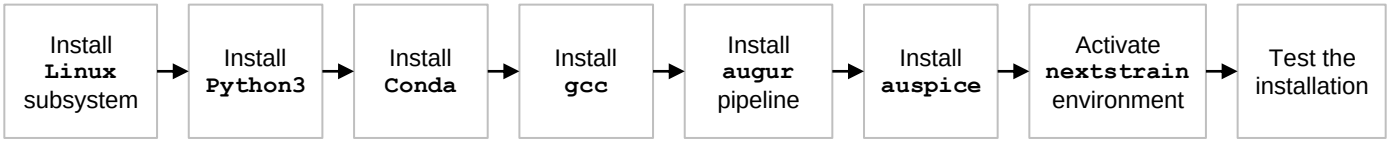
Nextstrain installation

Yale SCHOOL OF PUBLIC HEALTH

This tutorial is designed to assist you in installing `nextstrain` and its dependencies. The workflow below explains the main steps to accomplish that. Windows users must install a Linux subsystem first (see step 1).



(1) `nexstrain` only operates on UNIX systems (MacOS or Linux). As a workaround, Windows users must install Linux (Ubuntu) as a subsystem. Visit the link below ans check the instructions "*For windows users*" to **install** and **set up** Linux on Windows:

`https://github.com/grubaughlab/nextstrain_course`

(2) Access the Terminal in your system, and **run** the commands below to check if `Python3` is installed (see box):

```
python --version
```

If no version information is shown, it means the software is not installed. Please **access** the sites below to install it:

Python3 → https://www.python.org/downloads/

(3) While it may be available on MacOS, Linux subsystems may not come with a `gcc` compiler. **Test** if `gcc` is available by typing:

```
gcc --version
```

(4) If such command does not tell you which `gcc` version is installed, Linux users must **install** it by typing the commands below, one line at a time (MacOS users, please see note):

```
sudo apt-get update
sudo apt install gcc
gcc --version
```

`apt` (Advanced Package Tool) is a software used for installing and removing other software in Linux only. MacOS users should use `brew` instead:

```
brew update
brew upgrade
brew install gcc
```

(5) Check if `conda` is installed by typing `conda list` in your Terminal. If that returns a list of software and packages, proceed to step 7. Otherwise, visit the link below, **download** a Python3 Miniconda installer (in bash format `.sh`, or in executable format `.pkg`) compatible with your operating system (Linux or Mac), and proceed to step 6 to install Miniconda.

`https://docs.conda.io/en/latest/miniconda.html`

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(6) Access the directory where the Miniconda installer is located. **Execute** the file (if in `.pkg` format), or **type** `bash` followed the name of the file you downloaded (if in `.sh` format), as shown below:

```
bash Miniconda3-latest-<YourOperatingSystem>-x86_64.sh
conda list
```

(7) If `Python3`, `gcc` and `conda` are installed, **run** the commands below, one line at a time, to **install** `augur`:

```
python3 -m pip install nextstrain-cli
curl http://data.nextstrain.org/nextstrain.yml --compressed -o nextstrain.yml
conda env create -f nextstrain.yml
```

(8) Activate the `nextstrain` environment using the command below. It will change the prefix of the command prompt (please see the 'nextstrain' prefix in your Terminal):

```
conda activate nextstrain
```

(9) Now let's **install** `auspice`. First, **check** if `npm` is available (see box):

```
npm --version
```

If `npm` is not installed, type the command below to **install** it:

```
sudo apt install nodejs
```

(10) With `npm` installed, **run** the following command to install `auspice`, the software we are going to use to visualize the results generated by `augur`:

```
npm install --global auspice
```

(11) That's it. Now **run** the commands below to test the software installation. These commands will print information about how to use each software:

```
augur -h
auspice -h
nextstrain -h
conda deactivate
```

All set! 🎉

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