Making Request to Database

To make a request to a local BLAST database do the following:

- If you're using *BLAST* open *Tools BLAST BLAST Search*.
- If you're using *BLAST+* open Open *Tools BLAST BLAST+ Search*.

If there is a sequence opened you can also initiate the request to a local BLAST database from the *Sequence View*:

- If you're using *BLAST* select the *Analyze Query with BLAST* item in the context menu or in the *Actions* main menu.
- If you're using *BLAST+* select the *Analyze Query with BLAST+* item in the context menu or in the *Actions* main menu.

The *Request to local BLAST database* dialog appears:
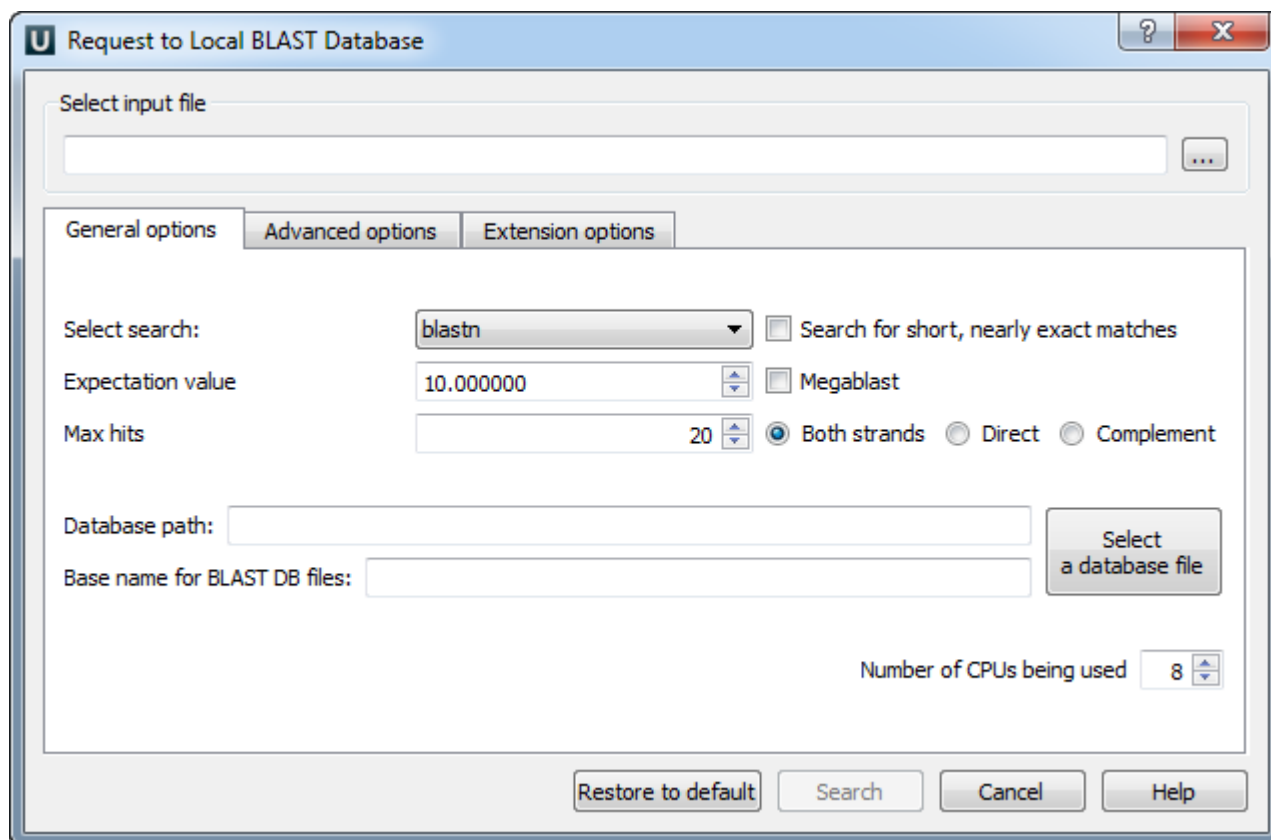
The dialog is very similar to the dialog described in the [Remote BLAST](#) chapter, except the following parameters:

Select input file — this parameter is only presented if the dialog has been opened from the *Tools* main menu. Here you must input a query sequence file that would be used to search the BLAST database.

If the dialog has been opened e.g. using the *Sequence View* context menu, then the currently active sequence is used as a query sequence.

Search type — here you should select the tool you would like to use.

If the query sequence is a nucleotide sequence then *blastn*, *blastx* and *tblastx* items are available. For a protein sequence the items are *blastp* and *tblastn*.

Select database path — path to the database files.

Base name for BLAST DB files — base name for the BLAST database files.

Number of CPUs being used — number of processors to use.

To learn about other parameters, please, refer to the [Remote BLAST](#) chapter.