HPC Lab Manual: Distributed Computing and Parallel Programming

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System Access

SSH Connection

ssh username@master-node

Replace (username) with your actual username.

Navigate to Summer School Directory

bash

cd /mnt/lustre/nabeel/summer_school

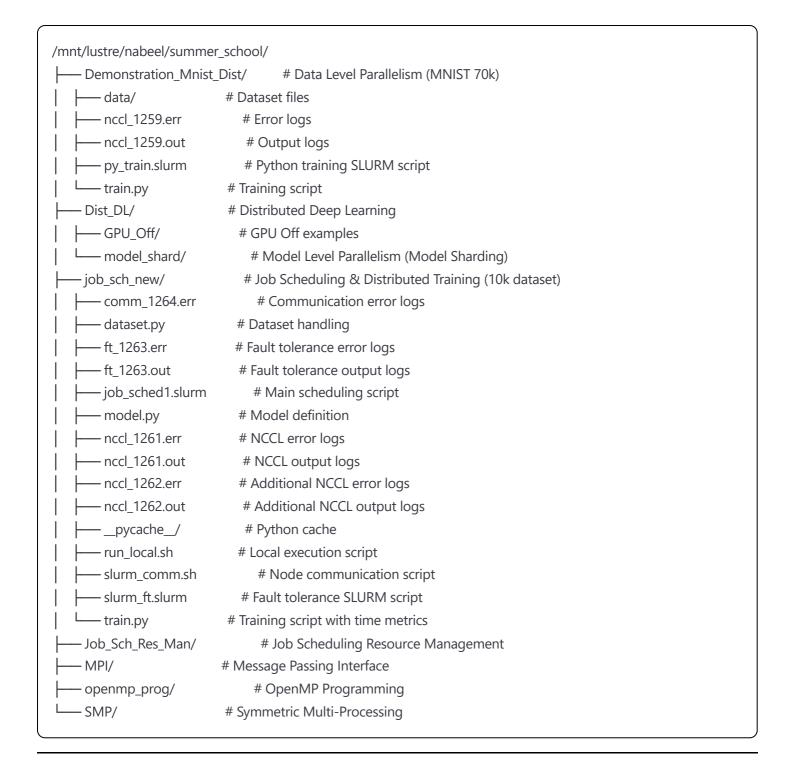
Directory Listing

bash

ls -la

Directory Structure Overview

The summer school materials are organized in the following hierarchy:



SLURM Job Scheduler

Basic SLURM Script Structure

Create a file named (job_script.slurm):

bash		

```
#!/bin/bash
#SBATCH --job-name=my_job
                               # Job name
#SBATCH --nodes=1
                            # Number of nodes
#SBATCH --ntasks-per-node=4
                              # Tasks per node
#SBATCH --cpus-per-task=4 # CPUs per task
#SBATCH --qpus-per-node=1
                             # GPUs per node (if needed)
#SBATCH --time=01:00:00 # Time limit (HH:MM:SS)
#SBATCH --output=nccl_%j.out
                              # Output file
#SBATCH --error=nccl_%j.err
                              # Error file
# Master node address and port
export MASTER_ADDR=192.168.20.15
export MASTER_PORT=29500
# Set Ethernet interface for NCCL
export NCCL_SOCKET_IFNAME=ensif1
# Disable InfiniBand (if not available)
export NCCL_IB_DISABLE=1
# Optional: Enable debug output
export NCCL_DEBUG=INFO
export PYTHONUNBUFFERED=1
# Export distributed environment variables
export RANK
export WORLD_SIZE
export MASTER_ADDR
export MASTER_PORT
echo "RANK=$RANK on $(hostname) using interface $NCCL_SOCKET_IFNAME"
# Run your program
python3 train.py
```

SLURM Parameter Explanation

Parameter	Description	Example Values
job-name	Name for your job	(mnist_training), (mpi_test)
nodes	Number of compute nodes	1,2,4
ntasks-per-node	Tasks per node	1,4,8
cpus-per-task	CPU cores per task	1,4,8
gpus-per-node	GPUs per node	1,2,4
time	Maximum runtime	00:30:00, 02:00:00
partition	Queue/partition name	gpu, cpu, debug
mem Memory per node		8G, 16G, 32G

Essential SLURM Commands

Submit a Job

bash sbatch job_script.slurm

Check Job Status

bash

squeue # All jobs

squeue -u username # Your jobs only

squeue -j jobid # Specific job

Cancel a Job

bash

scancel jobid # Cancel specific job scancel -u username # Cancel all your jobs

Job Information

bash

sinfo # Node information sacct -j jobid # Job accounting info

Distributed Machine Learning

Data Level Parallelism (MNIST 70,000 Images)

Navigate to the MNIST distributed training directory:

bash

cd /mnt/lustre/nabeel/summer_school/Demonstration_Mnist_Dist

Directory Contents:

- (data/) Contains the MNIST dataset
- (train.py) Main training script for distributed learning
- (py_train.slurm) SLURM batch script for Python training
- (nccl_*.out) Training output logs
- (nccl_*.err) Error logs

Running MNIST Distributed Training:

Step 1: Review the SLURM Script

bash

cat py_train.slurm

Step 2: Submit the Job

bash

sbatch py_train.slurm

Step 3: Monitor Job Progress

bash

Check job status

squeue -u \$USER

Monitor real-time output

tail -f nccl_*.out

Check for errors

tail -f nccl_*.err

Step 4: View Results

```
# View complete output
cat nccl_*.out

# Check training metrics and performance
grep -i "epoch\|loss\|accuracy" nccl_*.out
```

Key Features:

- Uses 70,000 MNIST images for training
- Implements data parallelism across multiple nodes
- NCCL backend for efficient communication
- Automatic logging of training progress

Distributed Deep Learning Options

GPU Off Examples

Navigate to the GPU off directory:

bash

cd /mnt/lustre/nabeel/summer_school/Dist_DL/GPU_Off

Model Level Parallelism (Model Sharding)

Navigate to the model sharding directory:

bash

cd /mnt/lustre/nabeel/summer_school/Dist_DL/model_shard

Running Model Sharding

```
bash

# Submit the job
sbatch model_shard.slurm

# Check logs
cat model_shard_*.out
```

Job Scheduling and Time Metrics (10,000 Image Dataset)

Navigate to the job scheduling directory:

bash

cd /mnt/lustre/nabeel/summer_school/job_sch_new

Directory Contents:

- (train.py) Training script with comprehensive time metrics
- (model.py) Neural network model definition
- (dataset.py) Dataset handling and preprocessing
- (job_sched1.slurm) Main scheduling script for training
- (slurm_ft.slurm) Fault tolerance SLURM script
- (slurm_comm.sh) Node communication script
- (run_local.sh) Local execution script
- (nccl_*.out/err) Output and error logs
- (ft_*.out/err) Fault tolerance logs
- (comm_*.err) Communication logs

Running Job Scheduling Experiments:

Option 1: Standard Distributed Training with Scheduling

```
# Submit the main scheduling job
sbatch job_sched1.slurm

# Monitor progress
squeue -u $USER
tail -f nccl_*.out
```

Option 2: Fault Tolerance Training

```
bash

# Submit fault tolerance job
sbatch slurm_ft.slurm

# Monitor fault tolerance logs
tail -f ft_*.out
```

Option 3: Node Communication Testing

```
# Run communication script
bash slurm_comm.sh

# Check communication logs
tail -f comm_*.err
```

Option 4: Local Testing

```
bash
```

Run locally for debugging

bash run_local.sh

Changing Number of Nodes for Performance Testing:

Edit SLURM Scripts to Test Different Node Configurations:

```
# Edit the main scheduling script
nano job_sched1.slurm

# Modify these parameters:
#SBATCH --nodes=1 # Change to 1, 2, 4, 8 nodes
#SBATCH --ntasks-per-node=4 # Adjust tasks per node
```

Example configurations for testing:

Single Node:

```
bash
```

#SBATCH --nodes=1
#SBATCH --ntasks-per-node=4

Two Nodes:

```
bash
```

#SBATCH --nodes=2

#SBATCH --ntasks-per-node=4

Four Nodes:

bash

```
#SBATCH --nodes=4
#SBATCH --ntasks-per-node=2
```

Analyzing Time Metrics:

View Training Time Results:

bash

Check training completion times
grep -i "training time\|epoch time\|total time" nccl_*.out

Compare performance across different node configurations

grep -i "throughput\|images/sec\|batch time" nccl_*.out

Performance Comparison Workflow:

- 1. Submit job with 1 node: (sbatch job_sched1.slurm)
- 2. Record job ID and wait for completion
- 3. Edit script to use 2 nodes, submit again
- 4. Compare time metrics in output files
- 5. Repeat for 4, 8 nodes to analyze scaling

Key Features:

- Uses 10,000 image dataset for faster experimentation
- Comprehensive time metrics and performance monitoring
- Multiple execution modes (standard, fault tolerance, communication testing)
- Easy node configuration changes for scaling experiments
- Detailed logging for performance analysis

Job Scheduling Resource Management

Navigate to the resource management directory:

bash

cd /mnt/lustre/nabeel/summer_school/Job_Sch_Res_Man

This directory focuses on:

- Resource allocation strategies
- Job queue management

- System resource optimization
- Scheduling algorithms

Parallel Programming with C/C++

MPI (Message Passing Interface)

bash

cd /mnt/lustre/nabeel/summer_school/MPI

Compilation:

```
bash
```

```
mpicc -o program program.c # C program
mpicxx -o program program.cpp # C++ program
```

SLURM Script for MPI:

```
bash
```

```
#!/bin/bash
```

```
#SBATCH --job-name=mpi_job
#SBATCH --nodes=2
#SBATCH --ntasks=8
#SBATCH --time=00:30:00
```

mpirun -np 8 ./program

OpenMP Programming

bash

cd /mnt/lustre/nabeel/summer_school/openmp_prog

Compilation:

```
bash
```

```
gcc -fopenmp -o program program.c # GCC icc -qopenmp -o program program.c # Intel compiler
```

SLURM Script for OpenMP:

```
bash

#!/bin/bash

#SBATCH --job-name=openmp_job

#SBATCH --nodes=1

#SBATCH --cpus-per-task=8

#SBATCH --time=00:30:00

export OMP_NUM_THREADS=8

//program
```

Symmetric Multi-Processing (SMP)

bash

cd /mnt/lustre/nabeel/summer_school/SMP

Compilation:

bash

gcc -o program program.c # Basic compilation
gcc -O3 -o program program.c # Optimized compilation

SLURM Script for SMP:

bash

#!/bin/bash

#SBATCH --job-name=smp_job #SBATCH --nodes=1 #SBATCH --cpus-per-task=4 #SBATCH --time=00:30:00

./program

Common Commands Reference

File Operations

bash

```
Is -la # List files with details

cp file1 file2 # Copy file

mv file1 file2 # Move/rename file

rm file # Delete file

mkdir dirname # Create directory
```

Viewing Files

```
cat filename # Display entire file
head -n 20 filename # First 20 lines
tail -n 20 filename # Last 20 lines
tail -f filename # Follow file updates
less filename # Page through file
```

Process Management

```
bash

ps aux  # List all processes

top  # System monitor

htop  # Enhanced system monitor

kill -9 PID  # Kill process
```

System Information

```
bash

nvidia-smi # GPU status

free -h # Memory usage

df -h # Disk usage

lscpu # CPU information
```

Troubleshooting

Common Issues and Solutions

Job Fails to Start

- 1. Check SLURM script syntax
- 2. Verify resource availability: sinfo
- 3. Check job queue: squeue

Out of Memory Errors

bash

#SBATCH --mem=32G # Increase memory allocation

GPU Not Detected

```
#SBATCH --gpus-per-node=1 # Explicitly request GPU

export CUDA_VISIBLE_DEVICES=0 # Set GPU device
```

NCCL Communication Issues

```
bash
```

Python Path Issues

```
bash
```

```
export PYTHONPATH=/path/to/modules:$PYTHONPATH
which python3  # Verify Python location
```

Log File Locations

Check these files for debugging:

- (nccl_*.out) Standard output
- (nccl_*.err) Error messages
- (slurm-*.out) SLURM job output
- Individual directory logs for specific applications

Getting Help

- 1. Check log files first
- 2. Use (squeue) to verify job status
- 3. Review SLURM script parameters
- 4. Test on smaller datasets/shorter time limits
- 5. Check system resource availability with sinfo

Quick Start Checklist

- 1. **Connect to HPC**: ssh username@master-node
- 2. **Navigate to directory**: cd /mnt/lustre/nabeel/summer_school
- 3. Choose your task:
 - Data parallelism: cd Demonstration_Mnist_Dist
 - Model parallelism: (cd Dist_DL/model_shard)
 - Job scheduling: (cd job_sch_new)
 - MPI/OpenMP/CUDA: (cd MPI/) or (cd OpenMP/) etc.
- 4. **Review the SLURM script**: (cat job_script.slurm)
- 5. **Submit job**: (sbatch job_script.slurm)
- 6. **Monitor**: squeue -u username
- 7. Check results: (tail -f output_file.out)

Remember to always check the specific requirements and parameters for each exercise in their respective directories!