



Research Computing  
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# Submitting Jobs to the Supercomputer

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# Outline

Submit specific jobs to the supercomputer!

- Batch jobs
  - Interactive jobs
  - External script jobs
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## Summit Access

We will use the Secure Shell (SSH) network protocol to connect to Summit

Please login to summit using the following command:

```
ssh -l user00XY tutorial-login.rc.colorado.edu
```

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# Submit Your First Job!

Submit a slurm job with the following instructions:

- The job should run the Unix command `hostname`
- The job script will be named `hostname.sh`
- The job will run on one node
- The job will request one minute of walltime
- The output of the job will go in a file called `hostname.out`

Before starting, SSH to the machine `scompile`

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# Contents of 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=tutorial1  # Reservation
```

hostname

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## Running the job script

Submit the job:

```
sbatch hostname.sh
```

Check the output:

```
nano hostname.out
```

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## Peer into the slurm queue

`squeue`

- Use this command to view the current jobs in the slurm scheduling queue

Options:

- **USER:** `-u <user_list>`
- **QUEUES:** `-q <qos_list>` or `--qos=<qos_list>`

Example:

```
squeue -q normal
```

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# Your Turn!

Submit a job with the following instructions:

- The job needs to run the following commands in order:
    - `whoami`
    - `sleep 90`
    - `hostname`
  - The job script name will be `sleep.sh` and will write output to a file named `sleep.out`
  - The job will run on 1 node and will have a walltime of 1 minute
  - Email yourself the results of the job
    - Hint: This will require two sbatch options
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# Contents of sleep.sh

```
#!/bin/bash
#SBATCH -N 1
#SBATCH --time=00:01:00
#SBATCH --output=sleep.out
#SBATCH --reservation=tutorial1
#SBATCH --mail-type=end
#SBATCH --mail-user=ralphie@colorado.edu
```

```
whoami
sleep 90
hostname
```

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## What went wrong?

What error did you run into?

- The command `sleep 90` will cause the script to wait 90 seconds before proceeding to the next task
- We only requested a walltime for our job of 60 seconds

Time to correct the job script

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# Improved version of sleep.sh

```
#!/bin/bash
#SBATCH -N 1
#SBATCH --time=00:01:00
#SBATCH --output=sleep.out
#SBATCH --reservation=tutorial1
#SBATCH --mail-type=end
#SBATCH --mail-user=ralphie@colorado.edu
```

```
whoami
```

```
sleep 30
```

```
hostname
```

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## Interactive Jobs

Interactive jobs are useful for when we want to run scripts or simulations in real time

Interactive jobs start up as soon as resources are available

For the upcoming working example we will ask for an interactive job which we will use then to run Matlab

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**DO NOT RUN MATLAB  
UNLESS YOU ARE  
RUNNING AN  
INTERACTIVE JOB**

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## Interactive Job

First log out of summit completely

We will connect again using the following command:

```
ssh -Y -l user00XY tutorial-login.rc.colorado.edu
```

The `-Y` option enables X11 GUI forwarding to your laptop allowing for graphic user interface programs to work as if you were running the program on your local machine.

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## Interactive Job

To work with Matlab interactively, we need to request time from the supercomputer

You can use the following command:

```
sinteractive --reservation=tutorial1
```

Once you receive a prompt:

```
m1 load matlab  
matlab
```

Once you are done, exit the job!

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## Your Turn!

Request an interactive job and open Totalview

- Make sure you request the interactive job against the `tutorial1` reservation!
- Make sure that once you are done, that you exit the interactive job.

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## Running a Matlab batch job

In the following example we will submit a batch job that will in turn execute a matlab script called `matlab_tic.m`

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# Contents of the job script

```
#!/bin/bash
#SBATCH -N 1
#SBATCH --time=00:10:00
#SBATCH --job-name=Matlab
#SBATCH --output=Matlab.out
#SBATCH --reservation=tutorial1

#Run Matlab without the GUI
matlab -nojvm -nodisplay -nodesktop -r "clear; matlab.tic;"
```

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## Running the matlab batch job

Load the Matlab module:

```
ml matlab
```

Submit the job:

```
sbatch matlab.sh
```

Check the output:

```
nano Matlab.out
```

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## Running a R job script

In the same way we wrote a job that would execute a matlab script, we can use the same logic to also run an R script within a batch job.

We will create a small R script called `R_program.R` that will create a vector called `planets` and then print the vector.

Remember that you will need to load the R module first before submitting your job!

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## Contents of R\_program.R

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

# Print the vector
planets
```

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# Contents of R batch job file

```
#!/bin/bash
#SBATCH -N 1
#SBATCH --job-name=R-planets
#SBATCH --time=00:10:00
#SBATCH --output=R-planets.out
#SBATCH --reservation=tutorial1
#SBATCH --mail-type=end
#SBATCH --mail-user=ralphie@colorado.edu
```

```
Rscript R_program.R
```

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## References and further reading

Squeue Documentation

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

Sbatch Documentation

<http://slurm.schedmd.com/sbatch.html>

Research Computing support documentation

<https://rc.colorado.edu/support>

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# Questions?

Email: [rc-help@colorado.edu](mailto:rc-help@colorado.edu)

Twitter: CUBoulderRC



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# Please let us know what you thought!

<http://tinyurl.com/curc-survey17>

# Thanks!



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# Top Tip

Include jobid as part of output file name, and job output file name.

Example:

```
#!/bin/bash
```

```
#SBATCH -N 1
```

```
#SBATCH --job-name=R-planets-%j
```

```
#SBATCH --time=00:10:00
```

```
#SBATCH --output=R-planets-%j.out
```

```
#SBATCH --reservation=tutorial1
```

```
#SBATCH --mail-type=end
```

```
#SBATCH --mail-user=ralphie@colorado.edu
```

```
Rscript R_program.R
```

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