Introduction to DelftBlue

Dennis Palagin 20 September 2024





Practical use of DelftBlue

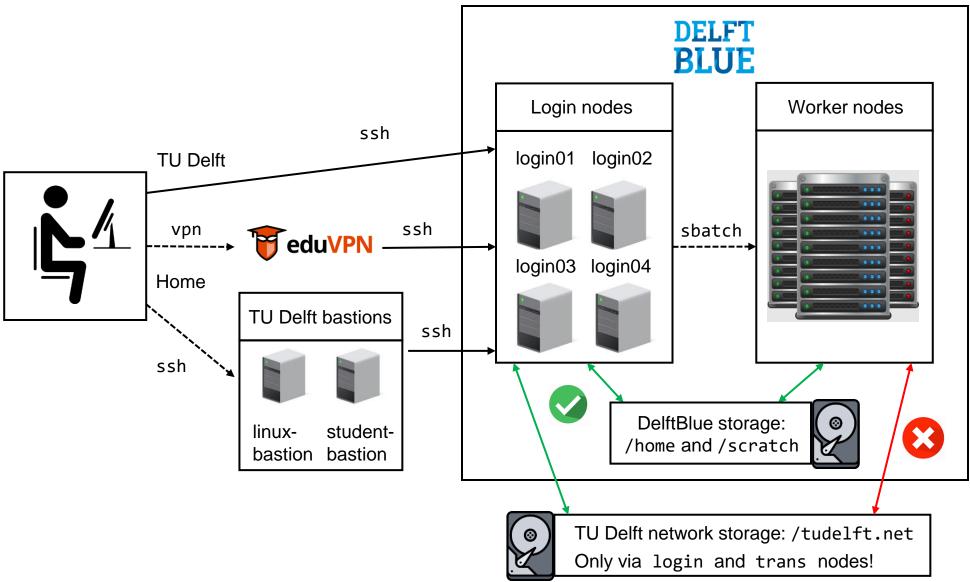
- Recap: what is a cluster computer
- DHPC and DelftBlue: organization
- Accessing the system
- File systems and data transfer
- Queuing, accounting
- Module system (Imod)



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DelftBlue

- Fast and flexible
- 16.000 CPU cores
- 20 GPU nodes
- High-Speed Interconnect based on Mellanox InfiniBand
- And a 700TB high-speed parallel storage subsystem



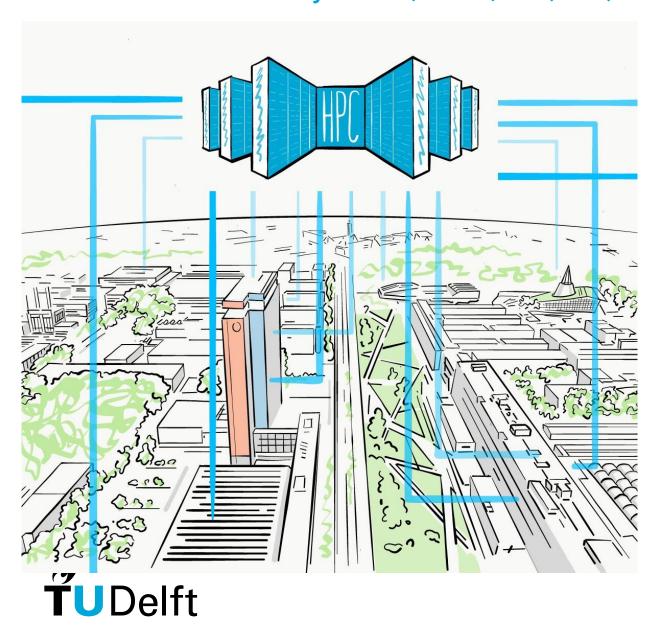


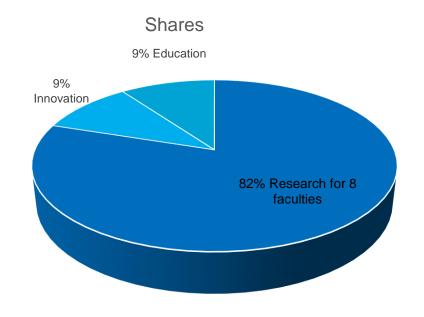
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DelftBlue community: 3mE, ABE, AE, AS, CEG, EEMCS, IDE, TPM, QuTech





December A.E./I.D	4.20/
Research AE/LR	12%
Research EEMCS/EWI	12%
Research TPM/TBM	12%
Research CEG/CiTG	12%
Research 3mE	12%
Research AS/TNW	12%
Research ABE/BK	6%
Research IDE/IO	2%
Research Qutech	2%
Education	9%
Innovation	9%
	100%

Documentation:

Documentation:

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

Mattermost:

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

Self Service Portal (TopDesk):

https://tudelft.topdesk.net

Training and courses:

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



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ssh

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

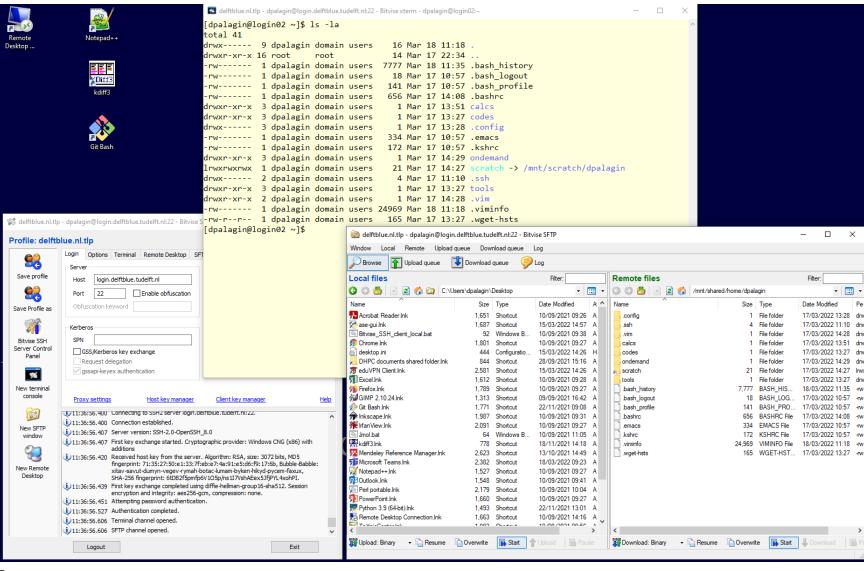
```
user@laptop:~ $ ssh <netid>@login.delftblue.tudelft.nl
```

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>/):



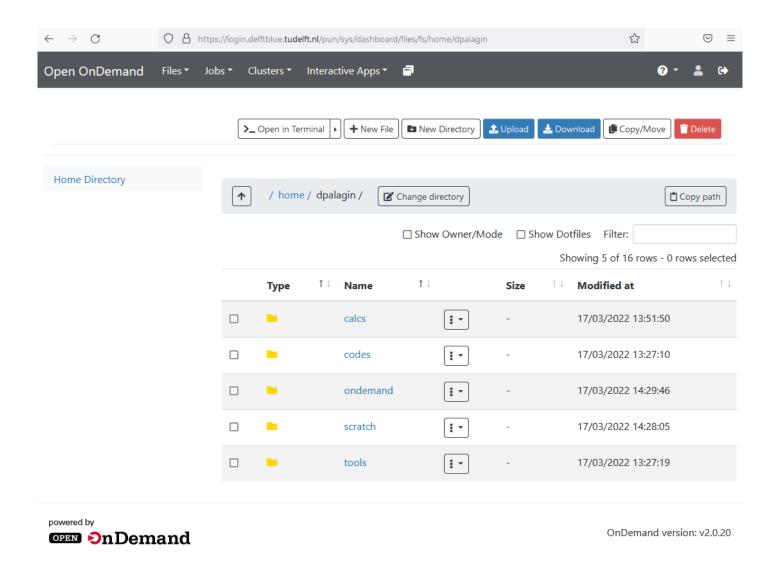
Graphical tools Windows: PuTTy, Bitvise SSH, MobaXterm,

etc...





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 ./
```

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
```



Exercise 101

ssh to DelftBlue

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

- Download exercises from https://doc.dhpc.tudelft.nl/delftblue/
- Copy to DelftBlue and unzip.



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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		pr107	Debug		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		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=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



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)
```



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 --ntasks=4
#SBATCH --cpus-per-task=1
#SBATCH --partition=compute
#SBATCH --mem=1GB
#SBATCH --account=Education-EEMCS-Courses-WI4049TU
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
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=2
#SBATCH --cpus-per-task=1
#SBATCH --partition=compute
#SBATCH --mem=1GB
#SBATCH --account=Education-EEMCS-Courses-WI4049TU
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
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://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("*")</pre>
: 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-WI4049TU
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 prepare a little program to calculate number pi in Python called calculate_pi.py:

```
from mpi4py import MPI
from math import pi as PI
from numpy import array
def comp_pi(n, myrank=0, nprocs=1):
    h = 1.0 / n
    s = 0.0
    for i in range(myrank + 1, n + 1, nprocs):
        x = h * (i - 0.5)
        s += 4.0 / (1.0 + x**2)
    return s * h
def prn pi(pi, PI):
    message = "pi is approximately %.16f, error is
%.16f"
    print (message % (pi, abs(pi - PI)))
```



```
comm = MPI.COMM WORLD
nprocs = comm.Get size()
myrank = comm.Get rank()
n = array(0, dtype=int)
pi = array(0, dtype=float)
mypi = array(0, dtype=float)
if myrank == 0:
   n = 20 # Enter the number of intervals
   n.fill(_n)
comm.Bcast([n, MPI.INT], root=0)
_mypi = comp_pi(n, myrank, nprocs)
mypi.fill(_mypi)
comm.Reduce([mypi, MPI.DOUBLE], [pi, MPI.DOUBLE],
            op=MPI.SUM, root=0)
if myrank == 0:
   prn_pi(pi, PI)
```



Submission script sub_calc_pi.sh:

```
#!/bin/bash
#SBATCH --job-name="Py pi"
#SBATCH --time=00:10:00
#SBATCH --ntasks=4
#SBATCH --cpus-per-task=1
#SBATCH --partition=compute
#SBATCH --mem-per-cpu=1G
#SBATCH --account=Education-EEMCS-Courses-WI4049TU
module load 2023r1
module load openmpi
module load python
module load py-numpy
module load py-mpi4py
srun python calculate pi.py
```



Let's submit the job:

```
user@login01:~ $ sbatch sub_calc_pi.sh
```

And check out the result:

```
pi is approximately 3.1418009868930934, error is
0.0002083333033003
```



Example 4: 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 4: ASE molecules generator

Now we are able to run our script:

```
# Import modules:
import os
import sys
import subprocess
import ase
from ase.io import read, write
from ase.build import molecule
from ase.optimize import BFGS
from ase.calculators.emt import EMT
def main():
    # Print info:
    info = """
    This script does the following:
    1. Creates a parent directory "molecules".
    2. Reads an array of molecules and does the following steps for each molecule:
        3. Creates a sub-directory for current molecule.
        4. Generates .xyz file containing Cartesian coordinates of current molecule.
        5. Decides if to write or to append the .log file.
        6. Optimizes the initial geometry of current molecule with EMT and ...
        6. ... writes optimization .log and ASE trajectory files for current molecule.
    11 11 11
    print(info)
```

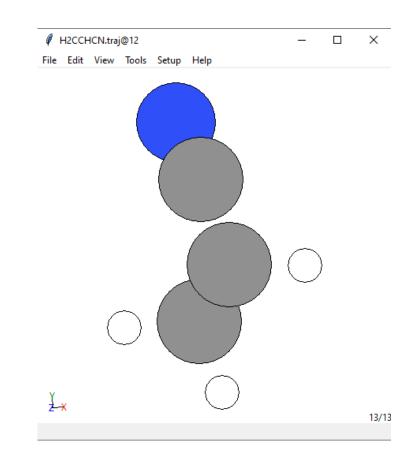
Example 4: ASE molecules generator

[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.





(Bonus) Example 5: PyTorch

Let's prepare a little program to check how many GPUs are available to us:

```
import torch
cuda avail = torch.cuda.is available()
if cuda avail:
        print("Torch CUDA is available")
        num of devices = torch.cuda.device count()
        if num of devices:
            print("Number of CUDA devices: {}".format(num_of_devices))
            current device = torch.cuda.current device()
            current device id = torch.cuda.device(current device)
            current device name = torch.cuda.get device name(current device)
            print("Current device id: {}".format(current_device_id))
            print("Current device name: {}".format(current_device name))
        else:
            print("No CUDA devices!")
else:
        print("Torch CUDA is not available!")
```



(Bonus) Example 5: PyTorch

Submission script sub_pytorch_gpus.sh:

```
#!/bin/bash
#
#SBATCH --job-name="PyTorch"
#SBATCH --time=00:10:00
#SBATCH --ntasks=1
#SBATCH --cpus-per-task=1
#SBATCH -gpus-per-task=1
#SBATCH --partition=gpu
#SBATCH --mem=4G
#SBATCH --account=Education-EEMCS-Courses-WI4049TU
module load 2023r1
module load openmpi
module load py-torch
srun python test pytorch gpus.py
```



(Bonus) Example 5: PyTorch

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

```
Torch CUDA is available
Number of CUDA devices: 1
Current device id: <torch.cuda.device object at 0x155555379dc0>
Current device name: Tesla V100S-PCIE-32GB
```



Discussion and questions

Thanks for your attention

