Submitting Jobs to the Supercomputer

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Questions? #RC_BasicSC

Link to survey on this topic: http://tinyurl.com/rcpresurvey

Slides:

https://github.com/ResearchComputing/Final_Tutorials/tree/master/Basics_Supercomputing

Outline

- Submit specific jobs to the supercomputer!
 - Batch job
 - Interactive job
 - Running external scripts

Janus/Summit Access

To access RC's computing, for this tutorial:

ssh tutorial-login.rc.colorado.edu —l user00XX

Practice Examples

Submit Your First Job!

- Submit a slurm job with the following instructions:
- 1. The job should run the Unix "hostname" command
- 2. The job will be submitted from a bash script named hostname.sh
- 3. The job will run on 1 node
- 4. We will request 1 minute wall time
- 5. We will name the job hostname
- 6. The output will be put in a file called hostname.out

Contents of Batch Script

Bash Script hostname.sh:

```
#!/bin/bash
#SBATCH -N 1  # Number of requested nodes
#SBATCH --time=0:01:00  # Max walltime
#SBATCH --job-name=hostname  # Job submission name
#SBATCH --output=hostname.out  # Output file name
#SBATCH --reservation=scbasics  # Reservation
```

hostname

Running the script

Load up the slurm module

ml slurm

Submit the job:

sbatch hostname.sh

Check output:

nano hostname.out

Another slurm command

squeue

 View information about jobs located in the slurm scheduling queue

OPTIONS:

- User: -u <user list>
- Queues: -q <qos_list> or --qos=<qos_list>

EXAMPLE:

squeue -q janus-debug

http://slurm.schedmd.com/squeue.html

Your turn

- Submit a slurm job with the following instructions:
- 1. The job should run first the whoami command, then the Unix "sleep" command for 90 seconds, then the hostname command
 - Syntax for sleep: sleep 90
 - hostname runs as before. Whoami runs same as hostname
- 2. The job will be submitted from a bash script named sleep.sh
- 3. The job will run on 1 node
- 4. We will request a 1 minute wall time
- 5. The output will be put in a file called sleep.out
- 6. Email yourself the results at the end of the job run
 - Hint: Requires two SBATCH options to do this

Hmmm

- Why didn't that work?
- Sleep 90 causes the script to wait 90 seconds before running
- We only asked for a wall time of 1 minute
- So we ran out of time requested before the job ran!
- Let's fix it!

Solution – contents of script

```
#!/bin/bash
#SBATCH -N 1
#SBATCH --time=0:01:00
#SBATCH --job-name=sleep
#SBATCH --output=sleep.out
#SBATCH --reservation=scbasics
                                  # Reservation
#SBATCH --mail-type=end
#SBATCH --mail-user=ralphie@colorado.edu
whoami
sleep 30
hostname
```

Interactive jobs!

- Sometimes we want our job to run in the background
- Sometimes we want to work in program in real time
- For example, Matlab
- Let's run an interactive Matlab job

Interactive job

- NEVER EVER EVER EVER EVER
- EVER EVER EVER EVER EVER EVER EVER
- Run matlab from the command line without running an interactive job first
- BAD USER!

Interactive job

- To do this, we are going to log out and log back in
 - Only necessary for demo
 - Need to add something to the sign in process

```
ssh tutorial-login.rc.colorado.edu —X —l user00XX
```

This enables x-windows on our laptops

Interactive job

- To work with Matlab interactively, we're going to request some time from the supercomputer
- When the resources become available then we will start up Matlab
- Commands to run:

```
<what command do we need to run first?>
sinteractive --reservation=schasics
```

Once we receive a prompt, then:

```
ml matlab
matlab
```

Once we finish we must exit!

Your turn – Interactive Job

- 1. Run an interactive job that opens up TotalView
 - Make sure you run the job using the reservation name schasics
- 2. Don't forget to exit!

Running an external script

- Let's run a Matlab program
- We will run the batch script matlab.sh
- This script calls and runs matlab_tic.m
- This is NOT an interactive job

Running the script

Load up the Matlab module

ml matlab

Submit the job:

sbatch matlab.sh

Check output:

nano Matlab.out

Contents of Batch Script

Bash Script matlab.sh:

```
#!/bin/bash
#SBATCH -N 1  # Number of requested nodes
#SBATCH --time=0:02:00  # Max walltime
#SBATCH --job-name=Matlab  # Job submission name
#SBATCH --output=Matlab.out  # Output file name
#SBATCH --reservation=scbasics  # Reservation name
```

```
# Run matlab without a GUI
matlab -nojvm -nodisplay -nodesktop -r "clear; matlab tic;"
```

Your turn

- Submit a slurm job with the following instructions:
- 1. Create an R program called R program. R that creates a vector called "planets" and then list the planets in the vector
 - Syntax: planets -> planets <- c("Mercury", "Venus",
 "Earth", "Mars", "Jupiter", "Saturn", "Uranus",
 "Neptune", "Pluto")</pre>
- 2. Print off the vector
 - Syntax: planets
- 3. Create a bash script called R code.sh that runs the R script
 - Syntax: Rscript R code.sh
- 4. The job will run on 1 node
- 5. We will request a 1 minute wall time
- 6. The output will be put in a file called R.out
- 7. Name your job R_code
- 8. Email yourself the results at the end of the job run
 - Hint: Requires two SBATCH options to do this

Solution – R_code.sh

```
#!/bin/bash

#SBATCH -N 1

#SBATCH --time=0:01:00

#SBATCH --job-name=R_code

#SBATCH --output=R_code.out

#SBATCH --reservation=scbasics
work during workshop
```

```
# Number of requested nodes
# Max walltime
# Job submission name
# Output file name
# Reservation - will only
```

Rscript R program.R

Solution – R_program.R

```
#Simple R code example by Shelley Knuth
(shelley.knuth@colorado.edu)

# Create vector
planets <- c("Mercury", "Venus", "Earth", "Mars", "Jupiter",
"Saturn", "Uranus", "Neptune", "Pluto")

# Print off vector
planets</pre>
```

Questions?

- Email <u>rc-help@colorado.edu</u>
- Twitter: CUBoulderRC
- Link to survey on this topic:

http://tinyurl.com/curc-survey16

Slides:

https://github.com/ResearchComputing/Final_Tutorials/tree/master/Basics_Supercomputing