# ilifu Online Training – Introduction to slurm

Dane Kennedy

Bioinformatics Support, ilifu University of Cape Town, 19 March 2024



# UNIVERSITY OF CAPE TOWN



IDIA Inter-University Institute for Data Intensive Astronomy





- Framework : Login node & Compute nodes
- Login node
  - Accessed via ssh (\$ ssh <username>@slurm.ilifu.ac.za)
  - Submit jobs and manage work directories

#### • Compute nodes

- Where processes/code runs
- via singularity containers or modules

#### • Partitions / Queues

Main, Jupyter, Devel 32 core, ~232GiB RAM	<b>GPU</b> 32 core, ∼232GiB RAM, Nvidia GPUs	<b>HighMem</b> 32 core, 503GiB RAM 96 core, 1.5TiB RAM
85 + 12 Nodes	7 nodes	3 nodes







### **SLURM - Use cases**



Login node Run SLURM & bash commands cd, mkdir, ls, etc

### Jupyter/Dev. node

Development space New code / workflows / routines Debugging / testing software





## Main partition

Stable, computationally heavy processing

### HighMem/GPU

For single-high memory jobs that can't be split into multiple jobs for MPI





# SLURM <u>http://docs.ilifu.ac.za/#/getting\_started/submit\_job\_slurm</u>



4

https://jupyter.ilifu.ac.za

\$ ssh <username>@slurm.ilifu.ac.za





- \$ sinfo  $\rightarrow$  shows partitions and resources
- \$ squeue  $\rightarrow$  shows all jobs in SLURM queue/partition
- $\qquad$  squeue -u  $\qquad$  shows your jobs
- s sbatch slurm\_job\_script.sh  $\rightarrow$  submit job to SLURM
- s sbatch --help  $\rightarrow$  info. on job submission parameters
- $\$  scancel <jobid>  $\rightarrow$  cancel running/pending job



CBIO

IDIA



#!/bin/bash

module add python/3.11.2

python hello\_world.py







<u>https://docs.ilifu.ac.za/#/tech\_docs/running\_jobs?id=customising-you</u> <u>r-job-using-sbatchsrun-parameters</u>

> -time=0-03:00:00 # 3 hours -mem=3G # 3 GiB -ntasks=1 # one task -nodes=1 # one node -partition=Main -account=<your default>



IDIA

University of Cape

Aon Kaapstad



## SLURM - running a job



https://github.com/ilifu/ilifu\_user\_training/tree/main/introduction/tutorial2





### **DEMO TIME!**

### https://github.com/ilifu/ilifu\_user\_training/tree/main/i ntroduction/tutorial2







### Do's :

- Run jobs using sbatch rather than interactive jobs
- Identify job resources requirements:
  - No. of nodes and CPUs, amount of RAM and wall-time.
- Remove files that aren't needed
  - /scratch3 folder after data processing is complete
  - Old raw data, temporary products , etc.
- Use Singularity (cannot install software on nodes)
- Use username@transfer.ilifu.ac.za for data transfers

### Don't:

- Don't run software/heavy processes on login node
- Don't place large files in your home directory (/users)
- Don't transfer using scp/rsync on the login node







# Thank you for coming and for your time.

Happy computing!

https://docs.ilifu.ac.za/





CBIO

support@ilifu.ac.za