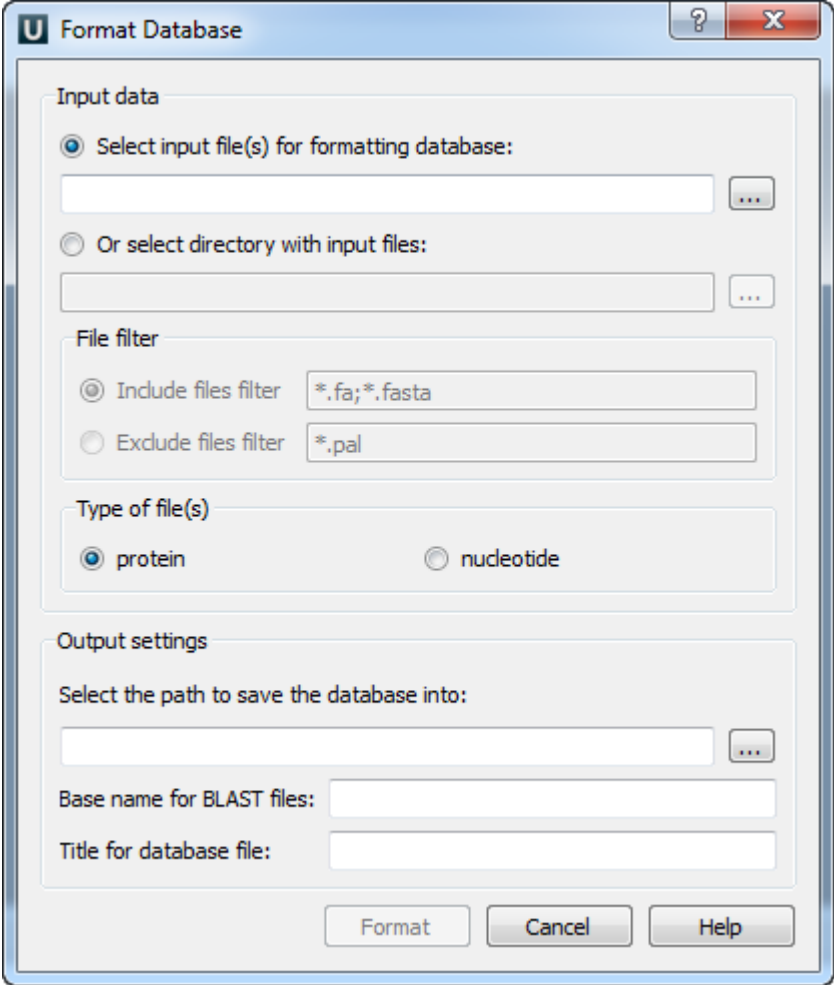


Creating Database

To format a BLAST database do the following:

- If you're using *BLAST* open *Tools BLAST FormatDB*.
- If you're using *BLAST+* open *Tools BLAST BLAST+ make DB*.

The *Format database* dialog appears:



The image shows a Windows-style dialog box titled "Format Database". It has a standard title bar with a question mark icon and a close button (X). The dialog is divided into several sections:

- Input data:** Contains two radio buttons. The first is "Select input file(s) for formatting database:" with an empty text field and a browse button (...). The second is "Or select directory with input files:" with an empty text field and a browse button (...).
- File filter:** Contains two radio buttons. The first is "Include files filter" with a text field containing "*.fa;*.fasta". The second is "Exclude files filter" with a text field containing "*.pal".
- Type of file(s):** Contains two radio buttons: "protein" (selected) and "nucleotide".
- Output settings:** Contains a text field for "Select the path to save the database into:" with a browse button (...). Below this are two more text fields: "Base name for BLAST files:" and "Title for database file:".

At the bottom of the dialog are three buttons: "Format", "Cancel", and "Help".

Here you must select the input files. If all the files you want to use are located in one directory, you can simply select the directory with the files. By default only the files are taken into account with *.fa and *.fasta extensions. You can change this by specifying either *Include files filter* or *Exclude files filter*.

You can choose either *protein* or *nucleotide* type of the files.

Then you must select the path to save the database file and specify a *Base name for BLAST files* and a *Title for database file*.