

HCC Kickstart

Introduction to HCC

University of Nebraska
Holland Computing Center

September 3-4, 2019

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Helpers: Carrie Brown, Adam Caprez, Tom Harvill
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Schedule ([link](#))

~~09:00 – 09:30 Overview of HCC~~

09:30 – 12:00 Introduction to HCC Coffee break from 10:30 to 10:45

12:00 – 1:00 Lunch

1:00 – 1:30 Using Globus for Data Management

1:30 - 2:45 Overview of Anvil

3:00 - 3:30 Using Jupyter Notebook on HCC

3:30 - 4:00 Introduction to OSG

4:00 - 5:00 Facility Tour / One-on-One Consultations

Intro to HCC: Teaching Objectives

- Login to HCC clusters using PuTTY(Windows)/Terminal(Mac).
- File management on the cluster.
- Use modules (software) installed on the clusters.
- Submit jobs using a job scheduler.

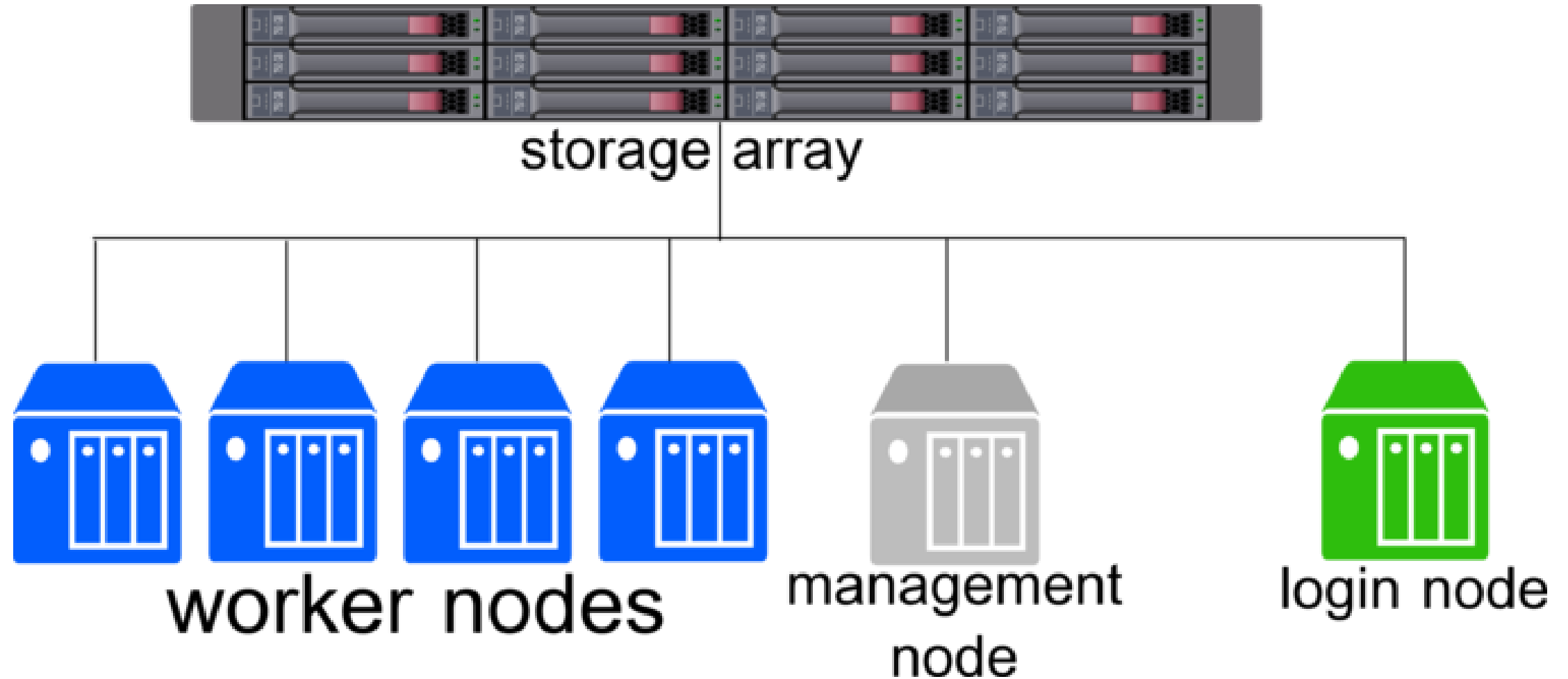
Logistics

- Location: Jackie Gaughan Multicultural Center – Unity Room
- Name tags, sign-in sheet
- Sticky notes: **Blue = need help**, **Yellow = all good**
- Lunch is provided
- Link to schedule and lessons/slides:
<http://hcc.unl.edu/hcc-kickstart-2019>

Intro to HCC: Teaching Objectives

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What is a Cluster?





Tusker/Sandhills Rhino

- Designed for memory intensive jobs
- 82 node AMD architecture cluster
- Up to 64 cores per node
- 256 GB RAM in most nodes
 - 2 nodes with 512 GB RAM
 - 1 node with 1024 GB RAM
- 500 TB shared storage
 - 500 GB scratch per node



Crane

- HCC's newest and fastest resource
- 548 node Intel cluster
- 16-36 cores per node
- 64 to 512 GB RAM per node
- 1452 TB shared storage
 - 4 TB scratch per node



Red

- Used to store and analyze data from the Large Hadron Collider CMS experiment
- 337 node Linux cluster
- 5888 cores
- 10.9 PB raw storage

Total Resources

almost 30k cores
approximately 10 PetaBytes of storage
64 GB to 1 terabyte memory per node



Anvil

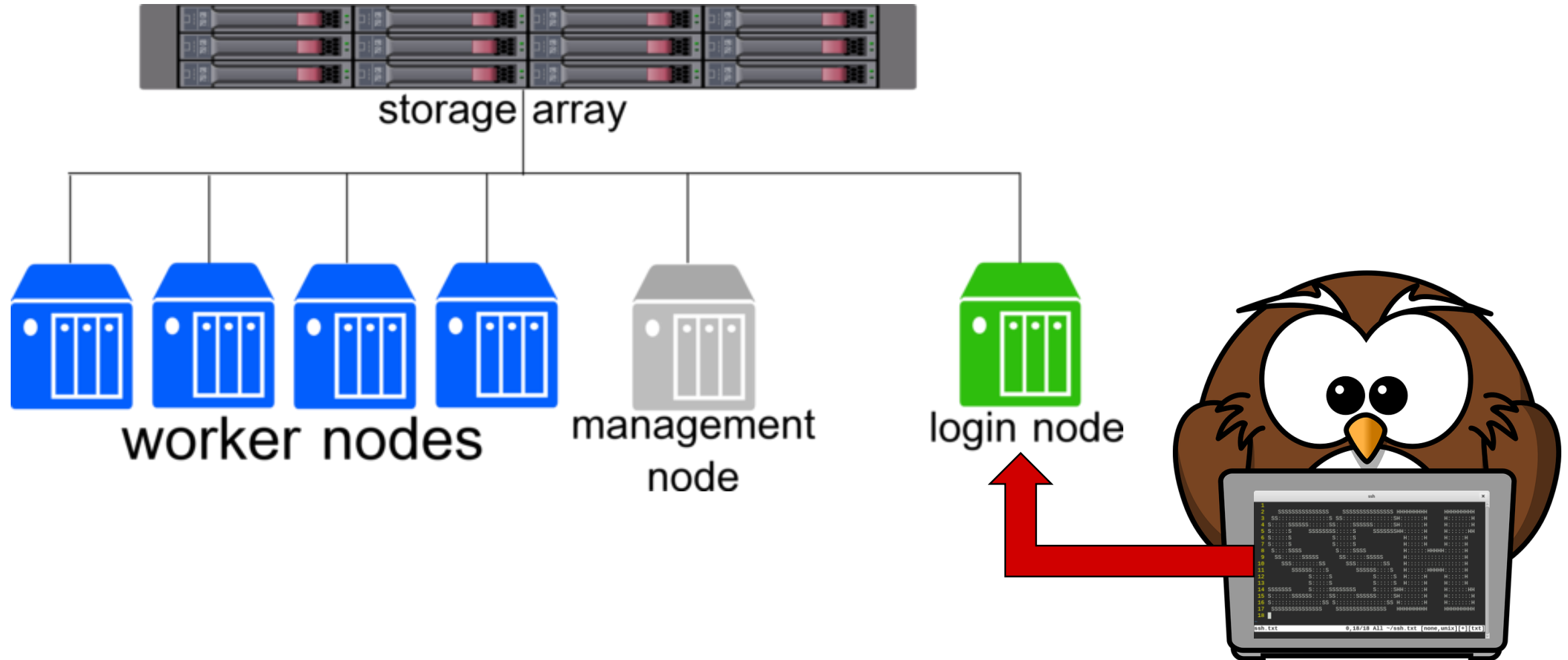
- HCC's Cloud
- Customizable virtual machines based on the OpenStack Software
- For projects that are not well served by a traditional Linux environment:
 - Highly interactive environments
 - Projects that require root access
 - Alternate operating systems
 - Test cluster environments
 - Cluster applications that require dedicated resources

Attic

- Near-line data archive
- Backed up in both Lincoln and Omaha for disaster tolerance
- 10 GB/s transfer speed to and from the clusters when using Globus Connect
- Cost per TB is significantly lower than commercial cloud services.
- No transfer limits or charges



Connecting to the Clusters



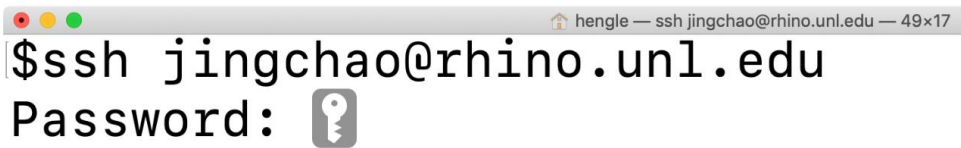
How to connect

Mac OS / Linux

- Open Terminal
- Type in the following command and press Enter:

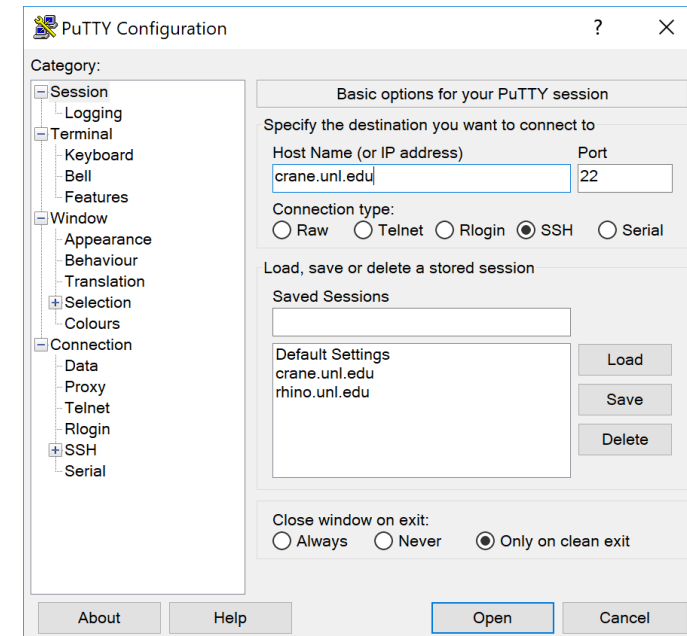
```
ssh <user_name>@rhino.unl.edu
```

(Replace <user_name> with your HCC login)



Windows

- Open PuTTY ([direct download link](#))
- Type **rhino.unl.edu** for Host Name and click Open



- On the second screen, click Yes

Once you connect, you will be prompted for your password.

Nothing will appear on your screen as you type your password. This is normal.

Two-Factor Authentication

If you are using a cell phone:

- Press 1 to receive a push notification on your device
- Press 2 to receive an automated phone call. Then enter the passcode provided.
- Press 3 to receive a list of passcodes via text message. Enter the passcode which starts with the number indicated

```
carriebrown — ssh cathrine98@tusker.unl.edu — 74x16
~ — ssh cathrine98@tusker.unl.edu
Carries-MacBook-Pro:~ carriebrown$ ssh cathrine98@tusker.unl.edu
Password:
Duo two-factor login for cathrine98

Enter a passcode or select one of the following options:

1. Duo Push to XXX-XXX-4833
2. Phone call to XXX-XXX-4833
3. SMS passcodes to XXX-XXX-4833

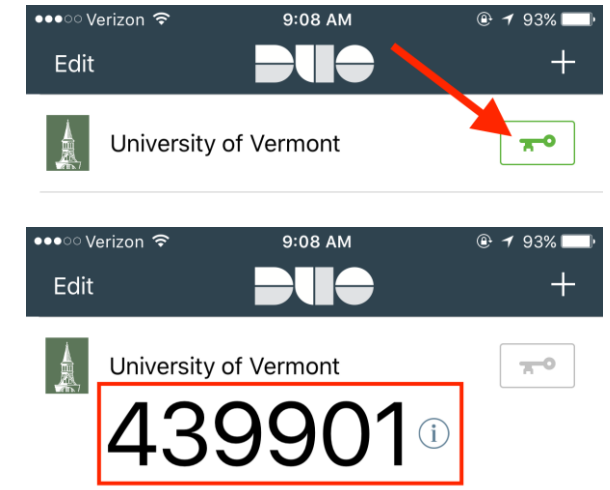
Passcode or option (1-3):
```

If you are using a hardware token (Yubikey):

- Insert the Yubikey into the computer's USB slot on your computer. A green light should come on inside the gold circle.
- Press your finger against the gold circle and a passcode will be generated.



The Duo Mobile app can also be used to generate passcodes, even when cell service is unavailable.



Shell Command Review

More commands and information can be found at:

https://hcc.unl.edu/docs/quickstarts/connecting/basic_linux_commands/

Command	What it does	Example Usage
ls	list: Lists the files and directories located in the current directory	ls <ul style="list-style-type: none">• Lists all files and directories in the current directory ls *.txt <ul style="list-style-type: none">• Lists all files which end with .txt in the current directory
cd	change directory: this allows users to navigate in or out of file directories	cd <dir_name> <ul style="list-style-type: none">• Navigates into the directory "dir_name" cd .. <ul style="list-style-type: none">• Navigates out of the current directory and into the parent directory cd \$WORK <ul style="list-style-type: none">• Navigates to your default /work directory
nano	nano text editor: opens the nano text editor Note: To access the menu options, ^ indicates the control (CTRL) key.	nano <ul style="list-style-type: none">• opens the text editor in a blank file nano <file_name> <ul style="list-style-type: none">• opens the text editor with "file_name" open. If "file_name" does not exist, it will be created if the file is saved
less	less: opens an extended view of a file Note: scroll using up and down arrows. To exit, press 'q'	less <file_name> <ul style="list-style-type: none">• opens an extended view of the file "file_name"

Exercises

1. Type **exit** to logoff of the Rhino cluster.
2. Connect to the Crane cluster (hostname: **crane.unl.edu**)
 - Try using a different Two-factor authentication method if you have another option.

Once you have finished, put up your **yellow sticky note**.

If you have issues, put up your **blue sticky note** and one of the helpers will be around to assist.

Intro to HCC: Teaching Objectives

- ~~Login to HCC clusters using PuTTY(Windows)/Terminal(Mac).~~

- Create files on the cluster. Transfer files between your laptop and the cluster.

- Utilize modules (software) installed on the clusters.
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Home vs Work vs Common ([documentation](#))

\$HOME - /home/group/user

- Not intended for I/O to active jobs
- Quota-limited to 20GB *per user*
- **Backed up for best-effort disaster recovery**
- Meant for items that take up relatively small amounts of space.
 - Source code
 - Program binaries
 - Configuration files
- **Read-Only to worker nodes**

\$WORK - /work/group/user

- Designed for I/O for running jobs
- 50TB quota *per group*
- **Not backed up**
- To check group usage:
 - **hcc-du**
- **Purge policy**
 - Files will be deleted after 6 months inactivity
 - Files eligible for purge can be checked using **hcc-purge**

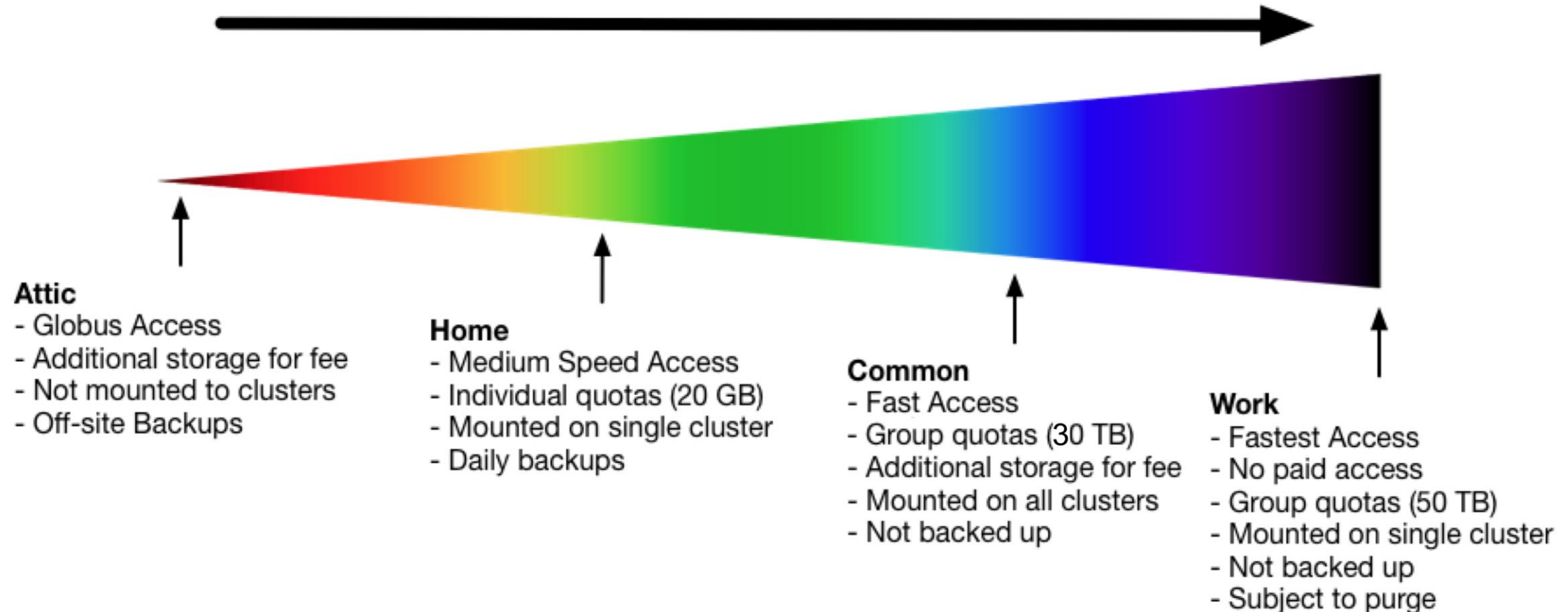
Home vs Work vs Common (cont.)

\$COMMON- /common/group/user ([documentation](#))

- Mounted on all HCC clusters
- Quota-limited to 30TB *per group*
- **Not backed up**
- **Not purged**
- **#SBATCH --licenses=common**
- Meant for items that read to be accessed from multiple clusters.
 - Shared data files
 - Reference databases
 - etc.

Home vs Work vs Common vs Attic

- Faster File Access (higher bandwidth / IOPS)
- Ease of Access
- Diminishing Redundancy (backups)



\$WORK/\$COMMON Usage Best Practices

- **Avoid large numbers of files**
 - Having hundreds of files in your directories can drastically degrade the performance of the file system
- **Storage resources are finite**
 - Be judicious about the data you store.
 - Periodically review your files and carefully consider what you need; remove what is no longer needed.
- **Use Globus for file transfers**
 - Globus Connect is a fast and robust file transfer service that allows users to quickly move large amounts of data between computer clusters and to and from personal workstations
- **Backup valuable data**
 - Users are responsible to backup their valuable research data on \$WORK periodically

Transferring Files

- **Transfer files using an SCP client**

- WinSCP (<https://winscp.net>) – Windows ([direct download link](#))
 - [Documentation page](#)
- Cyberduck (<https://cyberduck.io>) – MacOS ([direct download link](#))
 - [Documentation page](#)
- Filezilla (<https://filezilla-project.org/>) – Windows, MacOS and Linux

- **Globus Connect**

- <https://globus.org>
- Fast, secure and robust transfers with user-friendly web interface
- Uses the High-Speed transfer nodes by default
- Can transfer directly between clusters, Attic and personal machine

- **scp**

- Usage: `scp user@host:source_file user@host:target_file`
- Example: `scp my_file.txt demo01@crane.unl.edu:$WORK/my_file.txt`

Exercises

1. In your \$HOME directory create a file called 'bio.txt' – edit this file to include your name and department. (type command 'cd' to switch to \$HOME)
2. If you are using a Windows laptop, download and setup WinSCP. Or if you are using a Mac, download and setup Cyberduck.
 - Windows instructions: <https://go.unl.edu/hcc-windows-scp>
 - Mac instructions: <https://go.unl.edu/hcc-maclinux-scp>
3. Copy the 'bio.txt' file from Crane \$HOME to your local laptop.
4. Copy the 'bio.txt' file from your local laptop to Crane \$WORK.
5. Change to your \$WORK directory (Type command: cd \$WORK)
6. Clone the tutorial files by entering the command:
 - `git clone https://github.com/unlhcc/job-examples.git`
 - Contributions to this repository are welcome!

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Running Applications

- All applications installed on HCC clusters are loaded in individual modules implemented with Lmod
 - Lua based module system
- Modules dynamically change the user environment
 - \$PATH
 - \$LD_LIBRARY_PATH
- Hierarchical structure
 - If module A is dependent on module B, then module B must be loaded first to load module A
- Typically follows the naming convention <software>/<version>
 - Example: python/2.7
- Load using the **module** command

Lmod Commands

Command	What it does
<code>module avail</code>	Lists all modules available to be loaded
<code>module spider <name></code>	Information about a specific module – can also be used to search
<code>module load <module_name></code>	Load module(s) – can load a list of space delimited modules
<code>module unload <module_name></code>	Unload module(s) – can unload a list of space delimited modules
<code>module purge</code>	Unloads all currently loaded modules
<code>module list</code>	Lists all currently loaded modules

For more information:

- `module --help`
- Available software lists for each cluster:
 - Crane: <https://go.unl.edu/hcc-cranesoftware>
 - Rhino: <https://go.unl.edu/hcc-rhinosoftware>

Exercises

1. Find a list of 'Core' modules that do not have any dependences.
2. Load one or more of the modules from the list you just found. Now unload them. Try doing it two different ways.
3. Lookup information about the MATLAB module.
 - How many different versions are available?
 - Load a specific version using the `<module_name>/<version>` name
4. Try loading the lammmps/10Feb2017 module. Did it work?
 - Now load these modules first
 - compiler/intel/15
 - openmpi/1.10
 - Now try loading lammmps/10Feb2017 again. Does it work now? Why?
 - Unload all modules with only one command.

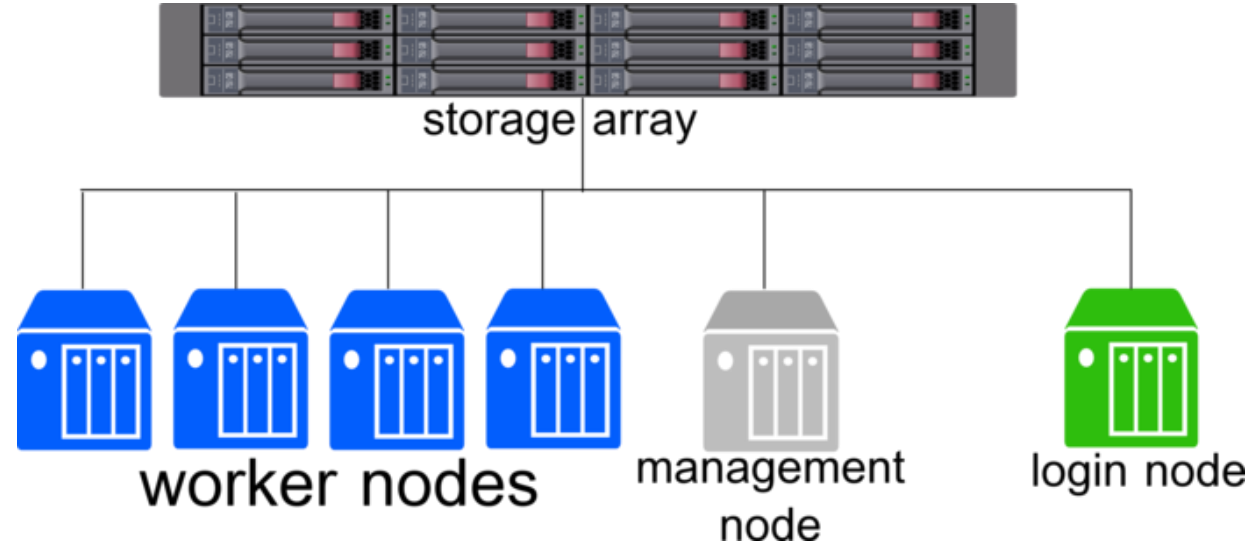
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Running Jobs



- All calculation and analysis must be done on the worker nodes
- Processes started on the login node will be killed
 - Limit usage to brief, non-intensive tasks like file management and editing text files
- HCC uses the SLURM scheduler to manage and allocate resources
 - Resources are allocated based on the Fair Use Algorithm
- Jobs can be run in interactive or batch format

Interactive vs Batch Jobs

Batch Jobs

- The user creates a **submit file** which contains all commands and job information and add its to the queue
 - Similar to running Bash scripts
- Holds job information until resources become available
 - User can disconnect and the job will remain queued
- Uses the **sbatch** command

Interactive Jobs

- Allows the user to type in commands and run programs **interactively**
- Must remain connected and wait for resources to be allocated
- Job can be interrupted
- Uses the **srun** command

Batch Jobs

- To create a batch job, the user must first make a submit script
 - Submit scripts include all job resource information:
 - number of nodes/cores
 - required memory
 - Runtime
 - **If the job exceeds the requested memory or time, it will be killed.**
- Submit script is then added to the job queue using the **sbatch** command
- **squeue** will show queued and running jobs
- **sacct** can be used to find information about completed jobs

Common SBATCH Options

Command	What it does
--nodes	Number of nodes requested
--time	Maximum walltime for the job – in DD-HHH:MM:SS format – maximum of 7 days on batch partition
--mem	Real memory (RAM) required per node - can use KB, MB, and GB units – default is MB Request less memory than total available on the node - The maximum available on a 512 GB RAM node is 500, for 256 GB RAM node is 250
--ntasks-per-node	Number of tasks per node – used to request a specific number of cores
--mem-per-cpu	Minimum of memory required per allocated CPU – default is 1 GB
--output	Filename where all STDOUT will be directed – default is slurm-<jobid>.out
--error	Filename where all STDERR will be directed – default is slurm-<jobid>.out
--job-name	How the job will show up in the queue

For more information:

- **sbatch -help**
- SLURM Documentation: <https://slurm.schedmd.com/sbatch.html>

Submit Scripts

Shebang

The shebang tells Slurm what interpreter to use for this file. This one is for the shell (Bash)

Name of the submit file

This can be anything. Here we are using "invert_single.slurm" the .slurm makes it easy to recognize that this is a submit file.

Commands

Any commands after the SBATCH lines will be executed by the interpreter specified in the shebang – similar to what would happen if you were to type the commands interactively

SBATCH options

These must be immediately after the shebang and before any commands.

```
[cathrine98@c3712.crane matlab-tutorial]$ cat invert_single.slurm
#!/bin/sh
#SBATCH --time=0:10:00
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --mem=10GB
#SBATCH --mem-per-cpu=10GB
#SBATCH --job-name="invert_single"
#SBATCH --error="invert_single.err"
#SBATCH --output="invert_single.out"

module load matlab/r2014b

cd $WORK/matlab-tutorial
mkdir -p /tmp/$SLURM_JOB_ID
matlab -nodisplay -r invertRand
[cathrine98@c3712.crane matlab-tutorial]$
```

Determining Parameters

How many nodes/memory/time should I request?

- **Short answer:** We don't know.
- **Long answer:** The amount of time and memory required is highly dependent on the application you are using, the input file sizes and the parameters you select.
 - Sometimes it can help to speak with someone else who has used the software before.
 - Ultimately, it comes down to trial and error
 - Check the output and utilization of each job will help you determine what parameters you will need in the future.
 - Trying different combinations and seeing what works and what doesn't.

Submit Files Best Practices

- **Put all module loads immediately after SBATCH lines**
 - Quickly locate what modules and versions were used.
- **Specify versions on module loads**
 - Allows you to see what versions were used during the analysis
- **Use a separate submit file for each job**
 - Instead of editing and resubmitting a submit files – copy a previous one and make changes to it
 - Keep a running record of your analysis
- **Redirect output and error to separate files**
 - Allows you to see quickly whether a job completes with errors or not
- **Separate individual workflow steps into individual jobs**
 - Avoid putting too many steps into a single job

Exercises

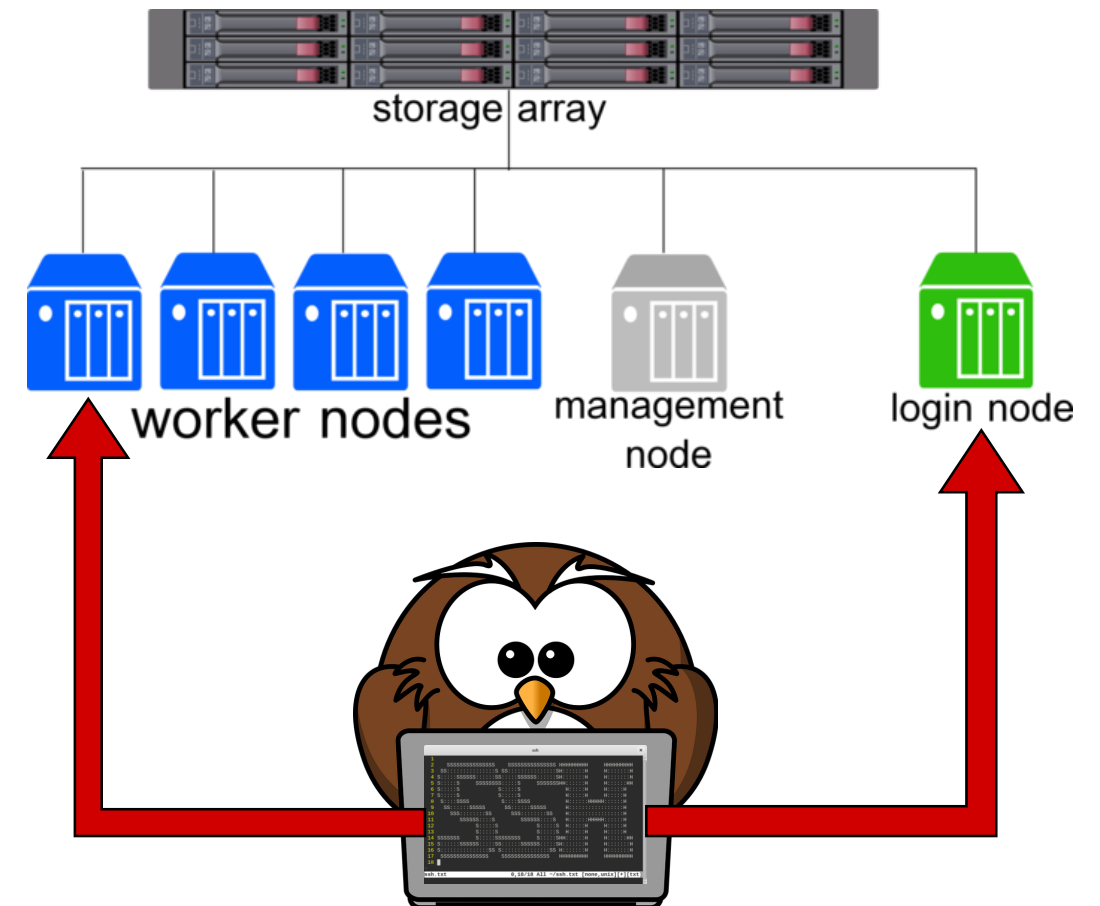
1. Navigate into the matlab directory of the job-examples directory and locate the serial.slurm file
 - This submit file runs a MATLAB script which inverts a 10,000 x 10,000 randomly generated matrix and outputs the length of time it took to perform the inversion.
 - Look at the contents of serial.slurm - How many nodes this will run on? How many cores? How much memory and time is requested?
 - Submit the serial.slurm job. Check the output to see how long it took to invert the matrix.
2. Location the parallel.slurm file.
 - Submit the job again and compare the time to your initial run. How much faster or slower is it?
 - Compare times with your neighbor. Did you see the same amount of improvement?
3. If there's time, try different combinations of SBATCH commands and see how the running time changes.

Once you have finished, put up your green sticky note.
If you have issues, put up your red sticky note and
one of the helpers will be around to assist.

Interactive Jobs

```
[cathrine98@login.crane ~]$ srun --nodes=1 --mem=1gb --pty bash  
srun: job 7741317 queued and waiting for resources  
srun: job 7741317 has been allocated resources  
[cathrine98@c3712.crane ~]$
```

- Interactive jobs work very similarly to batch jobs
- Once resources are allocated, commands can be input interactively
 - All output is directed to the screen



Exercises

1. Request an interactive job for certain amount of resources
 - If you can't think of a setup, use one of these:
 - 1 node, 1 core with 2 GB RAM each core
 - 2 nodes, 1 core per node with 2 GB RAM each core
 - How long did it take to allocate resources? Compare your set up and wait time with your neighbor. Did they get resources faster or slower than you did?
2. Using your interactive job from above, load the module for your favorite programming language (Python, R, MATLAB, etc.)
 - Run the program interactively

Once you have finished, put up your yellow sticky note.

If you have issues, put up your blue sticky note and one of the helpers will be around to assist.

A few links

1. [Software installation request form](#)
2. [Acknowledgement credit form](#)
3. [Priority access price list](#)

Asking for help

- **Contact Us**

- Drop by our offices
 - UNL: Room 118 in the Schorr Center on City Campus
 - UNO: Room 158 in the Peter Kewit Institute on Center Campus
- Email hcc-support@unl.edu