Agilent CytoGenomics 5.2

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 5.2 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 5.2 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 5.2 on computers running the macOS Catalina 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.
Figure 1  Agilent CytoGenomics Workflow — from image to result
Getting Help

To get help within Agilent CytoGenomics 5.2

Agilent CytoGenomics 5.2 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.

<table>
<thead>
<tr>
<th>Resource</th>
<th>To find technical support contact information</th>
</tr>
</thead>
</table>
| 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) | 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 5.2. 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
- Entering login credentials for 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 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 5.2.

**Table 1  User roles and capabilities**

<table>
<thead>
<tr>
<th>Role</th>
<th>Tasks and capabilities</th>
</tr>
</thead>
<tbody>
<tr>
<td>Technician</td>
<td>• Run manual or auto-processing workflows</td>
</tr>
<tr>
<td></td>
<td>• Add sample information</td>
</tr>
<tr>
<td></td>
<td>• Monitor workflow jobs</td>
</tr>
<tr>
<td></td>
<td>• Display reports and aberration results</td>
</tr>
<tr>
<td></td>
<td>• View sample results in Triage View</td>
</tr>
<tr>
<td></td>
<td>• Display auto-processing logs</td>
</tr>
<tr>
<td></td>
<td>(Technicians cannot sign off samples.)</td>
</tr>
<tr>
<td>Scientist</td>
<td>Technician tasks, plus:</td>
</tr>
<tr>
<td></td>
<td>• Configure system preferences, including</td>
</tr>
<tr>
<td></td>
<td>• Default input/output folders</td>
</tr>
<tr>
<td></td>
<td>• Auto-processing workflow settings</td>
</tr>
<tr>
<td></td>
<td>• Default view preferences</td>
</tr>
<tr>
<td></td>
<td>• Default genome build</td>
</tr>
<tr>
<td></td>
<td>• Standard notes, classifications, and queries</td>
</tr>
<tr>
<td></td>
<td>• Dynamic and static tracks</td>
</tr>
<tr>
<td></td>
<td>• Cartagenia BENCH data transfer settings</td>
</tr>
<tr>
<td></td>
<td>• Set analysis and workflow settings</td>
</tr>
<tr>
<td></td>
<td>• Create standard notes, classifications, and queries</td>
</tr>
<tr>
<td></td>
<td>• Create customized Cyto report templates</td>
</tr>
<tr>
<td></td>
<td>• Manage samples</td>
</tr>
<tr>
<td></td>
<td>• Evaluate and chart QC trends</td>
</tr>
<tr>
<td></td>
<td>• Sign off and unlock results</td>
</tr>
<tr>
<td>Administrator</td>
<td>Complete system access, including all Technician and Scientist tasks, plus</td>
</tr>
<tr>
<td></td>
<td>• Add users and create user roles</td>
</tr>
<tr>
<td></td>
<td>• Change database connection settings for client systems</td>
</tr>
<tr>
<td></td>
<td>• Backup and restore database</td>
</tr>
<tr>
<td></td>
<td>• Set up connections to partner software programs</td>
</tr>
</tbody>
</table>
2

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This chapter shows you how to install Agilent CytoGenomics 5.2 and migrate data from a previous version of CytoGenomics on computers running a compatible Microsoft Windows operating system.
Installing Agilent CytoGenomics 5.2 – Windows

This section includes detailed instructions and important notes for installing Agilent CytoGenomics 5.2 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 5.2 and Migrating Data – Windows” on page 42.

Step 1. Prepare for installation

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


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.

If an operating system is not listed in Table 2, it is not supported.
2  Installation Instructions for Windows
Installing Agilent CytoGenomics 5.2 – Windows

Table 2  Requirements for Agilent CytoGenomics computers – Windows

<table>
<thead>
<tr>
<th>Requirement</th>
<th>Specification</th>
</tr>
</thead>
<tbody>
<tr>
<td>Operating system</td>
<td>64-bit Windows 10 Enterprise or Professional, or Windows Server 2019</td>
</tr>
<tr>
<td></td>
<td><strong>Note</strong>: For all of these operating systems, the regional format must be set to <strong>English (United States)</strong>. You can find the regional format setting in <strong>Windows Settings &gt; Time &amp; Language &gt; Region</strong>.</td>
</tr>
<tr>
<td>Programs</td>
<td>Any program that enables you to open PDF files (for example, Adobe Reader)</td>
</tr>
<tr>
<td>Processor</td>
<td>Minimum: &gt; 2 GHz</td>
</tr>
<tr>
<td></td>
<td>Recommended: &gt; 3 GHz</td>
</tr>
<tr>
<td>Working memory (RAM)</td>
<td>Minimum: 4 GB</td>
</tr>
<tr>
<td></td>
<td>Recommended: 8 GB</td>
</tr>
<tr>
<td>Hard disk space</td>
<td>500 GB</td>
</tr>
<tr>
<td>Display Resolution</td>
<td>1280 x 768 or higher</td>
</tr>
</tbody>
</table>

c. **Set up permissions for Installer and users**

- Make sure that the user account used to install the Agilent CytoGenomics 5.2 software has administrator permissions on the installation computer.
- Make sure that every user account running the Agilent CytoGenomics 5.2 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**

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 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 5.2 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 5.2 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 19. Double-click the Agilent CytoGenomics 5.2.X.X application file to start the installation wizard.

The following message is displayed.
2 Installation Instructions for Windows
Installing Agilent CytoGenomics 5.2 – Windows

![Image of InstallAnywhere dialog box - preparing to install]

**Figure 2**  InstallAnywhere dialog box - preparing to install

The installation wizard opens to the Introduction screen.

![Image of 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. 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.
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.
8 By default, the program is installed in: C:\Agilent\AgilentCytoGenomics5.2.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 5.2. 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.

9 Click Next.

The Enter Administrator details screen opens.
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 5.2 software, type the correct user, using the format example shown.

For domain user: DOMAIN\username
For local machine: MACHINENAME\username

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 28**. Note that the administrator can set up new users from within CytoGenomics once installation is complete (see “To manage users and roles” on page 100).

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.
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.

Click Next.

The Choose common storage folder screen opens.

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

Figure 10  Choose common storage folder screen – Windows
17 By default, the common storage folder is created inside the folder 
\texttt{C:\Agilent\AgilentCytoGenomics5.2.X.X\Server} (where X.X is the 
revision number). Leave this folder as-is, or Click \textbf{Choose}, browse to 
the desired folder, and then click \textbf{Save}.

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

18 Click \textbf{Next}.

The Choose client data folder screen opens.

\begin{figure}[h]
\centering
\includegraphics[width=0.7\textwidth]{choose_client_data_folder.png}
\caption{Choose client data folder screen – Windows}
\end{figure}

19 By default, the client data folder is created inside the folder 
\texttt{C:\Agilent\AgilentCytoGenomics5.2.X.X\Client} (where X.X is the 
revision number). Leave this folder as-is, or Click \textbf{Choose}, browse to 
the desired folder, and then click \textbf{Save}.

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

20 Click \textbf{Next}. 
The Choose Shortcut Folder screen opens.

![Choose Shortcut Folder screen – Windows](image)

**Figure 12** Choose Shortcut Folder screen – Windows

By default, program icons are installed in the Agilent CytoGenomics 5.2.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 5.2 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.
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.
When the installation is complete, the Installation Complete screen opens.
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 5.2 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.

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 5.2 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.
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 5.2 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 5.2 program, run the installation wizard, as described in “Step 2. Install the database server and client on a single Windows computer” on page 21.

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

![Choose Install Set screen](image)

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

3. Click **Next**.

   The Choose Install Folder screen opens.
By default, the program is installed in `C:\Agilent\AgilentCytoGenomics5.2.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 5.2.

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.
6 Under **Host**, type the assigned computer name or IP address of the computer (from step 2) where you installed the Agilent CytoGenomics 5.2 database server. (To find the computer name of your current computer, click **Start > Control Panel > System and Security > 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 21.

**Step 4. Start the Agilent CytoGenomics 5.2 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 5.2 icon, or select Agilent CytoGenomics 5.2 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.

![Enter License dialog box](image)

**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**.

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.
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 100.
Upgrading from CytoGenomics 3.0 or 4.0 to CytoGenomics 5.2 and Migrating Data – Windows

These instructions are for users of CytoGenomics 3.0 or 4.0 who want to upgrade to CytoGenomics 5.2 and migrate all sample records from the previous database to the new CytoGenomics 5.2 database.

For upgrading from CytoGenomics 5.0 to 5.2, see “Upgrading from CytoGenomics 5.0 or 5.1 to CytoGenomics 5.2 – Windows” on page 52.

NOTE

CytoGenomics 5.2 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 v5.2.

Step 1. Install CytoGenomics 5.2 on the server computer

Follow these steps to install Agilent CytoGenomics 5.2 on the computer where the CytoGenomics server software is installed.

1. Download Agilent CytoGenomics 5.2.X.X from Agilent Technologies and check the system requirements.
   See “a. Download the Windows version of the software and release notes” on page 19 for detailed instructions on this step.

2. Double-click the Agilent CytoGenomics 5.2 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.
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.

**Figure 23**  Choose Install Set screen – Windows – select **Both Client and Server**

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

**Figure 24**  Dialog box – Agilent CytoGenomics software installation
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 21.

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 5.2 server.

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 5.2 server. The migration utility tool launches on your PC. Proceed to “Step 2. Migrate data to CytoGenomics 5.2 server” on page 45.

- 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 5.2 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 5.2 on the client computers” on page 49.

**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 5.2 installation.

If you click Skip with the intention of migrating your data at a later time, be aware that if CytoGenomics 5.2 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 5.2 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 5.2. If you do not want to transfer data, bypass this step and proceed to “Step 3. Upgrade to CytoGenomics 5.2 on the client computers” on page 49.

1. On the Sign In screen of the migration utility application (Figure 25), review the list of migration prerequisites and make sure they are all met before you continue.

![Figure 25](image)

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.
2 Installation Instructions for Windows
Upgrading from CytoGenomics 3.0 or 4.0 to CytoGenomics 5.2 and Migrating Data – Windows

Figure 26 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 5.2 server is installed. If CytoGenomics 5.2 server is installed on the same PC as the previous version of CytoGenomics server, then the host names are the same.

**NOTE**

If CytoGenomics 5.2 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.
Once the application has successfully connected to the servers, click **Start Migration**.

The Warning message box opens.

---

**Figure 28** 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 5.2 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 Process) displays the progress of the migration and the migration process summary.

![Data Migration Progress](image)

**Figure 29** CytoGenomics Migration Utility application – Migration in progress

Upon completion of the migration process, the following message box opens.
Click OK to close the message box.

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

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

**Step 3. Upgrade to CytoGenomics 5.2 on the client computers**

Follow these steps to install Agilent CytoGenomics 5.2 on each client computer.

1. Double-click the Agilent CytoGenomics 5.2.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.
2 Installation Instructions for Windows
Upgrading from CytoGenomics 3.0 or 4.0 to CytoGenomics 5.2 and Migrating Data – Windows

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 5.2 client.

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\AgilentCytoGenomics5.2.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 35.

**Step 4. Start the Agilent CytoGenomics 5.2 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 5.2 client software” on page 38.

2 Log in.
   
   See “Step 5. Log in to Agilent CytoGenomics” on page 38.

3 Enter your updated license information.
   
   See “Step 6. Add your software license” on page 39.
Upgrading from CytoGenomics 5.0 or 5.1 to CytoGenomics 5.2 – Windows

If you are using CytoGenomics 5.0 or 5.1 and want to upgrade to CytoGenomics 5.2, you need to uninstall the existing CytoGenomics client application, then install the CytoGenomics 5.2 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 CytoGenomics 5.0 or 5.1 client and install CytoGenomics 5.2 client and server

1. Download Agilent CytoGenomics 5.2 from Agilent Technologies and check the system requirements.
   See “a. Download the Windows version of the software and release notes” on page 19 for detailed instructions on this step.

2. Double-click the Agilent CytoGenomics 5.2 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.
   A message box opens notifying you that the existing version of CytoGenomics client must be uninstalled before installing CytoGenomics 5.2 client.

4. Click OK in the message box.
   The CytoGenomics uninstaller opens.
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.
7 Select **Uninstall Specific Features**.

The Choose Product Features screen opens.
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 or 5.1.

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 5.2 installer.

11 Continue the installation wizard, as described in “Step 2. Install the database server and client on a single Windows computer” on page 21.

12 When the Choose Install Set screen opens, select **Both Client and Server**.
Figure 36 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 21.
Step 2. On the client computers, uninstall CytoGenomics 5.0 or 5.1 client and install CytoGenomics 5.2 client

1. Download Agilent CytoGenomics 5.2 from Agilent Technologies and check the system requirements.
   See “a. Download the Windows version of the software and release notes” on page 19 for detailed instructions on this step.

2. Double-click the Agilent CytoGenomics 5.2 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.
   A message box opens notifying you that the existing version of CytoGenomics client must be uninstalled before installing CytoGenomics 5.2 client.

4. Click OK in the message box.
   The CytoGenomics uninstaller opens.
5 Click **Next**.

6 In the confirmation message box that opens, click **Yes** to continue uninstalling CytoGenomics client for version 5.0 or 5.1.

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 2. Install the database server and client on a single Windows computer” on page 21.

9 When the Choose Install Set screen opens, 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 35.
Step 3. Start the Agilent CytoGenomics 5.2 client software, log in, and add new software license

1. Start the Agilent CytoGenomics program.
   See “Step 4. Start the Agilent CytoGenomics 5.2 client software” on page 38.

2. Log in.
   See “Step 5. Log in to Agilent CytoGenomics” on page 38.

3. Enter your updated license information.
   See “Step 6. Add your software license” on page 39.
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 5.2 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 5.2.

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.
Installation Instructions for Windows
Uninstalling Agilent CytoGenomics on Windows computers

Figure 39  Uninstall Options screen – Windows – select Complete Uninstall

4 Select Complete Uninstall.
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 AgilentCytoGenomics5.2.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 AgilentCytoGenomics5.2.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 5.2 icon, or select Agilent CytoGenomics 5.2 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.
This chapter shows you how to install Agilent CytoGenomics 5.2 on computers running the macOS Catalina operating system.

**CAUTION**

Versions of CytoGenomics prior to version 5.2 are not compatible with the macOS Catalina operating system. To upgrade to CytoGenomics 5.2 from a previous version of CytoGenomics running on macOS Mojave, you first need to upgrade CytoGenomics then upgrade your Macintosh operating system. Please email informatics_support@agilent.com for guidance.

**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 5.2 – Macintosh

This section includes detailed instructions and important notes for installing Agilent CytoGenomics 5.2 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 “Uninstalling Agilent CytoGenomics on Macintosh computers” on page 96.

Step 1. Prepare for installation

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


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_5.2_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>
<thead>
<tr>
<th>Table 3</th>
<th>Requirements for Agilent CytoGenomics on Macintosh computers</th>
</tr>
</thead>
<tbody>
<tr>
<td>Operating System</td>
<td>macOS Catalina or macOS Mojave</td>
</tr>
</tbody>
</table>
| 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 5.2 software has administrator permissions on the installation computer.

- Make sure that every user account running the Agilent CytoGenomics 5.2 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 5.2 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 5.2 server. Use an account that has administrator permissions.

2. Locate the compressed folder (Agilent_CytoGenomics_5_2_X_X_MAC.zip) that you downloaded in Step 1, “a. Download the Macintosh version of the software and release notes” on page 64. 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.
4 Read the introductory information.
5 Click Next to display the next section.

The License Agreement screen opens.
3 Installation Instructions for Macintosh

Installing Agilent CytoGenomics 5.2 – Macintosh

Figure 41  License Agreement screen – Macintosh

6 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.
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.
By default, the program is installed in the AgilentCytoGenomics5.2.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 5.2 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.
If only the administrator will be accessing Agilent CytoGenomics 5.2 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 5.2 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.
3 Installation Instructions for Macintosh
Installing Agilent CytoGenomics 5.2 – Macintosh

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 45** 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 5.2 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 74. Note that the administrator can set up new users from within CytoGenomics once installation is complete (see “To manage users and roles” on page 100).

14 Click Next.

The Add CytoGenomics Users screen opens.

![Add CytoGenomics Users screen](image)

**Figure 46** 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.
3 Installation Instructions for Macintosh
Installing Agilent CytoGenomics 5.2 – Macintosh

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.

Click Next.

The Choose common storage folder screen opens.

By default, the common storage folder is created inside the Server folder in the AgilentCytoGenomics5.2.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.

![Choose client data folder screen – Macintosh](image)

**Figure 49** Choose client data folder screen – Macintosh

21 By default, the client data folder is created inside the Client folder in the AgilentCytoGenomics5.2.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.
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.
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.
3 Installation Instructions for Macintosh
Installing Agilent CytoGenomics 5.2 – Macintosh

Figure 52  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 5.2.X.X screen opens and is displayed until the installation is complete.
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**.
3 Installation Instructions for Macintosh
Installing Agilent CytoGenomics 5.2 – Macintosh

Figure 54 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 55 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 5.2 server.

![Launch Migration Utility dialog box – Macintosh](image)

**Figure 56** Launch Migration Utility dialog box – Macintosh

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

Because these instructions are for installing Agilent CytoGenomics 5.2 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.

28 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.
3 Installation Instructions for Macintosh
Installing Agilent CytoGenomics 5.2 – Macintosh

**Step 3. Install the client software on additional Macintosh computers**

To use other computers to run Agilent CytoGenomics 5.2 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 5.2 program, run the installation wizard, as described in “Step 2. Install the database server and client on a single Macintosh computer” on page 66.

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

![Choose Install Set screen – Macintosh](image.png)

**Figure 57** Choose Install Set screen – Macintosh

3. Click **Next**.

The Choose Installation Folder opens.

...
By default, the program is installed in the AgilentCytoGenomics5.2.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 5.2. 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.
6 Under Database Host, type the assigned computer name or IP address of the computer (from step 2) where you installed the Agilent CytoGenomics 5.2 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 12 through step 28 in the section “Step 2. Install the database server and client on a single Macintosh computer” on page 66.

**Step 4. Start the Agilent CytoGenomics 5.2 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 5.2 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.

![Login screen](image)

**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 Installation Instructions for Macintosh

Installing Agilent CytoGenomics 5.2 – Macintosh

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.

![Figure 61 Enter License dialog box](image)

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.

---

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 100.
Upgrading from CytoGenomics 5.1 to CytoGenomics 5.2 – Macintosh

If you are using CytoGenomics 5.1 and want to upgrade to CytoGenomics 5.2, you need to uninstall the existing CytoGenomics client application, then install the CytoGenomics 5.2 client and server. You do not need to migrate data from the previous version to the new version.

NOTE
CytoGenomics 5.2 is compatible with and can co-exist on the same machine as CytoGenomics 3.0 or 4.0. It is not necessary to uninstall CytoGenomics 3.0 or 4.0 in order to install CytoGenomics 5.2.

Step 1. On the server computer, uninstall CytoGenomics 5.1 client and install CytoGenomics 5.2 client and server

1. Log on to the Macintosh system where the CytoGenomics 5.1 server software is installed. Use an account that has administrator permissions.

2. Download Agilent CytoGenomics 5.2 from Agilent Technologies and check the system requirements.
   See “a. Download the Macintosh version of the software and release notes” on page 64 for detailed instructions on this step.

3. Locate the compressed folder (Agilent_CytoGenomics_5_2_X_X_MAC.zip) that you downloaded in step 2. Double-click the folder to expand the contents of the folder and save the installer on your computer.

4. Double-click the Mac installer.
   The installation wizard opens to the Introduction screen.

5. 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 5.2 client.

6. Click OK in the message box.
   The following window opens.
7 Click directly on the lock icon near bottom of the dialog box. The following dialog box opens.

![Authentication dialog box - preparing to uninstall](image)

**Figure 63** Authentication dialog box - preparing to uninstall

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

The uninstaller starts.

9 Read the introductory information, and then click **Next**.
10 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.

![Uninstall Options screen – Macintosh – select Uninstall Specific Features](image)

**Figure 65**  Uninstall Options screen – Macintosh – select **Uninstall Specific Features**

11 Select **Uninstall Specific Features**.

The Choose Product Features screen opens.
12 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.

13 In the confirmation message box that opens, click **Yes** to continue uninstalling CytoGenomics client for version 5.1.

14 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.

15 Continue the installation wizard, as described in “Step 2. Install the database server and client on a single Macintosh computer” on page 66.
When the Choose Install Set screen opens, select **Both Client and Server**.

![Choose Install Set screen – Macintosh – select Both Client and Server](image)

**Figure 67**  Choose Install Set screen – Macintosh – select **Both Client and Server**

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.

Continue the installation wizard. For information, refer to “Step 2. Install the database server and client on a single Macintosh computer” on page 66.
Step 2. On the client computers, uninstall CytoGenomics 5.1 client and install CytoGenomics 5.2 client

1. On each client computer, download Agilent CytoGenomics 5.2 from Agilent Technologies and check the system requirements.
   See “a. Download the Macintosh version of the software and release notes” on page 64 for detailed instructions on this step.

2. Locate the compressed folder (Agilent_CytoGenomics_5_2_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. Double-click the Mac installer.
   The installation wizard opens to the Introduction screen.

4. 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 5.2 client.

5. Click OK in the message box.
   The uninstaller starts.

6. Read the introductory information, and then click Next.

7. In the confirmation message box that opens, click Yes to continue uninstalling CytoGenomics client for version 5.1.

8. 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.

9. Continue the installation wizard, as described in “Step 2. Install the database server and client on a single Macintosh computer” on page 66.

10. When the Choose Install Set screen opens, select Only Client.
Installation Instructions for Macintosh

Upgrading from CytoGenomics 5.1 to CytoGenomics 5.2 – Macintosh

3 Installation Instructions for Macintosh

Upgrading from CytoGenomics 5.1 to CytoGenomics 5.2 – Macintosh

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Choose Install Set screen – Macintosh – select Only Client

11 Click Next.

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

12 Continue the installation wizard. For information, refer to “Step 2. Install the database server and client on a single Macintosh computer” on page 66.

Figure 68 Choose Install Set screen – Macintosh – select Only Client

Step 3. Start the Agilent CytoGenomics 5.2 client software, log in, and add new software license

1 Start the Agilent CytoGenomics program.

See “Step 4. Start the Agilent CytoGenomics 5.2 client software” on page 85.
2 Log in.
   See “Step 5. Log in to Agilent CytoGenomics” on page 85.
3 Enter your updated license information.
   See “Step 6. Add your software license” on page 86.
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 5.2 is compatible with and can co-exist on the same machine as CytoGenomics 3.0 or 4.0. It is not necessary to uninstall CytoGenomics 3.0 or 4.0 in order to install CytoGenomics 5.2.

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.

   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.
Uninstalling Agilent CytoGenomics on Macintosh computers

Figure 69  Uninstall Options screen – Macintosh – select **Complete Uninstall**

4 Select **Complete Uninstall**.

5 Click **Next**.

6 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.
Installation Instructions for Macintosh
Uninstalling Agilent CytoGenomics on Macintosh computers
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 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

<table>
<thead>
<tr>
<th>To do this task</th>
<th>Follow these instructions</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Click <strong>Admin</strong>.</td>
<td>• A user cannot be deleted but can be disabled.</td>
</tr>
<tr>
<td>2</td>
<td>Click <strong>Manage Users &amp; Roles</strong>.</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Click <strong>Add New User</strong>.</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Next to <strong>Add New User</strong>, type the user name, and then click <strong>Find</strong>. (See comments for information about adding users for local machines.)</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>At the bottom of the Add User dialog box, click <strong>Add User</strong>.</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>When the Add User dialog box opens asking you to confirm, click <strong>Yes</strong>.</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>When the notice of success opens, click <strong>OK</strong>.</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>When you are finished adding users, click <strong>Close</strong>.</td>
<td></td>
</tr>
</tbody>
</table>

Add new users

The user now appears in the list of users with the role of Technician, with a status of **Enabled**.

- For local machines with no Domain,
  - Next to **User**, type the computer name and user in the format `machinename\username`, or `\username` for Macintosh systems. (Do NOT click **Find**.)
  - 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.
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 4   Tasks for managing users and roles (continued)

<table>
<thead>
<tr>
<th>To do this task</th>
<th>Follow these instructions</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>• 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.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Change user roles</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Click Admin.</td>
</tr>
<tr>
<td>2 Click Manage Users &amp; Roles.</td>
</tr>
<tr>
<td>3 On the line for the user whose role you intend to change, click View/Edit.</td>
</tr>
<tr>
<td>4 Highlight the role on the right side of the panel, and then click &lt; to remove the role on the right.</td>
</tr>
<tr>
<td>5 Highlight a role on the left side of the panel, and then click &gt; to add the role to the right.</td>
</tr>
<tr>
<td>6 Click Save.</td>
</tr>
</tbody>
</table>

Table 5   Tasks for managing the database

<table>
<thead>
<tr>
<th>To do this task</th>
<th>Follow these instructions</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>• 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)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Change database locations and information</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Click Admin.</td>
</tr>
<tr>
<td>2 Click Database Settings.</td>
</tr>
<tr>
<td>3 Under Database Settings, click Change.</td>
</tr>
<tr>
<td>4 Type:</td>
</tr>
<tr>
<td>• Common Storage Location</td>
</tr>
<tr>
<td>• Database Host</td>
</tr>
<tr>
<td>• Database Port</td>
</tr>
<tr>
<td>Click Apply to save your changes.</td>
</tr>
</tbody>
</table>

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 5.2 and gives you instructions for installing and administering the software.