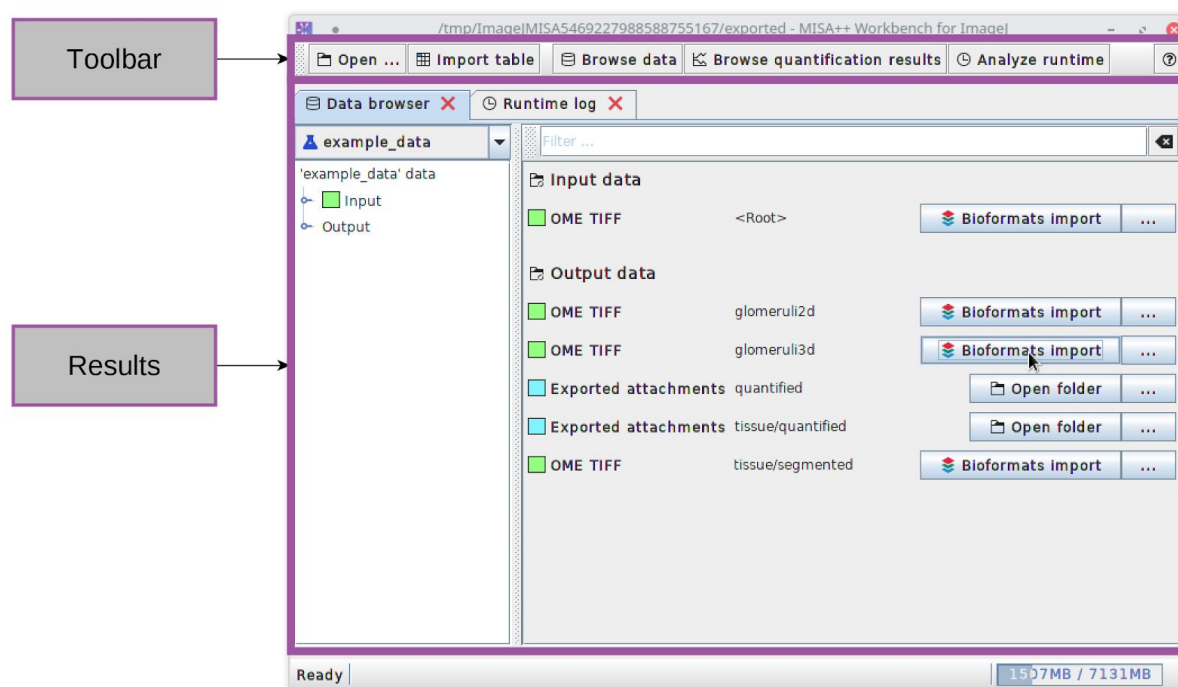


Analyzing results

The MISA++ ImageJ plugin comes with a tool to analyze the results of a MISA++ analysis. If you run an analysis (single-application or pipeline) on the current computer, you are offered to open the results immediately. If you executed the analysis on another computer, without the ImageJ plugin or want to re-visit an old result, you can access the analysis tool via the module manager (see [Managing applications](#)).

Due to the high standardization of MISA++ applications, you can analyze results of MISA++ application that are not installed or where the installed application is newer or older.






The user interface is divided into two sections:



1. A toolbar with global actions
2. Tabs containing the results


Following toolbar actions are available:

Action	Description
<i>Open ...</i>	Opens a MISA++ application output folder.
<i>Import table ...</i>	Imports an external table into the table analyzer (see Summarizing quantification results).
<i>Browse data</i>	Opens the data browser (see Evaluating output data).





 <i>Browse quantification results</i>	Opens a tool to browse quantification results (see Browsing quantification results). You can open as many tools as you want.
 <i>Analyze runtime</i>	Opens the runtime analysis tool (see Analyzing the runtime).
 <i>Help</i>	Opens the documentation.

Evaluating output data

The  *Data Browser* tool lists all input and output data. Its navigation is similar to the parameter editor's  *Data* category (see [Importing data](#)).

Depending on the data type, the data browser offers actions such as importing the data back into ImageJ via  *Bioformats Importer*. The “...” button opens a list of other available options.


Following actions are available by default:

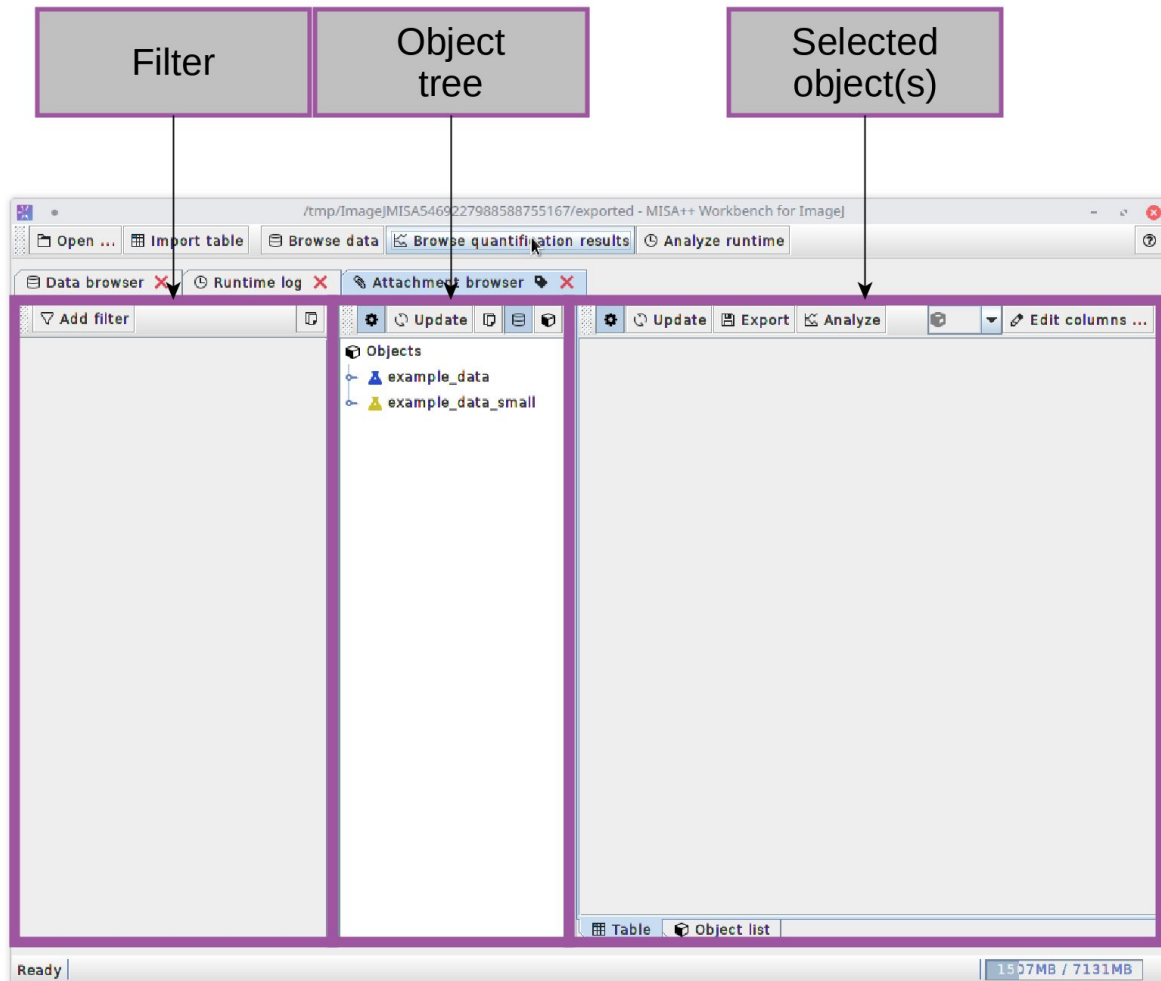
Action	Description
 <i>Bioformats import</i>	Only available for OME TIFF data. Imports the OME TIFF via the Bioformats importer.
 <i>Set current image name</i>	Only available for image data. Sets the name of the currently selected image in ImageJ to a name unique to the data.
 <i>Open folder</i>	Opens the folder that contains the data.
 <i>Copy path</i>	Copies the folder path into the clipboard.

Browsing quantification results

MISA++ applications store quantification results in a standardized and flexible format that is capable of organizing large amounts of metadata. The data is stored as objects such as quantities with units, locations or application-specific objects such as glomeruli.

MISA++ for ImageJ includes a tool to filter, browse and process the quantification results and create tables of only the relevant information.

Important: The tool is designed to handle millions of data entries and uses a SQLite database to handle such an amount of data. The database is created by the  **MISA++ Result Analyzer** application. Please check if it is installed and in the list of available applications (see [Managing applications](#)).

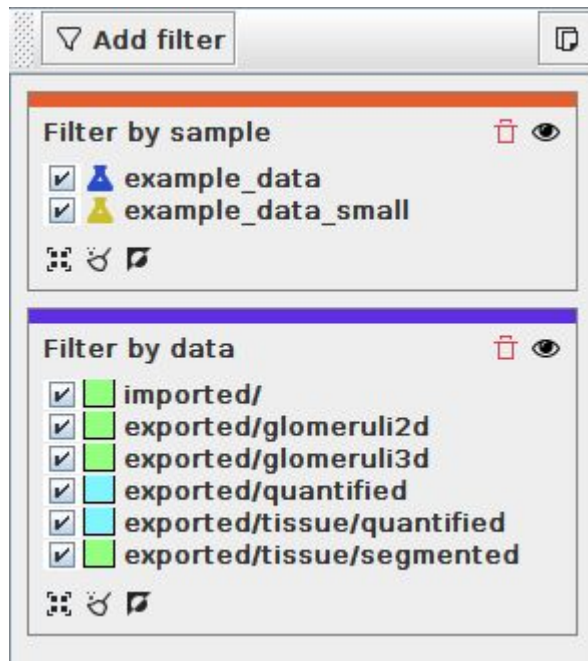


The user interface is divided into three sections:

1. An interface to filter the quantification results
2. A tree to navigate the filtered results
3. The selected object(s) displayed as table or object

The data flows from left to right: Quantification results are filtered by the filter tool and then displayed in the object tree. You can browse the tree and further refine your selection that will be displayed as table or object.

Filtering



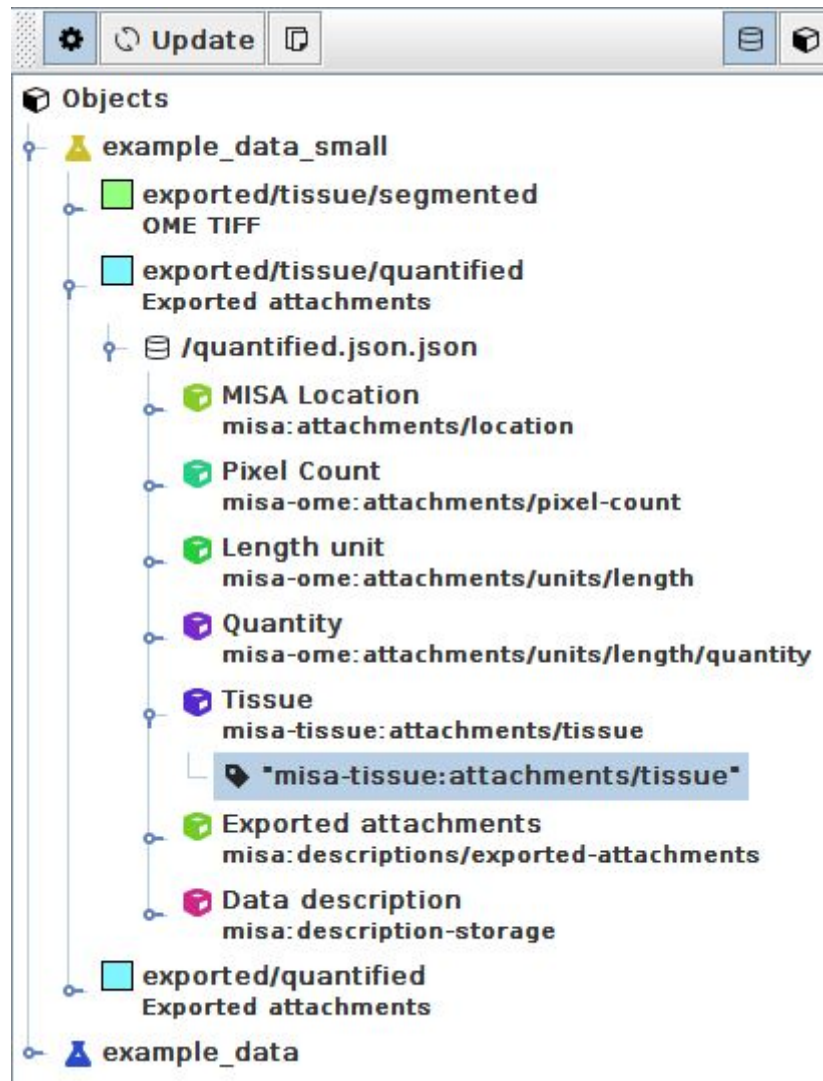
To add a filter, click Add filter and select one of the filter types. Each filter has a button Remove filter that deletes the filter from the list and a toggle Disable filter that temporarily disables the filter without deleting it.

Following filters are included in MISA++ for ImageJ:

Filter	Description
<i>Filter by SQL</i>	Allows insertion of a custom SQL filter query.
<i>Filter by data</i>	Filters quantification results that are attached to specific data.
<i>Filter by object type</i>	Restricts the object types (e.g. only list glomeruli).
<i>Filter by sample</i>	Only shows quantification results of specified samples.
<i>Filter only direct attachments</i>	MISA++ quantification results are hierarchical. With this filter, objects deeper down in the hierarchy are hidden.




Tip: If you want to re-use the filters for your own SQLite query, click Copy filters as SQL query to obtain the query.



Object tree



The object tree lists all unfiltered objects in a hierarchy and acts as input for the table and object browser.





The toolbar has following actions:

Action	Description
 <i>Automatically update</i>	If enabled (default), the tree is automatically updated when a filter is changed. Disable this feature if you change lots of filter settings at once and don't want to wait for the database update.
 <i>Update</i>	Updates the tree manually.
 <i>Copy as SQL query</i>	Copies the current selection as SQL query.







	This includes the SQL query from filtering.
 <i>Display by data</i>	If enabled (default), the tree is organized by sample → data → sub-data → type → property.
 <i>Display by object type</i>	If enabled, the tree is organized by MISA++ application → type → data → sample → property.



Creating a table and browsing objects

The data browser allows you to either browse the quantification results as objects or create a table (default option).

 Update  Export  Analyze Tissue (misa-tissue:attachments/tissue)  Edit columns ...						
Data	Property	Sample	Sub-data	volume/unit/order	volume/unit/unit	volume/value
exported/tissue/quantified	"misa-tissue:attachments/tissue"	example_data_small	/quantified.json,json	3	µm	1480703750.0
exported/tissue/quantified	"misa-tissue:attachments/tissue"	example_data	/quantified.json,json	3	µm	7330032875.0

















The table creator has following actions:

Action	Description
 <i>Automatically update</i>	If enabled (default), the table is automatically updated when a filter is changed or the selection the tree changes.
 <i>Update</i>	Updates the table manually.
 Export	Saves the table as *.csv or *.xlsx
 Analyze	Opens a tool to further analyze the table (see Summarizing quantification results).
 Current object	Tables can only be created for one object type. Use this selection to change the object type.
 Edit columns	By default, the table does not contain all properties of the current object. The column editor allows you to include more columns or exclude unnecessary information.

















By changing the current mode from  *Table* to  *Object list*, all selected quantification data is displayed as objects. You can browse the list and export objects in JSON format.






Summarizing quantification results

You can modify, split and summarize tables extracted from quantification results or loaded via the import function.

 Export	 Clone	 Undo	 Add row	 Add column											
Data	Property	Sample	Sub-data	invalid-glomeruli-number	valid-glomeruli-diameter-average	valid-glomeruli-diameter-variance									
exported/quantified	"misa-kidney-glomeruli:attachments/glomeruli"	example_data_small	/quantified.json,json	288	32.812939482981236	8.435064720193623									
exported/quantified	"misa-kidney-glomeruli:attachments/glomeruli"	example_data	/quantified.json,json	724	33.360173181187974	8.287420400890596									

Following actions are available:

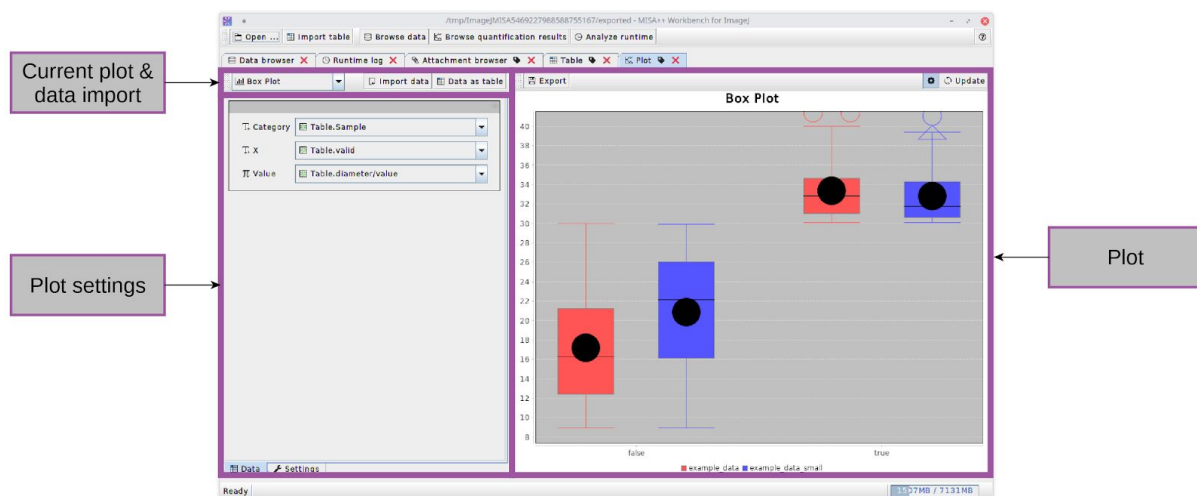
Action	Description
 Export	Exports the current table as *.csv or *.xlsx
 Clone	Clones the current table into a new table document. This will open a new tab.
 Undo	Undo the previous action. Please note that this function does not work for manually editing a table cell.
 Add row	Adds an empty row or copies rows from another table.
 Add column	<p>Allows creation of a  new empty column,  copying the currently selected column or  importing columns from another table.</p> <p>The  <i>Combine selected columns</i> function creates a new column that combines the values of the existing column in the format <i>Column1=Value1, Column2=Value2</i>. Use this function to quickly merge multiple conditions into a single one.</p>
 Remove rows	Removes the selected rows
 Remove columns	Removes the selected columns
 Rename column	Renames the selected column
 Select whole row	Expands the selection to the whole row
 Select whole column	Expands the selection to the whole column
 Invert selection	Inverts the current selection
 Filter select	Selects all rows that match with the

	<p>selected values.</p> <p><u>Example</u></p> <p>The table has two columns “Valid” and “Sample”. You want to select all rows where “Valid” = True and “Sample” = “Kidney1”. Select those values and click the filter selection button.</p>																								
 Autosize columns	Resizes the columns, so they fit their contents.																								
 Split columns	<p>Splits the values of one column by a set of category columns.</p> <p><u>Example</u></p> <table border="1"><thead><tr><th>Sample</th><th>Valid</th><th>Count</th></tr></thead><tbody><tr><td>S1</td><td>True</td><td>100</td></tr><tr><td>S1</td><td>True</td><td>30</td></tr><tr><td>S1</td><td>False</td><td>50</td></tr><tr><td>S2</td><td>True</td><td>200</td></tr></tbody></table> <p>The column “Count” is split by “Sample” and “Valid”. Following table is generated:</p> <table border="1"><thead><tr><th>Count WHERE Sample=S1, Valid=True</th><th>Count WHERE Sample=S1, Valid=False</th><th>Count WHERE Sample=S2, Valid=True</th></tr></thead><tbody><tr><td>100</td><td>50</td><td>200</td></tr><tr><td>30</td><td></td><td></td></tr></tbody></table>	Sample	Valid	Count	S1	True	100	S1	True	30	S1	False	50	S2	True	200	Count WHERE Sample=S1, Valid=True	Count WHERE Sample=S1, Valid=False	Count WHERE Sample=S2, Valid=True	100	50	200	30		
Sample	Valid	Count																							
S1	True	100																							
S1	True	30																							
S1	False	50																							
S2	True	200																							
Count WHERE Sample=S1, Valid=True	Count WHERE Sample=S1, Valid=False	Count WHERE Sample=S2, Valid=True																							
100	50	200																							
30																									
 Integrate columns	Creates column statistics such as sum, average, variance or median.																								
 Convert selection	Converts the selected cells by the selected conversion function (e.g. to a number)																								
 Create plot	Creates a plot from the table. See Plotting quantification results for more information.																								

	Info: The plot gets a copy of the table, so changes to the table do not affect an existing plot.
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Plotting quantification results

The integrated plot tool can create various plots from table data.



The user interface is divided into three sections:

1. The plot
2. The plot type and data import/export options
3. Plot data and additional settings

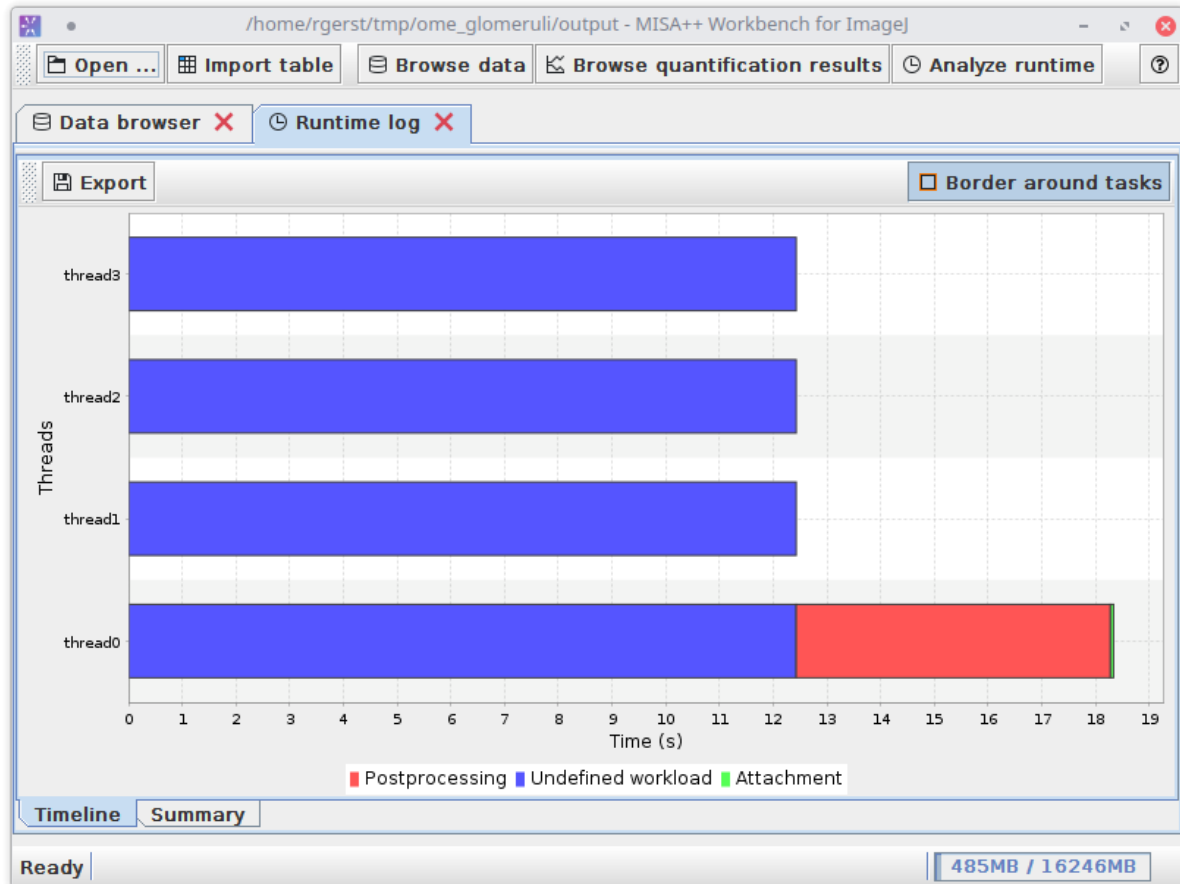
The plot is displayed on the right side and can be exported into publication-ready formats via the *Export* action. You can disable the automatic update when plot settings or data is changed by disabling the *Automatically update plot* button.

The plot type can be selected in ②, which also has following actions:

Actions	Description
Plot type	The current plot type
Import data	Imports columns from a table. Imported data series will be named <i><Table Name>.<Column Name></i> . Tip: Use the <i>Rename</i> buttons in the tab list to rename tabs.
Data as table	Exports the currently loaded data as table.

Analyzing the runtime

MISA++ applications always track basic information about the time needed to do an analysis with the option to enable a detailed runtime log. It can be accessed via the analysis tool (see [Evaluating output data](#)) or in a standalone-version that is accessible via the list of installed MISA++ applications (see [Managing applications](#)).



The timeline is a Gantt-chart that lists the duration and thread allocation of each calculation step. A full-detailed version that lists each individual task (e.g. tissue segmentation) is only available if enabled in the MISA++ application parameters.

The tool also creates statistics such as the total runtime, estimated single-threaded runtime and the estimated multithreading speedup.