



Agilent CytoGenomics 5.3

Product Overview and Installation Guide

Revision A0, November 2022

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Notices

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In This Guide...

This *Product Overview and Installation Guide* provides an overview of Agilent CytoGenomics 5.3 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 5.3 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 5.3 on systems running the macOS Big Sur or Monterey operating system.

4 Administering the System

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

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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.

What is Agilent CytoGenomics?

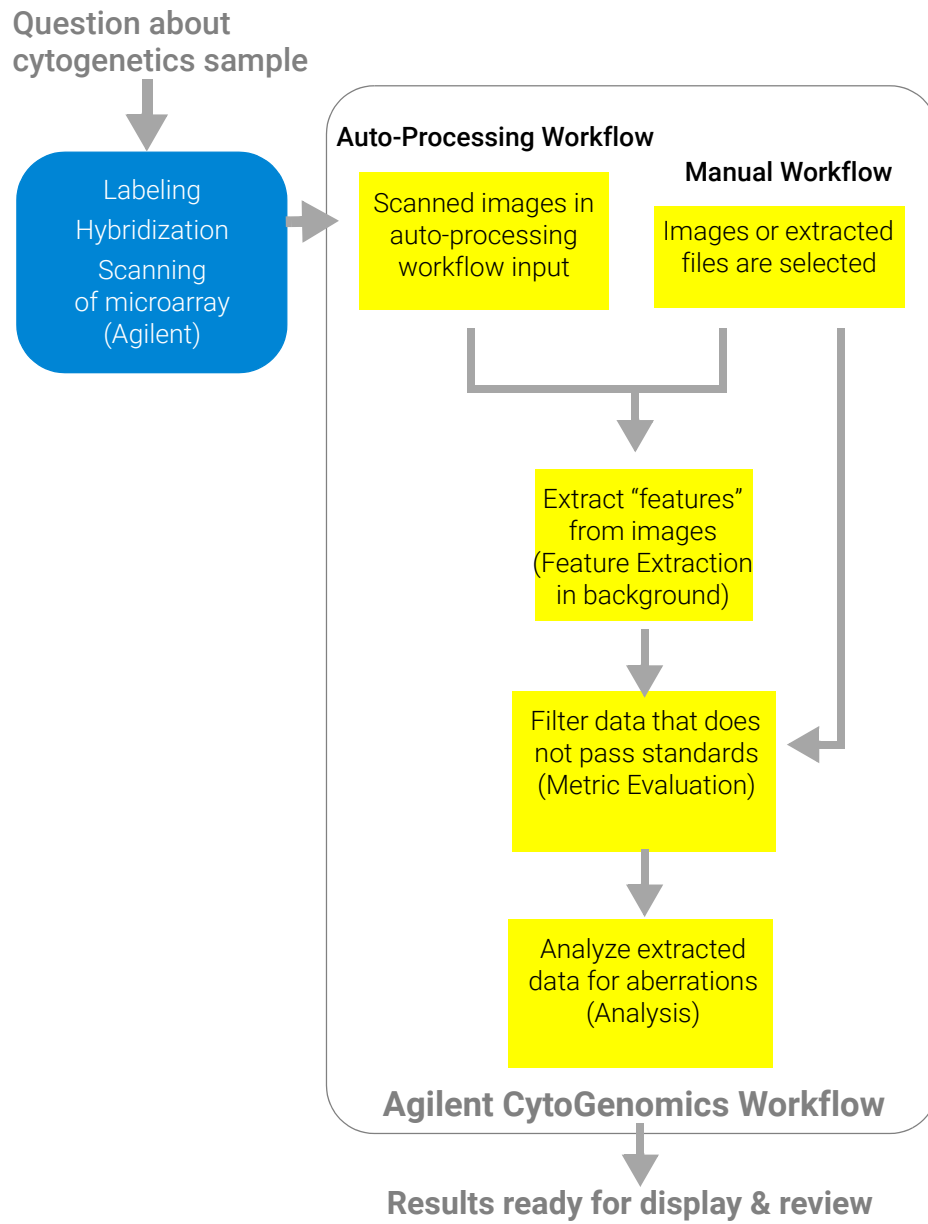


Figure 1 Agilent CytoGenomics Workflow – from image to result

Getting Help

To get help within Agilent CytoGenomics 5.3

Agilent CytoGenomics 5.3 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, 5, 3) E-mail message: informatics_support@agilent.com
Contact Agilent Technical Support by telephone or e-mail message (for your country)	<ol style="list-style-type: none"> 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 5.3. 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 14.)

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
- Entering login credentials for Agilent SureDesign accounts

The Auto Processing tab – setting up Auto-Processing workflows

Capabilities within the Auto Processing tab include:

- Starting and stopping Auto-Processing
- 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 SureDesign
- Exporting sample attribute files
- Configuring spike-in identifiers
- Importing design files and genotype reference files
- Importing and exporting probe ID lists and 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
- Setting up connections to partners software programs

User Roles and Capabilities

The following table lists the capabilities allowed for the three different default user roles within Agilent CytoGenomics 5.3.

Table 1 User roles and capabilities

Role	Tasks and capabilities
Technician	<ul style="list-style-type: none"> • 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: <ul style="list-style-type: none"> • Configure system preferences, including <ul style="list-style-type: none"> • 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 <ul style="list-style-type: none"> • Add users and create user roles • Change database connection settings for client systems • Backup and restore database • Set up connections to partner software programs

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This chapter shows you how to install Agilent CytoGenomics 5.3 and migrate data from a previous version of CytoGenomics on computers running a compatible Microsoft Windows operating system.

Installing Agilent CytoGenomics 5.3 – Windows

This section includes detailed instructions and important notes for installing Agilent CytoGenomics 5.3 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 5.3 and Migrating Data – Windows”** on page 41.

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	The following 64-bit Windows operating systems are supported. Windows 10 Enterprise or Professional Windows 11 Enterprise or Professional Windows Server 2019 Note: For all of these operating systems, the regional format must be set to English (United States). You can find the regional format setting in Windows Settings > Time & Language > Region .
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: 8 GB Recommended: 12 GB
Hard disk space	500 GB
Display Resolution	Windows 10 and Windows Server 2019 systems: 1280 × 768 or higher Windows 11 systems: 1600 × 900 or 1366 × 768

c. Set up permissions for Installer and users

- Make sure that the user account used to install the Agilent CytoGenomics 5.3 software has administrator permissions on the installation computer.
- Make sure that every user account running the Agilent CytoGenomics 5.3 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 10 or Windows 11

If you are using the 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 **Security and Maintenance**).
- 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 26.)

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 5.3 users. All client computers must have network access to the server computer and users must have read/write permissions.

- 1 Log on to the Windows system where you want to install Agilent CytoGenomics 5.3 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 16. Double-click the Agilent CytoGenomics 5.3.X.X application file to start the installation wizard.

The following message is displayed.

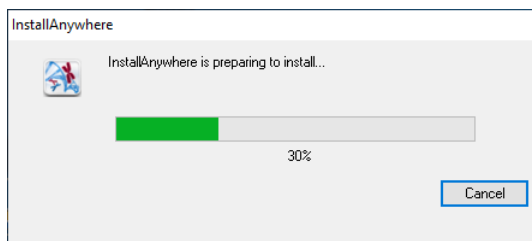


Figure 2 InstallAnywhere dialog box - preparing to install

The installation wizard opens to the Introduction screen.

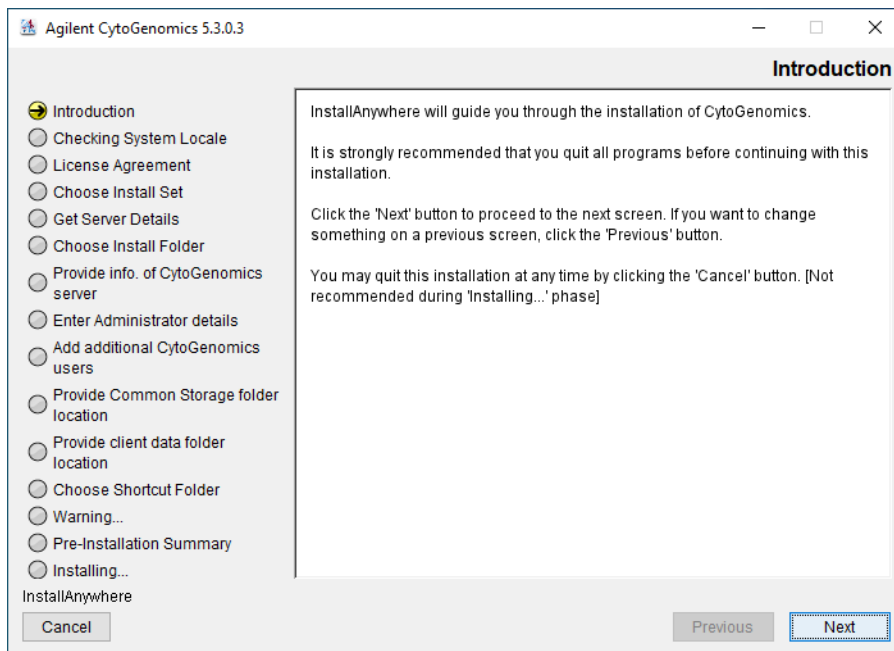


Figure 3 Introduction screen for the installation wizard – Windows

3 Read the introductory information.

4 Click **Next**.

The License Agreement screen opens.

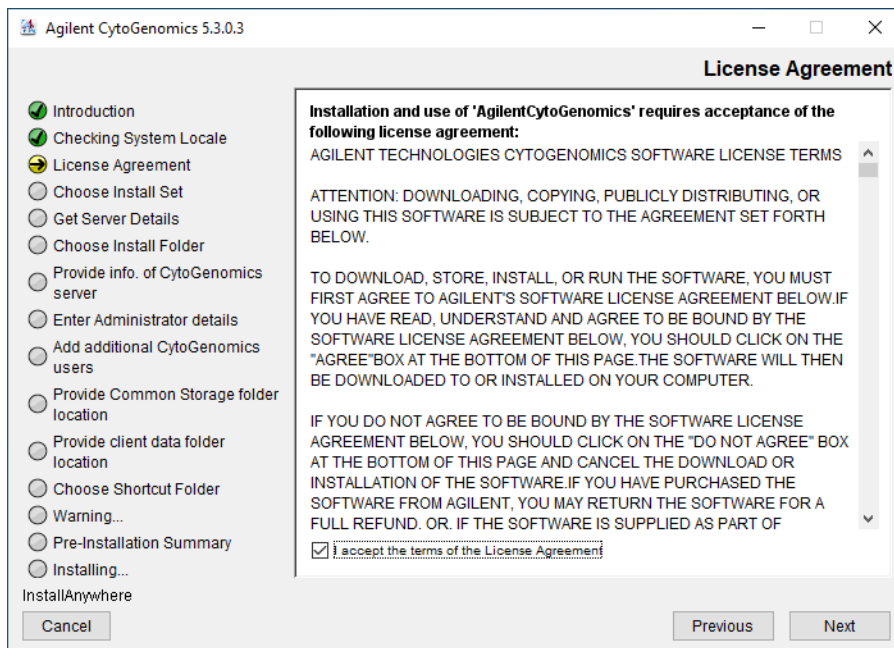


Figure 4 License Agreement screen – Windows

- 5 Read the license agreement. Mark **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.

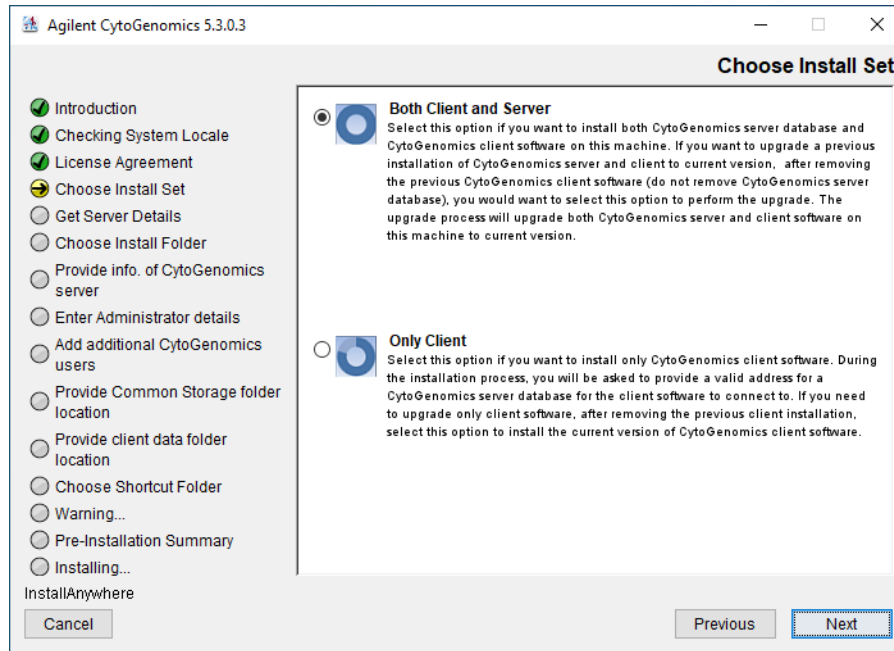


Figure 5 Choose Install Set screen – Windows - select **Both Client and Server**

- 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.

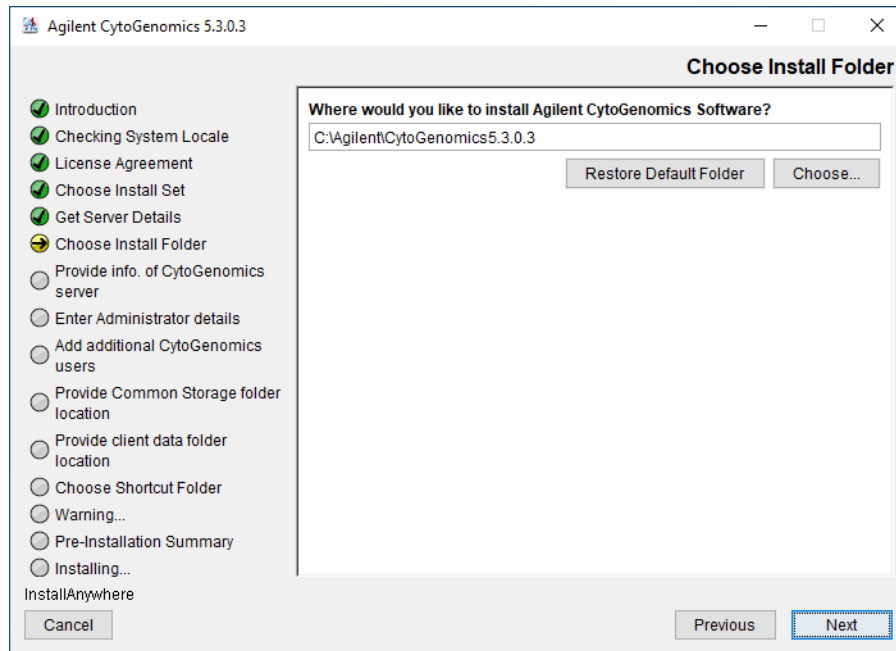


Figure 6 Choose Install Folder screen – Windows

- By default, the program is installed in: **C:\Agilent\AgilentCytoGenomics5.3.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 5.3. 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**.

- Click **Next**.

The Enter Administrator details screen opens.

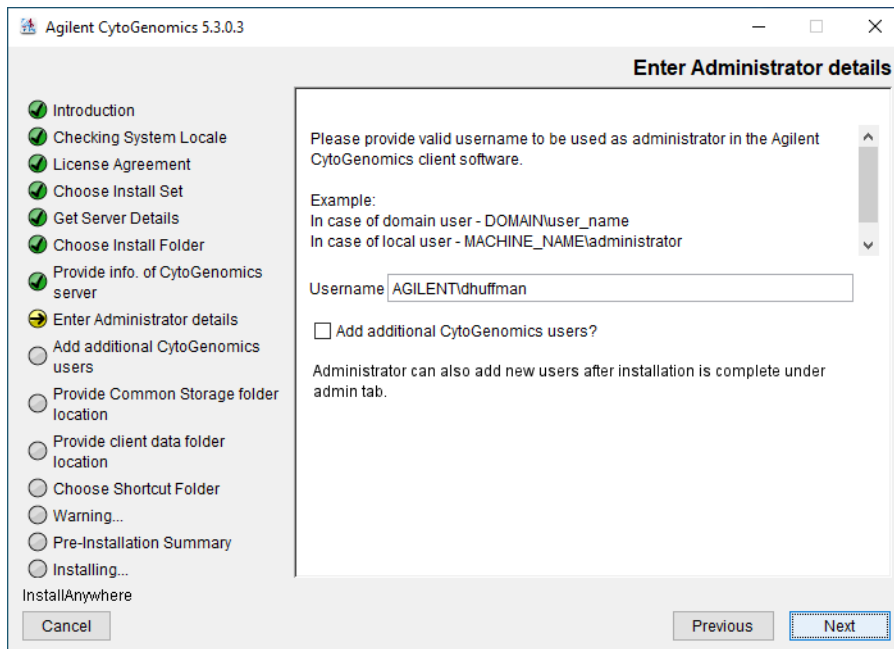


Figure 7 Enter Administrator details screen – Windows

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 5.3 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 23**. Note that the administrator can set up new users from within CytoGenomics once installation is complete (see **“To manage users and roles”** on page 82).

12 Click **Next**.

The Add additional CytoGenomics users screen opens.

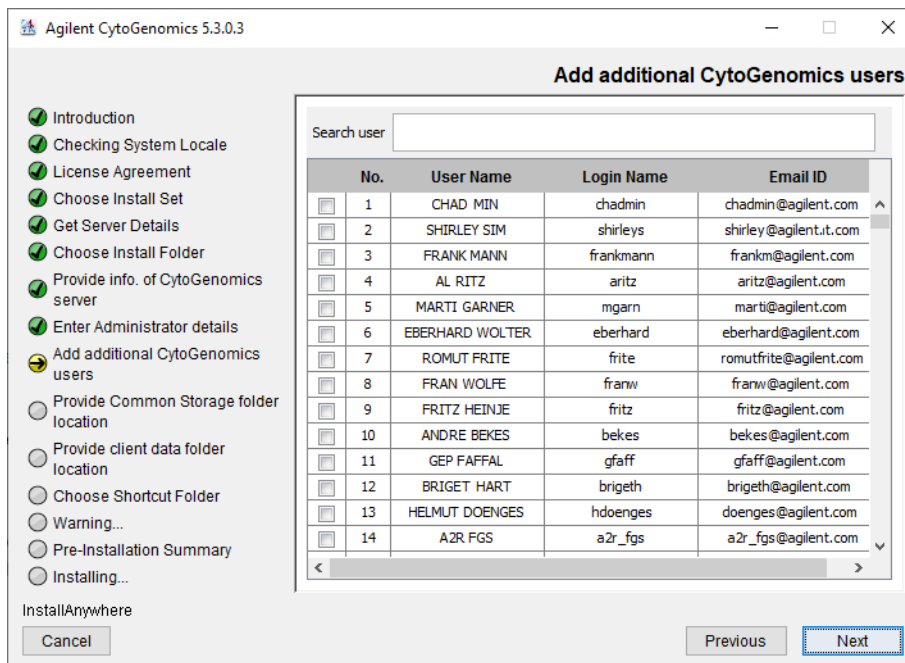


Figure 8 Add additional CytoGenomics users screen – Windows

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.

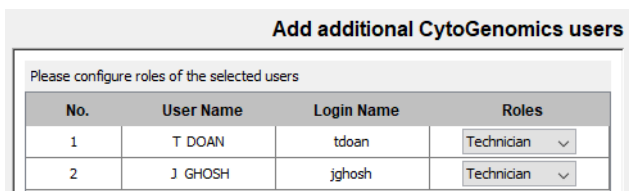


Figure 9 Add additional CytoGenomics users screen – Configure roles step – Windows

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 14 for a description of each role.

16 Click **Next**.

The Choose common storage folder screen opens.

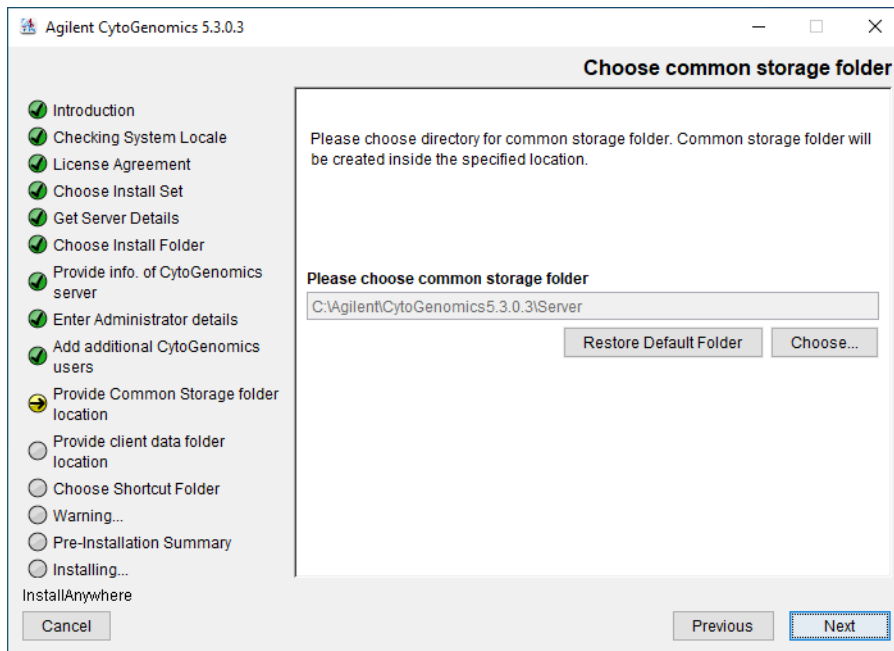


Figure 10 Choose common storage folder screen – Windows

17 By default, the common storage folder is created inside the folder **C:\Agilent\AgilentCytoGenomics5.3.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.

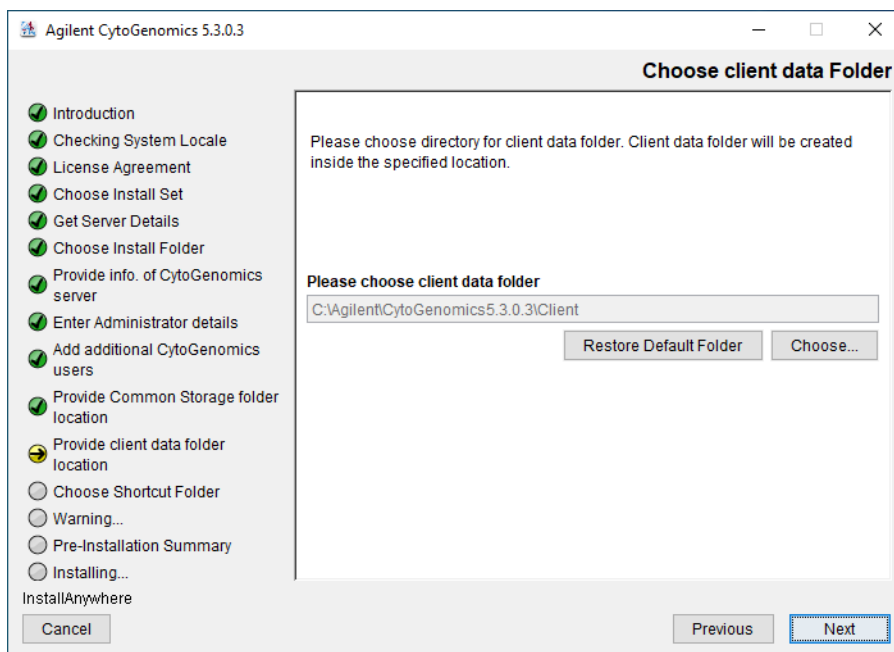


Figure 11 Choose client data folder screen – Windows

19 By default, the client data folder is created inside the folder **C:\Agilent\AgilentCytoGenomics5.3.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.

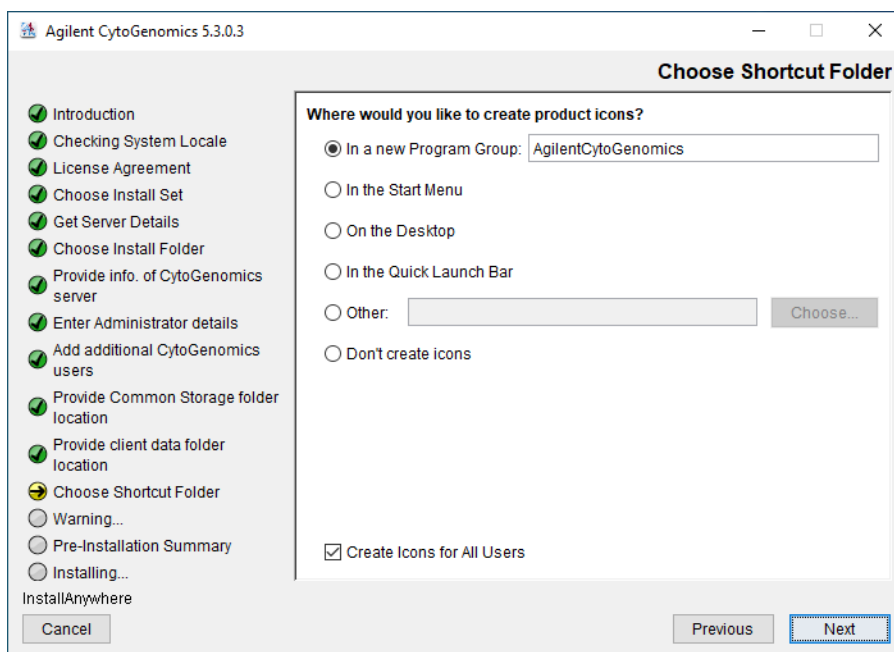


Figure 12 Choose Shortcut Folder screen – Windows

21 By default, program icons are installed in the Agilent CytoGenomics 5.3.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 5.3 on this computer, select **Create Icons for All Users**. Otherwise, other users do not see the program icons.

The Warning screen opens.

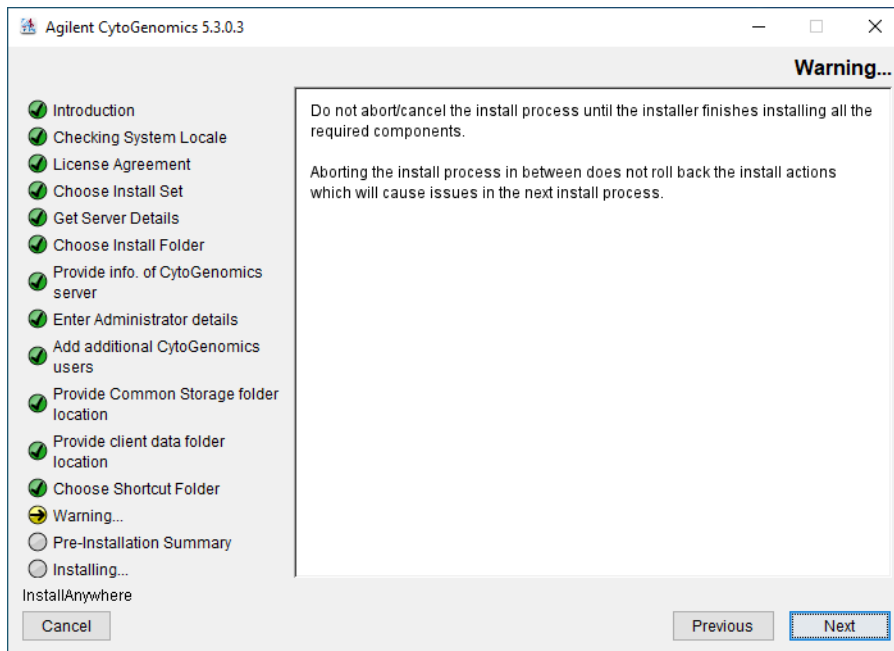


Figure 13 Warning screen – Windows

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.

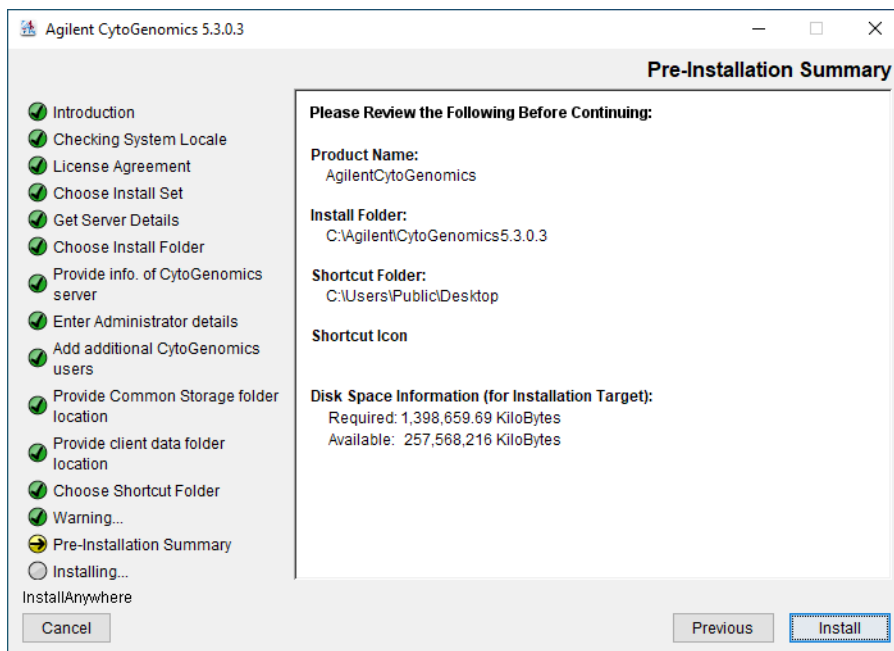


Figure 14 Pre-Installation Summary screen – Windows

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**.

Installing Agilent CytoGenomics 5.3 – Windows

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

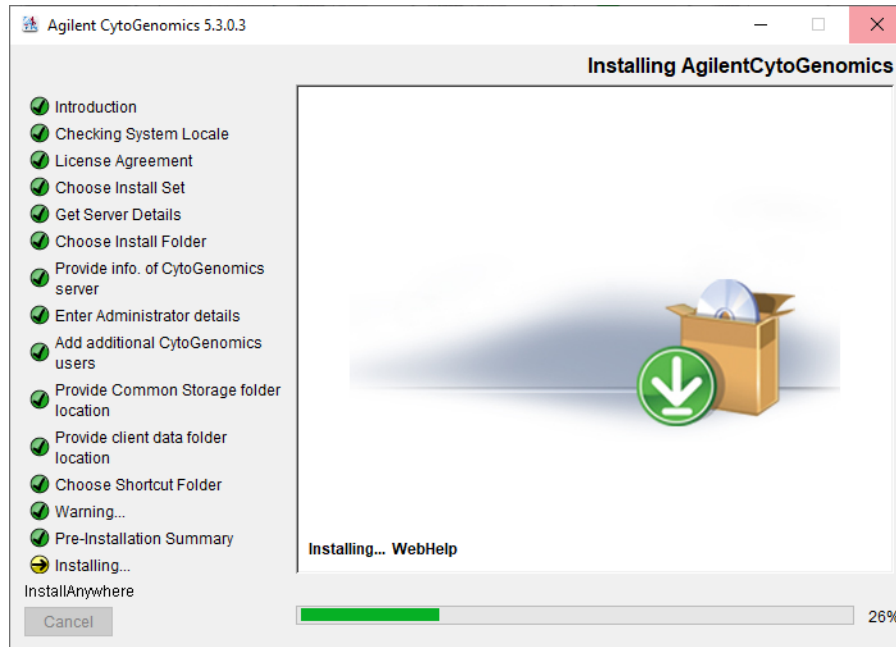


Figure 15 Installing Agilent CytoGenomics screen – Windows

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

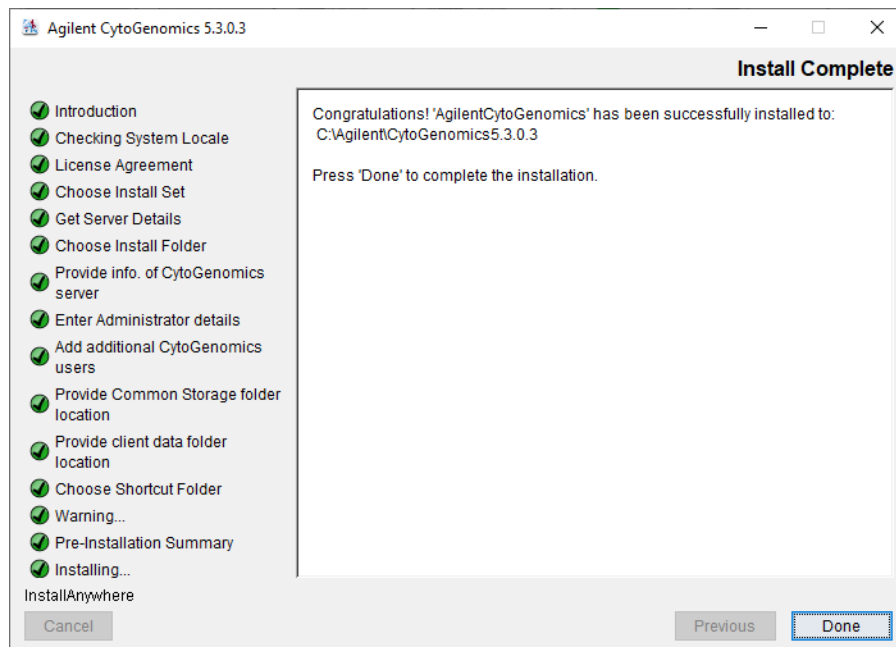


Figure 16 Install Complete screen – Windows

24 Click **Done**.

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.

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 5.3 server.

- 25 Click **Skip** to close the Launch Migration Utility dialog box without launching the migration utility tool.

Because these instructions are for installing Agilent CytoGenomics 5.3 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 5.3 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 5.3 program, run the installation wizard, as described in “**Step 2. Install the database server and client on a single Windows computer**” on page 18.
- 2 When the Choose Install Set screen opens, select **Only Client**.

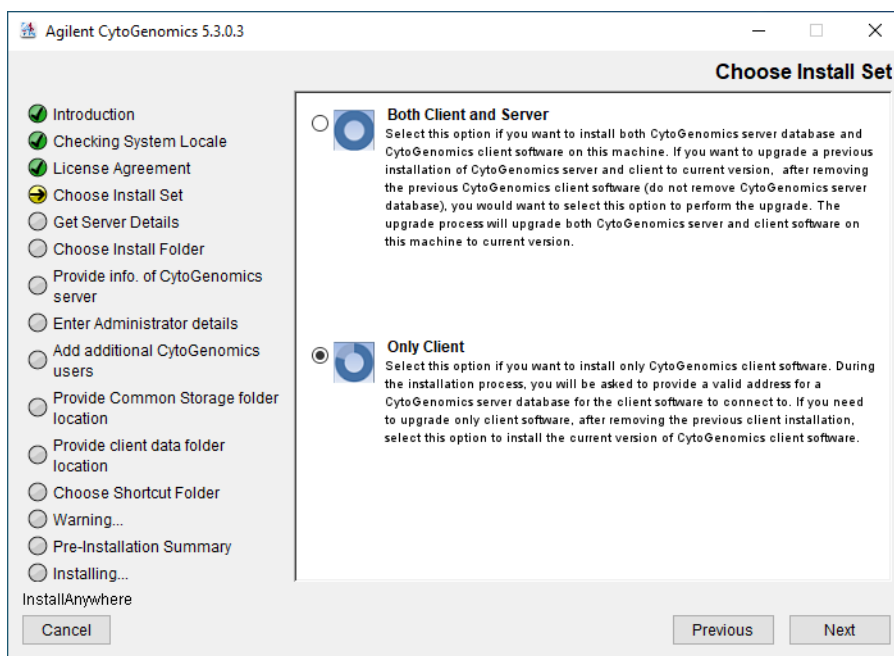


Figure 17 Choose Install Set screen – Windows – select **Only Client**

- 3 Click **Next**.

The Choose Install Folder screen opens.

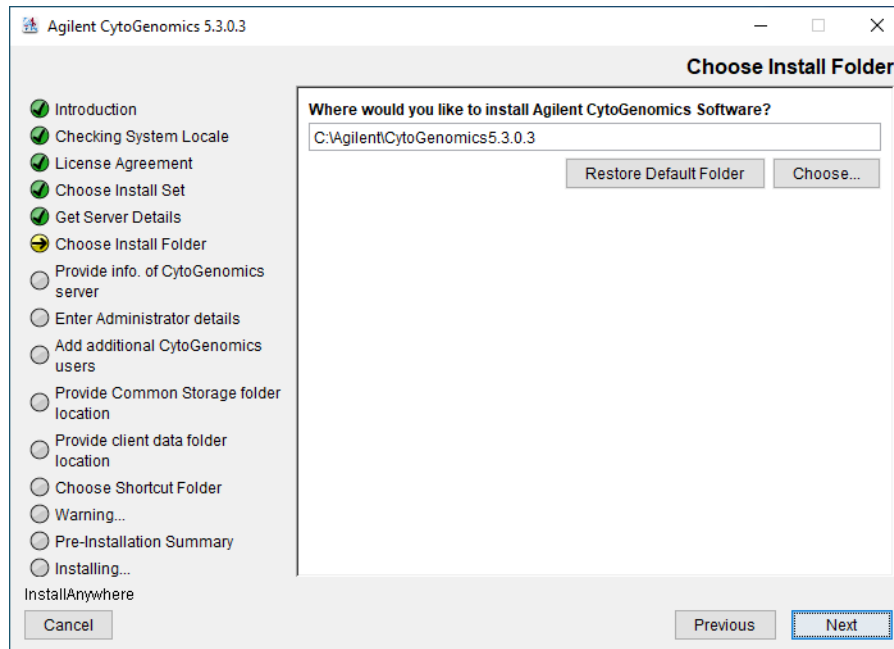


Figure 18 Choose Install Folder screen – Windows

- 4 By default, the program is installed in **C:\Agilent\AgilentCytoGenomics5.3.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 5.3.

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.

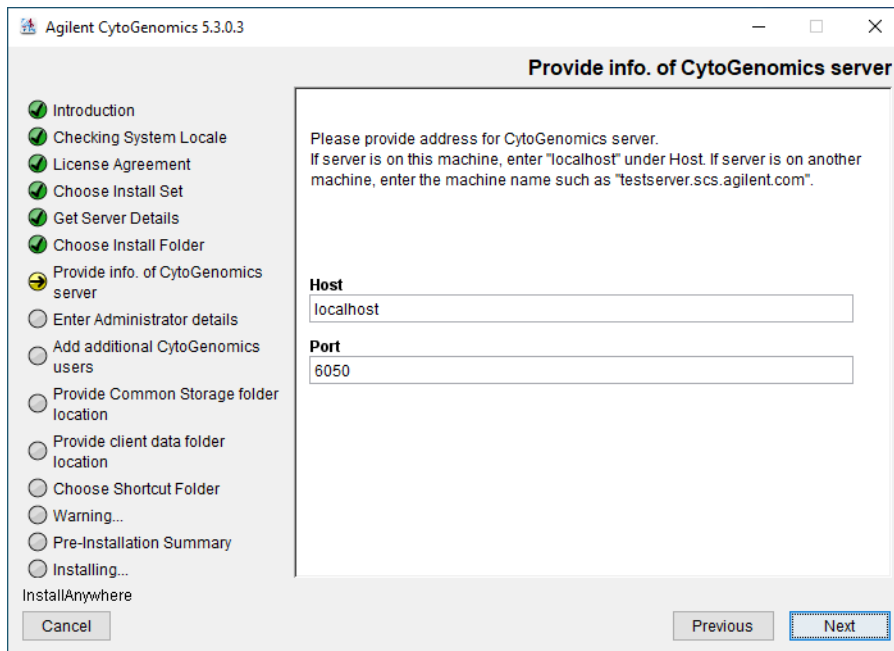


Figure 19 Provide Info. of CytoGenomics server screen – Windows

- 6 Under **Host**, type the assigned computer name or IP address of the computer (from **step 2**) where you installed the Agilent CytoGenomics 5.3 database server.

To find the computer name of your current computer, click **Start > Control Panel > System and Security > System** (Windows 10 and Windows Server 2019) or **Start > Control Panel > System** (Windows 11).

- 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.

- 9 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 18.

Step 4. Start the Agilent CytoGenomics 5.3 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 5.3 icon, or select **Agilent CytoGenomics 5.3** 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.

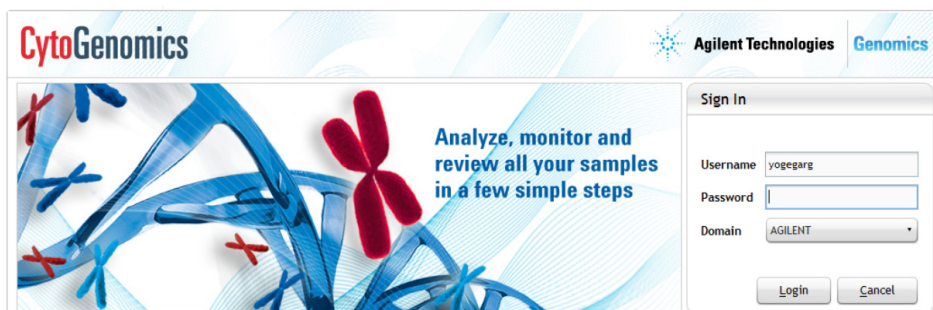


Figure 20 Login screen

- 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 21**).

- 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.

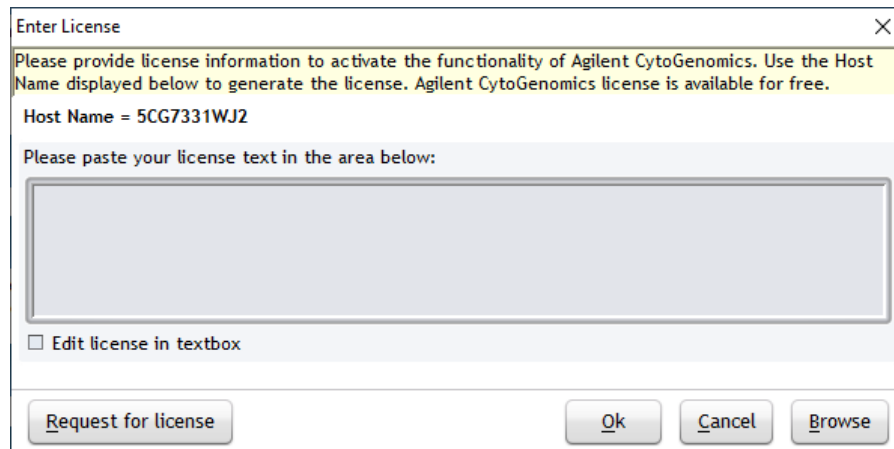


Figure 21 Enter License dialog box

- 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** in the Enter License dialog box.

The Agilent CytoGenomics program opens to the Home screen (**Figure 22**).

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.

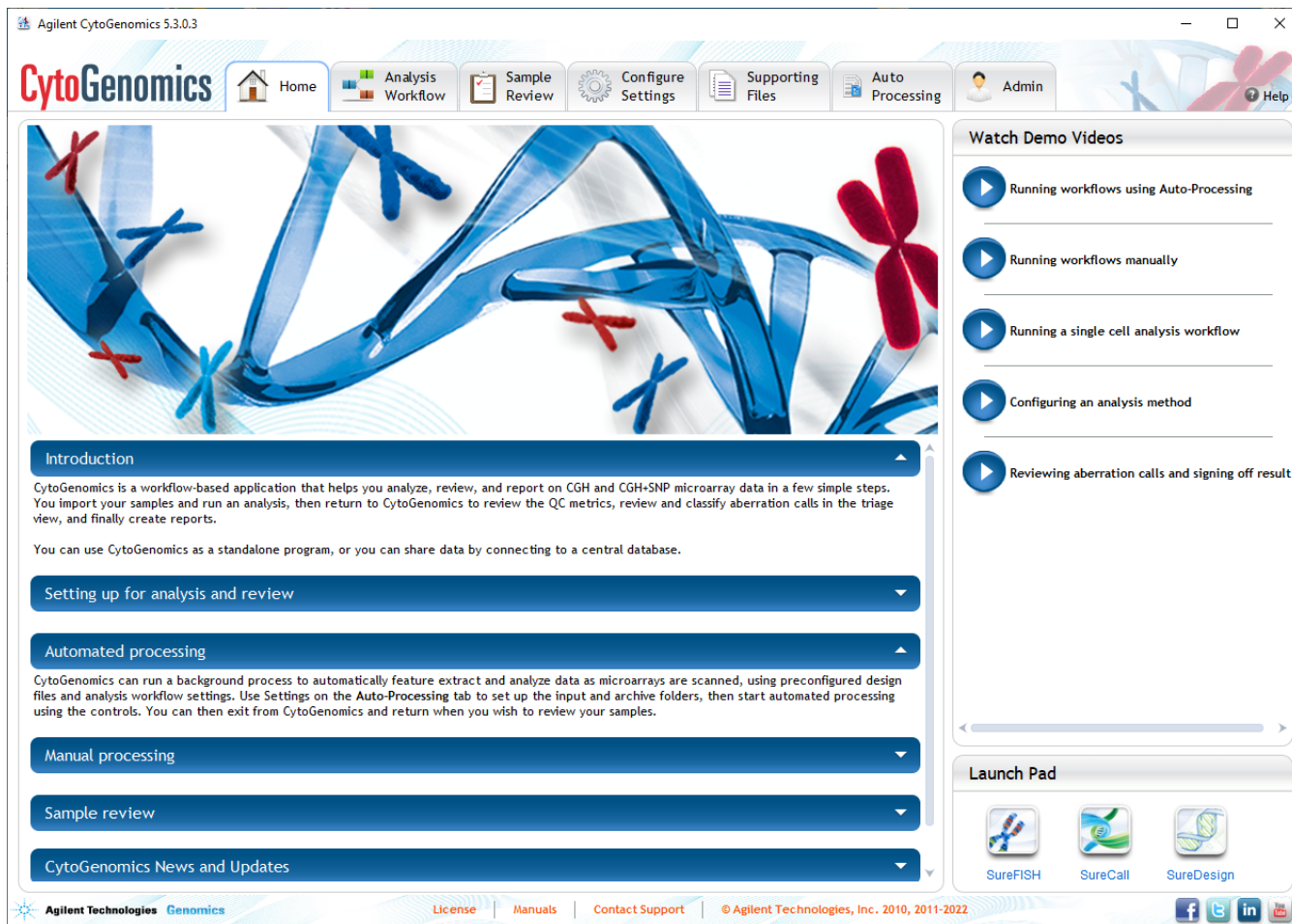


Figure 22 Agilent CytoGenomics program Home screen

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 14. For information on how to add users and assign roles, see ***“To manage users and roles”*** on page 82.

Upgrading from CytoGenomics 5.2.1 to CytoGenomics 5.3 – Windows

CytoGenomics 5.2.1 is the version just prior to CytoGenomics 5.3.0. You can upgrade from version 5.2.1 to version 5.3 through the cloud (i.e., without downloading the installer for version 5.3).

NOTE

Cloud update to CytoGenomics 5.3 is only supported from CytoGenomics 5.2.1. If CytoGenomics 5.2.1 is installed on a machine that is behind a proxy server, make sure required proxy credentials are provided on the Admin > Partners > Set Proxy Settings screen.

- 1 Launch CytoGenomics 5.2.1 and ensure you have an internet connection.

The Updates Available dialog box opens.

If this dialog box does not open, go to the Configure Settings > Settings > Local Settings screen and mark the check box under **Auto-Updates Software and Track Settings**. Click **Apply Settings** to save. Then, close and re-launch CytoGenomics 5.2.1.

- 2 In the Updates Available dialog box, mark the **Software update** check box.
- 3 Click **Download**.

The Confirm message box opens asking you to confirm that you want to start downloading software update files.

- 4 Click **OK** to start the download process.

A Progress Status message opens. During the download process, you are blocked from using CytoGenomics. Download time is dependent on internet speed.

Once the download is complete, a Download Successful message displays, and counts down from 5 seconds to close the application. You may skip the countdown by clicking **OK**.

A notification message opens confirming that the application has been updated.

- 5 Click **OK** in the notification message to launch CytoGenomics 5.3.

Upgrading from CytoGenomics 5.0.X, 5.1.X, or 5.2.0 to CytoGenomics 5.3 – Windows

If you are currently using CytoGenomics 5.0, 5.1, or the first release of 5.2 (i.e., 5.2.0) and you want to upgrade to CytoGenomics 5.3, you need to uninstall the existing CytoGenomics client application, then install the CytoGenomics 5.3 client and server. You do not need to migrate data from the previous version to the new version.

Step 1. On the server computer, uninstall existing CytoGenomics client and install CytoGenomics 5.3 client and server

- 1 Download Agilent CytoGenomics 5.3 from Agilent Technologies and check the system requirements.

See **“a. Download the Windows version of the software and release notes”** on page 16 for detailed instructions on this step.
- 2 Double-click the Agilent CytoGenomics 5.3 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**.

A message box opens notifying you that the existing version of CytoGenomics client must be uninstalled before installing CytoGenomics 5.3 client.
- 4 Click **OK** in the message box.

The CytoGenomics uninstaller opens.

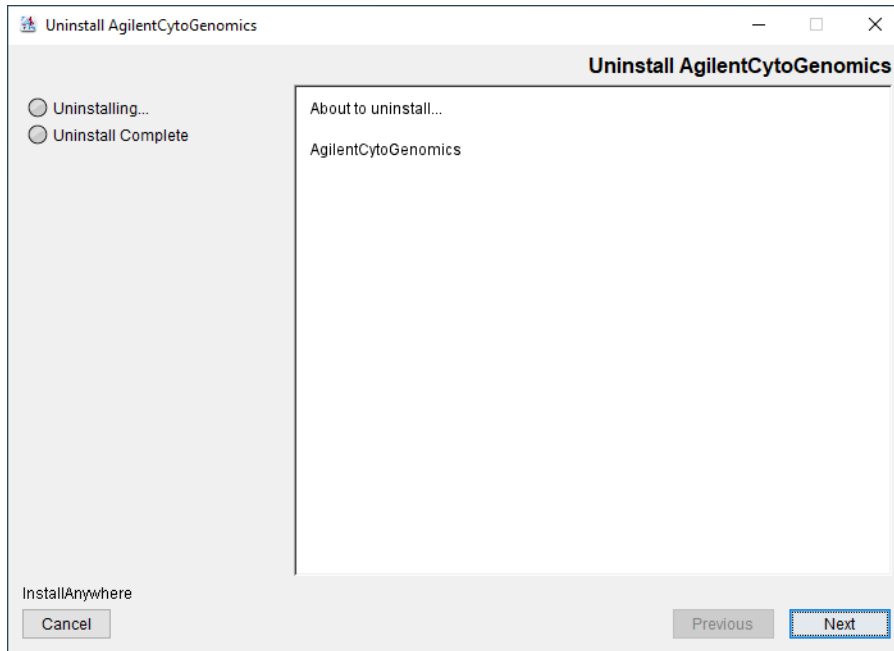


Figure 23 CytoGenomics Uninstaller – Windows

- 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.

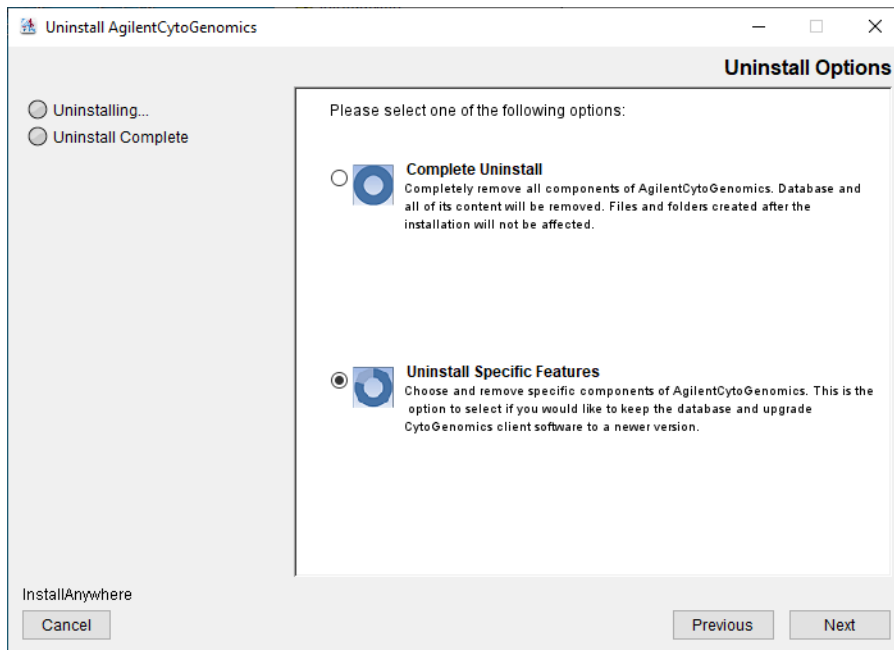


Figure 24 Uninstall Options screen – Windows – select Uninstall Specific Features

- 7 Select **Uninstall Specific Features**. Click **Next**.

The Choose Product Features screen opens.

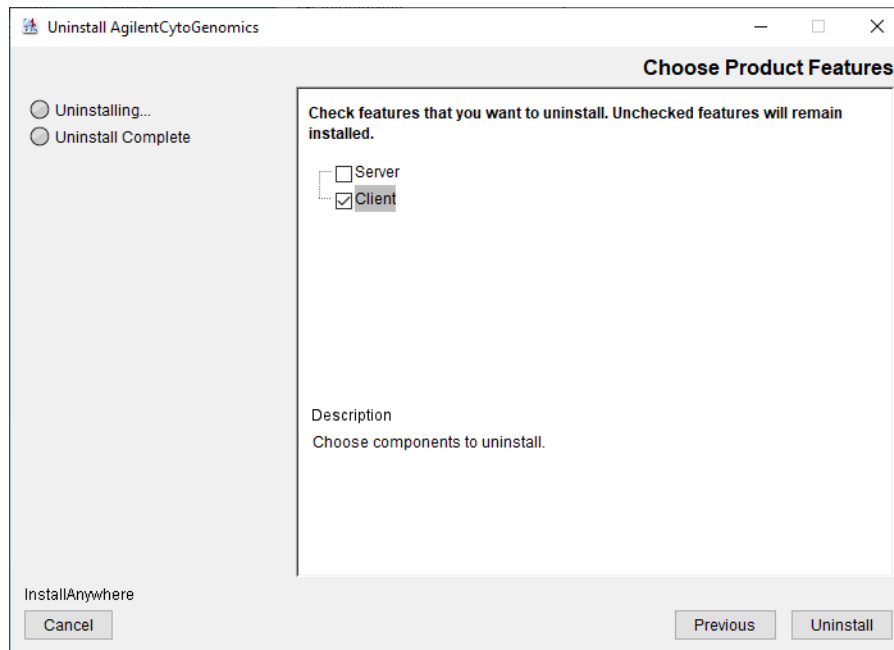


Figure 25 Choose Product Features screen – Windows – select **Client**

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, 5.1, or 5.2.0.
- 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 5.3 installer.
- 11** Continue the installation wizard, as described in **“Step 2. Install the database server and client on a single Windows computer”** on page 18.
- 12** When the Choose Install Set screen opens, select **Both Client and Server**.

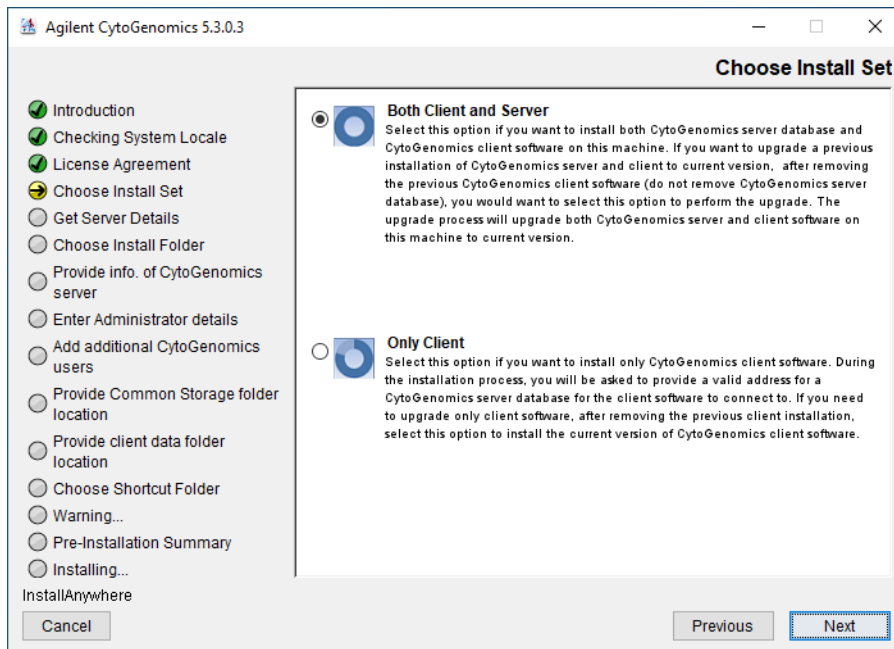


Figure 26 Choose Install Set screen – Windows – select **Both Client and Server**

13 Click **Next**.

An Information message opens notifying you that you selected to install both the server and client applications. Click **OK** to continue.

A second Information message opens notifying you that the CytoGenomics server application already exists on the local machine. Click **OK** to continue.

14 Continue the installation wizard. For information, refer to **“Step 2. Install the database server and client on a single Windows computer”** on page 18.

Step 2. On the client computers, uninstall existing CytoGenomics client and install CytoGenomics 5.3 client

1 Download Agilent CytoGenomics 5.3 from Agilent Technologies and check the system requirements.

See **“a. Download the Windows version of the software and release notes”** on page 16 for detailed instructions on this step.

2 Double-click the Agilent CytoGenomics 5.3 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**.

A message box opens notifying you that the existing version of CytoGenomics client must be uninstalled before installing CytoGenomics 5.3 client.

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

The CytoGenomics uninstaller opens.

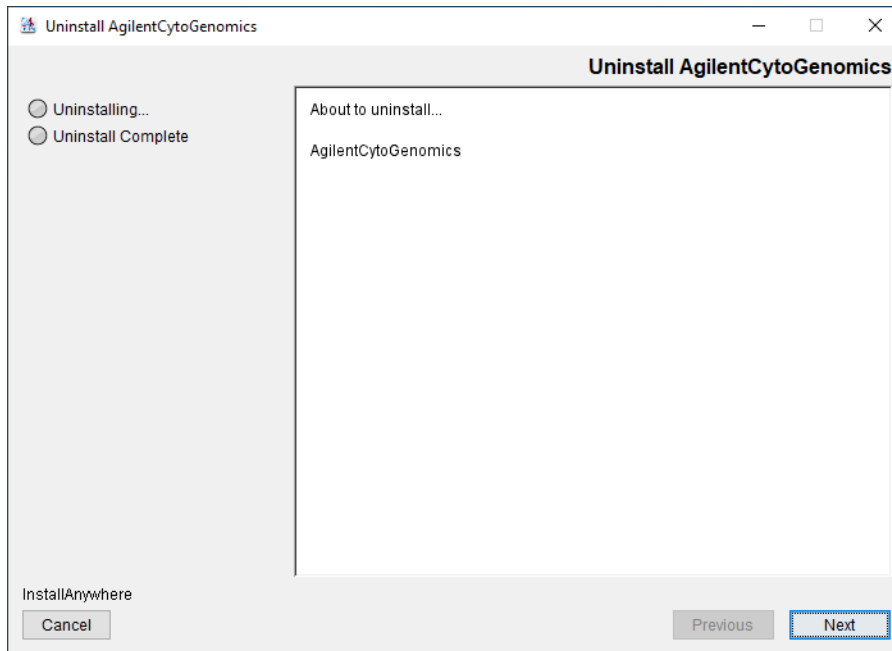


Figure 27 CytoGenomics Uninstaller – Windows

- 5 Click **Next**.
- 6 In the confirmation message box that opens, click **Yes** to continue uninstalling CytoGenomics client for version 5.0, 5.1, or 5.2.0.
- 7 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 5.2 installer.
- 8 Continue the installation wizard, as described in **“Step 3. Install the client software on additional Windows computers”** on page 28.
- 9 When the Choose Install Set screen opens, select **Only Client**.

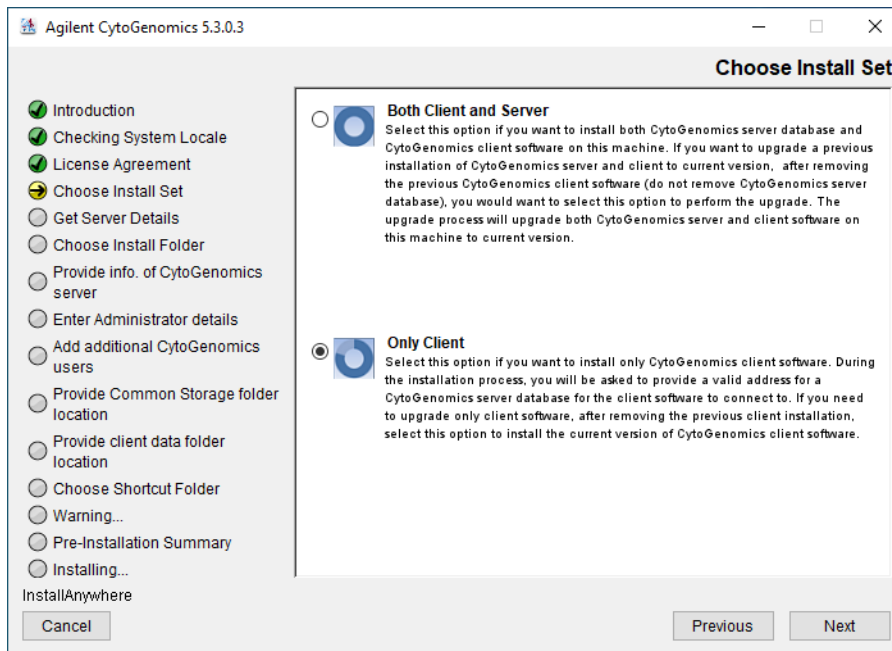


Figure 28 Choose Install Set screen – Windows – select **Only Client**

10 Click **Next**.

An Information message opens notifying you that you selected to install only the client application. Click **OK** to continue.

11 Continue the installation wizard. For information, refer to “**Step 3. Install the client software on additional Windows computers**” on page 28.

Step 3. Start the Agilent CytoGenomics 5.3 client software, log in, and add new software license

1 Start the Agilent CytoGenomics program.

See “**Step 4. Start the Agilent CytoGenomics 5.3 client software**” on page 31.

2 Log in.

See “**Step 5. Log in to Agilent CytoGenomics**” on page 31.

3 Enter your updated license information.

See “**Step 6. Add your software license**” on page 32.

Upgrading from CytoGenomics 3.0 or 4.0 to CytoGenomics 5.3 and Migrating Data – Windows

These instructions are for users of CytoGenomics 3.0 or 4.0 who want to upgrade to CytoGenomics 5.3 and migrate all sample records from the previous database to the new CytoGenomics 5.3 database.

NOTE

CytoGenomics 5.3 is compatible with and can co-exist on the same machine as CytoGenomics 3.0 or 4.0. You will not be prompted to uninstall the previous version of CytoGenomics (i.e., v3.0 or 4.0) during installation of v5.3.

Step 1. Install CytoGenomics 5.3 on the server computer

Follow these steps to install Agilent CytoGenomics 5.3 on the computer where the CytoGenomics server software is installed.

- 1 Download Agilent CytoGenomics 5.3.X.X from Agilent Technologies and check the system requirements.

See **"a. Download the Windows version of the software and release notes"** on page 16 for detailed instructions on this step.

- 2 Double-click the Agilent CytoGenomics 5.3 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. Mark **I accept the terms of the License Agreement** and then click **Next**.

The Choose Install Set screen opens.

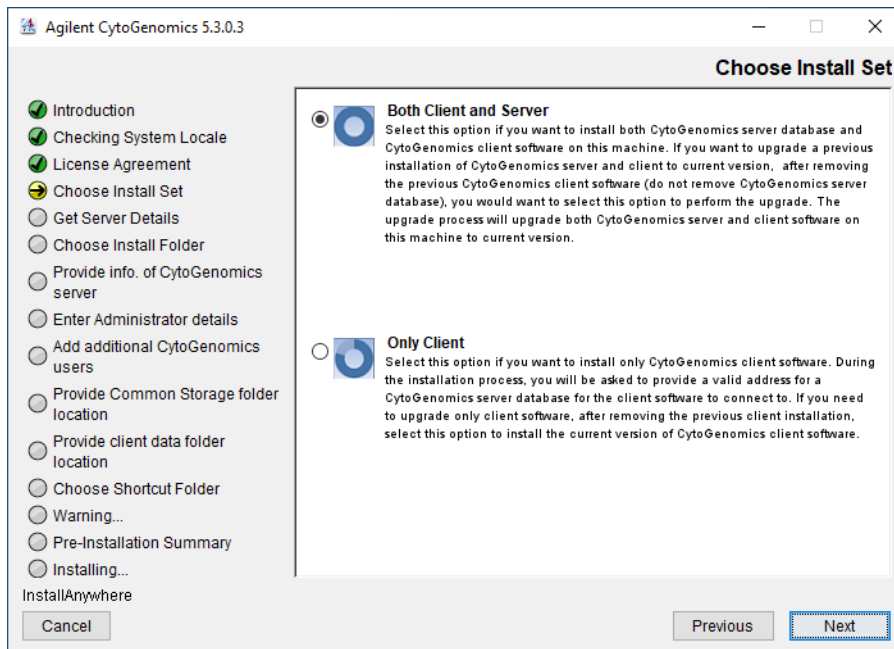


Figure 29 Choose Install Set screen – Windows – select **Both Client and Server**

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

An Information message opens. Click **OK** to continue.

- 6 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 18.

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 5.3. server.

- 7 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 5.3 server. The migration utility tool launches on your PC. Proceed to **“Step 2. Migrate data to CytoGenomics 5.3 server”** on page 43.
 - 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 5.3 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 5.3 on the client computers”** on page 46.

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 5.3 installation.

If you click **Skip** with the intention of migrating your data at a later time, be aware that if CytoGenomics 5.3 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 5.3 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 (v3.0 or 4.0) to CytoGenomics server 5.3. If you do not want to transfer data, bypass this step and proceed to **“Step 3. Upgrade to CytoGenomics 5.3 on the client computers”** on page 46.

- 1 On the Sign In screen of the migration utility application (**Figure 30**), review the list of migration prerequisites and make sure they are all met before you continue.

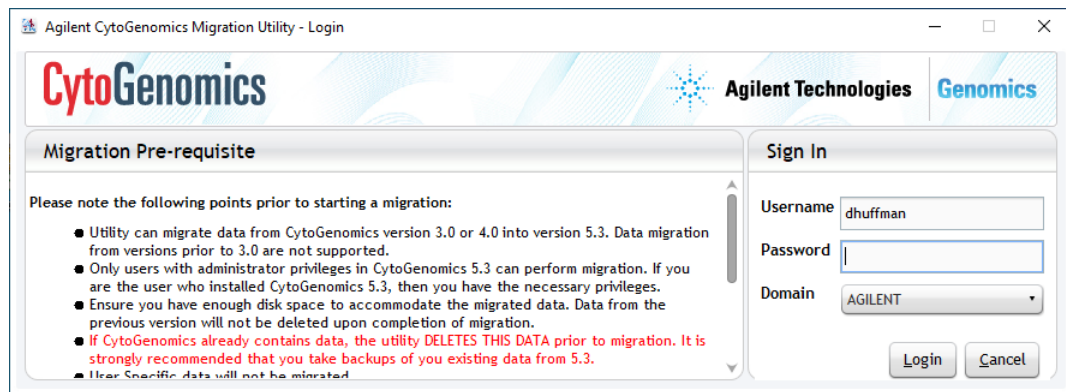


Figure 30 CytoGenomics Migration Utility application login screen

- 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.

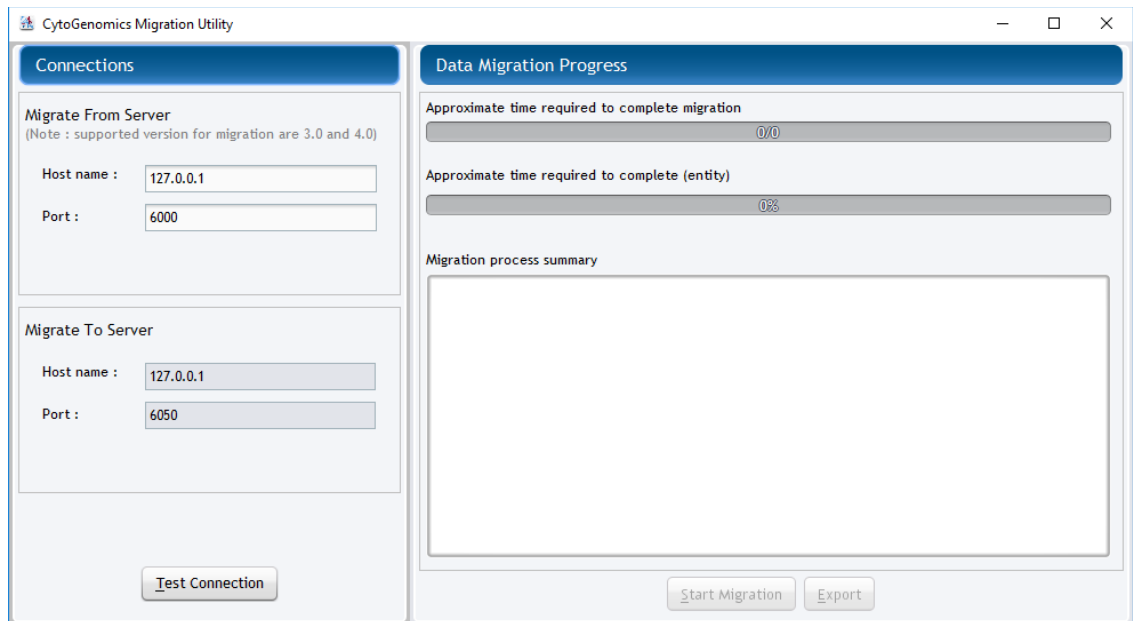


Figure 31 CytoGenomics Migration Utility application

- 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.

NOTE

Under **Migrate To Server**, the fields are automatically populated with the host name and port number where the CytoGenomics 5.3 server is installed. If CytoGenomics 5.3 server is installed on the same PC as the previous version of CytoGenomics server, then the host names are the same.

- 4 Click **Test Connection**.

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

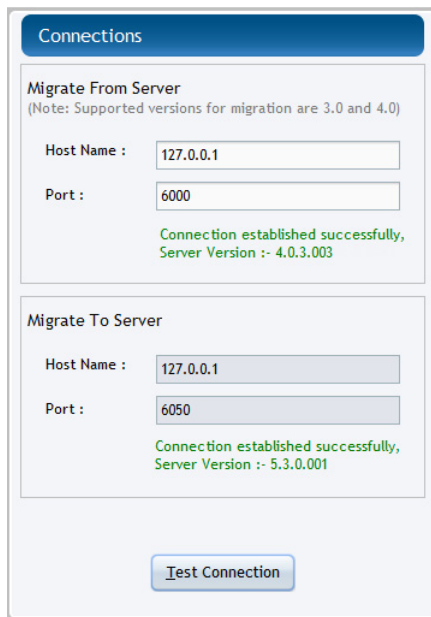


Figure 32 CytoGenomics Migration Utility application – Connections established

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.

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

The Warning message box opens.

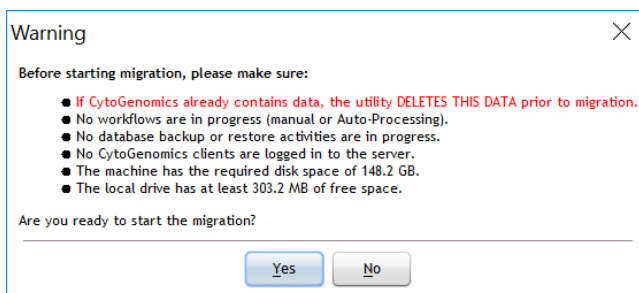


Figure 33 Warning message box

- 6 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 5.3 database already contains data, 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 Progress**) displays the progress of the migration and the migration process summary.

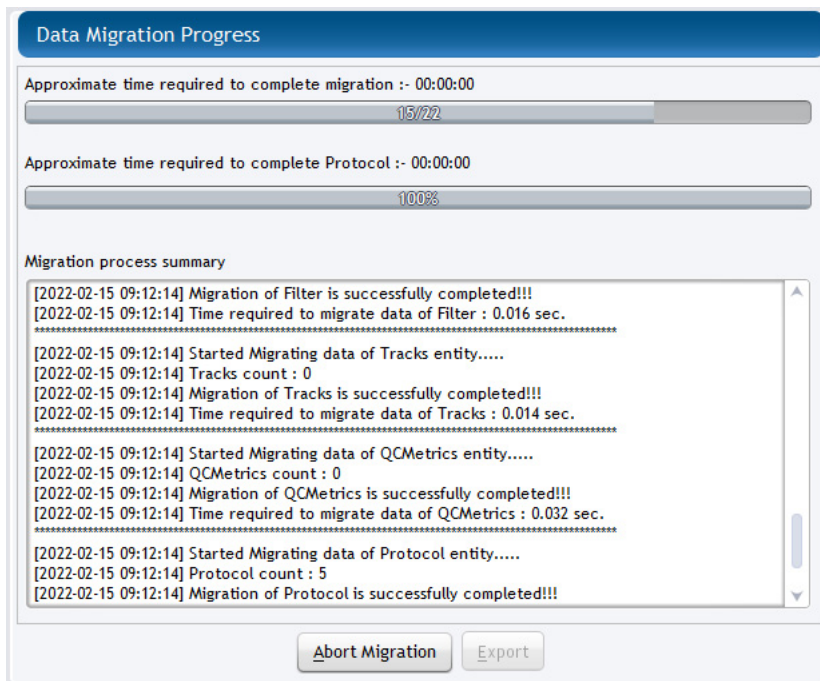


Figure 34 CytoGenomics Migration Utility application – Migration in progress

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

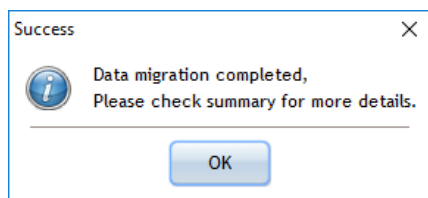


Figure 35 CytoGenomics Migration Utility application – Data migration complete

- 7 Click **OK** to close the message box.
- 8 If desired, click **Export** to export a summary of the migration job.
A summary of the migration job is automatically saved to the CytoGenomics 5.3 installation folder within the **Client\data** subfolder.
- 9 Click the X in the top right corner of the Migration Utility application window to close the application.

Step 3. Upgrade to CytoGenomics 5.3 on the client computers

Follow these steps to install Agilent CytoGenomics 5.3 on each client computer.

- 1 Double-click the Agilent CytoGenomics 5.3.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. Mark **I accept the terms of the License Agreement** and then click **Next**.

The Choose Install Set screen opens.

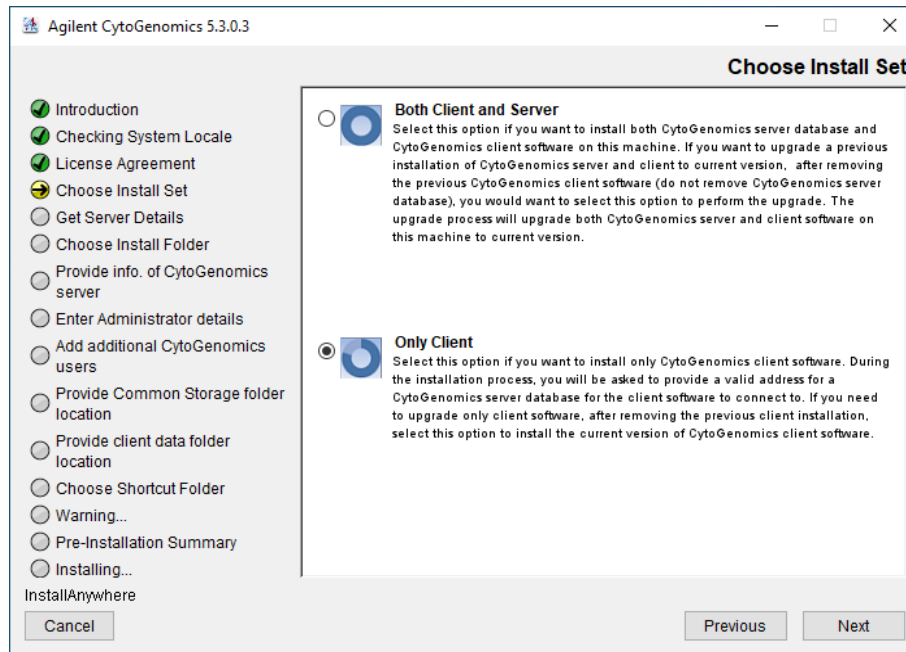


Figure 36 Choose Install Set screen – Windows – select **Only Client**

- 4 On the Choose Install Set screen, select **Only Client**. Click **Next**.
An Information message opens. Click **OK** to continue. The Choose Install Folder screen opens.
- 5 At the Choose Install Folder screen, the default folder for installation of the program is **C:\Agilent\AgilentCytoGenomics5.3.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**.
- 6 Click **Next**.
- 7 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 28.

Step 4. Start the Agilent CytoGenomics 5.3 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 5.3 client software”** on page 31.
- 2 Log in.
See **“Step 5. Log in to Agilent CytoGenomics”** on page 31.
- 3 Enter your updated license information.
See **“Step 6. Add your software license”** on page 32.

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 5.3 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 3.0 or 4.0 in order to install CytoGenomics 5.3.

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.

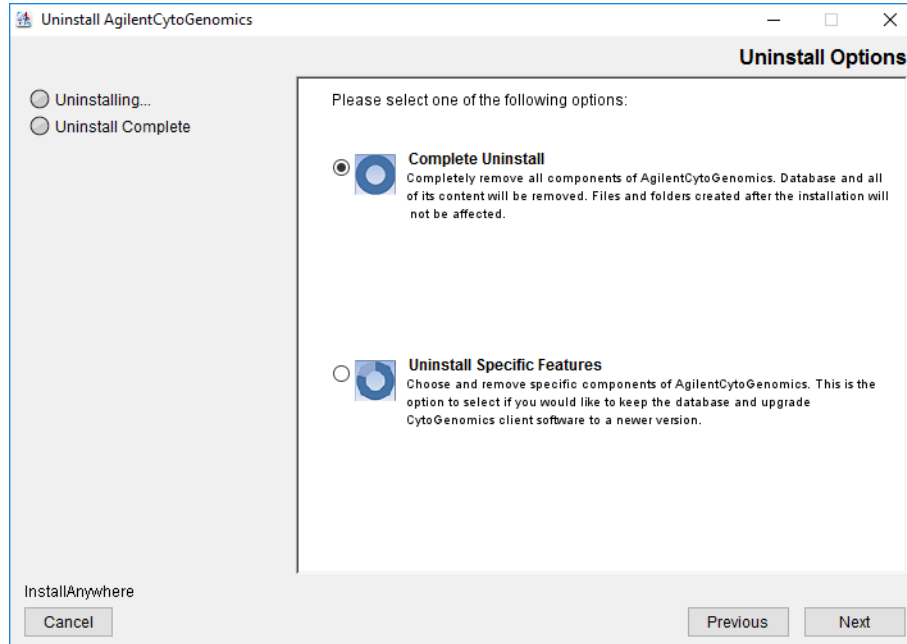


Figure 37 Uninstall Options screen – Windows – select **Complete Uninstall**

- 4 Select **Complete Uninstall**.

Uninstalling Agilent CytoGenomics on Windows computers

Depending on which version of CytoGenomics you are uninstalling, you may see one or both of the following message boxes before the uninstallation continues.

- A warning message advising you to backup the database before proceeding with the uninstall.
 - A message box prompting you to enter your username and password before proceeding.
- 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 AgilentCytoGenomics5.3.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.

If the CytoGenomics database service unable to start

- ✓ This installation error can occur when the user account does not have administrator rights on the PC where CytoGenomics was installed. Contact Agilent **Technical Support** for assistance.

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This chapter shows you how to install Agilent CytoGenomics 5.3 on systems running the macOS Big Sur or Monterey operating system.

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 5.3 – Macintosh

This section includes detailed instructions and important notes for installing Agilent CytoGenomics 5.3 on a Macintosh system that does not have a previous version of CytoGenomics installed. For instructions on how to upgrade an existing Agilent CytoGenomics installation, see **“Uninstalling Agilent CytoGenomics on Macintosh computers”** on page 78.

Agilent CytoGenomics consists of two parts: a PostgreSQL database server and the client software. The client is the program you run when you want to use Agilent CytoGenomics, while the database server software runs silently in the background and manages the shared database for all Agilent CytoGenomics 5.3 users. For Macintosh systems, you can install the two parts of CytoGenomics using one of the following approaches:

- **Option A:** Install both the database server and client software.
This option is suitable for users who want to run analysis workflows on extracted FE files and review the workflow results on a single Macintosh computer, without sharing the database across computers. See instructions in **“Step 2, Option A. Install both the database server”** on page 53.
- **Option B:** Install only the client software and designate another computer as the database host on which the database server software for CytoGenomics 5.3 is installed.
This option is suitable for users who want to access a shared CytoGenomics database. The database host computer must be a Windows PC, not a Macintosh. See instructions in **“Step 2, Option B. Install only the client software”** on page 66.

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_3_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	The following macOS operating systems are supported. Big Sur Monterey
Programs	Any program that enables you to open PDF files (for example, Adobe Reader)
Processor	Apple M1 chip with 8-core CPU and 8-core GPU and 16-core Neural Engine, or better
Unified memory (UMA)	8GB (16 GB recommended)
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 5.3 software has administrator permissions on the installation computer.
- Make sure that every user account running the Agilent CytoGenomics 5.3 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, Option A. Install both the database server

- 1 Log on to the Macintosh system. Use an account that has administrator permissions.
- 2 Locate the compressed folder (Agilent_CytoGenomics_5.3_X_X_MAC.zip) that you downloaded in Step 1, **“a. Download the Macintosh version of the software and release notes”** on page 52. 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 installation wizard opens to the Introduction screen.

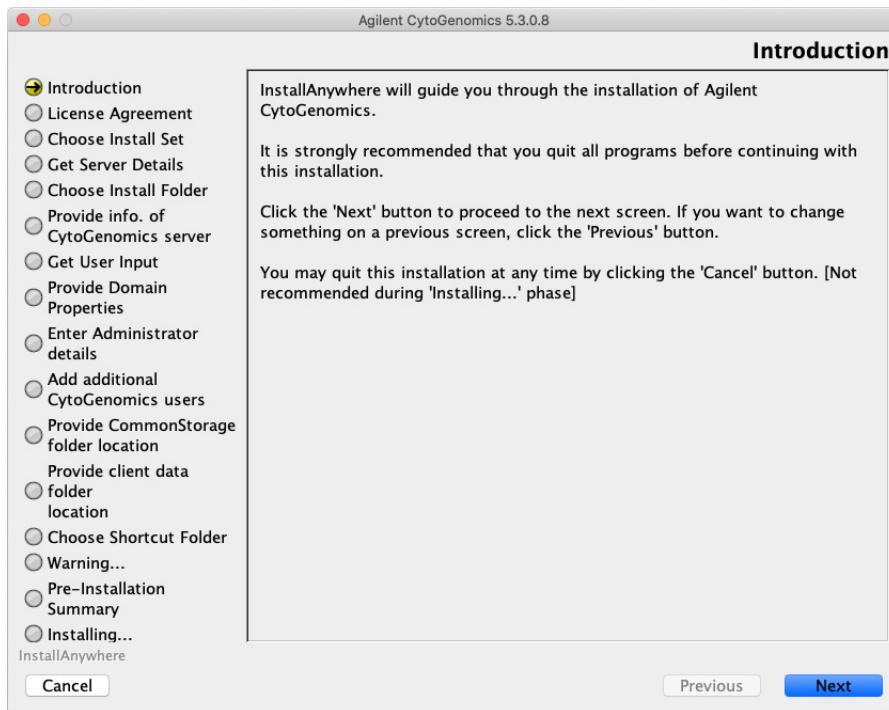


Figure 38 Introduction screen for the installation wizard – Macintosh

- 4 Read the introductory information.
- 5 Click **Next** to display the next section.
The License Agreement screen opens.

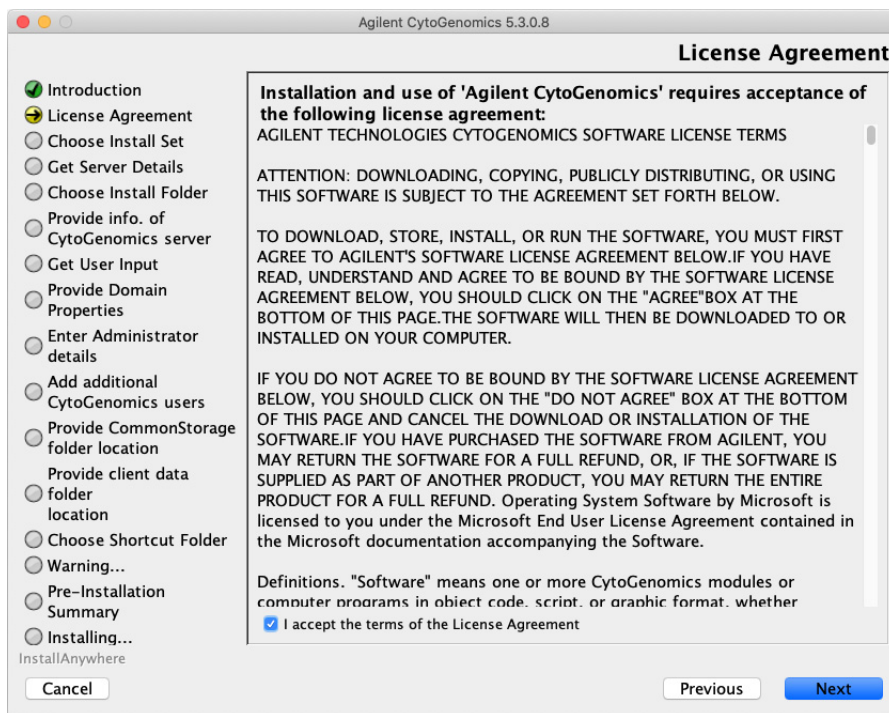


Figure 39 License Agreement screen – Macintosh

- 6 Read the license agreement. Mark **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.

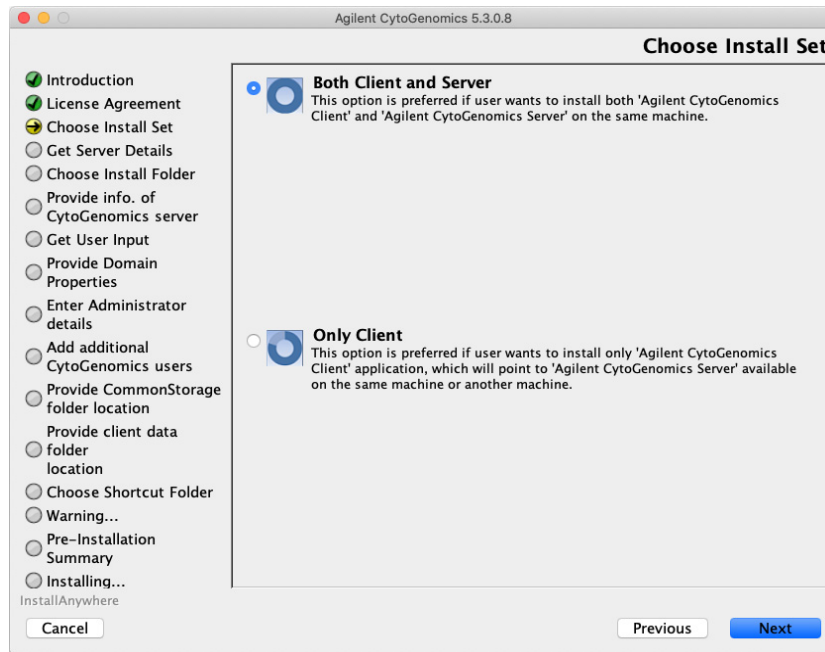


Figure 40 Choose Install Set screen – Macintosh

- 7 Click the icon next to **Both Client and Server** to install both the database server and client software on this computer.
- 8 Click **Next**.
- 9 An Information message opens confirming that you installing both the client and server software.
Click **OK**. The Choose Install Folder screen opens.

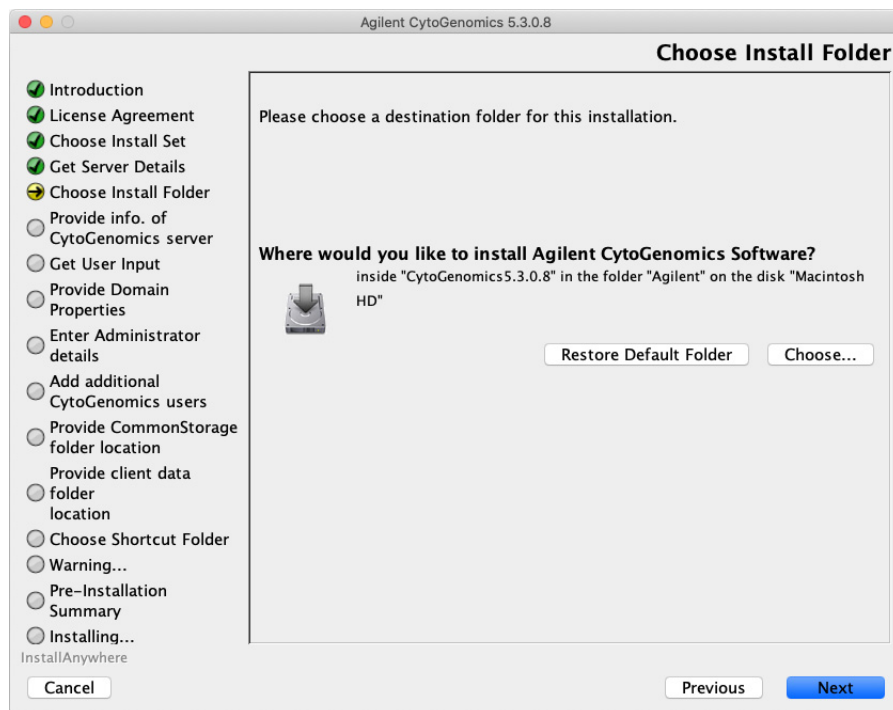


Figure 41 Choose Install Folder screen – Macintosh

10 By default, the program is installed in the AgilentCytoGenomics5.3.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 5.3 folder. Within this folder, one folder is created for the server software and one folder is created for the client software.

The Provide Domain Properties screen opens.

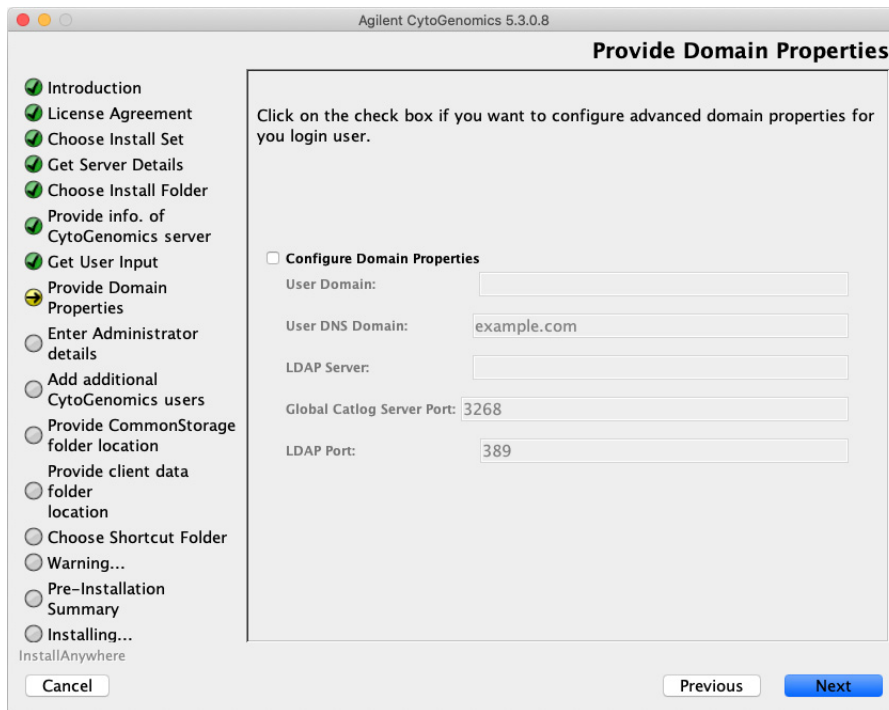


Figure 42 Provide Domain Properties screen – Macintosh

11 If only the administrator will be accessing Agilent CytoGenomics 5.3 from this computer, click **Next**. The Enter Administrator details screen opens, and you can proceed to **step 23**.

If more than one user plans to use Agilent CytoGenomics 5.3 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.

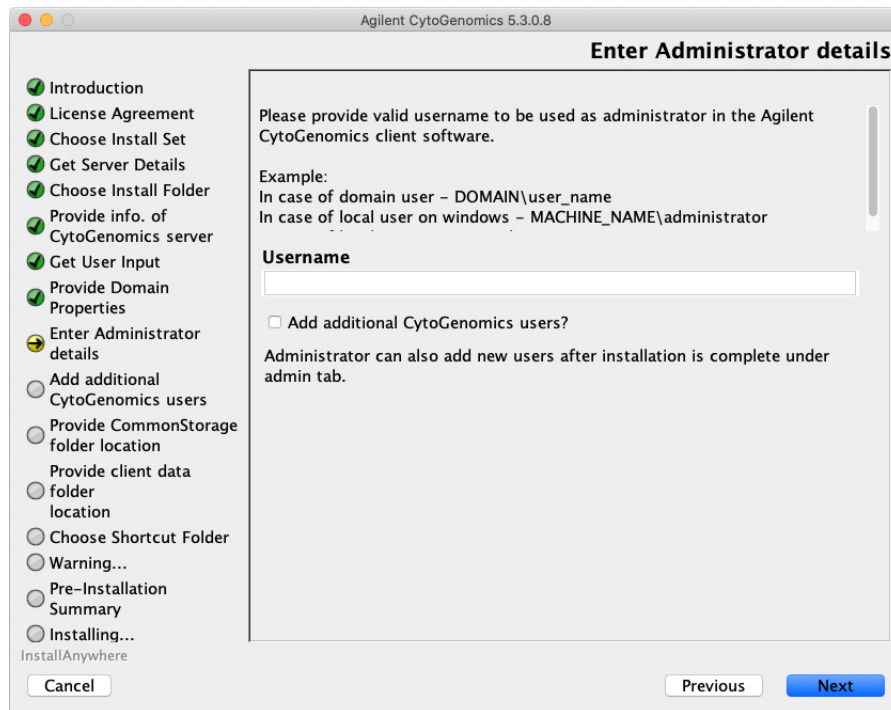


Figure 43 Enter Administrator details screen – Macintosh

12 In the Username field, type the user name of the person who will be the administrator for the Agilent CytoGenomics 5.3 software, using the format example shown.

For domain user: DOMAIN\username

For local machine: \username

13 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 18** on **page 59**.

Note that the administrator can set up new users from within CytoGenomics once installation is complete (see **“To manage users and roles”** on page 82).

14 Click **Next**.

The Add CytoGenomics Users screen opens.

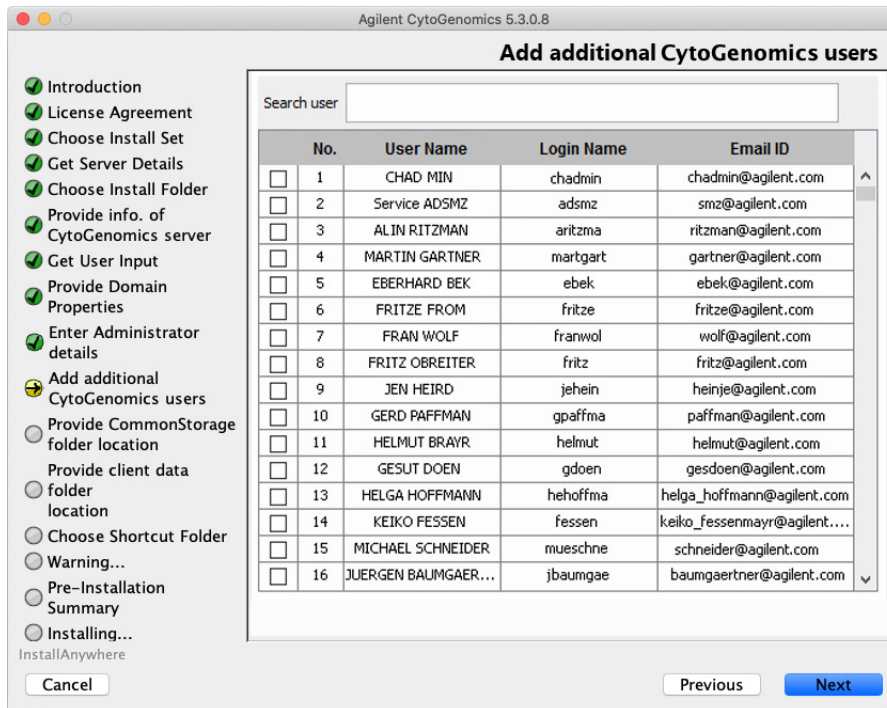


Figure 44 Add CytoGenomics Users screen – Macintosh

15 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.

16 Click **Next**.

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

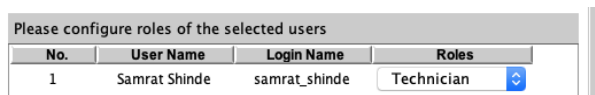


Figure 45 Add CytoGenomics Users screen – Configure roles step – Macintosh

17 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 14 for a description of each role.

18 Click **Next**.

The Choose common storage folder screen opens.

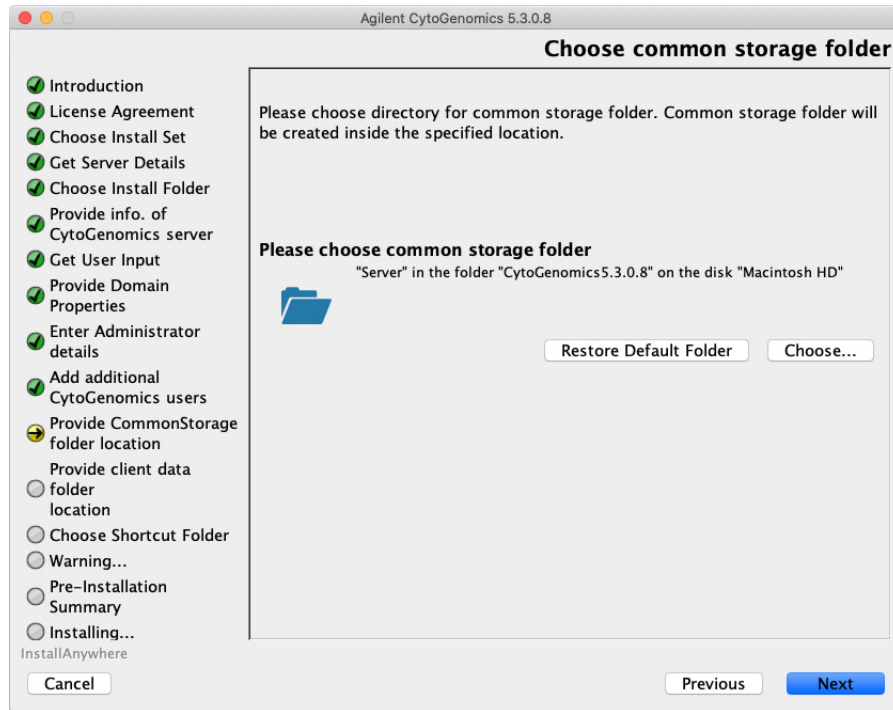


Figure 46 Choose common storage folder screen – Macintosh

19 By default, the common storage folder is created inside the Server folder in the AgilentCytoGenomics5.3.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.

20 Click **Next**.

The Choose client data folder screen opens.

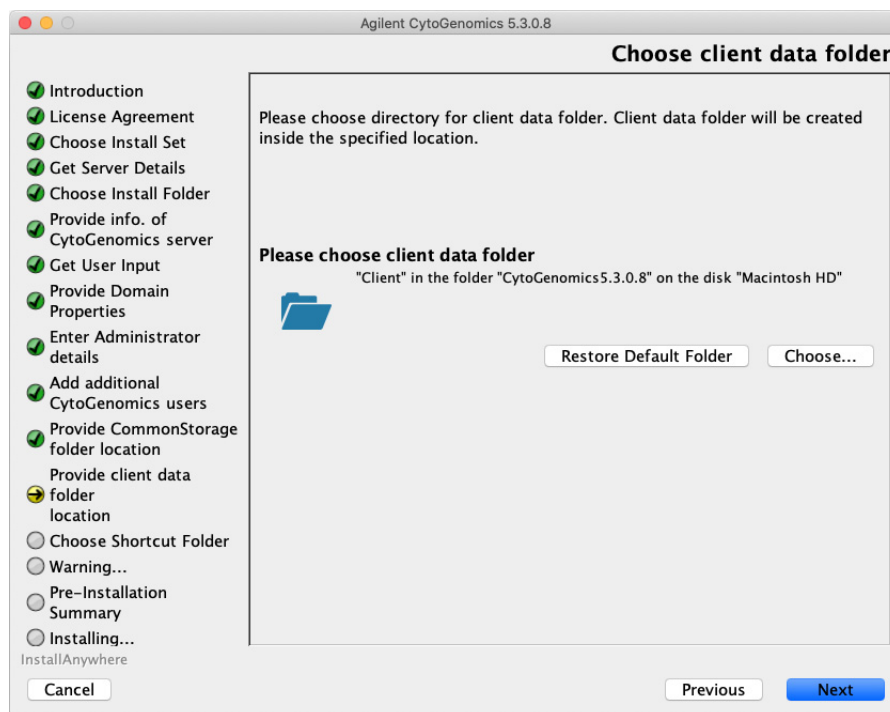


Figure 47 Choose client data folder screen – Macintosh

21 By default, the client data folder is created inside the Client folder in the AgilentCytoGenomics5.3.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.

22 Click **Next**.

The Choose Alias Folder screen opens.

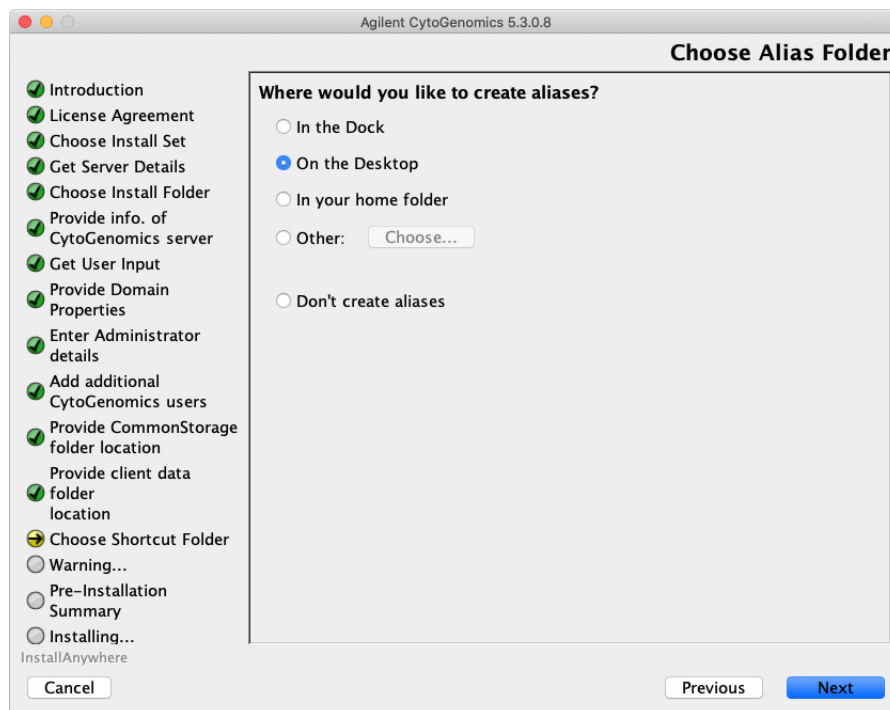


Figure 48 Choose Alias Folder screen – Macintosh

23 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.

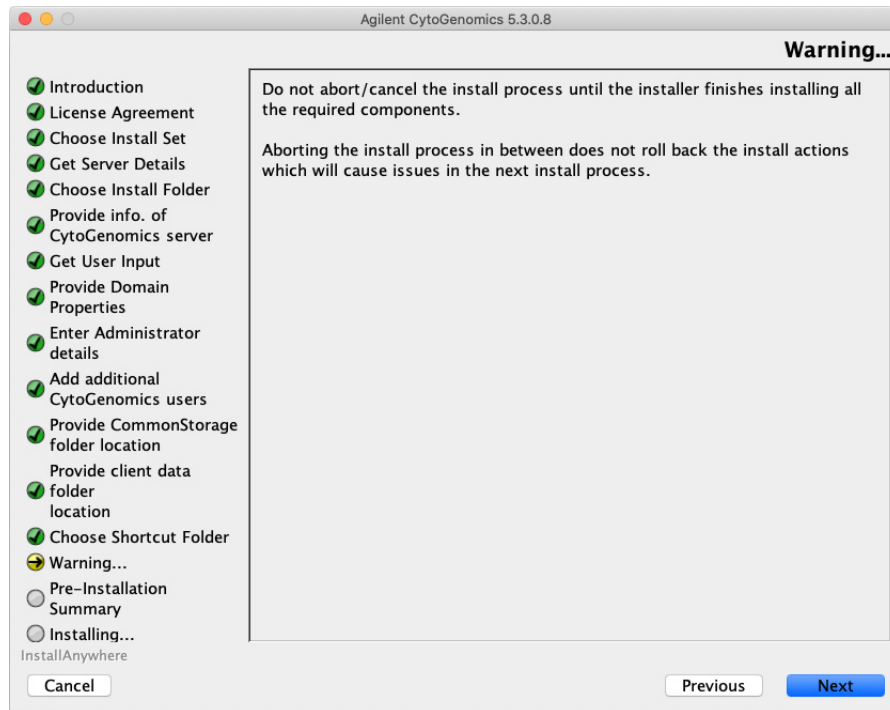


Figure 49 Warning screen – Macintosh

24 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.



Figure 50 Pre-Installation Summary screen – Macintosh

25 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 5.3.X.X screen opens and is displayed until the installation is complete.

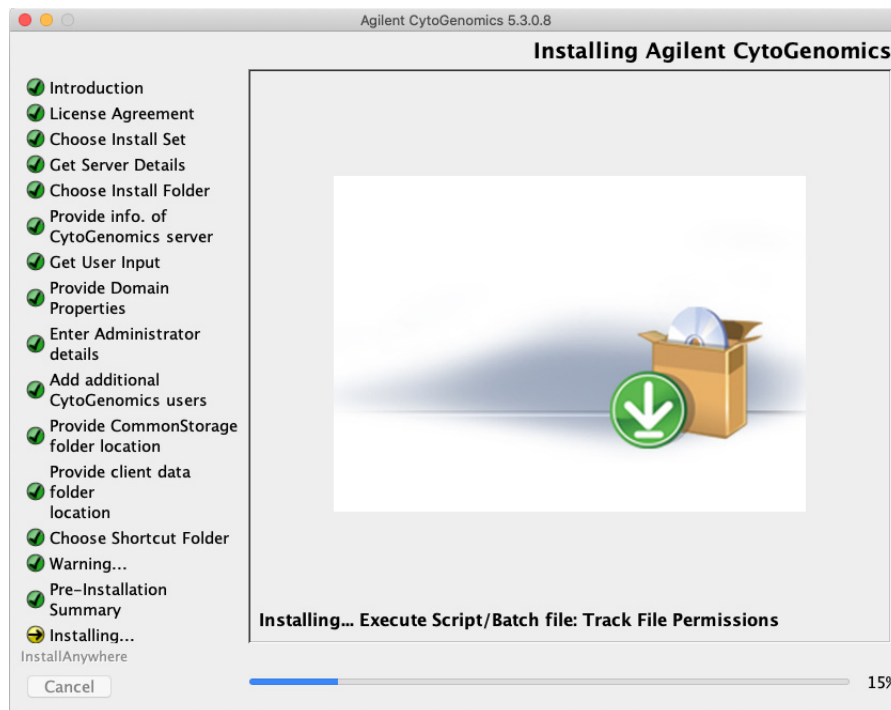


Figure 51 Installing Agilent CytoGenomics 5.3.X.X screen – Macintosh

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

26 Click **Done**.

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.

After the installation process, the PSQL Service installs a new helper tool. When prompted with the message box shown below, enter your username and password and click **Install Helper**.

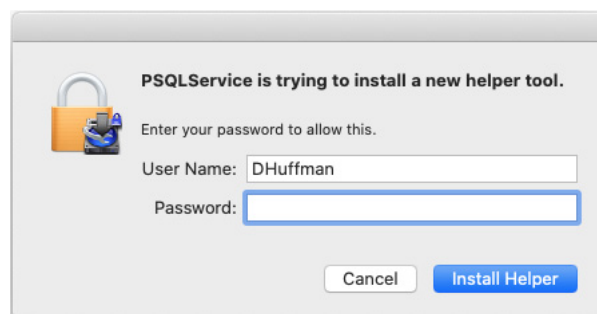


Figure 52 PSQL Service prompt

NOTE

After clicking **Install Helper**, you may see a message stating that the iCloud Drive may not work properly. Click **OK** to close the message and continue the installation.

The Installing PSQLService window opens displaying the progress of the helper tool install. The windows closes when installation is complete.

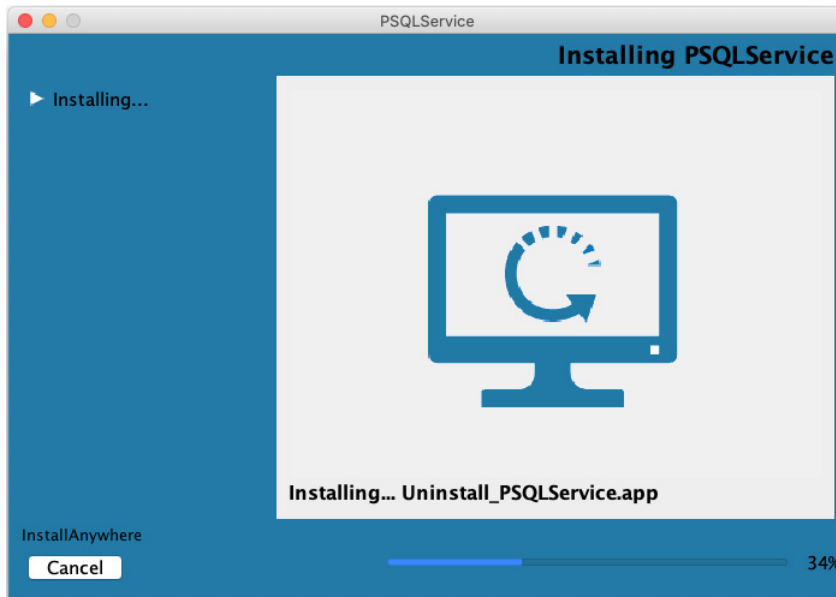


Figure 53 Installing PSQLService window

During or after the PSQLService 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 5.3 server.

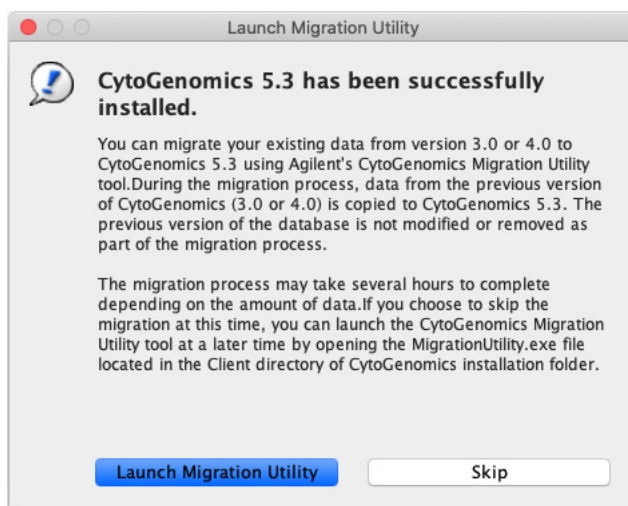


Figure 54 Launch Migration Utility dialog box – Macintosh

- 27 Click **Skip** to close the Launch Migration Utility dialog box without launching the migration utility tools.

Because only the client software was upgraded, there is no need to use the migration utility tool to transfer data.

Step 2, Option B. Install only the client software

When installing the client software, the client connects to a Windows PC that serves as the host for the CytoGenomics 5.3 database server.

- 1 On the Macintosh, set up access to the common storage folder (CommonStorage_5.3.X.X) located on the Windows PC database host. The default location for the commage storage folder is **C:\agilent\CytoGenomics5.3.0.10\Server\CommonStorage_5.3.X.X** (where X.X is the revision number).
 - a Mount a Windows shared folder to connect to the CommonStorage folder on the Windows PC that hosts the CytoGenomics database server.
 - b In the **System Preferences > Security & Privacy** settings, add the CommonStorage folder to the **Full Disk Access** section.
- 2 Run the installation wizard on the Macintosh, as described in **“Step 2, Option A. Install both the database server”** on page 53.
- 3 When the Choose Install Set screen opens, select **Only Client**.

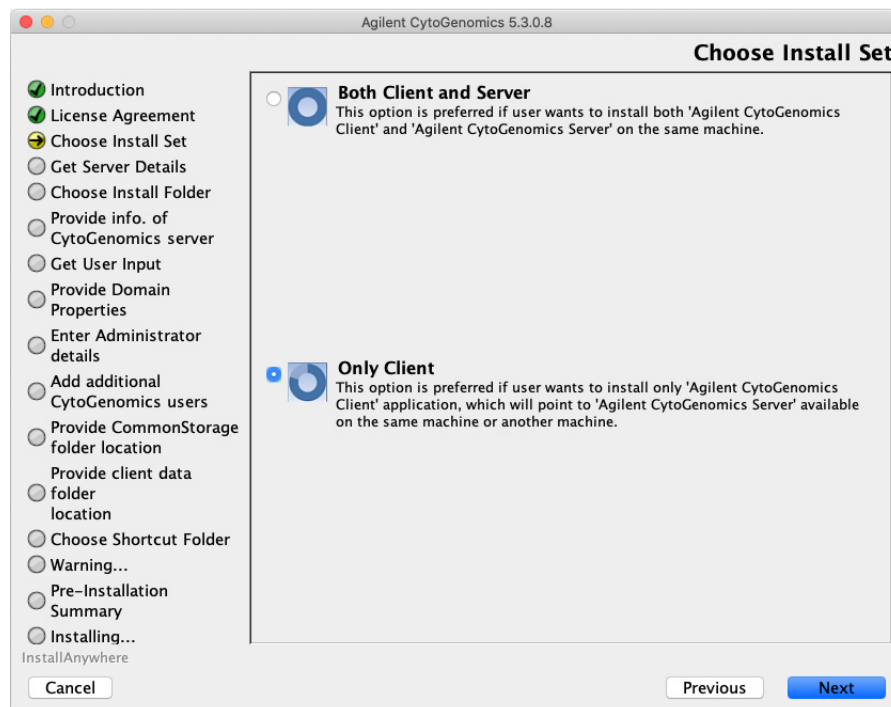


Figure 55 Choose Install Set screen – Macintosh

- 4 Click **Next**.

The Choose Installation Folder opens.

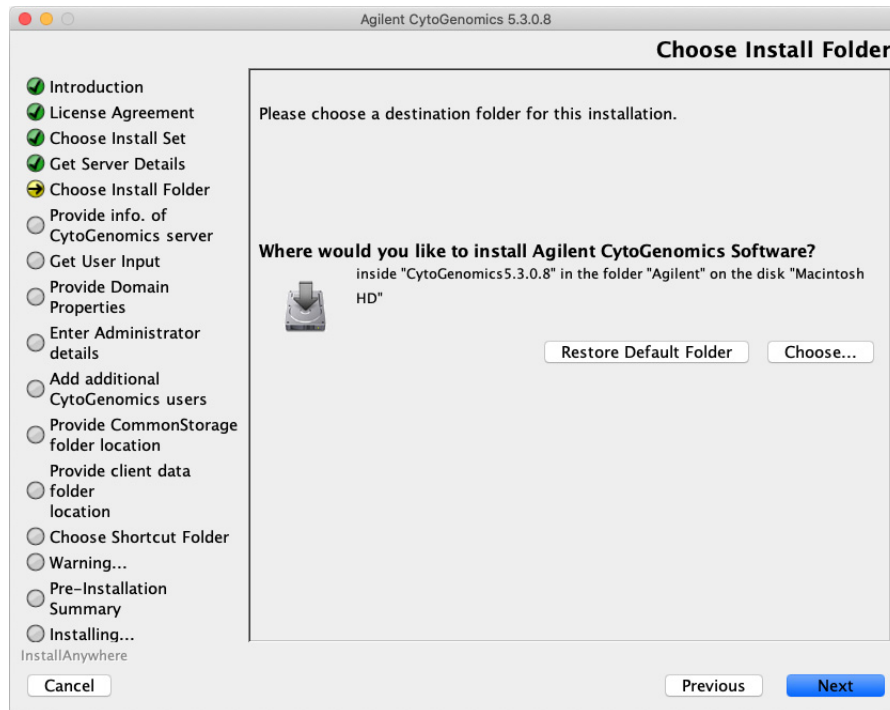


Figure 56 Choose Install Folder screen – Macintosh

- 5 By default, the program is installed in the AgilentCytoGenomics5.3.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 5.3.

OR

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

- 6 Click **Next**.

The Provide Information of CytoGenomics server screen opens.

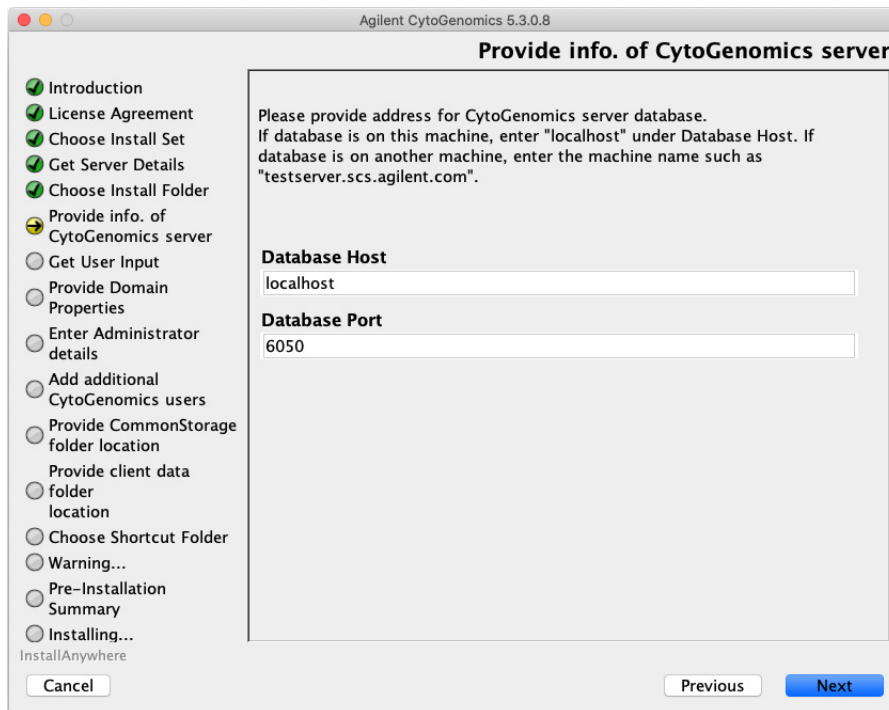


Figure 57 Provide information of CytoGenomics server screen – Macintosh

- 7 Under **Database Host**, type the assigned computer name or IP address of the Windows PC where the Agilent CytoGenomics 5.3 database server is installed.
- 8 Accept the default Database Port, unless your system administrator tells you otherwise.
- 9 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 12](#) through [step 27](#) in the section **“Step 2, Option A. Install both the database server”** on page 53.

Step 3. Start the Agilent CytoGenomics 5.3 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 5.3 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 4. 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.



Figure 58 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 **Login**.

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 5. Add your software license

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

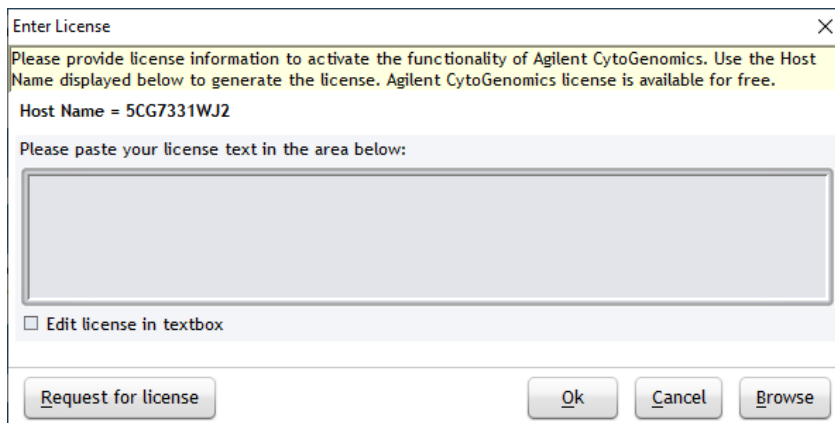


Figure 59 Enter License dialog box

- 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.

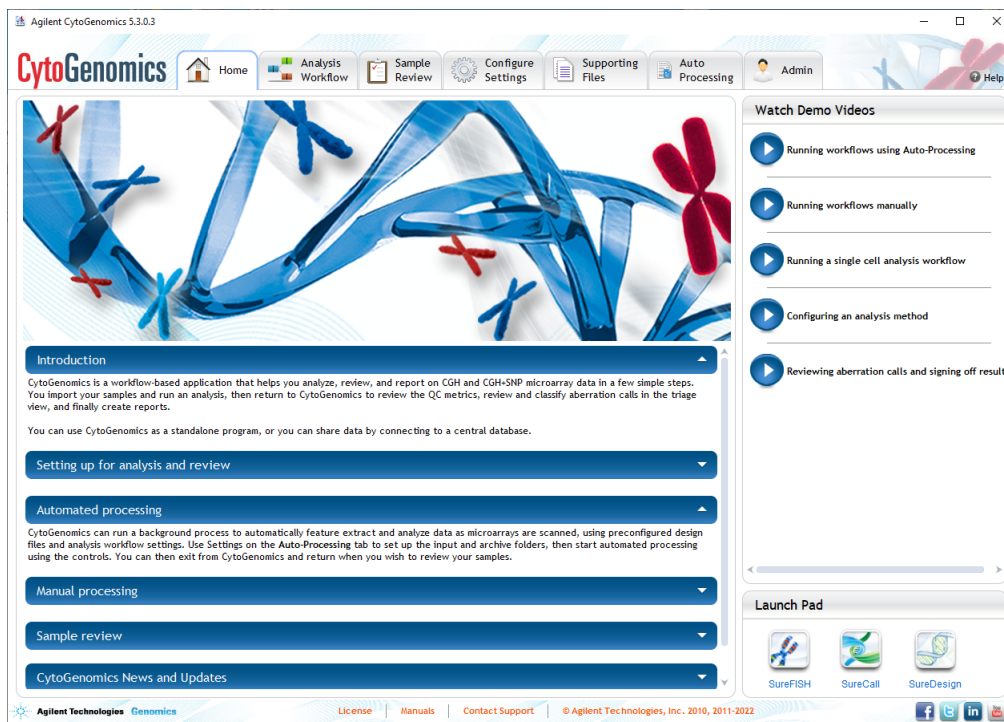


Figure 60 Agilent CytoGenomics program Home screen

Step 6. 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 14. For information on how to add users and assign roles, see **“To manage users and roles”** on page 82.

Upgrading from CytoGenomics 5.2 to CytoGenomics 5.3 – Macintosh (macOS Big Sur)

CAUTION

The upgrade from CytoGenomics 5.2 to CytoGenomics 5.3 will only work if CytoGenomics 5.2 was installed as a new installation (i.e., not an upgrade from version 5.1 or earlier) on a Macintosh running macOS Big Sur.

If CytoGenomics 5.2 was not a new installation, or if CytoGenomics 5.2 is installed on a Macintosh that uses a different operating system, contact **Technical Support** for further guidance.

If you are currently using CytoGenomics 5.2 and you want to upgrade to CytoGenomics 5.3, you need to uninstall the existing CytoGenomics client application, then either install the CytoGenomics 5.3 client and server or install the CytoGenomics 5.3 client only. You do not need to migrate data from the previous version to the new version.

For Macintosh users running CytoGenomics 5.1 or earlier If you are currently using a version of CytoGenomics prior to 5.2 (i.e., v5.1 or earlier), contact **Technical Support** for guidance on upgrading to CytoGenomics 5.3.

Upgrade CytoGenomics on a Macintosh with CytoGenomics 5.2 client and server

Step 1. Uninstall CytoGenomics 5.2 client software

- 1 Log on to the Macintosh system where both the CytoGenomics 5.2 client software and database server are installed. Use an account that has administrator permissions.
- 2 Double-click the Uninstaller file, located in the **\Uninstall_Agilent CytoGenomics** folder of your program folder.

The following window opens.

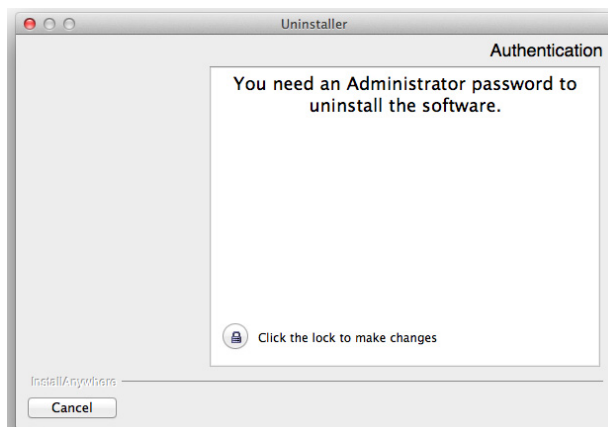


Figure 61 Authentication dialog box - preparing to uninstall

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

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.

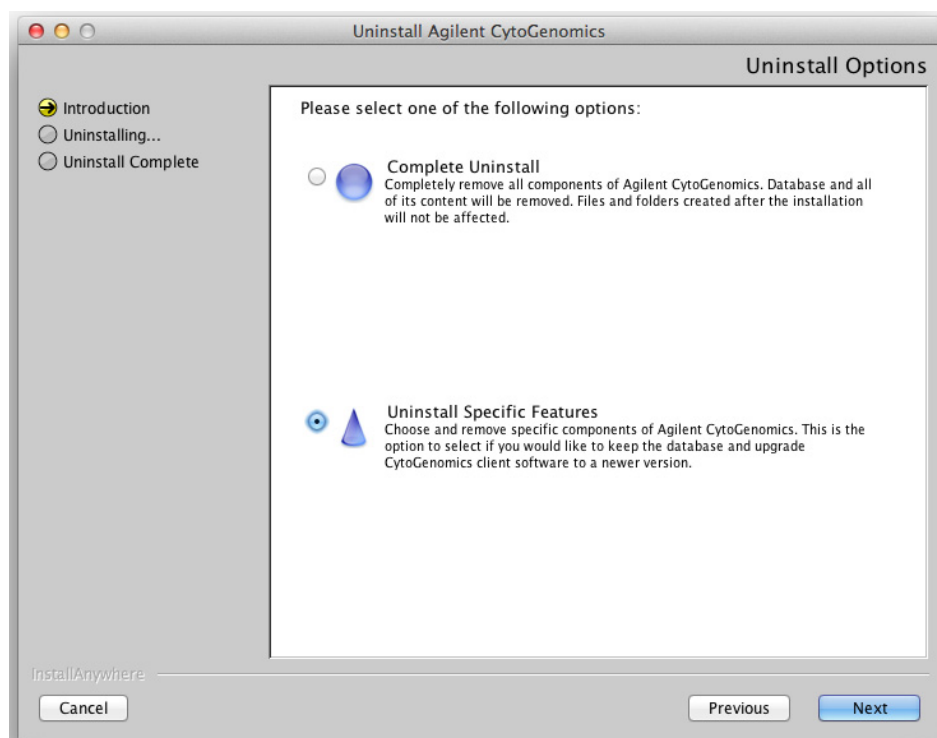


Figure 62 Uninstall Options screen – Macintosh – select Uninstall Specific Features

- 6 Select **Uninstall Specific Features**.

The Choose Product Features screen opens.

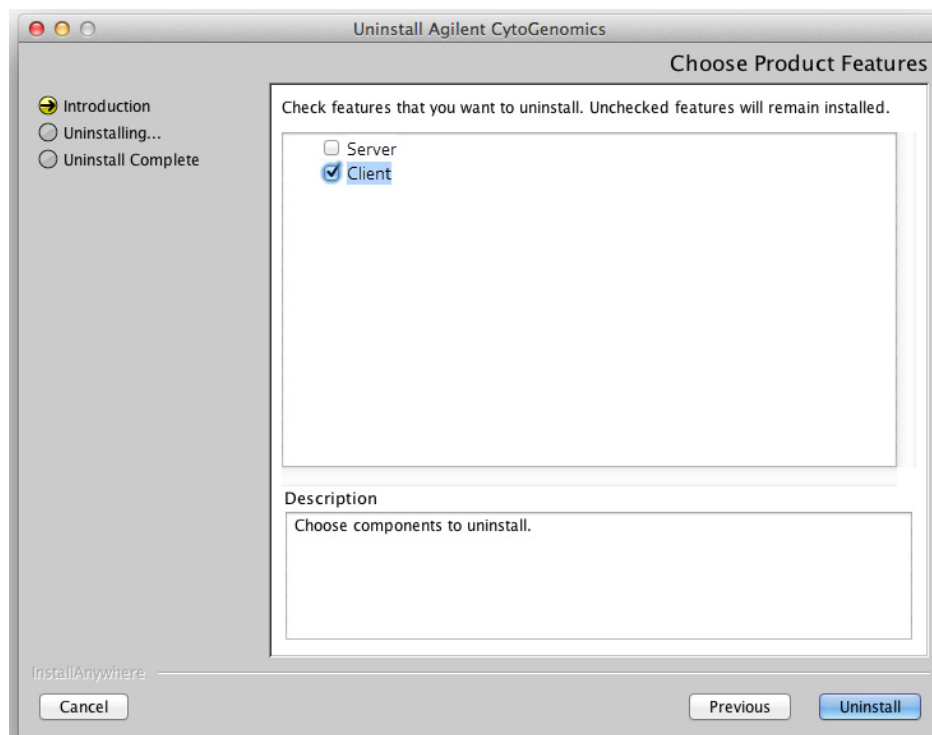


Figure 63 Choose Product Features screen – Macintosh – select Client

7 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.

8 In the confirmation message box that opens, click **Yes** to continue uninstalling the existing version of CytoGenomics client.

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

The uninstaller closes.

Step 2. Install CytoGenomics 5.3 client and server

1 Download Agilent CytoGenomics 5.3 from Agilent Technologies and check the system requirements.

See "**a. Download the Macintosh version of the software and release notes**" on page 52 for detailed instructions on this step.

2 Locate the compressed folder (Agilent_CytoGenomics_5_3_X_X_MAC.zip) that you downloaded in **step 1**. Double-click the folder to expand the contents of the folder and save the installer on your computer.

3 Continue the installation wizard, as described in "**Step 2, Option A. Install both the database server**" on page 53.

4 When the Choose Install Set screen opens, select **Both Client and Server**.

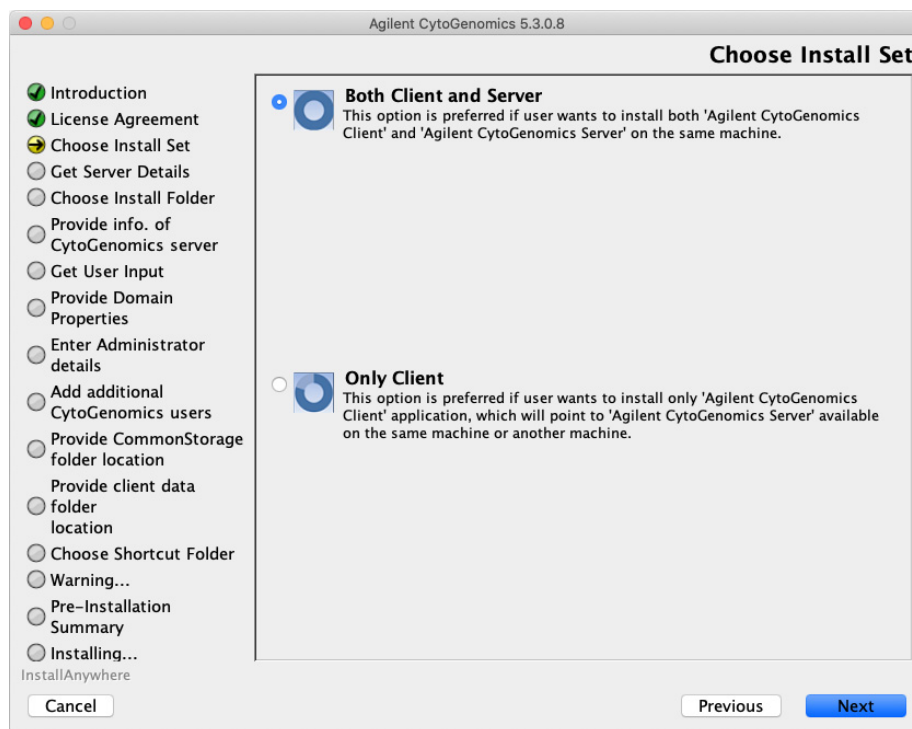


Figure 64 Choose Install Set screen – Macintosh – select **Both Client and Server**

5 Click **Next**.

An Information message opens notifying you that you selected to install both the server and client applications. Click **OK** to continue.

A second Information message opens notifying you that the CytoGenomics server application already exists on the local machine. Click **OK** to continue.

The Provide Domain Properties screen opens.

6 Continue the installation wizard. For information, refer to **“Step 2, Option A. Install both the database server”** on page 53.

7 Start the Agilent CytoGenomics program.

See **“Step 3. Start the Agilent CytoGenomics 5.3 client software”** on page 68.

8 Log in.

See **“Step 4. Log in to Agilent CytoGenomics”** on page 69.

9 Enter your updated license information.

10 See **“Step 5. Add your software license”** on page 69.

Upgrade CytoGenomics on a Macintosh with CytoGenomics 5.2 client only

Step 1. Uninstall CytoGenomics 5.2 client software

- 1 Log on to the Macintosh system where CytoGenomics 5.2 client software is installed.
- 2 Double-click the Uninstaller file, located in the **\Uninstall_Agilent CytoGenomics** folder of your program folder.

The uninstaller starts.

- 3 Read the introductory information, and then click **Next**.
- 4 In the confirmation message box that opens, click **Yes** to continue uninstalling the existing version of CytoGenomics client.
- 5 When the uninstallation is complete, a message opens. Click **Done**.

The uninstaller closes.

Step 2. Install CytoGenomics 5.3 client software

- 1 On the client computer, download Agilent CytoGenomics 5.3 from Agilent Technologies and check the system requirements.

See **“a. Download the Macintosh version of the software and release notes”** on page 52 for detailed instructions on this step.
- 2 Locate the compressed folder (Agilent_CytoGenomics_5_3_X_X_MAC.zip) that you downloaded in **step 1**. Double-click the folder to expand the contents of the folder and save the installer on your computer.
- 3 Continue the installation wizard, as described in **“Step 2, Option A. Install both the database server”** on page 53 until the Choose Install Set screen opens.
- 4 When the Choose Install Set screen opens, select **Only Client**.

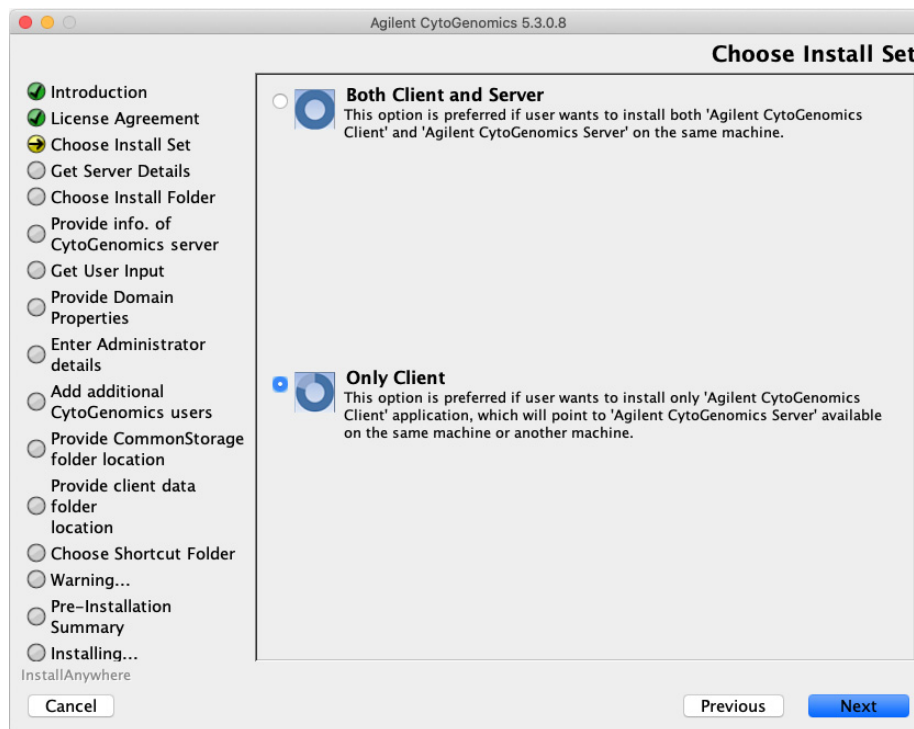


Figure 65 Choose Install Set screen – Macintosh – select **Only Client**

5 Click **Next**.

An Information message opens notifying you that you selected to install only the client application. Click **OK** to continue.

The Choose Installation Folder opens.

6 Continue the installation wizard. For information, refer to **“Step 2, Option B. Install only the client software”** on page 66.

7 Start the Agilent CytoGenomics program.

See **“Step 3. Start the Agilent CytoGenomics 5.3 client software”** on page 68.

8 Log in.

See **“Step 4. Log in to Agilent CytoGenomics”** on page 69.

9 Enter your updated license information.

10 See **“Step 5. Add your software license”** on page 69.

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

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** folder of your program folder.

Depending on which version of CytoGenomics you are uninstalling, you may be prompted to enter your login credentials. If so, follow the prompts on the screen to enter your username and password.

The uninstaller 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.

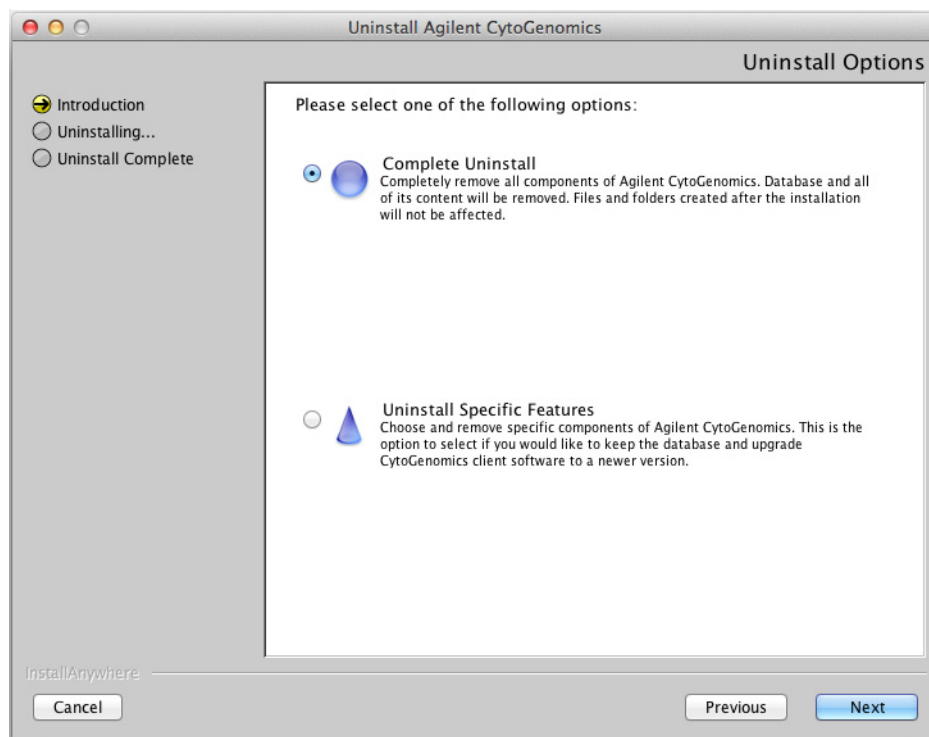


Figure 66 Uninstall Options screen – Macintosh – select Complete Uninstall

- 4 Select **Complete Uninstall**.
- 5 Click **Next**.

Uninstalling Agilent CytoGenomics on Macintosh computers

A warning message opens asking you to confirm that you want to completely remove Agilent CytoGenomics and its database.

- 6** Click **Yes** in the warning message to proceed with the uninstallation.
- 7** When the uninstallation is complete, a message opens. 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

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

See Chapter 1, “Product Overview” for an overview of the program and organization of the tasks within it.

Administering the System

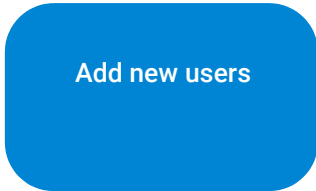
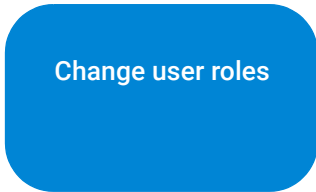
As an Administrator for Agilent CytoGenomics, you have access to everything. That is, you can perform any task available in the program. Your primary responsibility is to add users and their roles to the system, and you also manage the database.

See “**User Roles and Capabilities**” on page 14 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.

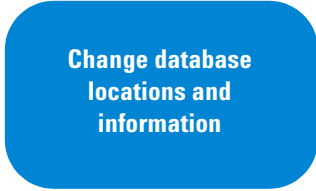
Table 4 Tasks for managing users and roles

To do this task	Follow these instructions	Comments
	<ol style="list-style-type: none"> 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 <i>Enabled</i>. 	<ul style="list-style-type: none"> • A user cannot be deleted but can be disabled. aClick Edit for the user you intend to disable. bClear the Enabled check box, and click Save. • For local machines with no Domain, aNext to User, type the computer name and user in the format <code>machinename\username</code>, or <code>\username</code> for Macintosh systems. (Do NOT click Find.) bClick 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.
	<ol style="list-style-type: none"> 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. 	<ul style="list-style-type: none"> • See “User Roles and Capabilities” on page 14 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
 <p>Change database locations and information</p>	<ol style="list-style-type: none"> 1 Click Admin. 2 Click Database Settings. 3 Under Database Settings, click Change. 4 Type: <ul style="list-style-type: none"> • Common Storage Location • Database Host • Database Port Click Apply to save your changes. 	<ul style="list-style-type: none"> • 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)

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

In this book

This book provides an overview of Agilent CytoGenomics 5.3 and gives you instructions for installing and administering the software.

