

# Cluster & HTCondor

Biochemistry laboratories - 201

Jean-Yves Sgro -jsgro@wisc.edu

Note: To see as slides click on "Gift icon"  at the top right. To revert back to page view click on "book icon"  when on the first slide.

## Set-up

- check your name on the attendees list
- choose an iMac
- login with your NetID ( @wisc.edu is not necessary)
- If this is the first time this Mac "sees" you it will go through a quick set-up: simply skip using "Apple ID"

## Finding Terminal on the iMac



Terminal

### Method 1

- Click on the "Finder"



at the bottom left of the "**Dock**" on the bottom of the screen. This will open a new window.

- On the left click on "**Applications**"
- In the alphabetical list open folder **Utilities**
- double click to open **Terminal**

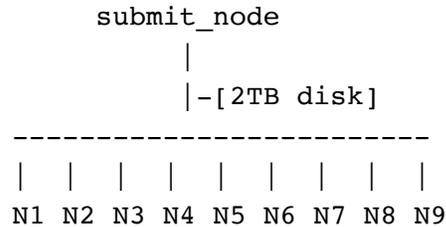
### Method 2

- *Spotlight Search*: Click the magnifying glass  at the top right corner of your screen
- type Terminal

- press the return key

## Cluster & HTCondor

The Biochemistry Computational Cluster (BCC) is a High Throughput Computing (HTC) environment within the UW-Madison Biochemistry Department.



## HTCondor

- HTCondor is a “scheduler” system that dispatches compute jobs to 1 or more "compute nodes."
- Using HTCondor is the only approved method for performing high throughput computing on the BCC Linux cluster.
- Jobs have to be ready to be processed by HTCondor as **jobs cannot be interactive on the cluster.**

## Cluster access overview

1. Text-based access only
2. No graphical interface
  - A. Login info `ssh myname@submit.biochem.wisc.edu`
3. Linux OS: Scientific Linux
4. VPN access

## Process

Submit a "job file" that contains information on how to run the software

- submit file: `myjob.sub`
- executable: `myjob.sh`

Information about software and file transfer

## Getting ready

Invert the process:

- define software and files (with dependencies)
- create script to run "hands-off"
- create submit file

## QuickStart

Login - [replace *myname* with your login name.]

```
ssh myname@submit.biochem.wisc.edu
```

Then move to `/scratch` and create a directory with your name and another directory within to work with.

```
$ cd /scratch
$ mkdir myname #replace myname with e.g. YOUR ID
$ mkdir quickstart
$ cd myname/quickstart
```

## Create an simple executable test file

Create execute file (e.g. with nano)

```
$ nano hello.sh
```

File content:

```
#!/bin/sh
echo "Hello World"
```

Make file executable:

```
$ chmod u+x hello.sh
```

## Create a simple submit file

```
$ nano hello.sub
```

File content:

```
executable = hello.sh
should_transfer_files = Yes

output = hello.out
error = hello.err
log = hello.log

queue
```

## Submit job

```
$ condor_submit hello.sub
```

## Check output

```
$ ls
```

```
hello.err hello.log hello.out hello.sh hello.sub
```

## On-line resources

Resource	Link
HTCondor Quick Start Guide	<a href="http://research.cs.wisc.edu/htcondor/manual/quickstart.html">http://research.cs.wisc.edu/htcondor/manual/quickstart.html</a> ( <a href="http://research.cs.wisc.edu/htcondor/manual/quickstart.html">http://research.cs.wisc.edu/htcondor/manual/quickstart.html</a> )
Complete manual*	<a href="http://research.cs.wisc.edu/htcondor/manual/">http://research.cs.wisc.edu/htcondor/manual/</a> ( <a href="http://research.cs.wisc.edu/htcondor/manual/">http://research.cs.wisc.edu/htcondor/manual/</a> )

\*You can check which manual you need by checking which version of HTCondor is installed with command: **condor\_version**

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