

# Scientific computing resources at FHCRC

Jerry Davison and Martin Morgan

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## 1 Scientific Computing's resources run the Linux operating system

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Many high-performance computers here and elsewhere run the [Linux](#) operating system. Interaction with it to access and manipulate files is through text *commands*. There are plenty of web sites offering help, here are two, and a publisher:

- [Linux ABC's](#)
- [Linux for newbies](#)
- O'Reilly *Linux in a Nutshell* - get the 1st or 2nd edition, later ones are badly bloated.

The Scientific Computing group ([http://centernet.fhcrc.org/CN/depts/it/scientific\\_computing/](http://centernet.fhcrc.org/CN/depts/it/scientific_computing/)) at the Hutch provides high-performance computing access to FHCRC researchers, without charge. These computers enable analyses difficult or impossible to perform on a typical laptop; all run the same version of the Ubuntu Linux operating system. There are four **rhino** machines, with these capabilities:

- *multicore* – 16 cores (cpu's)
- *large memory* – 378 GB main memory
- *large secondary storage* – 4 TB /home hard drive shared among users, plus additional large /shared volumes for data storage

### 1.1 Access

There are several ways to access a **rhino**:

**MAC OS X and Linux:** open a terminal and log in with the *secure shell* command

```
ssh -X myHutchID@rhino
```

and then enter your password. You'll be connected to one of the rhino's. The -X option enable *X11 forwarding* – so that plots can be presented on your laptop .

**MS Windows users:** use **PuTTY** – get putty.exe from <http://www.chiark.greenend.org.uk/~sgtatham/putty/download.html> to open a **rhino** terminal, and install **Xming** (<http://sourceforge.net/projects/xming/>) to process R plot commands – so plots can be presented on your laptop.

The first time you run **PuTTY** you'll need to navigate through the Category menu on the left to Connection, SSH, and X11; click on the *Enable X11 forwarding* box. Return to Session and *Save the Default Settings*. In the *Host Name* box enter rhino04 and click on *Open*. Log in with your Hutch ID and password. To enable plotting you need to start **Xming**.

## 1.2 Logging in to a rhino

When logging in to one of the rhino's you can specify a particular rhino (rhino01, rhino02, rhino03, or rhino04). This text is printed to your screen when you log in:

```
Welcome to Ubuntu 12.04.3 LTS (GNU/Linux 3.5.0-43-generic x86_64)
#####
```

### IMPORTANT NOTES:

(\*\*\*\*\* UPDATED \*\*\*\*\*)

- \* This computer is intended for interactive scientific computing, development and for compute jobs that require > 20GB memory.
- \* If you are running a long & CPU intensive job (> 1h) and your job requires less than 20GB of memory you can start an interactive session to Gizmo by using the 'grab\*' commands to get immediate access to a compute server with 1-12 cores.

However in most cases it will be more effective if you use the sbatch command.

\* Shared folders can be found in:  
     /shared/silo\_researcher  
     /shared/labs

- \* To use this system most effectively, please read this summary:  
     <http://scicomp.fhcrc.org/Gizmo%20Cluster%20Quickstart.aspx>

```
#####
```

Do have a look at the documentation at <http://scicomp.fhcrc.org/Gizmo%20Cluster%20Quickstart.aspx> and login for an introduction to using the scientific computing resources, especially if you plan to run long analyses. If you have questions about using them, send email to [scicomp@fhcrc.org](mailto:scicomp@fhcrc.org).

## 1.3 Starting and using R from the shell

To start an R session, at the shell prompt enter "R":

```
myShellPrompt$ R
```

```
> plot(1:10, type='h')
> q()
```

To use R studio instead, enter:

```
myShellPrompt$ rstudio
```