

HTCondor on BCC

Dec 14, 2023

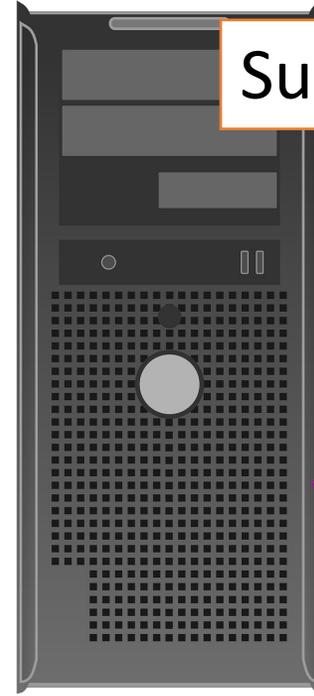


SSH to BCC



Submit node

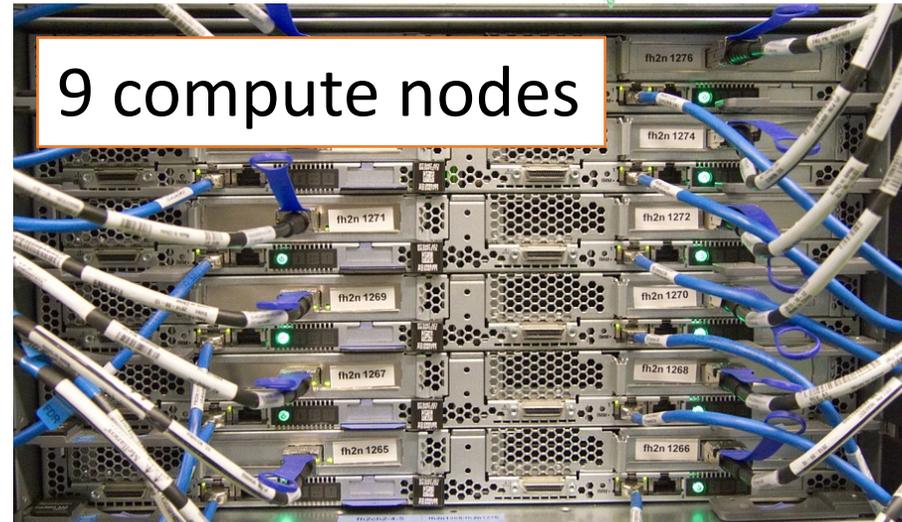
access point



HTCCondor

execute points

9 compute nodes



Credits



Lauren Michael – Open Science Grid, 2021

<https://osg-htc.org/virtual-school-2021/materials/htcondor/files/osgvsp21-htc-htcondor.pptx>



Christina Koch Researching Computer Facilitator

https://research.cs.wisc.edu/htcondor/HTCondorWeek2016/presentations/Koch_UserTutorial.pptx

OS Grid Materials

<https://osg-htc.org/virtual-school-2021/materials/>

Terminology: *Job*

Job: An independently-scheduled unit of computing work

Three main pieces:

Executable: the script or program to run

Input: any options (arguments) and/or file-based information

Output: files printed by the executable

In order to run *many* jobs, executable must run on the command-line **without any graphical input** from the user

Basic Job Submission

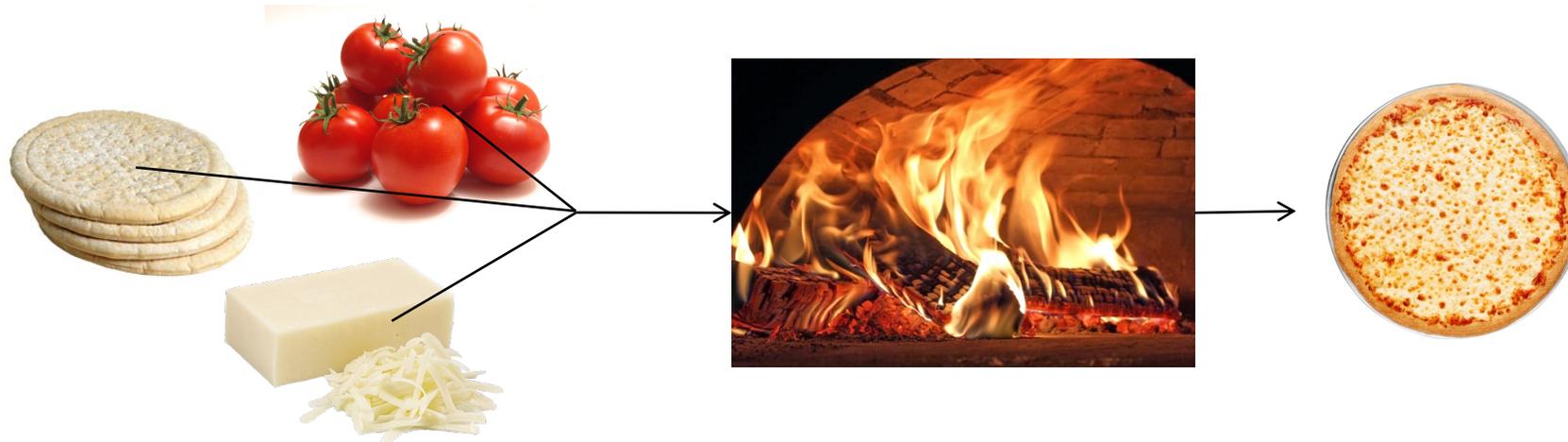


Jobs

A single computing task is called a “job”

Three main pieces of a job are:

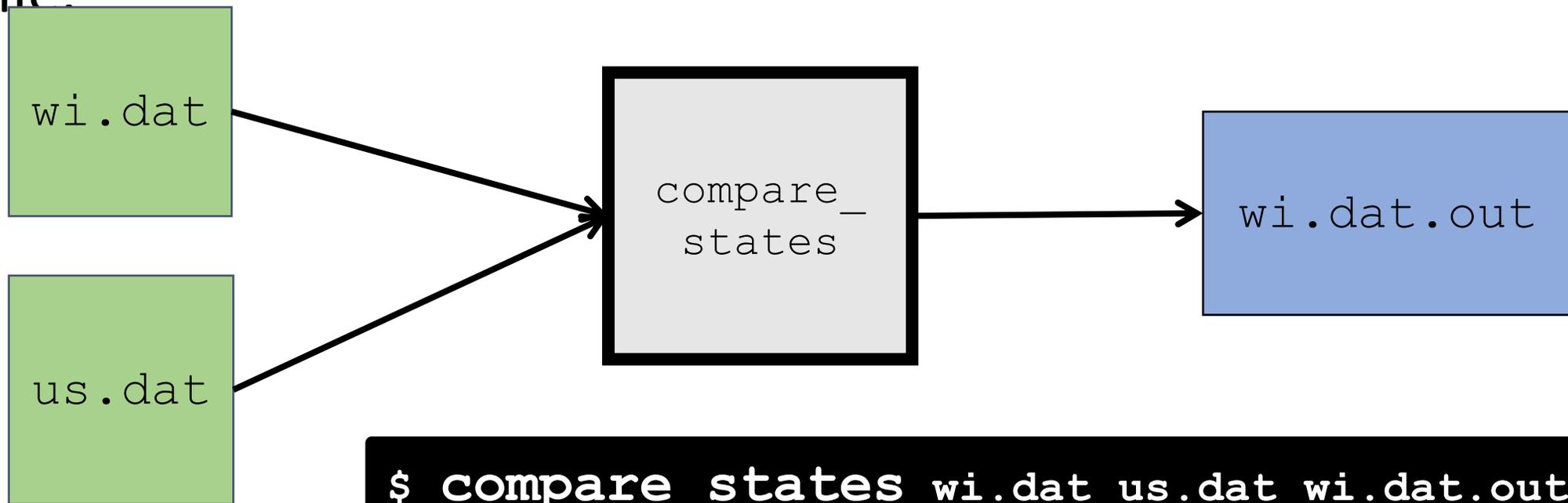
- input
- executable (program
- output



Executable must be runnable from the command line
without any interactive input

Job Example

- program called “compare_states” (executable), which compares two data files (input) and produces a single output file.



```
$ compare_states wi.dat us.dat wi.dat.out
```

Basic Submit File

```
executable = compare_states  
arguments = wi.dat us.dat  
wi.dat.out
```

```
transfer_input_files = us.dat,  
wi.dat
```

```
log = job.log  
output = job.out  
error = job.err
```

```
request_cpus = 1  
request_disk = 20MB  
request_memory = 20MB
```

```
queue 1
```

Basic Submit File

```
executable = compare_states  
arguments = wi.dat us.dat  
wi.dat.out
```

```
transfer_input_files = us.dat,  
wi.dat
```

```
log = job.log  
output = job.out  
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```

```
request_cpus = 1  
request_disk = 20MB  
request_memory = 20MB
```

queue 1

List your **executable** and any **arguments** it takes

Arguments are any options passed to the executable from the command line

```
$ compare_states wi.dat us.dat  
wi.dat.out
```

Basic Submit File

```
executable = compare_states  
arguments = wi.dat us.dat  
wi.dat.out
```

```
transfer_input_files =  
us.dat, wi.dat
```

```
log = job.log  
output = job.out  
error = job.err
```

```
request_cpus = 1  
request_disk = 20MB  
request_memory = 20MB
```

```
queue 1
```

comma-separated list of **input files to transfer** to the slot



wi.dat



us.dat

Basic Submit File

```
executable = compare_states  
arguments = wi.dat us.dat  
wi.dat.out
```

```
transfer_input_files =  
us.dat, wi.dat
```

```
log = job.log  
output = job.out  
error = job.err
```

```
request_cpus = 1  
request_disk = 20MB  
request_memory = 20MB
```

```
queue 1
```

HTCondor will transfer back all new and changed files (output) from the job, automatically.



wi.dat.out

Basic Submit File

```
executable = compare_states  
arguments = wi.dat us.dat  
wi.dat.out
```

```
transfer_input_files =  
us.dat, wi.dat
```

```
log = job.log  
output = job.out  
error = job.err
```

```
request_cpus = 1  
request_disk = 20MB  
request_memory = 20MB
```

```
queue 1
```

log: file created by HTCondor to track job progress

- *Explored in exercises!*

output/error: captures stdout and stderr from your program (what would otherwise be printed to the terminal)

Basic Submit File

```
executable = compare_states  
arguments = wi.dat us.dat  
wi.dat.out
```

```
transfer_input_files =  
us.dat, wi.dat
```

```
log = job.log  
output = job.out  
error = job.err
```

```
request_cpus = 1  
request_disk = 20MB  
request_memory = 20MB
```

request the resources your job needs.

(More on this later)

queue: *final* keyword indicating “create 1 job” according to the above

queue 1

Submitting and Monitoring

To submit a job/jobs: `condor_submit submit_file`

To monitor submitted jobs: `condor_q`

```
$ condor_submit job.submit
Submitting job(s).
1 job(s) submitted to cluster 128.
```

```
$ condor_q
-- Schedd: learn.chtc.wisc.edu : <128.104.101.92> @ 05/01/17 10:35:54
OWNER  BATCH_NAME          SUBMITTED   DONE    RUN    IDLE  TOTAL
JOB_IDS
alice  CMD: compare_states  5/9  11:05    _     _     1     1
128.0

1 jobs; 0 completed, 0 removed, 1 idle, 0 running, 0 held, 0 suspended
```

Job Idle

```
$ condor_q -nobatch
```

```
-- Schedd: submit-5.chtc.wisc.edu : <128.104.101.92>
```

ID	OWNER	SUBMITTED	RUN_TIME	ST	PRI	SIZE	CMD
128.0	alice	5/9 11:09	0+00:00:00	I	0	0.0	compare_states wi.dat us.dat

```
1 jobs; 0 completed, 0 removed, 1 idle, 0 running, 0 held, 0 suspended
```

Access Point

```
(submit_dir)/  
  job.submit  
  compare_states  
  wi.dat  
  us.dat  
  job.log  
  job.out  
  job.err
```

Job Starts by doing File Transfer

```
$ condor_q -nobatch
```

```
-- Schedd: submit-5.chtc.wisc.edu : <128.104.101.92:9618>
```

```
  ID          OWNER      SUBMITTED      RUN_TIME ST PRI  SIZE  CMD
128.0         alice        5/9  11:09      0+00:00:00 <  0  0.0  compare_states wi.dat us.dat
```

```
1 jobs; 0 completed, 0 removed, 0 idle, 1 running, 0 held, 0 suspended
```

Access Point

```
(submit_dir)/
  job.submit
  compare_states
  wi.dat
  us.dat
  job.log
  job.out
  job.err
```

compare_states
wi.dat
us.dat



Execute Point

```
(execute_dir)/
```

Job Running

```
$ condor_q -nobatch
```

```
-- Schedd: submit-5.chtc.wisc.edu : <128.104.101.92>
```

```
  ID            OWNER      SUBMITTED      RUN_TIME  ST  PRI  SIZE  CMD
128.0           alice      5/9  11:09      0+00:01:08  R   0    0.0  compare_states wi.dat us.dat
```

```
1 jobs; 0 completed, 0 removed, 0 idle, 1 running, 0 held, 0 suspended
```

Access Point

```
(submit_dir)/
  job.submit
  compare_states
  wi.dat
  us.dat
  job.log
  job.out
  job.err
```

Execute Point

```
(execute_dir)/
  compare_states
  wi.dat
  us.dat
  stderr
  stdout
  wi.dat.out
  subdir/tmp.dat
```

Job Completes

```
$ condor_q -nobatch
```

```
-- Schedd: submit-5.chtc.wisc.edu : <128.104.101.92>
```

```
  ID            OWNER      SUBMITTED      RUN_TIME  ST  PRI  SIZE  CMD
128            alice      5/9  11:09      0+00:02:02  >  0    0.0  compare_states wi.dat us.dat
```

```
1 jobs; 0 completed, 0 removed, 0 idle, 1 running, 0 held, 0 suspended
```

Access Point

```
(submit_dir)/
  job.submit
  compare_states
  wi.dat
  us.dat
  job.log
  job.out
  job.err
```

stderr
stdout
wi.dat.out

Execute Point

```
(execute_dir)/
  compare_states
  wi.dat
  us.dat
  stderr
  stdout
  wi.dat.out
  subdir/tmp.dat
```

Job Completes (cont.)

```
$ condor_q -nobatch
```

```
-- Schedd: submit-5.chtc.wisc.edu : <128.104.101.92:9618?...
```

```
  ID          OWNER          SUBMITTED      RUN_TIME ST PRI SIZE CMD
```

```
0 jobs; 0 completed, 0 removed, 0 idle, 0 running, 0 held, 0 suspended
```

Access Point

```
(submit_dir)/  
  job.submit  
  compare_states  
  wi.dat  
  us.dat  
  job.log  
  job.out  
  job.err  
  wi.dat.out
```



RESEARCH
D R I V E

Connecting research drive

<https://chtc.cs.wisc.edu/uw-research-computing/transfer-data-researchdrive>

Research drive

The information on the CHTC web page has all the details needed to connect to your research drive from your Biochemistry Cluster login using the **smbclient** communication software.

```
Connect to ResearchDrive:          $ smbclient -k //research.drive.wisc.edu/PI-Name  
Prompt changes to:                  smb: \>
```

Move files: To move files, you will use the get and put commands:

```
To move files from BCC to ResearchDrive:    smb: \> put filename
```

```
To move files from ResearchDrive to BCC:    smb: \> get filename
```

```
Finish: End connection to ResearchDrive:  smb: \> exit
```

See the CHTC web page <https://chtc.cs.wisc.edu/uw-research-computing/transfer-data-researchdrive> on using **mput** and **mget** or the wild card ***** for batch transfer of multiple files.