

Quick Setup Guide:

To run the HIV model simulation on your own system, you will need:

Python 2.7.5 (actually, any variant of 2.7.x will do),
numpy 1.6.2 or higher,
scipy 0.11.0 or higher,
matplotlib 1.1.1 or higher

Mac users

If you are trying to run the HIV model from a MAC,
Python 2.7.x comes pre-installed on MAC OS X.

You will still however need to get the other packages (numpy, scipy, matplotlib).

One way of doing so is by installing MacPorts here:

<http://www.macports.org/install.php>

Just follow steps 1 to 3 to complete the installation.

Note: Step 1 is just asking you to install Xcode Command Line Tools prior to steps 2 and 3. You just need Xcode Commands Line Tools and not Xcode itself to install MacPorts, and you can get the Tools here:

<https://developer.apple.com/downloads/index.action> (need an Apple ID, which is the same ID you use to access App Store/iTunes)

After you have MacPorts installed, execute the following command in the terminal:

```
sudo port install py27-numpy py27-scipy py27-matplotlib py27-ipython
```

This will install all the prerequisite packages required to run the HIV model simulation.

Windows users

If you are trying to run the HIV model from a Windows machine,
Python 2.7.x does not come pre-installed, so you will need to install Python plus the other packages listed at the top.

One way to get everything (including Python 2.7.x) from one installer is to download and install the Anaconda Python distribution package (freeware) here:

<http://continuum.io/downloads>

Note: Make sure that the Windows icon is selected on the page before proceeding to download.