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.

Parameters in GUI

Parameter	Description	Default value
Output directory	Directory to save MACS output files.	
Reference annotation	Merge the input assemblies together with this reference annotation.	
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.	
Minimum isoform fraction	Discard isoforms with abundance below this.	0.05
Cuffcompare tool path	The path to the Cuffcompare external tool in UGENE.	default
Cuffmerge tool path	The path to the Cuffmerge external tool in UGENE.	default
Temporary directory	The directory for temporary files.	default

Parameters in Workflow File

Type: cuffmerge

Parameter	Parameter in the GUI	Type
out-dir	**Output directory**	*string*
ref-annotation	**Reference annotation**	*string*
ref-seq	**Reference sequence**	*string*
min-isoform-fraction	**Minimum isoform fraction**	*numeric*
cuffcompare-tool-path	**Cuffcompare tool path**	*string*
path	**Cuffmerge tool path**	*string*
tmp-dir	**Temporary directory**	*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*