

# Getting Started on DiRAC systems

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**Slides: <https://github.com/edbennett/dirac-202306>**

# Assumptions

- You are familiar with the Unix (bash) shell
- You have used an HPC system and batch scheduler before
- You have registered with SAFE and provided an SSH key

# Connecting

- Tursa:  
ssh username@tursa.dirac.ed.ac.uk  
ed25519: SHA256:QFXBZzU5vChePHu/Y/FF42Xac7w2Shb/XT4G2+vTM48
- COSMA8:  
ssh username@login8.cosma.dur.ac.uk  
ed25519: SHA256:t50+QQcNZ6QAVCfD8n4fr4gfTT22TInc2xHke8g8ZhQ
- “Two-factor” authentication: SSH key *and* login password required
  - Passphrase-protect your keys!

# Login environment

- Tursa: 1TB RAM, 128 cores
- COSMA8: 2TB RAM, 64 cores
- Only for compilation/installation, not for compute-intensive/production jobs

# Software environment

- Software provided via Environment Modules
- To check available modules:  
`module avail`
- To load a module:  
`module load module1_name module2_name ...`
- Tursa: barebones stack—recommended modules:  
`cuda/11.4.1 openmpi/4.1.1-cuda11.4.1 ucx/1.12.0-cuda11.4.1`
- COSMA8 stack more full-featured

# Filesystems

## Tursa

- Your home directory:  
*/home/project\_core/project\_code/username*
- To share within your project:  
*/home/project\_code/project\_code/shared*
- To share with other projects:  
*/home/project\_code/shared*

# Filesystems

## COSMA8

- Your home directory: NFS mount, slow, small quota  
*/cosma/home/project/username*
- Fast Lustre storage, larger quota:  
*/cosma8/data/project/username*
- Super-fast scratch storage for checkpointing:  
*/snap8/scratch/project/username*

# Filesystems

## Striping

- Ensure that large files ( $\geq 1\text{TB}$ ) are striped
  - Otherwise they can take out the filesystem
  - Unless you have a one-file-per-node write pattern
- Talk to your RSEs about how to do this



# Compute nodes

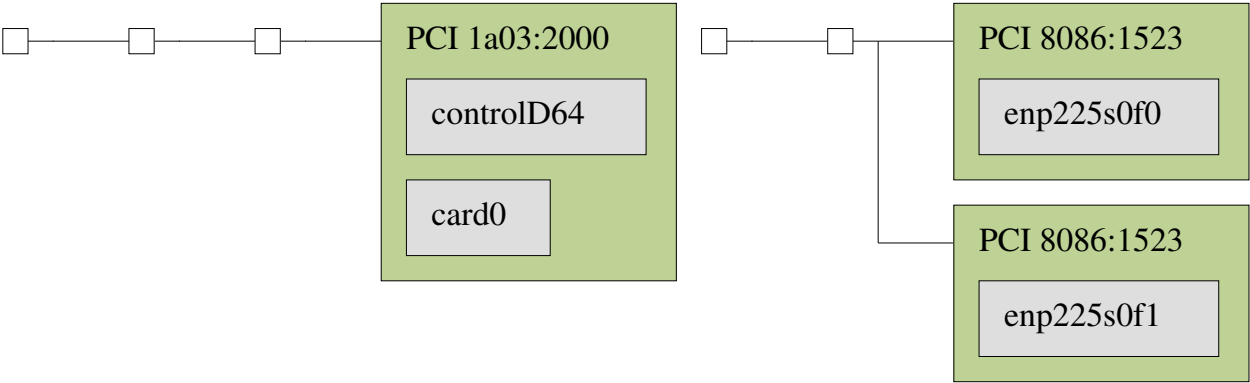
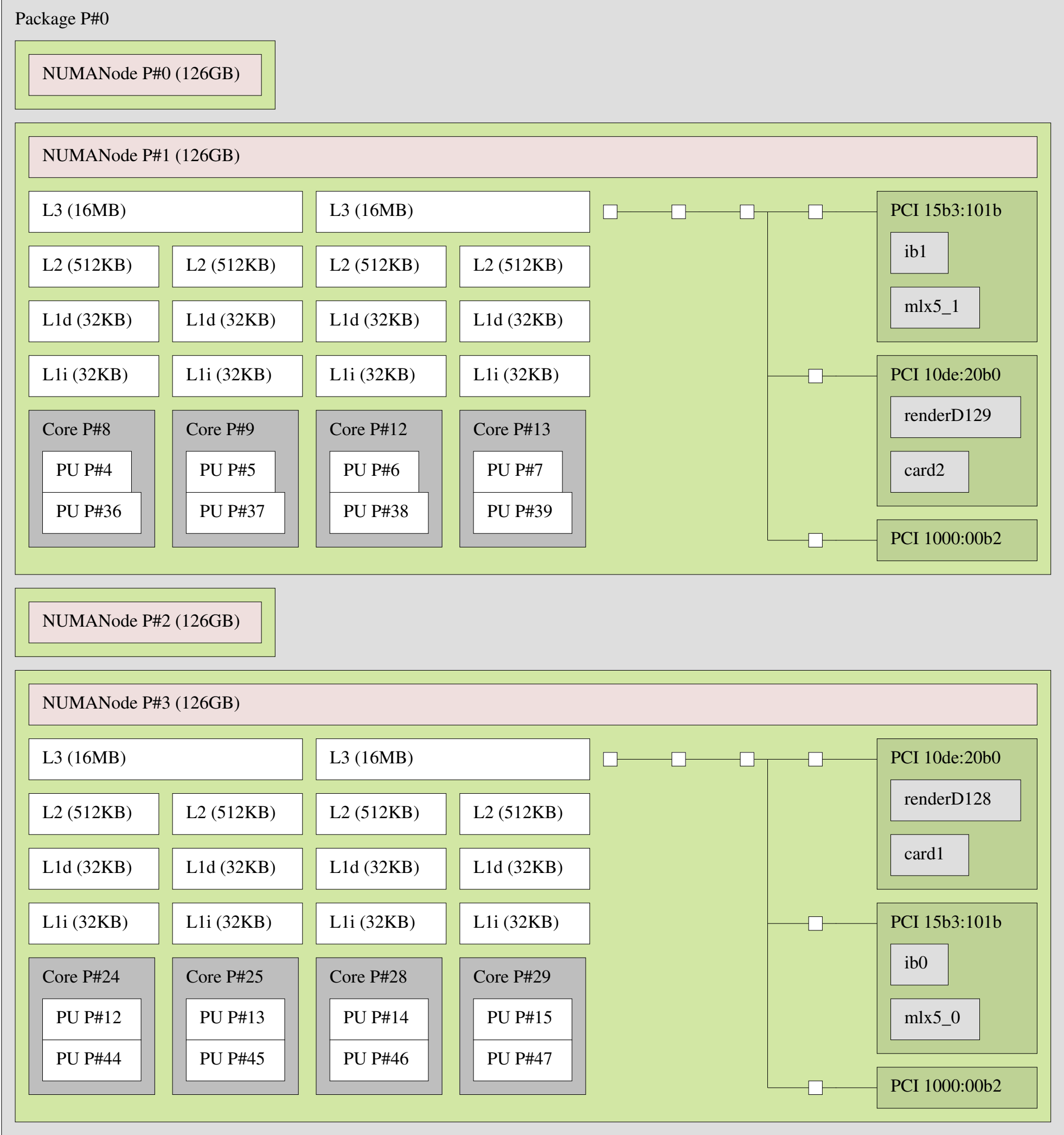
## Tursa

- 2 × AMD EPYC 7302
  - Each (16 cores/4 NUMA nodes/8 chiplets) × 2 hardware threads
- 4 × NVIDIA A100 [40/80GB] GPUs
- 4 × NVIDIA Networking ConnectX-6 Infiniband HDR adapters
  - Both on NUMA nodes 1, 3, 5, 7
- 1TiB RAM (128GiB per NUMA node)

# Compute nodes

## Tursa

Machine (1008GB total)



Host: tu-c0r0n45

Indexes: physical

Date: Mon 12 Jun 2023 13:19:30 BST



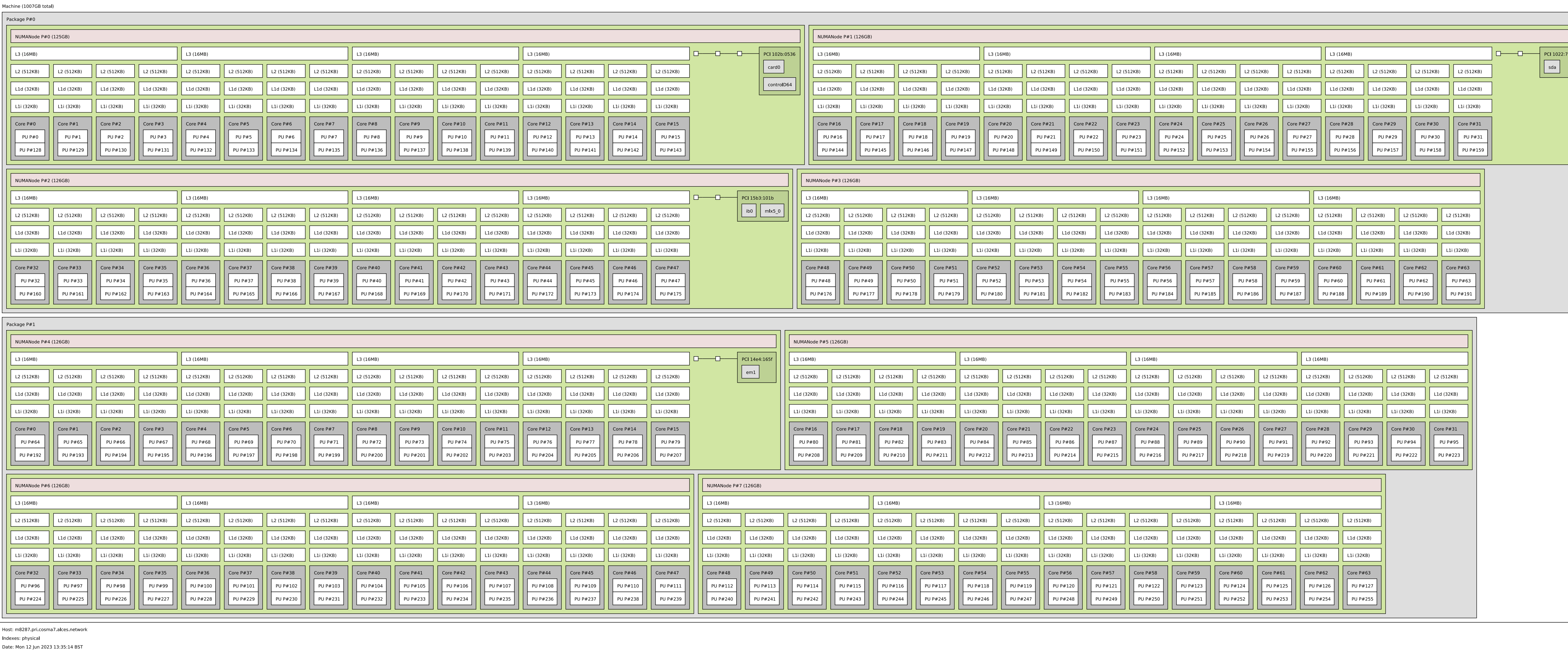
# Compute nodes

## COSMA8

- 2 × AMD EPYC 7H12
  - Each (64 cores/4 NUMA nodes/8 chiplets) × 2 threads
- 1 TiB RAM (128 GiB per NUMA node)
- 1 × NVIDIA Networking ConnectX-6 Infiniband HDR adapters

# Compute nodes

## COSMA8



# Slurm

<code>sinfo</code>	Get overall partition status
<code>squeue --me</code>	Get status of my jobs in queue
<code>sbatch <i>job_script_filename</i></code>	Submit a job to the queue
<code>scancel <i>job_id</i></code>	Cancel a running or pending job

# Example job script

## Tursa

Replace with standard in production

```
#!/bin/bash
#SBATCH --job-name NAME
#SBATCH --qos reservation
#SBATCH --time 10:00
#SBATCH --account PROJECT
#SBATCH --nodes NUM_NODES
#SBATCH --ntasks NUM_TASKS
#SBATCH --ntasks-per-node 4
#SBATCH --cpus-per-task 8
#SBATCH --partition gpu
#SBATCH --gres gpu:4
#SBATCH --output %x.%j.out
#SBATCH --error %x.%j.err
#SBATCH --reservation workshop
umask 0002
```

```
module purge
module load cuda/11.4.1 \
    openmpi/4.1.1-cuda11.4.1 \
    ucx/1.12.0-cuda11.4.1

export OMP_NUM_THREADS=4
export OMPI_MCA_btl=^uct,openib
export UCX_TLS=gdr_copy,rc,rc_x,sm,cuda_copy,cuda_ipc
export UCX_RNDV_SCHEME=put_zcopy
export UCX_RNDV_THRESH=16384
export UCX_IB_GPU_DIRECT_RDMA=yes
export UCX_MEMTYPE_CACHE=n

mpirun -np ${SLURM_NTASKS} \
    --bind-to none \
    ./wrapper.sh ./my_tool
```

# Wrapper script

## Tursa

- Bind processes to GPUs and fabric adapters with direct connection

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

```
lrank=$OMPI_COMM_WORLD_LOCAL_RANK
```

```
numa1=$(( 2 * $lrank ))
```

```
numa2=$(( 2 * $lrank + 1 ))
```

```
netdev=mlx5_${lrank}:1
```

```
export CUDA_VISIBLE_DEVICES=$OMPI_COMM_WORLD_LOCAL_RANK
```

```
export UCX_NET_DEVICES=mlx5_${lrank}:1
```

```
BINDING="--interleave=$numa1,$numa2"
```

```
echo "`hostname` - $lrank device=$CUDA_VISIBLE_DEVICES binding=$BINDING"
```

```
numactl ${BINDING} $*
```

# Example job script

## COSMA8

```
#!/bin/bash
#SBATCH --job-name NAME
#SBATCH --account PROJECT
#SBATCH --partition cosma8
#SBATCH --nodes NUM_NODES
#SBATCH --ntasks NUM_TASKS
#SBATCH --cpus-per-task 8
#SBATCH --time 10:00
#SBATCH --exclusive
#SBATCH --reservation onboarding

module purge
module load ucx/1.13.0rc2 oneAPI/2022.3.0

mpirun ./my_tool
```



# Project codes

dp287	CompBioMed
dp288	HECBioSim
dp289	MRCGlasgow
dp290	UKAEA
dp291	Materials Science/PAX
dp292	BritLLM

# Other thoughts

- We are all sharing a reservation
  - 16 nodes on COSMA8, 32 nodes on Tursa
  - Think before running long large jobs
- Tools like Miniconda, NVIDIA HPC SDK can be installed in your user space
- You can SSH into nodes that you have active jobs on
  - e.g. To run `nvidia-smi`

# More details

- Tursa user guide:  
<https://epcced.github.io/dirac-docs/tursa-user-guide>
- COSMA8 user guide:  
<https://www.dur.ac.uk/icc/cosma/support/cosma8/>