

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	string
URL of a file with reads	readspairedurl	string

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	string