

NcbiExplorer

Summary

NcbiExplorer is a Java Desktop application to query the NCBI nucleotide database and automatically download sequences into a multi-FASTA file. The application features an internationalised GUI.

Version

Version 0.4



Manual

Program description

Using the GUI, users can enter up to 10 query strings for three query fields ([Full Text], [Gene Name], [Organism]) and linearly link them with either one of the three Boolean operators AND, OR, NOT.

Using the Esearch API, the NCBI nucleotide database is searched to obtain relevant entries up to a maximum of RETMAX=100000.

Then, the received entries are downloaded from the NCBI nucleotide database one-by-one and the sequences saved in a user-specified output file in multi-FASTA format. The FASTA header is formatted as per:

```
>{Genus}_{species}_{accession_number}
```

Exceutable jar-archive

The software is provided as a pre-compiled jar-archive that has been digitally signed.

The integrity of the archive can be checked using the following command:

```
jarsigner -verify {application-name}.jar
```

which should return **jar verified**. if successful.

Running the software under Windows and Mac OS

The stand-alone Java application packaged in the jar-archive can be xecuted by a **left mouse-button double-click**.

Running the software under Linux

Depending on the Java installation, the application might run by typing

```
java -jar {application-name}.jar
```

Alternatively, a shell script can be setup, e.g.:

```
#!/bin/csh -f
setenv JAVA {path-to-java-bin-directory}/java
setenv CLASSPATH {path-to-pcsb-application-file}/{application-name}.jar
$JAVA {application-name} $*
```