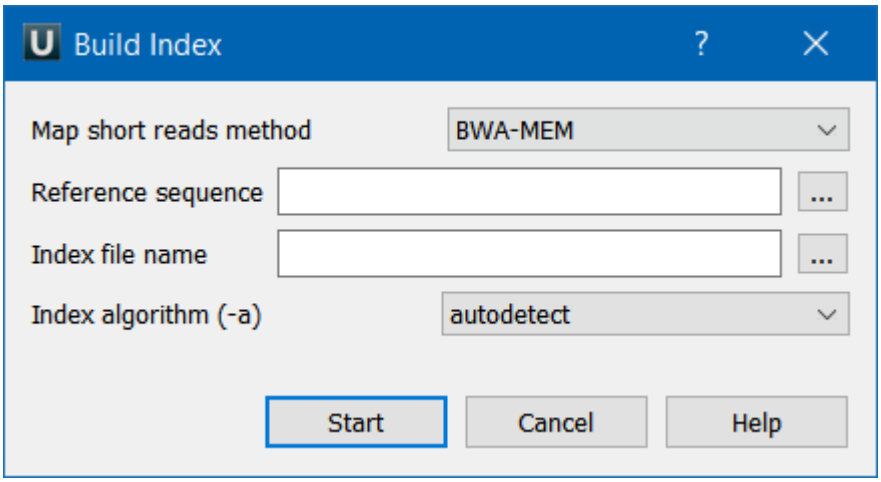
Building Index for BWA-MEM

To build *BWA-MEM* index select the *Tools NGS data analysis Build index for reads mapping* item in the main menu. The *Build Index* dialog will appears. Set the *Map short reads method* parameter to *BWA-MEM*.

The dialog looks as follows:



There are the following parameters:

Reference sequence — DNA sequence to which short reads would be aligned to. This parameter is required.

Index file name — file to save index to. This parameter is required.

Index algorithm (-a) — Algorithm for constructing BWA index. Available options are:

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.

The value *"autodetect"* by default means that the index (one of three) is chosen automatically depending on the length of the sequence.