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
Output directory	Directory to save Bowtie2 output files.		**output-dir**	*string*
Reference genome	Path to an indexed reference genome.		**reference**	*string*
Output file name	Base name of the output file. 'out.sam' by default.	out.sam	**outname**	*string*
Library	Is this library mate-paired?	single-end	**library**	*string*
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	**mode**	*string*
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	**mismatches_number**	*numeric*
Seed length (--L)	Sets the length of the seed substrings to align. Smaller values make alignment slower but more senstive.	20	**seed_len**	*numeric*
Add columns to allow gaps (--dpad)	"Pads" dynamic programming problems by the specified number of columns on either side to allow gaps.	15	**dpad**	*numeric*
Disallow gaps (--gbar)	Disallow gaps within a specified number of positions of the beginning or end of the read.	4	**gbar**	*numeric*
Seed (--seed)	Use as the seed for pseudo-random number generator.	0	**seed**	*numeric*
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	**threads**	*numeric*
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	**nomixed**	*boolean*
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	**nodiscordant**	*boolean*
No forward orientation (--nofw)	If --nofw is specified, bowtie will not attempt to align against the forward reference strand.	False	**nofw**	*boolean*
No reverse-complement orientation (--norc)	If --norc is specified, bowtie will not attempt to align against the reverse-complement reference strand.	False	**norc**	*boolean*
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	**nooverlap**	*boolean*
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	**nocontain**	*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*