



Ilifu Online Training

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Inter-University Institute
for Data Intensive Astronomy



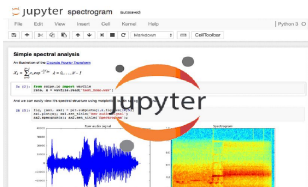
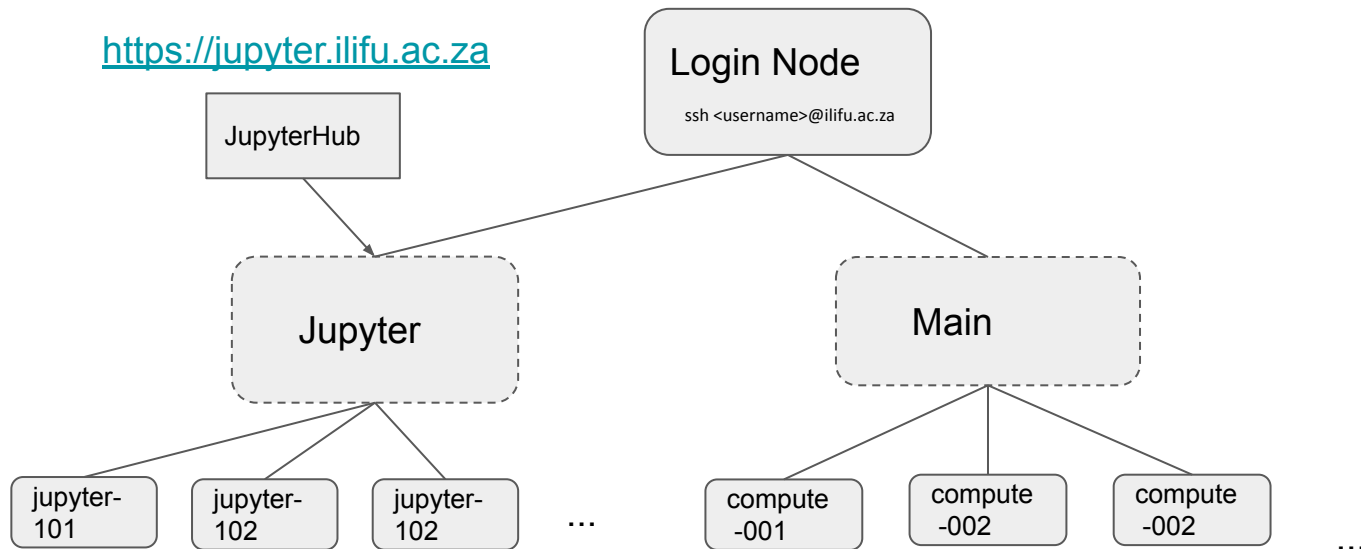
Job scheduling & cluster management tool

- 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
- **Partitions (1 node = 32 CPUs, 236 GB RAM)**

Main partition	Jupyter Spawner
~80 nodes	12 nodes



<https://jupyter.ilifu.ac.za>

[illegible]

\$ sinfo → shows partitions and resources

\$ squeue → shows all jobs in SLURM queue

\$ squeue -u → shows your jobs

\$ sbatch slurm_job_script.sh → submit job to SLURM

\$ sbatch --help → info. on job submission parameters

\$ scancel <jobid> → cancel running/pending job

\$ sacct → shows status of recent completed or running jobs

SLURM - running a job



```
$ cat slurm_job_script.sh
```

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

```
#SBATCH --job-name=demo_job
#SBATCH --time=00:00:10
#SBATCH --mem=4GB
#SBATCH --partition=Main
#SBATCH --output=demo-job-%j.out
#SBATCH --error=demo-job-%j.err
#SBATCH --mail-user=oarabile@idia.ac.za
#SBATCH --mail-type=BEGIN,END,FAIL,TIME_LIMIT_80
#SBATCH --account=b34-admins-ag
```

Describe job parameters / resources

```
echo "Running demo job"
```

container

software

script

```
singularity exec /idia/software/containers/python3/python3-2020-01-28.simg python job_script.py
```

```
$ sbatch slurm_job_script.sh # submit job to SLURM queue
```

DEMO TIME!

SLURM - running a job



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#!/bin/bash


#SBATCH --job-name=demo_job
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#SBATCH --mail-type=BEGIN,END,FAIL,TIME_LIMIT_80
#SBATCH --account=b34-admins-ag

echo "Running demo job"

module load python3
python job_script.py

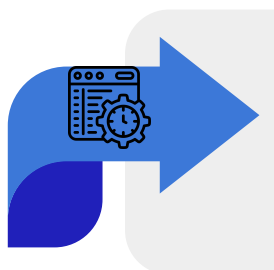

$ sbatch slurm_job_script.sh # submit job to SLURM queue
```





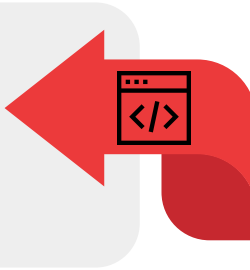
Login node
Run SLURM & bash commands
cd, mkdir, ls, etc

Jupyter/Dev. node
Development space
New code / workflows / routines
Debugging / testing software



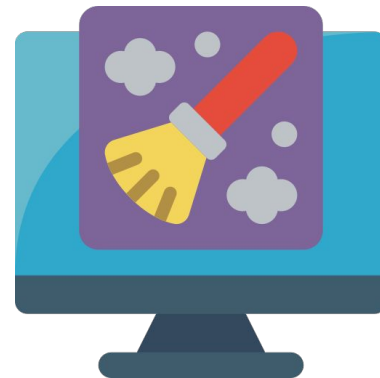
Main partition
Stable, computationally
heavy processing

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



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)



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!