Logging into TACC and exploring your directories

You should have already set up a TACC account (with username and password) and also have set up multi-factor authentication.

Log in to TACC Frontera using a **secure shell** on your computer. You will need your TACC user ID, your password, and to have set up multi-factor authentication. Paste the line you used to login to TACC below.
```
ssh eac3496@frontera.tacc.utexas.edu
```

Once you're logged in, navigate to your different directories within TACC (home, work, work2, and scratch). Put some examples of how to do this navigation below.
```
cdh # navigate to home
cds # navigate to scratch
cdw2 # navigate to work2
```

What's the full path to your scratch directory?
```
cds
pwd
# scratch1/03123/eac3496/
```

Copying files

Download the [Day2_TACC_worksheet_files](#) folder from the course website to your personal computer. Unzip the folder.
```
unzip Day2_TACC_worksheet_files.zip
```

Now, **secure copy** this entire directory to your TACC account, in the *scratch* directory (remember, you'll need to use the **recursive flag** -r because you're trying to copy an entire folder, and not just files).
```
cd Downloads/
scp -r Day2_TACC_worksheet_files/
eac3496@frontera.tacc.utexas.edu:/scratch1/03123/eac3496
```

In your TACC account, navigate to your scratch directory.
```
cds
```

Move to `Day2_TACC_worksheet_files` folder.
```
cd Day2_TACC_tutorial_files/
```

Take a look at the files inside `Day2_TACC_worksheet_files`. What is the full file path for the files contained within the `Day2_TACC_worksheet_files` folder?
```
ls
/scratch1/03123/eac3496/Day2_TACC_tutorial_files
```

Start an idev node that will last 1 hour (in the allocation Phylogenomics).

```
idev -t 1:00:00 -A Phylogenomics
```

Check your queue. What appears?
```
squeue -u eac3496

JOBID    PARTITION      NAME      USER ST      TIME  NODES
NODELIST(REASON)
3709306 development idv24830  eac3496  R        0:18      1 c202-017
```

Exit the idev node.
```
exit
```

There's a file within your `Day2_TACC_worksheet_files` that's called `skeletonslurm`.
We'll use this to make new slurm files and submit jobs for the course. What do the contents of
this file look like?
```
cat skeletonslurm
```

You may have noticed that `skeletonslurm` is an incomplete slurm file; there are several
more lines required for TACC to run a job. A typical slurm file should look something like this:

```
#!/bin/bash
#SBATCH -J jobname
#SBATCH -o jobname.o%j
#SBATCH -N 6
#SBATCH -n 64
#SBATCH -p normal
#SBATCH -t 2:00:00
#SBATCH --mail-user=youremailaddress
#SBATCH -A Phylogenomics
```

Copy the above missing lines, add them into the `skeletonslurm` file, and save the file. Now
doublecheck that the file looks correct.
```
nano skeletonslurm
cat skeletonslurm # to check that it looks good
```

```
[(base) login2.frontera(1044)$ cat ranaddrad_s3-7.slurm
#!/bin/bash
#SBATCH -J ranaddrad_s3-7
#SBATCH -o ranaddrad_s3-7.o%j
#SBATCH -N 6
#SBATCH -n 64
#SBATCH -p normal
#SBATCH -t 12:00:00
#SBATCH --mail-user=eachambers@utexas.edu
#SBATCH -A Phylogenomics

module unload python3

ipyrad -p params-ranaddrad.txt_-s 34567
```

Next, let's actually make and submit a job. Copy the `skeletonslurm` file and make a new file
called `fake_job.slurm`.
```
cp skeletonslurm fake_job.slurm
```

Edit the contents of `fake_job.slurm` such that the job name is `fake_job`, and the time for the job to run is 30 minutes.

```
nano fake_job.slurm
```

Now, submit the job.

```
sbatch fake_job.slurm
```

Check the status of the submitted job.

```
squeue -u eac3496
```

Cancel the job you've submitted. Print the output below.

```
scancel XXX
```