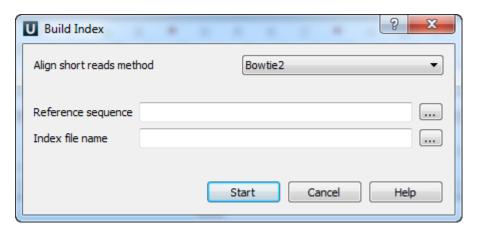
Building Index for Bowtie 2

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.