

INTRODUCTION

- What it is
- Why we need it
- How we use it

My_first_job.sl

- Log in
- Navigate folder
- Upload data
- Submit job
- Download results

Resources and example code are

here: https://github.com/BIAPT/Tutorial Compute Canada.git

Preparation:

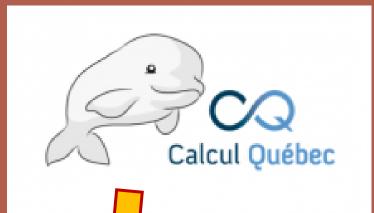
Windows users need to install this:

https://ubuntu.com/tutorials/ubuntu-on-windows#1-overview

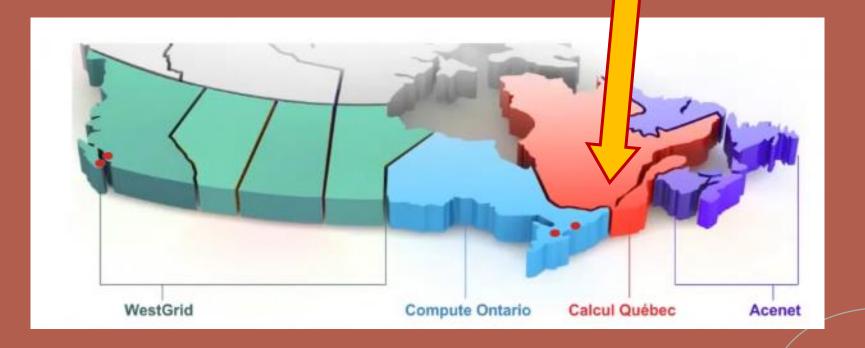
(follow the steps on the website and set up a password)

- Resources and example code are
 here: https://github.com/BIAPT/Tutorial Compute Canada.git
- For the detailed documentation, please refer to this: https://docs.computecanada.ca/wiki/Getting_started
- For further, more technical tutorials, have a look at this: https://www.youtube.com/watch?v=J9VCHe1ovBg

What it is

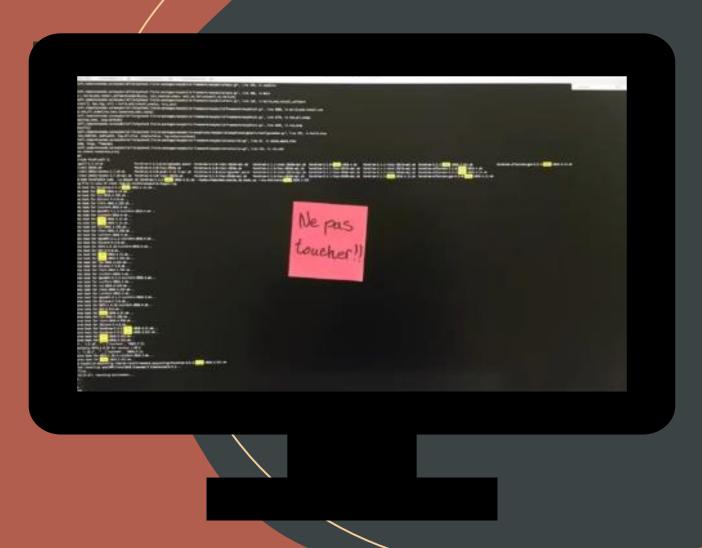


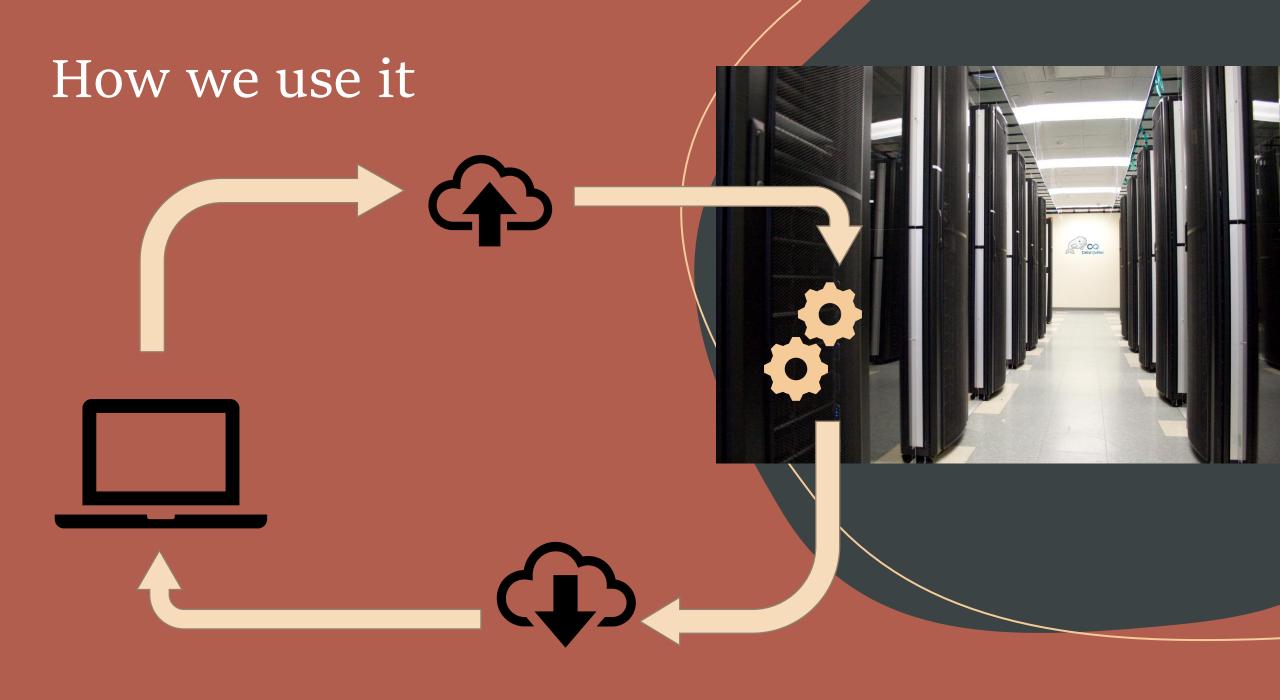




Why we need it

- Large amount of data
- Large amount of computation
- Limited time
- Limited resources





Log in:

WINDOWS:

- Open UBUNTU Terminal

- type:

MAC:

- open terminal

- type:

lotte@Horst:~\$ ssh lotte@beluga.computecanada.ca

Your account name The cluster in Montréal

- Type your password (hidden text)
- Press ENTER

- Type your password (hidden text)
- Press ENTER

Log out:

[lotte@beluga3 Dim_DOC]\$ exit
logout
Connection to beluga.computecanada.ca closed.
lotte@Horst:/mnt/c/Users/User/Desktop\$

Log in:

Welcome to Beluga!

[lotte@beluga2 ~]\$

```
lotte@Horst:~$ ssh lotte@beluga.computecanada.ca
lotte@beluga.computecanada.ca's password:
Last login: Sun Jan 17 22:58:38 2021 from modemcable012.187-179-173.mc.videotron.ca
                                   Bienvenue sur Béluga / Welcome to Béluga
                                  Aide/Support:
                                                   support@calculcanada.ca
                                   Globus endpoint: computecanada#beluga-dtn
                                                   docs.calculcanada.ca
                                   Documentation:
2020-10-01
             Mode turbo des CPU - CPU Turbo Mode
(FR) Le mode turbo des CPU est maintenant activé pour les noeuds GPU et les
noeuds à 752 Go de mémoire-vive. Le temps de calcul peut donc varier selon
la charge de calcul sur le noeud de calcul.
(EN) The CPU turbo mode is now enabled on all GPU nodes and all 752 GB
large-memory CPU nodes. The compute time may vary according to the compute
load on the compute node.
```

Log in:

Welcome to Beluga!





Navigate folders:

Navigation commands

pwd print working directory

- cd change directory (go to)

- cd .. Change directory (step outside)

- Is list

- mkdir make directory

- rm remove (add -r if directory)

→ Navigate to your personal project folder and create a directory called "Test_project" (don't use spaces or / or . In a foldername)

Prepare code:

- Each job needs a corresponding slurm file.
- This specifies how much time and power your job needs and gives you a place in the waiting line
- Never try to run jobs on the login node (it will make everything really slow)





Login NODE





Prepare code:

- Each job needs a corresponding slurm file.
- This specifies how much time and power your job needs and gives you a place in the waiting line



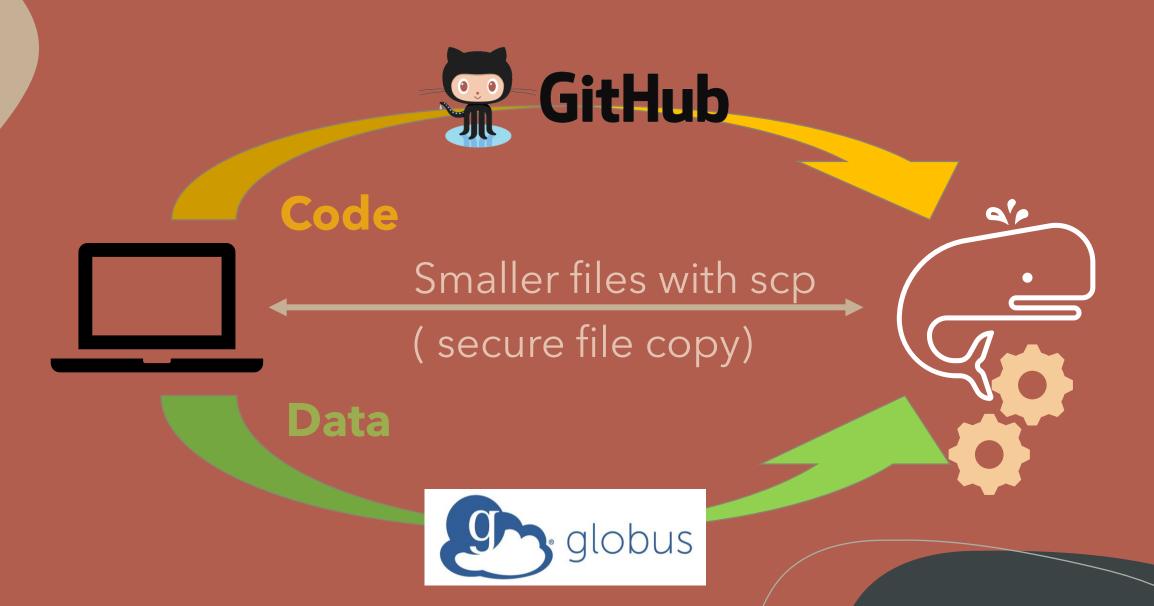
→ Prepare your own slurm files

Prepare code:

```
README 🖾 📙 README 🖾 🔚 CC_test.sl 🖾 📙 CC_test2.sl 🖾
    □#!/bin/bash -l
     ‡SBATCH --job-name=testComputeCanada ← Any name to recognize your job
     #SBATCH --account=def-sblain # adjust this to match the accounting group you are using to submit jobs
     #SBATCH --nodes=1
                                              Time Limit
                                                        Nr of Nodes (stays at 1 for now)
     #SBATCH --ntasks-per-node=1
     #SBATCH --cpus-per-task=40
                                 # adjust this if you are using parallel command
     #SBATCH --mem=90000
                              # adjust this according to the memory requirement per node you need (this is MegaByte)
     #SBATCH --mail-user=g2h3s6p4k0e9o7a5@biaptlab.slack.com ◀
                                                                             Your E-Mail
10
    #SBATCH --mail-type=ALL
12
     # Choose a version of MATLAB by loading a module:
13
     module load matlab/2018a
                                                           Matlab verison
14
15
     # Create temporary job info location
16
     mkdir -p /scratch/$USER/$SLURM JOB ID
17
                                                            How your .m is called
18
     srun matlab -nodisplay -r "CC test"
19
20
     # Cleanup
     rm -rf /scratch/$USER/$SLURM JOB ID
22
```

→ Prepare your own slurm files (open the .sl with a text editor)

Upload data/code:



Upload data/code:

scp from to scp oldfile newfile

scp test.txt lotte@beluga.computecanada.ca:projects/def-sblain/lotte/test.txt

→ Move your slurm and test matlab script into your folder

Upload data/code:

helpful commands

- unzip *name*.zip *unzip folder*

- zip -r name.zip name zip folder

→ Move your slurm and test matlab script into your folder

- sacct --format JobID,State -j 29231822 | grep TIMEOUT
- Log in your CC account and move to the directory of your code
- → submit your job

sbatch yourjobname.sl

→ Check the status of your job

```
lotte@beluga1 ~]$ sq

JOBID USER ACCOUNT NAME ST TIME_LEFT NODES CPUS TRES_PER_N MIN_MEM NODELIST (REASON)

15383554 lotte def-sblain_c testComputeCan PD 10:00 1 40 N/A 90000M (Priority)

15383558 lotte def-sblain_c test2ComputeCa PD 10:00 1 40 N/A 90000M (Priority)
```

→ Check the progress of your job / Check why it crashed

cat yourjobid.out

Do some other stuff





Do some other stuff







Do some other stuff







Slackbot 3:26 PM

Charlotte Maschke | Email •

slurm@calculquebec.ca (SLURM workload manager)

Slurm Job_id=15350790 Name=make-dPLI Began, Queued time 00:00:02

(No content)



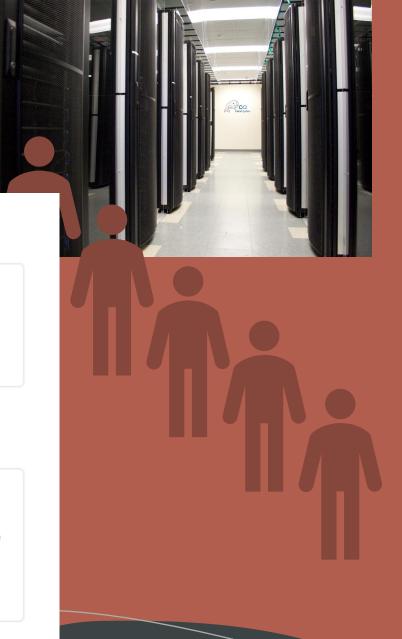
Slackbot 5:29 PM

Charlotte Maschke | Email -

slurm@calculquebec.ca (SLURM workload manager)

Slurm Job_id=15350790 Name=make-dPLI Ended, Run time 02:03:41, COMPLETED, ExitCode 0

(No content)



Download results:

Log out from Beluga and use the scp command on your computer

scp from to scp oldfile newfile

scp test.txt lotte@beluga.computecanada.ca:projects/def-sblain/lotte/test.txt



scp lotte@beluga.computecanada.ca:projects/def-sblain/lotte/test.txt test.txt

→ Download the output.txt to your computer

When to use it?

- Always try on your own Computer first! (use a reduced dataset ...)
- Debug on your own Machine

ONCE you have a finished pipeline

- Parallelize the code (search the bottleneck)
- When piloting a job on CC always start with a small number and time (proof of concept for additional debugging)

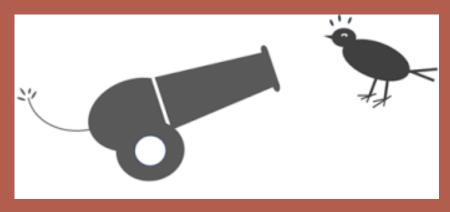




How to specify your needs?

"seff JOB_ID

```
[lotte@beluga4 4_Neuroimage_submission_2021]$ seff 19464051
perl: warning: Setting locale failed.
perl: warning: Please check that your locale settings:
        LANGUAGE = (unset),
        LC_ALL = (unset),
        LANG = "C.UTF-8"
    are supported and installed on your system.
perl: warning: Falling back to the standard locale ("C").
Job ID: 19464051
Cluster: beluga
User/Group: lotte/lotte
State: COMPLETED (exit code 0)
Nodes: 1
Cores per node: 40
CPU Utilized: 00:02:28
CPU Efficiency: 2.00% of 02:03:20 core-walltime
Job Wall-clock time: 00:03:05
Memory Utilized: 214.71 MB
Memory Efficiency: 0.24% of 87.89 GB
[lotte@heluga4 4 Neuroimage submission 2021]$
```



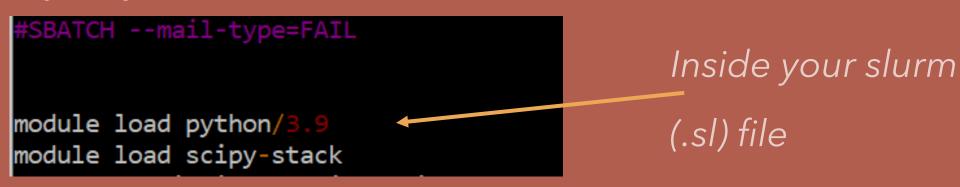
Check the efficiency of your job and adapt it for next time!

(it is ok to overestimate time a little)

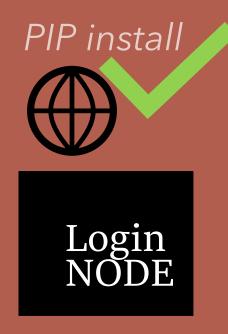
- Look whether the package you want to use is available on CC (pre-installed)

https://docs.computecanada.ca/wiki/Available_software

- If yes, you can use it like this:



- If No, need to install it yourself







- If No, need to install it yourself
- 1. Create a venv on your login node

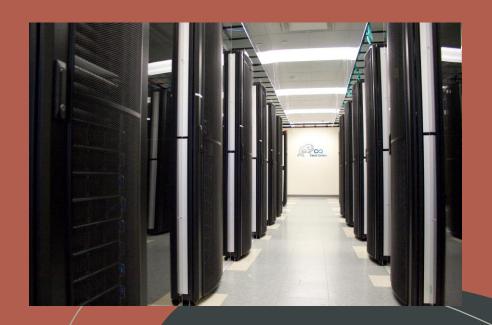
2. Send it in your slurm file to the compute node

3. Use it on compute node









- If No, need to install it yourself

1. Create a venv on your login node

[lotte@beluga4 Tutorial Compute Canada]\$

https://docs.computecanada.ca/wiki/Python#Creating and using a virtual environment

Load the python version you need

Activate your venv

You are now in your venv

... and you can start installing your packages

- If No, need to install it yourself

```
#SBATCH --mail-user=q2h3s6p4k0e9o7a5@biaptlab.slack.com
#SBATCH --mail-type=FAIL

2. Send it in your slurm
file to the compute node

module load python/3.9
module load scipy-stack
source aperiodic_env/bin/activate

python _1_spectral_decomposition.py data_aperiodic results_aperiodic data_aperiodic/data_Baseline.txt Base
```

END