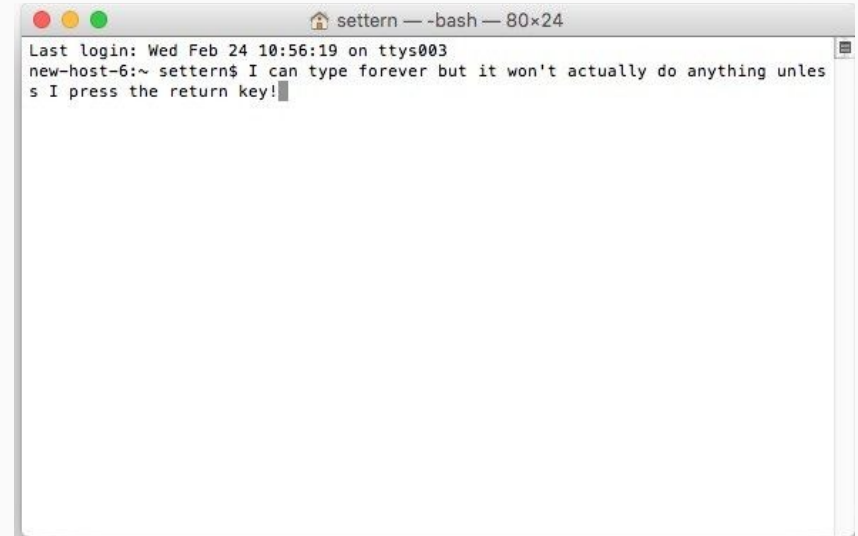
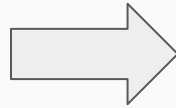


# **BF528 - Applications in Translational Bioinformatics**

Computational Skills Primer

# Computer was born in the mind of man, not the other way around!!



```
settern -- -bash -- 80x24
Last login: Wed Feb 24 10:56:19 on ttys003
new-host-6:~ settern$ I can type forever but it won't actually do anything unless I press the return key!
```

## Goal of this lecture:

- Overcome the fear of black screen (if you have one !!)
- Learn techniques for working on SCC you will need
- Introduce shared computing concepts you will use

# Prerequisites

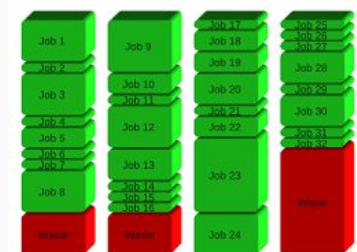
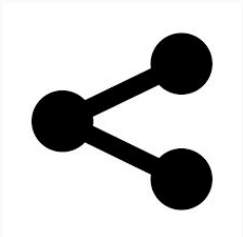
- Patience with self and with each other
- Keep an open mind
- Attitude of collaboration
- It's OK to not know - we will learn together
- **Rome ne s'est pas faite en un jour !!!**



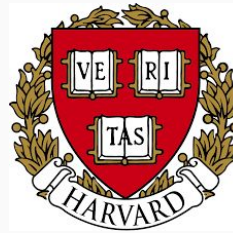
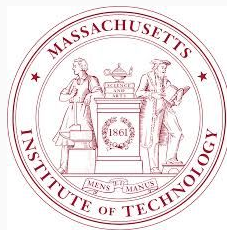
# What is SCC ?

## Shared Computing Cluster (SCC)

- **Shared:** Multi-user environment.
- **Computing:** Calculation, file manipulation, etc
- **Cluster:** Many individual computers connected together working in coordination



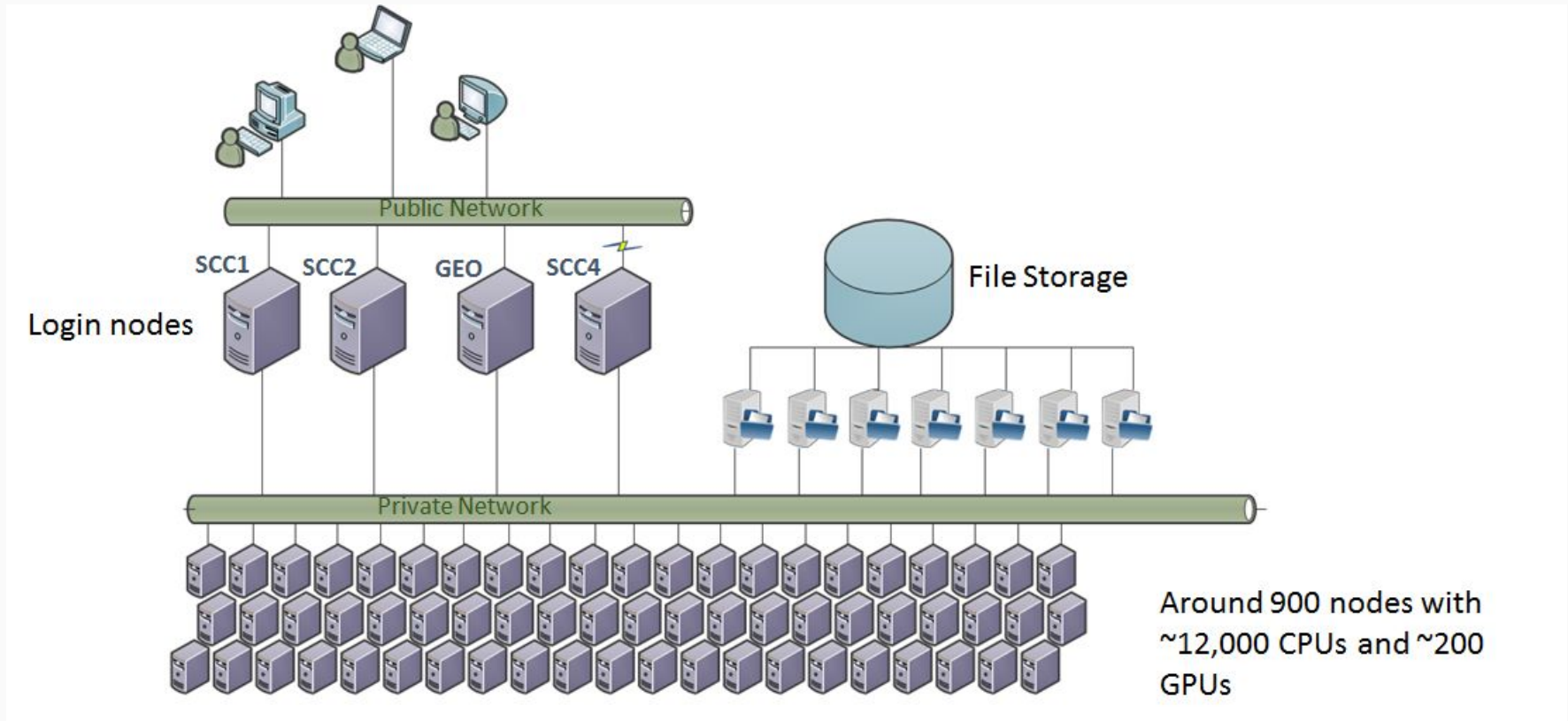
# Massachusetts Green High Performance Computing Center



# Terminology

- **Cluster** - connected set of computers
- **Node** - a single computer (on a rack)
  - **Head/login node** - “gateway” computer to cluster
  - **Compute node** - single computer where jobs run
- **terminal** - program used to interact with a computer using text commands
- **ssh** - secure shell, how we connect to cluster
  - NB: both a noun and a verb, e.g. “use ssh to ssh into scc1...”

# SCC Architecture



# Why use SCC? I have a laptop!

- Collaborate on projects
- Run code exceeding workstation capability
- Secured Network
- Fast and easy data sharing
- Analyze protected data (e.g. dbGaP)
- Run code that runs for long periods of time
- Perform many computations in parallel

# Software to Access SCC

- SSH

	SSH	X-Win	SFTP
Microsoft Windows	—	MobaXterm <a href="https://mobaxterm.mobatek.net">https://mobaxterm.mobatek.net</a>	—
Apple OS X	Terminal (Built in)	XQuartz <a href="https://www.xquartz.org">https://www.xquartz.org</a>	Cyberduck <a href="https://cyberduck.io">https://cyberduck.io</a>
Linux	Terminal (Built in)	X11 (Built in)	Various (Built in)

- SCC OnDemand

<https://scc-ondemand.bu.edu>

# How to connect with SCC OnDemand

The screenshot shows a web browser window with the URL `scc-ondemand.bu.edu/pun/sys/dashboard`. The browser's address bar and tabs are visible at the top. The dashboard has a red navigation bar with the following items: **SCC OnDemand**, **Files**, **Quotas**, **Login Nodes**, and **Interactive Apps**. A dropdown menu is open under **Login Nodes**, listing `>_scc1`, `>_scc2`, `>_geo`, and `>_scc4`.

The main content area displays four quota limit warnings, each with a red progress bar indicating usage percentage:

- Quota limit warning for /usr3/gr**: Using 9.55 GB of quota 10 GB. Consider deleting or archiving files to free up disk space. Progress bar: 95%.
- Quota limit warning for /projectnb/ikezulab**: Using 5.62 TB of quota 5.86 TB (5.93 GB are yours). Consider deleting or archiving files to free up disk space. Progress bar: 95%.
- Quota limit warning for /projectnb/staghorn**: Using 1.9 TB of quota 1.9 TB (171 GB are yours). Consider deleting or archiving files to free up disk space. Progress bar: 99%.
- Quota limit warning for /restricted/projectnb/mlhd**: Using 23.8 TB of quota 24.9 TB (5.54 TB are yours). Consider deleting or archiving files to free up disk space. Progress bar: 95%.

At the bottom of the dashboard, there is a photograph of a server room with rows of server racks and blue and green indicator lights, viewed through a metal mesh fence.

# SCC OnDemand Demonstration: Connecting

# Navigation

Essential navigation commands:

- **pwd** - print current working directory
- **ls** - list files
- **cd** - change directory

The “address” of a file/directory in linux is called a **path**:

- *Absolute path* - starts with /
- *Relative path* - does not start with /

# List of useful commands - Part I

Useful options for the “ls” command:

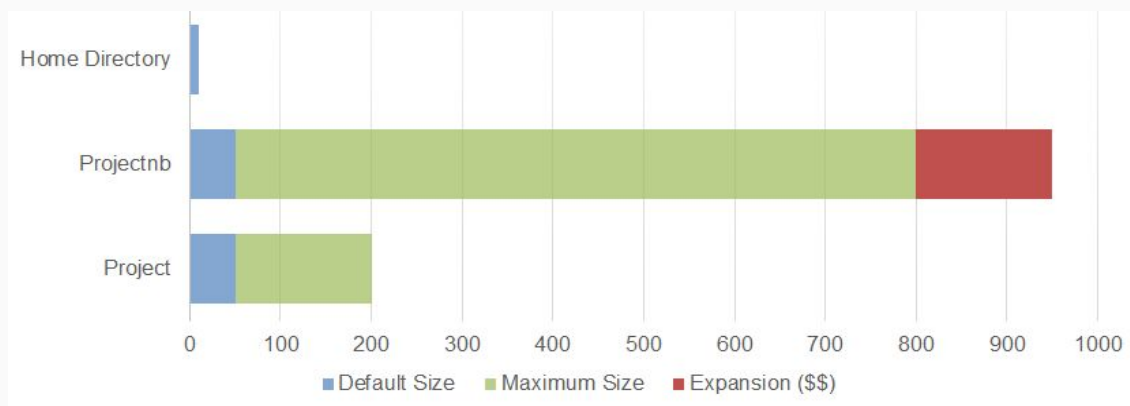
- **ls -a** List all files, including hidden files beginning with a period “.”
- **ls -ld \*** List details about a directory and not its contents
- **ls -F** Put an indicator character at the end of each name
- **ls -l** Simple long listing
- **ls -lR** Recursive long listing
- **ls -lh** Give human readable file sizes
- **ls -lS** Sort files by file size
- **ls -lt** Sort files by modification time (very useful!)

# Storage (GB)

- `~/` - Home directory, your personal space (10 GB max)
- `/project` - Source code, files you can't replace.
- `/projectnb` - Output files, downloaded data sets
- Available from all head nodes (scc1, scc2, etc)

## Restricted data (protected data, e.g. dbGaP)

- `/restricted/project`
- `/restricted/projectnb`
- Only accessible through `scc4.bu.edu` and compute nodes.



# Permissions

## Files Access Control:

- Every file has an owner
- Every file belongs to a group
- Every file has “permissions” controlling access to it:
  - **r** - read
  - **w** - write
  - **x** - execute

```
[kkarri@scc4 ~]$ ls -l newdir
```

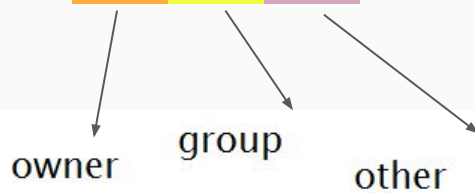
```
drwxr-xr-x 3 kkarri waxmanlab 512 Jan 21 16:03 newdir
```

# chmod

Change the permissions on the directory “newdir” so that members of your group can write to it:

```
[kkarri@scc4 ~]$ ls -l newdir
```

```
drwxr-xr-- 3 kkarri waxmanlab 512 Jan 21 16:03 newdir
```



Members of my group don't have access to this file, change that:

```
[kkarri@scc4 ~]$ chmod g+w newdir
```

```
[kkarri@scc4 ~]$ ls -l newdir
```

```
drwxrwxr-- 3 kkarri waxmanlab 512 Jan 21 16:03 newdir
```

# SCC OnDemand Demonstration: Navigation

# List of useful commands

**cp** [file1] [file2] copy file

**mkdir** [name] make directory

**rmdir** [name] remove (empty) directory

**mv** [file] [destination] move/rename file

**rm** [file] remove (-r for recursive)

**file** [file] identify file type

**less** [file] page through file

**head -n** [file] display first n lines

**tail -n** [file] display last n lines

**ln -s** [file] [new] create symbolic link

**cat** [file] [file2...] display file(s)

**tac** [file] [file2...] display file in reverse order

# Additional Reading

**Assignment:** familiarize yourself with the material on basic command line usage found here:

[Workshop 0. Basic Linux and Command Line Usage](#)

For in-depth understanding of these concepts go through the following modules on cluster computing and advance command line text editors:

- [Cluster Computing Tutorial](#)
- [Advanced CLI Tutorial](#)