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*