

## Lab 0: Preparing your laptop for the course – OS X

Five pieces of software are needed to complete this course:

1. VMD – Views and analyses molecular models.
2. NAMD – Performs molecular dynamics simulations.
3. Textmate 2.0
4. Gnuplot – Plots data
5. A modern web browser – Internet Explorer 10 or newer, recent versions of Chrome or Firefox.

Several assumptions in this document:

1. You have admin access (i.e. permission to install new packages to you system)
2. You know what a terminal is.
3. You understand the difference between a text editor and word processor.
4. You will have a web browser already installed, if you need a more modern version then one is only a web search and standard installation away.

We will also add NAMD and Gnuplot to your PATH for ease of use.

### VMD

#### Download

Click on this link <http://www.ks.uiuc.edu/Research/vmd/> or use your web browser to navigate to the web page.

- Locate the 'Downloads' section that is highlighted (below the 'Overview' section) on the left side of the page
- Click on the 'Download (all versions)' link

Then you need to select the 'MacOS X OpenGL' link appropriate for your version of OS X for the most recent version of VMD (Version 1.9.2 at the time of writing).

- Click the appropriate link
- You now need to register an account
  - Enter a username and password
  - Click "Continue with registration or download"
  - Fill in the form (including confirming your password)
  - Click 'Register'
- Confirm that you are you and agree to the license
- The download should begin automatically

#### Installation

- Once the file has downloaded double click on it to run it
- Drag the icon that resembles a water molecule into your Applications folder

To open VMD from a terminal window (optional)

- Add the following to your ~/.bashrc file:
  - alias vmd='Applications/VMD\ 1.9.2.app/Contents/vmd/vmd\_MACOSXX86'
  - VMDFILECHOOSER=FLTK
  - Export VMDFILECHOOSER

- Then type “source ~/.bashrc”

## NAMD

### Download

Click on this link <http://www.ks.uiuc.edu/Research/namd/> or use your web browser to navigate to the web page.

- Follow the 'Download NAMD' link on the left side of the page
- Select the MacOSX-x86\_64 link from the “Version 2.9 (2012-04-30) Platforms” section
  - We use version 2.9 to ensure that all input and output formats are compatible with other software used in the tutorial
- Enter the username and password you created before when installing VMD.
- Agree to the license and the download should start automatically

### Installation

- In the terminal navigate to the directory where the file was downloaded and run the command:

```
sudo tar xvf NAMD_2.9_MacOSX-x86_64-multicore.tar -C /usr/local/bin
```

- You will need to enter your password to gain admin rights
- Now we need to make the program easily accessible from the command prompt, this involves setting an Environment Variable:

1. Open the file ~/.bashrc in your text editor
2. Add the following line:

```
export PATH=$PATH:/usr/local/bin/NAMD_2.9_MacOSX-x86_64-multicore
```

3. Save the file
4. Type source ~/.bashrc
5. Open the file ~/.bash\_profile in your text editor
6. Add the following line:

```
if [-f ~/.bashrc];then . ~/.bashrc;fi
```

Textmate (optional – the TextEdit app that comes with OS X can be used)

### Download

Navigate to <http://macromates.com/>

- Click on the download icon

### Installation

- Once the file has downloaded double click on it to run it
- Drag the icon that resembles a water molecule into your Applications folder

## Gnuplot

### Download

There are a variety of ways of installing Gnuplot. All of which have different dependencies. Ask one of the course administrators which option is best for you.

Perhaps the nicest is via homebrew (<http://brew.sh/>) but even this requires a working installation of Xcode.

### Testing NAMD and Gnuplot Installations

If the installation has worked then NAMD and Gnuplot should be available from the command line.

- To test NAMD type:

```
namd2
```

- If NAMD is installed and setup correctly then a message stating:

```
FATAL ERROR: No simulation config file specified on command line.
```

- To test Gnuplot type:

```
gnuplot
```

- If Gnuplot is installed correctly a message giving the version of the code should appear and the terminal prompt should look like:

```
gnuplot>
```

- Try making a plot by typing:

```
plot sin(x)
```

- Exit by typing:

```
exit
```

### Getting the Course Files

All course content is available from:

[https://sassie-web.chem.utk.edu/training/aps\\_2016/main.html](https://sassie-web.chem.utk.edu/training/aps_2016/main.html)

Download each days zip file onto your desktop as you progress.