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

Final Project - README

The codes for each implementation are already compiled on the comet system.

- 1. ProgrammingProject\_2DConvolution\_MPISendReceive\_BrijeshMavani.c Executable mpip2p is created after compilation for part A.
- 2. ProgrammingProject\_2DConvolution\_MPICollective\_BrijeshMavani.c Executable mpicoll is created after compilation for part B.
- 3. ProgrammingProject\_2DConvolution\_MPITask\_BrijeshMavani.c Executable mpitask is created after compilation for part C.

Following steps can be executed for code execution:

1) C codes are already compiled as mentioned above. In case re-compilation is required you can execute the following command:

mpicc -o <executable file name> <C code file name>

eg: mpicc -o mpip2p ProgrammingProject\_2DConvolution\_MPISendReceive\_BrijeshMavani.c – For part A implementation.

mpicc -o mpicoll ProgrammingProject\_2DConvolution\_MPICollective\_BrijeshMavani.c – For part B implementation.

mpicc -o mpitask ProgrammingProject\_2DConvolution\_MPITask\_BrijeshMavani.c - For part C implementation.

- 2) For code execution there are two ways. Both ways are provided below:
  - 1) Creating a job and submitting.
    - a. Create the job file for execution. There are jobs created for each processor size (1, 2, 4, and 8).

File name format: <MPIP2P/MPICollective/MPITask><no of processors>\_job.sh eg:

MPIP2P1\_job.sh -- For MPI point to point communication (Part A) for 1 processor MPIP2P2\_job.sh -- For MPI point to point communication (Part A) for 2 processors

MPICollective1\_job.sh -- For MPI collective communication (Part B) for 1 processor MPICollective2\_job.sh -- For MPI collective communication (Part B) for 2 processors

MPITask8\_job.sh - For implementation of task and data parallelism (Part C) for 8 processors

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#!/bin/bash

#SBATCH --job-name="<executable file>"

#SBATCH --output="MPI_P2P_1_.%j.%N.out"

#SBATCH --partition=compute

#SBATCH --nodes=X

#SBATCH --ntasks-per-node=1

#SBATCH --export=ALL

#SBATCH -t 00:10:00
```

ibrun -np X ./<executable file>

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eg:ibrun -np 1 ./mpip2p where.

- X is number of processors i.e. 1,2,4,8. For Part C implementation, this should be multiple of 4.
- executable file -- name of the executable file name given during compilation. eg. mpip2p, mpicoll, mpitask.

Same script can be created for other implementation (part B and C) by changing details for X and executable file.

b. Execute the job with sbatch <job name>.eg: \$ sbatch MPICollective1\_job.sh\$ sbatch MPIP2P1\_job.sh\$ sbatch MPITask8 job.sh

- c. The result of the implementation will be stored in the file as below:
  - 1. mpi\_sendrecv\_output Output of MPI point to point communication implementation (part A). The format is same as the provided input files.
  - mpi\_collective\_output Output of MPI Collective communication implementation (part B). The format is same as the provided input files.
  - 3. mpi\_task\_output Output of task and data parallelism implementation (part C). The format is same as the provided input files.
- d. Each job execution will create the output file with unique name for with the execution details about elapsed, communication and computation timings. For simplicity, execute the command: Is –Itr to find out which file created at last.
- e. cat <output file name> -- To view the contents of the job output file or the program output file. As program output file can be large, you can use the following command to view certain lines of the output file.

tail -n 10 <output file name> -- for viewing only last 10 lines of the output file.

2) Alternatively, below command can be executed to execute the code without submitting the job:

mpirun –np X ./<executable file> where,

- X is number of processors i.e. 1,2,4,8. For Part C implementation, this should be multiple of 4.
- executable file -- name of the executable file name given during compilation. eg. mpip2p, mpicoll, mpitask.

Eg: mpirun –np 1 ./mpip2p