Assembly Transcripts with Cufflinks Element

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

Parameters in GUI

Parameter	Description	Default value
Output directory	Directory to save MACS output files.	
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.	
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 assembly. Output will include all reference transcripts as well as any novel genes and isoforms that are assembled.	
Library type	Specifies RNA-Seq protocol.	Standart Illumina
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.	
Multi-read correct	Tells Cufflinks to do an initial estimation procedure to more accurately weight reads mapping to multiple locations in the genome.	False
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
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 accuracy of transcript abundance estimates.	
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 uses 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
Cufflinks tool path	The path to the Cufflinks external tool in UGENE.	default
Temporary directory	The directory for temporary files.	default

Parameters in Workflow File

Type: cufflinks

Parameter	Parameter in the GUI	Type
out-dir	**Output directory**	*string*
ref-annotation	**Reference annotation**	*string*
rabt-annotation	**RABT annotation**	*string*
library-type	**Library type**	*numeric*
mask-file	**Mask file**	*string*
multi-read-correct	**Multi-read correct**	*boolean*
min-isoform-fraction	**Min isoform fraction**	*numeric*
frag-bias-correct	**Frag bias correct**	*string*
pre-mrna-fraction	**Pre-mRNA fraction**	*numeric*
path	**Cufflinks tool path**	*string*
tmp-dir	**Temporary directory**	*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	Type
Assembly data	assembly	*assembly*
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	Type
Isoform-level expression values	isolevel.slot	*ann_table*