# Installing bioinformatics software on Linux

# Bioconda

Install *most* bioinformatics software with one command:

conda install -c bioconda [name of software]

To get started, Google:

bioconda lh3

# Bioconda: a capable bio-software package manager

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## Getting Started

Firstly, a few basic concepts. Conda is a portable package manager primarily for Python and precompiled binaries. Miniconda is the base system of conda. It includes a standard python and a few required dependencies such as readline and sqlite. In conda, a *channel* contains a set of software typically managed by the same group. Bioconda is a channel of conda focusing on bioinformatics software. The following shows how to install and use conda.

```
# Download the miniconda installation script for Python2
wget https://repo.continuum.io/miniconda/Miniconda-latest-Linux-x86_64.sh
# Install conda; it will ask a few questions, including the installation path
sh Miniconda-latest-Linux-x86_64.sh
. ~/.bashrc   # or relogin to get PATH updated
# A few examples
conda info
conda search -c bioconda bwa
conda install -c bioconda bwa
```

Copy-paste this and Conda is installed.

# Other techniques

**Linuxbrew**/Homebrew:

       brew install [name of software]

Classical technique:            linux4biologists.tumblr.com



**Linux for biologists**

       wget [url of software]

       tar xf [archive.tar.gz]

       ./configure

       make

Not a substitute to:

- knowing whether software is appropriate

- reading its manual