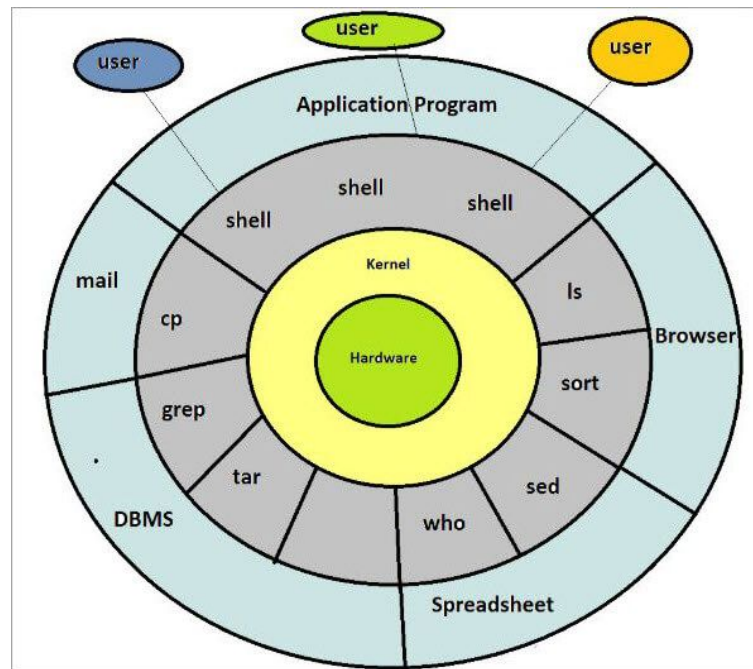


Unix tips and tricks

Cluster management, scripting and more!

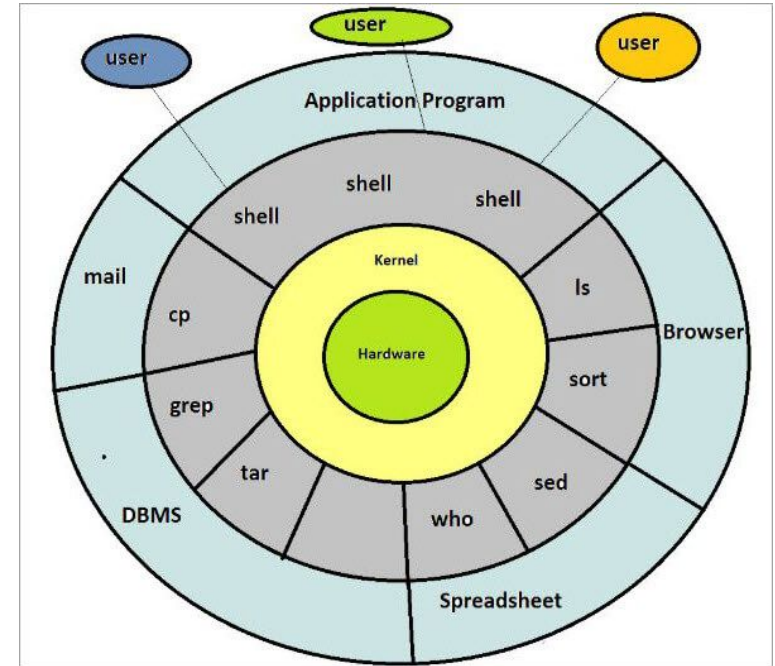
What is “Unix”?

- A family of operating systems
- The basis for many popular systems:
 - Mac OS X
 - CfN cluster
 - Neuroimaging programs like FSL, XCP



What is “Unix”?

- Kernel: core of the OS that interacts directly with hardware
- Shell: program that takes input from keyboard (command line) and passes it to kernel
- bash: Bourne Again SHell, enhanced version of the original shell program, written by Steve Bourne



Overview

Basic commands

Cluster management

Intro to scripting

Basic commands

Basic Unix commands (vs. DOS)

- **cat file**
cat file1 file2 ...
Concatenate or type out a file
- **cd directory1**
cd /usr/bin
cd
Type out a number of files
Change current directory to *directory1*
Change current directory to /usr/bin
Change back to your home directory
- **clear**
Clear the current screen
- **cp file1 file2**
cp file1 file2 ... dir
Copy *file1* to *file2*
Copy a number of files to a directory
- **ls**
ls /usr/bin
List the files in the current directory
List the files in the /usr/bin directory
- **lpr file1**
lpr file1 file2 ...
Print *file1* out
Print a number of files out
- **more file**
Look at the content of a file with paging, use 'q' to get out
- **mkdir directory**
Create a directory
- **mv file1 file2**
mv file1 file2 ... dir
mv dir1 dir2
Move *file1* to *file2*, like rename.
Move a number of files into a directory
Move or rename a directory

Unix/Linux Command Reference

File Commands	System Info
ls - directory listing ls -al - formatted listing with hidden files cd dir - change directory to <i>dir</i> cd - change to home pwd - show current directory mkdir dir - create a directory <i>dir</i> rm file - delete <i>file</i> rm -r dir - delete directory <i>dir</i> rm -f file - force remove <i>file</i> rm -rf dir - force remove directory <i>dir</i> * cp file1 file2 - copy <i>file1</i> to <i>file2</i> cp -r dir1 dir2 - copy <i>dir1</i> to <i>dir2</i> ; create <i>dir2</i> if it doesn't exist mv file1 file2 - rename or move <i>file1</i> to <i>file2</i> if <i>file2</i> is an existing directory, moves <i>file1</i> into directory <i>file2</i> ln -s file link - create symbolic link <i>link</i> to <i>file</i> touch file - create or update <i>file</i> cat > file - places standard input into <i>file</i> more file - output the contents of <i>file</i> head file - output the first 10 lines of <i>file</i> tail file - output the last 10 lines of <i>file</i> tail -f file - output the contents of <i>file</i> as it grows, starting with the last 10 lines	date - show the current date and time cal - show this month's calendar uptime - show current uptime w - display who is online whoami - who you are logged in as finger user - display information about <i>user</i> uname -a - show kernel information cat /proc/cpuinfo - cpu information cat /proc/meminfo - memory information man command - show the manual for <i>command</i> df - show disk usage du - show directory space usage free - show memory and swap usage whereis app - show possible locations of <i>app</i> which app - show which <i>app</i> will be run by default
Process Management	Compression
ps - display your currently active processes top - display all running processes kill pid - kill process <i>id pid</i> killall proc - kill all processes named <i>proc</i> * bg - lists stopped or background jobs; resume a stopped job in the background fg - brings the most recent job to foreground fg n - brings job <i>n</i> to the foreground	tar cf file.tar files - create a tar named <i>file.tar</i> containing <i>files</i> tar xf file.tar - extract the files from <i>file.tar</i> tar czf file.tar.gz files - create a tar with Gzip compression tar xzf file.tar.gz - extract a tar using Gzip tar cjf file.tar.bz2 - create a tar with Bzip2 compression tar xjf file.tar.bz2 - extract a tar using Bzip2 gzip file - compresses <i>file</i> and renames it to <i>file.gz</i> gzip -d file.gz - decompresses <i>file.gz</i> back to <i>file</i>
File Permissions	Network
chmod octal file - change the permissions of <i>file</i> to <i>octal</i> , which can be found separately for user, group, and world by adding: <ul style="list-style-type: none">• 4 - read (r)• 2 - write (w)• 1 - execute (x) Examples: chmod 777 - read, write, execute for all chmod 755 - rwx for owner, rx for group and world For more options, see man chmod .	ping host - ping <i>host</i> and output results whois domain - get whois information for <i>domain</i> dig domain - get DNS information for <i>domain</i> dig -x host - reverse lookup <i>host</i> wget file - download <i>file</i> wget -c file - continue a stopped download
SSH	Installation
ssh user@host - connect to <i>host</i> as <i>user</i> ssh -p port user@host - connect to <i>host</i> on port <i>port</i> as <i>user</i> ssh-copy-id user@host - add your key to <i>host</i> for <i>user</i> to enable a keyed or passwordless login	Install from source: ./configure make make install dpkg -i pkg.deb - install a package (Debian) rpm -Uvh pkg.rpm - install a package (RPM)
Searching	Shortcuts
grep pattern files - search for <i>pattern</i> in <i>files</i> grep -r pattern dir - search recursively for <i>pattern</i> in <i>dir</i> command grep pattern - search for <i>pattern</i> in the output of <i>command</i> locate file - find all instances of <i>file</i>	Ctrl+C - halts the current command Ctrl+Z - stops the current command, resume with fg in the foreground or bg in the background Ctrl+D - log out of current session, similar to exit Ctrl+W - erases one word in the current line Ctrl+U - erases the whole line Ctrl+R - type to bring up a recent command !! - repeats the last command exit - log out of current session
	* use with extreme caution.

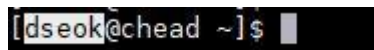


Basic commands - Navigation

Ctrl + a : move to beginning of line

Ctrl + e : move to end of line

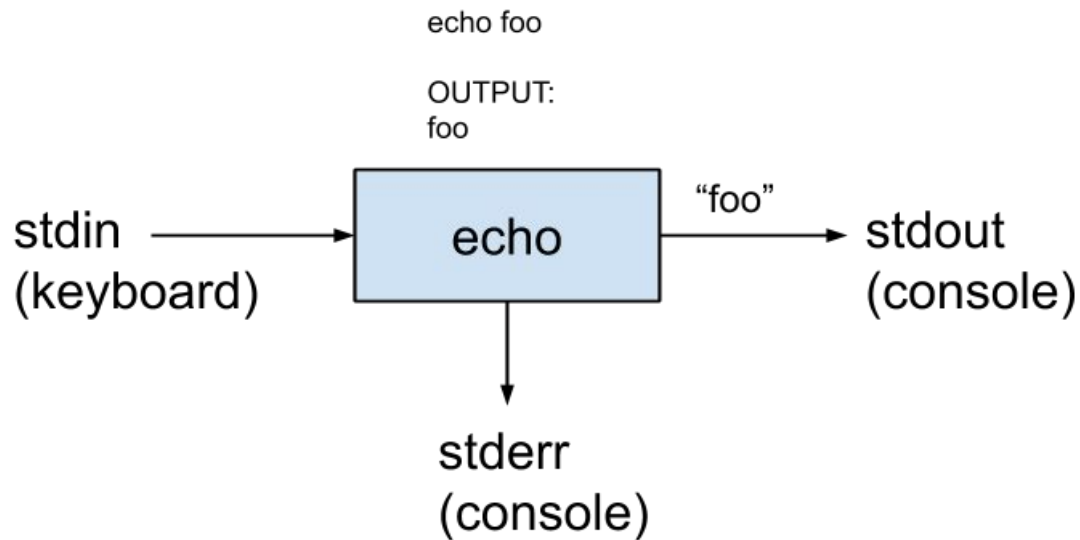
Highlight : copy (Mac -> command + c)

A terminal window with a black background. The prompt is [dseok@chead ~]\$ and the text 'dseok' is highlighted with a light blue selection box. A vertical cursor is visible at the end of the line.

```
[dseok@chead ~]$
```

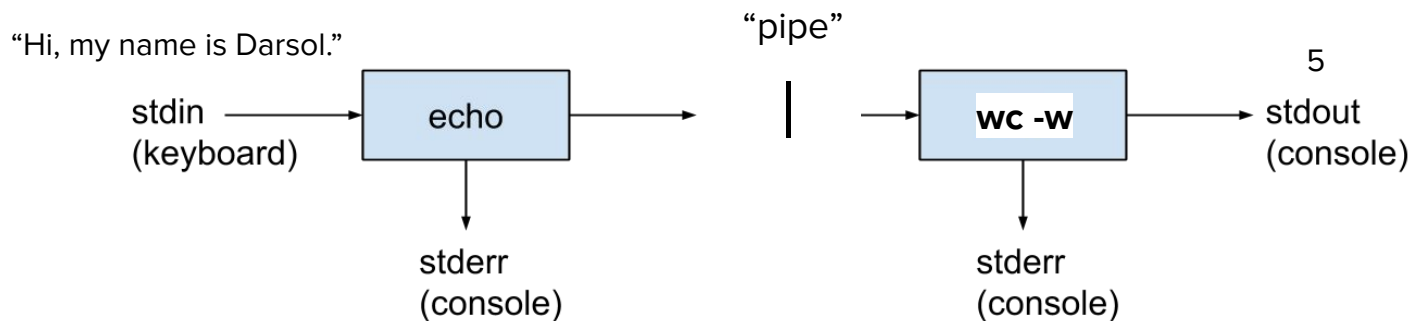
Middle mouse click : paste (Mac -> command + v)

Basic commands - stdin, stdout, stderr



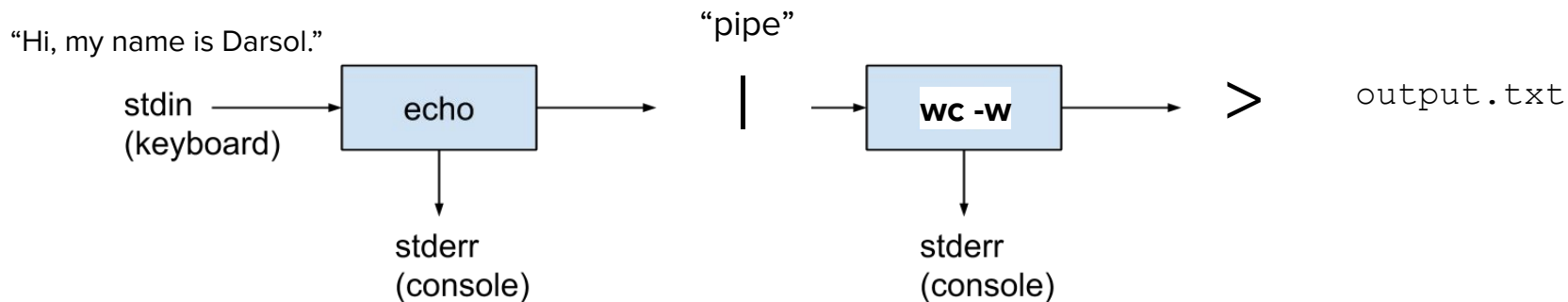
Basic commands - pipes and redirection

```
[dseok@chead ~]$ echo "Hi, my name is Darsol." | wc -w  
5
```



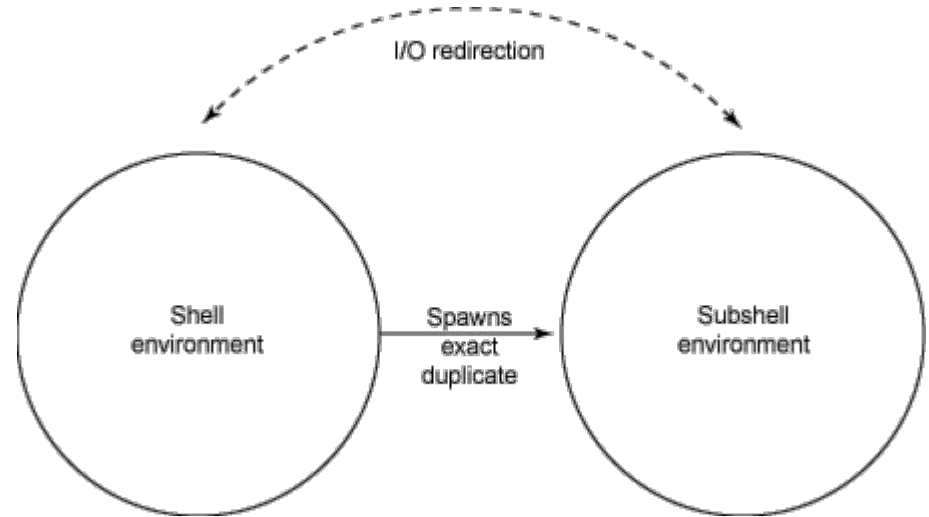
Basic commands - pipes and redirection

```
[dseok@chead ~]$ echo "Hi, my name is Darsol" | wc -w > output.txt  
[dseok@chead ~]$ cat output.txt  
5
```



Basic commands - pipes and redirection - subshells

```
var=$(ls | wc -w)
```



Basic commands - pipes and redirection

```
# check that the subject has an acceptable status
status_col=$(head -1 ${sublist} | tr ',' '\n' | grep -n "status" | awk -F ':' '{print $1}')
status=$(grep ${basesub} ${sublist} | awk -F ',' -v var=${status_col} '{print $var}' | sed 's/"//g')
```

Basic commands - the PATH

What happens when you type commands like `ls`, `cd` and `mkdir`?

The shell searches through all the directories in your `PATH`

`PATH` is defined in a file called your `bash_profile`

```
## .bash_profile

# Get the aliases and functions
if [ -f ~/.bashrc ]; then
    . ~/.bashrc
fi

# User specific environment and startup programs

PATH=$PATH:$HOME/bin

## CFNAPPS - defined in /etc/profile.d/cfn-common.sh

## R & RStudio
# Check that this is same version pointed to by the ANTsR build path
# NOTE: Define R_LIBS to include packages that aren't in R/library
PATH=$PATH:$CFNAPPS/R/R-3.1.1/bin
PATH=$PATH:$CFNAPPS/R/R-3.2.3/bin

## RStudio
# NOTE: Define R_LIBS to include packages that aren't in R/library
PATH=$PATH:$CFNAPPS/rstudio/rstudio-0.98.1091/bin/

## Pandoc
# Using the install that comes with rstudio because of
# difficulty building on its own.
# I believe this will use environment settings (i.e. PATH and R_LIBS)
# to run R as needed.
# Put it ahead of PATH so old default install isn't used.
PATH=$CFNAPPS/pandoc/1.12.4.2-in-rstudio/:$PATH
```

Basic commands - using aliases to set up shortcuts

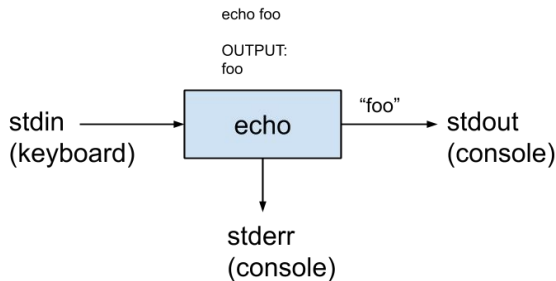
You can set up aliases (shortcuts) in your
bash_profile

```
alias hcp='cd /data/jag/cnds/connectome_U01/hcpPipeline'
alias beh='cd /data/jag/cnds/connectome_U01/MRIbehavior/task_timing_files'
alias ccbt='cd /data/jag/cnds/ccbt'
alias stress='cd /data/jag/cnds/stressInflammation'
alias jux='cd /data/jux/cnds'
alias cndsapps='cd /data/jag/cnds/applications'

alias queueup='qalter -u dseok -q all.q,basic.q,himem.q'

alias transform_results='/data/jag/cnds/stressInflammation/scripts/resting/sca/third_lev/transform_third_lev_results.sh ${pwd}'
alias transform_randomise='/data/jag/cnds/stressInflammation/scripts/resting/sca/randomise/transform_randomise_results.sh ${pwd}'
alias prepare_randomise='/data/jag/cnds/ccbt/scripts/task/third_lev/randomise/prepare_randomise_results.sh ${pwd}'
alias transform_ica='/data/jag/cnds/stressInflammation/scripts/resting/ica/transform_ica.sh ${pwd}'
```

Basic commands - background processes, nohup



```
[dseok@chead ~]$ jobs -l
[1] 6946 Running      sleep 20 &
[2] 6947 Running      sleep 20 &
[3] 6948 Running      sleep 20 &
[4] 6949 Running      sleep 20 &
[5] 6950 Running      sleep 20 &
[6] 6951 Running      sleep 20 &
[7] 6952 Running      sleep 20 &
[8] 6953 Running      sleep 20 &
[9] 6954 Running      sleep 20 &
[10] 6955 Running      sleep 20 &
[11] 6956 Running      sleep 20 &
[12] 6957 Running      sleep 20 &
[13] 6958 Running      sleep 20 &
[14] 6959 Running      sleep 20 &
[15] 6960 Running      sleep 20 &
[16] 6961 Running      sleep 20 &
[17] 6962 Running      sleep 20 &
[18] 6963 Running      sleep 20 &
[19]- 6964 Running      sleep 20 &
[20]+ 6965 Running      sleep 20 &
```

- Typically, while a process is running, the command line is not returned
- Using `&` after any command will place the process in the background
- `jobs -l` will show list of running jobs
- `kill [process_id]` will stop a running process
- `nohup [command]` will run the command, will not stop if you log off

Basic commands - background processes, nohup

```
for seed in $(cat seeds.txt); do  
  ./wrapper_run_analysis.sh ${seed} > ${seed}.log & done
```

```
[dseok@chead randomise]$ for seed in $(cat seeds.txt); do ./wrapper_run  
_randomise.sh group_diff ${seed} baseline > ${seed}.log & done
```

Basic commands - background processes, nohup

```
nohup [command] > [log_file] &
```

Running XCP:

```
nohup ${XCPEDIR}/xcpEngine -d design.dsn -c cohort.csv -o  
output_dir > output_dir.log &
```


Basic commands - useful tools

`awk` - when your file or string has delimiters

`sed` - search and replace, print specific lines

`grep` - search and output

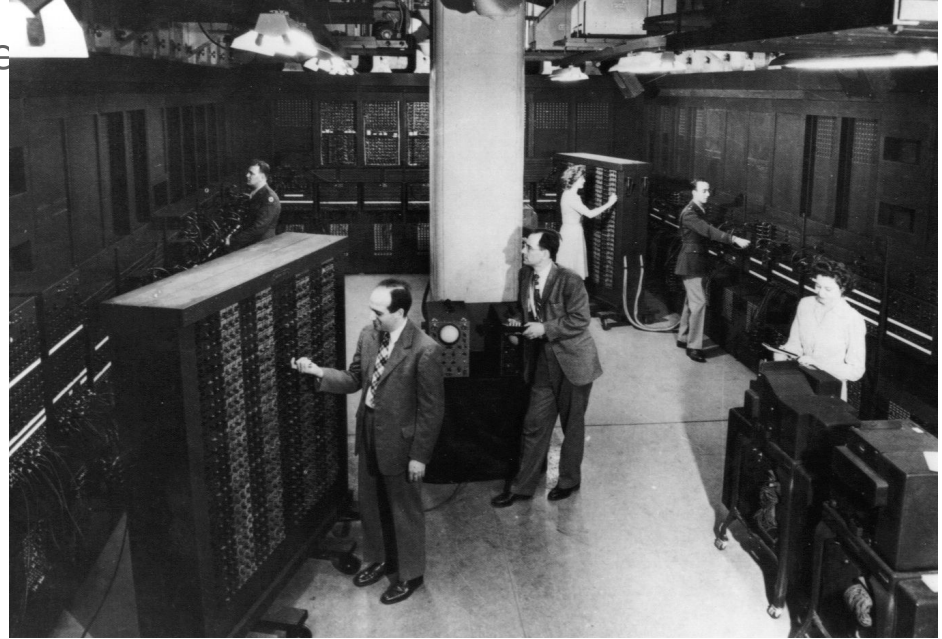
`bc` - integer and floating point calculations

`find` - finding files

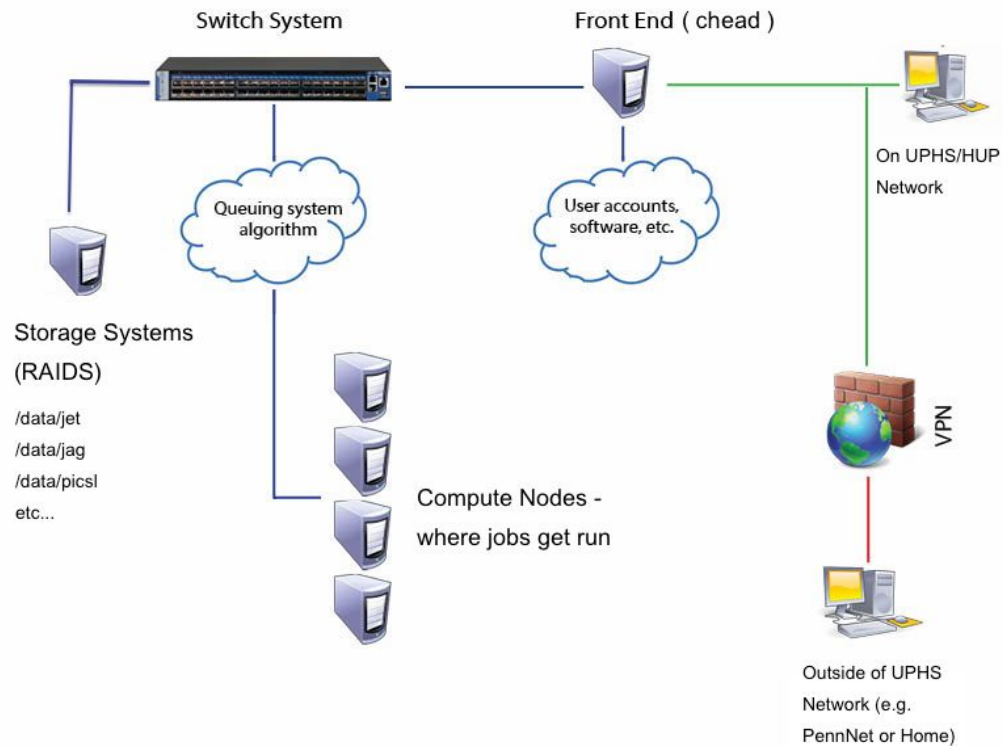
... and many more

Cluster management

Good management of your compute core
can make you more efficient!



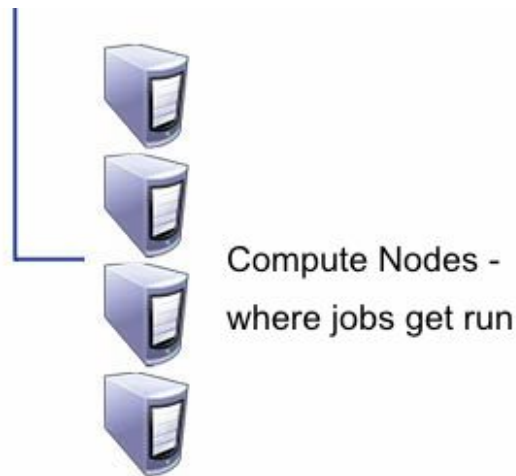
Cluster management - overview



Cluster management - interactive and batch nodes

Two flavors of nodes:

1. Interactive: directly login to a compute node. Use `qlogin`
2. Batch: submit a job to a compute node, stay on head node. Use `qsub`



Cluster management - interactive and batch nodes

Which node to use?



Cluster management - interactive and batch nodes

Which node to use?

Head node:

- Processes using > 5GB or lasting > 5 mins will be killed
- File management, submitting jobs, editing scripts, viewing images

Cluster management - interactive and batch nodes

Which node to use?

Head node:

- Processes using > 5GB or lasting > 5 mins will be killed
- File management, submitting jobs, editing scripts, viewing images

Interactive node:

- Directly log into compute node
- 8 slots, 230GB allocated
- Conducting analyses with GUIs - MATLAB
- Live debugging of scripts

Cluster management - interactive and batch nodes

Which node to use?

Head node:

- Processes using > 5GB or lasting > 5 mins will be killed
- File management, submitting jobs, editing scripts, viewing images

Interactive node:

- Directly log into compute node
- 8 slots, 230GB allocated
- Conducting analyses with GUIs - MATLAB
- Live debugging of scripts

Compute node:

- Submit a script (“job”) to the cluster
- 70 slots, ~600GB allocated
- Any other job

Cluster management - queues

In addition to interactive and batch, nodes come in different flavors:

all.q - default queue, standard cpu speed, 30GB memory limit. (220 GB, 32 slots)

himem.q - queue with higher memory limit - up to 220GB. (220GB, 6 slots)

basic.q - older set of compute cores, 19GB memory limit, slower. (130GB, 32 slots)

gpu.q - for use with GPU applications

Cluster management - queues

In addition to interactive and batch, nodes come in different flavors:

all.q - default queue, standard cpu speed, 30GB memory limit. (220 GB, 32 slots)

himem.q - queue with higher memory limit - up to 220GB. (220GB, 6 slots)

basic.q - older set of compute cores, 19GB memory limit, slower. (130GB, 32 slots)

gpu.q - for use with GPU applications

Also, **qlogin.q** (30GB, 5 slots) and **qlogin.himem.q** (220GB, 3 slots)

Cluster management - queues

By default, your account will only use **all.q** and **qlogin.q**

If your job isn't being scheduled, consider using other queues!

If you need to run many jobs as quickly possible, use all of the queues!

Cluster management - commands

`qsub test_script.sh` : submit a job

- `-l h_vmem=10G,s_vmem=9.5g` : set memory limits
- `-q all.q,basic.q,himem.q` : set queues
- `-o /data/jag/cnds/logs/test_script_\[extract_itex]JOB_ID.o` : set stdout
- `-e /data/jag/cnds/logs/test_script_\[extract_itex]JOB_ID.e` : set stderr
- `-j y` : merge stdout and stderr
- `-cwd` : launch in current working directory
- `-m e -M dseok@sas.upenn.edu` : send email when job is completed

Cluster management - commands

`qsub test_script.sh : submit a job`

- `-l h_vmem=10G,s_vmem=9.5g` : set memory limits
- `-q all.q,basic.q,himem.q` : set queues
- `-o /data/jag/cnds/logs/test_script_\[extract_itex]JOB_ID.o` : set stdout
- `-e /data/jag/cnds/logs/test_script_\[extract_itex]JOB_ID.e` : set stderr
- `-j y` : merge stdout and stderr
- `-cwd` : launch in current working directory
- `-m e -M dseok@sas.upenn.edu` : send email when job is completed

`qlogin -q qlogin.himem.q -l h_vmem=40G,s_vmem=40G`

Cluster management - commands

`qstat` : show all your running jobs

`cfn-resources` : show your available resources

`qalter -q all.q,basic.q,himem.q [job-id]` : change queue of job-id

`qdel [job-id]` : kill a running or queued job

Cluster management - example

Objective: change the queue of jobs started on 06/12/2019 that are currently queued (state = qw)

```
6724320 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-2-7.local 1
6724321 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-2-5.local 1
6724322 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-2-11.local 1
6724323 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-1-3.local 1
6724324 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-1-11.local 1
6724325 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-2-9.local 1
6724326 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-2-15.local 1
6724327 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-2-6.local 1
6724328 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-1-5.local 1
6724329 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 basic.q@compute-2-0.local 1
6724330 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 himem.q@compute-0-20.local 1
6724331 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 himem.q@compute-0-19.local 1
6724332 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 himem.q@compute-0-19.local 1
6724333 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 himem.q@compute-0-20.local 1
6724334 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 himem.q@compute-0-20.local 1
6724335 0.50500 sleep.sh dseok r 06/12/2019 09:56:16 himem.q@compute-0-19.local 1
6724336 0.50500 sleep.sh dseok qw 06/12/2019 09:56:12 1
6724337 0.50500 sleep.sh dseok qw 06/12/2019 09:56:12 1
6724338 0.50500 sleep.sh dseok qw 06/12/2019 09:56:12 1
6724339 0.50500 sleep.sh dseok qw 06/12/2019 09:56:12 1
6724340 0.50500 sleep.sh dseok qw 06/12/2019 09:56:12 1
6724341 0.50500 sleep.sh dseok qw 06/12/2019 09:56:12 1
6724342 0.50500 sleep.sh dseok qw 06/12/2019 09:56:12 1
```

Cluster management - example

```
[dseok@chead ~]$ qalter $(qstat | grep 06/12/2019 | grep qw | awk '{print $1}') -q basic.q
```

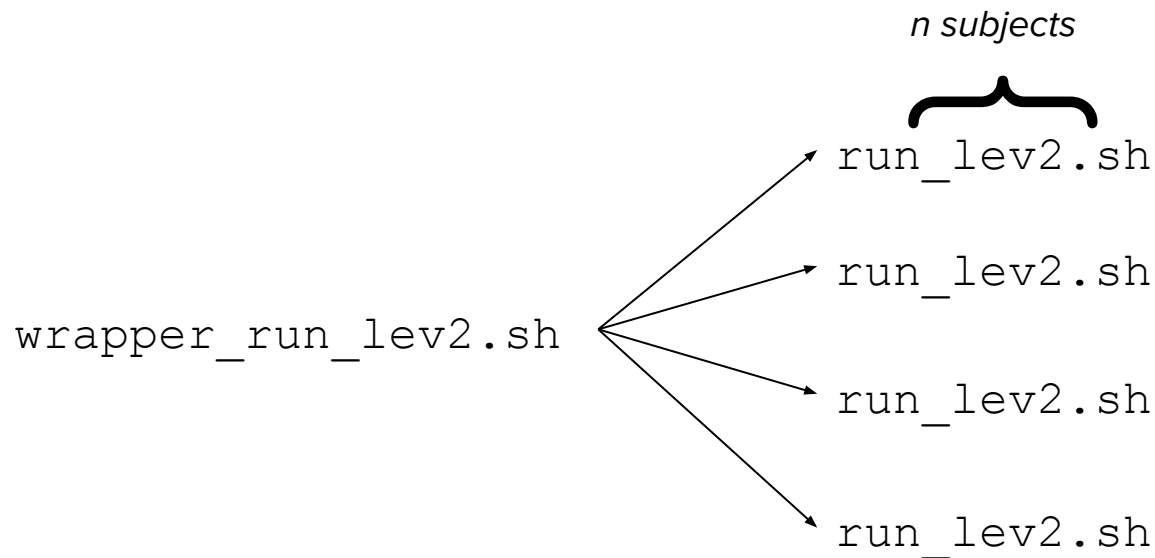

Intro to scripting

Script - a series of commands that performed sequentially to perform a task



Intro to scripting - example script

Script to run “level 2”, within subjects analysis



Intro to scripting - shebang



```
#!/bin/bash

# wrapper for run_lev2.sh. Will submit run_lev2.sh to the basic queue.

# args:
XCP_OUTPUT_NAME=${1}
LEV2_OUTPUT_NAME=${2}
```

`#!` : the shebang, a character sequence that indicates which interpreter to use

- `#!/usr/bin/env Rscript` : use `env` to launch interpreter for `Rscript`
- `#!/usr/bin/python` : use this version of `python` to interpret this script


Intro to scripting - comments



```
#!/bin/bash  
# wrapper for run_lev2.sh. Will submit run_lev2.sh to the basic queue.  
  
# args:  
XCP_OUTPUT_NAME=${1}  
LEV2_OUTPUT_NAME=${2}
```

You can use `#` to insert comments - human readable text that helps people (including yourself!) to read your code

Intro to scripting - arguments



```
#!/bin/bash

# wrapper for run_lev2.sh. Will submit run_lev2.sh to the basic queue.

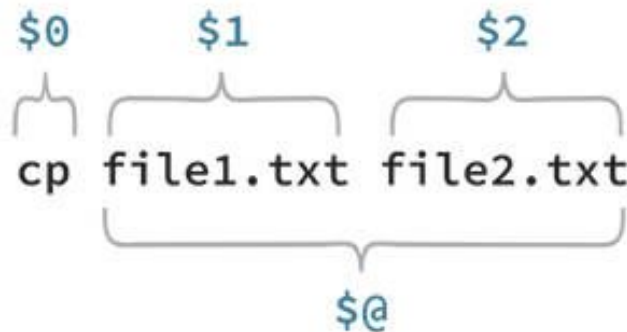
# args:
XCP_OUTPUT_NAME=${1}
LEV2_OUTPUT_NAME=${2}
```

When a script is launched as an executable, positional arguments are assigned to numbers


Intro to scripting - arguments

```
#!/bin/bash  
  
# wrapper for run_lev2.sh. Will submit run_lev2.sh to the basic queue.  
  
# args:  
XCP_OUTPUT_NAME=${1}  
LEV2_OUTPUT_NAME=${2}
```

When a script is launched as an executable, positional arguments are assigned to numbers



Intro to scripting - variables



```
PROJECT=/data/jag/cnds/ccbt
XCPDIR=/data/jux/cnds/xcp/outputs/${XCP_OUTPUT_NAME}
OUTPUTDIR=/data/jux/cnds/fsl/second_lev/${LEV2_OUTPUT_NAME}

mkdir -p ${OUTPUTDIR}
```

I like to assign variables to everything, so script is more portable

- Translating script to another project/data structure
- When your data structures change
- Also makes your script more readable

Intro to scripting - for loop

```
→ for sub in ${XCPDIR}/NDAR*; do
    for tp in $(ls ${sub}); do
        # check that sub and tp not already present
        basesub=$(basename ${sub})
        if [ -d ${OUTPUTDIR}/${basesub}_${tp}.gfeat ]; then
            echo ${basesub}_${tp} has already completed second level
analysis.
            continue
        fi
    done
done
```

The `for` loop is a control structure to iterate over a set of things

Intro to scripting - for loop

```
→ for sub in ${XCPDIR}/NDAR*; do
    for tp in $(ls ${sub}); do
        # check that sub and tp not already present
        basesub=$(basename ${sub})
        if [ -d ${OUTPUTDIR}/${basesub}_${tp}.gfeat ]; then
            echo ${basesub}_${tp} has already completed second level
analysis.
            continue
        fi
    done
done
```

```
for [thing] in [list_of_things]; do
```

```
    [stuff]
```

```
done
```

Intro to scripting - if statement

```
for sub in ${XCPDIR}/NDAR*; do
    for tp in $(ls ${sub}); do
        # check that sub and tp not already present
        basesub=$(basename ${sub})
        → if [ -d ${OUTPUTDIR}/${basesub}_${tp}.gfeat ]; then
            echo ${basesub}_${tp} has already completed second level
analysis.
            continue
        fi
    done
done
```

if statements can be used to check if a condition is met, and then perform some action

continue is used to skip to the next item in your for loop

Intro to scripting - if statement

```
for sub in ${XCPDIR}/NDAR*; do
    for tp in $(ls ${sub}); do
        # check that sub and tp not already present
        basesub=$(basename ${sub})
        → if [ -d ${OUTPUTDIR}/${basesub}_${tp}.gfeat ]; then
            echo ${basesub}_${tp} has already completed second level
            continue
        fi
    done
done
analysis.
```

```
if [ some_condition_to_meet ]; then
```

```
do_something
```

```
fi
```

Intro to scripting - multiple conditions

```
→ # check that xcp has completed
if [ ! -d ${echo ${sub}/${tp}/*/task/contrasts | awk '{print $1}'} ] \
|| [ $(ls ${sub}/${tp} | wc -w) -ne $(echo ${sub}/${tp}/*/task/contrasts | wc -w) ]; then
    echo "ERROR: ${basesub}_${tp} XCP run has failed or not completed."
    continue
fi

echo "Submitting ${sub} - ${tp}"
# otherwise, will we submit to run_lev2.sh
qsub -j y -o ${PROJECT}/scripts/task/logs/run_lev2/${basesub}_${tp}_\${JOB_ID}.stdout -cwd ${P
PROJECT}/scripts/task/second_lev/run_lev2.sh ${OUTPUTDIR} ${sub} ${tp}
done
done
```

You can string multiple conditions with logical connectors. Most common:

&& : and, both must be true

|| : or, either one or the other must be true

Intro to scripting - submitting “sub-script”


```
# check that xcp has completed
if [ ! -d $(echo ${sub}/${tp}/*/task/contrasts | awk '{print $1}')] \
|| [ $(ls ${sub}/${tp} | wc -w) -ne $(echo ${sub}/${tp}/*/task/contrasts | wc -w) ]; then
    echo "ERROR: ${basesub}_${tp} XCP run has failed or not completed."
    continue
fi

echo "Submitting ${sub} - ${tp}"
# otherwise, will we submit to run_lev2.sh
→ qsub -j y -o ${PROJECT}/scripts/task/logs/run_lev2/${basesub}_${tp}_\${JOB_ID}.stdout -cwd ${P
PROJECT}/scripts/task/second_lev/run_lev2.sh ${OUTPUTDIR} ${sub} ${tp}
done
done
```

Finally, we run our “sub-script”, `run_lev2.sh`

We pass our subject-specific parameters to the next script

Intro to scripting - submitting “sub-script”



```
#!/bin/bash

# runs second level analysis

OUTPUTDIR=${1}
sub=${2}
tp=${3}

LEV2_OUTPUT_NAME=$(basename ${OUTPUTDIR})
basesub=$(basename ${sub})
fsf_file=TEMP${LEV2_OUTPUT_NAME}_${basesub}_${tp}.fsf

# edit in the file names of the feat directories
feats=$(ls ${sub}/${tp}/*/task/fsf | grep "feat")
```

Receiving parameters from wrapper script

Thank you!
