Dennis Palagin 27 June 2022





- Recap: what is a cluster computer
- Accessing the system
- File systems and data transfer
- Queuing, accounting
- Module system (Imod)
- When (not to) use srun/mpirun/mpiexec
- Practical exercise



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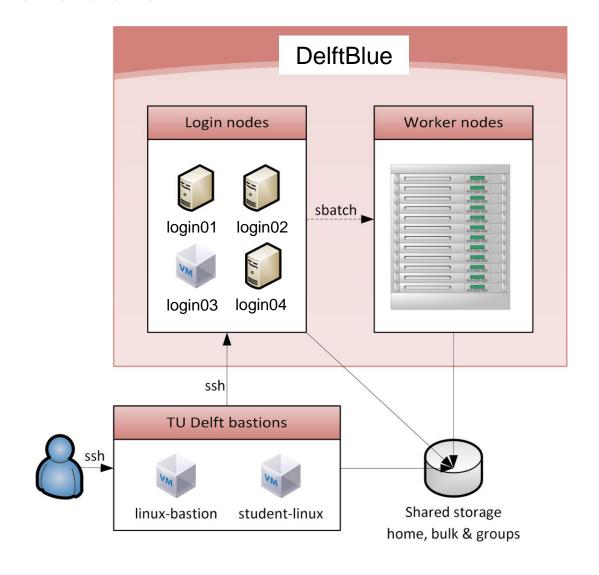


What is a cluster?

- Collection of (large) computing resources:
 - Processors (CPUs)
 - Graphics processors (GPUs)
 - Memory
 - Storage
- Shared with other users
- Makes it possible to:
 - Schedule lots of jobs
 - Do a lot of computational work
 - Use a lot of threads
 - Run long computations
 - Use multiple computers together
 - Compute on big data sets
 - Use GPUs when your own computer doesn't have one



What is a cluster?





DelftBlue

- Fast and flexible
- With a peak performance over 1 petaflop/s
- 10.000 CPU cores
- Over 200 compute nodes, 10 GPU nodes based on Nvidia Tesla v100 and 2 special nodes for interactive work.
- High-Speed Interconnect based on Mellanox InfiniBand
- And a 700TB high-speed parallel storage subsystem



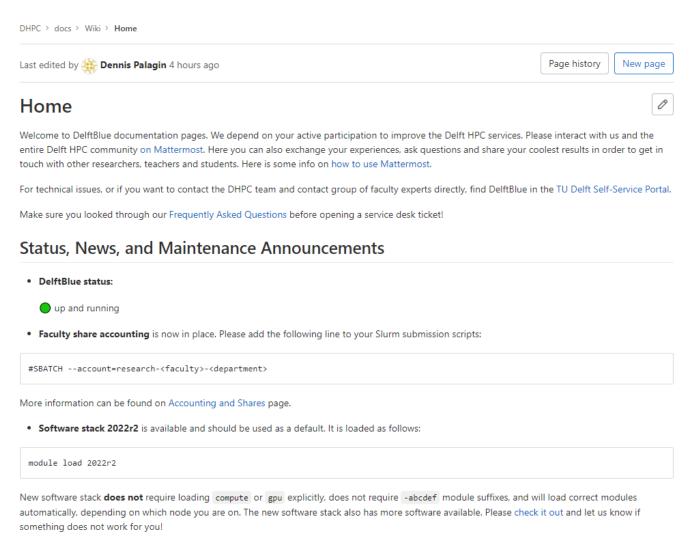


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Wiki:

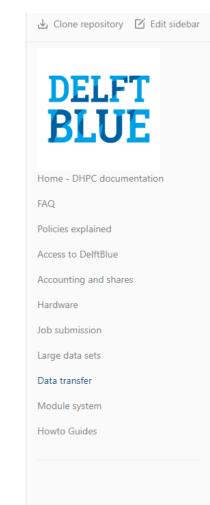
Website: https://www.tudelft.nl/dhpc/documentation





Upcoming maintenance:

12 July, from 11:00 to 17:00, DelftBlue will not be running any jobs due to maintenance. Login nodes and storage will be available.



ssh

Anyone with TU Delft <netid> should be able to SSH to DelftBlue:

```
user@laptop:~ $ ssh <netid>@login.delftblue.tudelft.nl
```

This will log you in into one of the four login nodes (login01, login02, login03, or login04). Your home directory is directly accessible (via /home/<netid>/):



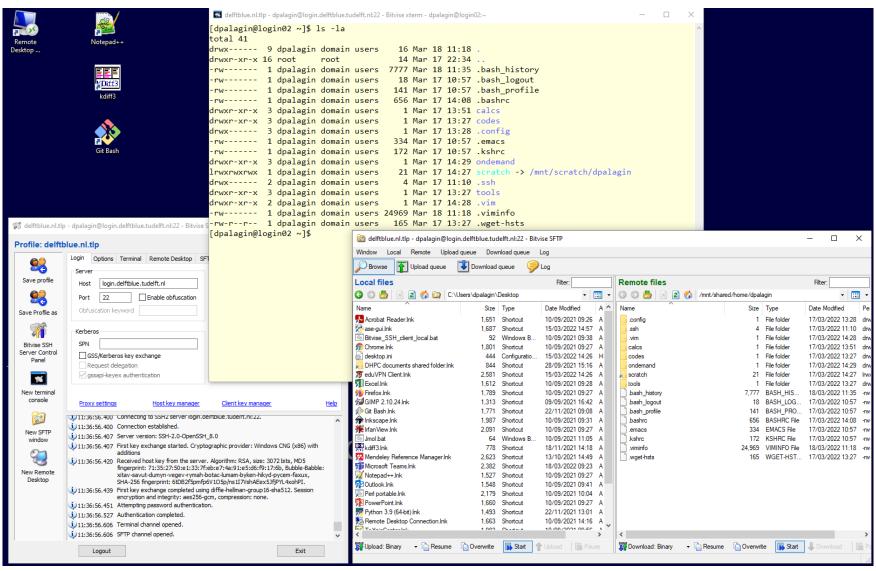
Jumping via bastion

Important note: a direct SSH to DelftBlue from outside of the university network is impossible! For the access from outside of the university network, you have two options:

- 1. Use TU Delft's EduVPN. Once connected via VPN, you can SSH to DelftBlue directly.
- 2. It is also possible to access DelftBlue without VPN, via the so-called linux-bastion server.

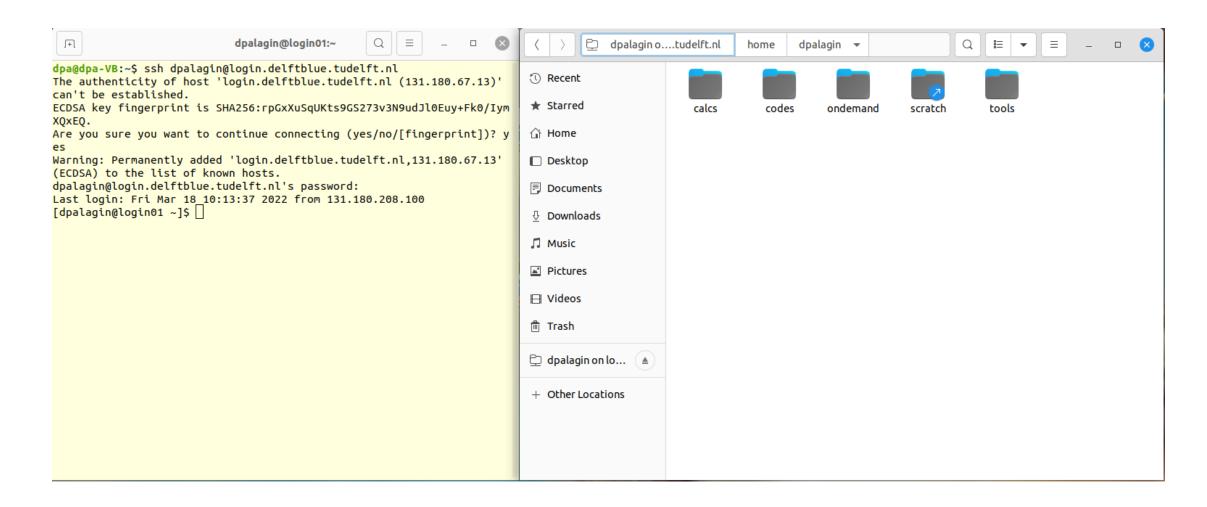


Graphical tools Windows: PuTTy, Bitvise SSH, MobaXterm, etc...



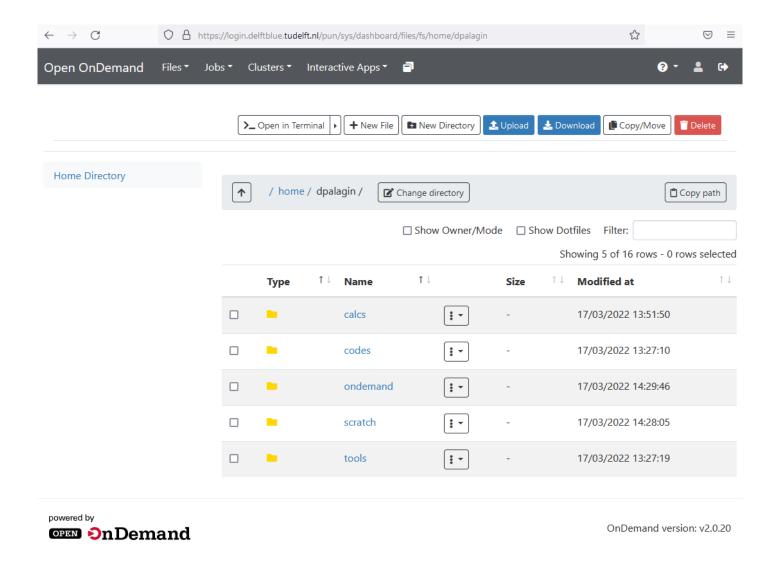


Graphical tools Linux: ssh in terminal + sftp via file manager





Web tools: OpenOnDemand





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scp

1. Transfer a file from your computer to DelftBlue:

```
user@laptop:~ $ scp localfile <netid>@login.delftblue.tudelft.nl:~/destination_on_DelftBlue/
```

2. Transfer a folder from your computer to DelftBlue:

```
user@laptop:~ $ scp -r localfile <netid>@login.delftblue.tudelft.nl:~/destination_on_DelftBlue/
```

3. Transfer a file from DelftBlue to your computer:

```
user@laptop:~ $ scp <netid>@login.delftblue.tudelft.nl:~/folder_on_DelftBlue/remotefile ./
```

4. Transfer a folder from DelftBlue to your computer:

```
user@laptop:~ $ scp -r <netid>@login.delftblue.tudelft.nl:~/folder_on_DelftBlue ./
```

rsync

rsync does not just blindly copy files, but instead synchronizes the source with the destination:

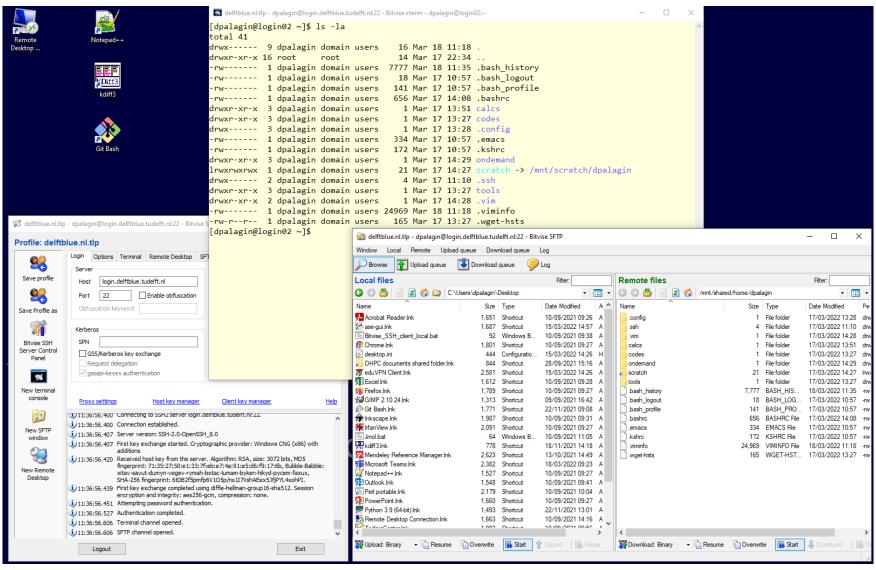
```
user@laptop:~ $ rsync -av ${source} ${target}
```

Please note: some file/folder permissions might not be compatible with project drives, e.g. on staff-umbrella. If you get rsync: failed to set permissions error when e.g. rsync'ing to your project drive, please use the --no-perms flag, e.g.:

```
user@laptop:~ $ rsync -av --no-perms ${source} ${target-on-network-drive}
```

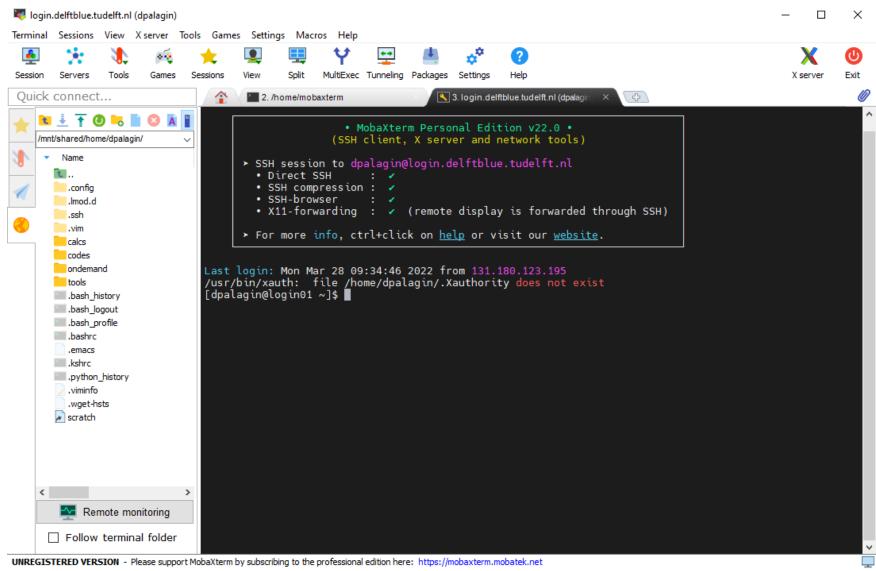


Graphical tools Windows: Bitvise SSH client



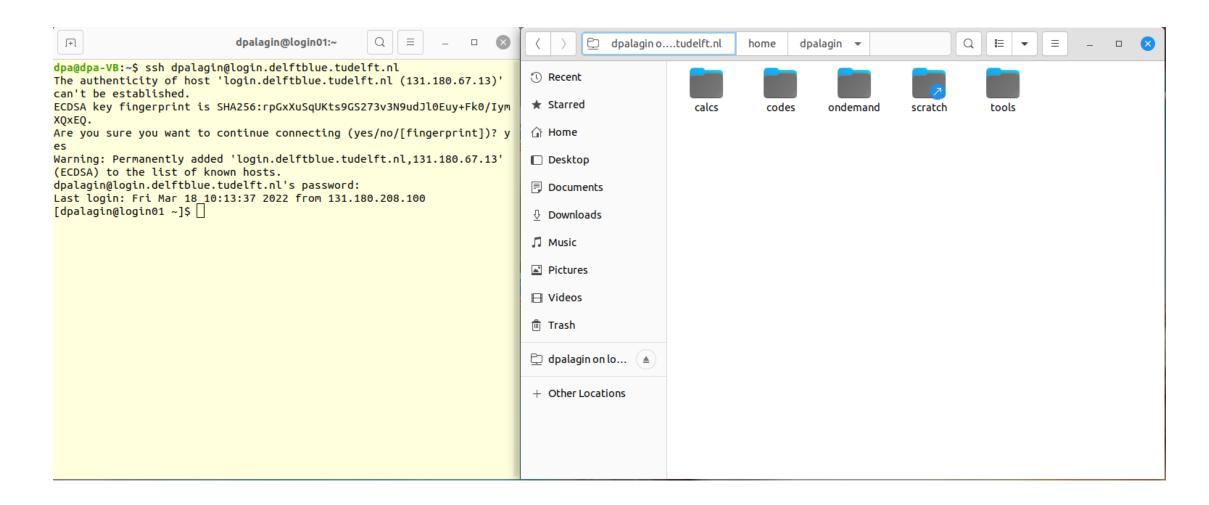


Graphical tools Windows: MobaXterm



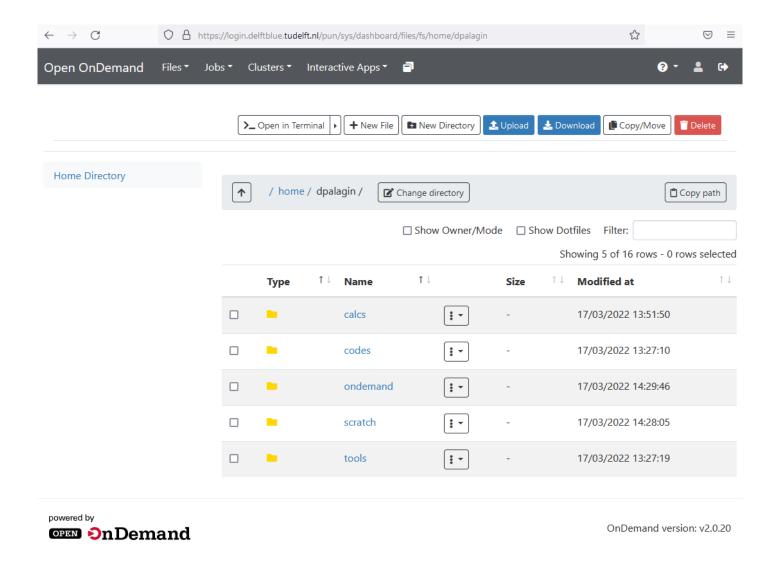


Graphical tools Linux: sftp via file manager





Web tools: OpenOnDemand





Network drives

```
[NetID@login02 tudelft.net]$ ls -1
total 104
drwxr-xr-x 12 root root 4096 Mar 16 15:16 staff-bulk
drwxr-xr-x 13 root root 4096 Mar 16 15:16 staff-groups
drwxr-xr-x 28 root root 4096 Mar 17 11:18 staff-homes
drwxr-xr-x 28 root root 4096 Mar 17 11:18 staff-homes-linux
drwxr-xr-x 1674 root root 65536 Mar 17 11:18 staff-umbrella
drwxr-xr-x 12 root root 4096 Mar 17 11:18 student-groups
drwxr-xr-x 28 root root 4096 Mar 17 11:18 student-homes
drwxr-xr-x 28 root root 4096 Mar 17 11:18 student-homes-linux
```



File transfer nodes

```
[NetID@login02 ~]$ sinfo
PARTITION AVAIL
                        NODES STATE NODELIST
               TIMELIMIT
           up infinite
compute*
                                 idle cmp[001-218]
                           226
           up infinite
                                 idle gpu[001-010]
                            10
gpu
           up infinite
                                 idle mem[001-010]
                            10
memory
                                 idle file[01-02]
                infinite
trans
           up
                infinite
                                 idle visual[01-02]
visual
           up
```

```
#!/bin/sh
#
#SBATCH --job-name="js_data"
#SBATCH --partition=trans
#SBATCH --time=01:00:00
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=1
rsync -av --no-perms /tudelft.net/staff-umbrella/<my-project-name>/data_folder
/scratch/<netid>/
```



Exercise 101

ssh to DelftBlue

```
user@laptop:~ $ ssh NetID@login.delftblue.tudelft.nl
```

copy (rsync) /scratch/dpalagin/DelftBlueWorkshop/ to your own /scratch

NetID@login01:~ \$ rsync -av /scratch/dpalagin/DelftBlueWorkshop /scratch/\$USER/



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What is a scheduler?

34101180	kchoudhu	pr89	5vb2 ctd unfol	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	16	192
34101393	kchoudhu		5vb2 ctd unfol		Priority	Tomorr	20:15	0:00	1-	00:00:00	16	192
34101545	ykarami	pr118	IgG1C1	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	6	72
34101588	ykarami	pr118	IgG3-1C1		Priority	Tomorr	20:15	0:00	1-	00:00:00	6	72
34101854	mperisdi	pr107	Debug	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	3	3
34102044	calleva	pr89	4q4g	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34102045	calleva	pr89	4g4q	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34102780	asridhar	pr89	Kv3_WT	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	12	144
34102782	asridhar	pr89	Kv3_WT_2	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	12	144
34102783	asridhar	pr89	D120_V253	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34102784	asridhar	pr89	D120_V253_2	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34102785	asridhar	pr89	F256A	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34102786	asridhar	pr89	F256A_2	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34102787	asridhar	pr89	gaba5	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	12	144
34102788	asridhar	pr89	gaba4	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	12	144
34102792	asridhar	pr89	gaba6	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	12	144
34102827	mbiliche	pr66	Gkclp5_825	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	25	300
34102868	mbiliche	pr66	Gkclp4_866	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	25	300
34102902	mbiliche	pr66	Gkclp3_854	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	25	300
34103693	kchoudhu	pr89	5vb2_ctd_unfol	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	16	192
34105695	akumawat	pr117	ICA-SOFT-AB2.1	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34105696	akumawat	pr117	ICA-SOFT-AB2.2	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34105700	akumawat	pr117	ICA-SOFT-AB2.3	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34105736	akumawat	pr117	MUT-NSc-AB2.9	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34105739	akumawat	pr117	MUT-NSc-AB2.10	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34105795	ykarami	pr118	IgG3-2C1	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	6	72
34105821	akumawat	pr117	AMB19-AB2.1	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	96
34108696	ykarami	pr118	MTDP	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	100	1200
34108877	ykarami	pr118	IgG3-1C2	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	6	72
34111511	sfurini	pr107	e4f	PD	Priority	Tomorr	20:15	0:00	1-	00:00:00	8	192
34087143	ykarami	pr118	IgG1B3	CG	None	Ystday	12:28	20:54:35		3:05:25	1	144
dpalagin@	daint105:	~>										



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)
- Download results to personal computer for further processing
- 8. Cleanup files



Typical commands?

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=24
#SBATCH --cpus-per-task=1
#SBATCH --mem-per-cpu=1GB
module load 2022r2
module load openmpi
srun ./executable > output.log
```

- → select name
- → select partition
- → specify account
- → request run time
- → number of tasks (parallel)
- → CPUs (threads) per task
- → request memory
- → Use DelftBlue software collection
- → load openmpi module
- → start tasks with srun



Typical commands?

- Log in to one of the login nodes
- Submit job using the job script

```
$ sbatch jobscript.sbatch
Submitted batch job 1
```

See queue status

```
$ squeue
JOBID PARTITION NAME USER ST TIME

1 general jobscrip somebody R 0:01
```

See job output

```
$ cat slurm-1.out
Hello world!
```

Cancel job

```
$ scancel 1
$ squeue

JOBID PARTITION NAME USER ST TIME
NODES NODELIST(REASON)
```



What do I need to know about accounting?

```
#!/bin/sh
#SBATCH --account=innovation
#SBATCH --account=research-eemcs-diam
#SBATCH --account=education-eemcs-msc
```



Example 1.1: Hello, World! on 8 CPUs

Our first submission script helloworld.sh:

```
#!/bin/bash
#SBATCH --job-name="01 hello"
#SBATCH --time=00:10:00
#SBATCH --ntasks=8
#SBATCH --cpus-per-task=1
#SBATCH --partition=compute
#SBATCH --mem=1GB
#SBATCH --account=innovation
#SBATCH --reservation=db-workshop
cd $SLURM SUBMIT DIR
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 1.1: Hello, World! on 8 CPUs

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

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



Example 1.2: Hello, World!

Our submission script helloworld2nodes.sh:

```
#!/bin/bash
#SBATCH --job-name="01 hello"
#SBATCH --time=00:10:00
#SBATCH --nodes=2
#SBATCH --ntasks-per-node=4
#SBATCH --cpus-per-task=1
#SBATCH --partition=compute
#SBATCH --mem=1GB
#SBATCH --account=innovation
#SBATCH --reservation=db-workshop
cd $SLURM SUBMIT DIR
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!

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

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



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Module system demo

```
[NetID@login02 ~]$ module avail
[NetID@login02 ~]$ module load
[NetID@login02 ~]$ module unload
[NetID@login02 ~]$ module list
[NetID@login02 ~]$ module spider {module}
```

- → list available modules
- → load module
- → unload module
- → list loaded modules
- → find module {module}

Trilinos example: https://gitlab.tudelft.nl/dhpc/docs/-/wikis/DHPC-modules



Let's prepare the R script generate. R to generate normal data sets:

```
options(bitmapType='cairo')
arg = commandArgs(TRUE)
samples = rep(NA, 100000)
for ( i in 1:100000 ) { samples[i] = mean(rexp(40, 0.2)) }
pdf(paste('plots/', arg, '.pdf', sep=""))
hist(samples, main="", prob=T, color="darkred")
lines(density(samples), col="darkblue", lwd=3)
dev.off()
```



Now let's prepare the submission script R_submit.sh:

```
#!/bin/bash
#SBATCH --job-name="02 R hist"
#SBATCH --time=00:10:00
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=1
#SBATCH --partition=compute
#SBATCH --mem=1GB
#SBATCH --account=innovation
#SBATCH --reservation=db-workshop
cd $SLURM SUBMIT DIR
mkdir plots
srun R --vanilla -f generate.R --args "plot$SLURM_ARRAY_TASK_ID"
```



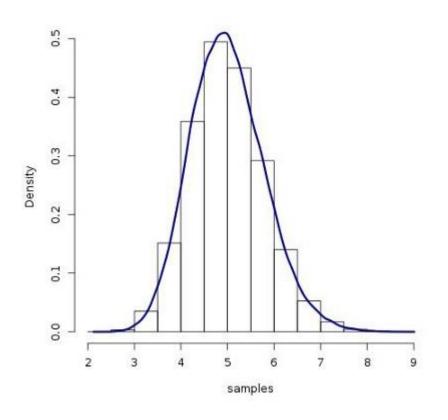
Finally, let's run the job:

```
NetID@login01 :~ $ sbatch --array=[1-8] R_submit.sh
```

And monitor the queue:

```
NODES NODELIST(REASON)
     JOBID PARTITION
                         NAME
                                  USER ST
354 [11-50] mycluster R submit
                                                         1 (Resources)
                                    pi PD
                                                0:00
     354_9 mycluster R_submit
                                    pi R
                                                0:02
                                                         1 cnat
    354 10 mycluster R submit
                                    pi R
                                               0:02
                                                         1 cnat
     354_1 mycluster R_submit
                                    pi R
                                                0:18
                                                         1 p1
     354 2 mycluster R submit
                                    pi R
                                                0:18
                                                         1 p2
     354_3 mycluster R_submit
                                    pi R
                                                0:18
                                                         1 p3
     354 4 mycluster R submit
                                                         1 p4
                                    pi R
                                                0:18
```







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When (not to) use srun/mpirun/mpiexec

Always use **srun** with parallel executables relying on mprun/mpiexec



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ASE molecules generator

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

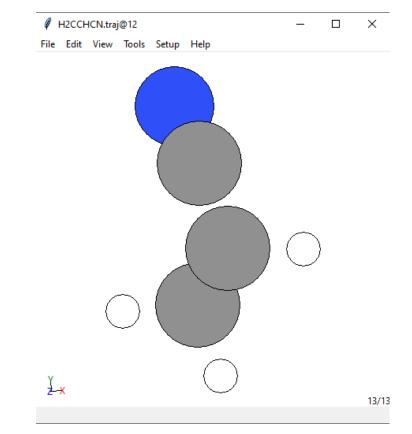
[NetID@login02 ~]$ sbatch sub_to_queue.sh

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

Exercise:

- 1. Submit the job. Inspect the output file and generated folders.
- 2. rsync resulting folders to your staff-home.
- 3. Submit the job again. Can you see what is different in the output now?
- 4. rsync resulting folders to your staff-home once again.







Discussion and questions

Thanks for your attention

