

MultiGeneBlast

Combined BLAST searches to find homologous operons and gene clusters

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Contents

1	Installation	4
1.1	Prerequisites	4
1.2	Source code.....	4
1.3	Installation of MultiGeneBlast.....	5
2	Third Party Software	5
2.1	Included Open Source Software	6
3	Information for General Use	7
3.1	Accepted input file formats	7
3.2	Specifying the settings for your MultiGeneBlast run Error! Bookmark not defined.	
3.3	MultiGeneBlast output	7
4	Command-line Usage	8
4.1	Basic usage.....	8
4.2	General settings	8
5	License.....	9

1 Installation

1.1 Prerequisites

1.1.1 General prerequisites

Operating system: Mac OS X 10.6+, LINUX or Windows XP/Vista/7

Internet Browser: Firefox >3.x, Internet Explorer >9.x, Safari, Google Chrome or Opera

For Windows users: the [Microsoft Visual C++ redistributable package](#) is required to run MultiGeneBlast.

To run sequences against the GenBank database, we recommend to use a system with at least two CPU cores and > 2 GB RAM.

1.1.2 Databases

A default GenBank database for MultiGeneBlast is available for download.

- GenBank sequence database for MultiGeneBlast
This is a default database that encompasses all sequences from the BCT, ENV, PAT, PHG, PLN, SYN, CON and WGS divisions of GenBank.
Download URL: http://gbic.biol.rug.nl/genbank_mf.tar.gz

1.2 Source code

This package provides binaries as well as source code of MultiGeneBlast. You are free to modify the source code under the terms of the supplied license and run it using a local Python installation.

1.3 Installation of MultiGeneBlast

1.3.1 Windows

Go to the [MultiGeneBlast download page](#), download the file with the name ending on `'_win32.exe'` and execute it. The installer will guide you through the installation process.

1.3.2 Mac OS X

If you intend to use the GUI, go to the [MultiGeneBlast download page](#), download the file with the name ending on `'_macosx.dmg'` and open it. Then simply drag the MultiGeneBlast application bundle to your 'Applications' folder (at the right bottom of your screen).

If you also want to use MultiGeneBlast from the command-line, download the file with the name ending on `'_macosx_commandline.zip'` and extract it in a directory to which you have full writing access (e.g., your user home directory). To access the GUI, run the `'mgb_gui'` executable. To run MultiGeneBlast from the command line, add the installation directory to your `$PATH` environment variable and run the `'multigeneblast'` executable.

1.3.3 LINUX

Go to the [MultiGeneBlast download page](#), download the file with the name ending on `'_linux.tar.gz'` and extract it in your user home folder. To access the GUI, run the `'mgb_gui'` executable. To run MultiGeneBlast from the command line, add the installation directory to your `$PATH` environment variable and run the `'multigeneblast'` executable.

2 Third Party Software

2.1 Included Open Source Software

MultiGeneBlast is powered by several open source tools and/or modules: NCBI BLAST+, Muscle 3, Python, PySVG, jQuery and jQuery SVG. The licenses of these softwares are included in the "licenses" folder within the antiSMASH installation directory.

- **NCBI BLAST**

Binaries for different platforms and documentation available at

http://blast.ncbi.nlm.nih.gov/Blast.cgi?CMD=Web&PAGE_TYPE=BlastDocs&DOC_TYPE=Download

Source code available in the NCBI C++ toolkit at

<http://www.ncbi.nlm.nih.gov/blast/developer.shtml>

- **Muscle 3**

Source code, binaries for different platforms and documentation available at

<http://www.drive5.com/muscle/downloads.htm>

- **Python**

Source code and binaries for different platforms available at

<http://www.python.org>

- **PySVG**

Python modules available at

<http://codeboje.de/pysvg/>

- **jQuery**

Available at

<http://jquery.com>

- **jQuery SVG**

Available at

<http://keith-wood.name/svg.html>

3 Information for General Use

The stand-alone version of MultiGeneBlast provides a graphical user interface for specifying input and options.

3.1 Accepted input file formats

3.1.1 GBK/EMBL files

The ideal input for a standard homology search with MultiGeneBlast is an annotated nucleotide file in Genbank format or EMBL format. The file names must end at either .gbk/.gb or .embl/emb.

General information on the EMBL format is available at <http://www.ebi.ac.uk/help/formats.html#EMBL> .

General information on the GenBank format is available at <http://www.ncbi.nlm.nih.gov/Sitemap/samplerecord.html> .

3.1.2 FASTA files

For architecture searches, you need to provide a FASTA file containing a set of multiple amino acid sequences.

3.2 MultiGeneBlast output

All output of your MultiGeneBlast run is saved in a subfolder within the MultiGeneBlast installation directory, with the name that was provided.

3.2.1 Interactive XHTML output

The output of the MultiGeneBlast analysis is organized in an interactive XHTML page with SVG graphics. The antiSMASH GUI will attempt to open this XHTML file automatically for you after finishing the calculation.

4 Command-line Usage

MultiGeneBlast can also be run from the command line.

4.1 Basic usage

The general way to run MultiGeneBlast is

```
multigeneblast <options>
```

4.2 General settings

Several options are available from the command line to set up a MultiGeneBlast run.

In the options below, "<x>" represents an integer number:

-in <file name>	: Query file name: GBK/EMBL file for homology search, FASTA file with multiple protein sequences for architecture search
-from <x>	: Start position of query region
-to <x>	: End position of query region
-genes <acc;acc;...>	: Accession codes of genes constituting query multigene module
-out <y/n>	: Output folder in which results will be stored
-db <db name>	: Blast database to be queried (default: genbank_mf)
-cores <x>	: Number of parallel CPUs to use for threading (default: all)
-minseqcov <x>	: Minimal % coverage of a Blast hit on hit protein sequence to be taken into account (default: 25)
-minpercid <x>	: Minimal % identity of a Blast hit on hit protein sequence to be taken into account (default: 30)
-distancekb <x>	: Maximum kb distance between two blast hits to be counted as belonging to the same locus (default: 10)
-syntenyweight <x>	: Weight of synteny conservation in hit sorting score (default: 0.5)
-muscle <y/n>	: generate Muscle multiple sequence alignments of all hits of each input gene (default: n)
-outpages <x>	: Maximum number of output pages (with 50 hits each) to be generated (default: 5)
-screenwidth <x>	: Screen width of output XHTML page (default: 1024)

5 License

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Note: This license accounts for MultiGeneBlast programs only.

As MultiGeneBlast relies on analysis data generated by 3rd party software (e.g. BLAST, HMMer) with own, separate licensing terms, you have to respect their licensing terms if you plan to use these 3rd party programs. These licenses are included in the download and can be found in the "Licenses" folder within the directory in which you haven chosen to install MultiGeneBlast.

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