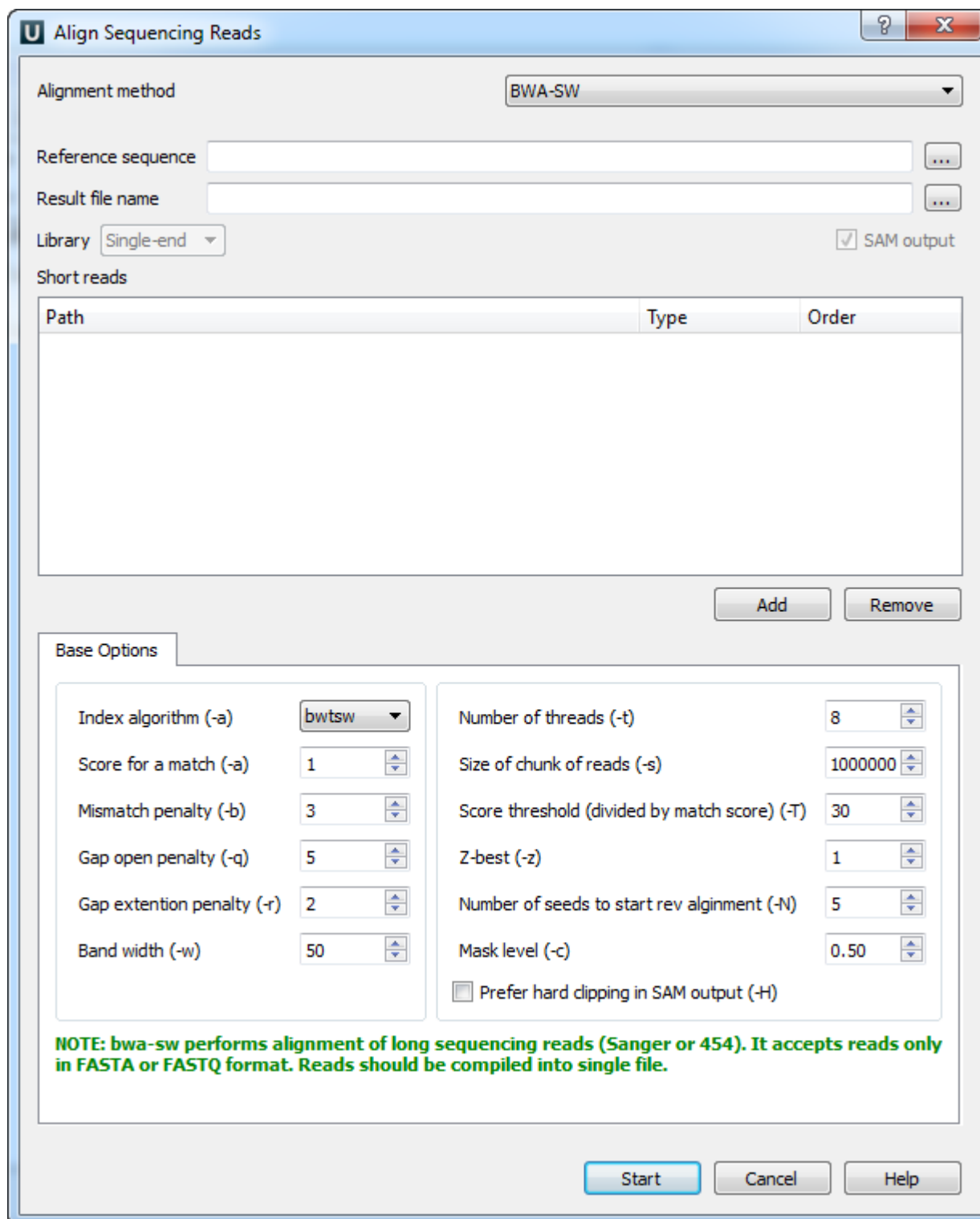


Aligning Short Reads with BWA-SW

When you select the *Tools > Align to reference > Align short reads* item in the main menu, the *Align Sequencing Reads* dialog appears. Set value of the *Align short reads method* parameter to *BWA-SW*. The dialog looks as follows:



The dialog box is titled "Align Sequencing Reads" and contains the following fields and options:

- Alignment method:** A dropdown menu set to "BWA-SW".
- Reference sequence:** A text input field with a browse button (...).
- Result file name:** A text input field with a browse button (...).
- Library:** A dropdown menu set to "Single-end".
- SAM output:** A checked checkbox.
- Short reads:** A table with columns "Path", "Type", and "Order".
- Base Options:** A section containing two columns of parameters:
 - Left Column:**
 - Index algorithm (-a): bwtsv
 - Score for a match (-a): 1
 - Mismatch penalty (-b): 3
 - Gap open penalty (-q): 5
 - Gap extension penalty (-r): 2
 - Band width (-w): 50
 - Right Column:**
 - Number of threads (-t): 8
 - Size of chunk of reads (-s): 1000000
 - Score threshold (divided by match score) (-T): 30
 - Z-best (-z): 1
 - Number of seeds to start rev alignment (-N): 5
 - Mask level (-c): 0.50
 - ☐ Prefer hard clipping in SAM output (-H)
- NOTE:** bwa-sw performs alignment of long sequencing reads (Sanger or 454). It accepts reads only in FASTA or FASTQ format. Reads should be compiled into single file.
- Buttons:** 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.

SAM output — always save the output file in the SAM format (the option is disabled for *BWA*).

Short reads — each added short read is a small DNA sequence file. At least one read should be added.

You can also configure other parameters.

Index algorithm (-a) — algorithm for constructing BWA-SW index.

It implements three different algorithms:

- *is* — designed for short reads up to ~200bp with low error rate (<3%). It does gapped global alignment w.r.t. reads, supports paired-end reads, and is one of the fastest short read alignment algorithms to date while also visiting suboptimal hits.
- *bwtsw* — is designed for long reads with more errors. It performs heuristic Smith-Waterman-like alignment to find high-scoring local hits. Algorithm implemented in [BWA-SW](#). On low-error short queries, *BWA-SW* is slower and less accurate than the *is* algorithm, but on long reads, it is better.
- *div* — does not work for long genomes.

Score for a match (-a) — score of a match.

Mismatch penalty (-b) — mismatch penalty.

Gap open penalty (-q) — gap open penalty.

Gap extension penalty (-r) — Gap extension penalty. The penalty for a contiguous gap of size k is $q+k*r$.

Band width (-w) - Band width in the banded alignment.

Number of threads (-t) - Number of threads in the multi-threading mode.

Size of chunk of reads (-s) - Maximum SA interval size for initiating a seed. Higher *-s* increases accuracy at the cost of speed.

Score threshold (divided by much score) (-T) - minimum score threshold.

Z-best (-z) - Z-best heuristics. Higher *-z* increases accuracy at the cost of speed.

Number of seeds to start rev alignment (-N) - Minimum number of seeds supporting the resultant alignment to skip reverse alignment.

Mask level (-c) - Coefficient for threshold adjustment according to query length. Given an l -long query, the threshold for a hit to be retained is $a*\max\{T, c*\log(l)\}$.

Prefer hard clipping in SAM output (-H) - use hard clipping in the SAM output. This option may dramatically reduce the redundancy of output when mapping long contig or BAC sequences.

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