

Map Reads with Bowtie2 Element

Performs alignment of short reads with Bowtie2.

Parameters in GUI

| Parameter | Description | Default value |
|---|--|---------------|
| Output directory | Directory to save Bowtie2 output files. | |
| Reference genome | Path to an 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 |
| Mode | 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 |
| Number of mismatches | 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 |
| Seed length (--L) | Sets the length of the seed substrings to align. Smaller values make alignment slower but more sensitive. | 20 |
| Add columns to allow gaps (--dpad) | "Pads" dynamic programming problems by the specified number of columns on either side to allow gaps. | 15 |
| Disallow gaps (--gbar) | Disallow gaps within a specified number of positions of the beginning or end of the read. | 4 |
| Seed (--seed) | Use as the seed for pseudo-random number generator. | 0 |
| Threads | 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 |
| No unpaired alignments (--no-mixed) | 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 |
| No discordant alignments (--no-discordant) | 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 |
| No forward orientation (--nofw) | If --nofw is specified, bowtie will not attempt to align against the forward reference strand. | False |
| No reverse-complement orientation (--norc) | If --norc is specified, bowtie will not attempt to align against the reverse-complement reference strand. | False |
| No overlapping mates (--no-overlap) | If one mate alignment overlaps the other at all, consider that to be non-concordant. Default: mates can overlap in a concordant alignment. | False |
| No mates containing one another (--no-contain) | 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 |

Parameters in Workflow File

Type: align-reads-with-bowtie2

| Parameter | Parameter in the GUI | Type |
|-------------------|--|---------|
| output-dir | Output directory | string |
| reference | Reference genome | string |
| outname | Output file name | string |
| library | Library | string |
| mode | Mode | string |
| mismatches_number | Number of mismatches | numeric |
| seed_len | Seed length (--L) | numeric |
| dpad | Add columns to allow gaps (--dpad) | numeric |
| gbar | Disallow gaps (--gbar) | numeric |
| seed | Seed (--seed) | numeric |
| threads | Threads | numeric |
| nomixed | No unpaired alignments (--no-mixed) | boolean |
| nodiscordant | No discordant alignments (--no-discordant) | boolean |
| nofw | No forward orientation (--nofw) | boolean |
| norc | No reverse-complement orientation (--norc) | boolean |
| nooverlap | No overlapping mates (--no-overlap) | boolean |
| nocontain | No mates containing one another (--no-contain) | boolean |

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> |