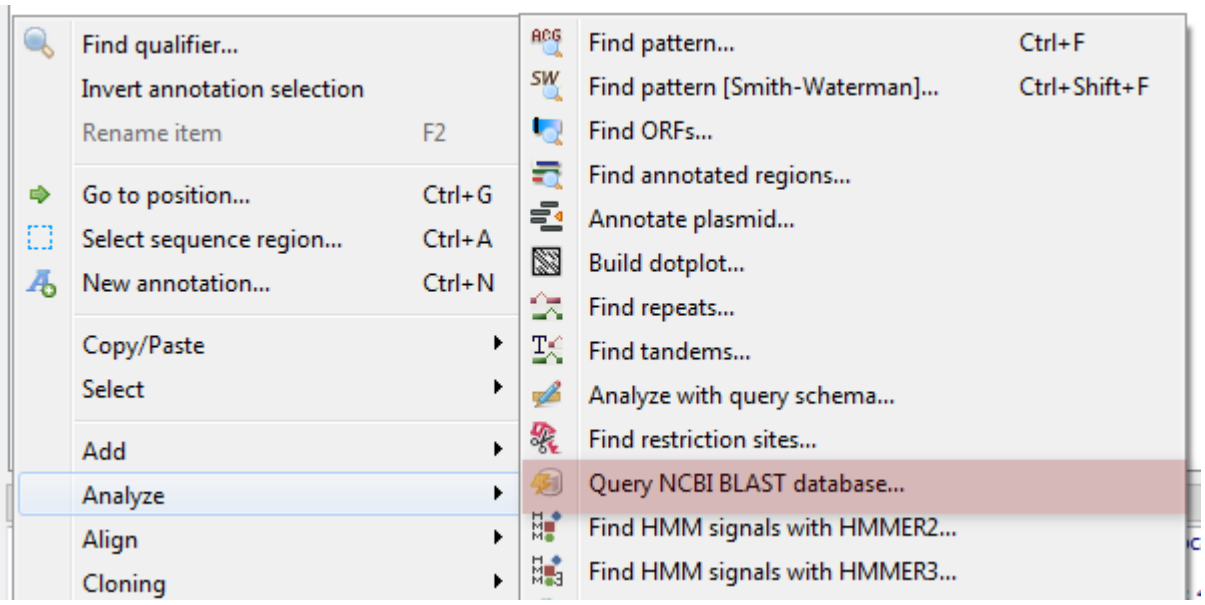
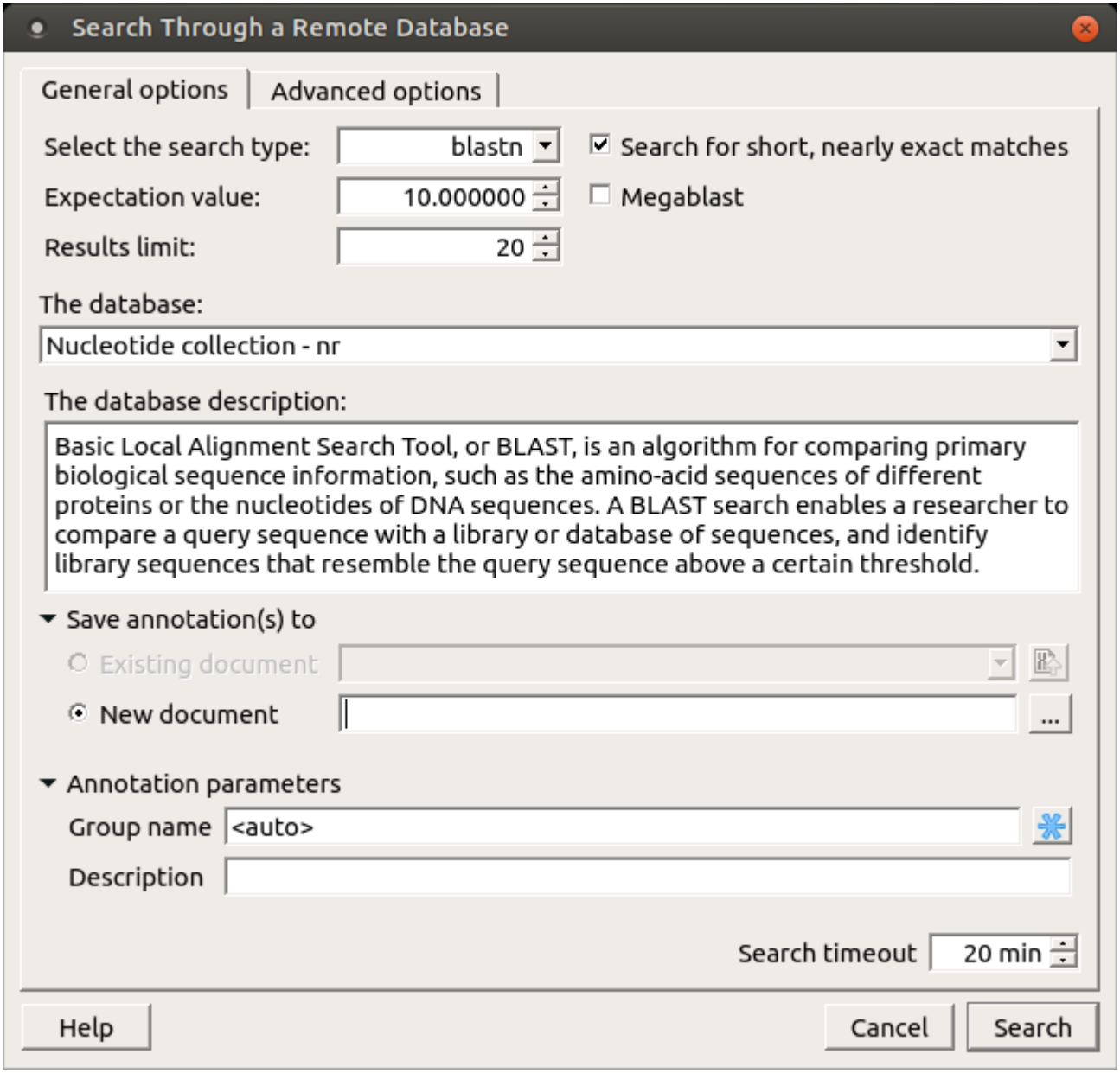
Remote BLAST

The *Remote BLAST* plugin provides a capability to annotate sequences with information stored in the NCBI BLAST remote database.

To perform a remote database search open a *Sequence View*, select a sequence region to analyze and click the *Analyze Query NCBI BLAST database* co ntext menu item. If a region is not selected the whole sequence will be analyzed.



The following dialog will appear where you can choose the search options:



General options are:

Select the search type — in the remote databases the *blastn* search is used for nucleotide sequences, *blastp* and *cdd* searches are used for amino sequences.

UGENE also provides a way to use *blastp* and *cdd* searches for nucleotide sequences. This is achieved by translating the nucleotide sequence into the amino sequences.

When a sequence is translated the translation table from the active *Sequence View* is used. Finally, all 6 translations are used to query the remote database with the selected *blastp* or *cdd* search.

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

Max hits — the maximum number of hits that will be shown (not equal to number of annotations). The maximum availablle number is 5000.

Database — the target database.

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

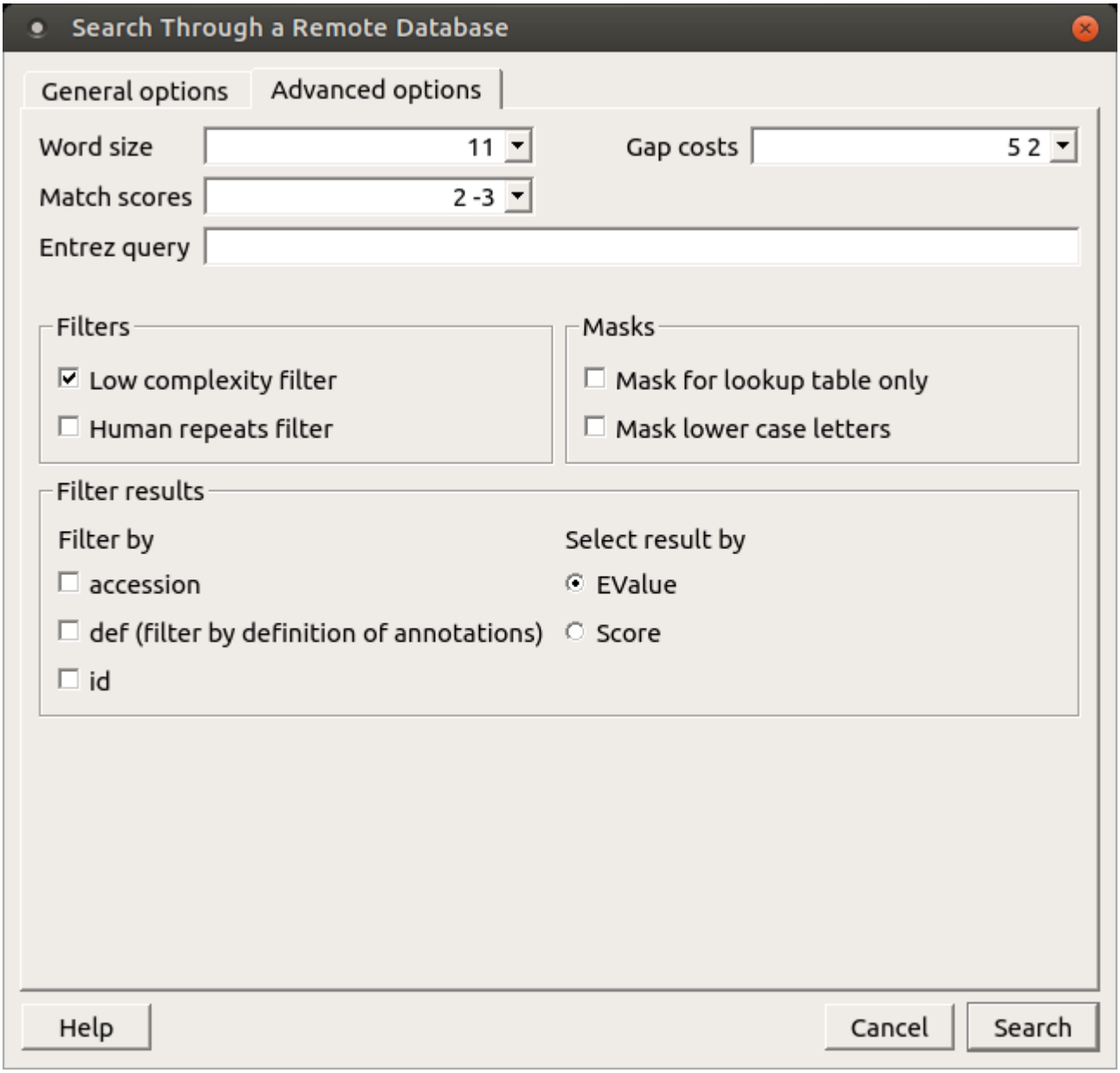
Megablast — select this option to compare query with closely related sequences. It works best if the target percent identity is 95% or more, but it is very fast.

You can see the description of the annotation saving parameters *here*.

Search timeout — the remote task terminated if the timeout is reached.

> There is a little difference in default values of parameters between NCBI Nucleotide BLAST web interface and UGENE:
>
> - The web interface uses the *megablast* option by default: the search is fast, but only highly similar sequences are found.
> - UGENE ignores the option by default: the search may take more time, but all somewhat similar sequences are found.
>
> Check the *Megablast* option, if you want exactly the same results to be found in UGENE as you had in the NCBI web interface.

Also there is *Advanced options* tab:



The view of the *Advanced options* tab depends on the selected search. For the *blastn* search it looks like on the picture above.

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.

Entrez query — a BLAST search can be limited to the result of an *Entrez query* against the database chosen. This restricts the search to a subset of entries from that database fitting the requirement of the *Entrez query*. Examples are given below:

protease NOT hiv1[organism] — this will limit a BLAST search to all proteases, except those in HIV 1.

1000:2000[slen] — this limits the search to entries with lengths between 1000 to 2000 bases for nucleotide entries, or 1000 to 2000 residues for protein entries.

Mus musculus[organism] AND biomol_mrna[properties] — this limits the search to mouse mRNA entries in the database. For common organisms, one can also select from the pulldown menu.

10000:100000[mlwt] — this is yet another example usage, which limits the search to protein sequences with calculated molecular weight between 10 kD to 100 kD.

src specimen voucher[properties] — this limits the search to entries that are annotated with a /specimen_voucher qualifier on the source feature.

all[filter] NOT enviromnental sample[filter] NOT metagenomes[orgn] — this excludes sequences from metagenome studies and uncultured sequences from anonymous environmental sample studies.

For help in constructing *Entrez queries* see the Entrez Help document.

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

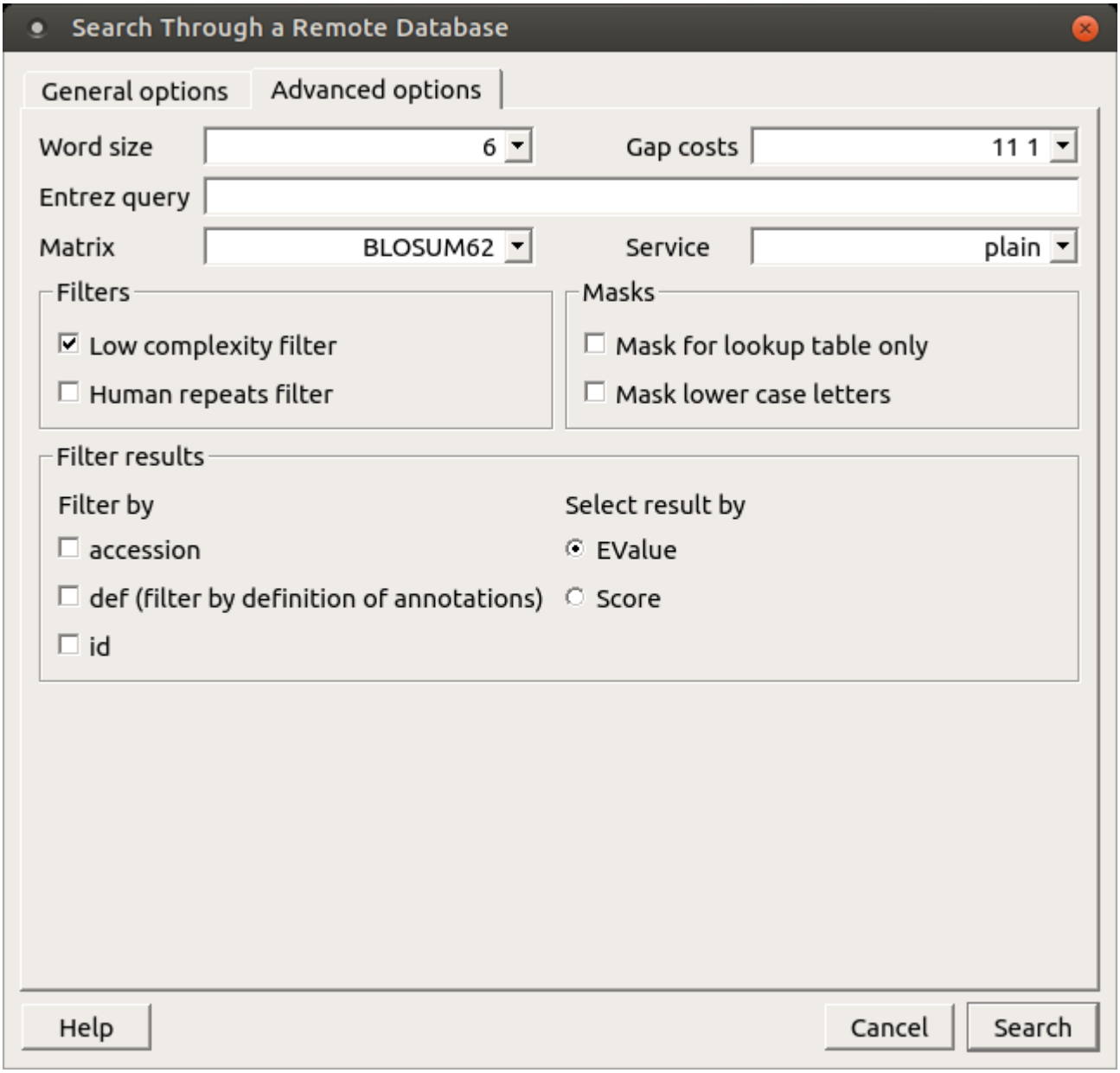
Masks for lookup table only — this option masks only for purposes of constructing the lookup table used by BLAST so that no hits are found based upon low-complexity sequence or repeats (if repeat filter is checked).

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.

Filter by — filters results by accession, by definition of annotations or by id.

Select result by — selects results by EValue or by score.

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



As you can see there is no *Match scores* option, but there are *Matrix* and *Service* options.

> *Matrix* — key element in evaluating the quality of a 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.

The *Advanced options* tab is not available when the *cdd* search is selected.

- Exporting BLAST Results to Alignment
- Fetching Sequences from Remote Database