

Making Request to Database

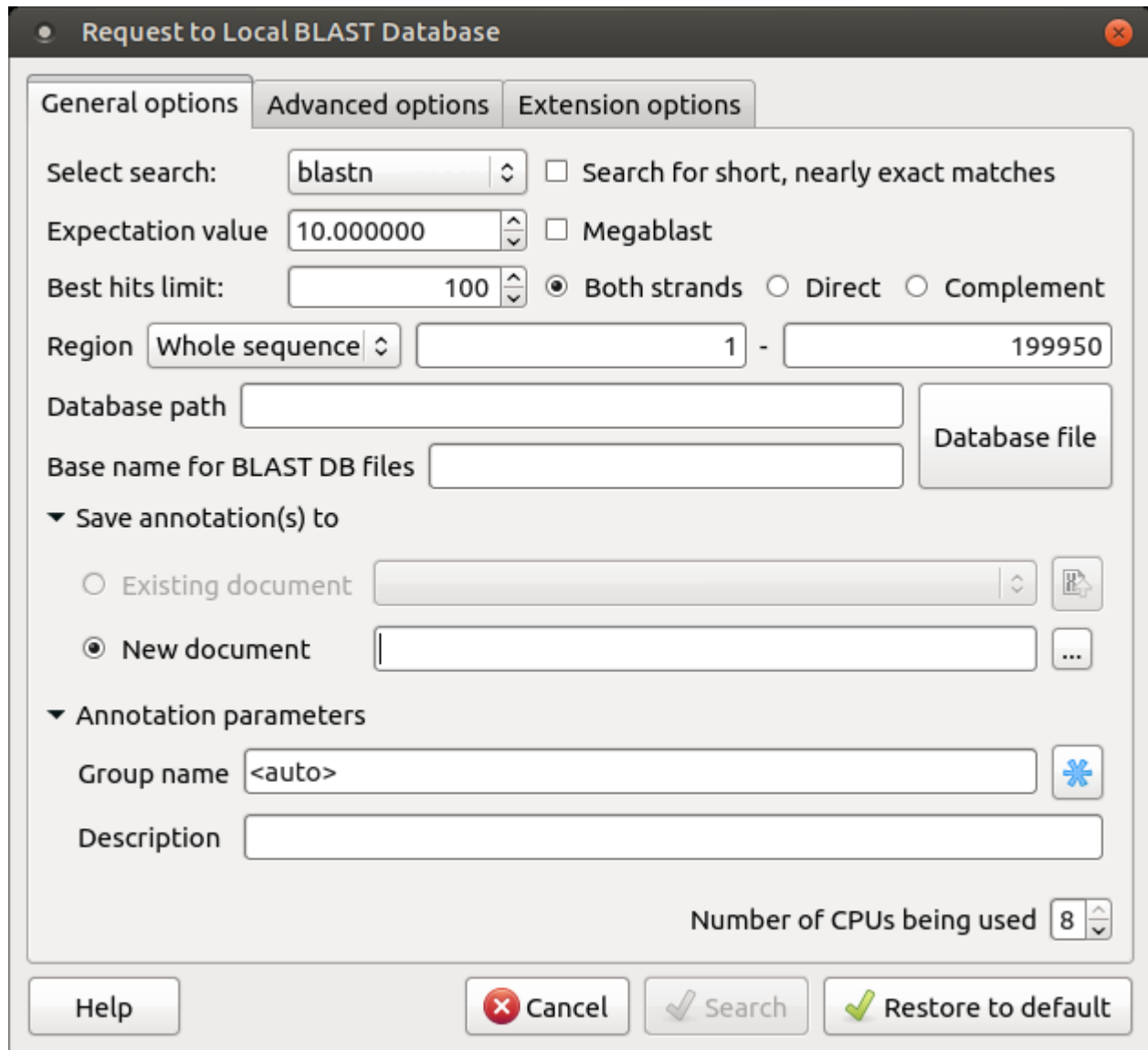
To make a request to a local BLAST database do the following:

- 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*:

- Select the *Analyze Query with BLAST+* item in the context menu or in the *Actions* the main menu.

The *Request to local BLAST+ database* dialog will appear:



The dialog box is titled "Request to Local BLAST Database" and has three tabs: "General options", "Advanced options", and "Extension options". The "General options" tab is active. It contains the following fields and controls:

- Select search:** A dropdown menu with "blastn" selected.
- Expectation value:** A text input field with "10.000000".
- Best hits limit:** A text input field with "100".
- Region:** A dropdown menu with "Whole sequence" selected, followed by a range input "1 - 199950".
- Database path:** A text input field.
- Base name for BLAST DB files:** A text input field.
- Database file:** A button with a folder icon.
- Save annotation(s) to:** A section with two radio buttons: "Existing document" (unselected) and "New document" (selected). The "New document" option has a text input field and a button with three dots.
- Annotation parameters:** A section with two text input fields: "Group name" (containing "<auto>") and "Description".
- Number of CPUs being used:** A text input field with "8".

At the bottom of the dialog are four buttons: "Help", "Cancel", "Search", and "Restore to default".

The following general options are available:

Select search - 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*.

Expectation value - this option specifies the statistical significance threshold for reporting matches against database sequences. Lower expectation thresholds are more stringent, leading to fewer chance matches being reported.

Culling limit - the maximum number of hits that will be shown (not equal to a number of annotations). The maximum available number is 5000.

Search for short, nearly exact matches - automatically adjusts the word size and other parameters to improve results for short queries.

Megablast - select this option to compare queries with closely related sequences. It works best if the target percent identity is 95% or more, but it is very fast.

Database path - path to the database files.

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

You can see the description of the annotation saving parameters [here](#).

The following advanced parameters are available:

Request to Local BLAST Database

General options | **Advanced options** | Extension options

Word size: 11 | Gap costs: 2 2 | Match scores: 1 -3

Filters

- ☐ Low complexity filter
- ☐ Human repeats filter

Masks

- ☐ Mask for lookup table only
- ☐ Mask lower case letters

Help | Cancel | Search | Restore to default

Word size - the size of the subsequence parameter for the initiated search.

Gap costs - costs to create and extend a gap in an alignment. Increasing the Gap costs will result in alignments which decrease the number of Gaps introduced.

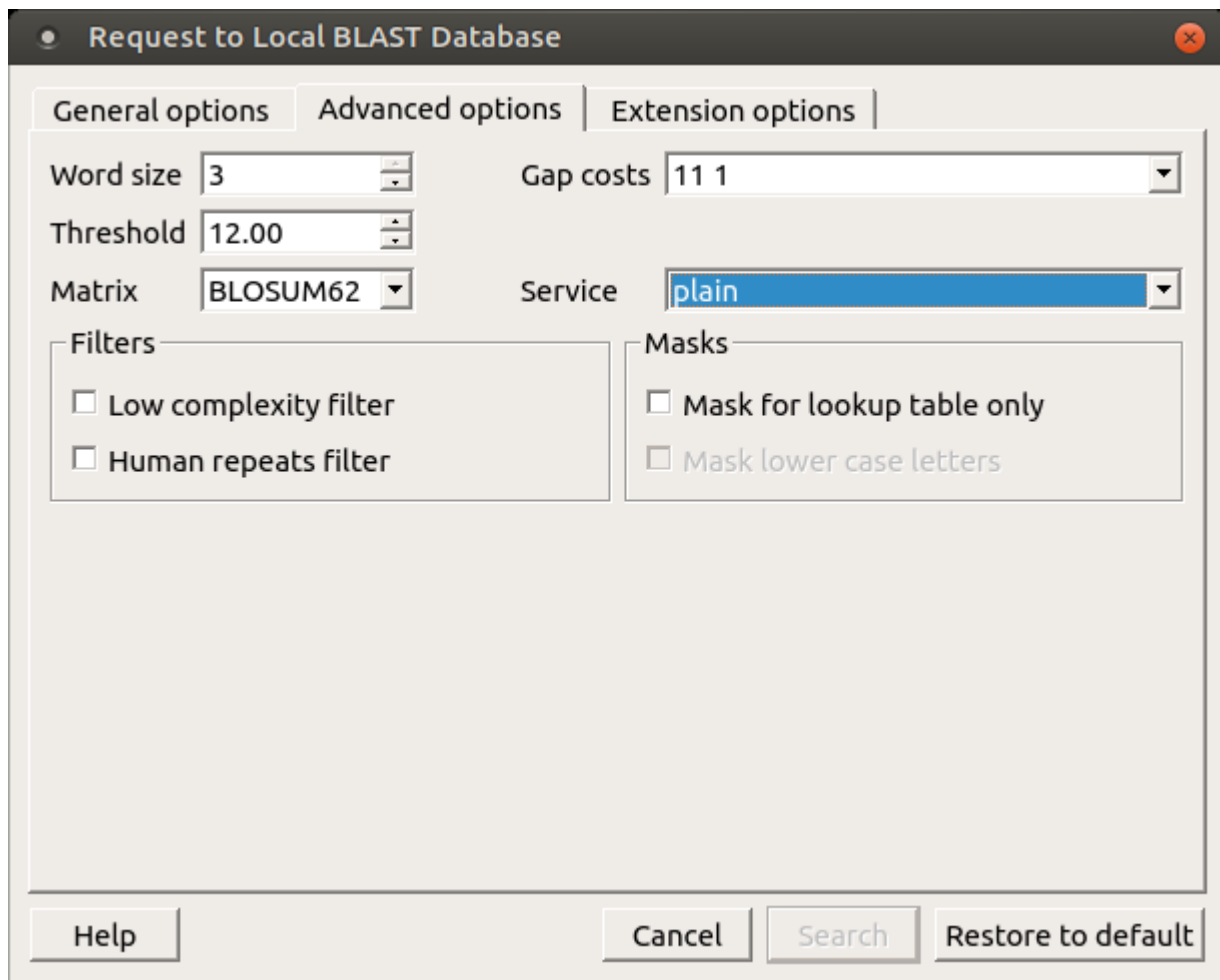
Match scores - reward and penalty for matching and mismatching bases.

Filters - filters for regions of low compositional complexity and repeat elements of the human's genome.

Masks for lookup table only — this option masks only for purposes of constructing the lookup table used by BLAST so that no hits are found based upon low-complexity sequence or repeats (if repeat filter is checked).

Mask lower case letters — with this option selected you can cut and paste a FASTA sequence in upper case characters and denote areas you would like filtered with lower case.

The view of the *Advanced options* tab depends on the selected search. For the *blastn* search, it looks like in the picture above. When the *blastx* search is selected in the general options, the view of the *Advanced options* tab is the following:



The image shows a dialog box titled "Request to Local BLAST Database". It has three tabs: "General options", "Advanced options", and "Extension options". The "General options" tab is selected. It contains the following settings:

- Word size: 3
- Threshold: 12.00
- Matrix: BLOSUM62
- Gap costs: 11 1
- Service: plain

There are two sections with checkboxes:

- Filters:**
 - ☐ Low complexity filter
 - ☐ Human repeats filter
- Masks:**
 - ☐ Mask for lookup table only
 - ☐ Mask lower case letters

At the bottom, there are four buttons: "Help", "Cancel", "Search", and "Restore to default".

As you can see there is no *Match scores* option, but there are *Threshold*, *Matrix*, *Composition-based statistics* and *Service* options.

Threshold - threshold for extending hits.

Matrix — key element in evaluating the quality of pair-wise sequence alignment is the “substitution matrix”, which assigns a score for aligning any possible pair of residues.

Service — blastp service which needs to be performed: plain, psi or phi.

Composition-based statistics - composition-based statistics.

When the *tblastx* search is selected in the general options, the view of the *Advanced options* tab is the following:

Request to Local BLAST Database

General options | Advanced options | Extension options

Word size

Threshold

Matrix Service

Filters

- ☐ Low complexity filter
- ☐ Human repeats filter

Masks

- ☐ Mask for lookup table only
- ☐ Mask lower case letters

Help Cancel Search Restore to default

The following extension options are available:

Request to Local BLAST Database

General options | Advanced options | Extension options

X dropoff value (in bits)

For gapped alignment 0

For ungapped extensions 7.00

For final gapped alignment 0

Multiple Hits Window Size 40

☒ Perform gapped alignment

Help Cancel Search Restore to default

For gapped alignment - X dropoff value (in bits) for gapped alignment.

For ungapped alignment - X dropoff value (in bits) for ungapped alignment.

For final gapped alignment - X dropoff value (in bits) for final gapped alignment.

Multiple hits window size - multiple hits window size.

Perform gapped alignment - performs gapped alignment.