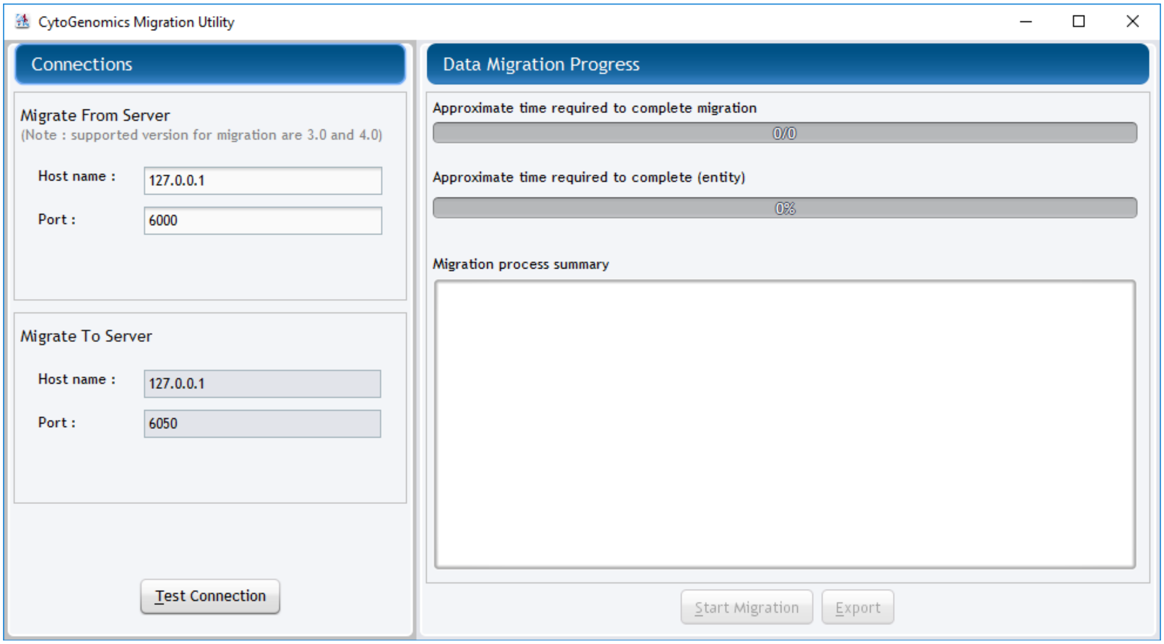
- Utility can migrate data from CytoGenomics version 3.0 or 4.0 into version 5.0. Data migration from versions prior to 3.0 are not supported.
- Only users with administrator privileges in CytoGenomics 5.0 can perform migration. If you are the user who installed CytoGenomics 5.0, then you have the necessary privileges.
- Ensure you have enough disk space to accommodate the migrated data. Data from the previous version will not be deleted upon completion of migration.
- If CytoGenomics already contains data, the utility DELETES THIS DATA prior to migration. It is strongly recommended that you take backups of you existing data from 5.0.
- User Specific data will not be migrated.

Username yogegarg
Password
Domain AGILENT

Figure 65 CytoGenomics Migration Utility application login screen

2 Log in with your username and password. The username and domain for the administrator set during installation appears in the Sign In area of the screen. (Only accounts with administrator privileges can migrate data.)

The CytoGenomics Migration Utility application opens.



(Note : supported version for migration are 3.0 and 4.0)

Migrate From Server:
Host name : 127.0.0.1
Port : 6000

Migrate To Server:
Host name : 127.0.0.1
Port : 6050

Figure 66 CytoGenomics Migration Utility application

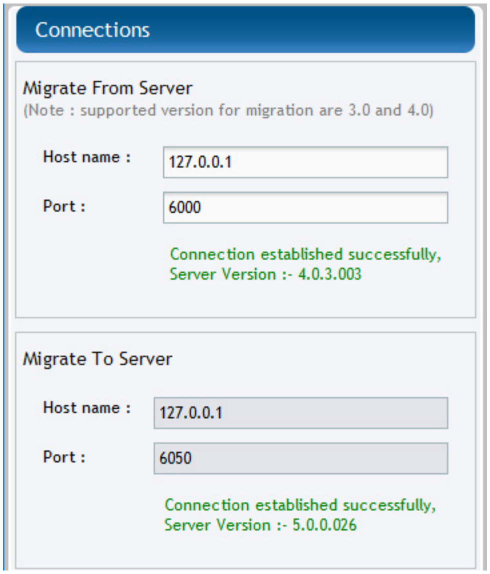
3 Under **Migrate From Server**, enter the host name (i.e., IP address) and port number where the previous version of CytoGenomics server is installed.

4 Under **Migrate To Server**, enter the host name (i.e., IP address) and port number where the CytoGenomics 5.0 server is installed. If CytoGenomics 5.0 server is installed on the same PC as the previous version of CytoGenomics server, then the host names are the same.

NOTE If CytoGenomics 5.0 server is installed on the same PC as the previous version of CytoGenomics server, then the host names of the two servers are the same.

5 Click **Test Connection**.

The screen displays the results of connection test with each server.



Migrate From Server
(Note : supported version for migration are 3.0 and 4.0)

Host name : 127.0.0.1

Port : 6000

Connection established successfully,
Server Version :- 4.0.3.003

Migrate To Server

Host name : 127.0.0.1

Port : 6050

Connection established successfully,
Server Version :- 5.0.0.026

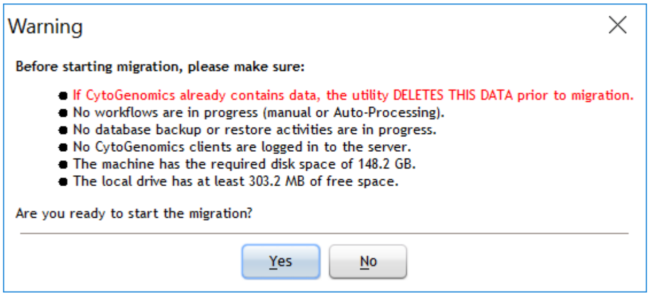
Figure 67 CytoGenomics Migration Utility application – Connections established

NOTE If the application was unable to successfully establish a connection to one or both servers, verify that the correct host name and port number are entered and test the connection again. You cannot proceed to data migration until the application connects to the servers.

---

6 Once the application has successfully connected to the servers, click **Start Migration**.

The Warning message box opens.



Before starting migration, please make sure:

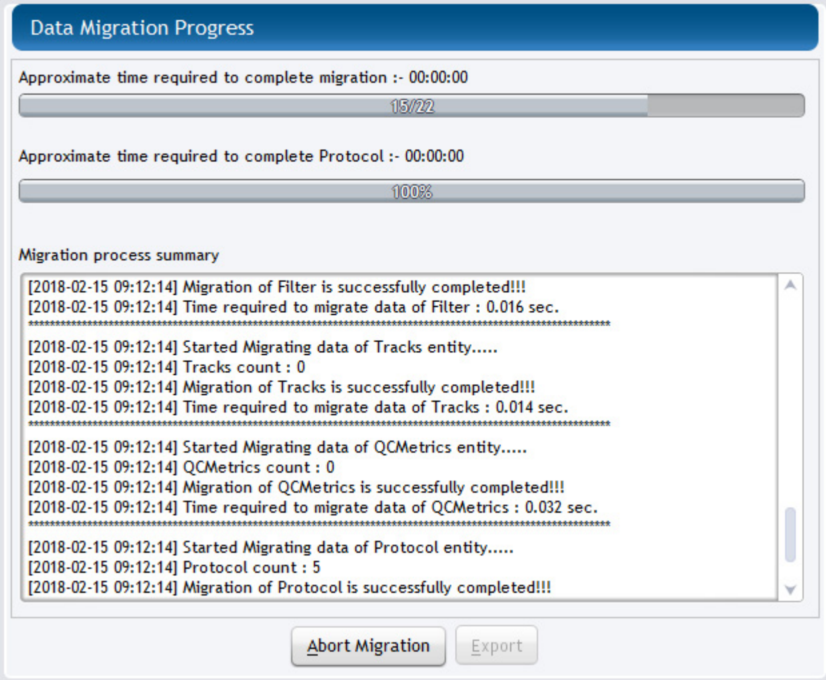
- If CytoGenomics already contains data, the utility DELETES THIS DATA prior to migration.
- No workflows are in progress (manual or Auto-Processing).
- No database backup or restore activities are in progress.
- No CytoGenomics clients are logged in to the server.
- The machine has the required disk space of 148.2 GB.
- The local drive has at least 303.2 MB of free space.

Are you ready to start the migration?

Figure 68 Warning message box

7 As instructed in the Warning message box, make sure that CytoGenomics is not actively running any workflows or performing any database backup or restore activities and that all clients are logged out. If your CytoGenomics 5.0 database already contains date, make sure that data has been backed up. Then, click **Yes** to continue with the migration.

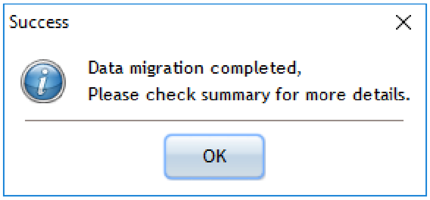
The right side of the screen (under **Data Migration Process**) displays the progress of the migration and the migration process summary.



```
[2018-02-15 09:12:14] Migration of Filter is successfully completed!!!
[2018-02-15 09:12:14] Time required to migrate data of Filter : 0.016 sec.
****************************************************************************************************
[2018-02-15 09:12:14] Started Migrating data of Tracks entity.....
[2018-02-15 09:12:14] Tracks count : 0
[2018-02-15 09:12:14] Migration of Tracks is successfully completed!!!
[2018-02-15 09:12:14] Time required to migrate data of Tracks : 0.014 sec.
****************************************************************************************************
[2018-02-15 09:12:14] Started Migrating data of QCMetrics entity.....
[2018-02-15 09:12:14] QCMetrics count : 0
[2018-02-15 09:12:14] Migration of QCMetrics is successfully completed!!!
[2018-02-15 09:12:14] Time required to migrate data of QCMetrics : 0.032 sec.
****************************************************************************************************
[2018-02-15 09:12:14] Started Migrating data of Protocol entity.....
[2018-02-15 09:12:14] Protocol count : 5
[2018-02-15 09:12:14] Migration of Protocol is successfully completed!!!
```

Figure 69 CytoGenomics Migration Utility application – Migration in progress

Upon completion of the migration process, the following message box opens.



Data migration completed,
Please check summary for more details.

Figure 70 CytoGenomics Migration Utility application – Data migration complete

8 Click **OK** to close the message box.

9 If desired, click **Export** to export a summary of the migration job.

10 Click the X in the top right corner of the Migration Utility application window to close the application.

Step 3. Upgrade to CytoGenomics 5.0 on the client computers

Follow these steps to install the CytoGenomics 5.0 client software.

- This procedure is the same as installing on client computers for a new installation.

  For more information, see "Step 3. Install the client software on additional Macintosh computers" on page 84.

Step 4. Start the Agilent CytoGenomics 5.0 client software, log in, and add new software license

1 Start the Agilent CytoGenomics program.

See "Step 4. Start the Agilent CytoGenomics 5.0 client software" on page 87.

2 Log in.

See "Step 5. Log in to Agilent CytoGenomics" on page 87.

3 Enter your updated license information.

See "Step 6. Add your software license" on page 89.

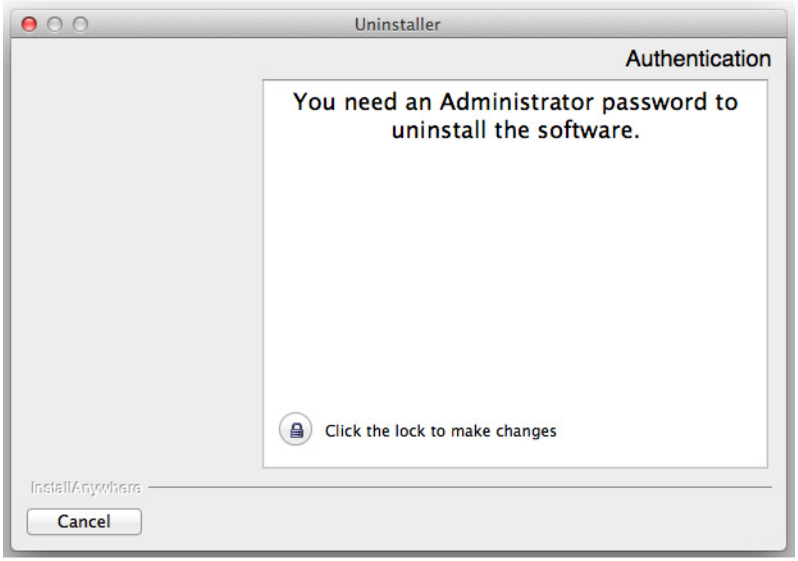
Upgrading from CytoGenomics 5.0.0 or 5.0.1 to CytoGenomics 5.0.2

If you are using CytoGenomics 5.0.0 or 5.0.1 and want to upgrade to CytoGenomics 5.0.2, you only need to upgrade the CytoGenomics client application. You do not need to upgrade to the CytoGenomics server application or migrate data from the previous version to the new version.

Step 1. Uninstall CytoGenomics 5.0.0 or 5.0.1 client

1 Double-click the Uninstaller file, located in the **\Uninstall_Agilent CytoGenomics** folder of your program folder.

The following window opens.



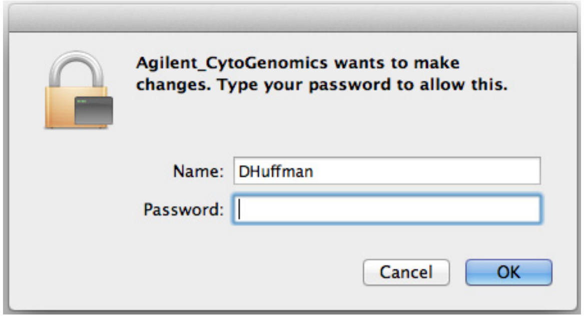
Authentication

You need an Administrator password to uninstall the software.

Figure 71 Authentication dialog box - preparing to uninstall

2 Click directly on the lock icon near bottom of the dialog box.

The following dialog box opens.



Agilent_CytoGenomics wants to make changes. Type your password to allow this.

Name: DHuffman

Password:

Figure 72 Administrator credentials dialog box - preparing to uninstall

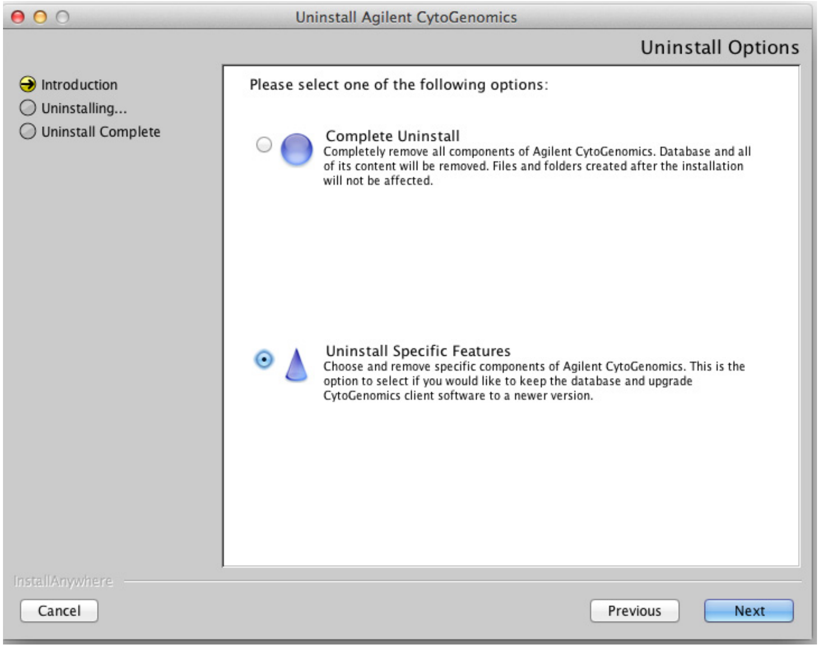
3. In this dialog box, enter the Name and Password for a user with administrator rights to the computer, then click **OK**.

   The uninstaller starts.

4. Read the introductory information, and then click **Next**.

5. Read the warning information. You are cautioned not to stop the uninstaller once it has started to remove the programs. Click **Next**.

   The Uninstall Options screen opens.



Please select one of the following options:

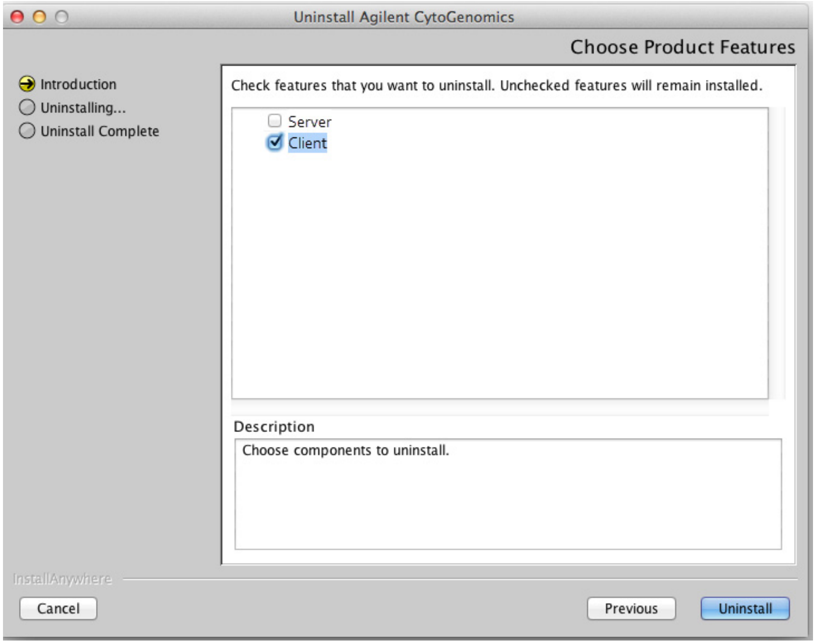
○ Complete Uninstall
Completely remove all components of Agilent CytoGenomics. Database and all of its content will be removed. Files and folders created after the installation will not be affected.

● Uninstall Specific Features
Choose and remove specific components of Agilent CytoGenomics. This is the option to select if you would like to keep the database and upgrade CytoGenomics client software to a newer version.

Figure 73 Uninstall Options screen – Macintosh – select **Uninstall Specific Features**

6 Select **Uninstall Specific Features** and click **Next.**

The Choose Product Features screen opens.



Check features that you want to uninstall. Unchecked features will remain installed.

☐ Server
☑ Client

Description

Choose components to uninstall.

Figure 74 Choose Product Features screen – Windows – mark **Client**

7 Mark **Client** and click **Uninstall**.

NOTE

Do not mark **Server** on the Choose Product Features screen. Doing so will result in removal of all previously analyzed data from your existing CytoGenomics server.

8 In the message box that opens click **Yes** to confirm that you want to uninstall the client software.

9 When the uninstallation is complete, click **Done** to close the uninstaller.

Step 2. Install CytoGenomics 5.0.2 client

1 Download Agilent CytoGenomics 5.0.2 from Agilent Technologies and check the system requirements.

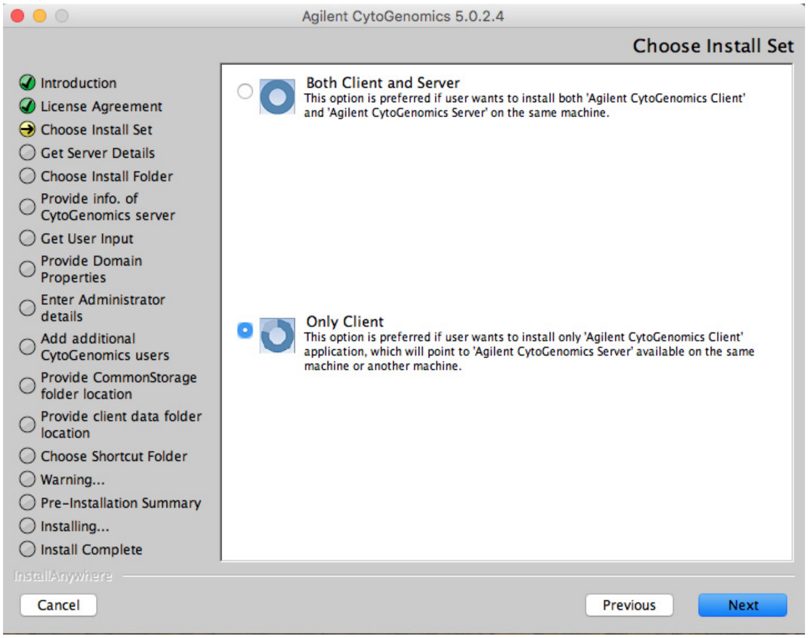
See "a. Download the Macintosh version of the software and release notes" on page 66 for detailed instructions on this step.

2 Double-click the compressed folder (Agilent_CytoGenomics_5_0_2_X_MAC.zip) that you downloaded and save the installer on your computer.

3 Double-click the Mac installer.

4 Run the installation wizard, as described in "Step 2. Install the database server and client on a single Macintosh computer" on page 68.

5 When the Choose Install Set screen opens, select **Only Client**.



Agilent CytoGenomics 5.0.2.4

Choose Install Set

○ Both Client and Server
This option is preferred if user wants to install both 'Agilent CytoGenomics Client' and 'Agilent CytoGenomics Server' on the same machine.

● Only Client
This option is preferred if user wants to install only 'Agilent CytoGenomics Client' application, which will point to 'Agilent CytoGenomics Server' available on the same machine or another machine.

Figure 75 Choose Install Set screen – Windows – select **Only Client**

6 Click **Next**.

7 Continue the installation wizard. For information, refer to "Step 3. Install the client software on additional Macintosh computers" on page 84.

Step 3. Start the Agilent CytoGenomics 5.0.2 client software, log in, and add new software license

1. Start the Agilent CytoGenomics program.

   See "Step 4. Start the Agilent CytoGenomics 5.0 client software" on page 87.

2. Log in.

   See "Step 5. Log in to Agilent CytoGenomics" on page 87.

3. Enter your updated license information.

See "Step 6. Add your software license" on page 89.

Uninstalling Agilent CytoGenomics on Macintosh computers

The Uninstall program for Agilent CytoGenomics provides an easy way to remove the CytoGenomics client, server, and PostgreSQL programs from your computer.

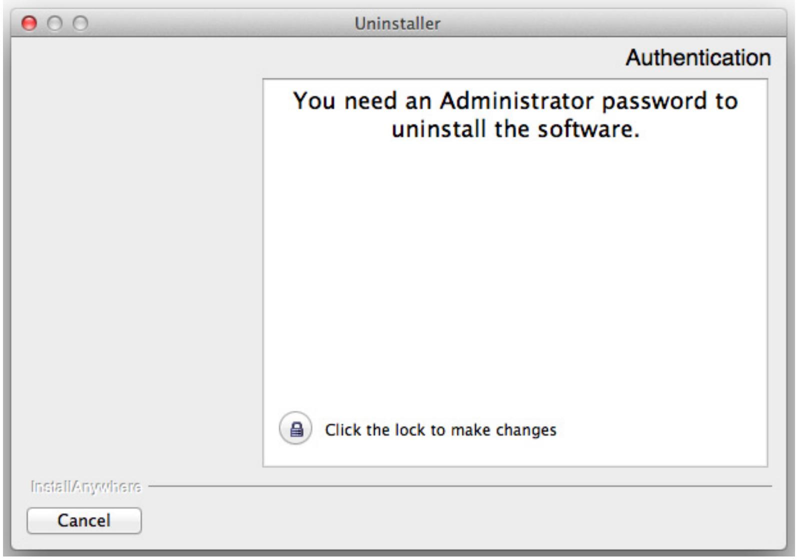
NOTE

CytoGenomics 5.0 is compatible with and can co-exist on the same machine as CytoGenomics 3.0 or 4.0. It is not necessary to uninstall the previous version of CytoGenomics (i.e., v3.0 or 4.0) in order to install v5.0.

When you completely uninstall Agilent CytoGenomics, the database and the data contained in it are completely removed. Do not uninstall the entire program unless you have backed up your database or no longer wish to use it.

1. Double-click the Uninstaller file, located in the **\Uninstall_Agilent CytoGenomics 3.0.X.X** or **\Uninstall_Agilent CytoGenomics** folder of your program folder.

   The following window opens.

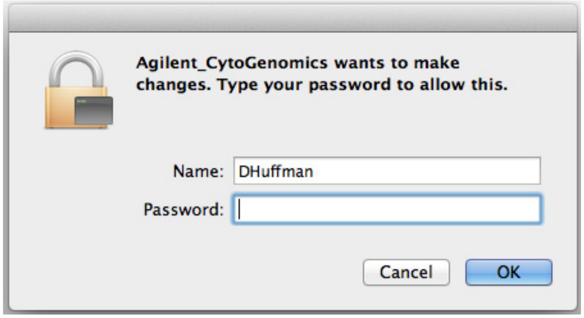


You need an Administrator password to uninstall the software.

Figure 76 Authentication dialog box - preparing to uninstall

2 Click directly on the lock icon near bottom of the dialog box.

The following dialog box opens.



Agilent_CytoGenomics wants to make changes. Type your password to allow this.

Name: DHuffman

Password:

Figure 77 Administrator credentials dialog box - preparing to uninstall

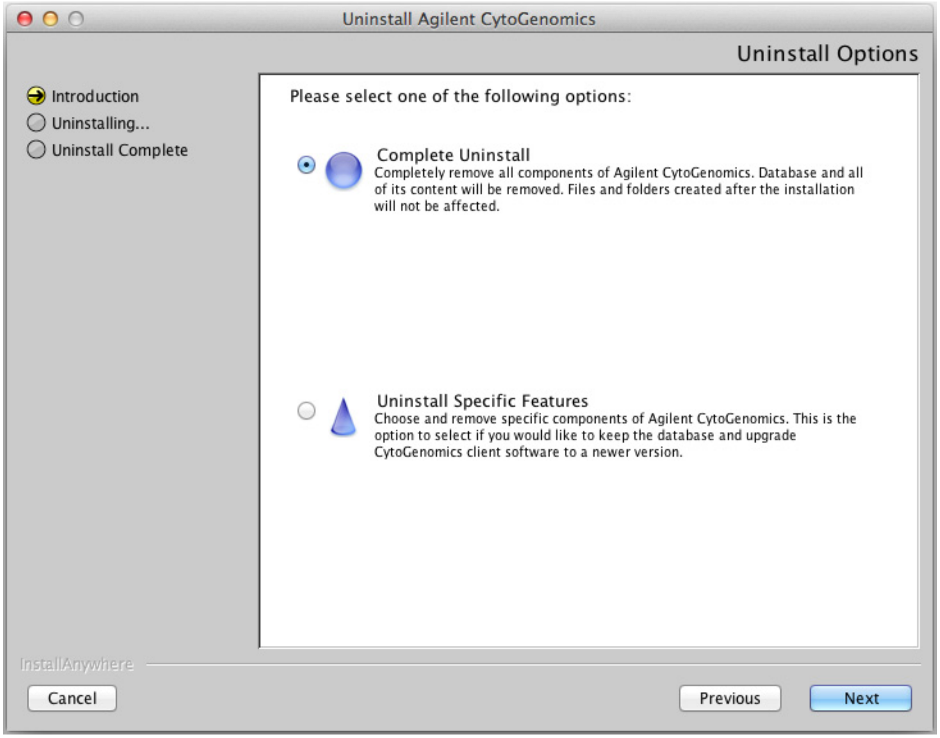
3 In this dialog box, enter the Name and Password for a user with administrator rights to the computer, then click **OK**.

The uninstaller starts.

4 Read the introductory information, and then click **Next**.

5 Read the warning information. You are cautioned not to stop the uninstaller once it has started to remove the programs. Click **Next**.

The Uninstall Options screen opens.



Please select one of the following options:

● Complete Uninstall
Completely remove all components of Agilent CytoGenomics. Database and all of its content will be removed. Files and folders created after the installation will not be affected.

○ Uninstall Specific Features
Choose and remove specific components of Agilent CytoGenomics. This is the option to select if you would like to keep the database and upgrade CytoGenomics client software to a newer version.

Figure 78 Uninstall Options screen – Macintosh – select **Complete Uninstall**

6 Select **Complete Uninstall**.

7 Click **Next.**

8 When the uninstallation is complete, a message appears. Click **Done** and then restart the system.

The Agilent CytoGenomics client program, server program and database, and PostgreSQL program were removed from your computer. Program folders and data folders (such as data output folders) created after installation were not removed.

4

Administering the System

This chapter shows you how to add users, assign roles and manage the database.

See the *Product Overview Guide* for an overview of the program and organization of the tasks within it.

Administering the System

As an Administrator for Agilent CytoGenomics, you have access to everything. That is, you can perform any task available in the program. Your primary responsibility is to add users and their roles to the system, and you also manage the database.

See “User Roles and Capabilities” on page 16 for an explanation of the tasks that each role can perform in the program. Users who are assigned the role of Technician can only run workflows and view the results. They cannot set up workflows, nor can they sign off on results. Those are tasks for users assigned the role of Scientist.

To manage users and roles

Only the Administrator role can perform these tasks.

Table 4 Tasks for managing users and roles

To do this task	Follow these instructions	Comments
Add new users	**1** Click **Admin**. **2** Click **Manage Users & Roles**. **3** Click **Add New User**. A list of all the users in the domain or on the local machine appears. **4** Next to **Add New User**, type the user name, and then click **Find**. (See comments for information about adding users for local machines.) **5** At the bottom of the Add User Dialog dialog box, click **Add User**. **6** When the Add User dialog box opens asking you to confirm, click **Yes**. **7** When the notice of success opens, click **OK**. **8** When you are finished adding users, click **Close**. The user now appears in the list of users with the role of Technician, with a status of *Enabled*.	• A user cannot be deleted but can be disabled. **a** Click **Edit** for the user you intend to disable. **b** Clear the **Enabled** check box, and click **Save**. • For local machines with no Domain, **a** Next to **User**, type the computer name and user in the format `machinename\username`, or `\username` for Macintosh systems. (Do NOT click **Find**.) **b** Click **Add User.** A warning dialog box opens stating that there was a problem fetching user details from the LDAP server. You can ignore this warning. Click **OK** to close the dialog box.

Table 4 Tasks for managing users and roles (continued)

To do this task	Follow these instructions	Comments
Change user roles	**1** Click **Admin**. **2** Click **Manage Users & Roles**. **3** On the line for the user whose role you intend to change, click **View/Edit**. **4** Highlight the role on the right side of the panel, and then click **<** to remove the role on the right. **5** Highlight a role on the left side of the panel, and then click **>** to add the role to the right. **6** Click **Save**.	• See "User Roles and Capabilities" on page 16 for descriptions of each user role. • You can create custom roles that allow for a desired set of privileges. See the CytoGenomics help system for instructions.

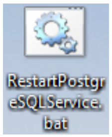
To manage the database

Although only the Administrator role can change the location of the database or the common storage folder, any user can restart the PostgreSQL service.

Table 5 Tasks for managing the database

To do this task	Follow these instructions	Comments
Change database locations and information	**1** Click **Admin**. **2** Click **Database Settings**. **3** Under **Database Settings**, click **Change**. **4** Type: • Common Storage Location • Database Host • Database Port Click **Apply** to save your changes.	• If you change the location of your common storage, copy the contents of the previous location to the new location manually. **Failure to do so can cause unexpected behavior in the program**. • Enter the location of the common storage using UNC standard notation. (\\machine2\CommonStorage)

Table 5 Tasks for managing the database

To do this task	Follow these instructions	Comments
Restart PostgreSQL	- If the PostgreSQL service stops, to restart it, click **Restart PostgreSQL Service** on the desktop.  RestartPostgreSQLService.bat	

For instructions on backing up and restoring the database, see the CytoGenomics help system.

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In this book

This book provides an overview of Agilent CytoGenomics 5.0 and gives you instructions for installing and administering the software.

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