



# Ilifu Online Training

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Inter-University Institute  
for Data Intensive Astronomy

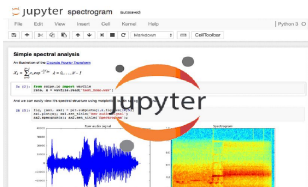
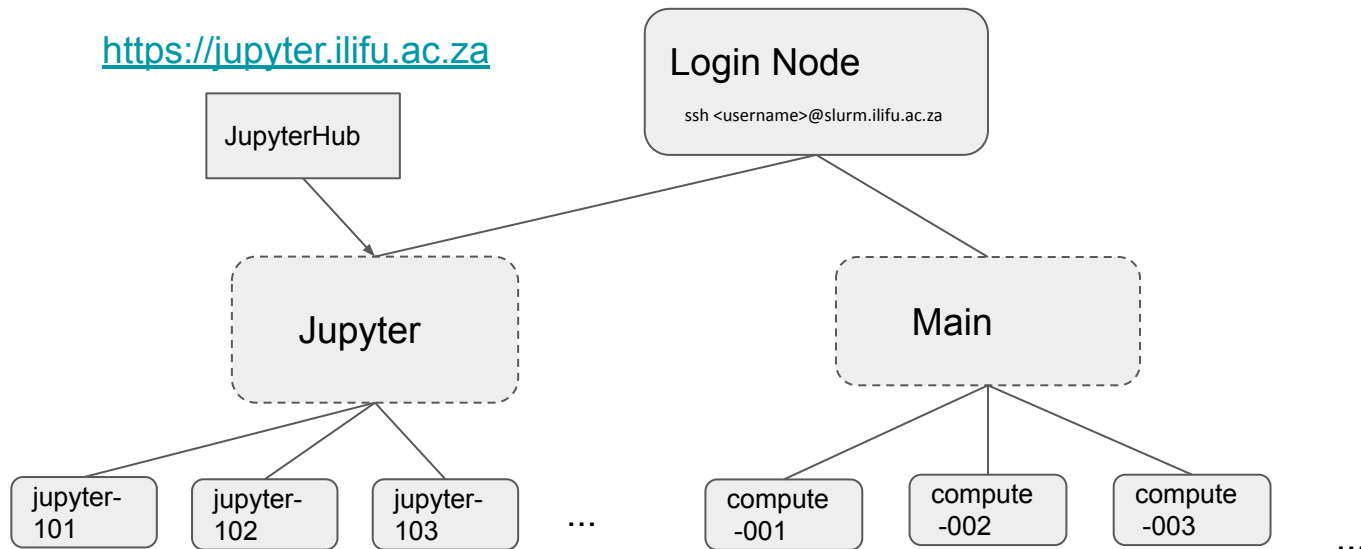


## Job scheduling & cluster management tool

- 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, 232 GB RAM )**

Main partition	Jupyter Spawner
~80 nodes	12 nodes



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


```

$ squeue
squeue: no jobs are in the queue
$ sinfo
sinfo: no jobs are in the queue
$ scontrol show nodes
NodeName=compute-001
State=Idle
Reason=
CurrentTime=2022-03-01T12:00:00.000000000
AllocTime=2022-03-01T12:00:00.000000000
...
  
```

\$ sinfo → shows partitions and resources

\$ squeue → shows all jobs in SLURM queue

\$ squeue -u \$USER → 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 --reservation=training
#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

```
singularity exec
```

```
/idia/software/containers/python-3.6.img
```

software

```
python3
```

script

```
job_script.py
```

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



DEMO TIME!

# 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

echo "Running demo job"

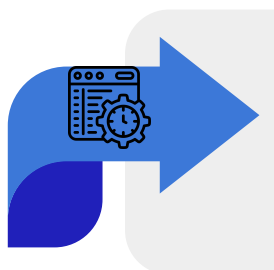

module load python
python job_script.py

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



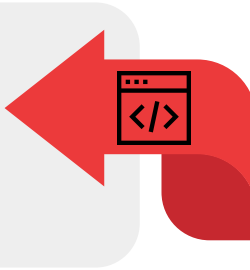
**Login node**  
Run SLURM & bash commands  
cd, mkdir, ls, etc

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



**Main partition**  
Stable, computationally  
heavy processing

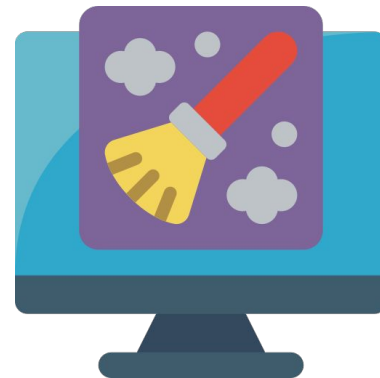
**HighMem/GPU**  
For single-high memory  
jobs that can't be split  
into multiple jobs for MPI





## 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!