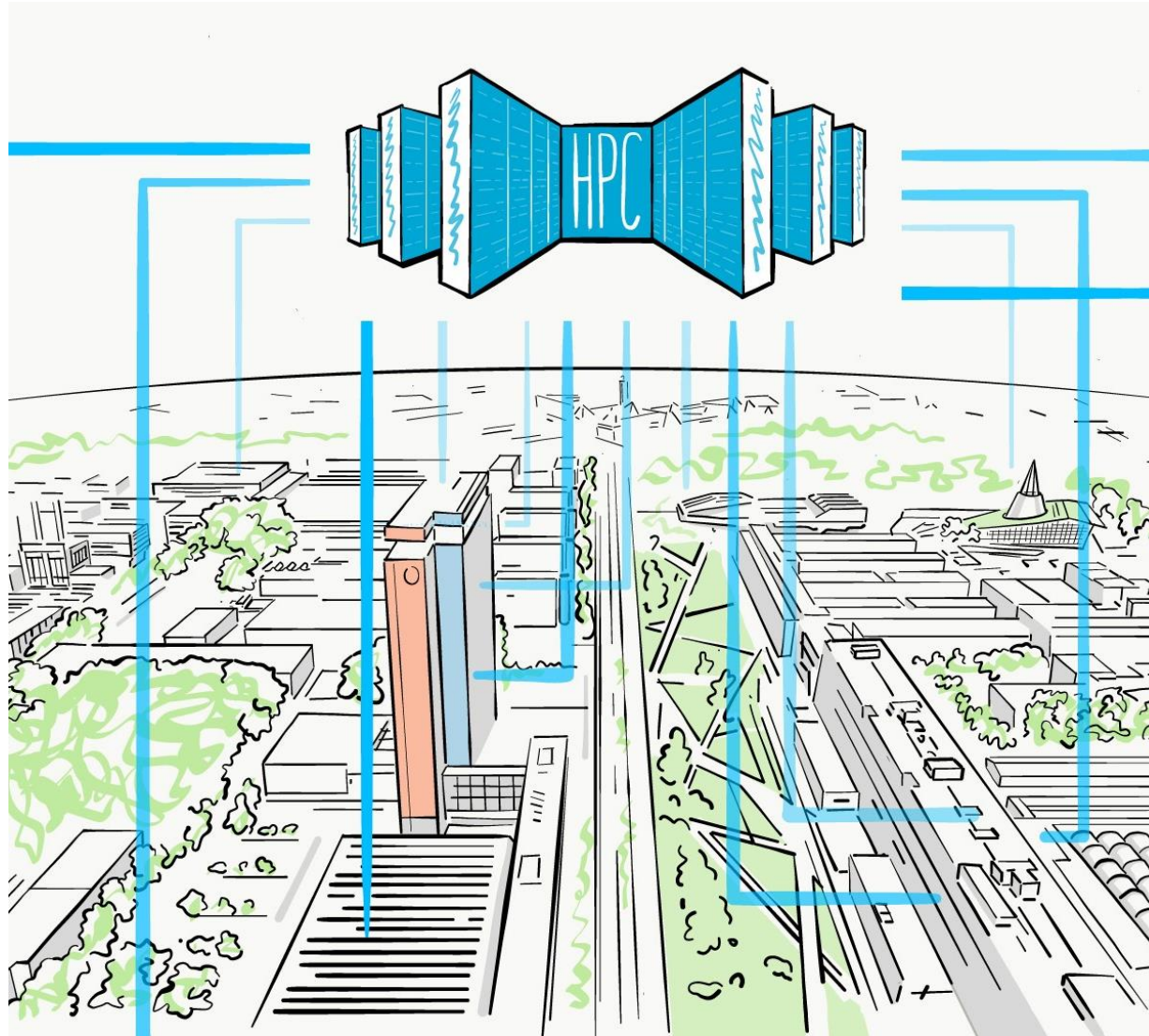


DelftBlue

- 10.000 CPU cores
- Over 200 compute nodes
- 10 GPU nodes



DelftBlue community: 3mE, ABE, AE, AS, CEG, EEMCS, IDE, TPM, QuTech



How do I work with cluster?

1. **Prepare input files for your code** on a personal computer
2. **Upload input files** and required data to the cluster's storage
3. **Determine** required **resources**
4. **Create job script**
5. **Submit** job(s) to scheduler
6. **Monitor** progress (via output files) and resource use (via statistics)
7. **Download** results to personal computer for further processing
8. **Cleanup** files

Typical submission script

- Create a job script in a file

```
#!/bin/sh

#SBATCH --job-name=job_name
#SBATCH --partition=compute
#SBATCH --account=research-eemcs-diam
#SBATCH --time=01:00:00
#SBATCH --ntasks=4
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1G

module load 2023r1
module load openmpi
srun ./executable > output.log
```

- system info: type of script
- select job name
- select partition to run your job on
- specify account
- request run time
- number of tasks (parallel)
- CPUs (threads) per task
- RAM per CPU
- Use DelftBlue software collection
- load openmpi module
- start tasks with srun

Example 1: Hello, World! on 4 CPUs

Our first submission script `helloworld.sh`:

```
#!/bin/bash
#SBATCH --job-name="01_hello"
#SBATCH --time=00:10:00
#SBATCH --partition=compute
#SBATCH --ntasks=4
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1GB
#SBATCH --account=education-eemcs-courses-linuxcli
#SBATCH --reservation=delftblueworkshop

echo "Hello, World!" >> helloworld.txt
echo "The following nodes are reporting for duty:" >> helloworld.txt
srun hostname >> helloworld.txt
echo "Have a great day!" >> helloworld.txt
```

Example 1: Hello, World! on 4 CPUs

```
NetID@login01:~ $ sbatch helloworld.sh
```

```
Hello, World!  
The following nodes are reporting for duty:  
cmpXXX  
cmpXXX  
cmpXXX  
cmpXXX  
Have a great day!
```

Example 1.2: Hello, World! On 2x2 CPUs

Our submission script `helloworld2nodes.sh`:

```
#!/bin/bash
#SBATCH --job-name="01_hello"
#SBATCH --time=00:10:00
#SBATCH --partition=compute
#SBATCH --nodes=2
#SBATCH --ntasks-per-node=2
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1GB
#SBATCH --account=education-eemcs-courses-linuxcli
#SBATCH --reservation=delftblueworkshop

echo "Hello, World!" >> helloworld.txt
echo "The following nodes are reporting for duty:" >> helloworld.txt
srun hostname >> helloworld.txt
echo "Have a great day!" >> helloworld.txt
```


Example 1.2: Hello, World! On 2x2 CPUs

```
NetID@login01:~ $ sbatch helloworld2nodes.sh
```

```
Hello, World!  
The following nodes are reporting for duty:  
cmpXXX  
cmpXXX  
cmpYYY  
cmpYYY  
Have a great day!
```

What is a scheduler?

```

2753413 compute KUS9e0 emadaï R 1-10:45:10 12 cmp[025,028,053,062,104-106,157,182,191,196-197]
2753412 compute KUS8e0 emadaï R 1-11:26:21 5 cmp[062,121,123,181,184]
2753410 compute KUS7e0 emadaï R 1-11:32:23 4 cmp[036,055-056,216]
2755343 compute gaT4War nikosvas R 16:10 1 cmp217
2753385 compute US11e000 emadaï R 1-14:34:15 13 cmp[010,016,021,030,037,054,069-070,158-159,195,212-213]
2753356 compute US10e000 emadaï R 1-18:45:28 21 cmp[002,018,065,084,087,095,101-103,105-106,109-110,125-127,129,162-164,182]
2753362 compute US11e000 emadaï R 1-18:43:25 9 cmp[016,109-110,134-136,174-176]
2753353 compute US9e000 emadaï R 1-19:31:59 12 cmp[008,019,066,077,093,115,118,134,150,163,181,183]
2753349 compute US6e000 emadaï R 1-19:42:11 6 cmp[097,173-175,190-191]
2753340 compute US0e000 emadaï R 1-19:45:14 10 cmp[046,107-110,124,173,201-203]
2753350 compute US7e000 emadaï R 1-19:42:11 13 cmp[009,025-026,030,082,085,093,099,109-110,129,161,195]
2753352 compute US8e000 emadaï R 1-19:40:09 8 cmp[009,011-012,064-065,207-209]
2753342 compute US1e000 emadaï R 1-19:44:13 5 cmp[169-173]
2753343 compute US2e000 emadaï R 1-19:44:13 11 cmp[036-039,157-159,204-207]
2753345 compute US3e000 emadaï R 1-19:44:13 5 cmp[085,140,199,215-216]
2753346 compute US4e000 emadaï R 1-19:43:12 7 cmp[061-064,115,136-137]
2753348 compute US5e000 emadaï R 1-19:43:12 5 cmp[003,014,058,088,093]
2753337 compute USm1e000 emadaï R 1-22:27:34 10 cmp[041-044,084,113,122-123,178,210]
2755699 compute ms-5_T_2 darshanr R 27:24 1 cmp122
2755698 compute ms-5_T_2 darshanr R 52:57 1 cmp158
2755697 compute ms-5_T_2 darshanr R 2:31:26 1 cmp012
2755696 compute ms-5_T_2 darshanr R 2:32:27 1 cmp201
2755695 compute ms-5_T_2 darshanr R 3:23:31 1 cmp122
2755694 compute ms-5_T_2 darshanr R 3:45:08 1 cmp022
2755692 compute ms-5_T_2 darshanr R 3:57:28 1 cmp144
2755693 compute ms-5_T_2 darshanr R 3:55:24 1 cmp025
2749288 compute M11 ydai2 R 4-01:45:13 50 cmp[004-006,016-019,026,047-055,066-067,069-070,074-076,084,104,107,109-110,114-115,
131-132,160-162,168-169,171-172,182,190,194-195,202-204,213,217-218]
2749330 compute M110 ydai2 R 4-01:35:12 36 cmp[007-011,020-022,072-073,081-082,091,095-099,116-120,152-157,163-166,210-212]
2757611 compute fmT4man nikosvas R 37:36 1 cmp167
2757612 compute fmT4war nikosvas R 36:35 1 cmp195
2753175 compute IPMC atajeddi R 2-00:47:23 4 cmp[116-119]
2756707 compute Q1 jjgreep R 9:55:20 1 cmp198
2756838 compute mcts_dis gmeppeli R 9:45:42 1 cmp041
2756448 compute random-w sajvanle R 11:20:27 1 cmp044
2756447 compute random-5 sajvanle R 12:11:13 1 cmp069
2756446 compute random-w sajvanle R 12:21:51 1 cmp134
2756445 compute random-w sajvanle R 12:28:16 1 cmp187
2756444 compute random-4 sajvanle R 13:45:02 1 cmp180
2757149 compute t_bin arodrigu R 15:05:59 1 cmp177
2757291 compute param arodrigu R 10:08:51 1 cmp068
2756837 compute mcts_dis gmeppeli R 18:15:47 1 cmp160
2756836 compute mcts_dis gmeppeli R 18:36:56 1 cmp131
2756835 compute mcts_dis gmeppeli R 18:38:00 1 cmp131
2756834 compute mcts_dis gmeppeli R 18:43:18 1 cmp159

```

Typical scheduler commands?

- Submit job using the job script

```
$ sbatch jobscript.sbatch
Submitted batch job 290573
```

- See queue status

```
$ squeue
JOBID PARTITION      NAME                USER ST  TIME
290573 general      jobscrip          somebody R   0:01
```

- See job output

```
$ cat slurm-290573.out
Hello world!
```

- Cancel job

```
$ scancel 290573
$ squeue
JOBID PARTITION      NAME                USER ST  TIME
NODES NODELIST(REASON)
```

Module system demo

```
[NetID@login02 ~]$ module avail
```

→ list available modules

```
[NetID@login02 ~]$ module load
```

→ load module

```
[NetID@login02 ~]$ module list
```

→ list loaded modules

```
[NetID@login02 ~]$ module spider {module}
```

→ find module {module}

More info: <https://doc.dhpc.tudelft.nl/delftblue/DHPC-modules/>

Example 2: Julia

Let's prepare a little program to draw a Mandelbrot set:

```
function mandelbrot(a)
    z = 0
    for i=1:50
        z = z^2 + a
    end
    return z
end

for y=1.0:-0.05:-1.0
    for x=-2.0:0.0315:0.5
        abs(mandelbrot(complex(x, y))) < 2 ? print("*") :
print(" ")
    end
    println()
end
```


Example 2: Julia

Submission script `run_julia_mandelbrot.sh`:

```
#!/bin/bash
#
#SBATCH --job-name="julia"
#SBATCH --time=00:10:00
#SBATCH --partition=compute
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1G
#SBATCH --account=education-eemcs-courses-linuxcli
#SBATCH --reservation=delftblueworkshop

module load 2023r1
module load julia

srun julia mandelbrot.jl
```

Example 2: Julia

Let's submit the job and check out the result:

Let's submit the job and check out the result:

[illegible]

Example 3: ASE molecules generator

Let's install a new python module, called ASE:

```
#!/bin/bash

# Install ASE:
module load 2023r1
module load python
module load py-pip
module load py-numpy
module load py-scipy
module load py-matplotlib

python -m pip install --user ase
```

```
[NetID@login02 ~]$ chmod +x install_ase.sh
```

```
[NetID@login02 ~]$ ./install_ase.sh
```

Example 3: ASE molecules generator

Submission script `sub_to_queue.sh`:

```
#!/bin/bash#
#SBATCH --job-name="gen_mol"
#SBATCH --time=00:10:00
#SBATCH --partition=compute
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1GB
#SBATCH --account=education-eemcs-courses-linuxcli
#SBATCH --reservation=delftblueworkshop

module load 2023r1
module load python
module load py-numpy
module load py-scipy
module load py-matplotlib

srun python gen_mol_folders.py
```

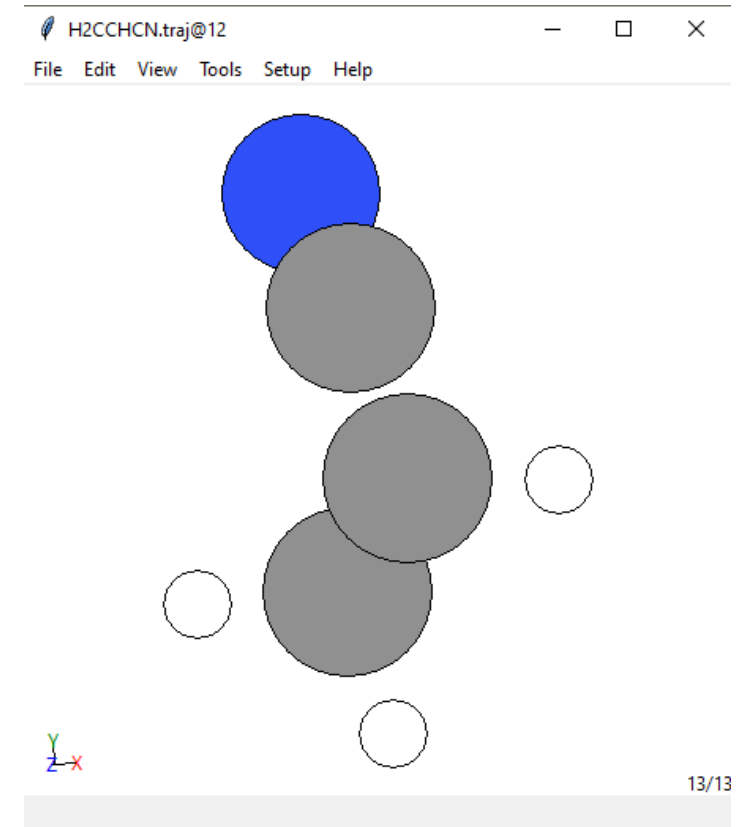
Example 3: ASE molecules generator

```
[NetID@login02 ~]$ sbatch sub_to_queue.sh
```

```
[NetID@login02 ~]$ cat slurm-XXX.out
```

Exercise:

Install ASE. Submit the job. Inspect the output file and generated folders.



References

- Documentation:

<https://www.tudelft.nl/dhpc/documentation>

- Mattermost:

<https://mattermost.tudelft.nl/dhpc/>

- Self Service Portal (TopDesk):

<https://tudelft.topdesk.net>

- DCSE Courses:

<https://www.tudelft.nl/cse/education/courses>

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NOVEMBER 2023 17:00

Programming on the GPU with
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16 NOVEMBER 2023 09:30 T/M
16:30

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