Slurm in 5 min.

Robert Dyro Stanford ASL

August 15, 2023

Outline

Introduction

Using Slurm

Stanford Sherlock

Introduction 2/13

Introduction - Overview

- ► a cluster allows to run independent processes across many computers
- ▶ many computers usually means 2 to 20
- by all means run your computation on only 1 computer if you want!
- ▶ processes are independent, can communicate over network
- ► usage through shell through ssh
- ► a cluster is managed by a cluster software Slurm
- ► computers in the cluster communicate via network (sockets)
- ▶ storage is shared, all computers see the same files
- sharing storage is managed by the shared storage software
- ▶ no sudo , install locally or load available packages

Introduction 3/13

Introduction - Terminology

- ► a node a computer on the network managed by Slurm [-N]
- ► a task a single of the many processes you want to run [-n]
- ► a CPU a single core on a computer (a physical core) [-c]
- ► a job a set of independent processes to run
- ► to submit to ask Slurm to run a job
- ► to schedule what Slurm does to execute all your tasks
- ► array job an alternative way of scheduling NOT covered here

Introduction 4/13

Introduction - How it works

- ▶ you submit a job
 - your job consists of instruction how many and what processes to run
 - you specify strict requirements: nodes nb, memory per node, time limit
 - you specify other requirements and job hints
- ▶ your jobs waits in a queue until resources (nodes) are available
 - if it is rejected, it is rejected immediately
- ▶ your job is scheduled
 - you can get an email about it
 - you check on the status by examining a combined output file

your job finishes or is cancelled (by you)

Introduction 5/13

Outline

Introduction

Using Slurm

Stanford Sherlock

Using Slurm 6/13

Important Commands

<u>Slurm user commands</u> (you're the user, as opposed to an admin)

- ▶ sinfo query available computational resources
- ► squeue check status of jobs (squeue --user \$USER)
- ▶ srun run a single process, low-level command
- ▶ [sbatch] run a job, a job is a shell script (that calls srun)

module - allows to load packages, no sudo apt on a cluster

- ► module avail available preinstalled packages
- ► module list currently loaded packages
- ▶ module load package load package
- ▶ module unload package unload package

Using Slurm 7/13

Example Job Script

run by issuing sbatch my_job.sh

```
#!/bin/bash
\#SBATCH --output = out \_ \% j. txt
#SBATCH --time=0-10:00
#SBATCH --mail-type=ALL
#SBATCH --ntasks=20
#SBATCH --cpus-per-task=2
module load julia # load needed packages
source environment # like a python virtualenv
echo ""; date; echo ""
srun -n1 -c2 python3 setup.py # 1 node, task and cpu
for i in {0..100}; do # 101 times, more than ntasks is OK
 srun -n1 -c2 python3 exp.py $i & # notice &
done # each srun ends with & to run all in the background
echo ""; date; echo ""
```

Using Slurm 8/13

Scheduling

- ▶ when you connect, you're on the login node, don't run stuff there
- ▶ srun --pty bash to run a computational node interactively
- ▶ srun -p gpu --gpus 1 --pty bash a gpu node interactively
- ▶ #SBATCH -p gpu in the my_job.sh file to have GPU nodes
- ► [tail -n 100 out_43598734.txt] to check on a job

Using Slurm 9/13

Outline

Introduction

Using Slurm

Stanford Sherlock

Stanford Sherlock 10/13

Sherlock - Stanford University Cluster

All info at: www.sherlock.stanford.edu

- ssh \$USER@login.sherlock.stanford.edu
- ► https://login.sherlock.stanford.edu web-based interface

Comments

- ▶ uses Slurm
- ► access via a linux shell without sudo privileges
- \blacktriangleright has 100s general computational nodes and \sim 100 GPU nodes
- ▶ account is free, but requires Sherlock admin's and your PI's approval
- ▶ usage is free for research, requires publication acknowledgement
- ► can request all the nodes, but will spend time in queue
- ▶ simple job wait: 1 node 10 s, 10 nodes 5 min, 20 nodes 1 hour

Stanford Sherlock 11/13

Sherlock Storage

Storage

- ▶ three types of storage *long*, *short* and *very short* term
- storage is very generous (a lot of GB or TB)
- short and very short storage locations are vastly faster
- ► short storage locations have file expiration (90 days)
- very short storage location is cleared on job end

Available storage locations - these are bash variables

- ► *long* term storage
 - \$\\$HOME | personal long term storage
 - \$GROUP_HOME | shared research group storage (your lab)
- ► *short* term storage
 - | \$SCRATCH | personal short term storage
 - | \$GROUP_SCRATCH | shared research group storage (your lab)
- very short term storage very good performance
 - \$L_SCRATCH local to node
 - \$L_SCRATCH_JOB local to node & job

Stanford Sherlock 12/13

Sherlock Tips

Persistent login

Under [~/.ssh/config] put

```
Host login.sherlock.stanford.edu
ControlMaster auto
ControlPath ~/.ssh/%1%r0%h:%p
```

Multiple terminal windows at computational node

- ▶ query what nodes are yours squeue --user \$USER
- ▶ issue ssh sh02-01n43

Installing things

- ► Sherlock does not give sudo access
- ▶ many installations do not *really* require sudo
- ▶ install and use stuff from [~/.local/lib] [~/.local/bin

Copying files back and forth

▶ use rsync! excellent tutorial from Digital Ocean here

Stanford Sherlock 13/13