

- 1.) In class today, we learned how to write an sbatch script and submit it with some basic parameters. Create a new directory in your home directory called "day_3_homework." Create an sbatch script that will output the date, sleep for 10 minutes, and run date again to show the 10 minutes difference. Save the error and output files and PBS script to show the instructors.
- 2.) Write a second sbatch script and download (using curl) some 1000 genomes data. If you don't want to pick some custom data, use ftp://ftp.sra.ebi.ac.uk/vol1/fastq/SRR792/SRR792473/SRR792473_1.fastq.gz. If you're feeling adventurous, you can try to find your own data! Move the downloaded fastq.gz to a new file called "test_data.fastq.gz". Run Fastq against the test_data.fastq.gz file. Make sure the error and output files look as you'd expect! *NOTE: The downloads will very likely take longer than in class today since we're pulling the data from an external resource. Be patient, be persistent, and you will be successful.
- 3.) Rsync the html file from the fastqc command to your local machine, open it, and view the results. You don't have to know how to interpret it, but familiarize yourself with the page for tomorrow's class.