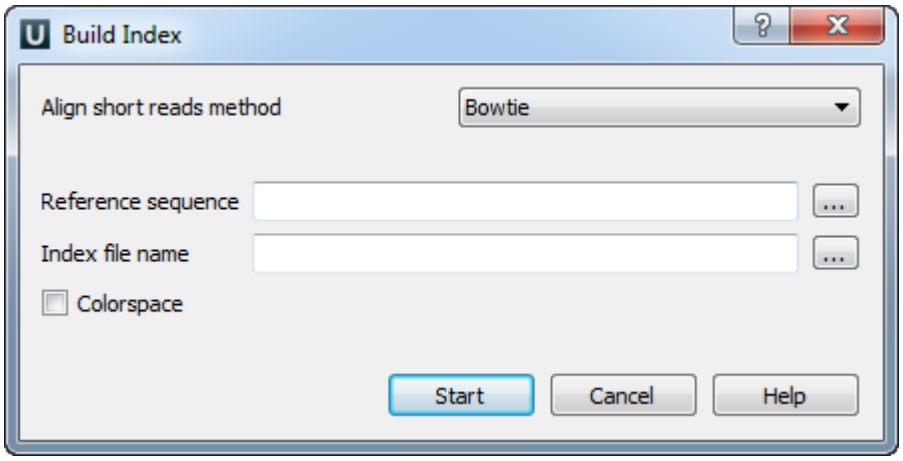
Building Index for Bowtie

To build *Bowtie* 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*.

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.

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).