HW01

1. I went through a) through c) and understand how to time code, how to submit my assignments with git, and what the recommended workflow is when it comes to working on my assignment

https://github.com/surendra-UW/repo759/tree/main/HW01

- 2. a. cd somedir
 - b. cat sometext.txt
 - c. tail -n 5 sometext.txt
 - d.tail -n 5 *.txt
 - e.for i in {0..6}; do echo \$i done
- 3. a.No modules loaded

```
b.gcc (GCC) 14.1.1 20240522 (Red Hat 14.1.1-4)
```

c.module avail cuda

```
gromacs/cuda-12.2-mpich/2023.3 nvidia/cuda/11.3.1 nvidia/cuda/12.1.0 nvidia/nvhpc-hpcx-cuda12/23.11
```

gromacs/cuda-12.2/2023.3 nvidia/cuda/11.6.0 nvidia/cuda/12.2.0 nvidia/nvhpc-hpcx-cuda12/24.5 (D)

nvidia/cuda/10.2.2 nvidia/cuda/11.8.0 nvidia/cuda/12.5.0 (D) nvidia/cuda/11.0.3 nvidia/cuda/12.0.0 nvidia/nvhpc-hpcx-cuda11/24.5

D. anaconda/mini/4.9.2 : **Anaconda** is a popular data science platform that includes Python, a collection of over 7,500 open-source packages, and conda, a package and environment manager.

4.

#SBATCH -p instruction #SBATCH -J FirstSlurm #SBATCH -o FirstSlurm.out -e FirstSlurm.err #SBATCH -N 1 -c 2 #SBATCH -t 0-00:10:00 echo \$HOSTNAME

5. a./srv/home/smparla

b.**SLURM JOB ID** is a unique identifier assigned to each job submitted to a Slurm cluster. It serves as a reference point for managing and monitoring the job's status and progress. We can check the status using the command "squeue -u <username>"

c. "squeue -u smparla"

d.scancel <job id>

e.requesting slurm to allocate a GPU as a node

f. The script should be executed as a array of 10 jobs with indexed as 0 to 9

6. Files in git

- #include<stdio.h>
- #include<iostream>