Tutorial 4 – BLAST Searching the CHO Genome

The CHO BLAST server can be accessed in two ways: from the CHO-K1 genome search page and by clicking on the BLAST button on the home page. A link to the NCBI BLAST web server is also provided on the CHO-K1 genome search page .
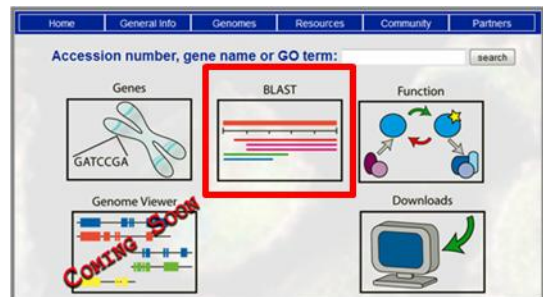
BLAST searching the CHO-K1 Genome

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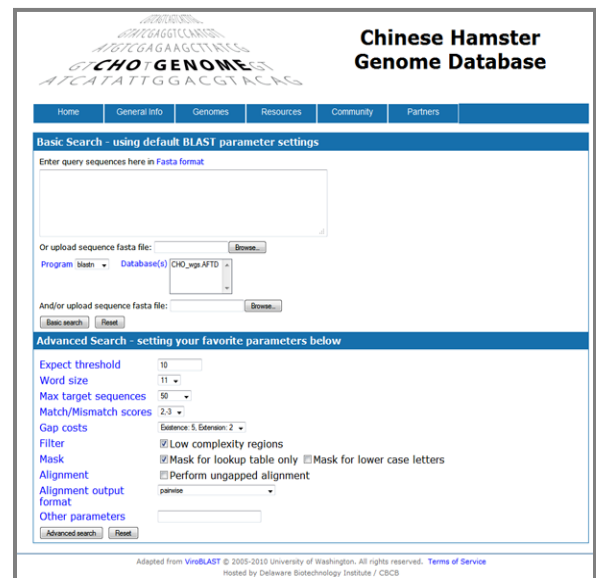Click on the BLAST server link on the CHO-K1 genome search page

Select the BLAST icon on the home page

2) The CHO BLAST page allows for basic and advanced BLAST searches against the CHO-K1 genome database.
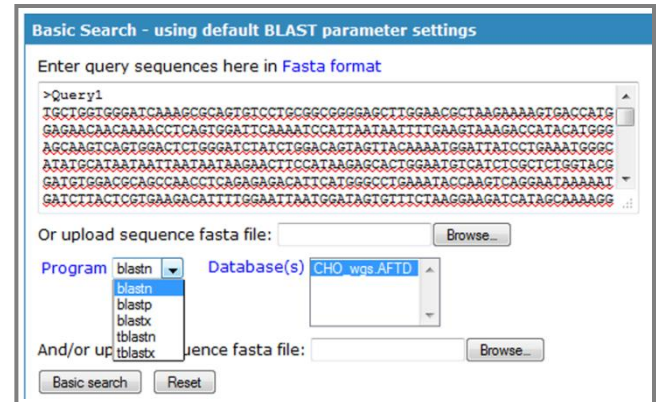
Clicking on the Program and Database(s) links will provide a brief description of the programs and databases currently available for BLAST searching.

3) Query sequences in FASTA format can be pasted into the search box at the top of the page or by uploading sequences in a FASTA file. Multiple query sequences may be entered at once.

The BLAST program to use and database to search are then selected from the currently available options.

To BLAST the CHO-K1 genome database, select the "blastn" program and the "CHO_wgs_AFTD" database.
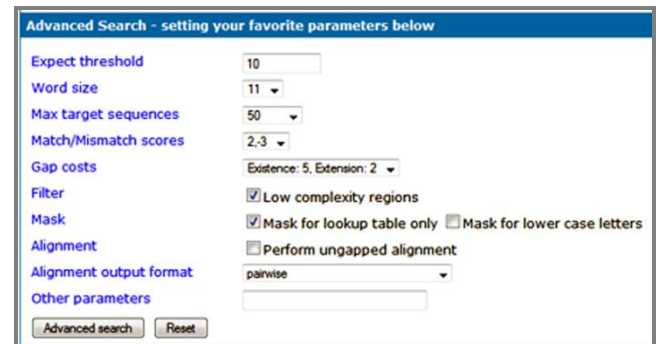
To perform a basic BLAST search, click the "Basic search" button once all information is entered.

4) In the Advanced Search sections, the BLAST parameters can be varied to perform an advanced BLAST search.

Clicking on the highlighted blue terms (such as Expect threshold) will provide a brief description of each the advanced search parameters that can be varied.

To perform an advanced BLAST search, click the "Advanced search" button once all information is entered.
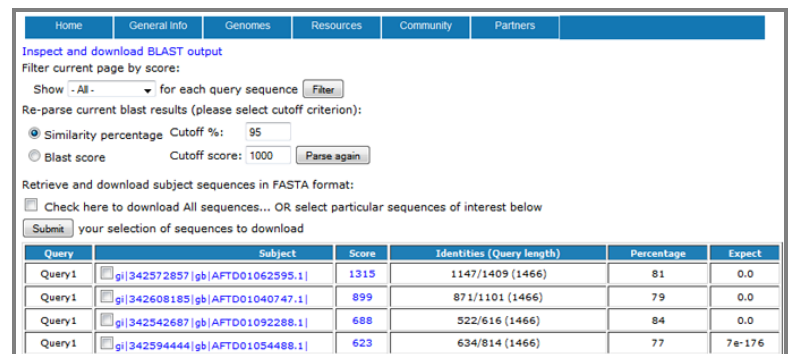
5) The results of the BLAST alignment are summarized in a table with the query sequence name, the subject sequence name, the bit score, the identity percentage, and the *E*-value.

The results can be filtered by score (showing only top 1, 5, or 10 alignments), by similarity percentage or by BLAST score.

After entering the filter parameter, click either the "Filter" of the "Parse again" buttons to refresh the results table.

To inspect all the BLAST pair-wise alignments, click on Inspect and download BLAST output.
To view the pair-wise alignment for a specific alignment, click on the value in the Score column for any alignment (such as 1315).

To view the GenBank entry for each subject sequence, click on the sequence name in the Subject column (such as gi|342572857|gb|AFTD01062595.1|).

6) To download the subject sequences, click the "Check here to download all sequences" box or select individual subject sequences from the table below and then hit the "Submit" button.   This will download a text file of the selected sequences in FASTA format in a new window.

If the BLAST search was against a genomic database (such as the CHO WGS contigs), the subject sequences will be the WGS genomic contig sequences.

6) Multiple query sequences can be BLAST searched at once.   The results from all query sequences will be displayed in a single results table. To inspect all the BLAST pair-wise alignments, click on Inspect and download BLAST output. Links provided at the top of the page can be used to quickly navigate to the alignment results for an individual query sequence.

BLAST searching the CHO-K1 Genome at NCBI

1) A link to the NCBI BLAST web server is also provided on the CHO-K1 genome search page. To BLAST the CHO-K1 genome using the NCBI BLAST web server, select the "Cricetulus griseus WGS" database under the "Choose Search Set" menu.