Map Reads with BWA-MEM Element

Performs alignment of short reads with BWA-MEM.

Element type: bwamem-id

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Output directory	Directory to save BWA-MEM output files.		**output-dir**	*string*
Reference genome	Path to an indexed reference genome.		**reference**	*string*
Output file name	Base name of the output file. 'out.sam' by default.	out.sam	**outname**	*string*
Library	Is this library mate-paired?	single-end	**library**	*string*
Number of threads	Number of threads (-t).	1	**threads**	*numeric*
Min seed length	Path to an indexed reference genome (-k).	19	**min-seed**	*numeric*
Index algorithm	Index algorithm (-a).	autodetect	**index-alg**	*string*
Band width	Bandwidth for banded alignment (-w).	100	**band-width**	*numeric*
Dropoff	Off-diagonal X-dropoff (-d).	100	**dropoff**	*numeric*
Internal seed length	Look for internal seeds inside a seed longer than {-k} (-r).	1.50000	**seed-lookup**	*numeric*
Skip seed threshold	Skip seeds with more than INT occurrences (-c).	10000	**seed-threshold**	*numeric*
Drop chain threshold	Drop chains shorter than FLOAT fraction of the longest overlapping chain (-D).	0.5	**drop-chains**	*numeric*
Rounds of made rescues	Perform at most INT rounds of mate rescues for each read (-m).	100	**mate-rescue**	*numeric*
Skip mate rescue	Skip mate rescue (-S).	False	**skip-mate-rescues**	*boolean*
Skip pairing	Skip pairing; mate rescue performed unless -S also in use (-P).	False	**skip-pairing**	*boolean*
Matching score	Score for a sequence match (-A).	1	**match-score**	*numeric*
Mismatch penalty	Penalty for a mismatch (-B).	4	**mistmatch-penalty**	*numeric*
Gap open penalty	Gap open penalty (-O).	6	**gap-open-penalty**	*numeric*
Gap extension penalty	Gap extension penalty; a gap of size k cost {-O} (-E).	1	**gap-ext-penalty**	*numeric*
Penalty for clipping	Penalty for clipping (-L).	5	**clipping-penalty**	*numeric*
Penalty unpaired	Penalty for an unpaired read pair (-U).	17	**inpaired-panalty**	*numeric*
Score threshold	Minimum score to output (-T).	30	**score-threshold**	*numeric*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: BWA data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
URL of a file with mate reads	**readsurl**	*string*
URL of a file with reads	**readspairedurl**	*string*

And 1 *output port*:

Name in GUI: BWA-MEM output data

Name in Workflow File: out-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Assembly URL	**assembly-out**	*string*