

## Microarray analysis

# Automated Axiom Analysis software

### Keywords

Axiom, software, automated, analysis, data, agrigenomics, biobanking, precision medicine, pharmacogenomics, microarray, long export, AxLE, genotyping

### Overview

Applied Biosystems™ Automated Axiom™ Analysis software enables walk-away capability for laboratory professionals and bioinformaticians who are routinely analyzing microarray data. This easy-to-use data analysis tool allows a laboratory technician or bioinformatician to set up their microarray analysis to run automatically so they can focus on other tasks. Following the run, CEL files are automatically uploaded to the Automated Axiom Analysis software for sample analysis and data storage. Users can then view batch analysis status, analysis summaries by batch, dish quality control (DQC), and sample quality control (QC) call rates by plate. In addition, users can monitor summarized marker metrics at a time of their choosing.

The automated data analysis workflow also integrates the Applied Biosystems™ Axiom™ Long Format Export ([AxLE](#)) Tool, providing flexibility of output format. The AxLE tool allows for data format congruity, is applicable for both human and non-human Applied Biosystems™ Axiom™ arrays, and reduces the need to change existing bioinformatics pipelines.

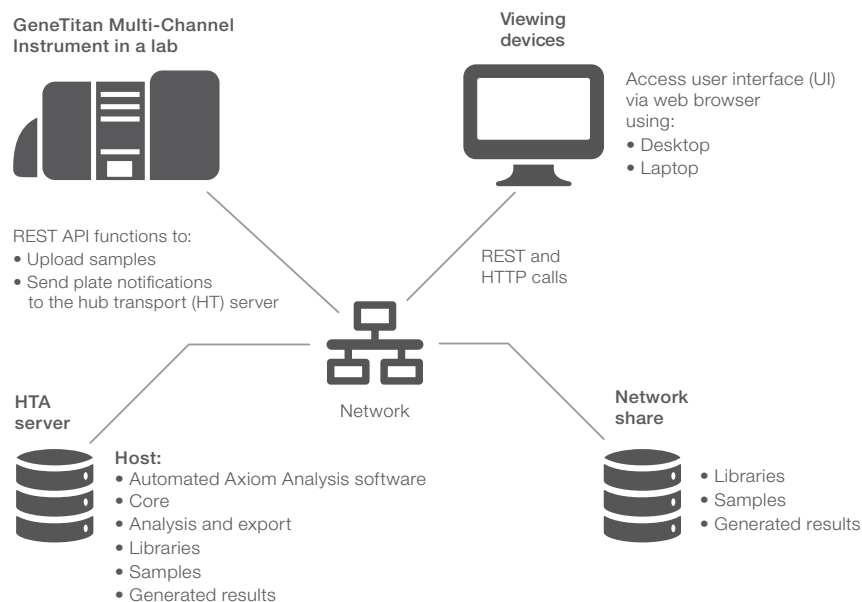
Automated Axiom software, with AxLE export integrated into the workflow, may be especially useful for laboratories that process a high volume of samples, as it removes the need to manually manage data flow and to initiate the application. For laboratories processing a relatively low volume of samples, the Applied Biosystems™ Axiom™ Analysis Suite is a strong choice for genotyping and copy number analysis. However, the data analysis workflow of the Axiom Analysis Suite requires manual transfer of data from the instrument, in addition to manual initiation and management of data once the analysis is complete. While manual data manipulation and management may be sufficient for laboratories with fewer samples, it is typically a burden for those with high sample volumes. In these situations, the Automated Axiom Analysis software may be the tool of choice.

### Features

Automated Axiom Analysis software allows analysis of CEL files following microarray scan completion without intervention by a user. Multiple workflow options are available, including Sample QC and Best Practices workflows. Once the workflow option is set by the user, the software runs the analysis based upon that workflow. Exports are preconfigured via AxLE format, and batches can be downloaded and viewed in the Axiom Analysis Suite.

The Automated Axiom Analysis software requires an Applied Biosystems™ GeneChip™ Command Console version 6.1 or higher. Once the system is set up, copies of the CEL files can then be uploaded to the server. Based on the preset analysis and chosen export configurations, the batch is analyzed. Automated Axiom Analysis software has an interactive interface that allows users to view the status of runs as well as sample and probeset metrics.

## High-level connectivity



## Benefits

The Axiom Analysis Suite is a powerful tool, but in high-volume sample processing scenarios, the manual data management and analysis may introduce a bottleneck. Automated Axiom Analysis software seeks to address efficiency issues by enabling laboratories to continually process microarray samples based on predetermined analysis configurations. Results can be viewed at a time of the user's choosing. Automated Axiom Analysis software improves data analysis efficiency and avoids introducing an analytics bottleneck via a streamlined data analysis workflow and automated report formatting and export.

## Applications

Automated Axiom Analysis software can be used in markets where microarrays are a research tool. These applicable markets include:

- Agrigenomics
- Pharmacogenomics
- Precision medicine
- Biobanking
- Genotyping

## System requirements

- GeneChip Command Console v6.1 or higher on an Applied Biosystems™ GeneTitan™ Multi-Channel Instrument workstation
- CentOS™ 7.7 or Ubuntu™ v18 to support Docker™ v19.03
  - Minimum of 2.0 GHz
  - At least 6 processor cores
  - At least 64 GB memory
  - At least 5 TB local storage or 5–10 TB network share; amount of disk space needed depends on throughput and customer archival procedures
  - At least 6 ports (starting at port 2,000) available for use

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