

# Merge Assemblies with Cuffmerge Element

Cuffmerge merges together several assemblies. It also handles running Cuffcompare for you and automatically filters a number of transfrags that are probably artifacts. If you have a reference file available, you can provide it to Cuffmerge in order to gracefully merge input (e.g. novel) isoforms and known isoforms and maximize overall assembly quality.

**Element type:** cuffmerge

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Output directory</b>	Directory to save MACS output files.		<b>out-dir</b>	<i>string</i>
<b>Reference annotation</b>	Merge the input assemblies together with this reference annotation.		<b>ref-annotation</b>	<i>string</i>
<b>Reference sequence</b>	The genomic DNA sequences for the reference. It is used to assist in classifying transfrags and excluding artifacts (e.g. repeats). For example, transcripts consisting mostly of lower-case bases are classified as repeats.		<b>ref-seq</b>	<i>string</i>
<b>Minimum isoform fraction</b>	Discard isoforms with abundance below this.	0.05	<b>min-isoform-fraction</b>	<i>numeric</i>
<b>Cuffcompare tool path</b>	The path to the Cuffcompare external tool in UGENE.	default	<b>cuffcompare-tool-path</b>	<i>string</i>
<b>Cuffmerge tool path</b>	The path to the Cuffmerge external tool in UGENE.	default	<b>path</b>	<i>string</i>
<b>Temporary directory</b>	The directory for temporary files.	default	<b>tmp-dir</b>	<i>string</i>

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** Set of annotations

**Name in Workflow File:** in-assembly

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Set of annotations</b>	<b>in-annotations</b>	<i>ann_table</i>

And 1 *output port*:

**Name in GUI:** Set of annotations

**Name in Workflow File:** out-assembly

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Set of annotations</b>	<b>out-annotations</b>	<i>ann_table</i>