

# Map Reads with Bowtie2 Element

Performs alignment of short reads with Bowtie2.

**Element type:** align-reads-with-bowtie2

## Parameters in GUI

| Parameter   | Description  | Default value | Parameter in Workflow File | Type           |
|---|--|---------------|----------------------------|----------------|
| <b>Output directory</b>                               | Directory to save Bowtie2 output files.  |               | <b>output-dir</b>          | <i>string</i>  |
| <b>Reference genome</b>                               | Path to an indexed reference genome.   |               | <b>reference</b>           | <i>string</i>  |
| <b>Output file name</b>                               | Base name of the output file. 'out.sam' by default.  | out.sam       | <b>outname</b>             | <i>string</i>  |
| <b>Library</b>  | Is this library mate-paired?   | single-end    | <b>library</b>             | <i>string</i>  |
| <b>Mode</b>   | When the -n option is specified (which is the default), bowtie determines which alignments are valid according to the following policy, which is similar to Maq's default policy. In -v mode, alignments may have no more than V mismatches, where V may be a number from 0 through 3 set using the -v option. Quality values are ignored. The -v option is mutually exclusive with the -n option. | --end-to-end  | <b>mode</b>                | <i>string</i>  |
| <b>Number of mismatches</b>                           | Sets the number of mismatches to allowed in a seed alignment. Can be set to 0 or 1. Setting this higher makes alignment slower (often much slower) but increases sensitivity.  | 0             | <b>mismatches_number</b>   | <i>numeric</i> |
| <b>Seed length (--L)</b>                              | Sets the length of the seed substrings to align. Smaller values make alignment slower but more sensitive.  | 20            | <b>seed_len</b>            | <i>numeric</i> |
| <b>Add columns to allow gaps (--dpad)</b>             | "Pads" dynamic programming problems by the specified number of columns on either side to allow gaps.   | 15            | <b>dpad</b>                | <i>numeric</i> |
| <b>Disallow gaps (--gbar)</b>                         | Disallow gaps within a specified number of positions of the beginning or end of the read.  | 4             | <b>gbar</b>                | <i>numeric</i> |
| <b>Seed (--seed)</b>                                  | Use as the seed for pseudo-random number generator.  | 0             | <b>seed</b>                | <i>numeric</i> |
| <b>Threads</b>  | Launch specified number of parallel search threads. Threads will run on separate processors/cores and synchronize when parsing reads and outputting alignments. Searching for alignments is highly parallel, and speedup is close to linear.   | 1             | <b>threads</b>             | <i>numeric</i> |
| <b>No unpaired alignments (--no-mixed)</b>            | If Bowtie2 cannot find a paired-end alignment for a pair, by default it will go on to look for unpaired alignments for the constituent mates. This is called "mixed mode." To disable mixed mode, set this option. Bowtie2 runs a little faster in the mixed mode, but will only consider the alignment status of pairs per se, not individual mates.  | False         | <b>nomixed</b>             | <i>boolean</i> |
| <b>No discordant alignments (--no-discordant)</b>     | By default, Bowtie2 looks for discordant alignments if it cannot find any concordant alignments. A discordant alignment is an alignment where both mates align uniquely, but that does not satisfy the paired-end constraints. This option disables that behavior.   | False         | <b>nodiscordant</b>        | <i>boolean</i> |
| <b>No forward orientation (--nofw)</b>                | If --nofw is specified, bowtie will not attempt to align against the forward reference strand.   | False         | <b>nofw</b>                | <i>boolean</i> |
| <b>No reverse-complement orientation (--norc)</b>     | If --norc is specified, bowtie will not attempt to align against the reverse-complement reference strand.  | False         | <b>norc</b>                | <i>boolean</i> |
| <b>No overlapping mates (--no-overlap)</b>            | If one mate alignment overlaps the other at all, consider that to be non-concordant. Default: mates can overlap in a concordant alignment.   | False         | <b>nooverlap</b>           | <i>boolean</i> |
| <b>No mates containing one another (--no-contain)</b> | If one mate alignment contains the other, consider that to be non-concordant. Default: a mate can contain the other in a concordant alignment.   | False         | <b>nocontain</b>           | <i>boolean</i> |

## Input/Output Ports

The element has 1 *input port*.

**Name in GUI:** Bowtie2 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:** Bowtie2 output data

**Name in Workflow File:** out-data

**Slots:**

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