

# 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       |
| 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  |
| 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> |