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High-Performance System Administration

Introduction to Slurm

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1 Learning Objectives

Learning Objectives

After the course the students should be able to:

- Comprehend there are login and compute nodes with different functionality
- Understand the basics of the HPC infrastrucutre
- Use a workload manager like SLURM to allocate HPC resources (e.g. CPUs) and to submit a batch job.
- Run parallel programs in an HPC environment.
- Compile programs on the HPC Cluster
- Run Interactive Sessions with a graphical user interface

What is a HPC Cluster?

Using Slurm - Basics

Getting Help

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What is a Cluster?



Basic Concepts

Cluster A collection of networked computers intended to provide compute capabilities.

Node One of these computers, also called host or server.

Frontend Special node provided to interact with the cluster. login-mdc.hpc.gwdg.de in our case.

Job Execution of a program consisting of one or several parallel tasks.

Partition A pool of nodes of equal or similar type.

Batch System Management system distributing job tasks across job slots.

Batch Systems

- Moab Cluster Manager.
- PBS Pro.
- Slurm.
- Spectrum LSF.
- Oracle Grid Engine.
- TORQUE Resource Manager.

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Basic Concepts 2

Serial job Job consisting of one task using one job slot.

- SMP job Job with shared memory parallelization, i.e. all processes need access to the memory of the same node. \Rightarrow several job slots **on the same node**.
- MPI job Job with distributed memory parallelization, realized with MPI. Can use several job slots on several nodes. Needs to be started with a helper program, e.g., mpirun or srun.

Single node vs. Multi node computations

- MPI jobs are a lot of independent tasks that usually use one core each.
 - Slurm calls these tasks with srun.
- Single node jobs are usually just one task with many cores.
- Both can be combined into hybrid jobs: multiple tasks using multiple cores each.

Getting started with Slurm

Getting Help

SCC Configuration



Available Partitions at SCC

General purpose partitions:

medium General purpose partition, well suited for most jobs. Up to 1024 cores per job.

fat Up to 512 GB in one host.

fat+ For extreme memory requirements. Up to 2048GB per host.

Special purpose partitions:

gpu For jobs using GPU acceleration.

int For interactive jobs, i.e. jobs which require a shell or a GUI.

The fat+ partition

The fat+ partition contains:

- 5 nodes with 1.5Tb Memory
- 1 node with 2Tb Memory

Usage recommendations:

- Work your way up. Start in fat and only use fat+ if your jobs runs out of memory.
- Use reportseff, see if your job really is memory bound

When unsure, ask us!

--mem or --mem-per-cpu is mandatory

Telling Slurm what to do

- srun submits information on your job to Slurm.
 - > What is to be done? (path to your program and required parameters)
 - What are its requirements? (e.g. which nodes, number of tasks, maximum runtime)
- Slurm matches the jobs requirements against the capabilities of the nodes.
- When suitable free resources are found, the job is started.
- Slurm prioritizes the jobs based on a number of factors.

Your first job

```
Use srun to submit a job to Slurm.
```

```
srun <program>
```

```
Example:
```

```
gwdu101:27 12:53:50 ~ > hostname
gwdu101
gwdu101:27 12:53:53 ~ > srun hostname
amp078
gwdu101:27 12:53:56 ~ > srun hostname -f
amp078.global.gwdg.cluster
```



Submitting a job

srun <parameters> <program>

common parameters

- -p <partition> partition.
- -t <hh:mm:ss> maximum runtime. If this is exceeded the job is killed.
- -n <i > number of tasks.

Interactive Jobs

srun: Interactive jobs

- --x11 adds X11 (GUI) forwarding. This requires that you connect to the frontend with ssh -Y and your local machine supports X-Windows.
- -p int use the interactive partition. In int the nodes have no slot limit. They will take jobs until their load crosses a specified threshold, so jobs start immediately.
- --pty interactive mode

Interactive X11 Job

Running Matlab

- > ssh -Y login-mdc.hpc.gwdg.de
- > module load matlab
- > srun --x11 -p int matlab -desktop

The job will be dispatched and as soon as an available node is found and the Matlab interface will start.

Interactive Console Job

Running python interactively

- > ssh login-mdc.hpc.gwdg.de
- > module load anaconda3
- > srun --pty -p int python3
- >>> import socket, os
- >>> print(socket.gethostname())
- >>> print(os.system("slurm_resources"))

Resource selection: CPU

srun options for parallel (SMP or MPI) jobs.

- -N <min>-<max>,
- --nodes=<min>-<max>
- -n,--ntasks=<n>
- --tasks-per-node=<n>

Minimum and maximum node count. You can also specify the exact number. Number of tasks (not equally distributed!) Tasks per node. If used with -n it denotes the maximum number of tasks per node. CPUs per tasks.

-c,--cpus-per-task=<n> C

A note on -n vs. -c

Rule of thumb

- c for single node jobs
- -n for MPI jobs

A note on -n vs. -c

Rule of thumb

- c for single node jobs
- -n for MPI jobs

Rule of thumb 2

If you are unsure if your program uses MPI, then it does not.

Resource Selection: Memory

srun options

```
--mem <size[K|M|G|T] > Memory per node.
```

- --mem-per-cpu<size[K|M|G|T] > Memory per core.
- without options:
 - each partition has a DefMemPerCPU option
 - can be retrieved via scontrol show partition <name>

Non interactive Jobs

Problem

- if you have big jobs, your queue time will be long
- srun needs you to stay logged in
- jobs can run for days

Non interactive Jobs

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Solution

Batch Jobs!

sbatch: Using Job Scripts

A job script is a shell script with a special comment section.

The #SBATCH lines have to come first!

sbatch: Basic job script example

1 #!/bin/bash
2 #SBATCH -p medium
3 #SBATCH -t 10:00
4 #SBATCH -o job-%J.out
5
6 slurm_resources

Submit with:

sbatch <script name>

Jobscripts

- a job script is essentially a normal script
- usually bash/shell, but can be any scripting language (R, python, perl)
- #SBATCH lines need to be at the top!
- only lines starting exactly with #SBATCH are parsed
- you can copy files, load modules, and do any scripting you want
- for MPI, use srun or mpirun to start your program

Getting Help

Useful options for batch job submssion

sbatch <slurm options> jobscript

```
--mail-type=<TYPE>
--mail-user=<address>
```

-o/-e <file>

get mail notifications (type: BEGIN, END, etc.) Default: \${USER}@gwdg.de Store job output in file (slurm-<jobid>.out by default). %J in the filename stands for the jobid.

Slurm Commands

```
sinfo Info about the system and partitions.
    sinfo -p <partition>, -t <state>
squeue Show the job queue.
    squeue -p <partition>, --me
scancel Cancel Job
    scancel <JobID>
    scancel -p <partition>|-u $USER
```

Getting Help

Batch Script for Task Distribution in medium partition

```
1 #SBATCH -p medium
2 #SBATCH -N 10
3 #SBATCH --ntasks-per-node 24
4 #SBATCH -o job-%J.out
5
6 module purge
7 module load intel-oneapi-compilers intel-oneapi-mkl intel-oneapi-mpi namd
8
9 srun namd2 +setcpuaffinity apoal.namd
```

Memory is faster then network!

Try to spread your tasks to as little nodes as possible.

Job Disk Space Usage Options

/local Local hard disk of the node. SSD based and therefore a very fast option for storing temporary data. Automatic file deletion. A temporary directory is created on all nodes at \$TMP_LOCAL.

/scratch Shared scratch space, available on most nodes, but there are two instances (use -C scratch). Very fast, no automatic file deletion, but also no backup! Files may have to be deleted manually when we run out of space.

\$HOME Available everywhere, permanent, with backup. Personal disk space can be increased. Comparably slow.

Getting Help

Recipe: Combine shared memory and MPI

Running hybrid jobs

```
#SBATCH -- p medium
  #SBATCH -- N 5
2
  #SBATCH ——ntasks—per—node=4
3
  #SBATCH — cpus—per—task=6
4
5
  #SBATCH -- o iob--%l.out
6
  module purge
7
8
  module load openmpi/gcc
9
   export OMP NUM THREADS=$SLURM CPUS PER TASK
10
11
   srun hybrid job
12
```

Longer or shorter jobs

The -- qos parameter

- Default maximum runtime: 2 days
 - --qos= <qos> can select a QoS
- Two extra QoS available:

short for shorter jobs (max. 2h), has higher priority, limited job slots long longer jobs (max. 5d), limited job slots.

But my job is even longer

- try parallelizing more
- break it down into smaller steps
- check, if your software supports checkpoints
- check again!

More Slurm Commands

scontrol show [partition|node|job] <x> where x should be a node name, JobID or partition name.

sprio Priority information about pending jobs

sacct Get information about a job after it finished

- -j <jobid>
- --format=JobID,User,JobName,MaxRSS,Elapsed,Timelimit

Using the gpu partition

GPU parameters

-G | --gpus=[type:]<n> requests n GPUs of type

--gpus-per-task=[type:]<n> requests n GPUs of type per task

--gpus-per-node=[type:]<n> requests n GPUs of type per node

- CPUs are evenly distributed for every GPU
- Available types are:
 - rtx5000
 - ▶ v100
 - gtx1080

```
See: sinfo -p gpu --format=%N,%G
```

Debugging

take a look at your output files, while the job is running:

- tail -f /path/to/output
- take a look at the jobs, while it is running
 - > you can ssh into every node that currently calculates your job
 - use htop to see the processor and ram usage

Debugging

Read the extra job information

Take a look at all the information. Is it as expected?

Debugging

Read your errors!

slurmstepd: error: Detected 1064 oom-kill event(s) in step XXXXXX.0 cgroup. Some of your processes may have been killed by the cgroup out-of-memory handler. srun: error: gwda024: task 3: Out Of Memory

Might have something to do with memory! Have a look at your jobs memory with: reportseff JOBID

Information sources

man pages

Slurm online help

- For example: sbatch --help
- GWDG scientific compute cluster documentation
 - https://docs.gwdg.de/doku.php?id=en:services:application_services: high_performance_computing:start
- GWDG scientific compute cluster user wiki
 - https://info.gwdg.de/wiki/doku.php?id=wiki:hpc:start
- HPC announce mailing list
 - https://listserv.gwdg.de/mailman/listinfo/hpc-announce

Rocket.Chat

- Rocket.Chat Channel at: https://chat.gwdg.de/channel/hpc-users
- Mainly for quick questions
- Usually faster response but we might tell you to open a ticket

Getting Help

Using the GWDG Support Ticket System

- Write an email to hpc-support@gwdg.de
- State your user id (\$USER)
- If you have a problem with jobs, **always** include:
 - Job IDs
 - standard output (-o <file>)
 - standard output (-e <file>)
- If you have a lot of failed jobs send at least two outputs. You may also list the jobid's of all failed jobs.
- If you don't mind us looking at your files, please state this in your request
 - > You may limit your permission to specific directories or files

GöHPCoffee

- Bi-weekly meeting between users and admins.
- Format: Short focus session and open discussions and Q&A afterwards
 More Information at https://docs.gwdg.de/doku.php?id=en:services:

application_services:high_performance_computing:hpc_coffee

The End

Thank you all for your attention!

Questions?

- We connected to the cluster
- We managed sessions
- Do you need additional information?