

# 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 mate 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	mismatch-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	<i>string</i>