A Brief Introduction to OSCAR and the Command Line

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BIOL 1435

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1 Installation

- If you are using a Mac, you can stop here and go to the next step.
- If you are using a Windows computer, please navigate to `https://mobaxterm.mobatek.net/` and download the free version of MobaXterm.

2 Logging on to OSCAR

- If you are using a Mac press the command key followed by the space bar, type "Terminal" into the search bar, and then click the Terminal application.
- If you are using a Windows system, navigate to wherever you downloaded MobaXterm and open the application.
- Your terminal window should look similar to figure 1.

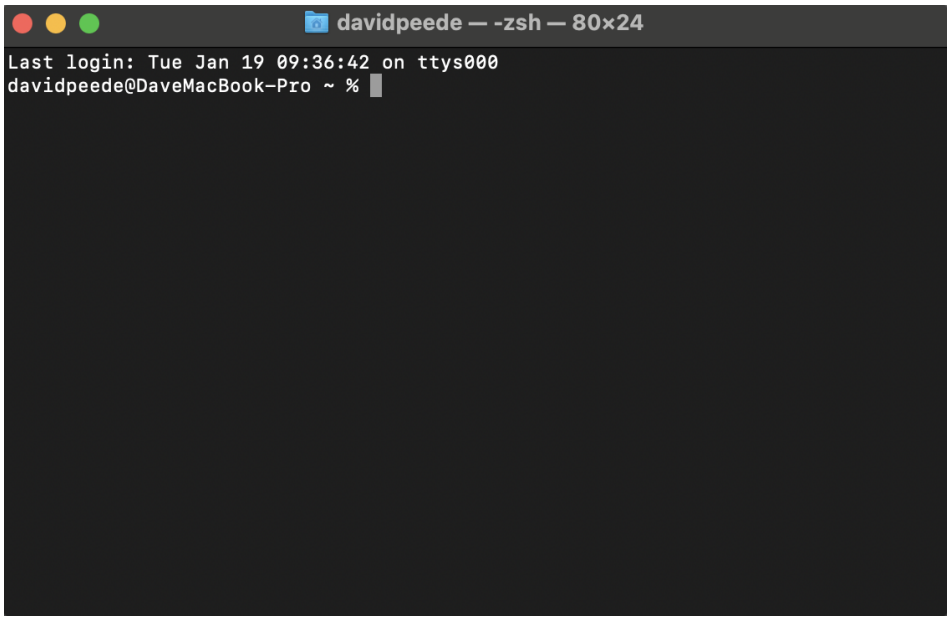

Figure 1: An example of a new terminal window.

- Next type `ssh yourBrownUsername@ssh.ccv.brown.edu` into your terminal and press enter, then type in your password associated with your Brown account **(NOTE: You will not be able to see that you are typing in your password, but I promise you are!)**, and lastly hit the enter key. If everything worked correctly your terminal should look similar to figure 2.

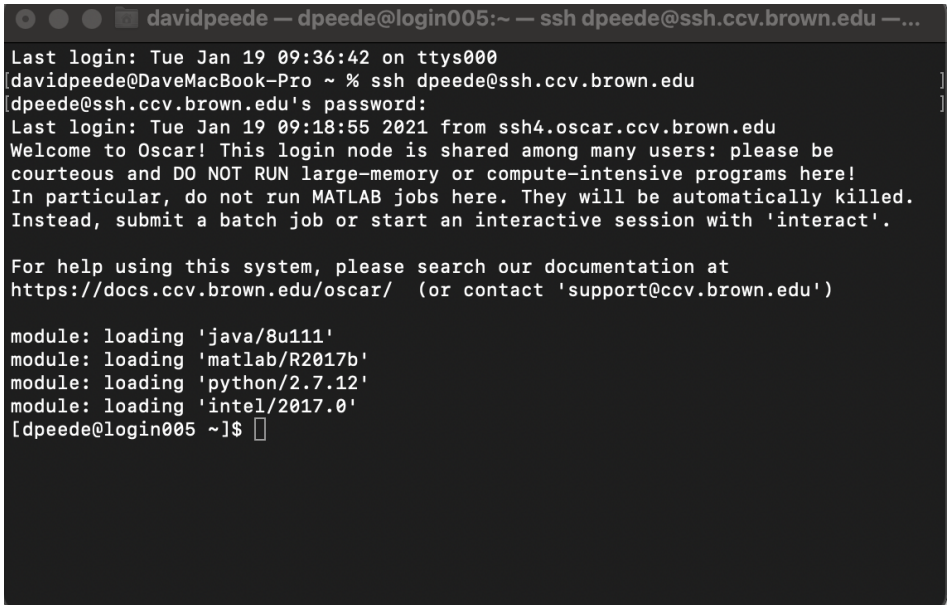

Figure 2: Successfully logging in to OSCAR.

3 Navigating around OSCAR

- Awesome! You have officially logged on to OSCAR lets now go over a few basic commands that will come in handy throughout the semester.
- So we know that we are on OSCAR but where are we really? If you ever want to know where you are on OSCAR simply type `pwd` on the command line and press enter. This command outputs your working directory to standard out (stdout), and if everything worked correctly you should see `/users/yourBrownUsername` printed to stdout, which means we are in our home directory! Your terminal should look similar to figure 3.

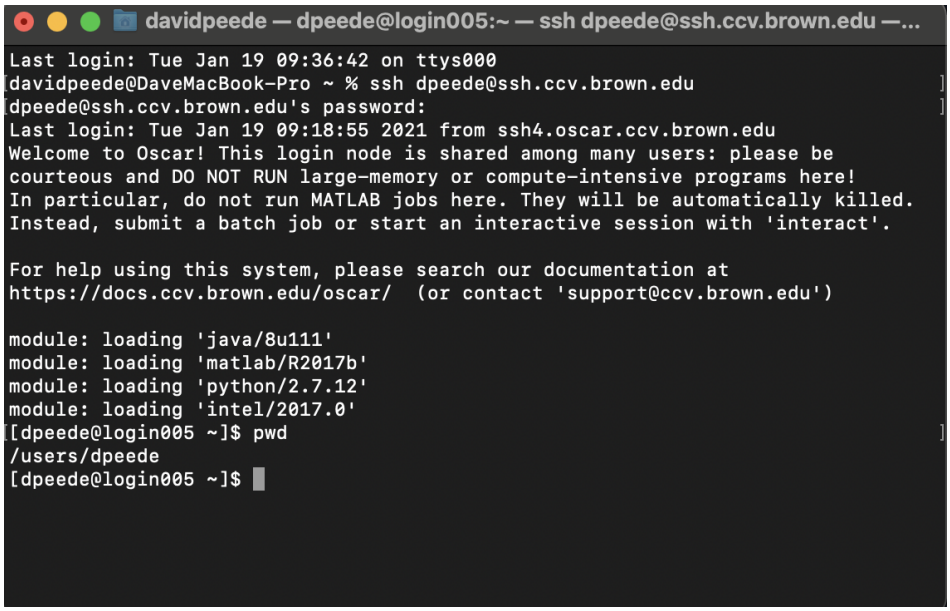

Figure 3: Printing your working directory.

- So we are in our home directory, but now what? Let's take a look at what is actually in our home directory. Type `ll` (which is equivalent to `ls -l`) and press enter. This command lists all the files that are located in your working directory to stdout in long form, which provides us some additional information that you can read more about here `https://linuxize.com/post/how-to-list-files-in-linux-using-the-ls-command/`. Your terminal should look similar to figure 4 (**NOTE: If you are a first time OSCAR user your home directory might look a tad different than mine**).

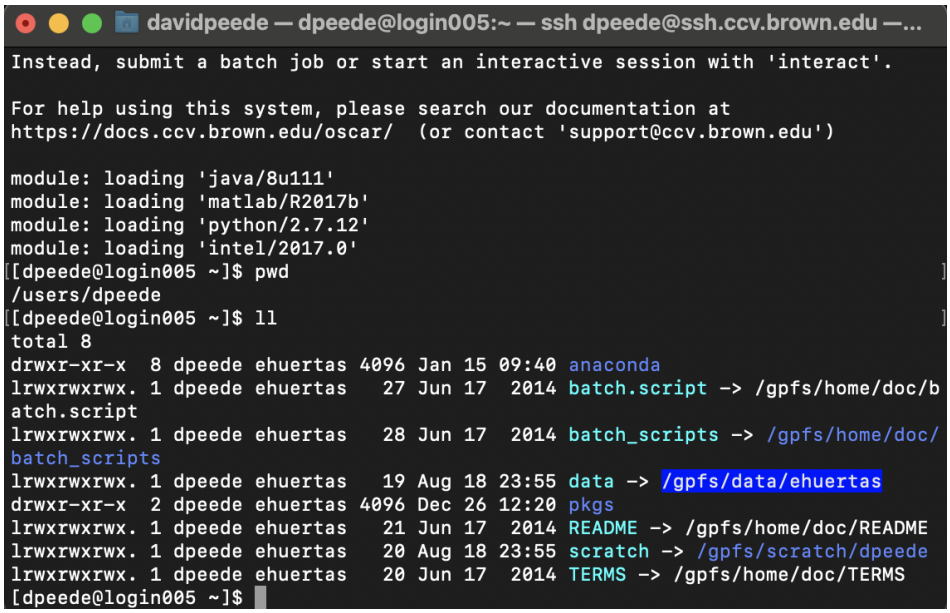

Figure 4: The contents of your home directory.

- In general we will be working in our scratch space for the majority of the semester, so lets move there! To change working directories type `cd yourDestination` so in this case type `cd scratch` and press enter. This command will change our working directory from home to scratch, and to confirm you can execute the `pwd` command, which should output `/users/yourBrownUsername/scratch` to stdout. Your terminal should look similar to figure 5

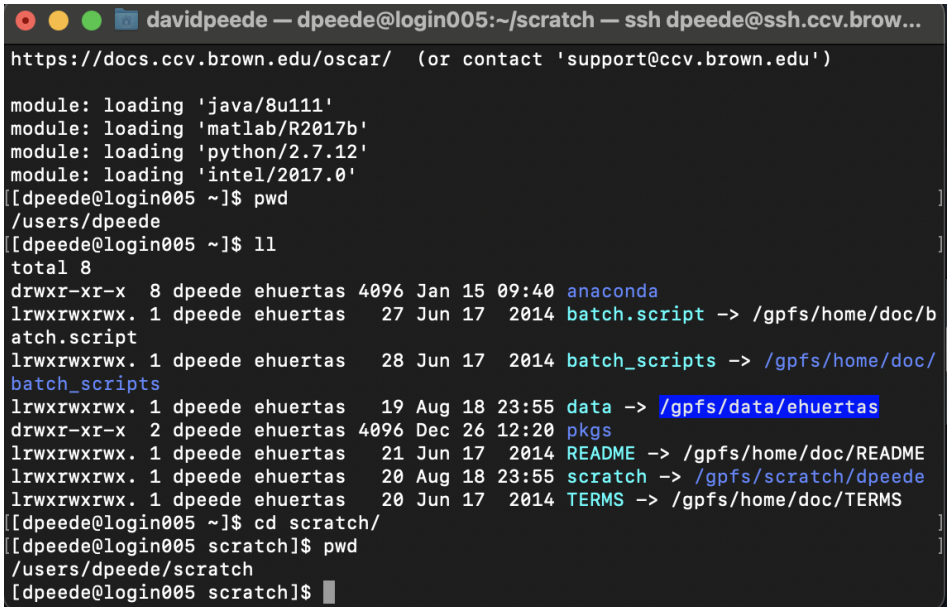

Figure 5: Moving to your scratch space.

- If you wanted to move back to your home directory you could either type the absolute path `cd /users/yourBrownUsername/` or simply `cd ../` since your home directory is the parent directory of your scratch space, but let's stay in our scratch space.

4 Files on OSCAR

- Now that we are in our scratch space lets execute the command `ll`. If you are a first time OSCAR user your scratch space should be empty, if you have previously used OSCAR before you might have some files already in your scratch space, regardless let's make a new directory! To make a new directory named `BIOL1435` type `mkdir BIOL1435` and press enter. To verify that you in fact created a new directory named `BIOL1435` execute the `ll` command and if everything worked correctly you should see `BIOL1435` in dark blue lettering in stdout! Your terminal should look similar to figure 6 (**NOTE: If you are a first time OSCAR user your scratch space might look a tad different than mine**).

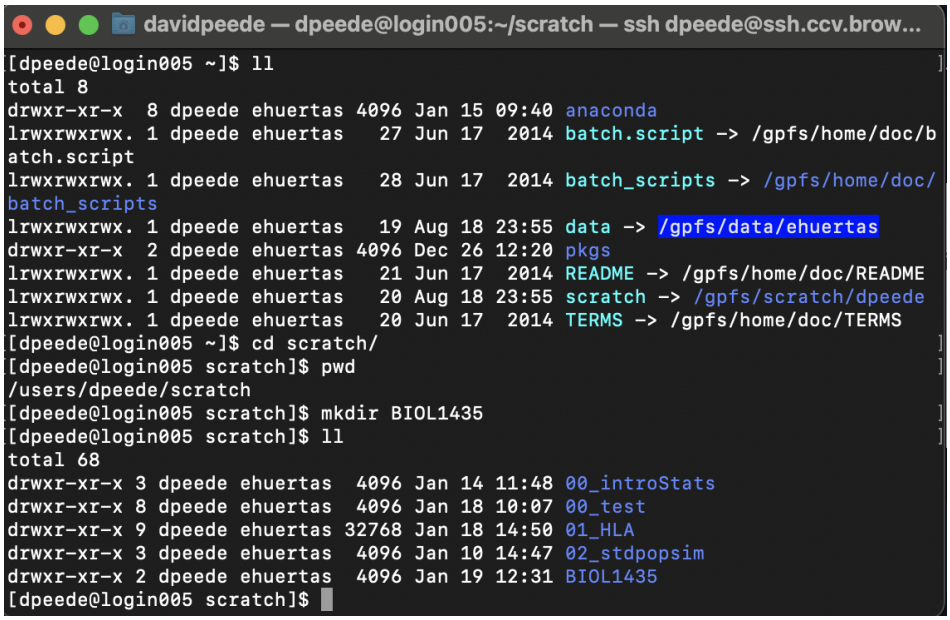

Figure 6: Making a new directory called BIOL1435.

- Now that we have a new directory let's create a text file called `README.txt` so that we don't forget why we created the `BIOL1435` directory. To do so we will use the text editor *Vi*, in your scratch space type `vi README.txt` and press enter. This will open up a blank text editor in normal mode, to edit your text file first press `i` which lets *Vi* know that we are changing from normal mode to insert mode, once you are in insert mode go ahead and add `This directory contains my work for BIOL 1435!` and then press the escape key to change back to normal mode. Your terminal should look similar to figure 7. Lastly, to save our text file and exit *Vi* type `:x` and then on the command line execute the `ll` command.

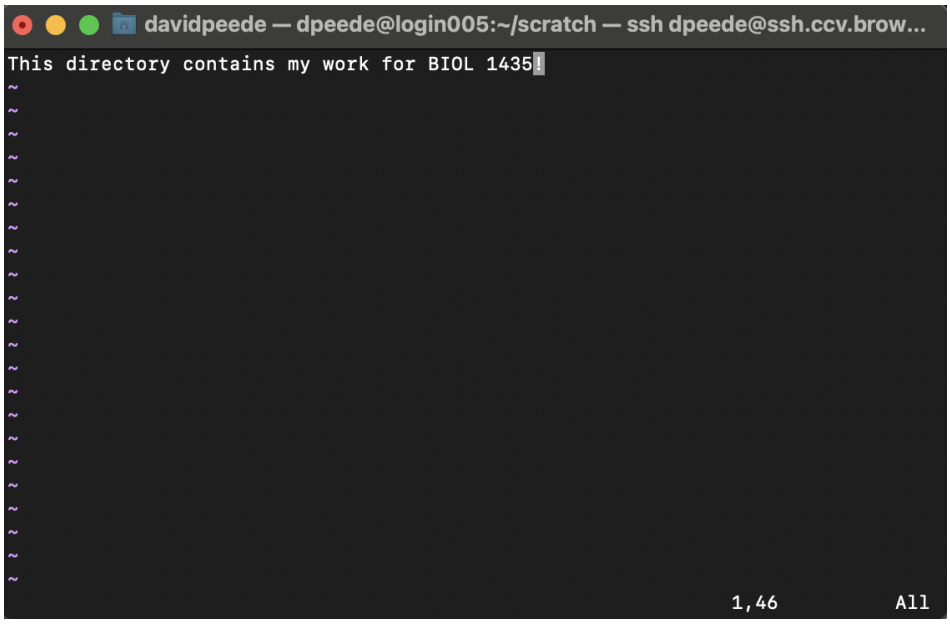

Figure 7: Vi text editor.

- Oh no! Our `README.txt` is in our scratch space, but we want it to be in our `BIOL1435` directory. No need to worry, we can easily fix my mistake. To do so we are going to use the command `mv` to move the `README.txt` file from our working directory to our target directory (in this case the target directory is `BIOL1435`). Type `mv README.txt /users/yourBrownUsername/scratch/BIOL1435/` and then press enter. Now navigate to your `BIOL1435` directory and execute the `ll` command to ensure you actually moved your `README.txt` file. Your terminal should look similar to figure 8

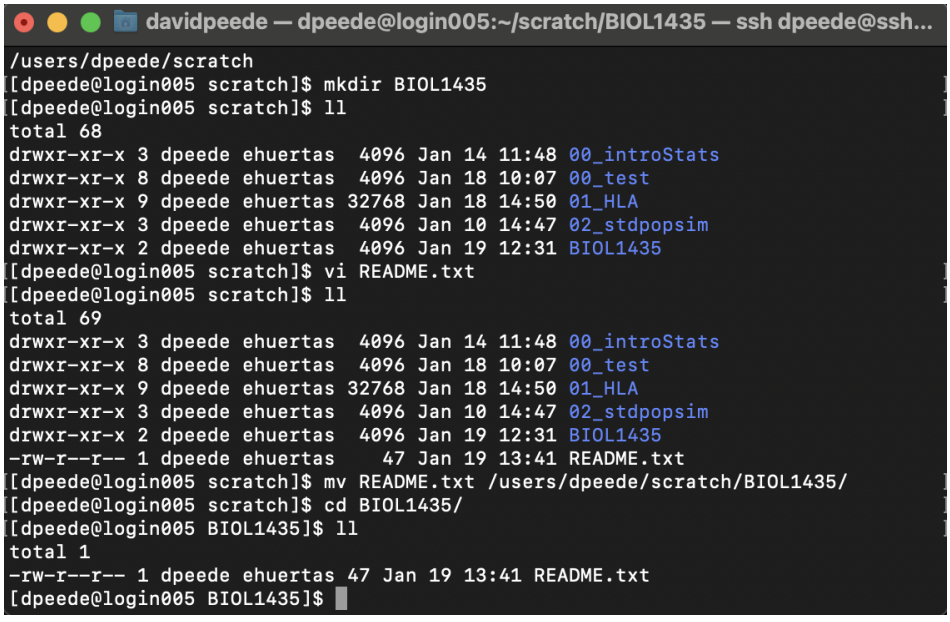

Figure 8: Moving README.txt from your scratch space to BIOL1435.

- Now as a sanity check let's quickly view the contents of the `README.txt` file to make sure nothing weird happened. To do so type `less README.txt` (which allows us to quickly inspect our file) and press enter. Your terminal should look similar to figure 9 and to exit `less` simply press the `q` key.

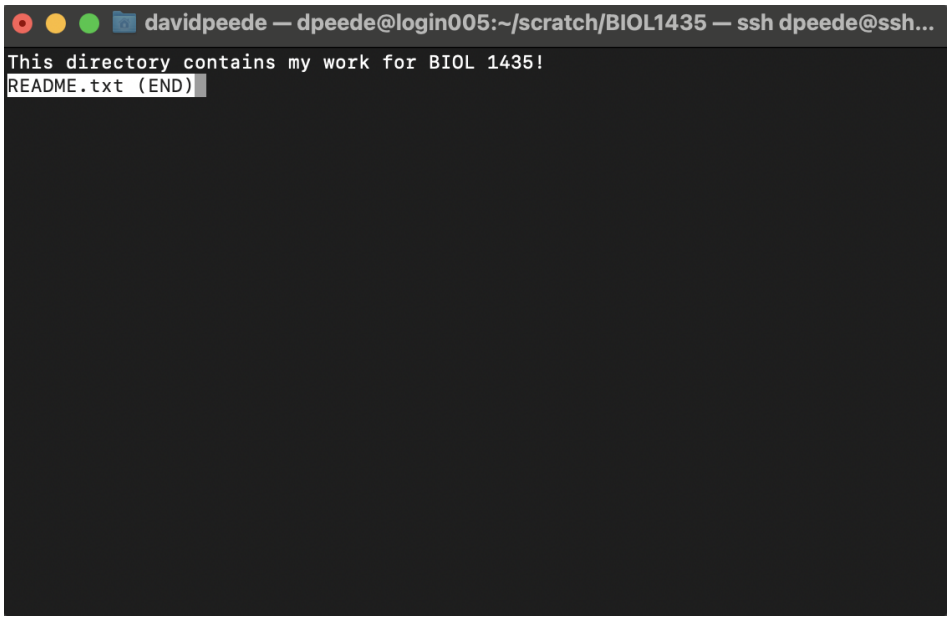

Figure 9: Viewing README.txt with less.

- Frequently this semester you will be asked to download files from Canvas and copy them to your OSCAR account to execute. Seems easy enough, so lets practice! Click on this link `https://downgit.github.io/#/home?url=https://github.com/David-Peede/BIOL1435/tree/main/OSCAR` and save the file to your downloads folder. Once the file is downloaded, go to your downloads folder, and unzip the file. Now open up a new terminal window, but do not log on to OSCAR, instead execute `pwd` to see where you are on your local computer, and then change directories into the `OSCAR` directory you just downloaded. I don't know how everyone's local computer is set up, but I imagine it will be fairly similar to how my local computer is organized in figure 10.

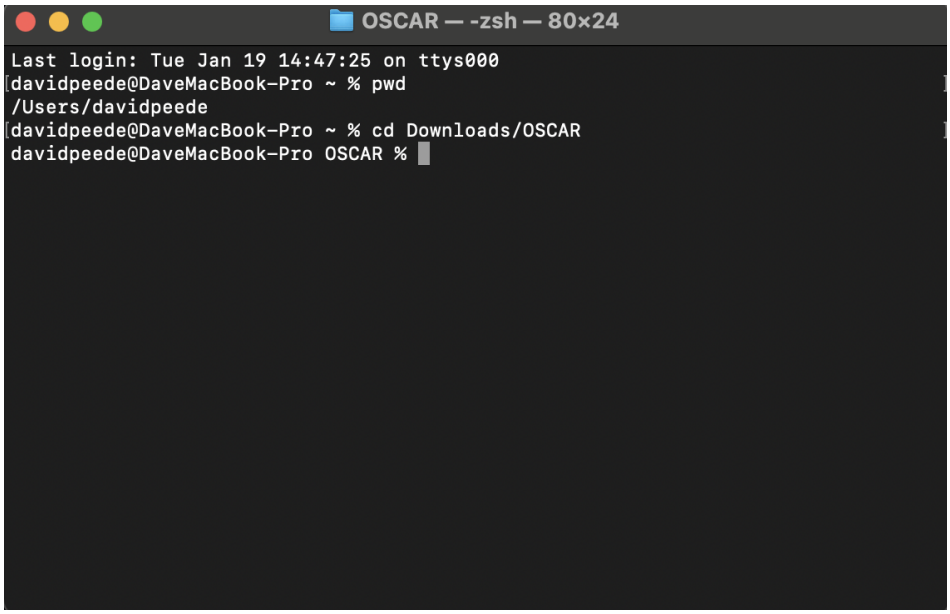

Figure 10: Moving into the OSCAR directory you downloaded from my GitHub.

- Now use the `ls` command to view the contents of the `OSCAR` directory. There are two files (one python script and one SLURM script) I want you to copy to your `BIOL1435` directory on OSCAR. To do so we will use the `scp` command which allows you to securely copy files between local and remote systems. The basic syntax for copying a file from your local computer to OSCAR is `scp myLocalFile Username@transfer.ccv.brown.edu:/pathToyourDirectory/` once you execute this command you will be prompted to enter the password associated with your Brown account and then EUREKA, the file was successfully copied to your directory in OSCAR. Notice how we used `@transfer.ccv.brown.edu` instead of `@ssh.ccv.brown.edu` this is because OSCAR has a node that is dedicated to transferring files! Your terminal should look similar to figure 11.

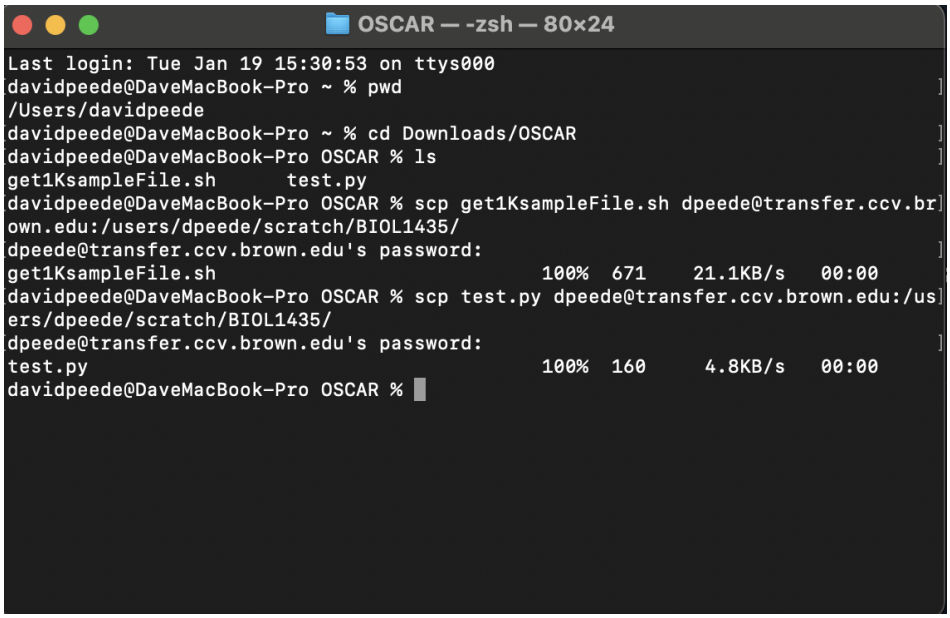

Figure 11: Copying files from your local computer to OSCAR.

- Now log back on to OSCAR and navigate to your `BIOL1435` directory and make sure those two files are actually there! If everything was successful your terminal should look similar to figure 12.

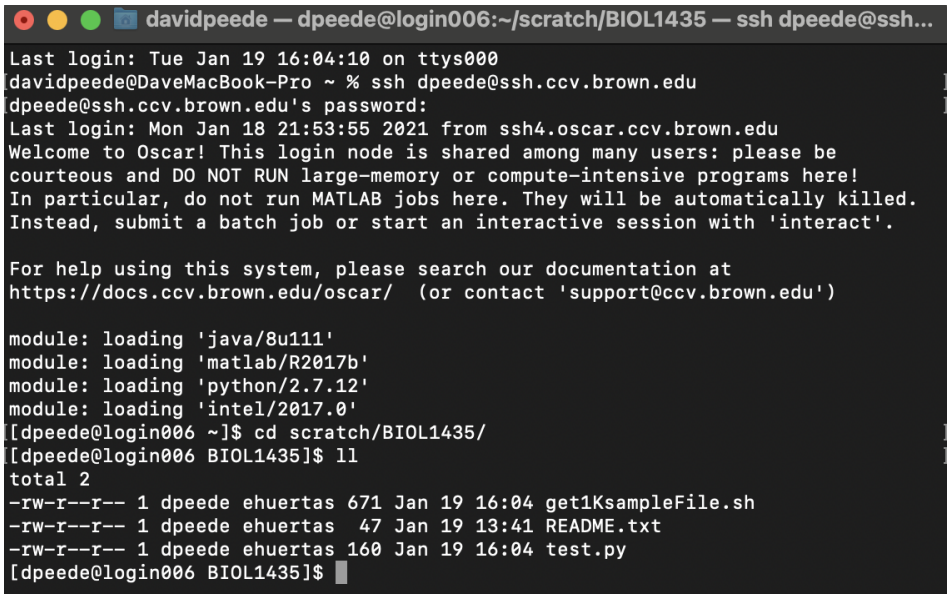

Figure 12: Confirming your copied files are on OSCAR.

5 Executing Scripts on OSCAR

- Since we just copied those two scripts from our local computer let's execute them, but first we need to make them executable. To do so we will use the basic syntax of `chmod +x myScript` which will change the file permissions so that we can execute the scripts. A quick way to tell if a file is executable is if the file has green lettering. Go ahead and change the permissions on `test.py` and `get1KsampleFile.sh` so that we can execute these scripts! If everything was successful your terminal should look similar to figure 13.

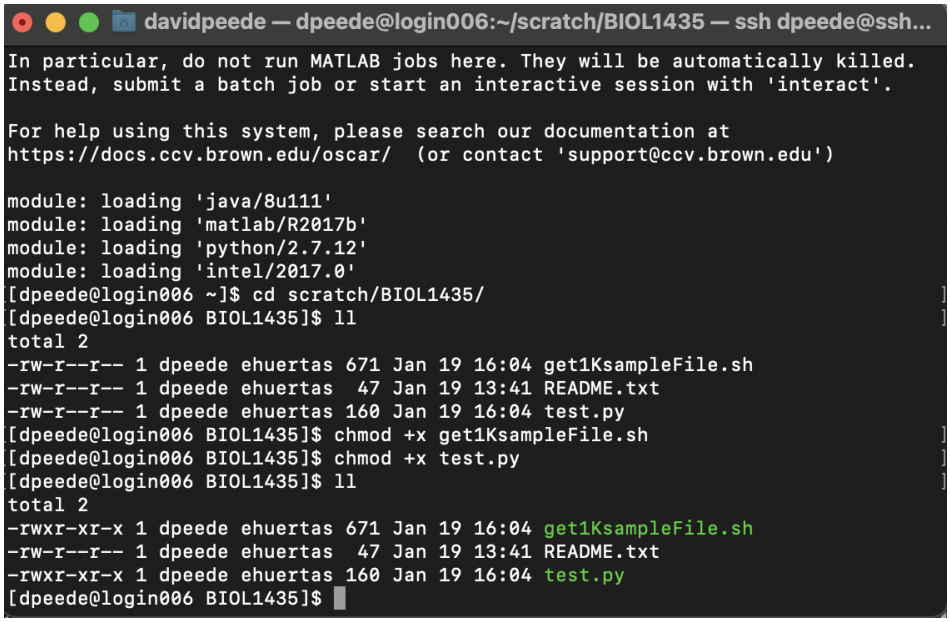

Figure 13: Changing file permissions.

- Now lets take a look at `get1KsampleFile.sh` and change the last line of the SLURM header to your email address. `get1KsampleFile.sh` is an example of a SLURM script, which is how we submit jobs to OSCAR. Don't worry too much about the header right now, but if you want to learn more you can read about it here `https://slurm.schedmd.com/sbatch.html` . To execute this script type `sbatch get1KsampleFile.sh` and press enter. This job should run fairly quickly, but if you wanted to view the status of your SLURM jobs you can execute the command `squeue -u Username` , to learn more about the `squeue` command you can visit this webpage `https://slurm.schedmd.com/squeue.html` . This SLURM scripts will download the panel file for all the individuals in the phase 3 realease of the 1000 Genomes Project and if everything was successful your terminal should look similar to figure 15.

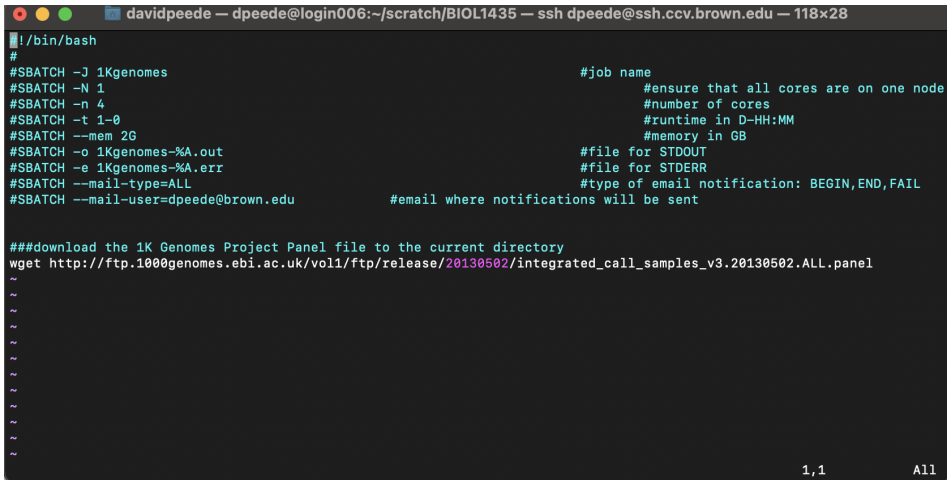

Figure 14: get1KsampleFile.sh

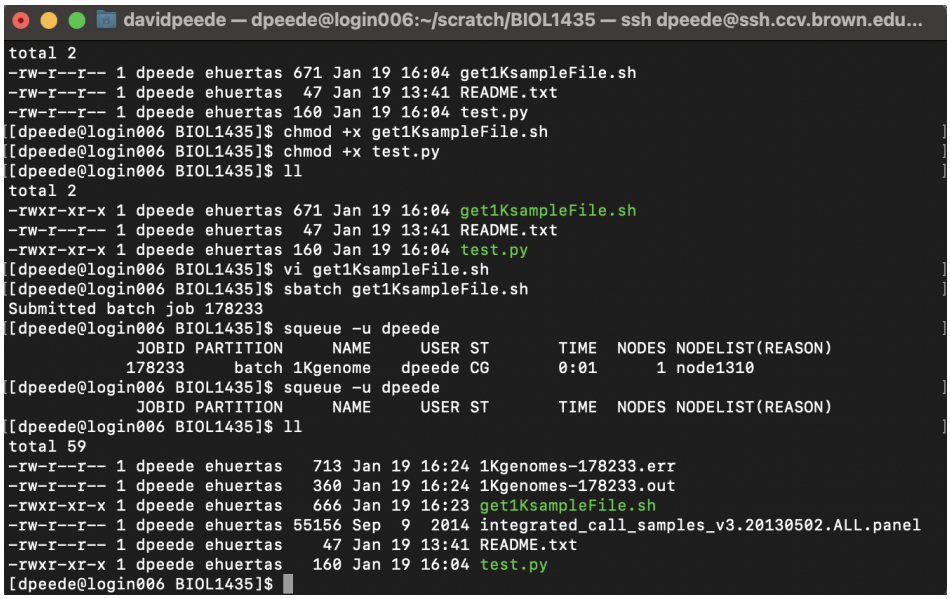

Figure 15: Submitting a SLURM job.

- Many times this semester we will find it more convenient to use an interactive session on OSCAR so we don't have to wait for jobs to run. To start an interactive session on OSCAR simply type `interact` and hit enter. It may take a second, but once your interactive session has started it should look similar to figure 16.

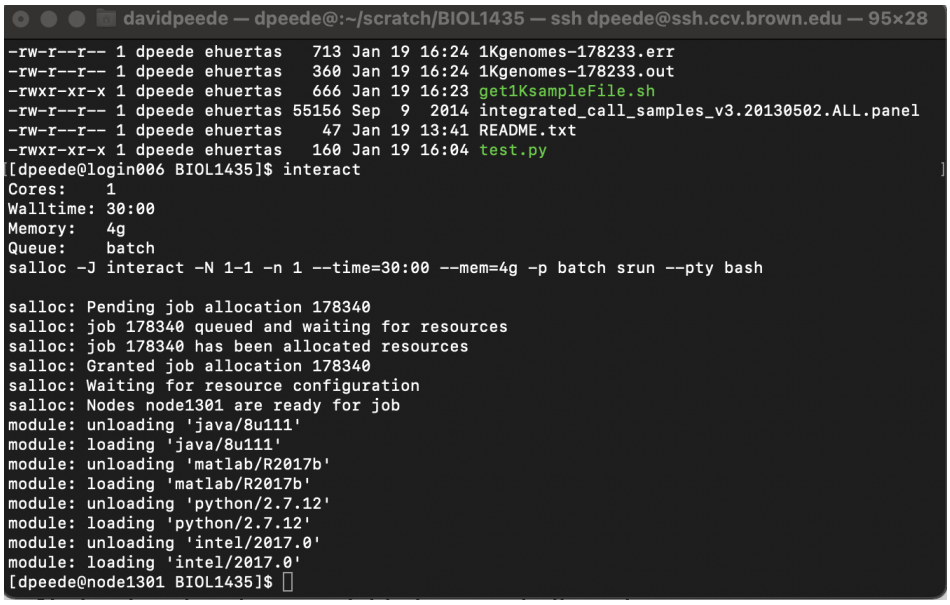

Figure 16: Interactive session on OSCAR.

- Now it is time to put your command line skills to test! Type `python test.py` and follow the prompts I gave you! If you are successful your terminal should look similar to figure 17.

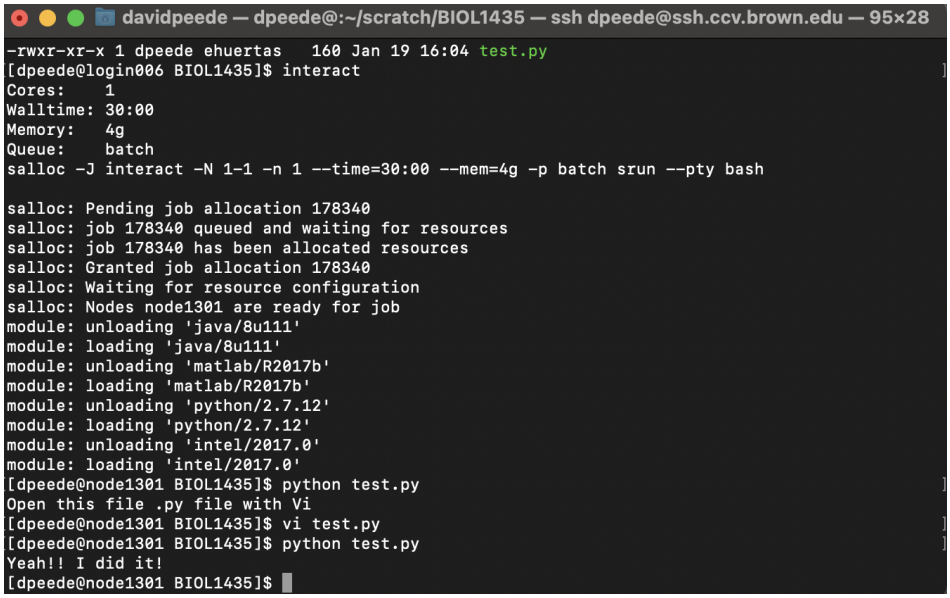

Figure 17: Correct answers for executing test.py

- Lastly, we will often want to copy a file from a directory in OSCAR to our local computer. Open a new terminal window and navigate to your downloads directory on your local computer. To copy a file from OSCAR to your local computer use `scp Username@transfer.ccv.brown.edu:/path/myFileOnOSCAR .` go ahead and download the `integrated_call_samples_v3.20130502.ALL.panel` file from your `BIOL1435` directory on OSCAR to your local downloads directory and then view the file on your

local computer. Figure 18 is an example of copying a file from OSCAR to your local downloads directory and if everything was successful your `integrated_call_samples_v3.20130502.ALL.panel` should look similar to figure 19.

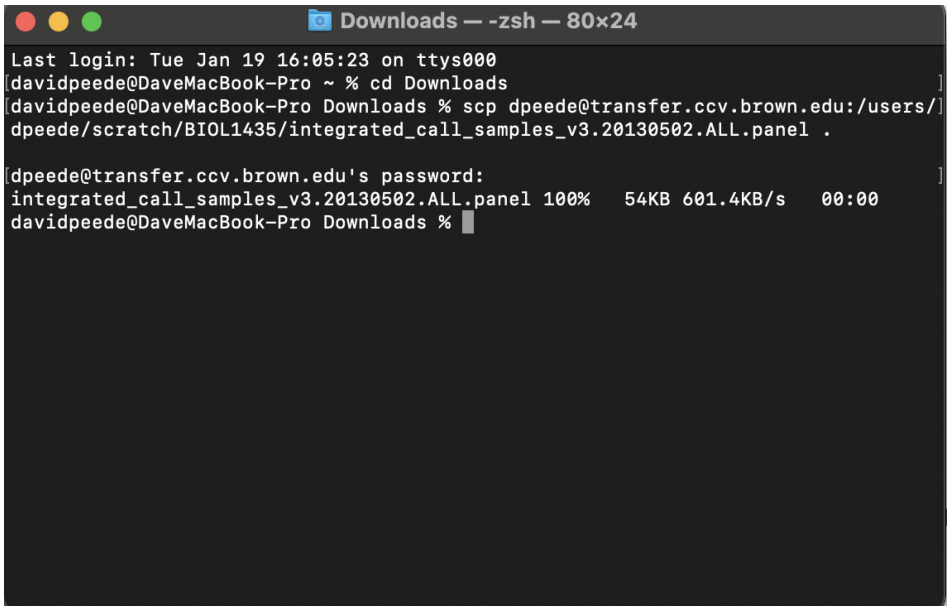

Figure 18: Copying files from OSCAR computer to your local computer.

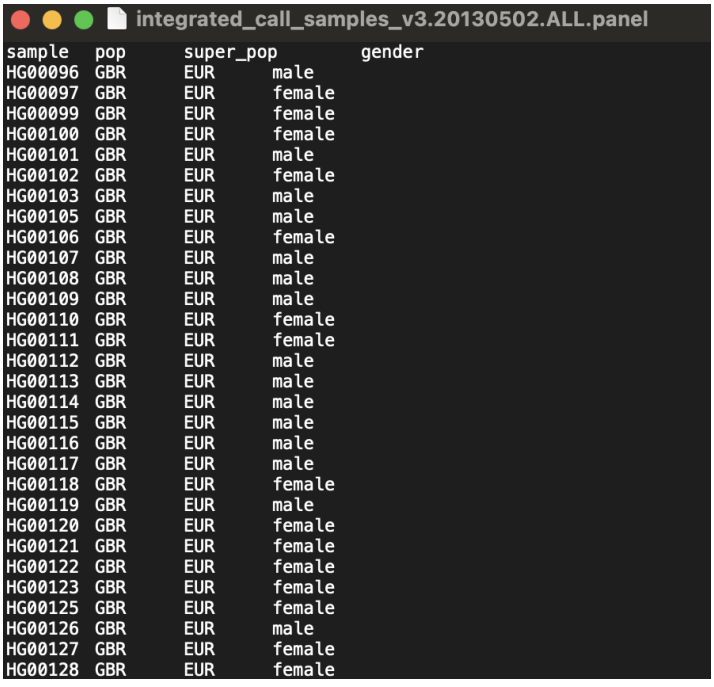

Figure 19: 1000 Genomes Project Panel File

6 Resources

- Here are some resources that are available to you if you ever run into issues with OSCAR or the command line.
    1. Google is your friend! If you run into an issue chances are someone else already had this issue and solved it!
    2. If you are having issues with the command line or want to learn more about shell scripting my go to is `https://linuxize.com/` .
    3. If you have OSCAR specific questions the documentation `https://docs.ccv.brown.edu/oscar/` is a great place to start and if you cannot find the answer to your question in the documentation feel free to submit a ticket to ITS here `support@ccv.brown.edu` .
    4. If all else fails feel free to drop me an email at `david_peede@brown.edu` or come to office hours and we will troubleshoot together!