

GENERAL SOFTWARE INSTALLATION

Be sure to download the software appropriate for your computer system.

Common repositories for bioinformatics software:

- GitHub <https://github.com>
- Source Forge <https://sourceforge.net>

Downloading and installing software from the command line using package managers:

- apt-get (Linux)
- Homebrew (Mac)

Installing software manually:

- Download software (download binaries when possible)
- Unpackage
- See README file for compatibility and dependency information
- See INSTALL file for installation instructions

Standard installation

Step 1: Configure software for installation.

Step 2: Build the software from the source code using the Makefile included in the distribution.

Step 3: Install the software on your machine and move the files to the correct locations.

NOTE: Installation is often done using the following set of three commands (\$ is the shell prompt):

```
$ ./configure
$ make
$ make install
```

NOTE: Mac users must install xcode tools before installing certain software. To install, use:

```
$ xcode-select -install
```

To make software accessible from any directory, the location of the software has to be added to your \$PATH variable. This can be done on a Mac as follows:

```
$ export PATH=$PATH:path_to_software
```

NOTE: It is a good practice to create a folder in your home directory called `bin` for command line-based software, in which case, the following code would be used to add the location to your path:

```
$ export PATH=$PATH:$HOME/bin/software_name
```