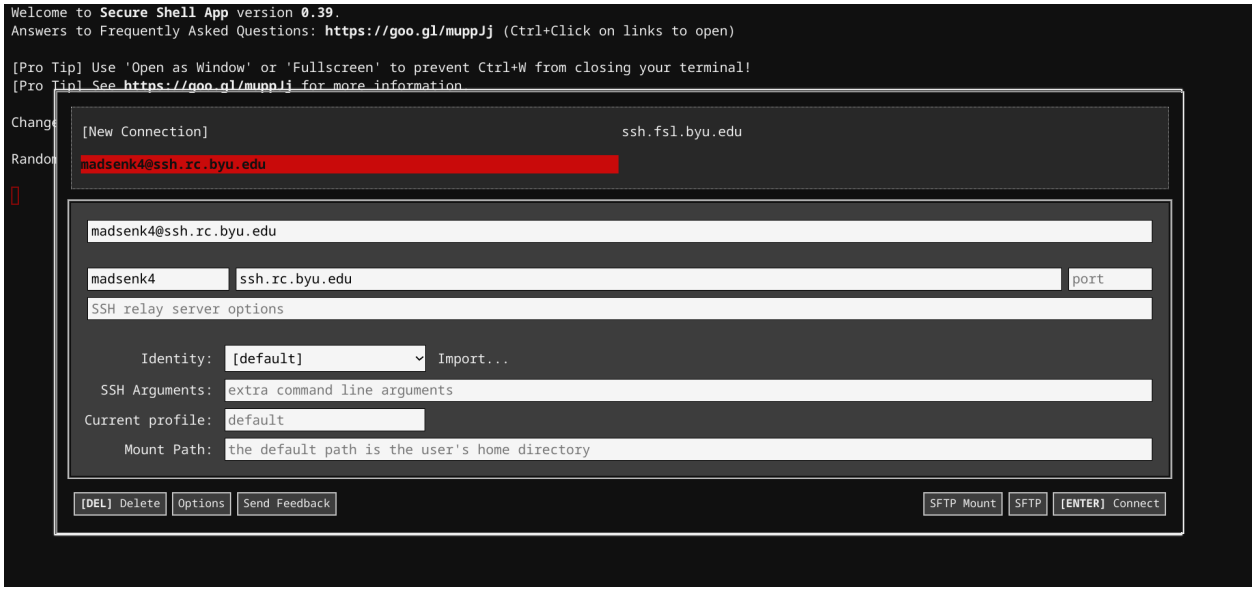
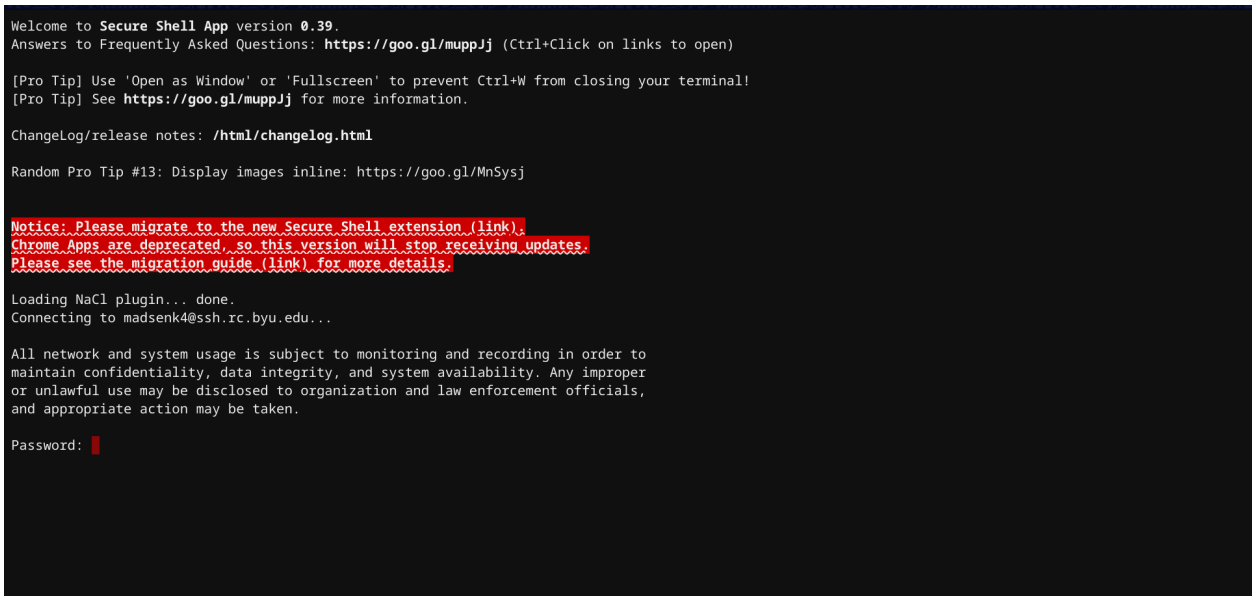
Introduction to the Supercomputer

Logging into the Supercomputer

Fill out the first three boxes with [your netID]@ssh.rc.byu.edu, and hit enter



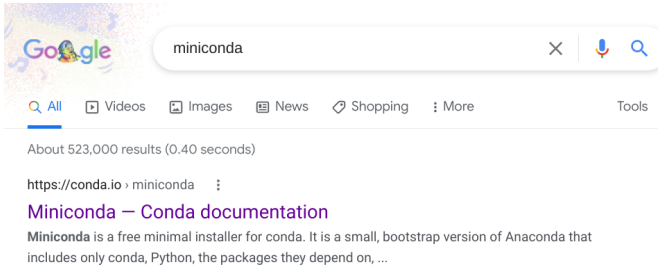
Enter the same password you use for the fulton supercomputing lab and the authentication code. No letters will appear on the screen - don't worry, it's still receiving the input.



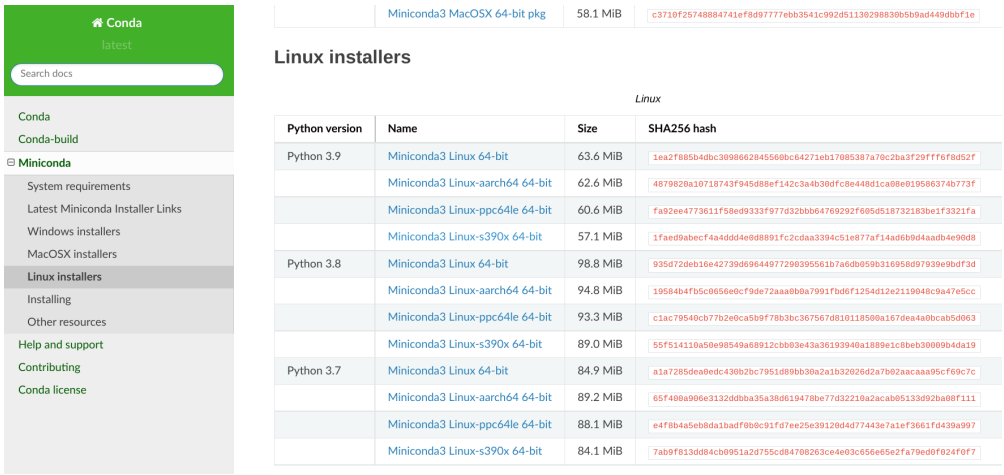
Importing CONDA

Step 1: Get miniconda

Google miniconda and click on the conda documentation.



Scroll down to 'Linux Installers' and right-click on Miniconda3-Linux64-bit to copy the link.



Make sure you're in the compute directory: cd ~/compute
Then use wget with the copied url:

```
-bash-4.2$ wget https://repo.anaconda.com/miniconda/Miniconda3-latest-
```
...

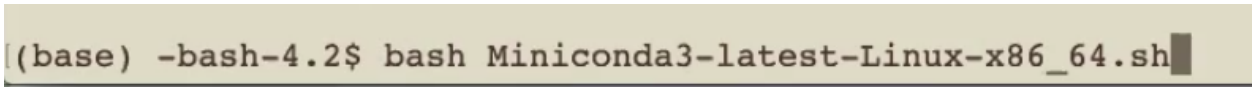
Your screen should look something like this:

```
Resolving repo.anaconda.com (repo.anaconda.com)... 104.16.131.3, 104.16.130.3
, 2606:4700::6810:8203, ...
Connecting to repo.anaconda.com (repo.anaconda.com)|104.16.131.3|:443... conn
ected.
HTTP request sent, awaiting response... 200 OK
Length: 93052469 (89M) [application/x-sh]
Saving to: 'Miniconda3-latest-Linux-x86_64.sh'

100%[====================================>] 93,052,469   210MB/s   in 0.4s

2020-09-17 14:50:09 (210 MB/s) - 'Miniconda3-latest-Linux-x86_64.sh' saved [9
3052469/93052469]
```

Step 2: Initialize CONDA

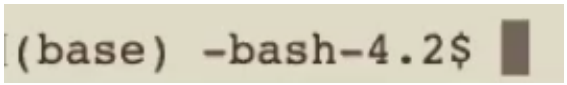
Type in bash Miniconda3-latest-Linux-x86_64.sh and hit enter. When prompted, accept any terms and conditions / questions (say yes by hitting the Y key or hit enter).

*the easiest thing to do is use tab complete: type “bash Mi”, then hit tab, and the rest should fill in



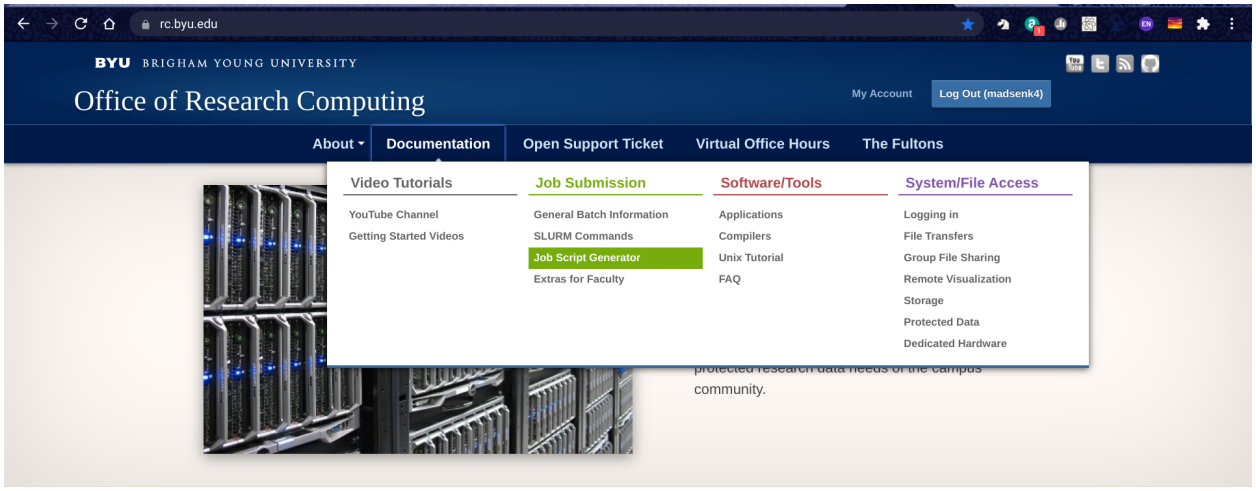
When the miniconda installation prompts you if you want to initiate conda and it it to your ~/.bashrc, type “y”

When you’re done, the command line will appear with a (base) after typing in source ~/.bashrc



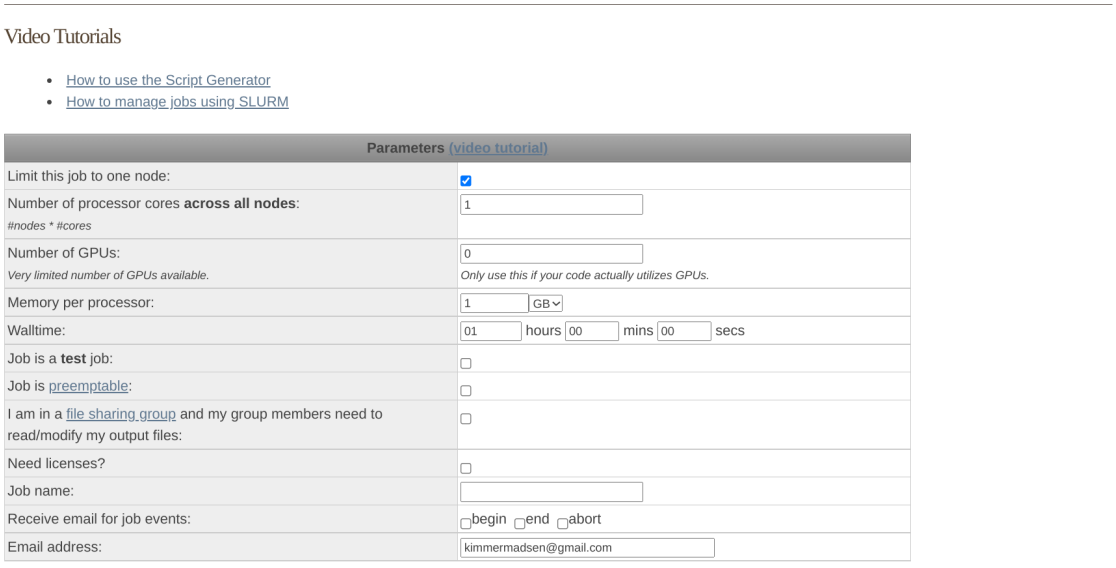
Writing a Job File

We'll be using the [Job Script Generator](https://rc.byu.edu/documentation/slurm/script-generator) (https://rc.byu.edu/documentation/slurm/script-generator) .



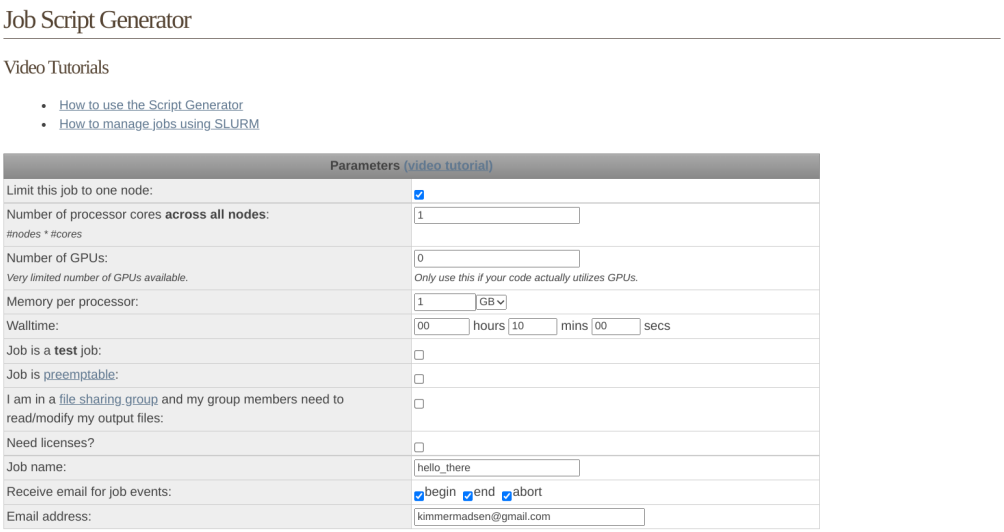
To get here, go to Documentation > Job Submission > Job Script Generator

By default, mine looks something like this:



If you would like to enter your email, you can opt to receive an email when the job has begun, ended, or if it aborted. It can be nice to get these kinds of alerts instead of checking the job status every few minutes from the command line.
Most labs will specify ranges for the number of processors, memory per processor, and walltime.

For practice, since we're submitting a very small job, you can just say 1 processor core with 1 GB memory and 10 minutes for simple practice code. If it aborts, you can modify these numbers. It's also helpful to name your job. In this case, I named mine "hello_there"



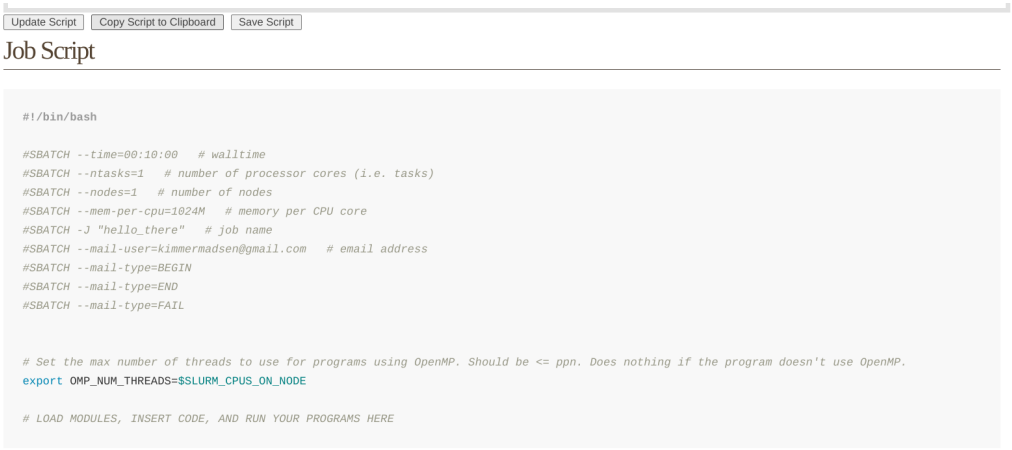
Job Script Generator

Video Tutorials

- How to use the Script Generator
- How to manage jobs using SLURM

Parameters (video tutorial)	
Limit this job to one node:	☑
Number of processor cores **across all nodes**: *#nodes * #cores*	1
Number of GPUs: *Very limited number of GPUs available.*	0 *Only use this if your code actually utilizes GPUs.*
Memory per processor:	1 GB
Walltime:	00 hours 10 mins 00 secs
Job is a **test** job:	☐
Job is preemptable:	☐
I am in a file sharing group and my group members need to read/modify my output files:	☐
Need licenses?	☐
Job name:	hello_there
Receive email for job events:	☑ begin ☑ end ☑ abort
Email address:	kimmermadsen@gmail.com

When you're satisfied with the settings, scroll down to where it says 'Job Script' and click "copy script to clipboard" (you can also highlight and copy - it doesn't really matter).

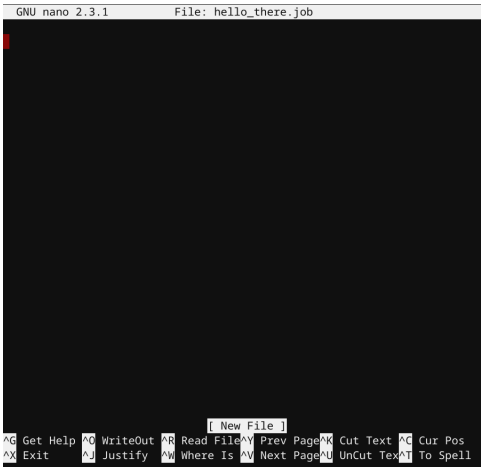


Update Script | Copy Script to Clipboard | Save Script

Job Script

```
#!/bin/bash

#SBATCH --time=00:10:00   # walltime
#SBATCH --ntasks=1   # number of processor cores (i.e. tasks)
#SBATCH --nodes=1   # number of nodes
#SBATCH --mem-per-cpu=1024M   # memory per CPU core
#SBATCH -J "hello_there"   # job name
#SBATCH --mail-user=kimmermadsen@gmail.com   # email address
#SBATCH --mail-type=BEGIN
#SBATCH --mail-type=END
#SBATCH --mail-type=FAIL


# Set the max number of threads to use for programs using OpenMP. Should be <= ppn. Does nothing if the program doesn't use OpenMP.
export OMP_NUM_THREADS=$SLURM_CPUS_ON_NODE

# LOAD MODULES, INSERT CODE, AND RUN YOUR PROGRAMS HERE
```

In the command line, create a text file called "hello_there.job" using the 'nano' command:
nano hello_there.job
(hit enter)
You'll be brought to a screen that looks like this:



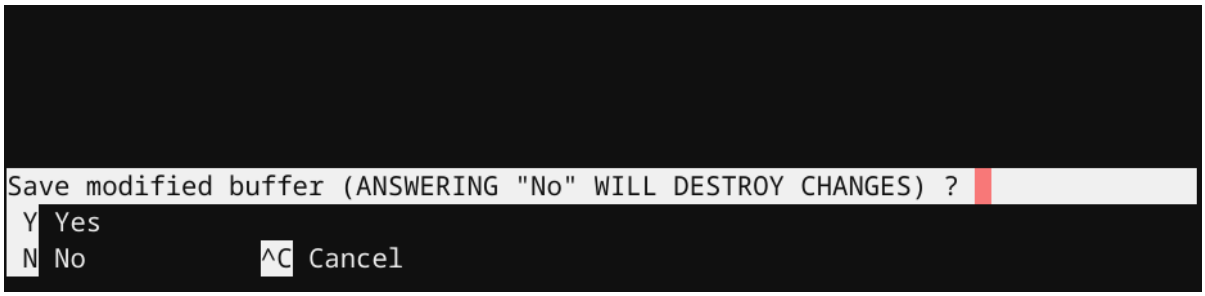
Paste in the job script you just copied, then type in the command: echo "hello there!", sleep 75, then echo "You're finished!". This will tell the computer to print out 'hello there!', wait 75 seconds, then print out "you're finished!"

Mine looks like this:

```
  GNU nano 2.3.1          File: hello_there.job                    Modified

#!/bin/bash

#SBATCH --time=00:10:00   # walltime
#SBATCH --ntasks=1   # number of processor cores (i.e. tasks)
#SBATCH --nodes=1   # number of nodes
#SBATCH --mem-per-cpu=1024M   # memory per CPU core
#SBATCH -J "hello_there"   # job name
#SBATCH --mail-user=kimmermadsen@gmail.com   # email address
#SBATCH --mail-type=BEGIN
#SBATCH --mail-type=END
#SBATCH --mail-type=FAIL


# Set the max number of threads to use for programs using OpenMP. Should b$
export OMP_NUM_THREADS=$SLURM_CPUS_ON_NODE

# LOAD MODULES, INSERT CODE, AND RUN YOUR PROGRAMS HERE

echo "hello there!"
sleep 75
echo "You're finished!"
```

Use ^O to save or rename your text file, and ^X to exit. After hitting ^X, be sure to hit ‘Y’ and enter to save the changes you’ve made

```
^G Get Help ^O WriteOut ^R Read File^Y Prev Page^K Cut Text ^C Cur Pos
^X Exit     ^J Justify  ^W Where Is ^V Next Page^U UnCut Tex^T To Spell
```



You can check that it saved by using the cat command to view the text file:

```
-bash-4.2$ nano hello_there.job
-bash-4.2$ cat hello_there.job
#!/bin/bash

#SBATCH --time=00:10:00   # walltime
#SBATCH --ntasks=1   # number of processor cores (i.e. tasks)
#SBATCH --nodes=1   # number of nodes
#SBATCH --mem-per-cpu=1024M   # memory per CPU core
#SBATCH -J "hello_there"   # job name
#SBATCH --mail-user=kimmermadsen@gmail.com   # email address
#SBATCH --mail-type=BEGIN
#SBATCH --mail-type=END
#SBATCH --mail-type=FAIL


# Set the max number of threads to use for programs using OpenMP. Should be
 <= ppn. Does nothing if the program doesn't use OpenMP.
export OMP_NUM_THREADS=$SLURM_CPUS_ON_NODE

# LOAD MODULES, INSERT CODE, AND RUN YOUR PROGRAMS HERE

echo "hello there!"
sleep 75
echo "You're finished!"
-bash-4.2$
```

Submitting a Job

Once you have the job file created, use the ‘sbatch’ command to submit your job.

```
-bash-4.2$ sbatch hello_there.job
Submitted batch job 43392291
-bash-4.2$
```

Checking the Job Status

Use the squeue command to check job status:
squeue -u [your netID or username]

```
-bash-4.2$ sbatch hello_there.job
Submitted batch job 43392292
-bash-4.2$ squeue -u madsenk4
             JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
          43392292       m8n hello_th madsenk4  R       0:02      1 m8-19-3
```

You can do this as much as you’d like:

```
-bash-4.2$ squeue -u madsenk4
             JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
          43392292       m8n hello_th madsenk4  R       0:02      1 m8-19-3
-bash-4.2$ squeue -u madsenk4
             JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
          43392292       m8n hello_th madsenk4  R       0:25      1 m8-19-3
-bash-4.2$ squeue -u madsenk4
             JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
          43392292       m8n hello_th madsenk4  R       0:25      1 m8-19-3
-bash-4.2$
```

If you signed up for email alerts, you’ll be notified if the job is begun, finished, or aborted.

Remember to properly exit out of the super computer by typing in ‘exit’:

```
-bash-4.2$ exit
logout
Connection to ssh.rc.byu.edu closed.
```