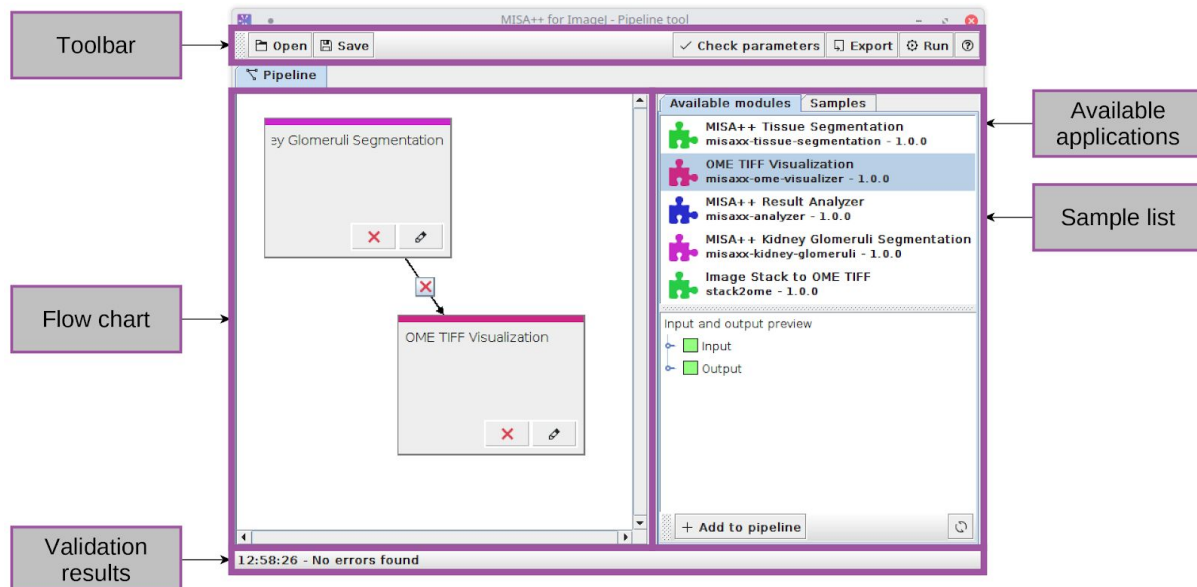


Creating pipelines

MISA++ applications can make usage of other MISA++ applications via a fixed code dependency. Creation of pipelines using code dependencies on the other hand requires modification of the source code. The MISA++ ImageJ plugin provides a tool that allows creation of pipelines of existing MISA++ applications without writing code.

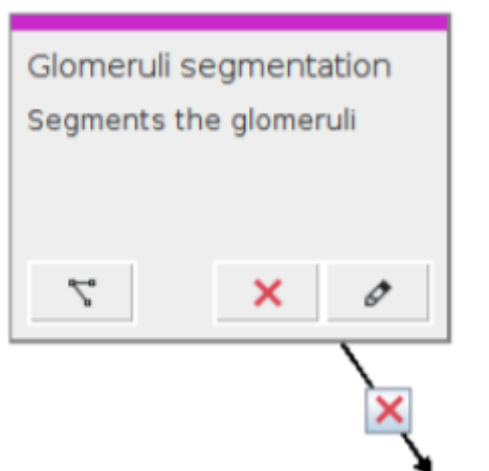


The user interface is divided into four sections:






1. Pipeline flow chart
2. List of available MISA++ applications (modules) and an overview of samples
3. Toolbar with global actions
4. Parameter validation results (for all pipeline nodes)

Pipeline flow chart



The pipeline flow chart (represents MISA++ applications as processing steps and data flow as arrow (connections) between processing steps.




Each processing step consists of following components (from top to bottom):


Component	Description
Name	The name of the processing step. Can be edited.
Description	Optional description of the processing step. Can be edited.
 <i>Connect from other node</i>	Click to connect another processing step to the current one. This button is not visible if there are no available connections.
 <i>Remove entry</i>	Removes the processing step.
 <i>Edit parameters</i>	Opens a parameter editor (see Analyzing data) for the MISA++ application behind the processing step.
Arrow(s) and  <i>Remove connection</i>	An arrow connects the data from one application to another. Click  <i>Remove connection</i> to remove the connection.

Managing samples

By default, all MISA++ applications within the pipeline have the same set of samples. You can disable this behavior by navigating the “*Samples*” tab next to the pipeline and disabling  *Autosync*. The interface contains a list of all  samples, color-coded by the MISA++ applications that work on the sample.


Below the list, you can find following actions:

Action	Description												
 <i>Synchronize selected</i>	<p>Ensures that the selected samples are represented in the same set of processing steps.</p> <p><u>Example</u> We have following configuration:</p> <table><tr><th></th><th>Sample 1</th><th>Sample 2</th><th>Sample 3</th></tr><tr><td>Step 1</td><td></td><td>✓</td><td></td></tr><tr><td>Step 2</td><td>✓</td><td>✓</td><td></td></tr></table>		Sample 1	Sample 2	Sample 3	Step 1		✓		Step 2	✓	✓	
	Sample 1	Sample 2	Sample 3										
Step 1		✓											
Step 2	✓	✓											

	<table><tr><td>Step 3</td><td></td><td>✓</td><td>✓</td></tr></table> <p>If we synchronize Sample 1 and Sample 3, both of them will be in Step 2 and Step 3, but not Step 1.</p>	Step 3		✓	✓
Step 3		✓	✓		
 Autosync	If enabled (default), keeps samples synchronized across all processing steps.				



Creating a pipeline

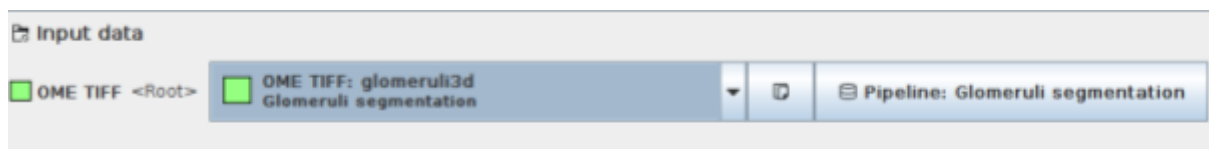
To add an application to the pipeline, select an application in ② and click **+ Add to pipeline**. This will create a new processing step in the flow chart (①). You can use your mouse to drag the processing step to any location in the flow chart.

To implement the flow of data from one application to another, a connection must be created. Click the  **Connect from other node** button on the target processing step and select the source processing step. This will create an arrow and will allow you to import data from another processing step.

Connecting data



Creating a connection between processing steps does not automatically connect the output of the source to the input of the target processing step.

To connect data, open the parameter editor of the target processing step via  **Edit parameters** and change the importer (see [Importers](#)) of the input data to  **Pipeline: <Name of the source processing step>**. Then select the appropriate data from the available options.



Pipeline actions

Following actions are available at in the toolbar (③):

Action	Description
 Open	Opens a pipeline description file. Please note that while structure of the pipeline and its connections are imported, all non-pipeline input data (from outside sources such as ImageJ) must be manually set after loading the pipeline.
 Save	Saves the structure of the pipeline, including

	<ul style="list-style-type: none"> • The processing steps • Samples • Algorithm parameters • Sample parameters • Runtime parameters • Pipeline connections (including importer settings) <p>This will not save importer settings for non-pipeline data sources.</p>
✓ <i>Check parameters</i>	Manually triggers a check if the settings of each processing step are correct. See Validating the current pipeline settings for more information.
📄 <i>Export</i>	<p>Exports a ready-to-use package that processes the pipeline. The packages require that the MISA++ applications are installed on the current computer and includes all settings, parameters and data.</p> <p>The tool generates two feature-identical scripts <i>run.sh</i> (Linux) and <i>run.py</i> (any operating system) and saves the pipeline structure in <i>pipeline.json</i>.</p>
⚙️ <i>Run</i>	Executes the pipeline on the current computer.
❓ <i>Help</i>	Opens the documentation.

Validating the current pipeline settings

Similar to the analysis with one application (see [Analyzing results](#)), the pipeline builder will validate if the processing steps have valid parameters. See [Validating the current settings](#) for more information.