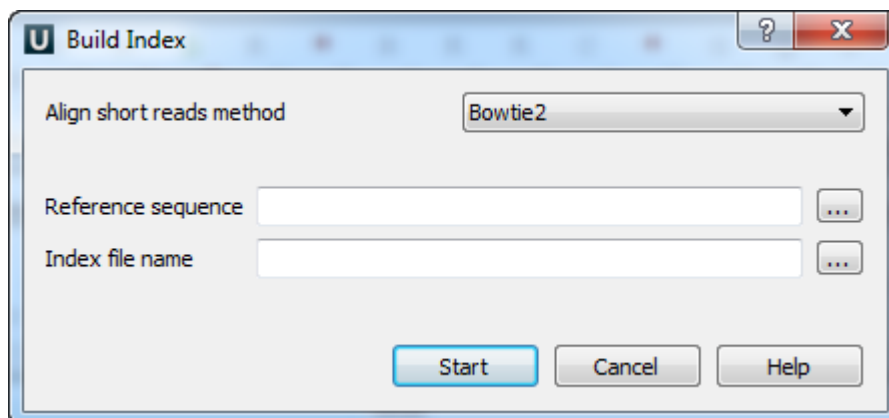


## Building Index for Bowtie 2

To build *Bowtie 2* index select the *Tools > NGS data analysis > Build index for reads mapping* item in the main menu. The *Build Index* dialog appears. Set the *Align short reads method* parameter to *Bowtie 2*.

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* — a file to save the created index to. This parameter is required.