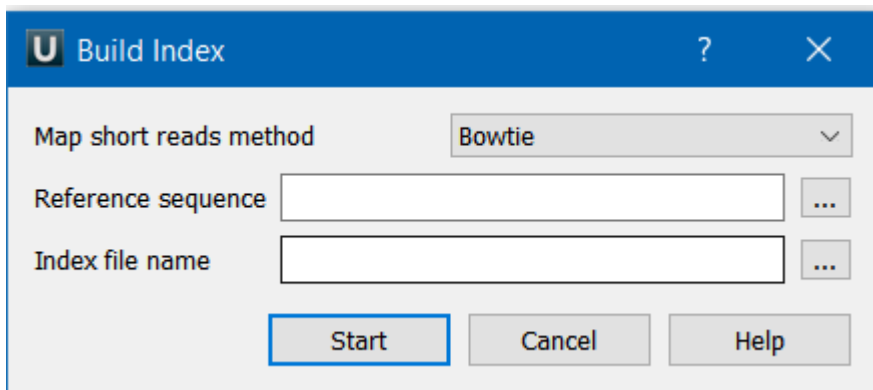


Building Index for Bowtie

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 Windows-style dialog box titled "Build Index". The title bar is blue and contains a small "U" icon, a question mark, and a close button. The main area of the dialog is light gray. It features three labeled input fields: "Map short reads method" with a dropdown menu currently showing "Bowtie", "Reference sequence" with a text box and a browse button (three dots), and "Index file name" with a text box and a browse button (three dots). At the bottom of the dialog, there are three buttons: "Start", "Cancel", and "Help". The "Start" button is highlighted with a blue border.

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.