How to use getSequenceInfo (English version)

This is a user manual showing students and researchers how to use the getSequenceInfo software tool (https://github.com/dcouvin/getSequenceInfo) provided as both a command line interface (CLI) and a graphical user interface (GUI).

Keywords: Bioinformatics, DNA sequence, GenBank, RefSeq, European Nucleotide Archive (ENA), Perl programming language, BioPerl, Annotation, FASTA, FASTQ, GC-content, Statistics, NucleScore

Introduction

getSequenceInfo is a Perl script allowing to easily download sequence data from public repositories such as the NCBI's GenBank and RefSeq, as well as the European Nucleotide Archive or ENA (hosted at the European Bioinformatics Institute). This Perl software programme allows users to download sequence data and statistics in various formats (FASTA, FASTQ, Genbank full format, XLS, TSV, HTML). The getSequenceInfo software tool can either be used as a command line programme or as a graphical user interface (GUI).

Installation

Perl is usually already installed on Unix systems (such as Linux and MacOS). However, for people using the Windows operating system, the language can be installed with Strawberry Perl (http://strawberryperl.com/).
This video shows you how to install Strawberry Perl:

If necessary, please see information on how to launch or how to use the Command Prompt in Windows. When using a Unix OS (Linux or Mac), Perl is generally already installed. But if it is not the case, you can see this page for its installation. You can follow this wiki page for information about the Shell Prompt. You can then check the installation by typing the following command:

```
perl -v
```

Users can then install required Perl modules (please note that these modules are already available within the provided installation files "**installer_Unix.sh**" and "**installer_Windows.bat**"):
- Tk
- BioPerl
- Date::Calc
- Bio::SeqIO
- LWP::Simple
- Data::Dumper
- IO::Uncompress::Gunzip
- IO::File
- Getopt::Long
- Net::FTP

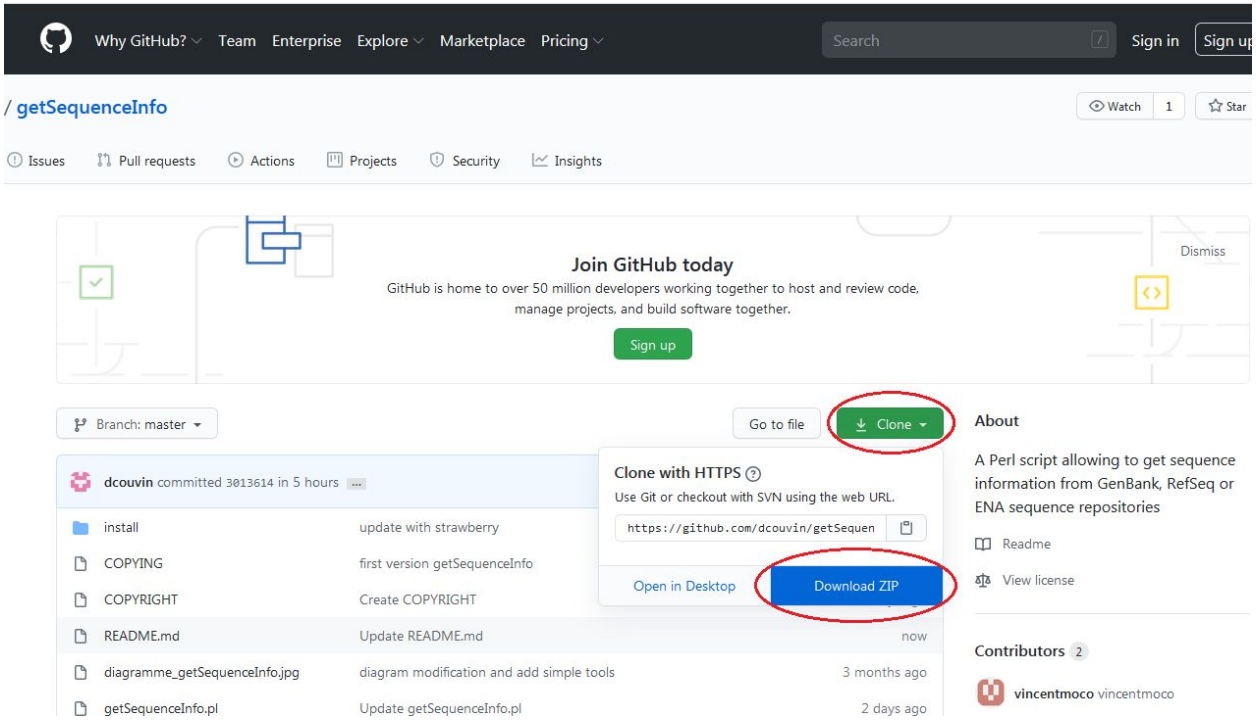
Each Perl module can be installed using the **cpan** or the **cpanm** command as follows:

- cpan -f -i <Module::Name>
- cpanm <Module::Name>

Please note that <Module::Name> should be replaced by the required Perl module (e.g. cpan -f -i Date::Calc or cpanm Date::Calc).
Further details concerning the installation of Perl modules are available at the webpage [How to install CPAN modules](#).

Download or clone getSequenceInfo

The tool can be downloaded or cloned from the git repository (https://github.com/dcouvin/getSequenceInfo).
The “Clone” button then the “Download ZIP” button can be used to download the repository:



Snapshot of the GitHub page allowing you to download the tool.

Otherwise, you can clone the tool using the “git clone” command. Please note that git (https://git-scm.com/) must be installed in your system to do this:

```
git clone https://github.com/dcouvin/getSequenceInfo.git
```

Once the archive has been cloned or downloaded, then unzipped in the place of your choice, you can go to the getSequenceInfo repository by typing the following command:

```
cd getSequenceInfo
```

Users can also navigate through classic windows to access the tool.

Launching the installation on Unix or Windows systems

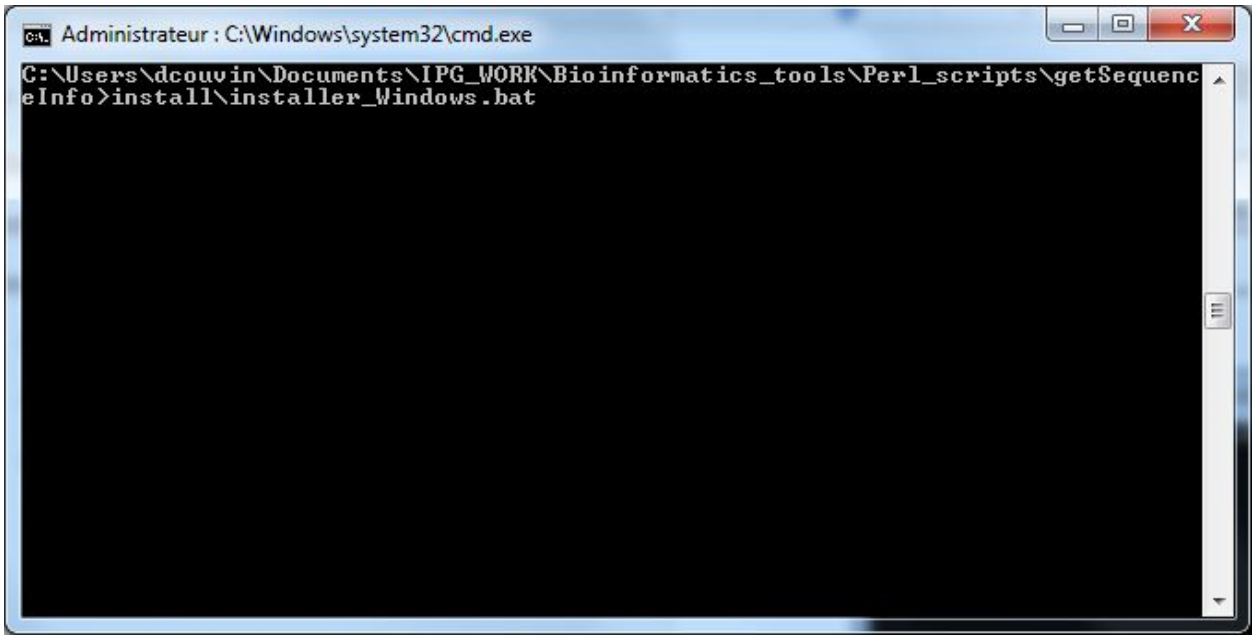
In order to install the getSequenceInfo software tool, the user must be placed into the corresponding uncompressed archive repository (getSequenceInfo).

Installation on Linux or MacOS (Unix system) Shell Prompt

```
bash install/installer_Unix.sh
```

Installation on Microsoft Windows system Command Prompt. Users can also install the tool by running the installer_Windows.bat file (double-click)

```
install\installer_Windows.bat
```



Snapshot of the Windows installation using the command line.

Installation instructions can also be provided when running the getSequenceInfo.pl Perl script.

Content of the getSequenceInfo archive

The archive contains the following files and folders:

- **install** (a folder containing the installation files “**installer_Unix.sh**” and “**installer_Windows.bat**”)
- **simple_tools** (a folder containing other Perl scripts dedicated to the execution of specific tasks)
- **COPYING** and **COPYRIGHT** (GPLv3 licence files)
- **README.md** (a simplified README file)
- **workflow.png** (a diagram representing the main functionalities of the software tool)
- **getSequenceInfo.pl** (main Perl program)
- **getSequenceInfoGUI.pl** (Graphical User Interface (GUI) version of the program)
- **launcher_Windows.bat** (executable file allowing to launch the GUI from Windows)
- **logo_getSequenceInfo.png** (a logo representing the tool)
- **User_manual.pdf** (this user manual)

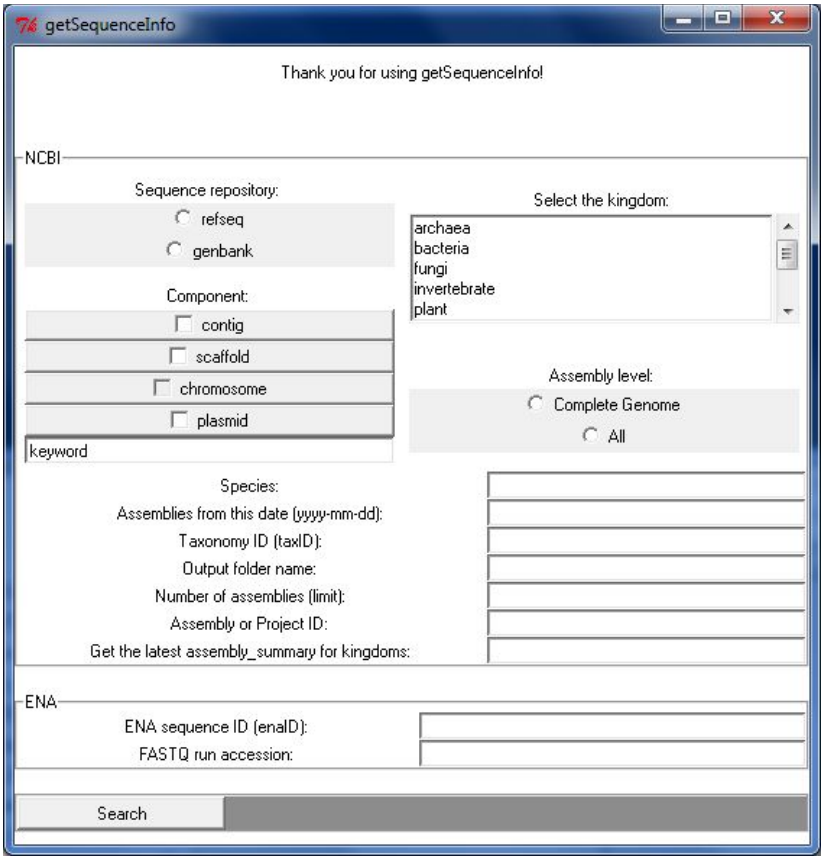
How to use the tool

As mentioned earlier, the tool can be used from the command line or with a graphical user interface (GUI). The same usage semantics are shared between the two interfaces. Please note that both Perl files (getSequenceInfo.pl and getSequenceInfoGUI.pl) should be localized in the same directory.

The user can launch the GUI version of the tool (getSequenceInfoGUI.pl) either by executing it (double click) or by typing the following command:

```
perl getSequenceInfoGUI.pl
```

The following window should appear in front of a command prompt:



Snapshot of the GUI window.

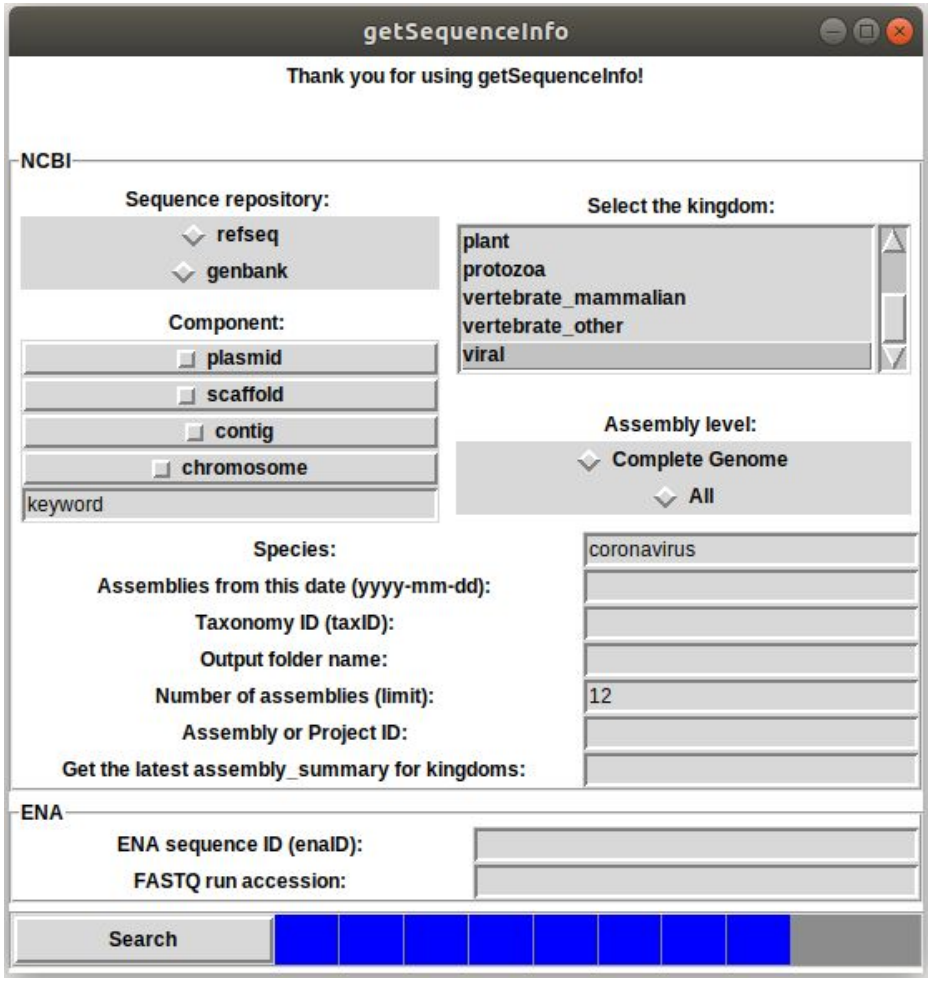
Examples of use (GUI)

There are many ways to use this tool to download assemblies and their related information.

The simplest way is to use the name of the species you want to search and its associated kingdom.

Suppose we want to search for information about the coronavirus.
We can use the following command in order to retrieve 12 genome assemblies available from the date 2019/12/01:

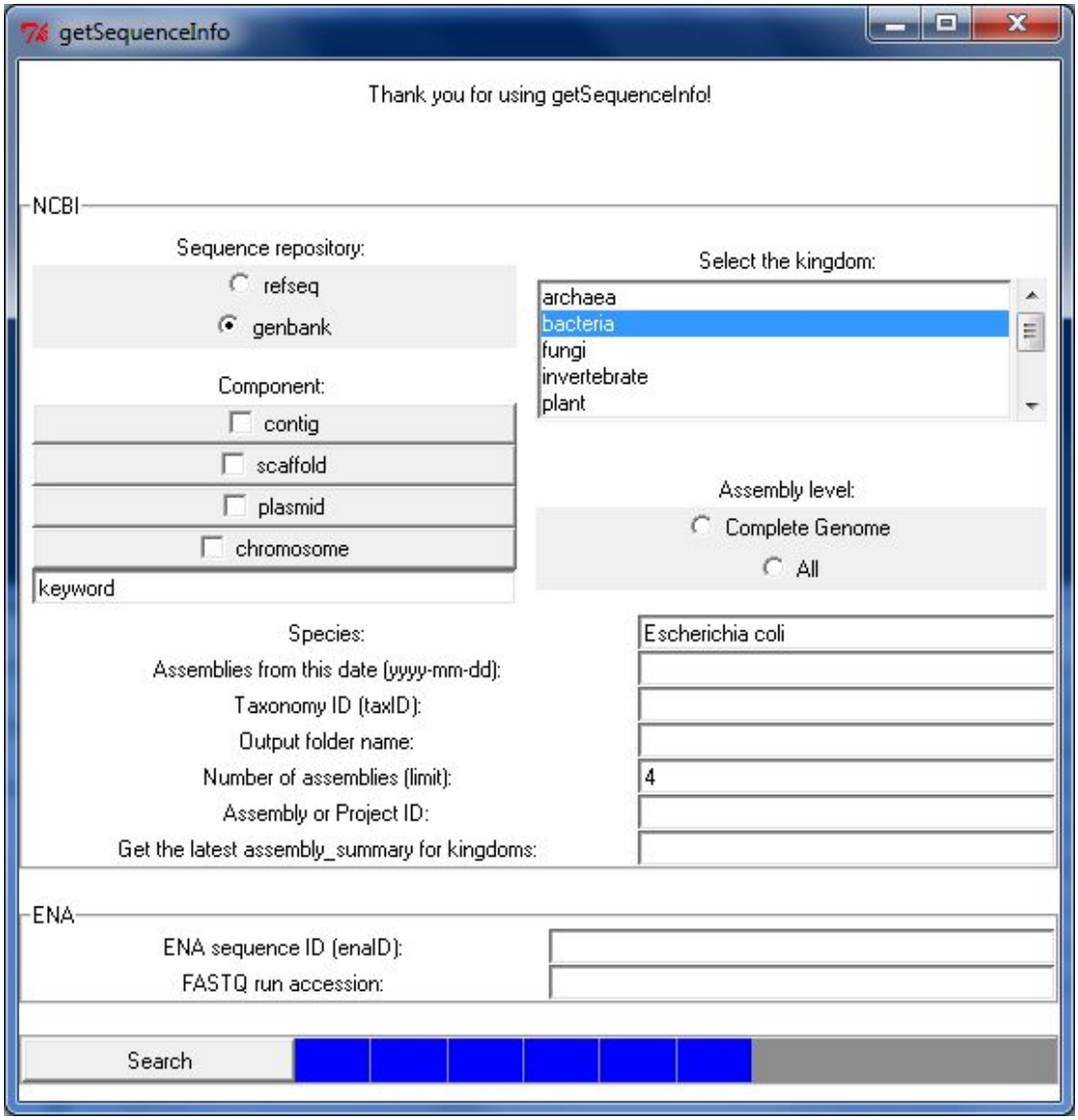
```
perl  getSequenceInfo.pl -s coronavirus -k viral -date 2019-12-01 -n 12
```



Snapshot of the GUI launched from Linux Ubuntu system to get sequence information regarding "coronavirus"

Another example to get sequence information regarding *Escherichia coli* bacterial species (limiting the number of assemblies to 4):

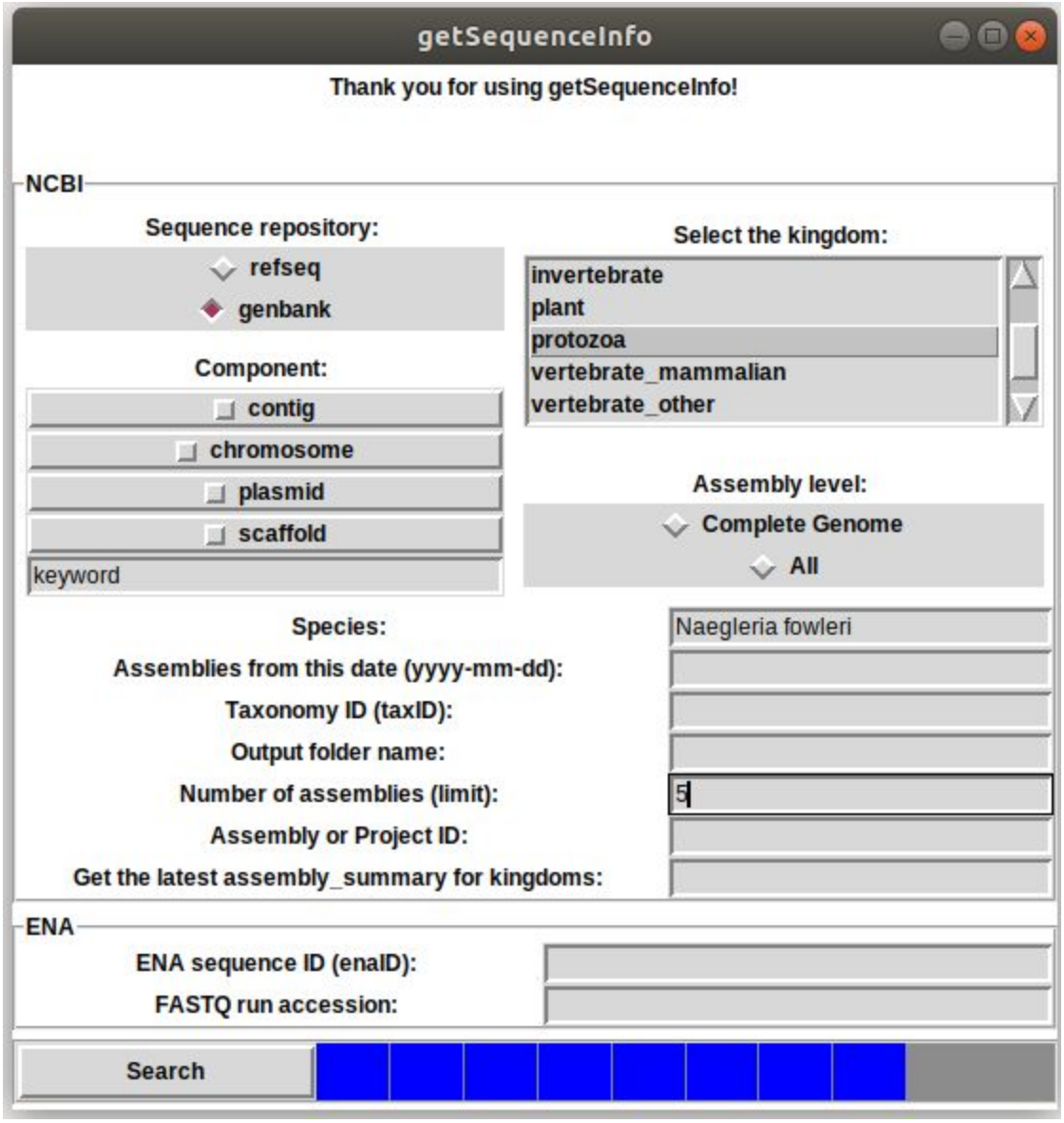
```
perl getSequenceInfo.pl -k “bacteria” -s “Escherichia coli” -d “genbank” -n 4
```



Snapshot of a search using a Microsoft Windows Operating System

Another example to get sequences from *Naegleria fowleri* species (limiting the number of assemblies to 5):

```
perl getSequenceInfo.pl -k “protozoa” -s “Naegleria fowleri” -d “genbank” -n 5
```



Snapshot regarding the search for *Naegleria fowleri* assemblies

Some command lines

We can type the following command to display the help message:

```
perl getSequenceInfo.pl -h
```

The following Help message will appear:

```
Name:
        getSequenceInfo.pl

   Synopsis:
        A Perl script allowing to get sequence information from GenBank RefSeq or ENA repositories.

   Usage:
     perl getSequenceInfo.pl [options]
     examples:
        perl getSequenceInfo.pl -k bacteria -s "Helicobacter pylori" -l "Complete Genome" -date 2019-06-01
        perl getSequenceInfo.pl -k viruses -n 5 -date 2019-06-01
        perl getSequenceInfo.pl -k "bacteria" -taxid 9,24 -n 10 -c plasmid -dir genbank -o Results
        perl getSequenceInfo.pl -ena BN000065
        perl getSequenceInfo.pl -fastq ERR818002
        perl getSequenceInfo.pl -fastq ERR818002,ERR818004

   Kingdoms:
        archaea
        bacteria
        fungi
        invertebrate
        plant
        protozoa
        vertebrate_mammalian
        vertebrate_other
        viral

   Assembly levels:
        "Complete Genome"
        Chromosome
        Scaffold
        Contig

   General:
        -help or -h                     displays this help
        -version or -v                  displays the current version of the program

   Options ([XXX] represents the expected value):
        -directory or -dir [XXX]    allows to indicate the NCBIs nucleotide sequences repository (default: genbank)
        -get or -getSummaries [XXX]    allows to obtain a new assembly summary file in function of given kingdoms
(bacteria,fungi,protozoa...)
        -k or -kingdom [XXX]            allows to indicate kingdom of the organism (see the examples above)
        -s or -species [XXX]            allows to indicate the species (must be combined with -k option)
        -taxid [XXX]                    allows to indicate a specific taxid (must be combined with -k option)
        -assembly_or_project [XXX]    allows to indicate a specific assembly accession or bioproject (must be combined with
-k option)
        -date [XXX]                     indicates the release date (with format yyyy-mm-dd) from which sequence information
are available
        -l or -level [XXX]      allows to select a specific assembly level (e.g. "Complete Genome")
        -o or -output [XXX]             allows users to name the output result folder
        -n or -number [XXX]             allows to limit the total number of assemblies to be downloaded
        -c or -components [XXX]         allows to select specific components of the assembly (e.g. plasmid, chromosome, ...)
        -ena [XXX]                      allows to download report and fasta file given a ENA sequence ID
        -fastq [XXX]                    allows to download FASTQ sequences from ENA given a run accession
(https://ena-docs.readthedocs.io/en/latest/faq/archive-generated-files.html)
        -log                            allows to create a log file
```