**For your homework you will assemble 20 genes.**

**Answer the following questions:**

1. What is the purpose of High Performance Computing (HPC) and when might you use an HPC cluster?

An HPC cluster allows for higher computer power which allows complex tasks to be done and at a faster rate than a normal computer. You would use an HPC cluster if you have a task that requires a lot of computing power or would take a long time on your personal computer.

2. What is a slurm script? Print the path of your slurm script here (including file name).

/data/gpfs/assoc/biol\_bids-2/abby/atram.slurm.sh

3. What is the path to your gene assemblies on pronghorn (i.e., output files).

/data/gpfs/assoc/biol\_bids-2/abby/atram\_out/

4. How many CPUs per task did you ask for?

10 CPUs per task

5. How many genes assembled?

20 genes assembled

6. Did all genes assemble? Why or why not?

Yes, I didn’t receive any error messages and I can see all files in my atram\_out directory.

7. How long did it take for them to assemble? What processes might have slowed this down?

It took 33 minutes and 17 seconds to complete. I could have increased the number of CPUs per task to increase the speed of completiong.