

Neuroimaging on the Shared Computing Cluster (SCC)

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Resources

- Tutorial Slides will be made available:
 - <https://www.bu.edu/tech/support/research/training-consulting/access-training-materials/>
- Questions, Problems, Need Help?
 - help@scc.bu.edu
 - mhorn@bu.edu

Topics

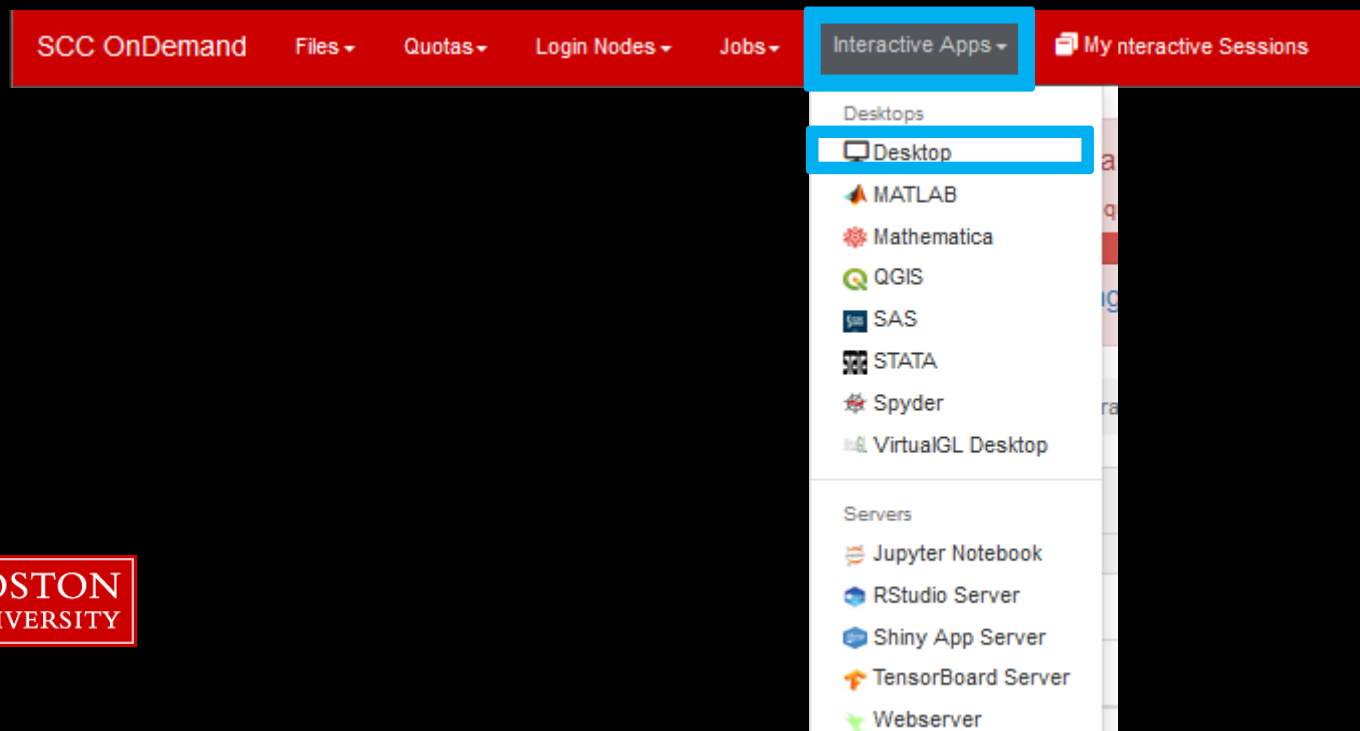
- Get On the SCC
- What/Where/How the SCC?
- OnDemand
- Unix
- Wrangling Imaging Data
- XNAT
- Using the Batch System
- Useful Tools

Topics

- Get On the SCC
- What/Where/How the SCC?
- OnDemand
- Unix
- Wrangling Imaging Data
- XNAT
- Using the Batch System
- Useful Tools

Connect to OnDemand

1. Go to: scc-ondemand-tutorial.bu.edu
2. Username: **tuta#** [random # between 30-99]
3. Password: **Yardbirds#**
4. Click: Interactive Apps
5. Click: Desktop



Connect to OnDemand

Desktop
This app will launch an interactive desktop on a compute node.

List of modules to load (space separated)

Working Directory

The directory to start in. (Defaults to home directory.)

Initial command to run

Number of hours

Number of cores

Number of gpus

Project

Extra qsub options

I would like to receive an email when the session starts

* The Desktop session data for this session can be accessed under the data root directory.

3 hours

1 core

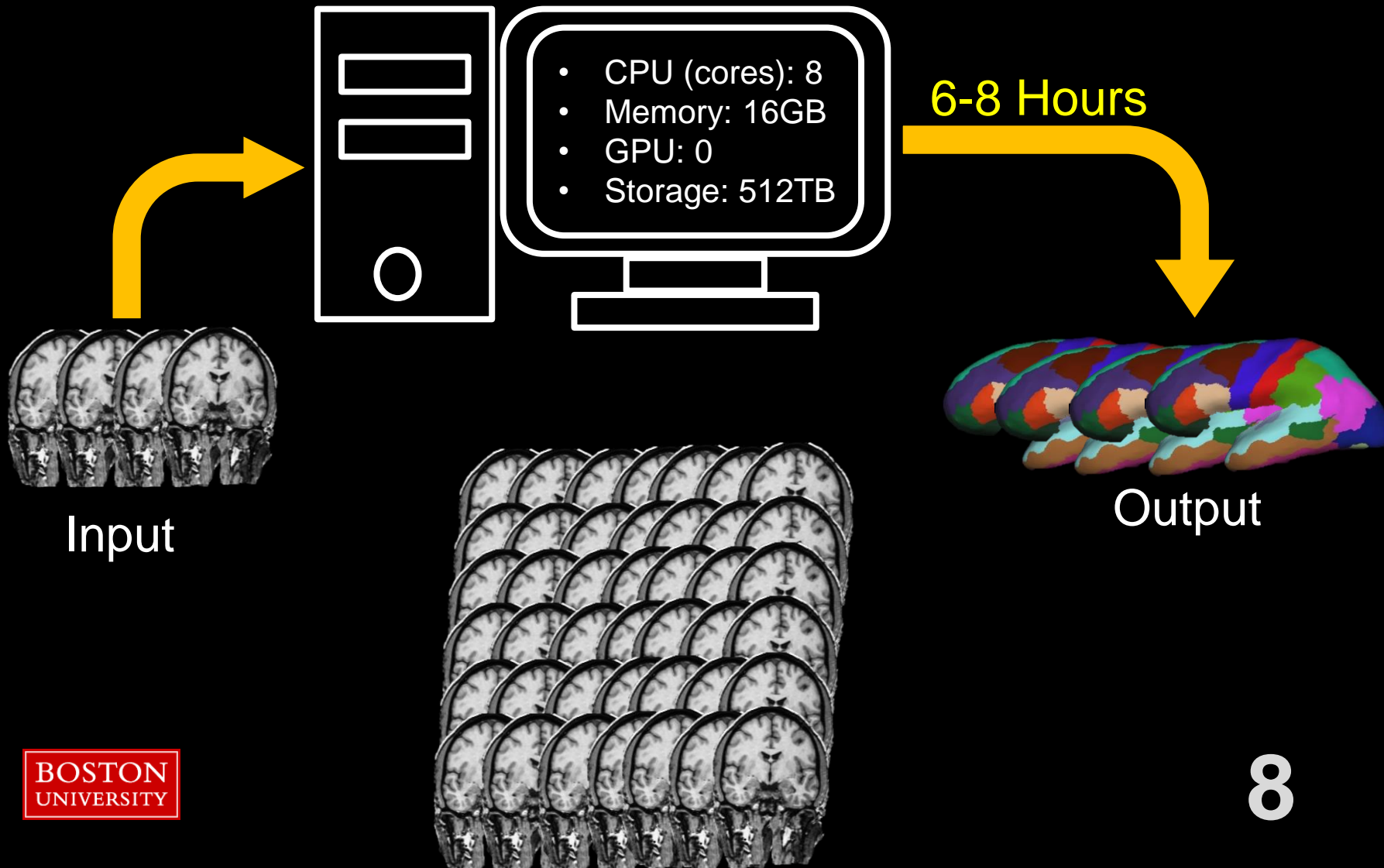
project-ID

click launch!

Topics

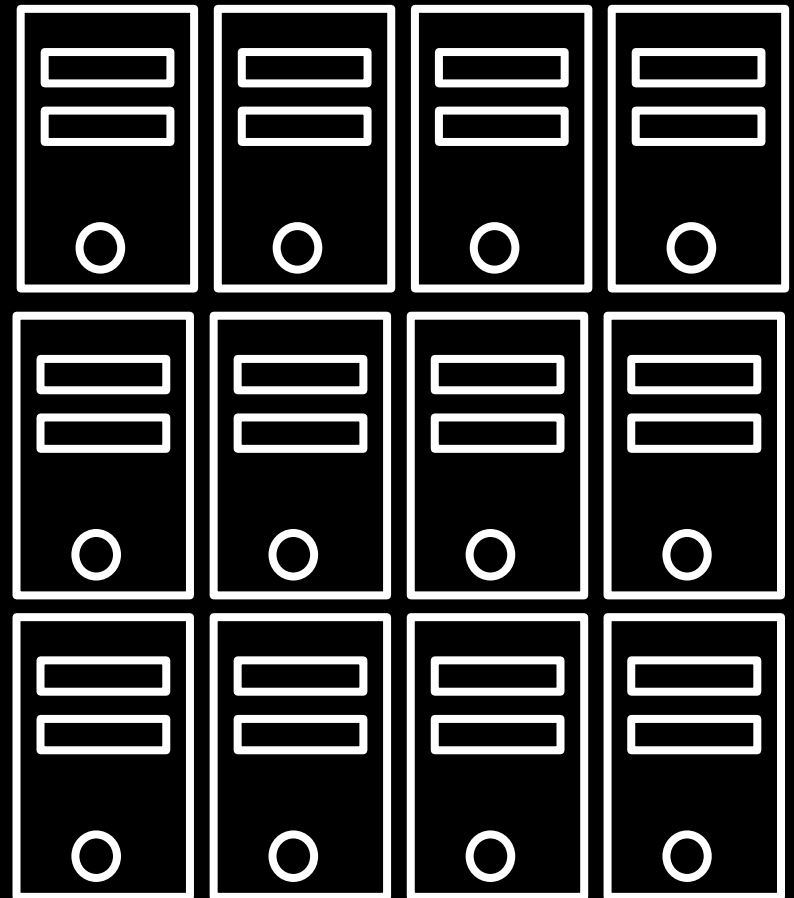
- Get On the SCC
- What/Where/How the SCC?
- OnDemand
- Unix
- Wrangling Imaging Data
- XNAT
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- Useful Tools

What is the SCC?

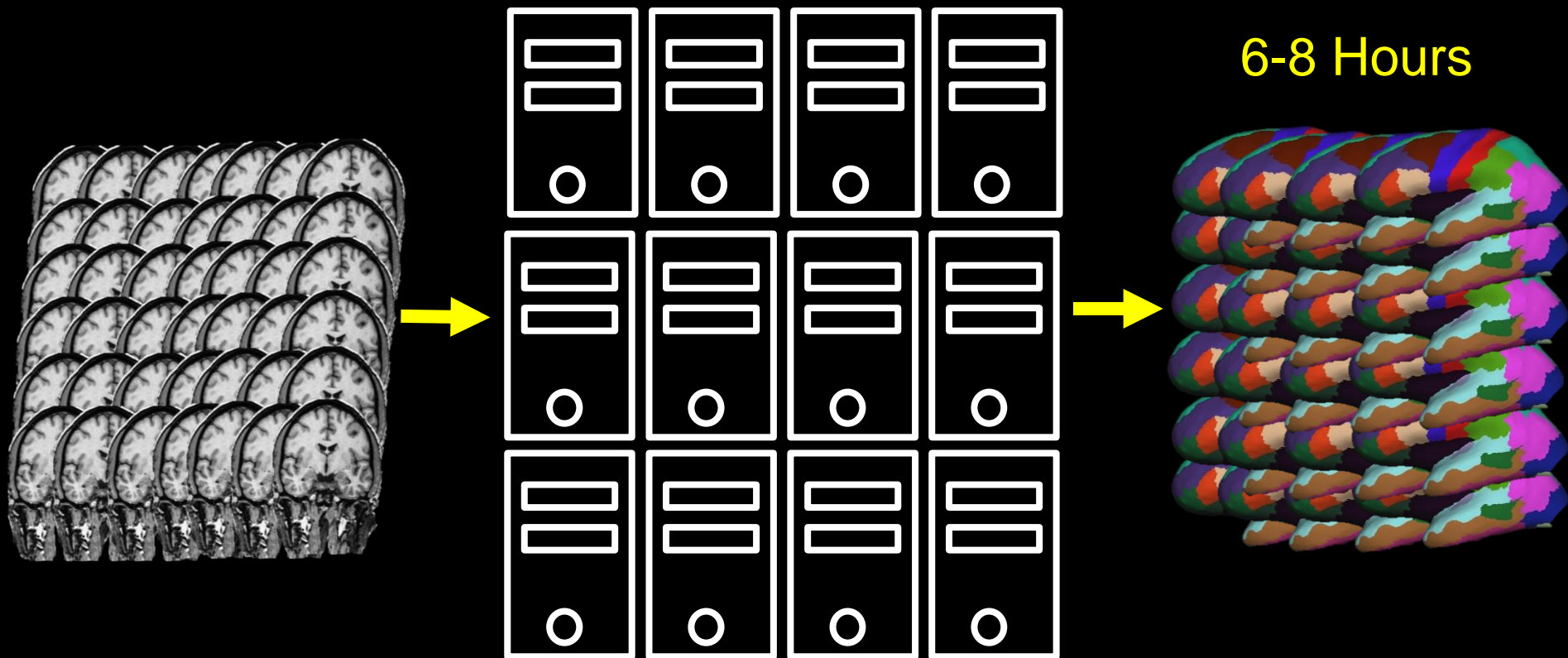


What is the SCC?

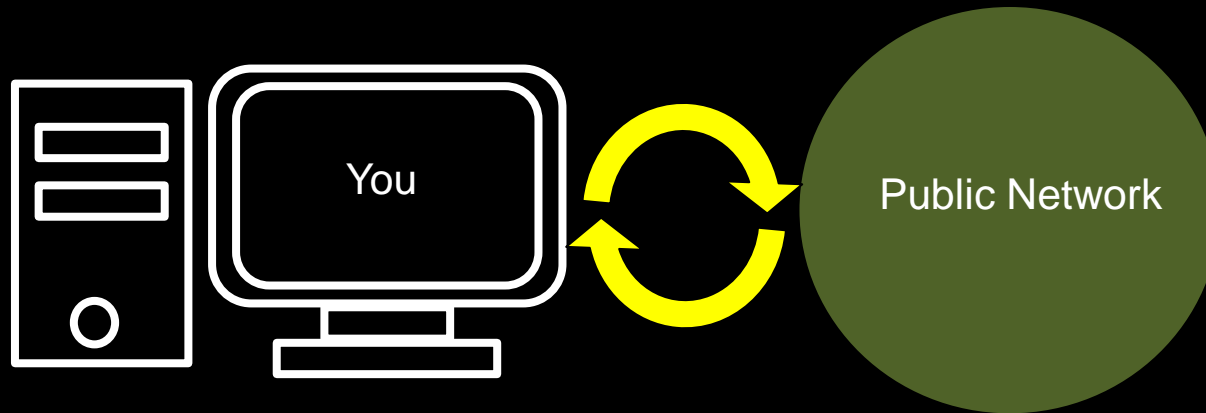
- > 900 Computers (nodes)
- > 25,000 CPUs (cores)
- > 100 GPUs
- > 9 PB (storage)



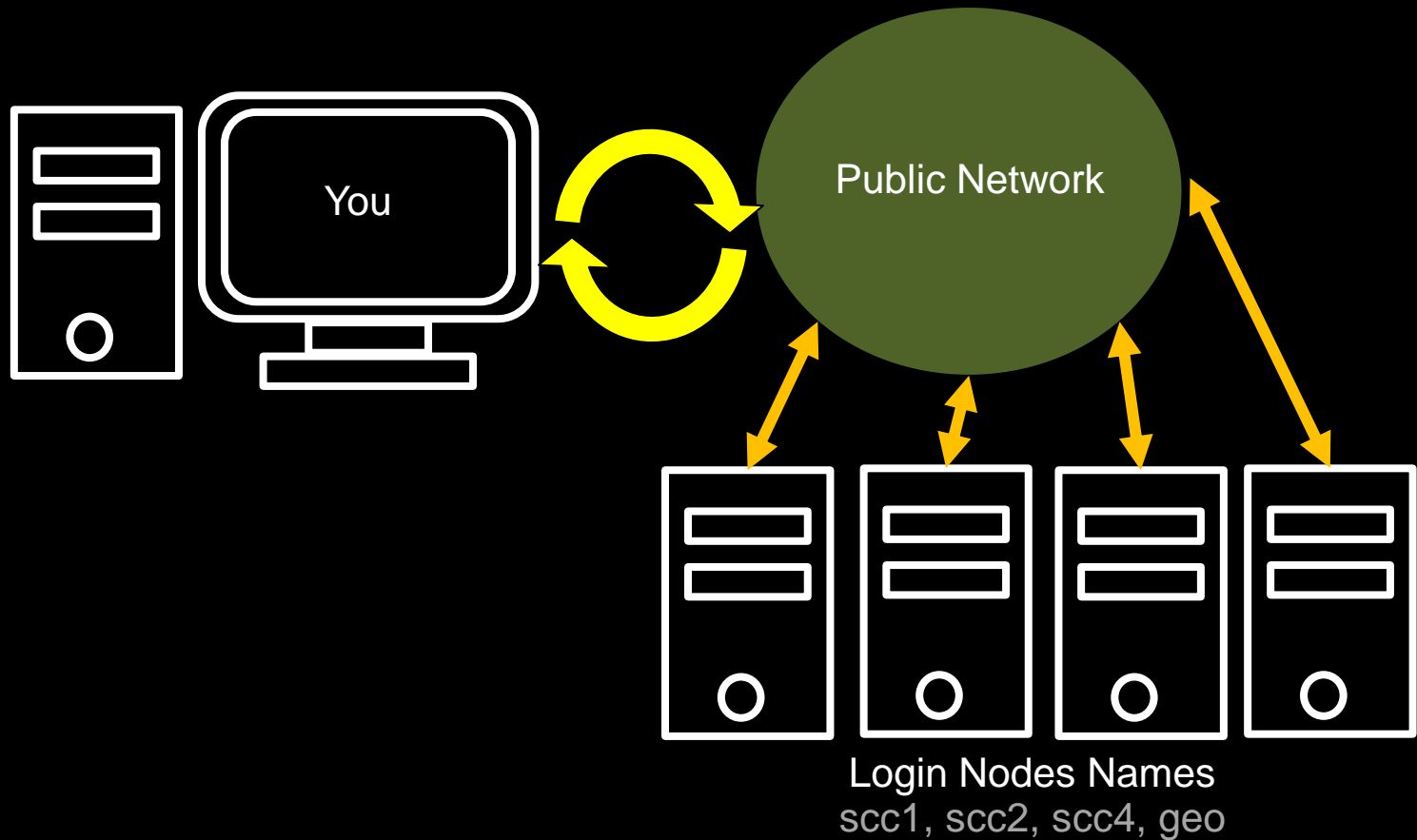
What is the SCC?



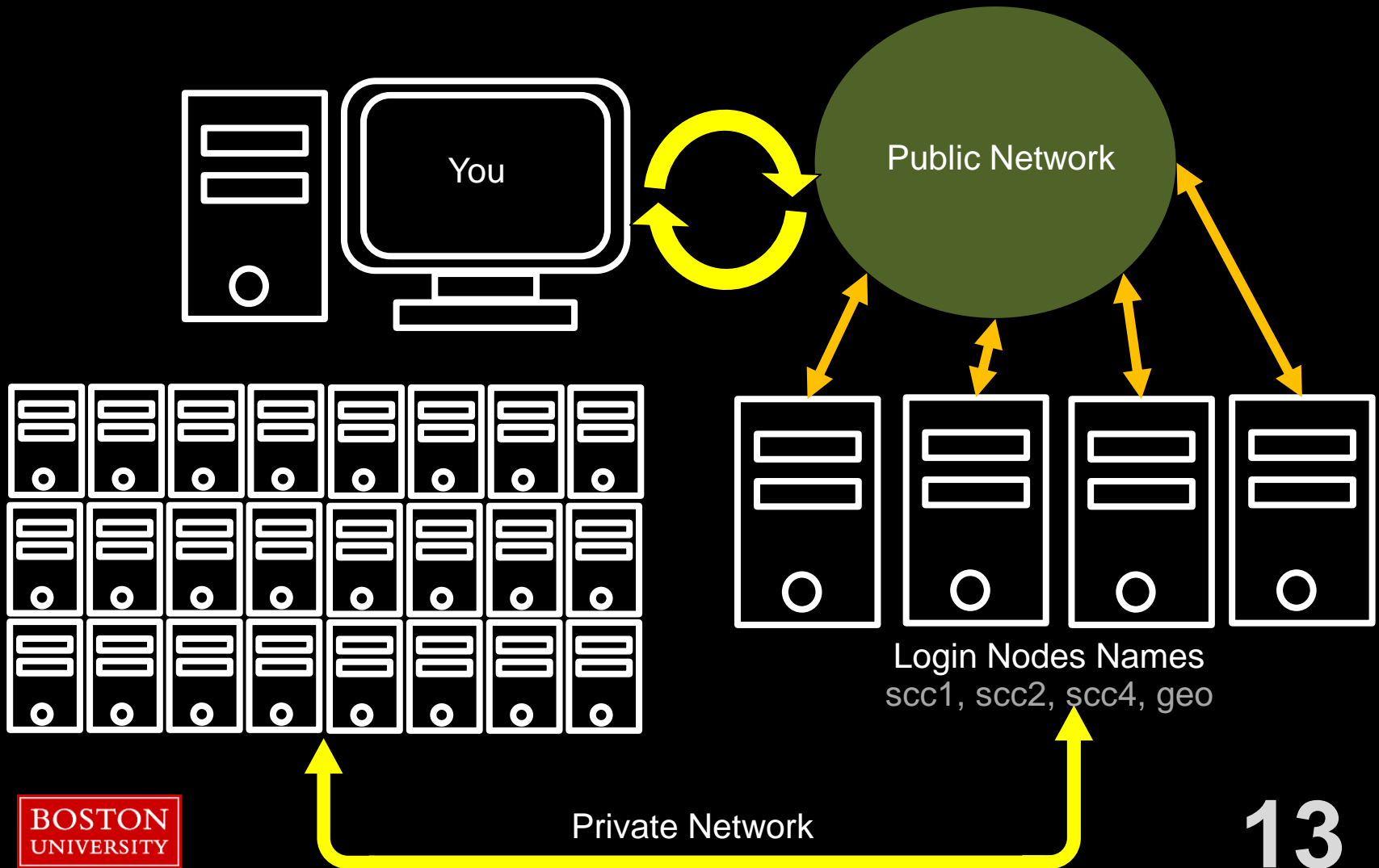
How to Connect to the SCC?



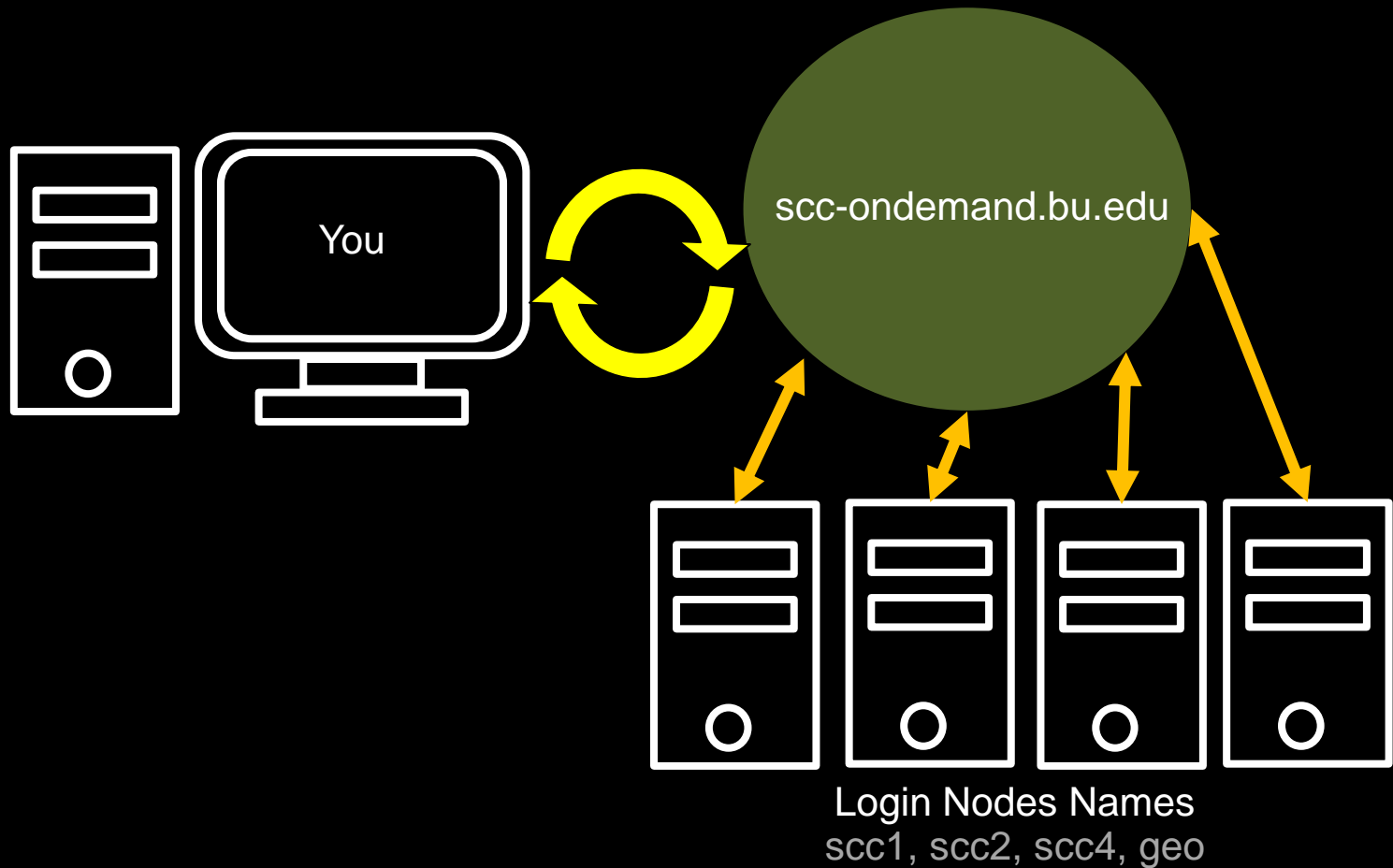
How to Connect to the SCC?



How to Connect to the SCC?



How to Connect to the SCC?



Getting an SCC Account?

- Using tutorial accounts today. These should not be used after today.
- All users of the SCC must be on a Research Project headed up by a full-time BU Faculty member.
- Exception: Some classes may have an academic project which you can be added to for the semester
- <http://www.bu.edu/tech/support/research/account-management/>

Questions so Far?

Topics

- Get On the SCC
- What/Where/How the SCC?
- OnDemand
- Unix
- Wrangling Imaging Data
- XNAT
- Using the Batch System
- Useful Tools

OnDemand


SCC OnDemand

Files ▾

Quotas ▾

Login Nodes ▾

Interactive Apps ▾


 My Interactive Sessions


OnDemand


SCC OnDemand


Files ▾

Desktops

 Desktop


 MATLAB

 Mathematica

 QGIS


 SAS


 STATA

 Spyder


 VirtualGL Desktop


Servers


 Jupyter Notebook

 RStudio Server


 Shiny App Server

 TensorBoard Server

 VS Code Server

 Webserver

Interactive Apps ▾

 My Interactive Sessions

OnDemand

Desktop

This app will launch an interactive desktop on a compute node.

List of modules to load (space separated)

Working Directory

The directory to start in. (Defaults to home directory.)

Initial command to run

Number of hours

Number of cores

Number of gpus

GPU compute capability

Project

Extra qsub options

I would like to receive an email when the session starts

Launch

* The Desktop session data for this session can be accessed under the data root directory.

OnDemand


SCC OnDemand

Files ▾

Quotas ▾

Login Nodes ▾


Interactive Apps ▾

 My Interactive Sessions

Desktop (6994379)

1 core | Running

Host: [>_scc-bb3](#)

 Delete

Created at: 2022-08-29 11:12:24 EDT

Time Remaining: 19 hours and 53 minutes

Session ID: [afff80fb-ca1f-44fd-a440-0637da849e84](#)

Compression

Image Quality



0 (low) to 9 (high)

0 (low) to 9 (high)

Connect to Desktop

View Only (Share-able Link)

OnDemand

Open in Terminal
Refresh
New File
New Directory
Upload
Download
Copy/Move
Delete

Home Directory

- /projectnb/abcd
- /projectnb/connectmedb
- /restricted/projectnb/diagnosectc
- /restricted/projectnb/hcp-aging
- /projectnb/natscenes
- /project/ozymandias
- /projectnb/ozymandias
- /projectnb/rcsmetrics
- /project/scv
- /projectnb/scv
- /restricted/projectnb/scv
- /project/tutorial
- /projectnb/tutorial
- Dropbox
- Google_Drive

↑ /usr1/scv/mhorn/ondemand/data/sys/dashboard/batch_connect/sys/desktop/output/5d6b8efb-6184-46e1-90a9-dde0b000acdb/
 Change directory
Copy path

Show Owner/Mode
 Show Dotfiles
 Filter:

Showing 11 rows - 0 rows selected

	Type	▲	Name	▲	Size	↕	Modified at	↕
<input type="checkbox"/>	📁		desktops	⋮	-		8/16/2019 9:52:26 AM	
<input type="checkbox"/>	📄		before.sh	⋮	100 Bytes		9/4/2023 10:00:10 AM	
<input type="checkbox"/>	📄		connection.yml	⋮	92 Bytes		9/4/2023 10:02:38 AM	
<input type="checkbox"/>	📄		job_script_content.sh	⋮	6.83 KB		9/4/2023 10:00:10 AM	
<input type="checkbox"/>	📄		job_script_options.json	⋮	440 Bytes		9/4/2023 10:00:10 AM	
<input type="checkbox"/>	📄		ood-desktop.e601374	⋮	727 Bytes		9/4/2023 10:02:06 AM	
<input type="checkbox"/>	📄		output.log	⋮	405 Bytes		9/4/2023 10:02:38 AM	
<input type="checkbox"/>	📄		script.sh	⋮	693 Bytes		9/4/2023 10:00:10 AM	
<input type="checkbox"/>	📄		user_defined_context.json	⋮	262 Bytes		9/4/2023 10:00:10 AM	
<input type="checkbox"/>	📄		vnc.log	⋮	3.65 KB		9/4/2023 10:02:38 AM	
<input type="checkbox"/>	📄		vnc.passwd	⋮	16 Bytes		9/4/2023 10:02:38 AM	

OnDemand – Login Nodes

SCC OnDemand

Files ▾

Quotas ▾

Login Nodes ▾

Interactive Apps ▾

 My Interactive Sessions

Login Nodes ▾

>_scc1

>_scc2

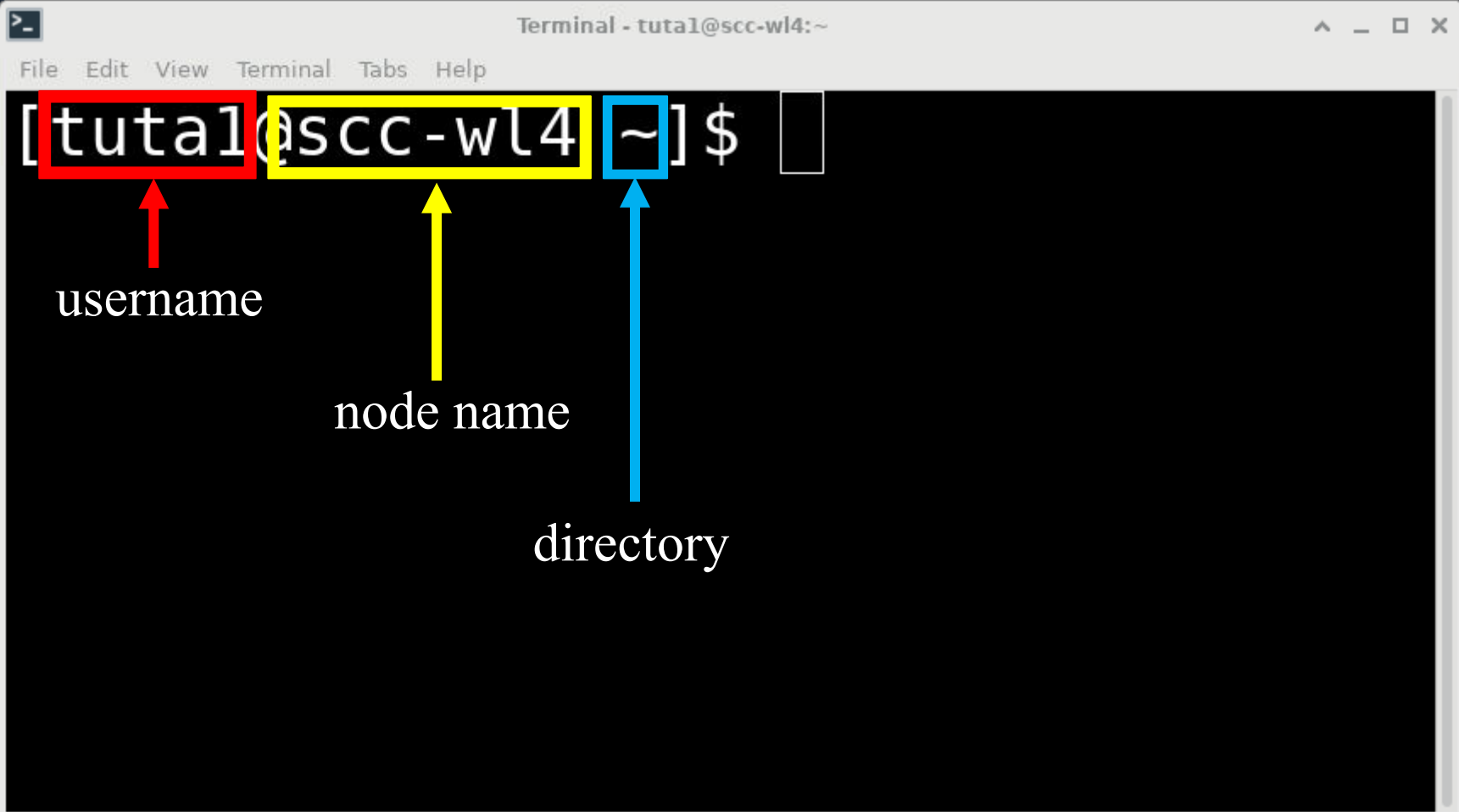
>_geo

>_scc4

Topics

- Get On the SCC
- What/Where/How the SCC?
- OnDemand
- **Unix**
- Wrangling Imaging Data
- XNAT
- Using the Batch System
- Useful Tools

Unix



A terminal window titled "Terminal - tuta1@scc-wl4:~" showing a shell prompt. The prompt is "[tuta1@scc-wl4 ~]\$". The prompt is annotated with three colored boxes and arrows: a red box around "tuta1" with an arrow pointing to the label "username"; a yellow box around "@scc-wl4" with an arrow pointing to the label "node name"; and a blue box around "~" with an arrow pointing to the label "directory".

```
Terminal - tuta1@scc-wl4:~
File Edit View Terminal Tabs Help
[tuta1@scc-wl4 ~]$
```

username

node name

directory

Unix

```
[tuta1@scc-v01 ~]$ groups  
tutorial
```

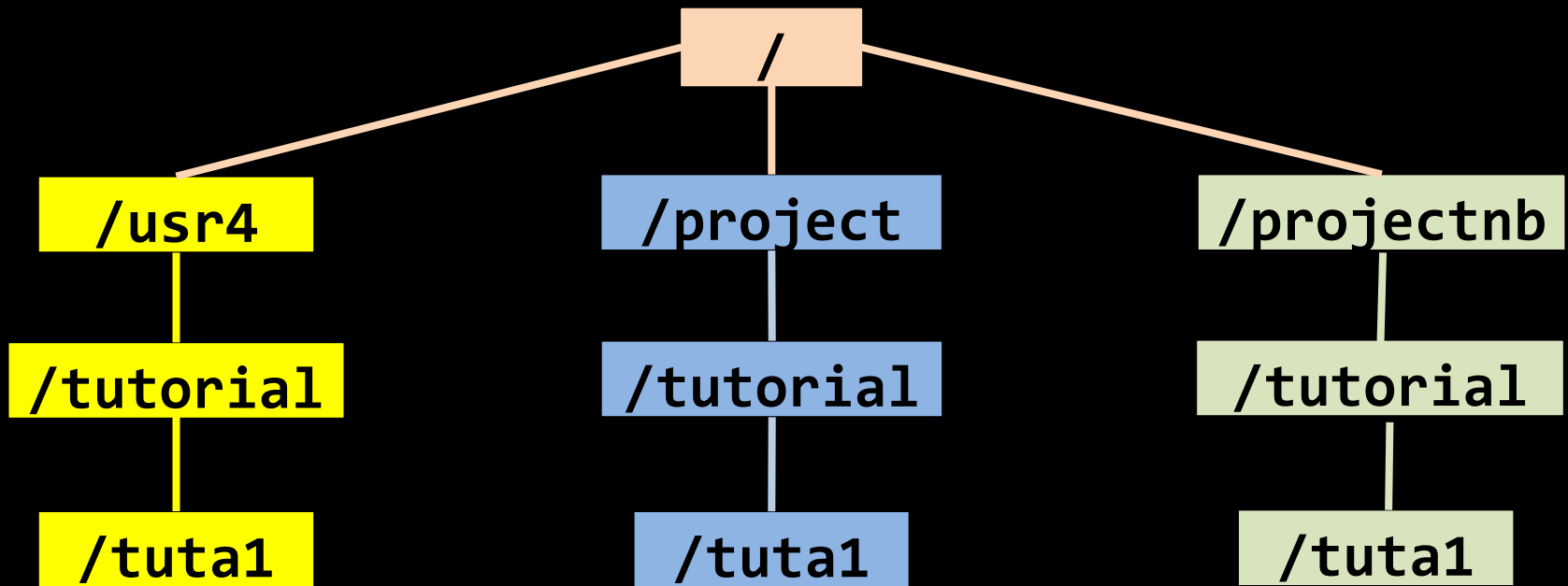
The first group listed is your default project

Unix

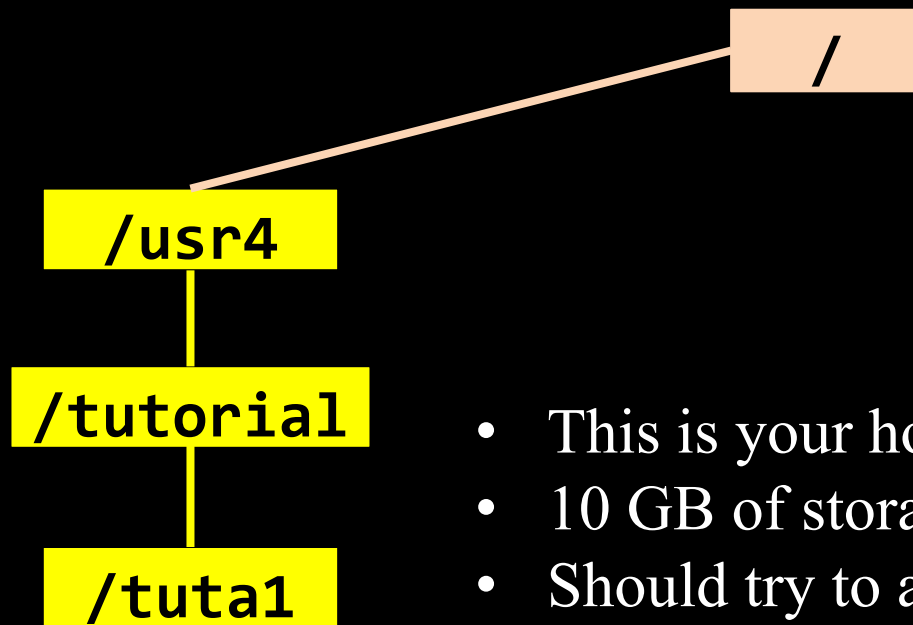
```
[tuta1@scc-v01 ~]$ pwd  
/usr4/tutorial/tuta1
```

Shows the directory you are in, with the full path

Unix

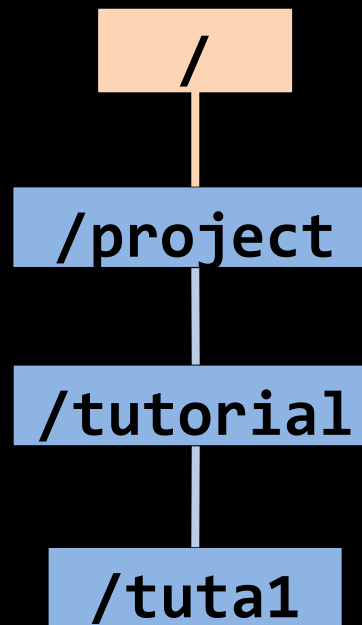


Unix



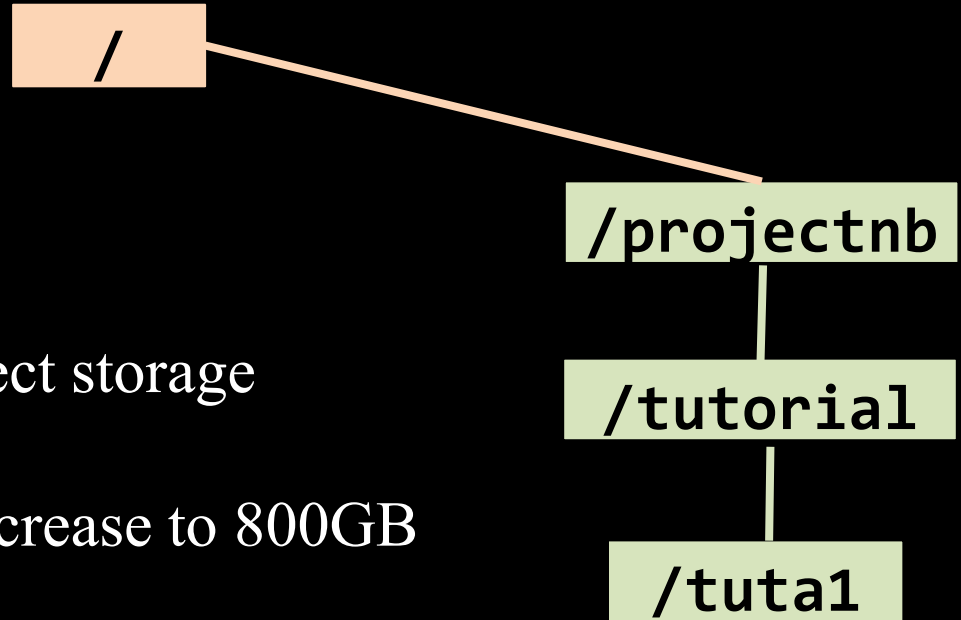
- This is your home directory
- 10 GB of storage
- Should try to avoid filling up this directory

Unix



- This is a backed-up project storage
- Backup in a separate location incase of physical damage
- Default 50GB of space, can increase to 200GB

Unix



- This is a NOT backed-up project storage
- Local snapshots
- Default 50GB of space, can increase to 800GB

Unix

```
[tuta1@scc-v01 ~]$ cd /projectnb/tutorial
```



swap in your default group!

cd = change directory

Unix

```
[tuta1@scc-v01 ~]$ mkdir tuta1
```



swap in your username

mkdir = make a directory

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

```
total 1
```

```
drwxr-xr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```

ls = list contents

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

```
total 1
```

```
drwxr-xr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```

↑
owner

↑
group

↑
file/folder name

ls = list contents

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

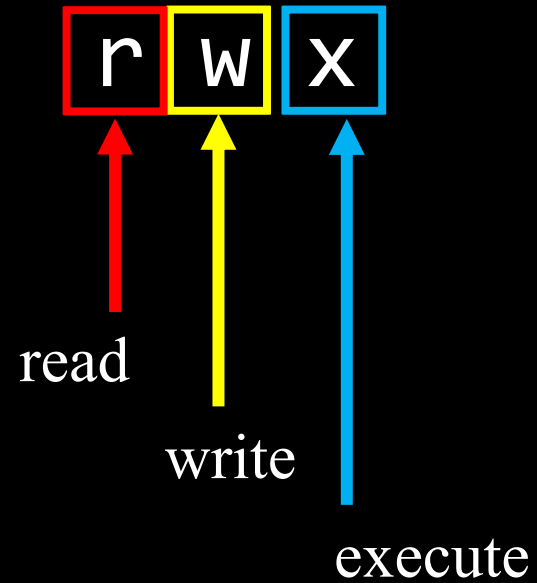
```
total 1
```

```
drwxr-xr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```

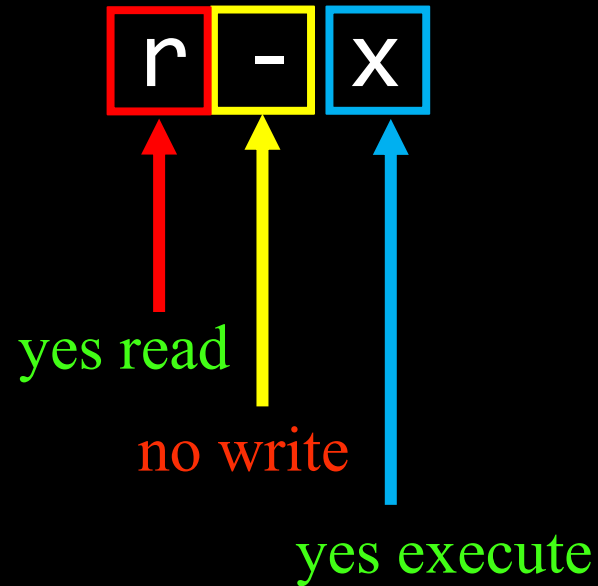
↑
permissions

ls = list contents

Unix



Unix



Unix

`drwxr-xr-x`

The diagram shows the Unix permission string `drwxr-xr-x` with three colored boxes highlighting different parts: a red box around `drwx`, a yellow box around `r-x`, and a blue box around `r-x`. Below each box is an arrow pointing to a label: a red arrow points to `user`, a yellow arrow points to `group`, and a blue arrow points to `other`.

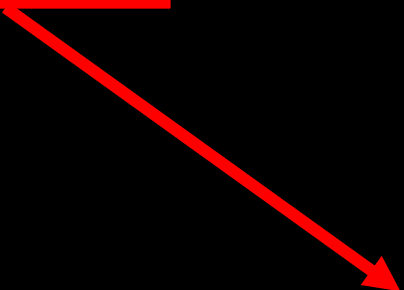
user group other

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

```
total 1
```

```
drwxr-xr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```



drwxr-xr-x

Object Type

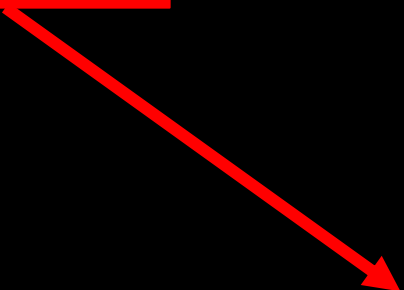
- d = directory
- - = file

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

```
total 1
```

```
drwxr-xr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```



drwxr-xr-x

User/Owner Permissions:

- tuta1 is owner
- currently all enabled

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

```
total 1
```

```
drwxr-xr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```



drwxr-xr-x

Group Permissions:

- tutorial is group
- read and execute are enabled
- write is not enabled

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

```
total 1
```

```
drwxr-xr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```



drwxr-xr-x

Other/World Permissions:

- read and execute are enabled
- write is not enabled

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

```
total 1
```

```
drwxr-xr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```



How can we change permissions?

Unix

```
[tuta1@scc-v01 ~]$ chmod g+w tuta1
```



To group add write permissions

Unix

```
[tuta1@scc-v01 ~]$ ls -l
```

```
total 1
```

```
drwxrwxr-x 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1
```



yes write

OnDemand – Interactive Desktop

SCC OnDemand

Files ▾

Quotas ▾


Login Nodes ▾

Interactive Apps ▾

 My Interactive Sessions

Desktop (6994379)

1 core | Running

Host: [>_scc-bb3](#) Delete

Created at: 2022-08-29 11:12:24 EDT

Time Remaining: 19 hours and 53 minutes

Session ID: afff80fb-ca1f-44fd-a440-0637da849e84

Compression



0 (low) to 9 (high)

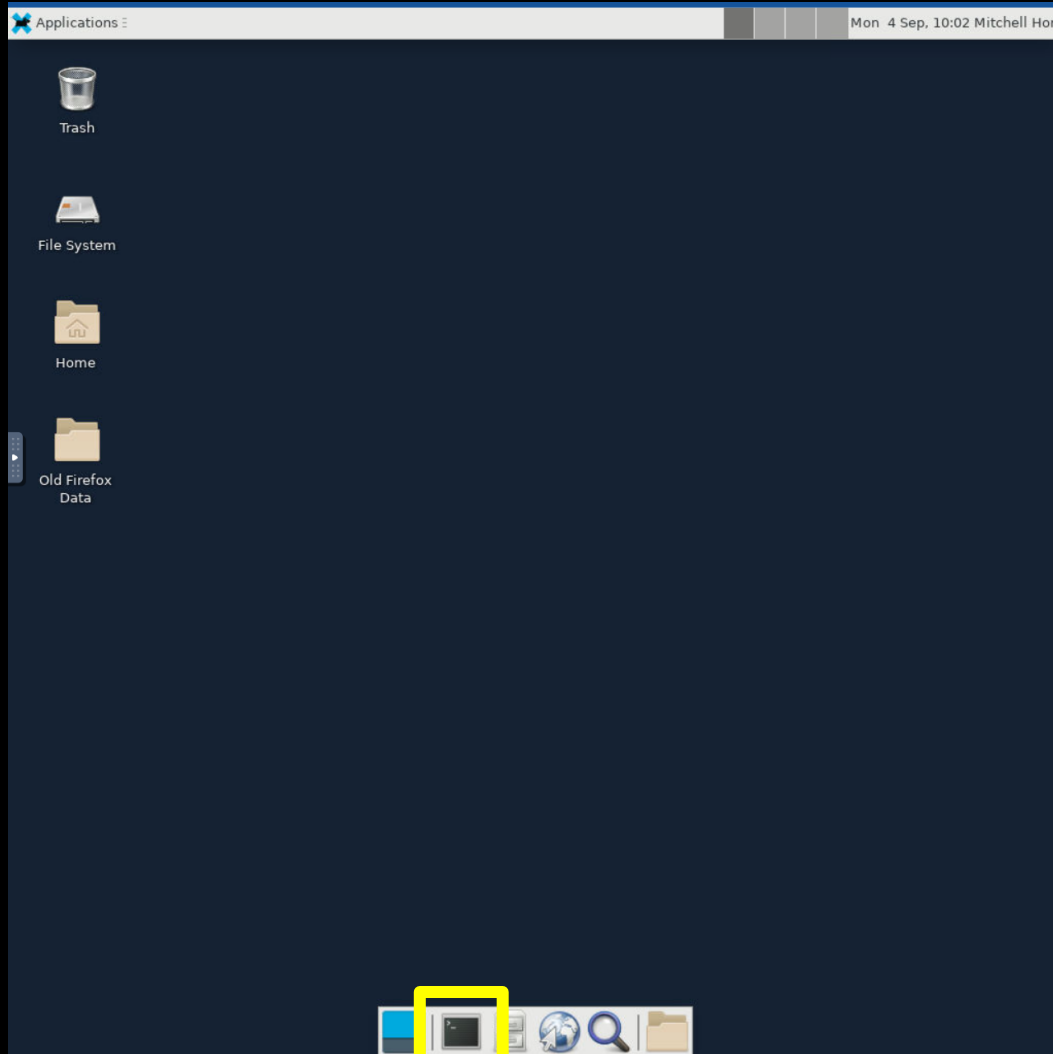
Image Quality



0 (low) to 9 (high)

[Connect to Desktop](#)[View Only \(Share-able Link\)](#)

Connect to OnDemand



Unix

```
[ ]$ cd /projectnb/tutorial/tuta1
```



swap in your username

cd = change directory

Unix

```
[tuta1@scc-v01 tuta1]$ gedit test.sh &
```



gedit = graphical text editor

Unix

1 echo "Welcome to the SCC!"

save; close (hit x in top-right)

Unix

```
[tuta1@scc-v01 tuta1]$ chmod u+x test.sh
```



To user add execute permissions

Unix

```
[tuta0@scc-v01 tuta1]$ ./test.sh
```

```
Welcome to the SCC!
```

Unix

```
[tuta1@scc-v01 tuta1]$ mv test.sh tuta1.sh
```



swap in your username

mv = move

- can also be used to rename files!

Unix

```
[tuta1@scc-v01 tuta1]$ ls -l
```

```
total 1
```

```
-rwxr--r-- 3 tuta1 tutorial 4096 Oct 28 16:03 tuta1.sh
```

Topics

- Get On the SCC
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- Wrangling Imaging Data
- XNAT
- Using the Batch System
- Useful Tools

Unix

```
[ ]$ cd /projectnb/tutorial/tuta1
```



swap in your username

cd = change directory

Wrangling Imaging Data

```
cp /project/scv/examples/imaging/tut_neuro_scc/tut.zip .
```



- `cp` = copy
- `.` = short-hand for current directory
- use `[tab]` key to autocomplete paths
 - `/project/scv/ex[tab]/im[tab]/tut_n[tab]/tut[tab]`

Wrangling Imaging Data

```
[tuta1@scc-v01 tuta1]$ unzip tut.zip
```

unzip the tutorial data

Wrangling Imaging Data

```
[tuta1@scc-v01 tuta1]$ cd tut
```

Wrangling Imaging Data

```
[tuta1@scc-v01 tuta1]$ ls -l  
  
-rwxrwsrwx  2 tuta1 tutorial      4096 Sep 11 12:54 bet.qsub  
drwxrwsrwx  2 tuta1 tutorial      4096 Sep 11 12:54 dicom
```

list the contents of the tut directory

Wrangling Imaging Data

```
[tuta1@scc-v01 tuta1]$ ls -l dicom
```

```
1.3.12.2.1107.5.2.43.166024.30000022072919140806900000007-9-97-10diwog.dcm
1.3.12.2.1107.5.2.43.166024.30000022072919140806900000007-9-98-2cfytv.dcm
1.3.12.2.1107.5.2.43.166024.30000022072919140806900000007-9-99-nkpf0x.dcm
...
```

list the contents of the dicom directory

Wrangling Imaging Data

1.3.12.2.1107.5.2.43.166024.30000022072919140806900000007-9-97-10diwog.dcm

1.3.12.2.1107.5.2.43.166024.30000022072919140806900000007-9-98-2cfytv.dcm

1.3.12.2.1107.5.2.43.166024.30000022072919140806900000007-9-99-nkpf0x.dcm

...

■ DICOM

- Standard medical image format on most* imaging machines
- Contains an image and metadata about the image (like most pictures)
- The metadata contains information about the scan
- Is not a conducive format for image processing

Wrangling Imaging Data

- **NIfTI**
 - Subject_001.nii, Subject_001.nii.gz
 - FreeSurfer, FSL, AFNI, SPM, CONN
- **MGH/MGZ**
 - Subject_001.mgh, Subject_001.mgh.gz, Subject_001.mgz
 - FreeSurfer
- **BRIK & HEAD**
 - Subject_001.BRIK & Subject_001.HEAD
 - AFNI
- **IMG & HDR (Analyze Format)**
 - Subject_001.img & Subject_001.hdr
 - SPM, FreeSurfer, FSL, AFNI

Wrangling Imaging Data

- Unpacking DICOMs
 - Reads through DICOM metadata to sort and stack slices/volumes into specified file format
- dcm2niix
 - MRICroGL
- ArcGet.py
- heudiconv
- dcmunpack / unpacksdcmDir
 - FreeSurfer
- spm_dicom_convert
 - SPM
- to3d
 - AFNI

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ module avail | less
```

ctrl+z to quit “less”

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ module avail dcm2niix
```

ctrl+z to quit “less”

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ module load dcm2nix
```

Module system to load software packages

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ module list
```

Currently Loaded Modules:

```
1) dcm2niix/1.0.20220720
```

Module system to load software packages

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ mkdir nifti
```

Make a new folder called nifti

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ dcm2niix -o nifti dicom/*
```



* = short-hand for include everything

convert dicoms to nifti; and save them in the nifti directory

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ ls -l nifti
```

```
-rw-r--r-- 2 tuta1 tutorial 4096 Sep 11 12:54 dicom.json  
-rw-r--r-- 2 tuta1 tutorial 4096 Sep 11 12:54 dicom.nii
```

header
↓
dicom.json
dicom.nii
↑
image

Software on the SCC

Neuroimaging Suites

- FreeSurfer
- FSL
- AFNI
- SPM
- CONN
- ANTS

Neuroimaging Tools

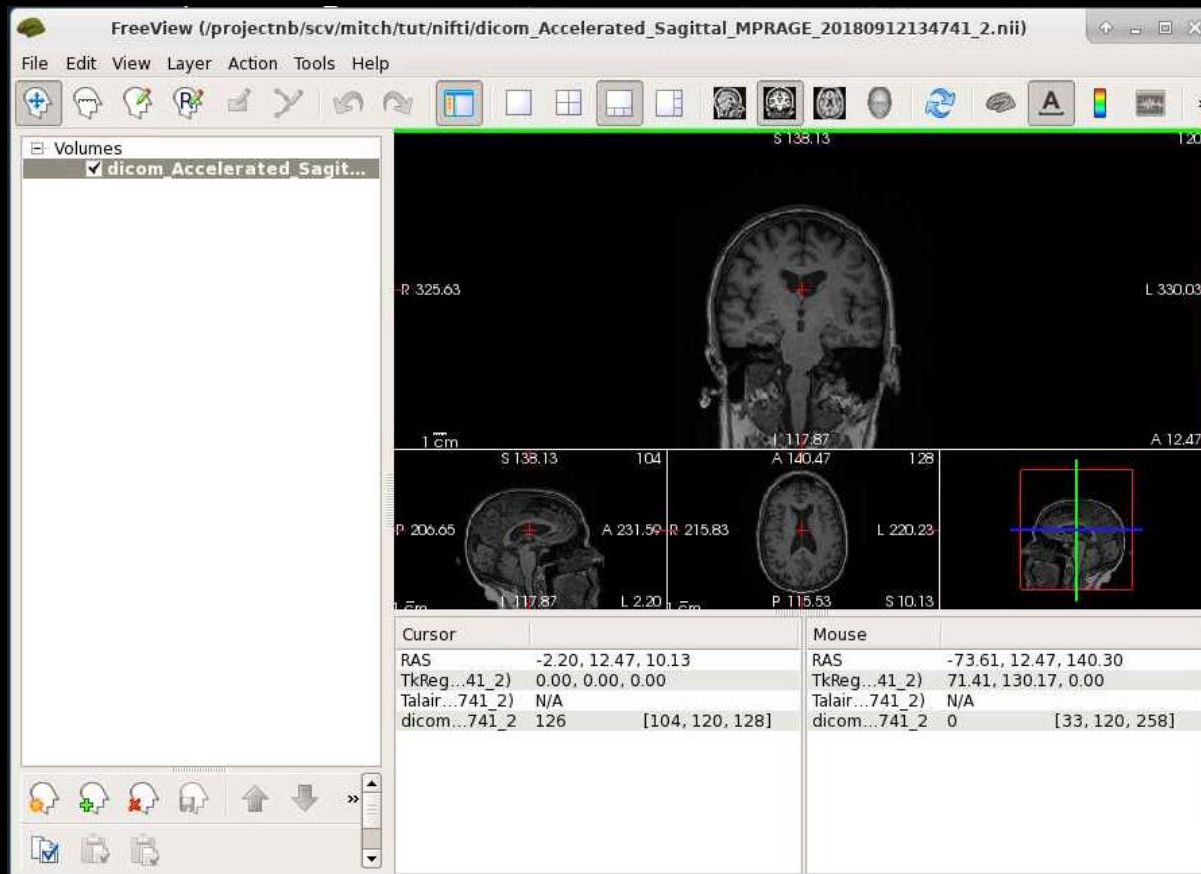
- MRICroGL
- MRICron
- Osirix
- Nipype
- MRIQC

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ module load freesurfer
```

Software on the SCC

```
[tuta1@scc-v01 tuta1]$ freeview nifti/*.nii
```



Software on the SCC

```
[tuta1@scc-v01 tuta1]$ module purge
```

```
[tuta1@scc-v01 tuta1]$ module list
```

Topics

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Using the Interactive Node

- 1 Computer - Non-Parallelized (~80 Hours for 8 Subjects):
- SCC - Parallelized (~5 Hours for 8 Subjects):

<https://rcs.bu.edu/examples/imaging/freesurfer/>

Using the Interactive Node

```
[tuta1@scc-v01 tuta1]$ pwd
```

```
/projectnb/tutorial/tuta1/tut
```

Check to make sure we are in the “tut” directory!

Using the Interactive Node

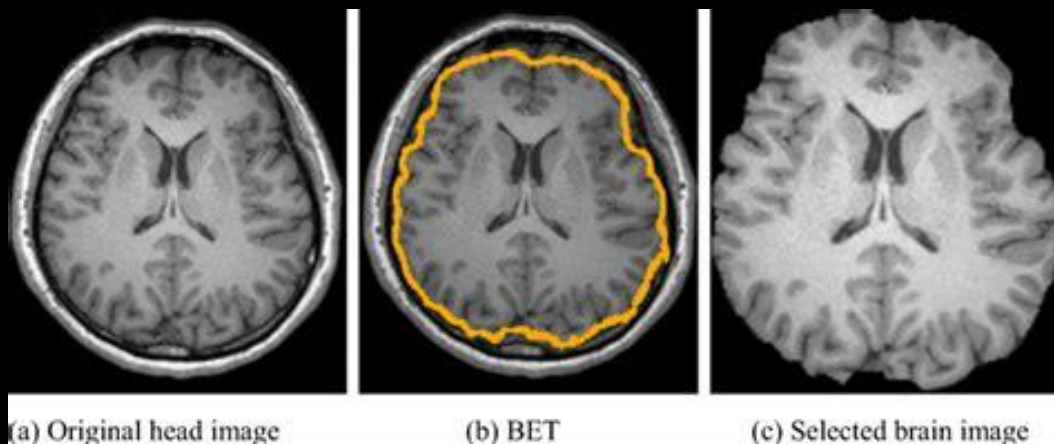
```
[tuta1@scc-v01 tuta1]$ module load fsl/6.0.4
```

```
[tuta1@scc-v01 tuta1]$ module list  
Currently Loaded Modules:  
1) fsl/6.0.4
```


Using the Interactive Node

bet = Brain Extraction Tool

[~]\$ bet input output



Using the Interactive Node

```
[tuta1@scc-v01 tuta1]$ bet nifti/dicom[tab].nii nifti/ss.nii
```

[tab] = use [tab] button to autocomplete filenames!

Using the Interactive Node

```
[tuta1@scc-v01 tuta1]$ ls -l nifti
```

```
-rw-r--r--  2 tuta1 tutorial      4096 Sep 11 12:54 dicom.json  
-rw-r--r--  2 tuta1 tutorial      4096 Sep 11 12:54 dicom.nii  
-rw-r--r--  2 tuta1 tutorial      4096 Sep 11 12:54 ss.nii.gz
```

Using the Interactive Node

```
[tuta1@scc-v01 tuta1]$ module load freesurfer
```

```
[tuta1@scc-v01 tuta1]$ freeview nifti/*.nii nifti/*.nii.gz
```

Using the Batch System

```
[tuta1@scc-v01 tuta1]$ gedit bet.qsub &
```

Open the bet.qsub file in gedit

Using the Batch System



```
Open  bet.qsub  Save  -  x
/projectnb/tutorial/tuta1/tut

#!/bin/bash -l

# Set SCC Project
#$ -P tutorial

# Give job a name
# $ -N bet_tut

# give it 12 hours to run per core/node
#$ -l h_rt=12:00:00

#####

# load fsl module and input subject ID on command-line
module load fsl

# perform skull-strip on the tutorial data
bet /projectnb/tutorial/tuta1/tut/nifti/dicom_Accelerated_Sagittal_MPRAGE_20180912134741_2 /projectnb/tutorial/tuta1/tut/nifti/skullstrip

sh  Tab Width: 8  Ln 18, Col 138  INS
```

Submitting a Job to the SCC

```
[tuta1@scc-v01 tuta1]$ qsub bet.qsub
```

```
Your job 1041461 ("bet.qsub") has been submitted
```

Submit job with qsub

qsub Details

- Submit non-interactive batch jobs using **qsub**

qsub *[options]* **command** *[arguments]*

- Setting default **qsub** options using a `.sge_request` file:

http://www.bu.edu/tech/support/research/system-usage/running-jobs/advanced-batch/#sge_request

- <http://www.bu.edu/tech/support/research/system-usage/running-jobs/submitting-jobs/>

qsub options

General Directives	
Directive	Description
-l h_rt=hh:mm:ss	Hard run time limit in <i>hh:mm:ss</i> format. The default is 12 hours.
-P project_name	Project to which this jobs is to be assigned. This directive is mandatory for all users associated with any Med.Campus project.
-N job_name	Specifies the job name. The default is the script or command name.
-o outputfile	File name for the stdout output of the job.
-e errfile	File name for the stderr output of the job.
-j y	Merge the error and output stream files into a single file.
-m b e a s n	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 user_email	Overwrites the default email address used to send the job report.
-V	All current environment variables should be exported to the batch job.
-v env=value	Set the runtime environment variable <i>env</i> to <i>value</i> .
-hold_jid job_list	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.

qsub options cont.

Directives to request SCC resources	
Directive	Description
<code>-l h_rt=hh:mm:ss</code>	Hard run time 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, and 1000G
<code>-l mem_per_core=#G</code>	Request a node that has at least this amount of memory per core. Current possible choices include 3G, 4G, 8G, 12G, 16G, 18G and 28G
<code>-pe omp N</code>	Request multiple slots for Shared Memory applications (OpenMP, pthread). This option can also be used to reserve a larger amount of memory for the application. <i>N</i> can vary 1-28, 36.
<code>-pe mpi_#_tasks_per_node N</code>	Select multiple nodes for an MPI job. Number of tasks can be 4, 8, 12, 16, or 28 and <i>N</i> must be a multiple of this value. See Running Parallel Batch Jobs for more information.
<code>-t N</code>	Submit an Array Job with <i>N</i> tasks. <i>N</i> can be up to 75,000. For more information see Array Jobs
<code>-l cpu_arch=ARCH</code>	Select a processor architecture (broadwell, haswell, ivybridge, ...). See Technical Summary for all available choices.
<code>-l cpu_type=TYPE</code>	Select a processor type (X5650, X5670, X5675, etc.) See Technical Summary for all available choices.
<code>-l gpus=G/C</code>	Requests a node with GPUs. <i>G/C</i> specifies the number of GPUs per CPU requested and should be expressed as a decimal number. See GPU Computing for more information.
<code>-l gpu_type=GPUMODEL</code>	Current choices for <i>GPUMODEL</i> are M2070, K40m, and P100.
<code>-l gpu_c=CAPABILITY</code>	Specify minimum GPU capability. Current choices for <i>CAPABILITY</i> are 2.0, 3.5, and 6.0

Checking Job Status

```
[tuta1@scc-v01 tuta1]$ qstat -u tuta1
```



swap in your username

Check status of job

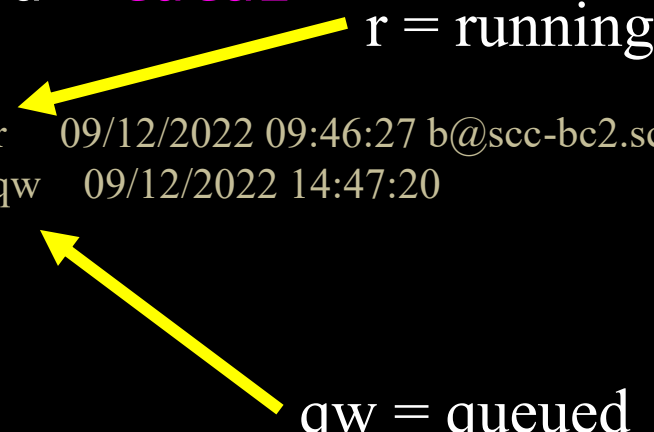
Checking Job Status

```
[tuta1@scc-v01 tuta1]$ qstat -u tuta1
```

7238828	0.14071	ood-deskto	tuta1	r	09/12/2022 09:46:27	b@scc-bc2.scc.bu.edu	1
7243957	0.00000	bet.qsub	tuta1	qw	09/12/2022 14:47:20		1

r = running

qw = queued



Check status of job

qsub output

- The job should run soon and produce an output file:

```
[tuta1@scc1 tut]$ cat bet.qsub.o1041461
```

- There will also be an error file which should be empty:

```
[tuta1@scc1 tut]$ cat bet.qsub.e1041461
```

Topics

- Get On the SCC
- What/Where/How the SCC?
- OnDemand
- Unix
- Wrangling Imaging Data
- **XNAT**
- Using the Batch System
- Useful Tools

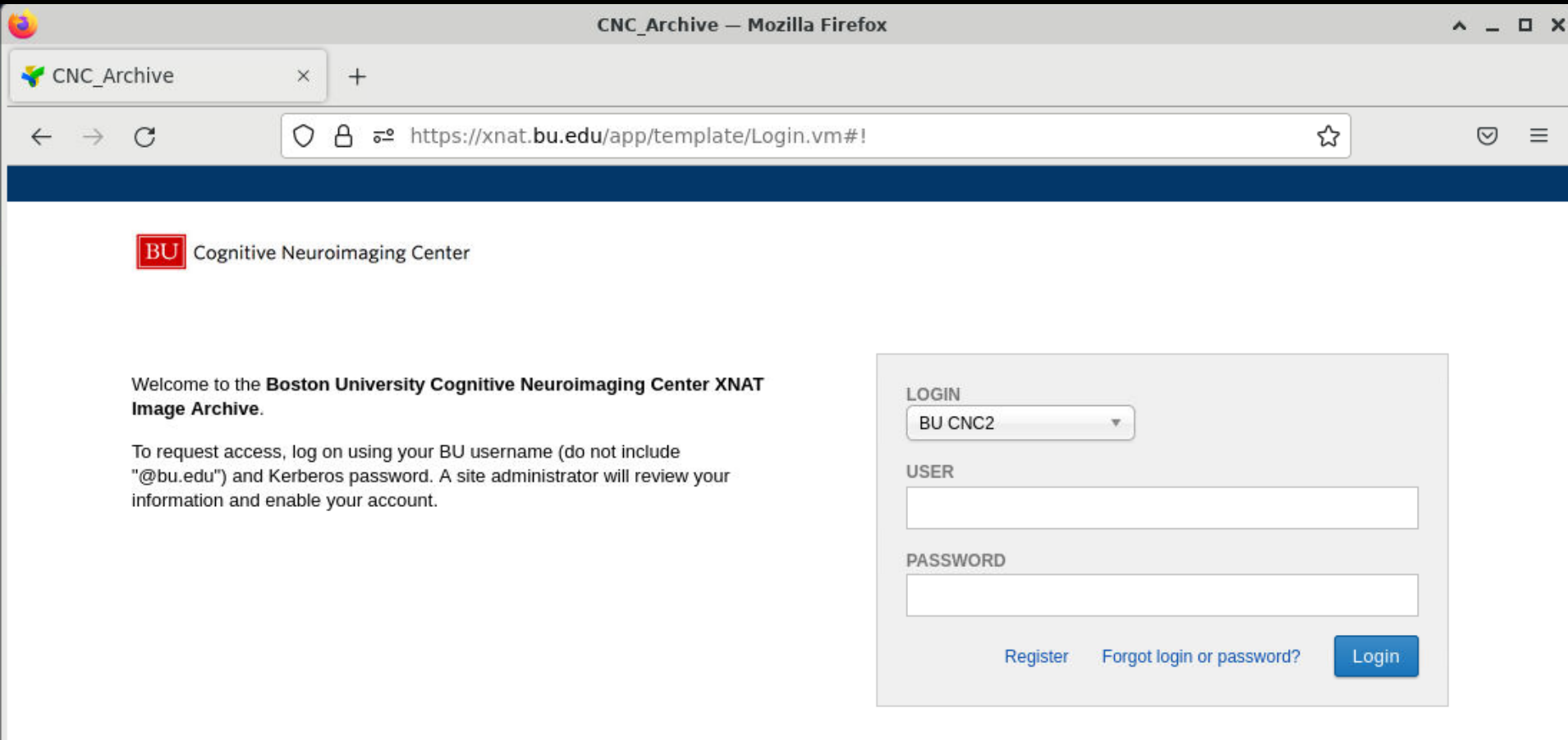
XNAT

- Software platform that will store CNC neuroimaging data
- Live Upload from MRI Scanner to XNAT
- Inspect/Download raw data for artifacts before processing in Web API (Demo)



The screenshot shows the XNAT website interface. At the top, there is a navigation menu with the following items: "What is XNAT?", "Institutional Repositories", "Clinical Research", "Multi-center Studies", and "Data Sharing". Below the menu is a large blue graphic illustrating the data flow. On the left, there is an image of an MRI scanner. In the center, there are two circular icons: "Imaging Data" (with a key and folder icon) and "Clinical Data" (with a clipboard and folder icon). Arrows point from these icons to a central brain icon, which then points to a large, colorful, abstract shape on the right. Below the graphic, there is a section titled "What is XNAT?" with the following text: "XNAT is an open-source imaging informatics software platform dedicated to helping you perform imaging-based research. XNAT's core functions manage importing, archiving, processing and securely distributing imaging and related study data. But its extended uses continue to evolve."

XNAT



The screenshot shows a Mozilla Firefox browser window titled "CNC_Archive". The address bar displays the URL "https://xnat.bu.edu/app/template/Login.vm#!". The page content includes the Boston University Cognitive Neuroimaging Center logo and a welcome message. A login form is present with fields for LOGIN (a dropdown menu showing "BU CNC2"), USER, and PASSWORD. There are also links for "Register", "Forgot login or password?", and a "Login" button.

CNC_Archive

https://xnat.bu.edu/app/template/Login.vm#!

BU Cognitive Neuroimaging Center

Welcome to the **Boston University Cognitive Neuroimaging Center XNAT Image Archive**.

To request access, log on using your BU username (do not include "@bu.edu") and Kerberos password. A site administrator will review your information and enable your account.

LOGIN
BU CNC2

USER

PASSWORD

[Register](#) [Forgot login or password?](#) [Login](#)

XNAT

CNC_Archive x +

← → ↻ https://xnat.bu.edu

Last login: 08/24/2023 15:48:12

Logged in as: [mhorn](#) | Auto-logout in: 0:29:46 - [renew](#) | [Logout](#)

[Browse](#) ▾ [New](#) ▾ [Upload](#) ▾ [Administer](#) ▾ [Tools](#) ▾ [Help](#) ▾ [Advanced](#)

BU Cognitive Neuroimaging Center

CNC_Archive currently contains 36 projects, 2374 subjects, and 2384 imaging sessions.

[Projects](#) | [Subjects](#) | [MR](#) | [PET](#) | [CT](#)

ID: Name: Description:
 Keywords: Investigator:

Projects
<p>Morgan_Spine Project ID: Spine You are a collaborator for this project.</p>
<p>NSF FONC Foraging Task Project ID: Stern_FONC PI: Chantal Stern You are a member for this project.</p>
<p>Efficacy Evaluation of Transdiagnostic CBT for Comorbid Alcohol Use and Anxiety Disorders Project ID: STAR2 PI: David Barlow You are a member for this project.</p>
<p>CNC Workshop Project ID: Workshop PI: CNC Staff</p>

Recent Data Activity		
qa	MR	230904_QA
Guenther_...	MR	230901_SEQM107_2
LOVET	MR	230901_LOVET08_V4
qa	MR	230901_QA
Somers_EMP	MR	230831GG
Stern_CITY	MR	CITY05_Session0...
Spine	MR	230831_morgan_63
LOVET	MR	230821_LOVET05_V9
Spine	MR	230831_morgan_60
Spine	MR	230831_morgan_49
Spine	MR	230831_morgan_53
Spine	MR	230831_morgan_62

Downloading from XNAT

```
[~]$ module load python3/3.8.10
```

```
[~]$ module load yaxil/0.9.0
```

Downloading from XNAT

```
[~]$ ArcGet.py -a xnat -l 220801_Rise_demo_01 -p Workshop -o .
```

```
Enter XNAT passphrase:
```

```
INFO:/share/pkg.7/yaxil/0.6.5_dwi_beta/install/bin/ArcGet.py:downloading scans  
1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22  
reading response data: done.
```

Topics

- Get On the SCC
- What/Where/How the SCC?
- OnDemand
- Unix
- Wrangling Imaging Data
- XNAT
- Using the Batch System
- Useful Tools

Additional Web Resources

- Research Computing Support Pages

<https://www.bu.edu/tech/support/research/>

- Running Jobs on the SCC

<https://www.bu.edu/tech/support/research/system-usage/running-jobs/>

- Software Packages on the SCC

<https://www.bu.edu/tech/support/research/software-and-programming/software-and-applications/>

1. Please open a web browser and:
2. Google “rcs tutorial evaluation”
3. Click 1st link
http://scv.bu.edu/survey/tutorial_evaluation.html
4. Fill out the survey!