

# Modelling, Uncertainty and Data for Engineers (MUDE)

Running code on cluster and queues

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# Cluster

Cluster is a set of computational nodes, which are interconnected to a network.

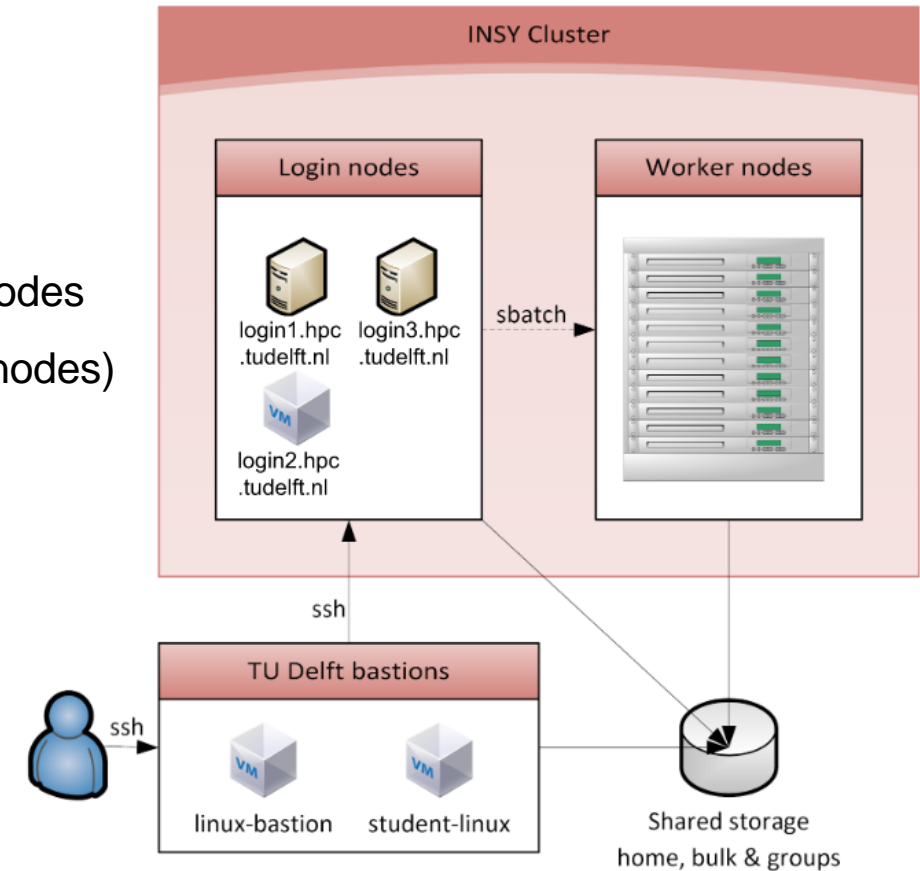
Each node is a computer with CPU, RAM, disk

HPC clusters are actual in case of:

- Computation takes a lot of time
- Series of calculations which can be run simultaneously on the different nodes
- Calculation requires a large amount of memory (one task runs on a few nodes)

Specifics:

- Usually command line interface is used through the login nodes
- Job manager to use the computational nodes
- Shared file system
- Monitoring system (web-interface)



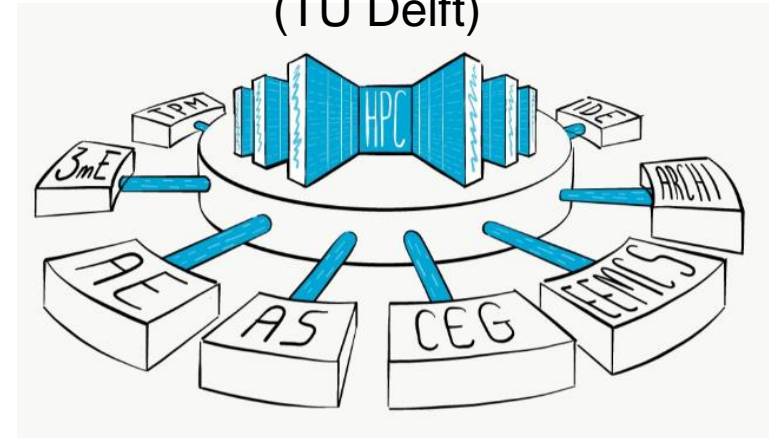
# Cluster



SURFsara national  
supercomputer



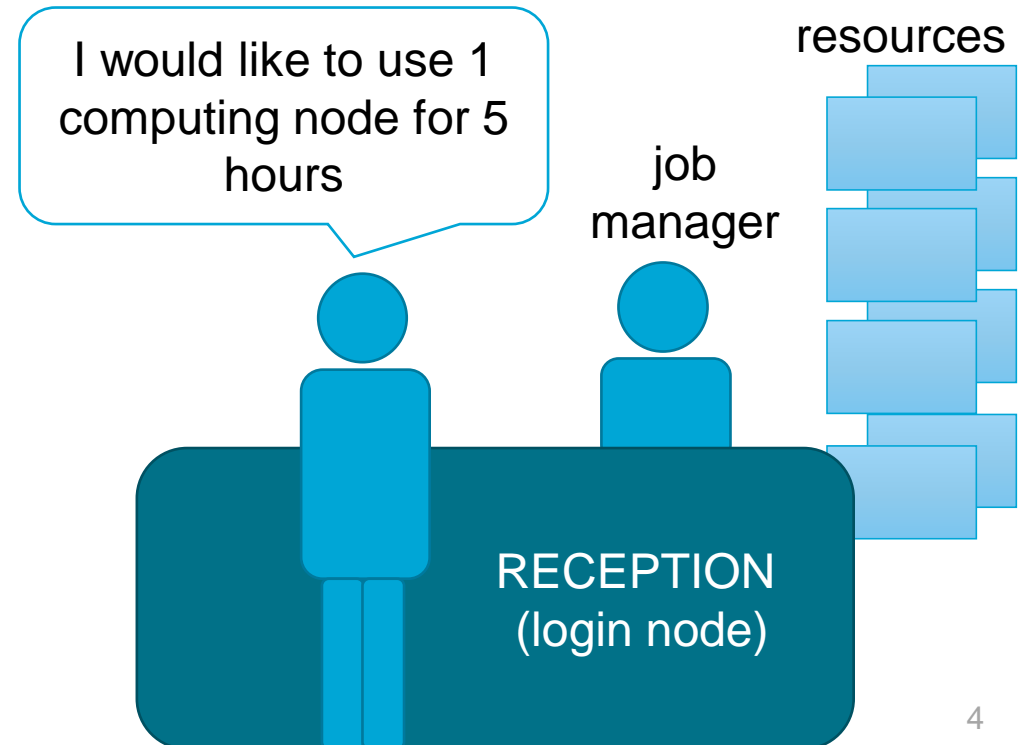
DelftBlue supercomputer  
(TU Delft)



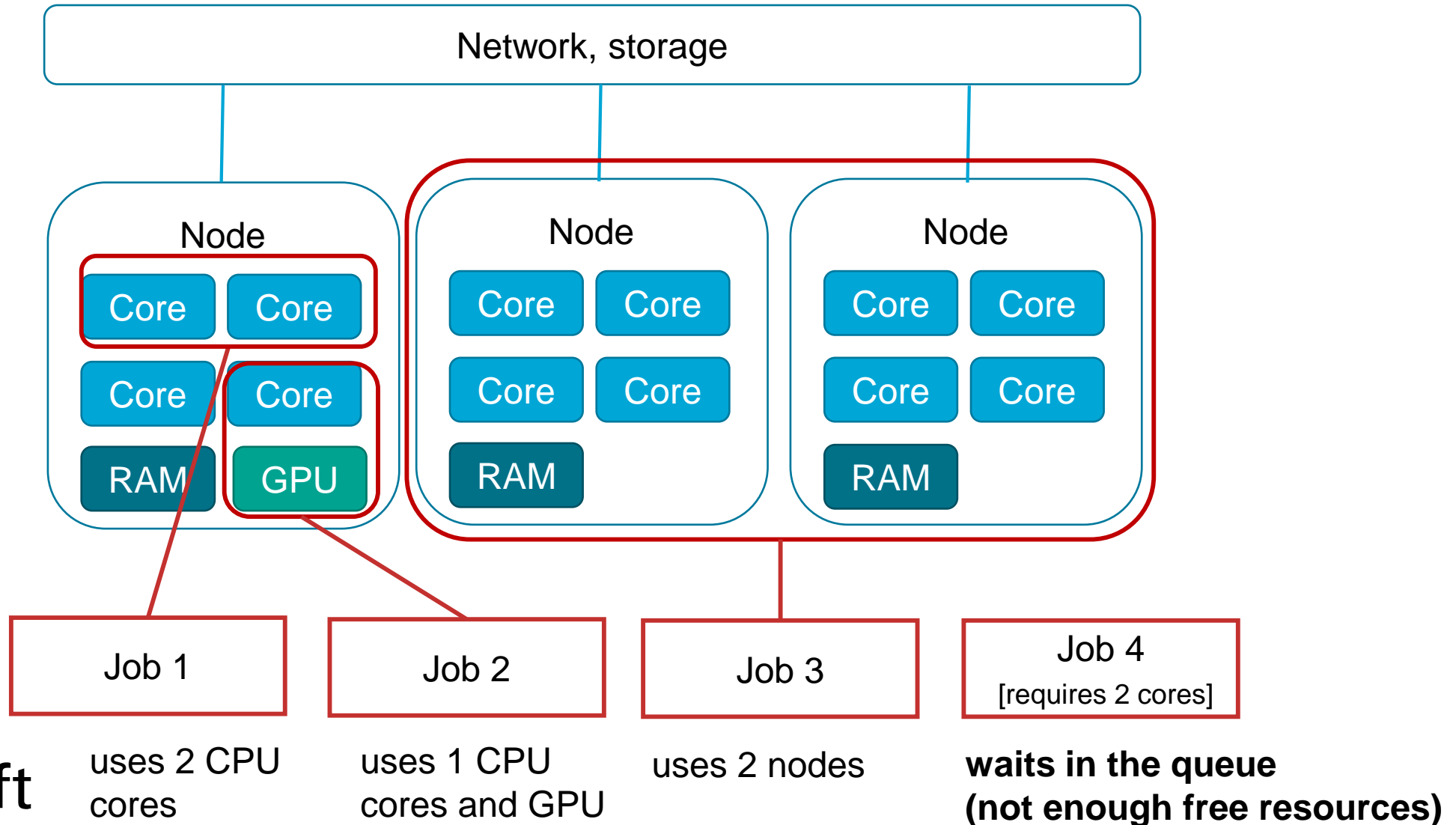
<https://www.tudelft.nl/dhpc/ark/delftbluephase1>

# Job manager

- The scheduler handles how compute resources are shared between users and tasks
- Users should not run any task on login nodes
- Users should run tasks on a computing node only through the scheduler
- Job will not run immediately, it depends on the resources available at that moment
- A task (job) usually has shell script syntax with:
  - commands need to be executed
  - resources request



# Job managers



# SLURM job manager: commands

Command	Description	Example
<b>sbatch</b> <i>RESOURCES SCRIPT</i>	submit a batch script	<b>sbatch</b> myfile.sbatch
<b>srun</b> <i>RESOURCES COMMAND</i>	run a single command	<b>srun --mem=1G --time=00:10:00</b> hostname
<b>squeue</b> [-u <i>USERNAME</i> ] [-t <i>STATUS</i> ]	check the status of jobs	<b>squeue -u student</b> <b>squeue -u student -t COMPLETED</b>
<b>scancel</b> <i>JOBID</i>	cancel a job and delete it from the queue	<b>scancel 15168</b>

srun and sbatch differences:

- srun is blocking
- srun is interactive (outputs directly to the current console)
- if ssh session interrupts, a job running with srun be cancelled

# Slurm: running a serial job (one core)

## 1. nano test.sbatch

Job specifications

```
#!/bin/sh
#SBATCH --job-name="my script"
#SBATCH --time=01:00:00
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1G

srun hostname
#srun python my_script.py
```

## 2. sbatch test.sbatch

Create a file with the next content

Job name

Set the job time limit to 1 hour

Number of MPI processes (nodes)

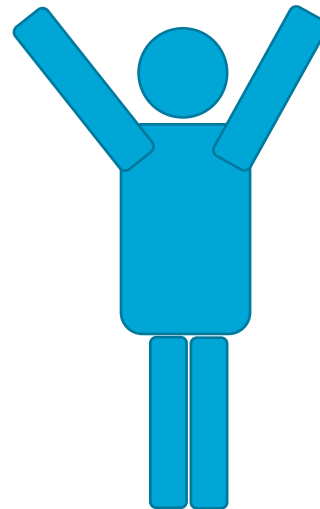
Allocate 1 core of processor

Set the memory limit to 1 GB.

Commands to run in Bash syntax  
(your computational task)

Put the job into queue and print *JOBID*

My laptop doesn't freeze because of my huge computing task! Now I can play study all the day!



# Additional batch parameters for DelftBlue

1. It is needed to load modules first

**module load 2022r2**

**module load python**

**module load py-numpy**

**module load py-matplotlib**

2. Add this line to your sbatch script

**#SBATCH --account=Education-CEG-Courses-CEGM1000**



# Examples of commands and output

## Output of sbatch

```
[dvoskov@login04 slurm]$ sbatch test.sbatch  
Submitted batch job 1688390
```

## Output of squeue

```
1662870    memory      S5T tianming  R 1-02:57:47    1 mem009  
1662844    memory      S5L tianming  R 1-02:57:54    1 mem010  
1664746    memory      S4T tianming  R   12:59:16    1 mem008  
1664750    memory      S4L tianming  R   12:59:16    1 mem008  
1629107    memory     1549 pklaver  R 2-22:36:04    8 mem[001-006,009-010]  
[dvoskov@login04 slurm]$
```

squeue doesn't show completed tasks by default. How to show them:

```
[dvoskov@login04 slurm]$ squeue -u dvoskov -t "COMPLETED"  
      JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)  
    1688390   compute     test    dvoskov CD        0:00      1 cmp033
```

# Squeue command output

Job ID                      Job name  
                            (specified in  
                            sbatch)

Status                      How long  
                            job runs

How much  
nodes uses

```
clln24:~$ squeue | head -n 10
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST (REASON)
10275029	fat	airf	bartk	R	8:51:05	1	r23n23
10276343	normal	allenbra	tphung	PD	0:00	1	(Resources)
10275351	normal	92_ad_pr	emilu	PD	0:00	1	(Priority)
10275350	normal	91_ad_pr	emilu	PD	0:00	1	(Priority)
10275349	normal	90_ad_pr	emilu	PD	0:00	1	(Priority)
10275348	normal	89_ad_pr	emilu	PD	0:00	1	(Priority)
10275355	normal	96_ad_pr	emilu	PD	0:00	1	(Priority)
10275356	normal	97_ad_pr	emilu	PD	0:00	1	(Priority)
10275357	normal	98_ad_pr	emilu	PD	0:00	1	(Priority)

Completed tasks are not shown by default

# Most important job statuses

Code	Status
PD	PENDING
R	RUNNING
CG	COMPLETING
CD	COMPLETED
F	FAILED
CA	CANCELLED

# How to connect to DelftBlue

ssh command

1. From Linux
2. From MobaXTerm application

# How to transfer your data to DelftBlue

1. Drag and drop from/to file tree in MobaXterm (left area)
2. OnDemand web-interface
3. SFTP clients (GUI)
4. scp command
5. rsync command

Details:

# Use MC solver for Poisson equation

- Lets run Poisson solver in Monte-Carlo simulation using left temperature and nu as an uncertain input based on seed:

```
# run Monte-Carlo simulation for number of samples
def run_MC(n_samples=20):
    # generate values and put the values into arrays
    t_left_values = np.zeros(n_samples)
    nu_values = np.zeros(n_samples)
    for i in range(n_samples):
        t_left_values[i], nu_values[i] = generate(i)

    for i in range(n_samples):
        x, u = solve_poisson(T_left=t_left_values[i], nu=nu_values[i])
        plt.plot(x, u)
    plt.xlabel('x')
    plt.ylabel('Temperature')
    plt.savefig('result.png')
```

# Slurm: Solving Poisson equation on cluster

How to solve with different parameters **simultaneously** (on different cores/nodes)?

1. Modify the Python script poisson.py to use cmd parameters
2. Pass the seed parameter from bash script
3. Make a loop in bash - to put the jobs into queue
4. Wait until computations finish
5. Plot the results

```
# job params
params="--mem=1G --time=00:30:00 --ntasks=1 --cpus-per-task=1"

# account specification for DelftBlue
params=$params --account=Education-CEG-Courses-CEGM1000"

# number of samples for seed
nsamples=10

# add jobs for seeds in specified range
for seed in `seq 1 $nsamples`
do
    echo "running $seed"

    # it's better to have an individual job name for each task
    jobparams=$params --job-name='poisson.$seed'"

    # put job into the queue. '&' - for non-blocking execution
    srun $jobparams python poisson.py $seed &
done

echo "Jobs are put into queue"

# wait until all the jobs finish
wait

echo "Calculation finished"

echo "Plotting started"
jobparams=$params --job-name='poisson.plot'"
srun $jobparams python plot_results.py ./results/sol*.npz
echo "Plotting finished"
```

# Running Poisson solver with slurm

## Output of ./run.sh

```
running 1
running 2
running 3
running 4
running 5
running 6
running 7
running 8
running 9
running 10
Jobs are put into queue
srun: job 1701398 queued and waiting for resources
srun: job 1701399 queued and waiting for resources
Hostname: cmp100 Seed: 1 Time: 0.03134 sec.
Hostname: cmp100 Seed: 6 Time: 0.03182 sec.
srun: job 1701398 has been allocated resources
srun: job 1701399 has been allocated resources
Hostname: cmp100 Seed: 4 Time: 0.03275 sec.
Hostname: cmp100 Seed: 7 Time: 0.03274 sec.
Hostname: cmp100 Seed: 5 Time: 0.03157 sec.
Hostname: cmp100 Seed: 9 Time: 0.03197 sec.
Hostname: cmp092 Seed: 8 Time: 0.04887 sec.
Hostname: cmp092 Seed: 2 Time: 0.04759 sec.
Hostname: cmp100 Seed: 3 Time: 0.03024 sec.
Hostname: cmp100 Seed: 10 Time: 0.03908 sec.
Finished
```

## Output of queue

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	ODELIST(REASON)
1701399	compute	'poisson	isaifull	PD	0:00	1	(AssocMaxJobsLimit)
1701398	compute	'poisson	isaifull	PD	0:00	1	(AssocMaxJobsLimit)
1701390	compute	'poisson	isaifull	R	0:14	1	cmp100
1701391	compute	'poisson	isaifull	R	0:14	1	cmp100
1701392	compute	'poisson	isaifull	R	0:14	1	cmp100
1701393	compute	'poisson	isaifull	R	0:14	1	cmp100
1701394	compute	'poisson	isaifull	R	0:14	1	cmp100
1701395	compute	'poisson	isaifull	R	0:14	1	cmp100
1701396	compute	'poisson	isaifull	R	0:14	1	cmp100
1701397	compute	'poisson	isaifull	R	0:14	1	cmp100

Pending jobs

Running jobs

Output from jobs