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University: Illinois Institute of Technology Course: Parallel and Distributed Processing

Assignment: 5 - README

The serial code (CGOL_BrijeshMavani_SerialCode.c) and parallel Cuda code (CGOL_BrijeshMavani_ParallelCode.cu) is already compiled on a comet system with executable file names cgolserial and cgolparallel respectively.

Following steps can be executed for code execution:

- 1) Check whether cuda module is present or not with command: \$module list. In case cuda is not present execute command: \$module load cuda
- 2) C and Cuda codes are already compiled as mentioned above. In case re-compilation is required you can execute the following command:

```
gcc -o <executable file name> <C code file name> eg: gcc -o cgolserial CGOL_BrijeshMavani_SerialCode.c
```

```
nvcc -o <executable file name> <Cuda code file name> nvcc -o cgolparallel CGOL_BrijeshMavani_ParallelCode.cu
```

3) For C code execution follow below steps:

./<executable file name> <number of iterations> <matrix size> > <log file name> Eg: ./cgolserial 1000 32 > 32x32Serial.txt – This will execute the code cgolserial for 1000 iterations on 32x32 Matrix and store the result in 32x32Serial.txt file.

- 4) For cuda code execution follow below steps:
 - a. Creating a job and submitting:
 Create the job file for execution. There are jobs created for different matrix sizes: (16,32,64,128,256,512,1024)

File name format : <matrix size >cuda.sh

eg:

16cuda.sh – This will execute code for 1000 iterations with matrix size as 16x16.

Sample .sh file content

```
#!/bin/bash
#SBATCH --job-name="Brijesh"
#SBATCH --output="MxN16x16Cuda_%j.%N.out"
#SBATCH -p gpu
#SBATCH --gres=gpu:k80:4
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --export=ALL
```

./<executable file> X Y

eg: ./cgolparallel 1000 16 where,

- X is number of iterations
- executable file -- name of the executable file name given during compilation. eg. cgolparallel
- Y Matrix size.
- b. Execute the job with sbatch <job name>.eg: \$ sbatch 16cuda.sh
- c. The output file will be created with a unique name for each job execution. For simplicity, run the command: Is –Itr to find out which file created at last.
- d. cat <output file name> -- To view the contents of the job output file. You can use the following command to view certain lines of the output file.

tail -n 20 <output file name> -- for viewing only last 20 lines of the output file.