

# Map Reads with BWA Element

Performs alignment of short reads with BWA.

Element type: align-reads-with-bwa

## 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
Use missing prob	Use missing prob instead maximum edit distance.	True	use-miss-prob	boolean
Missing prob	Missing prob (-n).	0.04	missing-prob	numeric
Seed length	Seed length (-l).	32	seed-length	numeric
Max gap opens	Max gap opens (-o).	1	max-gap	numeric
Index algorithm	Index algorithm (-a).	is	index-alg	string
Best hits	Best hits (-R).	30	best-hits	numeric
Long-scaled gap penalty for long deletions	Long-scaled gap penalty for long deletions (-L).	False	scaled-gap	boolean
Non iterative mode	Non iterative mode (-N).	False	non-iterative	boolean
Enable long gaps	Enable long gaps.	True	enable-long-gaps	boolean
Max gap extensions	Max gap extensions (-e).	0	gap-extensions	numeric
Indel offset	Indel offset (-i).	5	indel-offset	numeric
Max long deletions extensions	Max long deletions extensions(-d).	10	long-deletions	numeric
Barcode length	Barcode length (-B).	0	barcode-length	numeric
Max queue entries	Max queue entries (-m).	2000000	max-queue	numeric
Threads	Threads (-t).	4	num-threads	numeric
Max seed differencies	Max seed differencies (-k).	2	max-seed	numeric
Mismatch penalty	Mismatch penalty (-M).	3	mismatch-penalty	numeric
Gap open penalty	Gap open penalty (-O).	11	gap-open-penalty	numeric
Gap extension penalty	Gap extension penalty; a gap of size k cost (-E).	4	gap-ext-penalty	numeric
Quality threshold	Quality threshold (-q).	0	quality-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 output data

Name in Workflow File: out-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Assembly URL	assembly-out	<i>string</i>