

LAB 1: GETTING STARTED SHARED MEMORY MIMD AND DISTRIBUTED MEMORY MIMD

GOAL

In this lab:

- You start to work with the Heracles cluster by learning its architecture, getting access, and monitoring the cluster status.
- You will gain an introduction and become familiar with two different parallel programming languages: openMP (Open Multi-Processing) and MPI (Message Passing Interface), which are used to design and implement programs on two different parallel platforms. We use the matrix multiplication programs as examples to introduce these subjects. You will observe that different tools (parallel languages with various capabilities) and design considerations are needed for different parallel platforms. Note that openMP and MPI will be covered in more detail in future labs. Read all the sections at the end of this document in order to answer the questions.

If you need help with the labs, contact Thoria or Manh by sending email pdslab@ucdenver.edu with subject “**Question Lab01**”

SUBMISSION

- Provide answers for each question in **QUESTIONS** section. Place your answers in a word document (.docx) and name it as “Lab1_LastName_FirstName.docx.”
- Submit your document on Canvas.
- Show your own work.

QUESTIONS

Question 1 (5pts) According to the Heracles architecture, write a short paragraph in your own words about your understanding of this machine. Follow steps in Section 1 to answer this question.

My understanding of the Heracles architecture is that it is comprised of a total of 18 nodes. We have one node (node 1) which is the master node, 16 computed nodes (node 2-17), and another single node (node 18) that comprises 4 advanced GPUs in node 18. It connects 4 of the same GPU which is the Nvidia Tesla P100. To my understanding, the Nvidia Tesla P100 is one of the most advanced data accelerators ever built! Heracles also contains a Mellanox SwitchX-2 18-Port QSFP FDR which provides a high performing fabric solution in a 1U form with a non-blocking switch capacity of 2tb/s.

The master node (node 1) is used to manage all computing resources and operations on Heracles. The computed nodes (nodes 2-17) are nodes that execute jobs submitted by the user and the node with the 4 GPUs are used to run mainly Cuda programs because node 18 is the only node with the GPUs. The overall point is that Heracles is built with top quality technology, and it is meant to teach us students the different types of parallelism by allowing us to execute code sequentially or in parallel and allows us to review the result and efficiency between sequential and parallel processing.

Question 2 (5pts) Give few examples of applications that can benefit from this type of machine and what challenges come with this type of machine?

Banking systems, gaming and simulations, and medical technology such as MRI, CT, and x-ray machines can benefit from this type of machine. The processing of a 4k video would benefit because it would process the video at a much higher speed if it was done by parallelism. Supercomputers, and mainframe computers can also benefit from this type of machine because it has a lot of high performance processors and high performance GPUs which can process huge quantities of data in a very short amount of time. So any machine that runs heavy and intense softwares/programs would need a high performance processor this machine offers. Some of the challenges that come with this machine is that it is difficult to code an efficient algorithm that runs parallelism without hitting any race conditions. With high performance processors also comes with high performance power supplies.

Question 3 In this lab, you are given three versions of matrix multiplication programs:

mm-seq.cpp: *sequential C++ CPU Version.*

mm-omp.cpp: *OpenMP Version.*

mm-mpi.cpp: *MPI Version.*

a) (10pts) Understand the given source codes and explain the differences in computing and execution models of these programs (i.e. how these programs are designed and executed on parallel hardware? Which one uses distributed and shared memory?). To understand the codes, please get yourself used with basic syntax of OpenMP and MPI. The following materials are useful to learn these syntaxes:

- <https://computing.llnl.gov/tutorials/openMP/>
- <https://computing.llnl.gov/tutorials/mpi/#LLNL>
- http://mpi.deino.net/mpi_functions/index.htm

MPI uses distributed memory while OpenMp uses shared memory while the CPU version is sequential. In the mm-seq.cpp algorithm, this will perform the matrix multiplication individually which means that it will compute each element of matrix C one by one. For the mm-omp.cpp algorithm, this chooses to perform the matrix multiplication using parallelism through shared memory. It retrieves the maximum number of threads or cores it can use for its parallelism, then it will utilize all the maximum number of cores to perform the randomly generated matrix multiplication in parallel until all of the matrix c elements are populated. In the mm-mpi.cpp algorithm, this chooses to perform the matrix multiplication using parallelism through shared memory. It will run on 1 node that has 24 processes/cores for it to utilize. It will randomly generate a matrix multiplication and will send a different problem to each process to be computed. Once it is computed, it will retrieve the computed products and join them together to populate the matrix c. It will continue sending the problems to the processes to be computed, then retrieves the computed result and joins the multiple computed results from the process together to populate matrix c. This will not stop until the matrix multiplication is over and matrix c is completely populated.

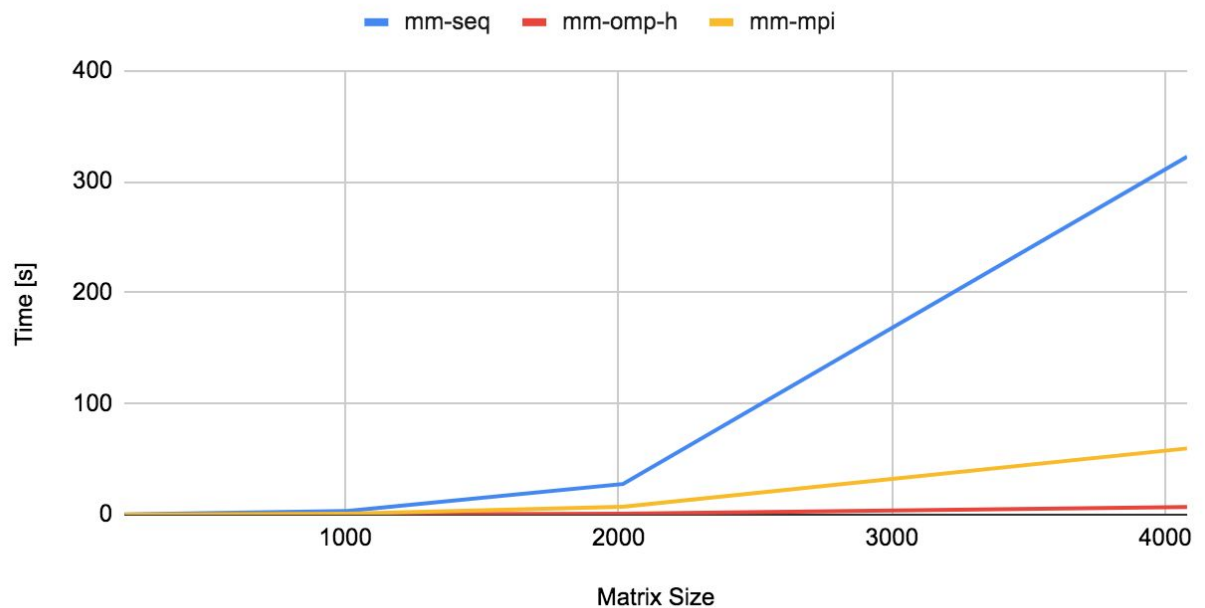
b) (5pts) For each version of matrix multiplication, run the program with matrix sizes according to the Table, then fill out the runtime in Table 1. Follow steps in Section 2 to compile and run the codes.

Table 1: Runtime (Heracles Machine)

Matrix size	mm-seq	mm-omp-h	mm-mpi (1 node x 24 processes)
192	0.04000	0.01002093	0.011169605
1008	3.21000	0.13961730	0.780141700
2016	27.5700	0.84896278	7.128184400
4080	322.560	6.82520272	59.62527600

c) (5pts) Plot the chart for each program version in Table 1 using the runtime (x-axis is the matrix size; y-axis is the runtime).

mm-seq, mm-omp-h and mm-mpi matrix size vs Time [s]



d) (10pts) Calculate the speedup of parallel versions compared to its sequential version on CPU and fill out Table 2. According to the runtime and speedups, which codes

performed better? Why?

$$\text{Speedup} = \frac{\text{Time}_{\text{Sequential}}}{\text{Time}_{\text{Parallel}}}$$

Table 2: Speedup

Matrix size	mm-omp-h	mm-mpi
192	3.9916	3.5811
1008	29.9914	4.1146
2016	32.4749	3.8677
4080	47.2601	5.4098

The mm-omp-h code performed better because it uses parallel processing with shared memory where the mm-mpi uses parallel processing with distributed memory. With shared memory, all the CPU cores are accessing the same memory. It is faster because shared memory is not being copied from one private memory and distributed over a network to the other different private memories, and memory allocation is done once. In a distributed memory, each processor has its own private memory. Each process will communicate with another through the network. The more processors we have, the more it will have to communicate with each other through the network and if the network cannot handle a huge traffic, this will slow down performance. This is the reason why mm-omp-h (shared memory) is much faster than the mm-mpi (distributed memory) when it is compared against the sequential algorithm. Shared memory is faster.

SECTION 1: ACCESSING HERACLES CLUSTER

Request for PDS Lab Access

You should already have received an email from pdslab@ucdenver.edu about your account information and instructions to login on Heracles. If you did not receive the email until now, please contact the TAs immediately for your account info.

Login

Once you obtained an account information, you will be able to login to Heracles with host name: **heracles.ucdenver.pvt**. Go to this link in order to learn how to connect to the Cluster

http://pds.ucdenver.edu/document.php?type=cluster&name=access#Accessing_the_hardware

If you are not on campus, remember to connect to the campus network via VPN before logging on Hereacles. More information about VPN and remote access is at:

<https://www.ucdenver.edu/offices/office-of-information-technology/software/how-do-i-use/vpn-and-remote-access>

- 1) Learn HERACLES Multi-Core Cluster architecture:
http://pds.ucdenver.edu/webclass/Heracles_Architecture.html
- 2) Monitoring Heracles by accessing the following link in order to observe some metrics (CPU, Network, memory, etc.)
 - a) Connect to the VPN if you are not on Campus before accessing the link.
<https://heracles.ucdenver.pvt/mcms/>
 - b) if you get this error bellow, just click on <Advanced> and <Proceed to Heracles(unsafe)>



Your connection is not private

Attackers might be trying to steal your information from **heracles** (for example, passwords, messages, or credit cards). [Learn more](#)

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[Proceed to heracles \(unsafe\)](#)

SECTION 2: COMPILING PROGRAMS ON HERACLES

If you are not familiar with Linux, you should get started with any online Linux tutorial before doing this and future Lab assignments. Some Linux tutorials are available at:
<http://pds.ucdenver.edu/document.php?type=links&name=tutorials>

1. Copy source code files to Heracles

- Logon to the cluster
- Make a folder named csc5551/lab1 in your home directory using the 'mkdir' command.

```
$ mkdir /path/to/directory
```

For example:

```
$ mkdir /home/john/csc5551/lab01
```

- Copy the source code files to your folder. If you are using MAC or Linux, you can copy these files using `scp` or `sftp` command. Also you can download Cyberduck for Mac (http://download.cnet.com/Cyberduck/3000-2160_4-10246246.html)
If you are using Windows, you can use WinSCP or SSH Secure Shell to login and copy files from your PC to the cluster. For more information on downloading WinSCP and how to use this software, visit:

<http://pds.ucdenver.edu/document.php?type=software&name=winscp>

- Change the working directory to `csc5551/csc7551` using `cd` command
\$ `cd /path/to/directory`

For example:

\$ `cd /home/john/csc5551/labnn`

2. Compiling programs.

Update intel compiler library, execute the following command every time you log on, or you can insert in in `~/.bashrc` for an automatic update.

\$ `source /opt/intel/compilers_and_libraries_2019.4.243/linux/bin/compilervars.sh -arch intel64 -platform linux`

Use the following commands to compile given source codes. Make sure the executable files are: `mm-seq`, `mm-omp`, `mm-mpi` for the slurm scripts to work. Otherwise, you need to modify the slurm scripts.

\$ `g++ -O mm-seq.cpp -o mm-seq`
\$ `g++ -O -fopenmp mm-omp.cpp -o mm-omp`
\$ `mpicxx mm-mpi.cpp -o mm-mpi`

For more detail instructions, please read:

- Compiling sequential programs on Heracles (C, C++ and Fortran)
http://pds.ucdenver.edu/webclass/Compiling%20C_C++%20and%20Fortran%20program%20s.html
- Compiling MPI code on HERACLES
<http://pds.ucdenver.edu/webclass/Compiling%20MPI%20program%20on%20Heracles.html>
- Compiling OpenMP programs on Heracles
<http://pds.ucdenver.edu/webclass/Compiling%20openMP%20programs.html>
- Compiling SIMD-SSE programs
http://pds.ucdenver.edu/webclass/Compiling%20openMP_SSE%20programs%20on%20Hydra.html
- Compiling CUDA programs on Heracles
<http://pds.ucdenver.edu/webclass/Heracles-Compiling%20Cuda%20code.html>

SECTION 3: RUNNING PROGRAMS ON HERACLES

We use Slurm to run the compiled codes (generated from Section 2) as it will guarantee that the codes will run on an available node(s) without any other concurrent jobs. It is crucial for accurate runtime measurements. In this lab, we have provided the Slurm script for each given source code as follows:

- `c_slurm.sh` (script to run C/C++ sequential code)
- `openmp_slurm.sh` (script to run openMP code)
- `mpi_slurm.sh` (script to run MPI code)

1. Run Slurm scripts.

From the master node, execute the following command:

```
$ sbatch scriptName argument1 argument2
```

where,

- `scriptName` is either `c_slurm.sh` or `openmp_slurm.sh` or `mpi_slurm.sh` depending on which program you want to execute.
- `argument1` is the dimension of the matrix
- `argument2`: is the option to specify if input/output matrices are printed or not (1=print; 0=not print). Program only prints if the matrix size is less than 10.

By default, output results will be written to file `slurm_output.jobID` and errors will be written to file `slurm_error.jobID`, where `jobID` is a job id number, which is assigned when you execute the command `sbatch`.

For example:

```
$ sbatch c_slurm.sh 4 1
```

will run `mm-seq` (executable file of C/C++ sequential version) with matrix size 4x4 and print out results.

2. Useful commands with Slurm scripts:

```
squeue           // check the job queue
scancel jobID    // cancel job execution
```

3 (Optional) Configuring Slurm.

You may change some parameters in your script, such as:

```
#SBATCH --mail-type=ALL      ### configure email
#SBATCH --mail-user=myemailaddress  ### put your email
#SBATCH --job-name=myjob     ### Job Name
#SBATCH --output=slurm_output.%j  ### File in which to store job output
#SBATCH --error=slurm_error.%j    ### File in which to store job error messages
```

For MPI job you may configure the grid by changing some parameters in your job according to the experiment, such as:

```
#SBATCH --ntasks=24          ## corresponds to MPI ranks/ each rank corresponds to one task
#SBATCH --ntasks-per-node=24 ## Number of tasks to be launched per Node, default = 1
```

In the above example the mpi job will launch 24 tasks divided in 24 tasks per node, in other word the MPI job will use one node run 24 tasks.

Check this link for more information about Slurm scripts:

<http://pds.ucdenver.edu/webclass/Heracles-RunningPrograms%20Slurm.html>