

Bowtie Aligning Short Reads

When you select the *Tools* *DNA Assembly* *Align short reads* item in the main menu, the *Align Short Reads* dialog appears. Set value of the *Align short reads method* parameter to *Bowtie*. The dialog looks as follows:

U Align Sequencing Reads

Alignment method

Bowtie

Reference sequence

...

Result file name

...

Library

Single-end

☐ Prebuilt index

☒ SAM output

Short reads

Path	Type	Order
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Add

Remove

Parameters

Mode:

-n mode

2

☐ Maq error (--maqerr)

70

☐ Seed length (--seedlen)

28

☐ Maximum of backtracks (--maxbts)

800

☐ Descriptors memory usage (--chunkmbs)

64

☐ Seed (--seed)

0

Flags

☐ Colorspace (--color)

☐ No Maq rounding (--nomaqround)

☐ No forward orientation (--nofw)

☐ No reverse-complement orientation (--norc)

☐ Try as hard (--tryhard)

☐ Best alignments (--best)

☐ All alignments (--all)

Start

Cancel

Help

There are the following parameters:

- Reference sequence* — DNA sequence to align short reads to. This parameter is required.
- Result file name* — file in SAM format to write the result of the alignment into. This parameter is required.
- Library* - single-end or paired-end reads.
- Prebuilt index* — check this box to use an index file instead of a source reference sequence. The index is a set of 6 files with suffixes .1.ebwt, .2.ebwt, .3.ebwt, .4.ebwt, .rev.1.ebwt, and .rev.2.ebwt. The index is created during the alignment. Also you can [build it manually](#).
- SAM output* — always save the output file in the SAM format (the option is disabled for *Bowtie*).
- Short reads* — each added short read is a small DNA sequence file. At least one read should be added.





Short reads length for *Bowtie* can't be more than 1024.

You can also configure other parameters. They are the same as in the original *Bowtie* (you can read detailed description of the parameters on the [Bowtie manual page](#)).

Select one of the following alignment modes:

The *-n* alignment mode:

When the *-n mode* is selected, *Bowtie* determines which alignments are valid according to the following policy. Alignments may have no more than N mismatches (where N is a number 0-3) in the first L bases (where L is a number 5 or greater, set with *Seed length*) on the high-quality (left) end of the read. The sum of the Phred quality values at all mismatched positions (not just in the seed) may not exceed E (set with *Maq error*). Where qualities are unavailable (e.g. if the reads are from a FASTA file), the Phred quality defaults to 40.

The *-v* alignment mode:

In *-v mode*, alignments may have no more than V mismatches, where V may be a number from 0 through 3. Quality values are ignored. The *-v mode* is mutually exclusive with the *-n mode*.

The following parameters are available:

Maq error (*-maqerr*) — maximum permitted total of quality values at all mismatched read positions throughout the entire alignment, not just in the “seed”. The default is 70. By default, *Bowtie* rounds quality values to the nearest 10 and saturates at 30. Note that the rounding can be disabled with *No Maq rounding*.

Seed Length (*-seedlen*) — the number of bases on the high-quality end of the read to which the *-n* applies. The lowest permitted setting is 5 and the default is 28.

Maximum of backtracks (*-maxbts*) — the maximum number of backtracks (default: 125 without *Best*, 800 with *Best*). A “backtrack” is the introduction of a speculative substitution into the alignment.

Descriptors memory usage (*-chunkmbs*) — the number of megabytes of memory a given thread is given to store path descriptors in the *Best* flag. Default: 64. This parameter is available if the *Best* flag is checked.

Seed (*-seed*) — pseudo-random number generator.

The following flags are available:

Colorspace (*-color*) — the input is read in colorspace, colors are encoded as characters A/C/G/T (A=blue, C=green, G=orange, T=red).

No Maq rounding (*-nomaqround*) — Maq (Mapping and Assembly with Quality) accepts quality values in the Phred quality scale, but internally rounds values to the nearest 10, with a maximum of 30. By default, *Bowtie* also rounds this way. *No Maq rounding* prevents this rounding in *Bowtie*.

No forward orientation (*-nofw*) — do not attempt to align against the forward reference strand.

No reverse-complement orientation (*-norc*) — do not attempt to align against the reverse-complement reference strand.

Try as hard (*-tryhard*) — try as hard as possible to find valid alignments when they exist, including paired-end alignments.

Best alignments (*-best*) — make *Bowtie* guarantee that reported singleton alignments are “best” in terms of stratum (i.e. number of mismatches, or mismatches in the seed for the case of *-n mode*) and in terms of the quality values at the mismatched position(s).

All alignments (*-all*) — report all valid alignments per read or pair. Validity of alignments is determined by the alignment policy (combined effects of *-n mode*, *-v mode*, *Seed length*, and *Maq error*).

Select the required parameters and press the *Start* button.