## **Assembly Transcripts with Cufflinks Element**

Cufflinks accept aligned RNA-Seq reads and assemble the alignments into a parsimonious set of transcripts. Cufflinks then estimate the relative abundances of these transcripts based on how many reads support each one, taking into account biases in library preparation protocols.

Element type: cufflinks

## **Parameters**

Parameter	Description	Default value	Parameter in Workflow File	Туре
Output directory	Directory to save MACS output files.		out-dir	string
Reference annotation	Tells Cufflinks to use the supplied reference annotation to estimate isoform expression. Cufflinks will not assemble novel transcripts and the program will ignore alignments not structurally compatible with any reference transcript.		ref- annotation	string
RABT annotation	Tells Cufflinks to use the supplied reference annotation to guide Reference Annotation Based Transcript (RABT) assembly. Reference transcripts will be tiled with faux-reads to provide additional information in an assembly. The output will include all reference transcripts as well as any novel genes and isoforms that are assembled.		rabt- annotation	string
Library type	Specifies RNA-Seq protocol.	Standart Illumina	library-type	numeric
Mask file	Ignore all reads that could have come from transcripts in this file. It is recommended to include any annotated rRNA, mitochondrial transcripts other abundant transcripts you wish to ignore in your analysis in this file. Due to variable efficiency of mRNA enrichment methods and rRNA depletion kits, masking these transcripts often improves the overall robustness of transcript abundance estimates.		mask-file	string
Multi-read correct	Tells Cufflinks to do an initial estimation procedure to more accurately weight reads mapping to multiple locations in the genome.	False	multi-read- correct	boolean
Min isoform fraction	After calculating isoform abundance for a gene, Cufflinks filters out transcripts that it believes are very low abundance, because isoforms expressed at extremely low levels often cannot reliably be assembled, and may even be artifacts of incompletely spliced precursors of processed transcripts. This parameter is also used to filter out introns that have far fewer spliced alignments supporting them.	0.1	min-isoform- fraction	numeric
Frag bias correct	Providing Cufflinks with a multifasta file via this option instructs it to run the bias detection and correction algorithm which can significantly improve the accuracy of transcript abundance estimates.		frag-bias- correct	string
Pre-mRNA fraction	Some RNA-Seq protocols produce a significant amount of reads that originate from incompletely spliced transcripts, and these reads can confound the assembly of fully spliced mRNAs. Cufflinks use this parameter to filter out alignments that lie within the intronic intervals implied by the spliced alignments. The minimum depth of coverage in the intronic region covered by the alignment is divided by the number of spliced reads, and if the result is lower than this parameter value, the intronic alignments are ignored.	0.15	pre-mrna- fraction	numeric
Cufflinks tool path	The path to the Cufflinks 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: Input reads

Name in Workflow File: in-assembly

Slots:

Slot In GUI	Slot in Workflow File	Туре
Assembly data	assembly	assembl y
Source url	url	string

And 1 output port.

Name in GUI: Output annotations

Name in Workflow File: out-annotations

Slots:

Slot In GUI	Slot in Workflow File	Туре
Isoform-level expression values	isolevel.slot	ann_tabl e