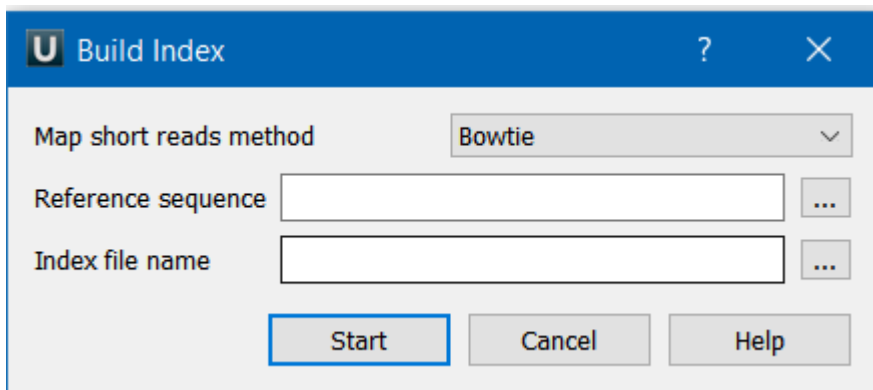


# Building Index for Bowtie

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 *Map short reads method* parameter to *Bowtie*.

The dialog looks as follows:



The screenshot shows a 'Build Index' dialog box. The title bar is blue with a 'U' icon, a question mark, and a close button. The main area is light gray. It contains three input fields: 'Map short reads method' (a dropdown menu set to 'Bowtie'), 'Reference sequence' (a text box with a browse button '...'), and 'Index file name' (a text box with a browse button '...'). At the bottom are three buttons: 'Start' (highlighted with a blue border), 'Cancel', and 'Help'.

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.