

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
Output directory	Directory to save MACS output files.		out-dir	string
Reference annotation	Merge the input assemblies together with this reference annotation.		ref-annotation	string
Reference sequence	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.		ref-seq	string
Minimum isoform fraction	Discard isoforms with abundance below this.	0.05	min-isoform-fraction	numeric
Cuffcompare tool path	The path to the Cuffcompare external tool in UGENE.	default	cuffcompare-tool-path	string
Cuffmerge tool path	The path to the Cuffmerge external tool in UGENE.	default	path	string
Temporary directory	The directory for temporary files.	default	tmp-dir	string

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
Set of annotations	in-annotations	ann_table

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
Set of annotations	out-annotations	ann_table