

# Parallel Machine Learning and Artificial Intelligence

Prof. Handan Liu, PhD

[h.liu@northeastern.edu](mailto:h.liu@northeastern.edu)

Northeastern University

Spring 2020

# Content

- Introduction to the Discovery cluster
- Using Discovery
  - Connecting to Discovery
  - Data transfer
  - Loading Module
  - Using Slurm
  - Running jobs: interactive mode and batch mode; Job scripts
- Linux Fundamentals for Discovery Cluster
- Learn how to compile and run OpenMP and MPI programs ( in C )

# Connecting to Discovery

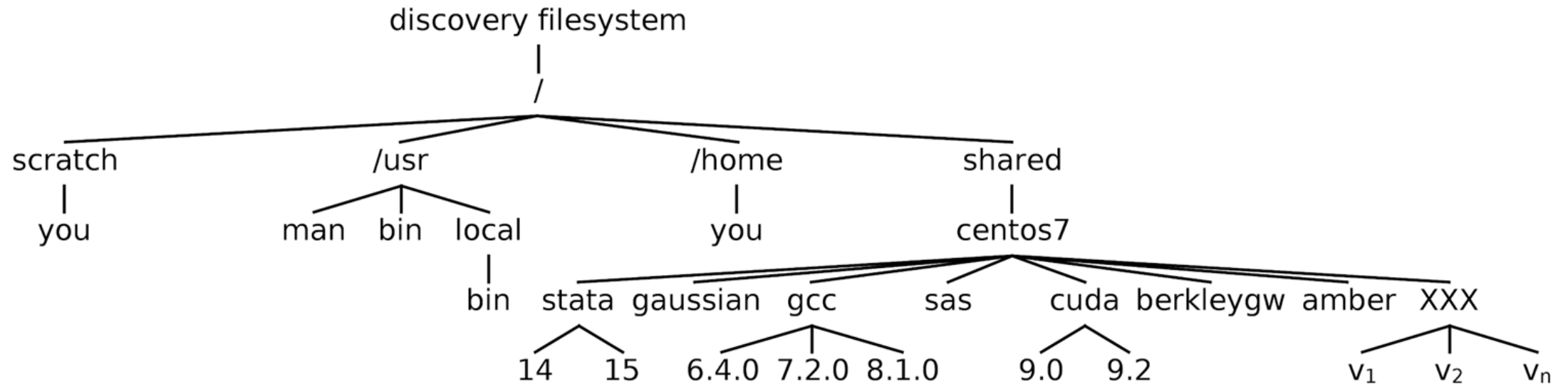
- Secure SHell (SSH)
  - Linux/Mac: Terminal
  - Windows: Putty, MobaXTerm

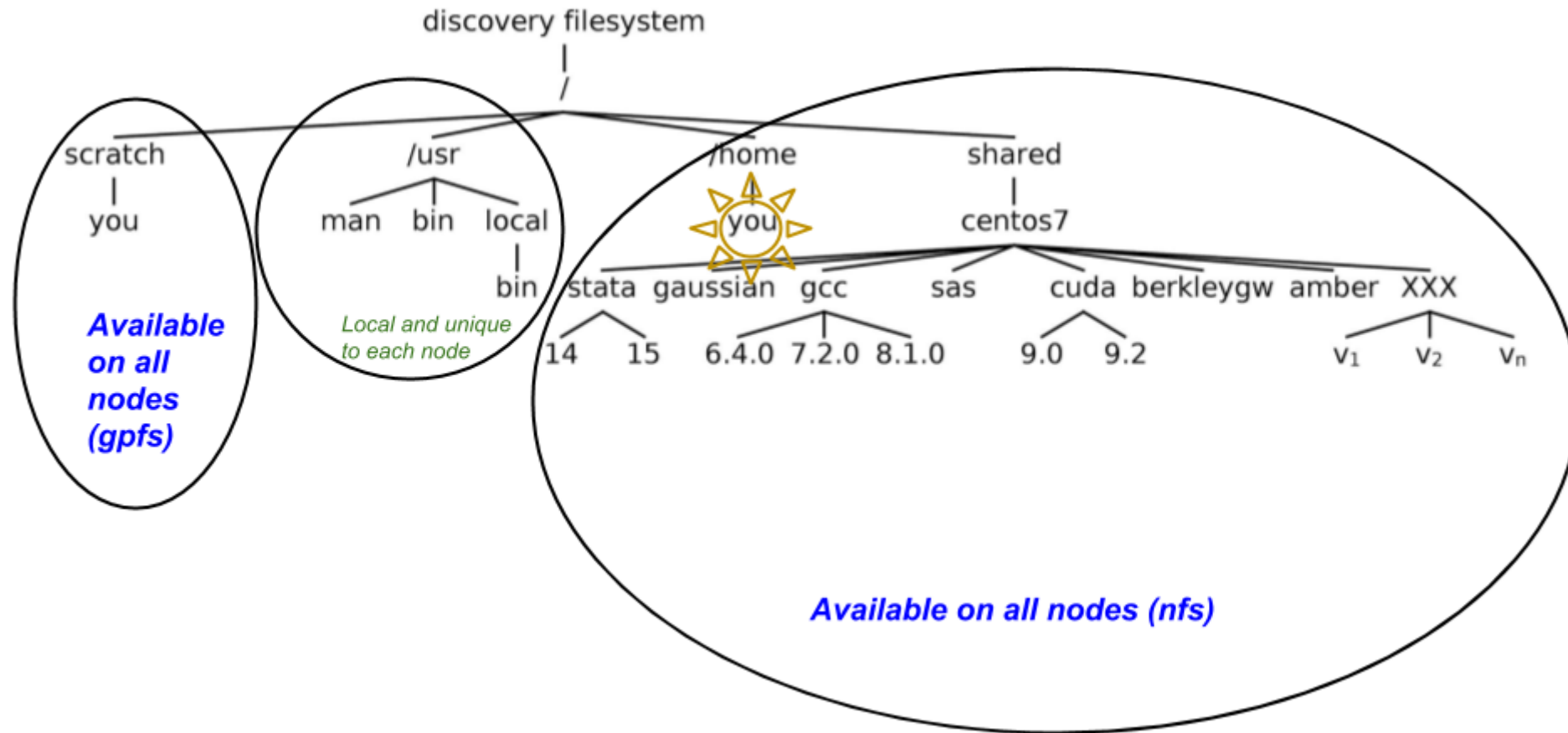
\$ ssh <username>@login.discovery.neu.edu

- Here, username is your Northeastern username

- Graphical User Interface (GUI), optional
  - Mac: Xquartz
  - Windows: X11

# Discovery Filesystem





# Data Transfer

- On command line (Linux like terminal) – scp, rsync
- Graphically – FileZilla
- Run the commands on your local machine:
  - \$ scp (-r for folder) source destination
  - \$ rsync -auv local remote
- Remote address:
  - username@xfer.discovery.neu.edu
  - sftp://xfer.discovery.neu.edu
- See RC document.

# Documentation

- Almost all utilities have the `--help` option which shows what the options are
- `man` utility shows the manual page for the utility, or a system call or any concept.
  - `q` → quit

# Filesystem navigation: viewing

- `ls` - list files
  - Options: `ls -[lart1d]` most common options
    - `-l`: long listing
    - `-a`: all files (including hidden files, (ones that begin with a .))
    - `-r`: show in reverse order (default sorting order is alphanumeric)
    - `-t`: sort by time modified
    - `-1`: show all in 1 column
    - `-d`: show directory names but not their content



# Viewing file content

`cat`: print content of file to the stdout (more on streams later)

`more`: print content of file to the screen but pause between pages

`less`: like more but with more options

`vi/vim/gedit`: open file in an editor

# File and directory manipulation

copy: `cp [-rpi v]`

- files: `cp file1 file2`
- Directories: `cp -r dir1 dir2`

move/rename: `mv oldpath/oldname newpath/newname`

Remove: `rm -[irf] / rmdir -[pmv]`

- Files: `rm file1 file2 file3 ... filek filen`
- Directories: `rmdir dir1 dir2 dir3 ... dirk dirn`

# Find a file in your directory tree

I want to find all the files which end with .err:

```
find . -type f -name '*.err'
```

- Using `find --help` or `man find` to get more information

# Archives

Sometimes it may be necessary to pack up an entire directory into a single file, for archiving, reducing the number of files in the filesystem, or easy transfer.

Create an archive from directory foo:

```
tar cvf foo.tar ./foo
```

c: create, f: name of file to create

Unpack an archive:

```
tar xvf foo.tar
```

x: xtract, v: verbose, f: filename of the archive

# Archives

Often tar archives are compressed to form what is known in the uinx/linux world as a “tarball”

To create or unpack a tarball, use the z option

```
tar czvf foo.tgz ./foo
```

```
tar zxvf foo.tgz
```

zip creates archives compatible with windows archives

# Slurm

- Slurm (Simple Linux Utility Resource Management) is the scheduling software that you use to schedule your jobs on Discovery.

- See the RC document.

- The sinfo shows the basic information of the cluster:

```
$ sinfo
```

```
$ sinfo -p partition-name
```

- Then scontrol shows configuration of partitions and nodes.

```
$ scontrol show res=reservation-name
```

```
$ scontrol show partition=partition-name
```

```
$ scontrol show nodes=node-name
```

# Using Module

# Running jobs

- Single node;
- Multiple nodes.
- Interactive mode
- Batch mode
- Move to a compute node by using `srun` or `sbatch`
- You should **NEVER** launch any jobs from the login nodes `login-00` or `login-01`. Any job launched from the login node will be terminated.



# Running jobs – Interactive

- Allocate resource, log onto compute node, run the job and exit
- To move to a compute node, at the command prompt type:

```
$ srun --pty /bin/bash
```

```
$ srun -p partition-name --pty /bin/bash
```

```
$ srun --reservation=CSYE7374 --pty  
/bin/bash
```

- Easy /small / debug
- Interactive

# Running jobs – Batch

- Submit to the cluster for later execution
  - \$ sbatch configuration file
- Configuration file
  - Parameters, what resource do you want
  - Commands, instructions to be executed
- A little more effort
- For longer and bigger jobs

# Submitting a job

- See the RC document.
- The general format for submitting a job to the scheduler is as follows:  

```
$ sbatch example.sbatch
```
- Example Job Scripts

# Sample batch script

```
#!/bin/bash
```

```
## Both in single-letter and whole-word formats, e.g. -N 1 and --nodes=1
```

```
## Normal configurations
```

```
#SBATCH --job-name=test
```

```
#SBATCH --output=test.out
```

```
#SBATCH --error=test.err
```

```
#SBATCH --time=00:15:00
```

```
## Parallel configurations
```

```
#SBATCH -p general
```

```
#SBATCH -N 1
```

```
##SBATCH -n 2  #OR --ntasks-per-node=10
```

```
##SBATCH --cpus-per-task=2
```

```
##SBATCH --mem-per-cpu=50G
```

## Constraint options

#SBATCH --mem=10G

#SBATCH --nodelist=c1[234-238]

#SBATCH --exclude=c1234

#SBATCH --constraint="E5-2690v3@2.60GHz"

## Dependencies options

#SBATCH --dependency=after:jobid

#SBATCH --dependency=afterok:jobid

#SBATCH --dependency=afternotok:jobid

Load modules

Change directory

Start the job

# Monitoring - Jobs

- `squeue`, jobs in the queue

```
$ squeue -u $USER -p partition -t PENDING
```

- `scontrol`, detailed job information,  
only for active jobs

```
$ scontrol show job id
```

- `seff`, efficiency related statistics,  
only for completed jobs

```
$ seff jobid
```

# Parallel Examples

# How to compile and run an OpenMP Program

Compiler	Compiler Options	Default behavior for # of threads (OMP_NUM_THREADS not set)
GNU (gcc, g++, gfortran)	-fopenmp	as many threads as available cores
Intel (icc ifort)	-openmp	as many threads as available cores
Portland Group (pgcc,pgCC,pgf77,pgf90)	-mp	one thread

## GNU Compiler Example:

```
$ gcc -o omp_helloc -fopenmp omp_hello.c  
$ export OMP_NUM_THREADS=2  
$ ./omp_helloc
```

## Intel Compiler Example:

```
$ icc -o omp_helloc -openmp omp_hello.c  
$ export OMP_NUM_THREADS=3  
$ ./omp_helloc
```



# How to Compile and Run a MPI Program

The table below lists OpenMPI compiler wrapper scripts for Linux clusters.

Language	Script Name	Underlying Compiler
C	mpicc	C compiler for loaded compiler package
C++	mpiCC mpic++ mpicxx	C++ compiler for loaded compiler package
Fortran	mpif77	Fortran77 compiler for loaded compiler package. Points to mpifort.
	mpif90	Fortran90 compiler for loaded compiler package. Points to mpifort.
	mpifort	Fortran 77/90 compiler for loaded compiler package.

# Compile and Run your cases

# Special tips – Install Python package

- Use the anaconda on cluster

```
$ module load anaconda
```

```
$ conda install package
```

- Install it on your own (download the source code)

```
>>> import sys
```

```
>>> sys.path.append(path_to_the_package)
```

- Install your own anaconda/virtual env/...

# The End!

## Assignment:

1. Practice Linux/Slurm commands on Discovery.
2. Don't run any job on login nodes!!!!