Cluster & HTCondor

> Biochemistry laboratories - 201
>
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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.

```
          submit_node
               |
               |-[2TB disk]
     -------------------------
     |  |  |  |  |  |  |  |  |
     N1 N2 N3 N4 N5 N6 N7 N8 N9
```

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 dependecies)
- 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	http://research.cs.wisc.edu/htcondor/manual/quickstart.html (http://research.cs.wisc.edu/htcondor/manual/quickstart.html)
Complete manual*	http://research.cs.wisc.edu/htcondor/manual/ (http://research.cs.wisc.edu/htcondor/manual/)

*You can check which manual you need by checking which version of HTCondor is installed with command: **`condor_version`**

```
In [ ]:
```