

# Automated Axiom™ Analysis

## New features in v2.0

- Automated Axiom v2.0 has a brand-new user interface that features three easy-to-use window tabs: Batches, Workflow Setup and Multiplate.
  - **Batches** is the primary window tab and dashboard. It is divided into three separate panes (left, middle, and right):
    - The left pane displays the batches as individual information cards. This pane can be viewed in full screen mode by clicking its expand arrow button.
    - The middle pane displays the details of the selected batch. It includes a pop-up Marker Metrics Summary, expanded Plate Plots, and configurable Sample Metrics and Probeset Summary tables.
    - The right pane displays batch parameters and input values of a highlighted/selected card.
  - **Workflow Setup** window tab features Analysis and Extension panes.
    - Exports are now labeled as *Extensions* and are included for arrays that support them (Allele Translation, and HLA).
    - **Reset to Defaults** enables users to reset to factory or previous custom settings.
  - **Multiplate** batches can be setup in the Multiplate window tab.
    - If the plate is already located on the Server, Automated Axiom automatically starts the analysis after the multiplate batch is created. **Note:** A manual start option is available.
    - Multiplate batches can be created prior to scanning.
    - Multiplate Normalization is now enabled.

- Parallelization of analyses is now enabled. Queued analyses are no longer performed one at a time. For details on batches performed at the same time, see the *Automated Axiom Performance Testing* metrics table below.

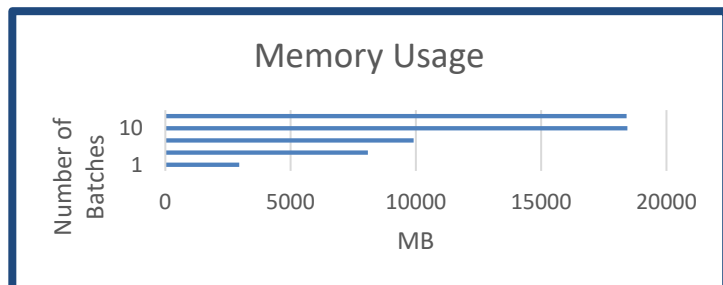
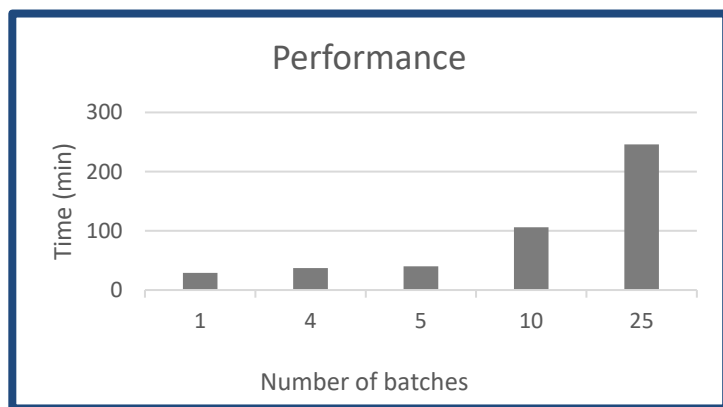
#### Automated Axiom Performance Testing

Number of analyses started at same time	Array type	Workflow	Number of Plates per Batch	Time	CPU (%) up to...	Memory (MB) up to...
1 batch	PMRA	Best Practices	1	44m	5.7	2275
1 batch	PMRA	Best Practices with HLA and AxLE Extensions	1	1h 8m	20.6	6638
1 batch	PMRA	Best Practices with AxLE Extension	50	20h 41m	5.5	5151
2 batches	Transfusion-focused research 384 array	BloodGenomiX Reporter	4	1h 53m	20.7	4014
	BovMD	Best Practices	10			
4 batches	Transfusion-focused research 384 array	BloodGenomiX Reporter	4	5h 58m	30.6	4799
	PMRA	Best Practices with AxLE Extension	20			
	BovMD	Best Practices	10			
	Transfusion-focused research 384 array	BloodGenomiX Reporter	1			
10 batches	PMRA	Best Practices with AxLE Extension	50	48h 5m	43.3	40466

**Note:** Automated Axiom Performance Testing was performed on a system with 2 cores: 20 threads (2 per 64GB RAM and 2GB Swap).

- BloodGenomiX Reporter is a new research-orientated workflow enabled for blood transfusion arrays. Its analysis includes Best Practices, Contamination QC, HLA, and Extended Blood Typing. The final output file is configured for easy integration.

**Note:** The following graphs illustrate performance testing results of a Blood GenomiX Reporter workflow run that utilized a Transfusion-focused research 384 array.



**Note:** Memory Usage: *Number of Batches* = Number of single plate analyses running in parallel.

- AutoAx v2.0 directory structure now includes a Transfers folder. Mapping a drive to this folder enables direct copying rather than requiring a download from the Batches window tab.
- Downloaded data can now be configured.

## Known issues and limitations in v2.0

- When two users are editing a template in the analysis or extension pane at the same time, edits made by one of the two users may not be saved.
- Running Automated Axiom on a virtual machine has been validated, however, it is critical the Checklist is properly followed and AutoAx is the only application currently running.
- The GTDataUploader log file clears frequently. To retain log file history, the **GTDataUploader.exe.config** file must be modified. To modify this file, search for **deleteOldFileOnStartup**, then change its associated value from true to **false**. After changing the value, make sure to restart the Services. **Tip:** Log files should be archived for a reasonable period of time, while log files that are no longer needed should be deleted to optimize available disk space.
- Archive scheduling for the GeneTitan™ is highly recommended. Archiving batches and rootdata should be an on-going scheduled routine. See **Archiving** in the *Automated Axiom User Guide* (P/N MAN1000174) for details.
- When batches are run using the ContaminationQC Extension, **ContaminationQC** will not be displayed in the Sample Metrics Table.
- A value entered in the Analysis pane's Inbred File Value field does not reset after clicking on the **Reset to Defaults** button. To reset, click on the **Use value for all samples** check box, change the value to 0, then click outside the value field to save.
- When exporting single sample VCF formats, the VCF Extension card may display an error message even though the export was successful.