

Align Reads with BWA Element

Performs alignment of short reads with BWA.

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
Library	Is this library mate-paired?	single-end
Use missing prob	Use missing prob instead maximum edit distance.	True
Missing prob	Missing prob (-n).	0.04
Seed length	Seed length (-l).	32
Max gap opens	Max gap opens (-o).	1
Index algorithm	Index algorithm (-a).	is
Best hits	Best hits (-R).	30
Long-scaled gap penalty for long deletions	Long-scaled gap penalty for long deletions (-L).	False
Non iterative mode	Non iterative mode (-N).	False
Enable long gaps	Enable long gaps.	True
Max gap extensions	Max gap extensions (-e).	0
Indel offset	Indel offset (-i).	5
Max long deletions extensions	Max long deletions extensions(-d).	10
Barcode length	Barcode length (-B).	0
Max queue entries	Max queue entries (-m).	2000000
Threads	Threads (-t).	4
Max seed differences	Max seed differences (-k).	2
Mismatch penalty	Mismatch penalty (-M).	3
Gap open penalty	Gap open penalty (-O).	11
Gap extension penalty	Gap extension penalty; a gap of size k cost (-E).	4
Quality threshold	Quality threshold (-q).	0

Parameters in Workflow File

Type: align-reads-with-bwa

Parameter	Parameter in the GUI	Type
output-dir	Output directory	string
reference	Reference genome	string
outname	Output file name	string
library	Library	string
use-miss-prob	Use missing prob	boolean
missing-prob	Missing prob	numeric
seed-length	Seed length	numeric
max-gap	Max gap opens	numeric
index-alg	Index algorithm	string
best-hits	Best hits	numeric
scaled-gap	Long-scaled gap penalty for long deletions	boolean
non-iterative	Non iterative mode	boolean
enable-long-gaps	Enable long gaps	boolean
gap-extensions	Max gap extensions	numeric
indel-offset	Indel offset	numeric
long-deletions	Max long deletions extensions	numeric
barcode-length	Barcode length	numeric
max-queue	Max queue entries	numeric
num-threads	Threads	numeric
max-seed	Max seed differencies	numeric
mismatch-penalty	Mismatch penalty	numeric
gap-open-penalty	Gap open penalty	numeric
gap-ext-penalty	Gap extension penalty	numeric
quality-threshold	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>