Align 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 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 senstive.	20
Add columns to allow gaps (--dpad)	"Pads" dynamic programming problems by specified number of columns on either side to allow gaps.	15
Disallow gaps (--gbar)	Disallow gaps within 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 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*