Align reads with BWA-MEM

Performs alignment of short reads with BWA-MEM.

Parameters in GUI

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

Parameters in Workflow File

Type: bwamem-id

Parameter	Parameter in the GUI	Type
output-dir	**Output directory**	*string*
reference	**Reference genome**	*string*
outname	**Output file name**	*string*
threads	**Number of threads**	*numeric*
min-seed	**Min seed length**	*numeric*
band-width	**Band width**	*numeric*
dropoff	**Dropoff**	*numeric*
seed-lookup	**Internal seed length**	*numeric*
seed-threshold	**Skip seed threshold**	*numeric*
drop-chains	**Drop chain threshold**	*numeric*
mate-rescue	**Rounds of made rescues**	*numeric*
skip-mate-rescues	**Skip mate rescue**	*boolean*
skip-pairing	**Skip pairing**	*boolean*
match-score	**Mismatch penalty**	*numeric*
mistmatch-penalty	**Mismatch penalty**	*numeric*
gap-open-penalty	**Gap open penalty**	*numeric*
gap-ext-penalty	**Gap extension penalty**	*numeric*
clipping-penalty	**Penalty for clipping**	*numeric*
inpaired-panalty	**Penalty unpaired**	*numeric*
score-threshold	**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*