

Map Reads with BWA-MEM Element

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 an indexed reference genome.	
Output file name	Base name of the output file. 'out.sam' by default.	out.sam
Library	Is this library mate-paired?	single-end
Number of threads	Number of threads (-t).	1
Min seed length	Path to an indexed reference genome (-k).	19
Index algorithm	Index algorithm (-a).	autodetect
Band width	Bandwidth 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
Matching score	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
library	Library	string
threads	Number of threads	numeric
min-seed	Min seed length	numeric
index-alg	Index algorithm	string
band-width	Bandwidth	numeric

dropoff	Dropoff	<i>numeric</i>
seed-lookup	Internal seed length	<i>numeric</i>
seed-threshold	Skip seed threshold	<i>numeric</i>
drop-chains	Drop chain threshold	<i>numeric</i>
mate-rescue	Rounds of made rescues	<i>numeric</i>
skip-mate-rescues	Skip mate rescue	<i>boolean</i>
skip-pairing	Skip pairing	<i>boolean</i>
match-score	Matching score	<i>numeric</i>
mismatch-penalty	Mismatch penalty	<i>numeric</i>
gap-open-penalty	Gap open penalty	<i>numeric</i>
gap-ext-penalty	Gap extension penalty	<i>numeric</i>
clipping-penalty	Penalty for clipping	<i>numeric</i>
inpaired-penalty	Penalty unpaired	<i>numeric</i>
score-threshold	Score threshold	<i>numeric</i>

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	<i>string</i>
URL of a file with reads	readspairedurl	<i>string</i>

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	<i>string</i>