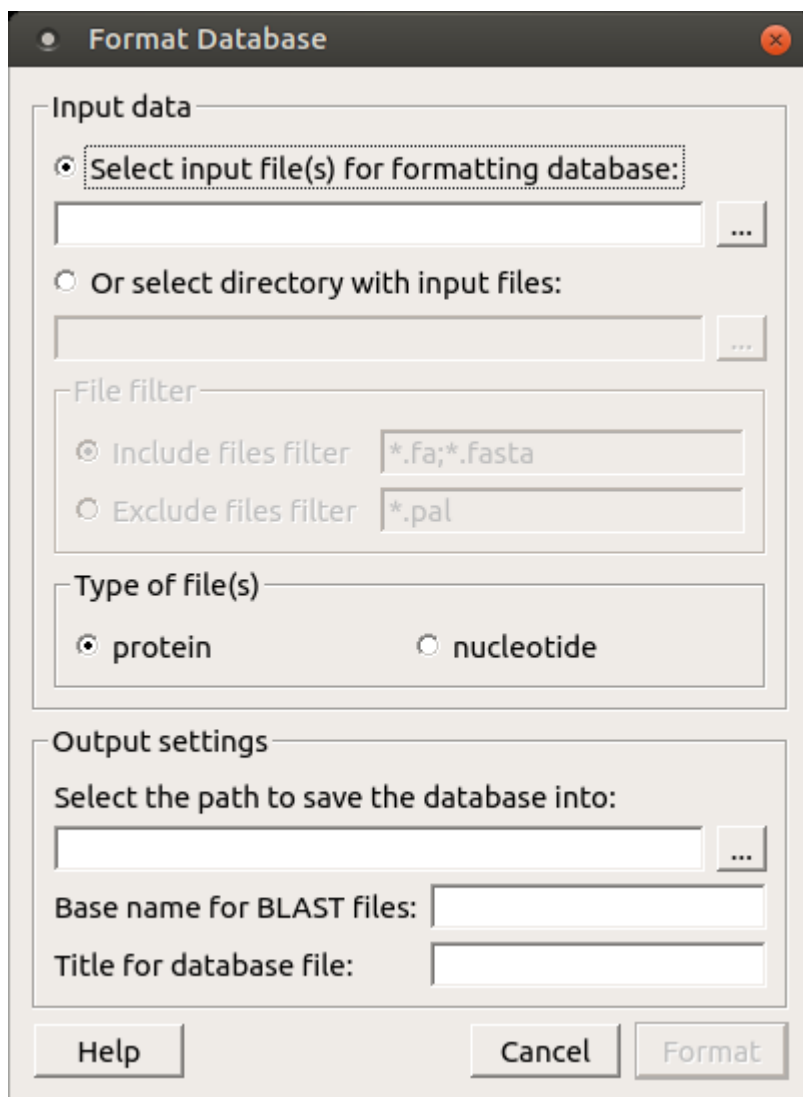


# Creating Database

To format a BLAST database do the following:

- Open *Tools* *BLAST* *BLAST make database*.

The *Make Blast Database* dialog appears:



The **Format Database** dialog box is shown. It has a title bar with a close button. The dialog is divided into two main sections: **Input data** and **Output settings**.

**Input data** section:

- ☒ **Select input file(s) for formatting database:** Below this is a text field with a browse button (three dots).
- ☐ **Or select directory with input files:** Below this is a text field with a browse button (three dots).
- File filter** section:
  - ☒ **Include files filter** with a text field containing `*.fa;*.fasta`.
  - ☐ **Exclude files filter** with a text field containing `*.pal`.
- Type of file(s)** section:
  - ☒ **protein**
  - ☐ **nucleotide**

**Output settings** section:

- Select the path to save the database into:** Below this is a text field with a browse button (three dots).
- Base name for BLAST files:** Below this is a text field.
- Title for database file:** Below this is a text field.

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

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 the database file*.