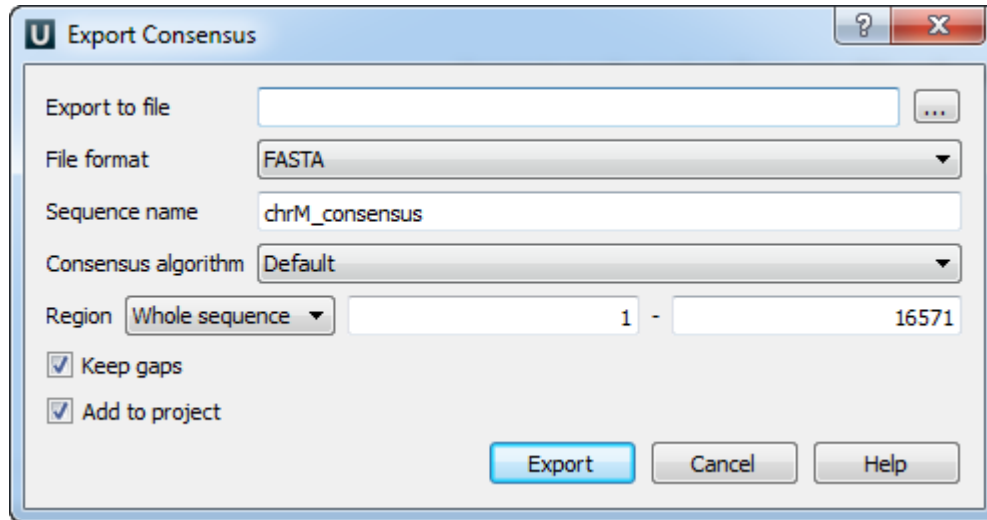


Exporting Consensus

To export a consensus sequence of the assembly, select either the *Export consensus* item in the *Consensus Area* context menu or the *Export Consensus* item in the *Reads Area* context menu.

The *Export Consensus* dialog appears:

The image shows a software dialog box titled "Export Consensus". It has a standard Windows-style title bar with a question mark icon and a close button (X). The dialog contains several input fields and checkboxes. The "Export to file" field is empty with a browse button (three dots) to its right. The "File format" is set to "FASTA" in a dropdown menu. The "Sequence name" field contains the text "chrM_consensus". The "Consensus algorithm" is set to "Default" in a dropdown menu. The "Region" is set to "Whole sequence" in a dropdown menu, followed by two input fields containing "1" and "16571" separated by a hyphen. There are two checked checkboxes: "Keep gaps" and "Add to project". At the bottom right, there are three buttons: "Export" (highlighted in blue), "Cancel", and "Help".

Select a file and the file format. The consensus can be exported to a FASTA, FASTQ, GFF or GenBank file.

Modify, if required, the exported sequence name and choose the [consensus algorithm](#).

The consensus is exported with gaps if the *Keep gaps* check box has been checked.

Also you can select the exporting region. It can be either a *Whole sequence*, a *Visible* region, or a *Custom* region.

When all the parameters are set click the *Export* button.

The consensus sequence is exported to the file and if the *Add to project* check box has been checked it is added to the current *project* and opened.