

Introduction to the **Shared Computing Cluster (SCC)**

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Topics for Today

Intro

- Research Computing Services
- Shared Compute Cluster Overview
- Getting and Account

Linux

- Connecting to the SCC
- Commands
- Permissions
- Tools/Methods

Compute Cluster

- Software and Modules
- Cluster Architecture
- Files/Storage
- The Batch System

Research Computing Services

Research Computing Services (RCS)

A group within Information Services & Technology at Boston University provides computing, storage, and visualization resources and services to support research that has specialized or highly intensive computation, storage, bandwidth, or graphics requirements.

Three Primary Services:

- Research Computation
- Research Visualization
- Research Consulting and Training

RCS Team and Expertise

Our Team

- Scientific Programmers
- Systems Administrators
- Graphics/Visualization Specialists
- Account/Project Managers
- Special Initiatives (Grants)

Consulting Focus:

- Bioinformatics
- Data Analysis \ Statistics
- Molecular modeling
- Geographic Information Systems
- Scientific/Engineering Simulation
- Visualization

Me

- Systems Programmer and Administrator
- Background in biomedical engineering, technology, and bioinformatics
- Office on the Boston University Medical Campus
 - We also have staff on the Charles River Campus
- Contact:
 - Email: cjahnke@bu.edu
 - Office: Crosstown Building, Suite 485

Our whole team: help@scc.bu.edu

You

- Who has experience programming?
- Working with "big data"?
- Using Linux?
- Using compute clusters?
- Have an account on SCC?



Shared Computing Cluster (SCC) Overview

The Shared Computing Cluster (SCC)

- A Linux compute cluster with 11,000 CPU cores and 250 GPUs.
- Over 3 Petabytes of disk space.
- Located at the Massachusetts Green High Performance Computing Center (MGHPCC) in Holyoke, MA
- Owned by Boston University and researchers.
- Went into production in June, 2013 for Research Computing.

MGHPCC

- Collaboration between 5 universities, MA state, and industry.

Boston University



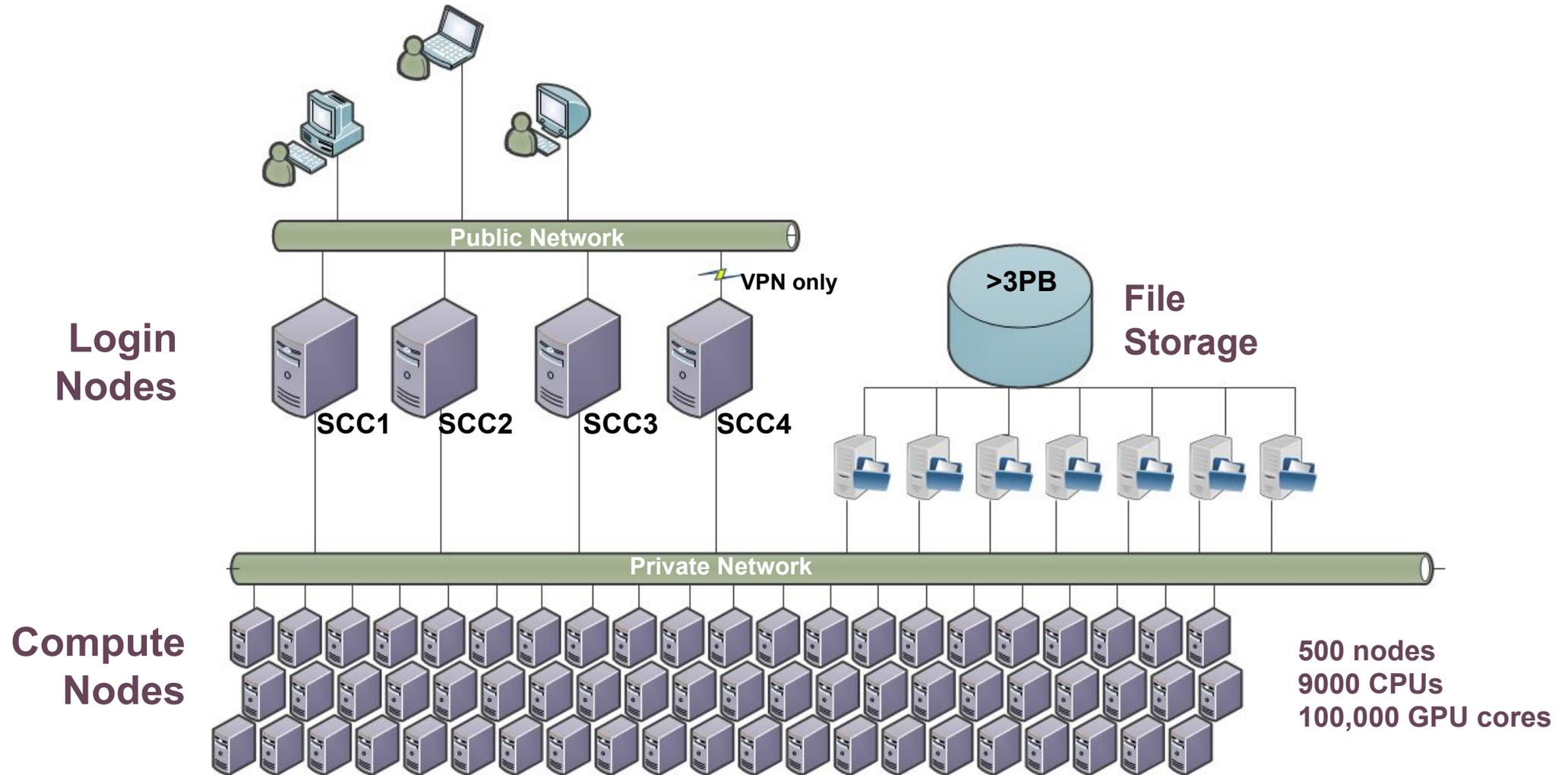
Northeastern University



- State-of-the-art data center in Holyoke, MA.
- MGHPCC provides physical infrastructure (i.e. space, power, cooling), not computing systems.
- Individual universities or consortiums provide their own computing and support.



SCC Architecture



That seems like a lot... why do all this?

Researchers need to:

- Collaborate on shared data.
- Run code that exceeds workstation capability (RAM, Network, Disk).
- Run code that runs for long periods of time (days, weeks, months)
- Run code in highly parallelized formats (use 100 machines simultaneously).
- Might want to do all of those things 1,000 times.

Getting an Account on SCC

Getting an Account on SCC

- BU Faculty members can create SCC projects online (no cost).
- All users of the SCC must be on a SCC research project managed by a full-time BU Faculty member.
- Exception: 3 month trial accounts for students/tutorial attendees.
 - Email help@scc.bu.edu if interested.

Today

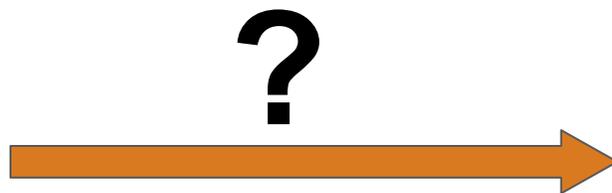
- Use your own account if you have one.
- Tutorial Accounts:
 - Username:
 - Password:
 - These should not be used after today.

Connecting to SCC

Windows, OS X, Linux



Local System



Remote Server

Connection Protocols and Software

Remote Connections:
Secure Shell
(SSH)

```
cjahnke:~ cjahnke$ ssh scc1.bu.edu
cjahnke@scc1.bu.edu's password:
Last login: Mon Jun 27 08:51:50 2016 from vpn-offcampus-168-122-67-176.bu.edu
*****
This machine is governed by the University policy on ethics.
http://www.bu.edu/tech/about/policies/computing-ethics/

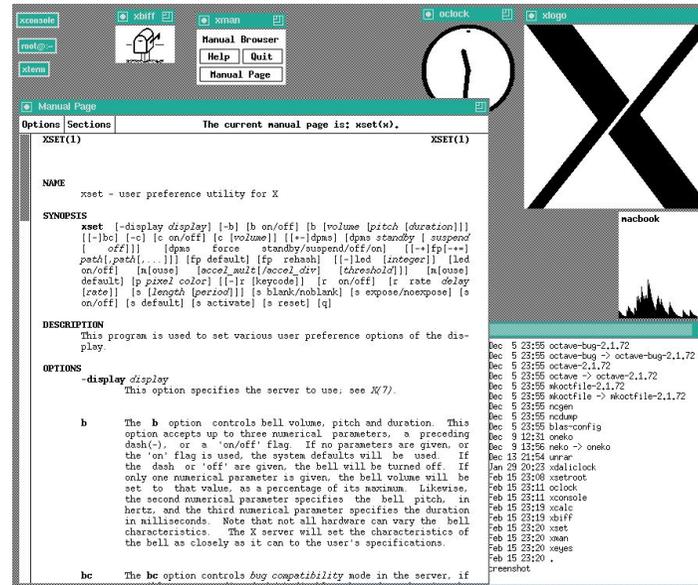
This machine is owned and administered by
Boston University.

See the Research Computing web site for more information about our facilities.
http://www.bu.edu/tech/support/research/

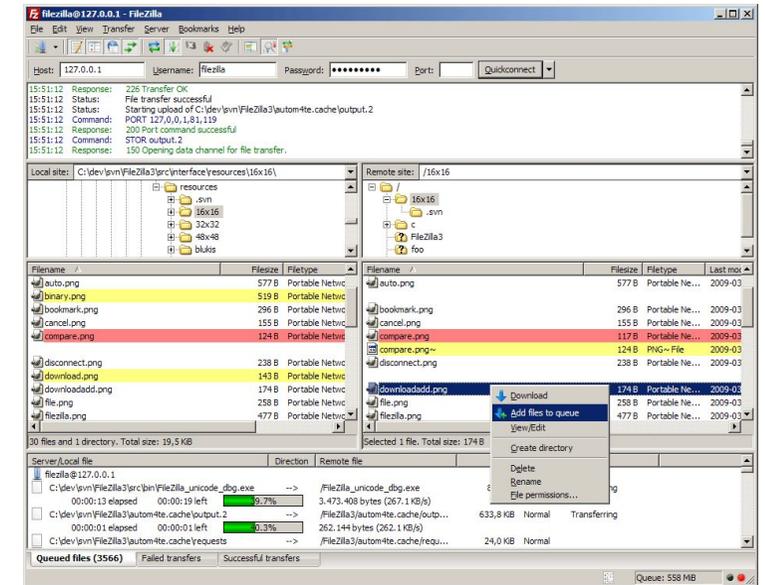
For Cluster specific documentation see:
http://www.bu.edu/tech/support/research/computing-resources/scc/

Please send questions and report problems to "help@scc.bu.edu".
*****
[cjahnke@scc1 ~]$
```

Remote Graphics:
X-Windowing
(X, X-Win)



Data Transfer:
Secure File Transfer Protocol
(SFTP)



Other protocols too, but let's start with these.

Connecting from Different Platforms

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

Hands-On: SSH Connection

Have a BU Account?

- Hostname: scc1.bu.edu
- Username: <Your BU Username>
- Password: <Your BU Password>

Use Tutorial Account

- Hostname: scc1.bu.edu
- Username: tuta30+
- Password:

```
[local_prompt]$ ssh username@scc1.bu.edu
```

```
MobaXterm
Terminal Sessions View X server Tools Games Settings Macros Help
Session Servers Tools Games Sessions View Split Fullscreen MultiExec Tunneling Settings Help X server Exit

1. cjahnke@scc1:~
[2017-06-12 15:06.59] ~
[cjahnke.IST_STAFF_VM058] > ssh cjahnke@scc1.bu.edu
cjahnke@scc1.bu.edu's password:
Last login: Mon Jun 12 15:06:38 2017 from cumm111-0b13-dhcp-206.bu.edu
*****
This machine is governed by the University policy on ethics.
http://www.bu.edu/tech/about/policies/computing-ethics/

This machine is owned and administered by
Boston University.

See the Research Computing web site for more information about our facilities.
http://www.bu.edu/tech/support/research/

For Cluster specific documentation see:
http://www.bu.edu/tech/support/research/computing-resources/scc/

Please send questions and report problems to "help@scc.bu.edu".
*****

[cjahnke@scc1 ~]$
```

Hands-On: X-Windows Application

X-Windows (X-Win, X11, etc) allows graphics to come through the SSH session.

- MobaXterm does not need to do this. Just type “**xclock**”
- **Windows and Linux and:** Use the “-X” option to enable X-Win

```
[local_prompt]$ ssh -X username@scc1.bu.edu
username@scc4.bu.edu's Password:
[username@scc1 ~]$ xclock &
```

- **Apple OS X:** Use the “-Y” option to enable X-Win

```
[local_prompt]$ ssh -Y username@scc1.bu.edu
username@scc4.bu.edu's Password:
[username@scc1 ~]$ xclock &
```



Commands

Basic Linux commands and system use

This one is long and very hands-on.

Linux: The “prompt”

```
[username@scc1 ~]$
```

This is the “prompt” -- the system is ready to accept commands.

- `username` Your login name
- `scc1` The machine you are on
- `~` The directory you are in

(In Linux “~” is a shorthand for your home directory.)

Linux: Command Basics

At the prompt, you can issue commands

```
[username@scc1 ~]$ command --option argument
```

- **Command:** command that does one thing
- **Options:** change the way a command does that one thing
 - Short form: single-dash and one letter e.g. `ls -a`
 - Long form: double-dash and a word e.g. `ls --all`
- **Argument:** provides the input/output that the command interacts with.

For more information about any command, use `man` or `info` (e.g. “`man ls`”)

Linux: Everyday Commands

- Refer to the “SCC Getting Started” handout/PDF.
- For time, I’ll only mention the most common/useful commands.
- Please ask questions (this is a lot of information)

http://rcs.bu.edu/documents/SCC_GettingStarted.pdf

Command Hands-On: Your Account

```
[cjahnke@scc1 ~]$ id cjahnke
uid=23175(cjahnke) gid=4939(scv) groups=4939(rcs),1003(apps),2000(tutorial)
```

```
[cjahnke@scc1 ~]$ groups cjahnke
rcs apps tutorial
```

```
[cjahnke@scc1 ~]$ finger cjahnke
Login: cjahnke                Name: Charles Jahnke
Directory: /usr3/bustaff/cjahnke  Shell: /bin/bash
On since Tue Jun 28 16:11 (EDT) on pts/161 from bumc.bu.edu
Mail forwarded to cjahnke@bu.edu
No mail.
No Plan.
```

```
[cjahnke@scc1 ~]$ quota -s
Home Directory Usage and Quota:
Name      GB  quota  limit  in_doubt  grace |  files  quota  limit  in_doubt  grace
cjahnke   7.37  10.0   11.0    0.0      none | 39144  200000 200000  40       none
```

```
[cjahnke@scc1 ~]$ pquota rcs
```

project space	quota (GB)	quota (files)	usage (GB)	usage (files)
/project/rcs	50	1638400	21.00	687
/projectnb/rcs	1050	33554432	2.01	1454

Command Hands-On: Directory Navigation

```
[cjahnke@scc1 ~]$ pwd  
/usr3/bustaff/cjahnke
```

```
[cjahnke@scc1 ~]$ ls  
TheJungleBook.txt  directory1
```

```
[cjahnke@scc1 ~]$ mkdir new_directory
```

```
[cjahnke@scc1 ~]$ ls -l  
total 69420  
drwxr-xr-x 3 cjahnke rcs      512 Nov 14  2015 directory1  
-rwxr-xr-x 5 cjahnke rcs      512 Nov 14  2015 TheJungleBook.txt  
drwxr-xr-x 3 cjahnke rcs      512 Jun 28  2016 new_directory
```

```
[cjahnke@scc1 ~]$ cd new_directory
```

```
[cjahnke@scc1 new_directory]$ ls  
<empty>
```

```
[cjahnke@scc1 new_directory]$ cd ..
```

```
[cjahnke@scc1 ~]$ rmdir new_directory
```


Command Hands-On: Viewing Text Files

```
[cjahnke@scc1 ~]$ wget http://rcs.bu.edu/documents/TheJungleBook.txt
```

```
[cjahnke@scc1 ~]$ cat TheJungleBook.txt  
# WHOA! That's too much!
```

```
# Let's "catenate" the book to look.
```

```
[cjahnke@scc1 ~]$ head TheJungleBook.txt  
The Project Gutenberg eBook of The Jungle Book, by Rudyard Kipling
```

```
# Just the top (head) of the file.
```

```
This eBook is for the use of anyone anywhere at no cost and with  
almost no restrictions whatsoever. You may copy it, give it away or  
re-use it under the terms of the Project Gutenberg License included  
with this eBook or online at www.gutenberg.org
```

```
Title: The Jungle Book
```

```
# OK, That's more manageable
```

```
[cjahnke@scc1 ~]$ tail TheJungleBook.txt  
Most people start at our Web site which has the main PG search facility:
```

```
# Now the bottom (tail) of the file.
```

```
http://www.gutenberg.org
```

```
This Web site includes information about Project Gutenberg-tm,  
including how to make donations to the Project Gutenberg Literary  
Archive Foundation, how to help produce our new eBooks, and how to
```

```
subscribe to our email newsletter to hear about new eBooks.
```

```
[cjahnke@scc1 ~]$ less TheJungleBook.txt  
# Press "q" to quit
```

```
# Now read page by page with a "pager"
```

Command Hands-On: Finding Things

```
# Search the directory for files:
```

```
[cjahnke@scc1 ~]$ find . -name "TheJungleBook.txt"  
./TheJungleBook.txt
```

```
# Search a file for text:
```

```
[cjahnke@scc1 ~]$ grep Mowgli TheJungleBook.txt
```

```
    Mowgli's Brothers
```

```
    Mowgli's Song
```

```
Mowgli's Brothers
```

```
frog. O thou Mowgli--for Mowgli the Frog I will call thee--the time will  
night of the Pack Meeting took them and Mowgli and Mother Wolf to the  
Wolf pushed "Mowgli the Frog," as they called him, into the center,
```

```
...
```

```
..
```

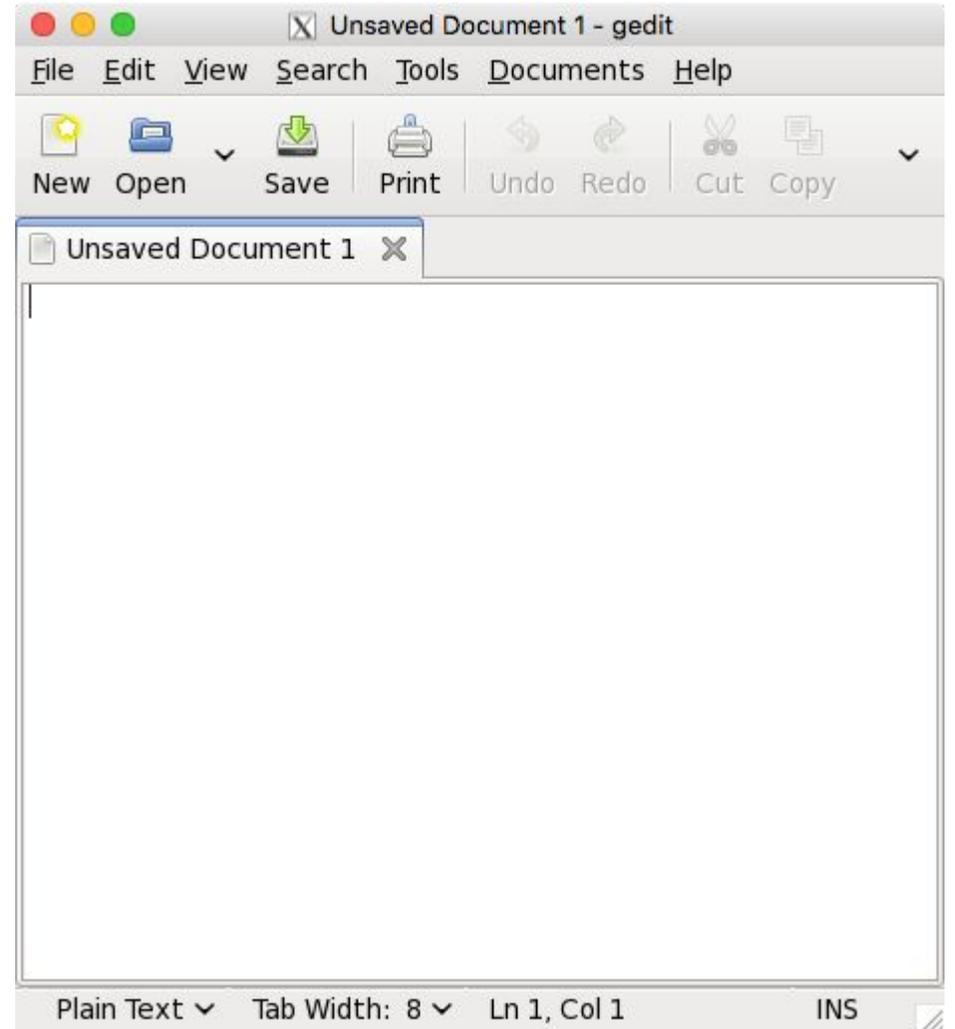
```
.
```

```
# 216 Lines
```

Command Hands-On: Editing Files

```
[cjahnke@scc1 ~]$ gedit
# Normal, foreground process.
# Close the GUI to get prompt.
```

```
[cjahnke@scc1 ~]$ gedit &
[cjahnke@scc1 ~]$
# Background process.
```



Command Hands-On: Editing Text Files

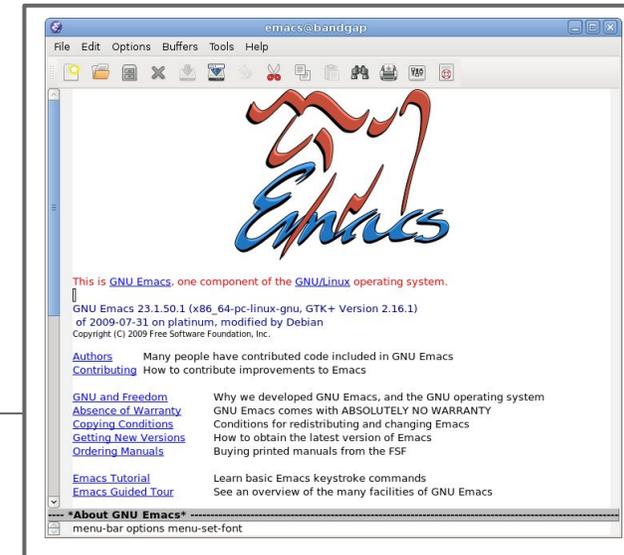
Command Interface

- **nano** - “Nano's ANOther” editor
- **emacs** - Programming Editor
- **vim** / **vi** - Visual IMproved
- Others

```
#!/bin/sh
if [ "$SOLAR_BIN" = "" ]
then
  SOLAR_BIN=/opt/app1/solar/4.2.2/bin
fi
if [ "$SOLAR_LIB" = "" ]
then
  SOLAR_LIB=/opt/app1/solar/4.2.2/lib
fi
PATH=$SOLAR_BIN:$PATH
LD_LIBRARY_PATH=$SOLAR_LIB:$LD_LIBRARY_PATH
#TCL_LIBRARY=$SOLAR_LIB/tcl8.0.5
#TK_LIBRARY=$SOLAR_LIB/tk8.0.5
TCL_LIBRARY=$SOLAR_LIB/tcl8.4
TK_LIBRARY=$SOLAR_LIB/tk8.4
SOLAR_PROGRAM_NAME=$0
export SOLAR_BIN
export SOLAR_LIB
export PATH
export LD_LIBRARY_PATH
export TCL_LIBRARY
export TK_LIBRARY
export SOLAR_PROGRAM_NAME
if [ ! -s $SOLAR_BIN/solarmain ]
then
  echo "The directory $SOLAR_BIN for solar binaries is not accessible."
else
  $SOLAR_BIN/solarmain $*
fi
~
~
1,1 All
```

Graphical Interface

- **gedit** - Gnome EDITor
- **emacs** - Programming Editor
- **gvim** - GUI VIM
- Others



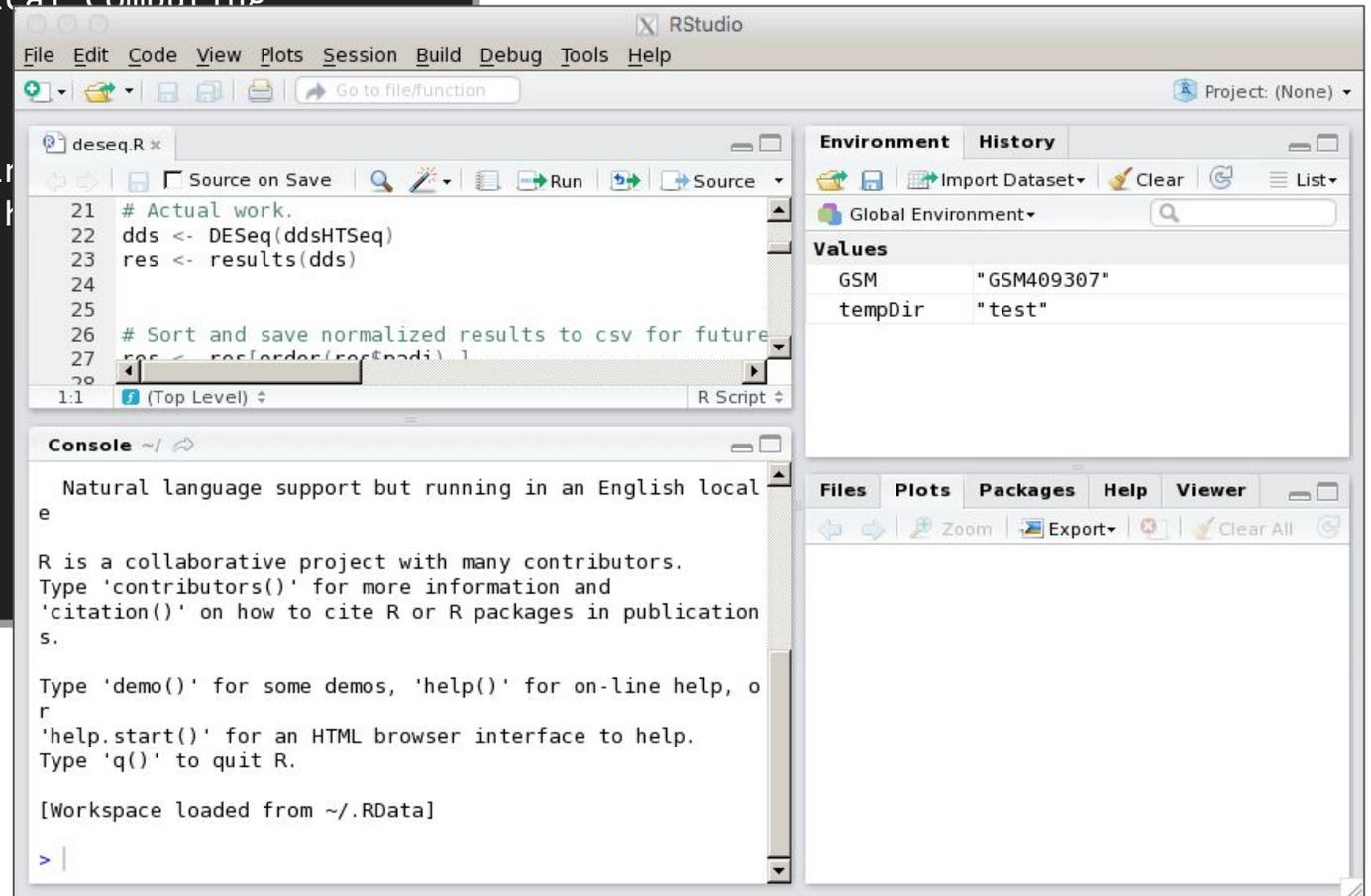
Command Hands-On: Applications

```
[cjahnke@scc1 ~]$ R
R version 2.15.3 (2013-03-01) -- "Security Blanket"
Copyright (C) 2013 The R Foundation for Statistical Computing
ISBN 3-900051-07-0
Platform: x86_64-unknown-linux-gnu (64-bit)
```

```
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
```

```
>
```

```
[cjahnke@scc1 ~]$ rstudio
```



The screenshot displays the RStudio environment. The main editor window shows a script named 'deseq.R' with the following code:

```
21 # Actual work.
22 dds <- DESeq(ddsHTSeq)
23 res <- results(dds)
24
25
26 # Sort and save normalized results to csv for future
27 res <- res[order(res$negLog10(padj)), ]
28
```

The console window shows the following output:

```
Natural language support but running in an English locale
R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Workspace loaded from ~/.RData]
> |
```

The Environment pane on the right shows the following values:

Variable	Value
GSM	"GSM409307"
tempDir	"test"

- More on this later.

Command Hands-On: Transferring Remote Files

- Transfer files from your local system (laptop)
 - Use the SFTP application you downloaded earlier.
- Transfer files from remote Linux system

```
[cjahnke@scc1 ~]$ scp username@remotehost.com:/path/to/file .  
[cjahnke@scc1 ~]$ rsync -a username@remotehost.com:/path/to/file .
```

- Download files from the internet/webpages



```
[cjahnke@scc1 ~]$ wget http://rcs.bu.edu/documents/sample.vcf  
--2016-06-28 18:25:47-- http://rcs.bu.edu/documents/sample.vcf  
Connecting to rcs.bu.edu|128.197.160.76|:80... connected.  
HTTP request sent, awaiting response... 200 OK  
Length: 298778 (292K) [text/plain]  
100%[=====>] 298,778      1.79M/s   in 0.2s  
  
2016-09-20 18:25:48 (1.79 MB/s) - `sample.vcf' saved [298778/298778]
```

dos2unix / unix2dos

- Windows and Linux define “end of line” differently
 - Windows: “\r\n” (“^M”)
 - Linux: “\n”
- **dos2unix** - DOS to UNIX text file format converter

```
[cjahnke@scc1 ~]$ dos2unix input.txt # Convert and replace input.txt
```

```
[cjahnke@scc1 ~]$ dos2unix input.txt output.txt # write output to new file.
```

Permissions

Users, Groups, and File Ownership

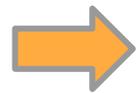
This one is quick, but important.

Users, Groups, and File Ownership

SCC is a Multi-user System

Real users:

- There are many users
- There are many groups
- Users can belong to multiple groups



Access control:

- Every file has an owner
- Every file belongs to a group
- Every file has “permissions”

Changing Ownership

- **chown** - Change file owner and group
 - `chown [OPTION]... [OWNER][:[GROUP]] FILE...`
 - Must have write access to file to make changes.
- Change user ownership of individual file

```
[username@scc1 ~]$ chown cjahnke testfile.txt
```

- Change user and group ownership of file

```
[username@scc1 ~]$ chown cjahnke:rsc testfile.txt
```

Changing Permissions

- **chmod** - Change mode (permission) for files
 - `chmod[OPTION] ... MODE[,MODE] ... FILE...`
 - Must have write access to file to make changes.
- Mode has 2 formats:
 - Octal: base-8 bit representation

```
[username@scc1 ~]$ chmod 750 testfile.txt
```

- Symbolic: u/g/o, r/w/x, and +/-/= define permissions

```
[username@scc1 ~]$ chmod u+rwx,g+rx,o-r testfile.txt
```

Using the System (Part 3)

Some basic tools, utilities, and methods

Basic Tools, Utilities, and Methods

We'll cover some basic tools

- Word Count (**wc**)
- Column Segmentation (**cut**)
- Line Sort (**sort**)

Use them to demonstrate methods

- **Pipes**
 - Command input and output
- **Redirection**
 - File input and output

Download Sample File:

```
[cjahnke@scc1 ~]$ wget http://rcs.bu.edu/documents/sample.vcf
```

Hands-On: New file to work with

Just a few lines from a VCF file, let's take a look.

```
[cjahnke@scc1 ~]$ cat sample.vcf
#CHROM POS ID REF ALT QUAL FILTER INFOFORMAT
3 14370 rs6054257 G A 29 PASSNS=3;DP=14;AF=0.5;DB;H2 GT:GQ:DP:HQ
2 17330 . T A 3 q10 NS=3;DP=11;AF=0.017 GT:GQ:DP:HQ
1 1110696 rs6040355 A G,T 67 PASSNS=2;DP=10;AF=0.333,0.667;AA=T;DB GT:GQ:DP:HQ
3 1230237 . T . 47 PASSNS=3;DP=13;AA=T GT:GQ:DP:HQ
6 1234567 microsat1 GTCTG,GTACT 50 PASSNS=3;DP=9;AA=G GT:GQ:DP
```

```
[cjahnke@scc1 ~]$ column -t sample.vcf
#CHROM POS ID REF ALT QUAL FILTER INFO
3 14370 rs6054257 G A 29 PASS NS=3;DP=14;AF=0.5;DB;H2
2 17330 . T A 3 q10 NS=3;DP=11;AF=0.017
1 1110696 rs6040355 A G,T 67 PASS NS=2;DP=10;AF=0.333,0.667
3 1230237 . T . 47 PASS NS=3;DP=13;AA=T
6 1234567 microsat1 GTCT G,GTACT 50 PASS NS=3;DP=9;AA=G
```

Hands-On: Word Count (**wc**)

- Count Everything

```
[cjahnke@scc1 ~]$ wc sample.vcf  
6 72 573 sample.vcf
```

- Count Lines

```
[cjahnke@scc1 ~]$ wc -l sample.vcf  
6 sample.vcf
```

- Count Words

```
[cjahnke@scc1 ~]$ wc -w sample.vcf  
72 sample.vcf
```

Hands-On: Column Segmentation (**cut**)

- Cut the second column to view the positions

```
[cjahnke@scc1 ~]$ cut -f2 sample.vcf
POS
14370
17330
1110696
1230237
1234567
```

- Cut multiple columns to few position, quality and status

```
[cjahnke@scc1 ~]$ cut -f2,6,7 sample.vcf
POS  QUAL  FILTER
14370    29  PASS
17330     3  q10
1110696  67  PASS
1230237  47  PASS
1234567  50  PASS
```

Hands-On: Sort (**sort**)

- Sort the file by FILTER (key #7)

```
[cjahnke@scc1 ~]$ sort -k7 sample.vc
#CHROM  POS      ID          REF  ALT  ID      QUAL  FILTER  INFO
1       1110696  rs6040355   A    G,T   67     PASS   NS=2;DP=10;AF=0.333,0.667
3       1230237  .           T    .     47     PASS   NS=3;DP=13;AA=T
3       14370    rs6054257   G    A     29     PASS   NS=3;DP=14;AF=0.5;DB;H2
6       1234567  microsat1   GTCT G,GTACT 50     PASS   NS=3;DP=9;AA=G
2       17330    .           T    A     3      q10    NS=3;DP=11;AF=0.017
```

- Too much info, I only want CHROM and POS for SNPs that passed.

```
[cjahnke@scc1 ~]$ sort -k7 sample.vcf | cut -f1,2,7
#CHROM  POS  FILTER
1       1110696  PASS
3       1230237  PASS
3       14370    PASS
6       1234567  PASS
2       17330    q10
```

Pipes

- Pipes (“|”) redirect the standard output of a command to the standard input of another command.
- Example:

```
[cjahnke@scc1 ~]$ cat sample.vcf | cut -f1,2,7 | sort -k3
```

cat sample.vcf

#CHROM	POS	ID	REF	...
3	14370	rs6054257	G	...
2	17330	.	T	...
1	1110696	rs6040355	A	...
3	1230237	.	T	...
6	1234567	microsat1	GTCT	...

cut -f1,2,7

#CHROM	POS	FILTER
3	14370	PASS
2	17330	q10
1	1110696	PASS
3	1230237	PASS
6	1234567	PASS

sort -k3

#CHROM	POS	FILTER
1	1110696	PASS
3	1230237	PASS
3	14370	PASS
6	1234567	PASS
2	17330	q10

Redirection

- The “>” symbol redirects the output of a command to a file.

Redirection	Description
COMMAND < filename	Input - Directs a file 
COMMAND << stream	Input - Directs a stream literal
COMMAND <<< string	Input - Directs a string
COMMAND > filename	Output - Writes output to file (will “clobber”) 
COMMAND >> filename	Output - Appends output to file 

- Example:

```
[cjahnke@scc1 ~]$ cat sample.vcf | cut -f1,2,7 | sort -k3 > sorted.txt
```

Variables and Environment Variables

Variables and Environment Variables

- Variables are named storage locations.
 - `USER=cjahnke`
 - `foo="this is foo's value"`
- “Environment variables” are used by the shell to store information
 - For example, `$PATH` tells the path where to look for commands.
- Environment variables are shared with programs that the shell runs.

Bash variables

- To create a new variable, use the assignment operator '='

```
[username@scc1 ~]$ foo="this is foo's value"
```

- The foo variable can be shown with **echo**

```
[username@scc1 ~]$ echo $foo  
this is foo's value
```

- To make \$foo visible to programs run by the shell (i.e., make it an “environment variable”), use **export**:

```
[username@scc1 ~]$ export foo
```

Environment Variables

- To see all currently defined environment variable, use **printenv**:

```
[username@scc1 ~]$ printenv
HOSTNAME=scc4
TERM=xterm-256color
SHELL=/bin/bash
HISTSIZE=1000
TMPDIR=/scratch
SSH_CLIENT=168.122.9.131 37606 22
SSH_TTY=/dev/pts/191
USER=cjahnke
MAIL=/var/spool/mail/cjahnke
PATH=/usr3/bustaff/cjahnke/apps/bin:/usr/local/apps/pgi-13.5/bin:/usr/java/default/jre/bin:/usr/java/default/bin:/usr/lib64/qt-3.3/bin:/usr/local/bin:/bin:/usr/local/sbin:/usr/sbin:/sbin:/usr3/bustaff/cjahnke/bin
PWD=/usr3/bustaff/cjahnke/linux-materials
LANG=C
MODULEPATH=/share/module/bioinformatics:/share/module/chemistry
SGE_ROOT=/usr/local/ogs-ge2011.11.p1/sge_root
HOME=/usr3/bustaff/cjahnke
```

Software and Modules

Software (without modules)

- Many tools/utilities are available from the basic system environment
- Some big-name software applications are too:
 - MATLAB
 - SAS
 - STATA
- Others require **Modules**

Software (without modules)

- Modules allow users to access *non-standard* tools or *alternative versions* of standard packages.
- This is also an method for customizing your environment as required for certain packages.
- Most software packages on SCC are configured this way.

Module Usage

Command	Description
<code>module list</code>	List currently loaded modules.
<code>module avail</code>	List available packages.
<code>module help [modulefile]</code>	Displays description of specified module.
<code>module show [modulefile]</code>	Displays environment modifications for specified module.
<code>module load [modulefile]</code>	Loads specified module into environment.
<code>module unload [modulefile]</code>	Unloads specified module from environment.
<code>module purge</code>	Unloads all loaded modules.

RCS Software Website

The screenshot displays the RCS Software Website interface. At the top, there is a dark navigation bar with links for "RCS Support", "Software Support", "Training", and "Request Software", along with a green "Get Help" button. Below the navigation bar, the main content area is titled "RCS SOFTWARE". On the left, there is a list of categories with checkboxes, including "Show All Categories", "chemistry", "math-eng", "desktop", "bioinformatics", "visualization", "programming", "gis", "imaging", "libraries", "utilities", "hadoop", and "statistics". A search bar labeled "Search Checked Categories" is positioned above the category lists. Below the "bioinformatics" category, a grid of software tools is listed, including abyss, annovar, bayescan, beam, blast, bowtie2, cc3d, clustalomega, cutadapt, diffreps, dsk, entrez-direct, fastx-toolkit, flux-capacitor, gatb-core, geneid, admixmap, augustus, bcftools, bedtools, blast+, breakdancer, celera, cobratoolbox, deeptools, discosnp, EIGENSOFT, epacts, fbat, flux-simulator, gatb-tools, genome, allpaths_lg, bamtools, bcl2fastq, bfast, blat, bwa, chunkchromosome, CPAT, defuse, dnanexus-dx, elph, fastqc, fcgene, gapcloser, gatk, genomestrip, amos, bamutil, beagle, blasr, bowtie, casava, circexplorer, cufflinks, delly, dnanexus-ua, emmax, faststructure, fhsp, gapfiller, gcta, and genowap.

Software Website: <http://rcs.bu.edu/software/#/>

Module Hands-On

```
[cjahnke@scc1 ~]$ plink
-bash: plink: command not found

[cjahnke@scc1 ~]$ module avail plink
----- /share/module/bioinformatics -----
plink/1.07          plink/1.90b          plink/1.90b3b
plink/1.90a        plink/1.90b2i

[cjahnke@scc1 ~]$ module load plink

[cjahnke@scc1 ~]$ module list
Currently Loaded Modulefiles:
  1) pgi/13.5          2) plink/1.90b3b

[cjahnke@scc1 ~]$ plink -h
PLINK v1.90b3b 64-bit (15 Jan 2015)      https://www.cog-genomics.org/plink2
(C) 2005-2015 Shaun Purcell, Christopher Chang   GNU General Public License v3

plink [input flag(s)...] {command flag(s)...} {other flag(s)...}
plink --help {flag name(s)...}
```

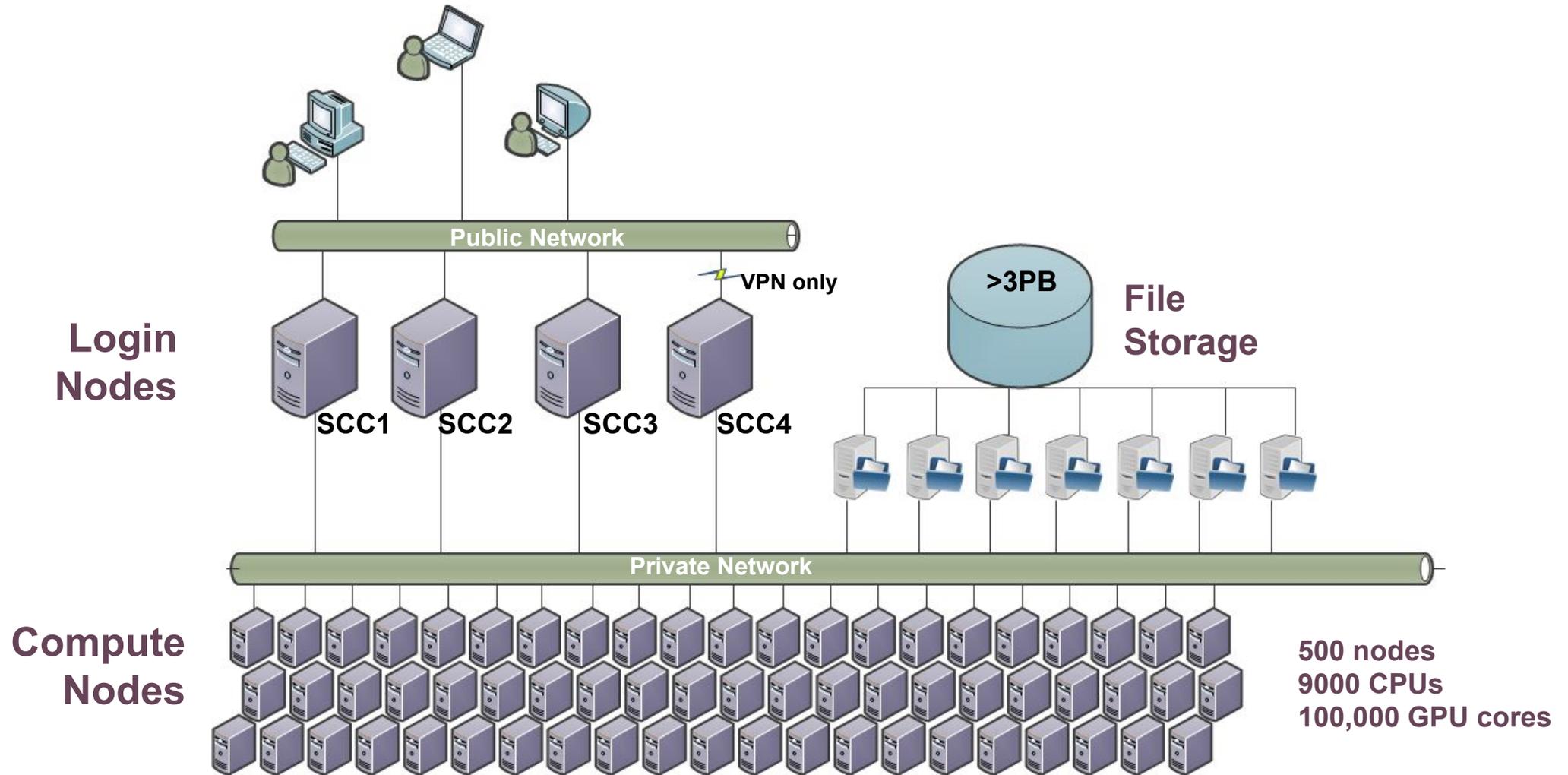
New Applications and Requests

- New packages are developed every day.
- Users can compile/install packages for personal use in home directories and project spaces.
- Users can request global installation of software:
 - Complete form on our website (Link below)
 - send an email to help@scc.bu.edu

The Shared Computing Cluster (SCC)

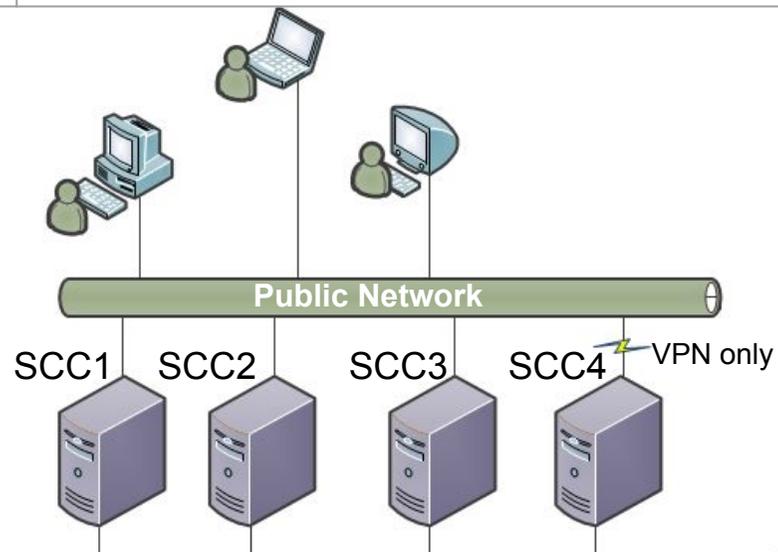
Cluster Architecture, File Storage and the Batch System

SCC Architecture



Choose a Login Node

Login Node	Hostname	Description
SCC1	scc1.bu.edu	General purpose login node, accessible from internet
SCC2	scc2.bu.edu	General purpose login node, accessible from internet
SCC3	geo.bu.edu	Earth and Environment department node.
SCC4	scc4.bu.edu	BUMC login node. Access to /restricted/project data. Requires BU network or VPN.



File Storage on SCC

Storage Locations on SCC

- More than just your home directory!

Location	Backed-up Internally	Disaster Recovery
Home Directory: ~	Yes - 180 Days	Yes
Project Space: /project/{projectname}	Yes - 180 Days	Yes
Project "NB" Space: /projectnb/{projectname}	Yes - 30 Days	No

- And some special cases too

Location	Backed-up Internally	Disaster Recovery
STASH /stash/{projectname}	Yes - 30 Days	Yes
Archive /archive/{type}/{projectname}	N/A	Conditional (\$)

Restricted Data

Some data requires dbGaP compliance or other restrictions.

- Policies for “project” and “projectnb” in previous slides is replicated for the /restricted filesystem.
- Only accessible through scc4.bu.edu and compute nodes

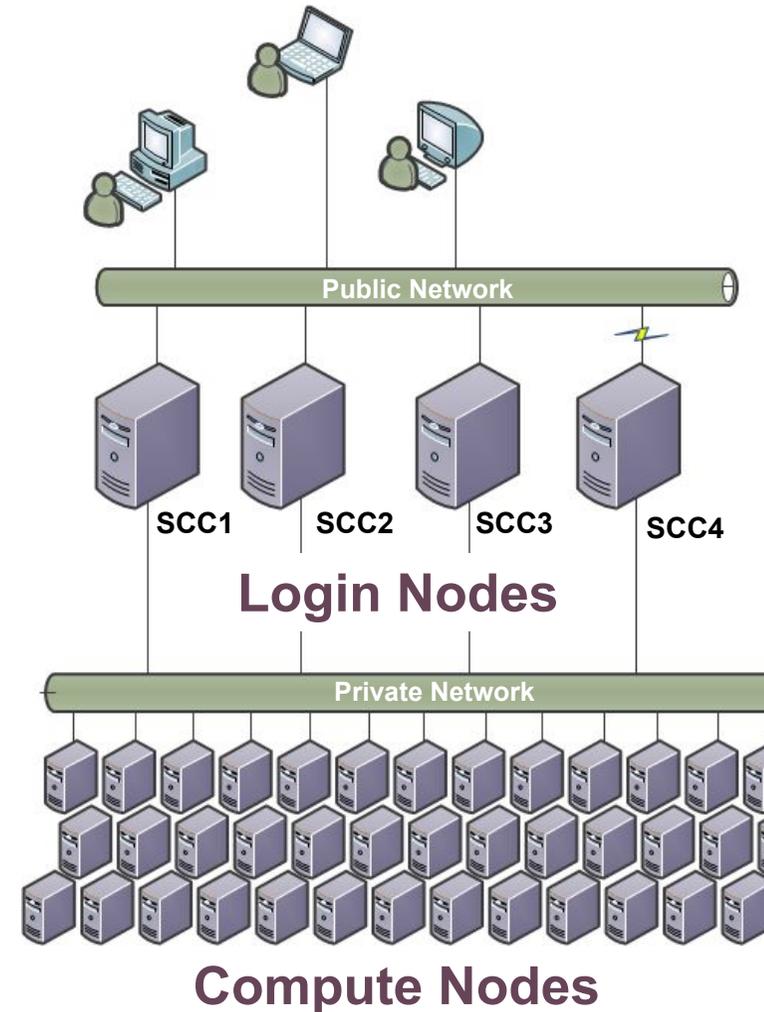
Restricted Space		Description
Restricted Project	<code>/restricted/project/{projectname}</code>	/project/ space equivalent for restricted data
Restricted ProjectNB	<code>/restricted/projectnb/{projectname}</code>	/projectnb/ space equivalent for restricted data

The Batch System

Submitting and Monitoring Batch Jobs

Batch System Overview

- Login nodes are busy!
 - Limited resource
 - Limited runtime (15 min)
- Compute Nodes provide reserved resources
 - Many more nodes
 - Many types of resources
- “Fair Share” scheduling



Types of Jobs

Interactive

- Just like the login node
- Can type, view output, open files, run commands
- “Interactive”

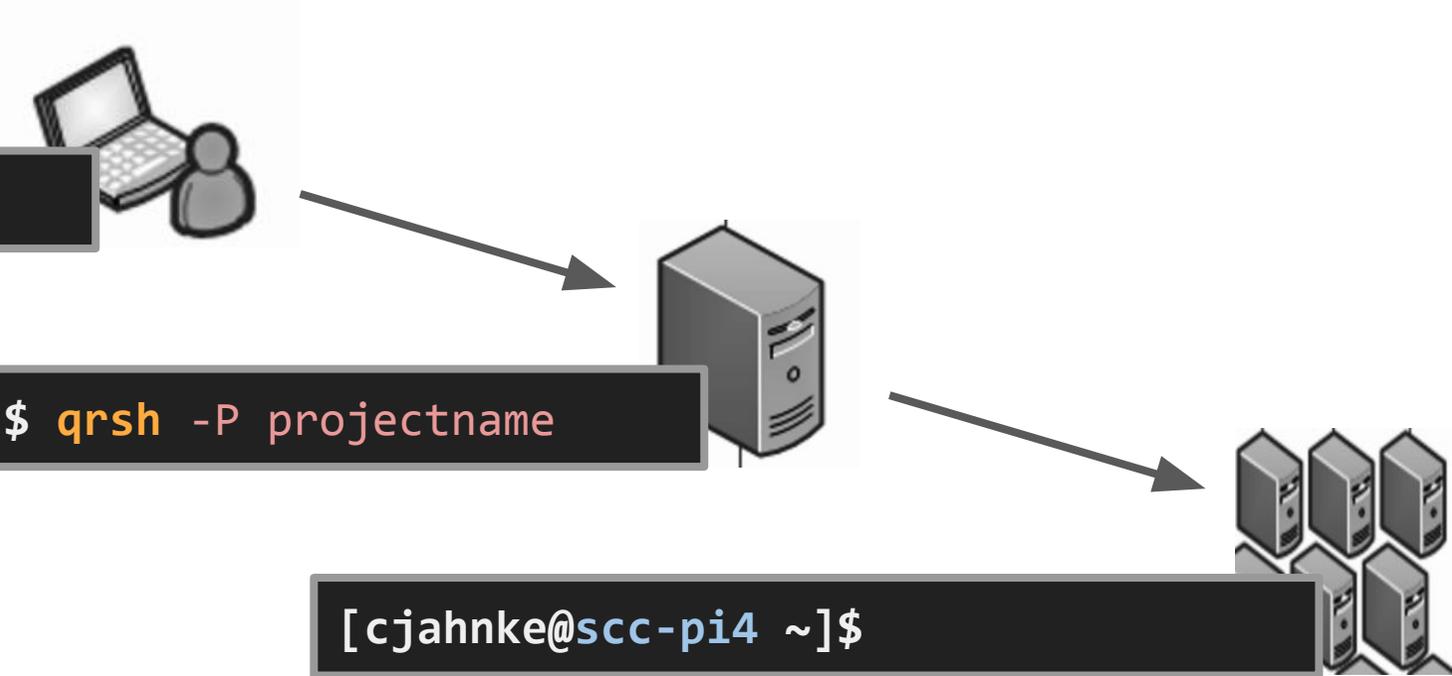
Non-Interactive “Batch”

- Blind
- Instructions coordinated with a script or binary
- Easy to run 1000’s at a time.

Interactive

Interactive jobs are submitted with the “**qrsh**” command:

```
qrsh [options] [ command [ command_arguments ] ]
```



```
[local_PC]$ ssh username@scc1.bu.edu
```

```
[cjahnke@scc1 ~]$ qrsh -P projectname
```

```
[cjahnke@scc-pi4 ~]$
```

Hands-On: Submitting an Interactive Job

A prompt! Now we can issue commands and run applications **interactively**.

```
cjahnke:~$ ssh -Y scc1.bu.edu
cjahnke@scc1.bu.edu's password:
*****
This machine is governed by the University policy on ethics.
http://www.bu.edu/tech/about/policies/computing-ethics/

This machine is owned and administered by
Boston University.

See the Research Computing web site for more information about our facilities.
http://www.bu.edu/tech/support/research/

Please send questions and report problems to "help@scc.bu.edu".

*****

[cjahnke@scc1 ~]$ qssh -P sibs
Last login: Tue Apr 26 14:42:05 2016 from scc4p.scc.bu.edu
*****
This machine is governed by the University policy on ethics.
http://www.bu.edu/tech/about/policies/computing-ethics/

This machine is owned and administered by
Boston University.

See the Research Computing web site for more information about our facilities.
http://www.bu.edu/tech/support/research/

Please send questions and report problems to "help@scc.bu.edu".

*****

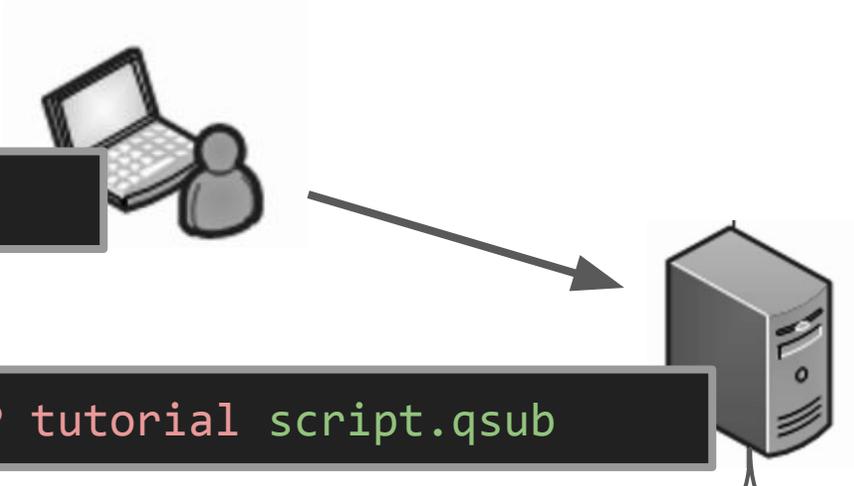
[cjahnke@scc-pi4 ~]$
```

Non-Interactive “Batch” Job

Non-Interactive jobs are submitted with the “**qsub**” command:

```
qsub [options] command [arguments]
```

```
[local_PC]$ ssh username@scc1.bu.edu
```



```
[cjahnke@scc1 ~]$ qsub -P tutorial script.qsub
```

Hands-On: Submitting a Batch Job

We need a script.

Submit script to scheduler

We get our prompt back.
(Still the head node)

After completion, we get an
output file.

```
[cjahnke@scc1 ~]$ wget http://rcs.bu.edu/documents/test.qsub
```

```
[cjahnke@scc1 ~]$ qsub -P projectname test.qsub  
Your job 9253374 ("test") has been submitted
```

```
[cjahnke@scc1 ~]$
```

```
[cjahnke@scc1 ~]$ ls  
test.qsub  test.o9253374
```

The qsub File

- Just a text file.
 - Usually with extension “.qsub” or “.sh”
- Contains scheduler “directives”
 - These tell the scheduler how to orchestrate the job
 - Notification (email), Accounting, Runtime, Number of cores, Number of tasks, and more
- Contains the commands you want to run
 - Load modules
 - Single commands line by line
 - Entire pipelines

Hands-On: The qsub File

Script Interpreter

Scheduler Directives

Task Commands

```
#!/bin/bash -l

#$ -P sibs
#$ -N test
#$ -j y
#$ -m bae

echo "====="
echo "Starting on : $(date)"
echo "Running on node : $(hostname)"
echo "Current directory : $(pwd)"
echo "Current job ID : $JOB_ID"
echo "Current job name : $JOB_NAME"
echo "====="

module load R
sleep 10
echo hello, world

echo "====="
echo "Finished on : $(date)"
echo "====="
```

Monitoring Running Jobs

- Use **qstat** to monitor the queue status
 - Think “Queue Status” == qstat
 - Shows all users jobs. Usually a very long list
 - The “**-u [username]**” option will show a single user

```
[cjahnke@scc1 ~]$ qstat -u cjahnke
job-ID  prior   name       user          state submit/start at           queue                slots ja-task-ID
-----
5186514 0.11176 test      cjahnke       r   06/29/2016 16:06:58  l@scc-ka4.scc.bu.edu    1
```

Completed Job Info

- Use **qacct** query the query the accounting system
 - Think “Queue Accounting” == qacct
 - Many options to tailor query
 - user
 - jobid
 - date run
 - See “man qacct”

```
[cjahnke@scc1 ~]$ qacct -j 9253374
=====
qname          linga
hostname       scc-ka4.scc.bu.edu
group          sibs
owner          cjahnke
project        sibs
department     defaultdepartment
jobname        test
jobnumber      9253374
taskid         undefined
account        sge
priority       0
qsub_time      Wed Jun 29 12:35:21 2016
start_time     Wed Jun 29 12:35:37 2016
end_time       Wed Jun 29 12:35:47 2016
granted_pe     NONE
slots          1
failed         0
exit_status    0
ru_wallclock   10
...
cpu            0.126
mem            0.000
io             0.000
iow            0.000
maxvmem        13.953M
arid           undefined
```

A Standard Single-Processor Job

If no specific resources are requested, your job is allocated:

- 1 “Slot” (Processor core, any type/architecture)
- 12 Hour Runtime
- 4 GB RAM
- No GPU, MPI, or Parallelization

All of these can be modified.

Scheduler Options - General Directives

General Directives	
Directive	Description
-P <i>project_name</i>	Project to which this jobs is to be assigned. Mandatory for all users associated with any BUMC project.
-N <i>job_name</i>	Specifies the job name. The default is the script or command name.
-o <i>outputfile</i>	File name for the stdout output of the job.
-e <i>errfile</i>	File name for the stderr output of the job.
-j <i>y</i>	Merge the error and output stream files into a single file.
-m <i>b e a s n</i>	Controls when the batch system sends email to you. The possible values are – when the job begins (b), ends (e), is aborted (a), is suspended (s), or never (n) – default.
-M <i>user_email</i>	Overwrites the default email address used to send the job report.
-V	All current environment variables should be exported to the batch job.
-v <i>env=value</i>	Set the runtime environment variable <i>env</i> to <i>value</i> .
-hold_jid <i>job_list</i>	Setup job dependency list. <i>job_list</i> is a comma separated list of job ids and/or job names which must complete before this job can run. See Advanced Batch System Usage for more information.

Scheduler Options - Resource Directives

Directives to request SCC resources	
Directive	Description
<code>-l h_rt=hh:mm:ss</code>	Hard runtime limit in <i>hh:mm:ss</i> format. The default is 12 hours.
<code>-l mem_total =#G</code>	Request a node that has at least this amount of memory. Current possible choices include 94G, 125G, 252G 504G.
<code>-l mem_per_core =#G</code>	Request a node that has at least these amount of memory per core.
<code>-l cpu_arch=ARCH</code>	Select a processor architecture (sandybridge, nehalem, etc). See Technical Summary for all choices.
<code>-l cpu_type=TYPE</code>	Select a processor type (E5-2670, E5-2680, X5570, X5670, etc). See Technical Summary for all choices.
<code>-l gpus=G/C</code>	Requests a node with GPU. <i>G/C</i> specifies the number of GPUs per each CPU requested and should be expressed as a decimal number. See Advanced Batch System Usage for more information.
<code>-l gpu_type=GPUMODEL</code>	Current choices for <i>GPUMODEL</i> are M2050, M2070 and K40m, P100. (specific)
<code>-l gpu_c=GPUCAPABILITY</code>	Define the minimum GPU Capability you need for you job (at least)
<code>-l eth_speed=N</code>	Ethernet speed (1 or 10 Gbps).
<code>-l scratch_free=#G</code>	Request a node that has at least this amount of space in scratch. Note that the amount changes!
<code>-pe omp N</code>	Request multiple slots for Shared Memory applications (OpenMP, pthread). This option can also be used to reserve larger amount of memory for the application. <i>N</i> can vary from 1 to 16.
<code>-pe mpi_#_tasks_per_node N</code>	Select multiple nodes for MPI job. Number of tasks can be 4, 8, 12 or 16 and <i>N</i> must be a multiple of this value. See Advanced Batch System Usage for more information.

Getting Help

How to Get Help

Support Website

- <http://rcs.bu.edu> (<http://www.bu.edu/tech/support/research/>)

Upcoming Tutorials:

- <http://rcs.bu.edu/tutorials>

Email (Submit a Ticket):

- help@scc.bu.edu

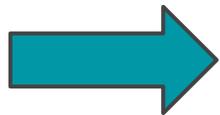
Email Direct:

- cjahnke@bu.edu

Questions?

Research Computing Services Website

<http://rcs.bu.edu>



RCS Tutorial Evaluation

http://rcs.bu.edu/survey/tutorial_evaluation.html

