Microarray Applications Server and Automated Axiom™ Analysis Software Installation

Expectations

- This document assumes the user of this document has an intermediate level of knowledge in the use of command line commands (specific to the Linux) on a server.

- SSH must already be installed and used while completing the steps contained in this document. If unable to access the server using SSH, either the user account name and password are incorrect, or the IP address specified is incorrect, or the SSH server subsystem has not been properly setup on the server.

- The Checklist specifications and requirements for the Server must be completed, returned, and approved prior to Axiom System installation.

- System account to be used by the software must be used for the installation process. The account needs to be in the sudo group. Personnel with access to the server, access to the system account, and have password privileges are required to be available at time of installation.

Conventions used

Abbreviations

- Microarray Applications = MA, Core

- Automated Axiom = AutoAx

- Commands are placed in single quotes. Example: '**cd /srv**'

- Command examples where text is contained in [ ] indicates the text must be edited. Text must be replaced by the user before running the command. For example, 'cd [change to roots folder]' where roots folder is /srv/core/roots would have an actual command of **'cd /srv/core/roots'**.

IMPORTANT!   The following steps must be performed to use the Microarray Applications and Automated Axiom software.

IMPORTANT!   Depending on the operating system used on some systems, the terminal may appear to freeze during an update and/or an install. If this frozen state continues for more than a minute, press **Enter** to continue the update and/or install process.

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

ThermoFisher
SCIENTIFIC

Microarray Applications and Automated Axiom

1. With the *Site Preparation Questionnaire and Checklist* (P/N MAN000083) in hand, start the SSH application from your client computer to connect to the server.

2. Change directory to the specified directory: cd to **'/srv/core'**

3. Place the unzipped Axiom System installer package (provided by your Thermo Fisher FAS or FSE) in a folder that is visible from the user's account designated for software on the server.

   Note: For example, on a network share option: '/srv/core/roots' where roots is mounted to a network share. The install folder contains *install.sh* and all necessary files to install Core and AutoAx applications.

4. Run the installation script: **/<location of install folder>/install.sh**
   For example, if the install package was located on the network share location "srv/core/roots/installer", then installer would be:
   /srv/core/roots/installer/install.sh

5. The first step in installation process is the licensing agreement. The EULA must be reviewed and accepted.

6. The installation wizard provides a prompt for the database password. Enter the password, then press **Enter**.

IMPORTANT! Record the password on your checklist or some other way in case it needs to be retrieved.

---

7. The installation wizard prompts you for the user password of the account used for installation. This is presumed to be the same user account that will be running the software (see "Expectations"). The password is not recorded and is only requested by the tools needed to perform actions on the server, such as installing or updating utilities and docker. **Note:** As a safeguard, the sudo password will not be displayed on the terminal display while it is entered.

   ■ If Docker is currently installed, it will be uninstalled. The installer will then install the version of Docker required and any required utilities.

   ■ All necessary directories and files are created, Docker images loaded for both Microarray Applications and AutoAx.

   ■ Microarray Applications and AutoAx are now started.

8. Open a compatible (e.g. Google Chrome) web browser.

   a. In the address bar, enter: 'http://[ip address or server name]/core-view'
      Replace the contents inside the '[ ]' (brackets) with the appropriate IP address or server name.

   b. Verify the Microarray Applications view is displayed

   c. Verify the AutoAx application is listed

   d. Verify the MA version is correct version by clicking on the ☰ icon (upper right).

   e. Verify the AutoAx version. To do this, click the Automated Axiom Analysis application card's **Open** button. From the AutoAx's main window, click on the ☰ icon (upper right), then click **About** to confirm its v2.0.0.

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

Thermo Fisher
SCIENTIFIC

f. At this point, you should be configured properly and running. If not, see .

Library files

To install library files, see the *Automated Axiom Library Package Installation* document (P/N APL03483).

GCC File Uploader

1. After the AutoAx Library Files are successfully installed on the server core, install the GCC File Uploader on each connected GeneTitan Workstation by following its installation procedure (P/N APL03484) and using the provided IP address.

```
***********************************************************************
* Core and AutoAx requires the installation and configuration
* of the GCC Uploader to be done prior to scanning. Follow the GCC
* Uploader configuration procedure and use the following IP address
```

Automated Axiom Analysis is now ready for use.

2. Exit, then close the SSH utility.

Troubleshooting

Common errors

- Permissions are not set for 'core' directory on down the directory structure such that the system account being run as, has proper access.
- If network share is used, verify mounting point is properly configured and system account has proper read/write/execute access to remote point.
- If batches exist, but not shown in the dashboard after server boot, verify the mount configuration is set to auto for auto connecting on boot to the network share. Follow the cache resync steps in the archiving document to ensure the cache information is refreshed.
- If batches are displayed in the navigation panel, but their details are not displayed when selected, see mounting troubleshooting in previous step.
- If a 404-like browser display is shown for the Application, verify the Docker daemon engine is set to auto start on boot. Performing a Linux service start on Docker should resolve the issue.

Google Chrome issues

- If the Core UI is not appearing, confirm the IP address or server name was entered correctly.
- Make sure IT has not blocked firewall access to the required http server.
- Make sure 'http' has been entered in the address bar and not 'https'.

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

ThermoFisher
SCIENTIFIC

The information in this guide is subject to change without notice.

DISCLAIMER

TO THE EXTENT ALLOWED BY LAW, LIFE TECHNOLOGIES AND/OR ITS AFFILIATE(S) WILL NOT BE LIABLE FOR SPECIAL, INCIDENTAL, INDIRECT, PUNITIVE, MULTIPLE, OR CONSEQUENTIAL DAMAGES IN CONNECTION WITH OR ARISING FROM THIS DOCUMENT, INCLUDING YOUR USE OF IT.

Revision history: MAN1000084

Revision	Date	Description
A.0	April 2024	Initial release.

Important Software Licensing Information

Your installation and/or use of this Automated Axiom Analysis software is subject to the terms and conditions contained in the End User License Agreement (EULA) which is incorporated within the Automated Axiom Analysis software, and you will be bound by the EULA terms and conditions if you install and/or use the software.

Legal entity

Affymetrix, Inc.| Santa Clara, CA 95051 USA | Toll Free in USA 1 800 955 6288

TRADEMARKS

All trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified.

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

Thermo Fisher
SCIENTIFIC