

# 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>