



Canadian Centre for  
Computational  
Genomics

# Unix like system

Command line is your friend

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## Introduction

- Lets Connect!
  - Simple computer
  - User Interface
  - Storage
- A system that computes
- Compute Canada
- Simple Super Computer

# Test your account

In a terminal:

```
ssh my_cc_account@mp2.ccs.usherbrooke.ca
```

on older windows systems:

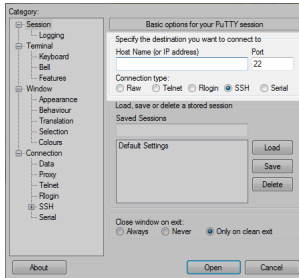


Figure: PuTTY

# Simple computer

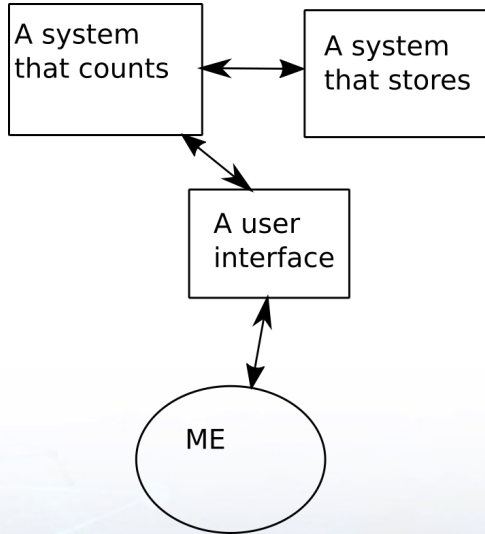
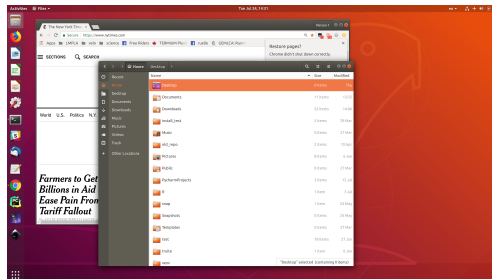


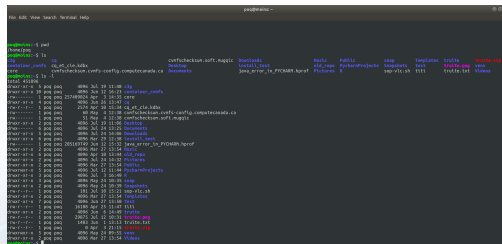
Figure: very simple

# A User Interface (UI)

GUI

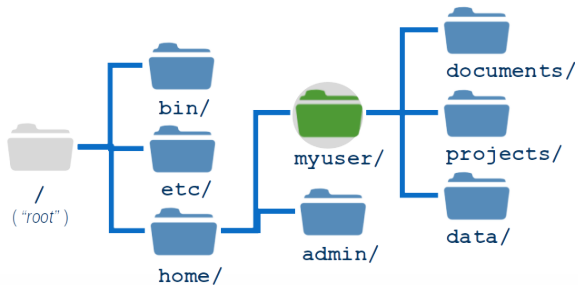


UI



# A System that Stores

The file system is like a serie of interlinked drawers



Root /

system configuration /etc

home \$HOME == /home/myuser

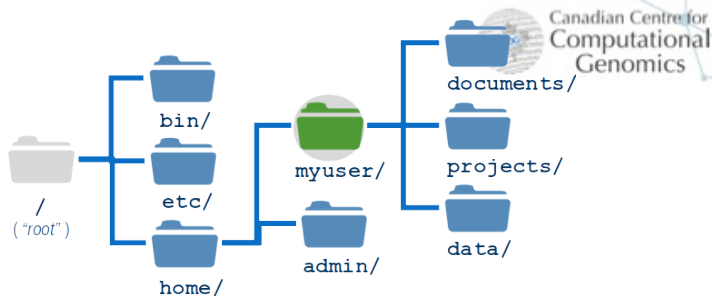
# File System



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```
[poq@ip15-mp2 ~]$ pwd
/home/poq
[poq@ip15-mp2 ~]$ ls
bin  projects  scratch
[poq@ip15-mp2 ~]$ ls -al
total 1011
drwx-----  6 poq  poq    4096 Jul 12 15:36 .
drwxr-xr-x 16925 root root 876544 Jul 24 14:17 ..
-rw-----  1 poq  poq    4748 Jul 12 13:37 .bash_history
-rw-r--r--  1 poq  poq     18 Feb 16 18:23 .bash_logout
-rw-r--r--  1 poq  poq    193 Feb 16 18:23 .bash_profile
-rw-r--r--  1 poq  poq    260 Jul 11 17:31 .bashrc
drwxrwxr-x  2 poq  poq    4096 Jul 11 17:32 bin
drwxrwxr-x  2 poq  poq    4096 May 22 09:54 .licenses
drwxr-xr-x  2 root poq    4096 Jun 14 16:17 projects
lrwxrwxrwx  1 poq  poq     12 Feb 25 17:28 scratch -> /scratch/poq
drwx-----  2 poq  poq    4096 Jul 12 13:37 .ssh
-rw-----  1 poq  poq   13217 Jul 12 13:37 .viminfo
[poq@ip15-mp2 ~]$ cd bin/
[poq@ip15-mp2 bin]$ pwd
/home/poq/bin
[poq@ip15-mp2 bin]$ ls
partition-stats  toto
```

# PATH



Relative or full path:

relative path `project/`

relative path `./project/`

relative path `../admin/`

absolute path `/home/myuser/project/`

absolute path `$HOME/project/`

- ▶ Relative to the user though



## Creating/deleting files/directory and moving them around

- ▶ create (make) directory: `mkdir a_dir/`
- ▶ create a file : `nano new_file.txt`
- ▶ delete (remove) a file : `rm a_file.txt`
- ▶ delete directory (and file in it recursively): `rm -r a_dir/`
- ▶ move (or rename) a file or directory: `mv old_name ../new_place_and_name`
- ▶ Remember not to panic!

```
[poq@ip18-mp2 hand_on]$ rm-r toto/  
rm-r: command not found
```

# Ownership and Permissions

```
[poq@ip18-mp2 hand_on]$ ls -al
total 55
drwxr-xr-x  2 poq poq 4096 Jul 25 18:46 .
drwx----- 7 poq poq 4096 Jul 25 17:08 ..
-rw-rw-r--  1 poq poq    2 Jul 25 16:20 a_file.txt
-rwxr-xr-x  1 poq poq  106 Jul 25 16:45 a_script.sh
```

- ▶ UID
- ▶ GID
- ▶ USER GROUP OTHER
- ▶ rwx -> read, write, execute
- ▶ To change: `chmod g+rx`

# Simple Computer

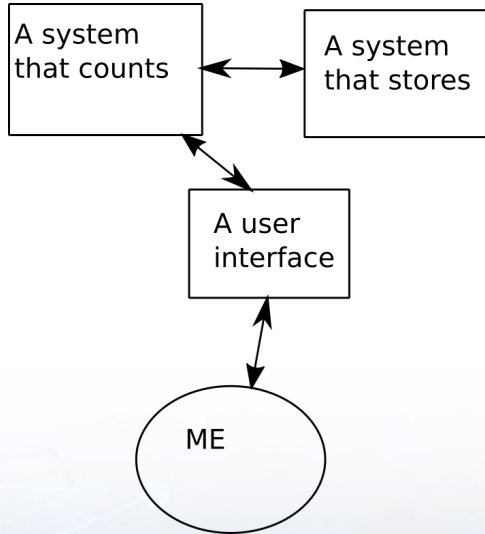
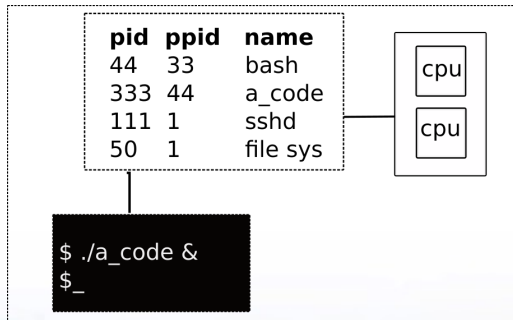


Figure: very simple

# A System that Counts

- ▶ All commands are script/binary/software that tell the computer to execute some code. The script can be written in BASH, python, Fortran, C++, ...
- ▶ Once a script is executed, it "transforms" into a process.



- ▶ This process has ways to talk to the external world: streams. There are three "standard" streams called stdin, stdout and stderr.



Bigger computers

- ▶ Compute Canada (CC) is an umbrella organisation that helps providing computing services to Canadians. It is undergoing a transformation right now, sweeping from the West: it closes smaller supercomputers managed by universities and opens regional SuperComputers
- ▶ New: Cedar (Simon Fraiser- West Grid)  
New: Graham (Waterloo - Compute Ontario)  
New: Niagara (Toronto - Compute Ontario)  
To come: Beluga (Montréal - Calcul Québec)  
Legacy: Guillimin (U. McGill), Mammouth (U. Sherbrooke), etc.
- ▶ The Mammouth cluster (mp2b) used for this workshop is a test bed for Beluga.

# Simple computer

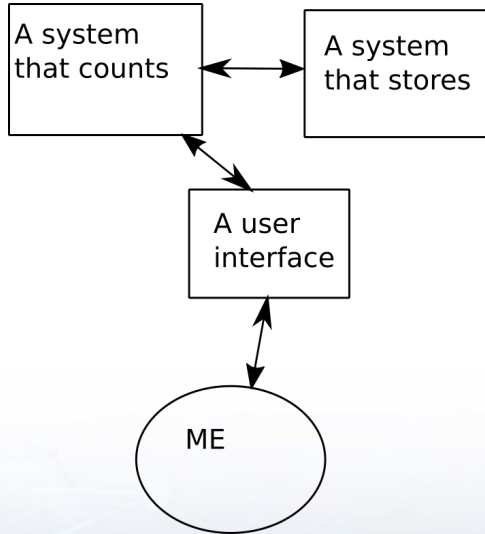


Figure: very simple

# Simple Super Computer

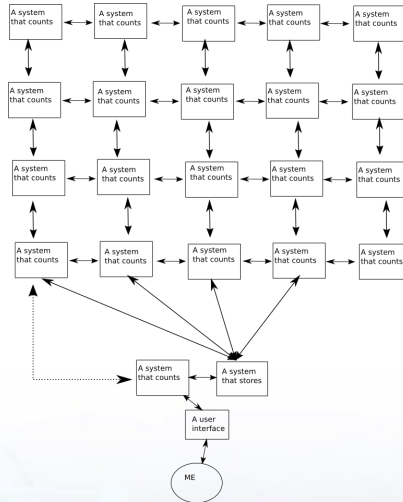


Figure: HPC for numerical simulation



# Simple Super Computer for Big data

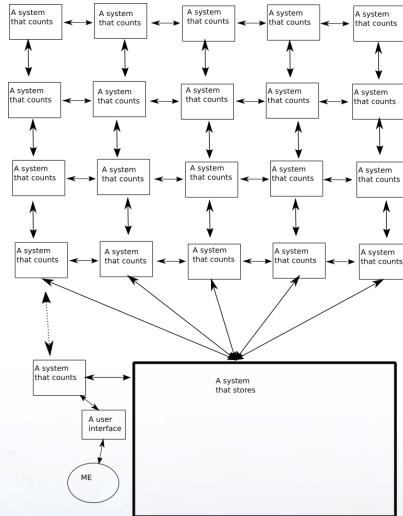
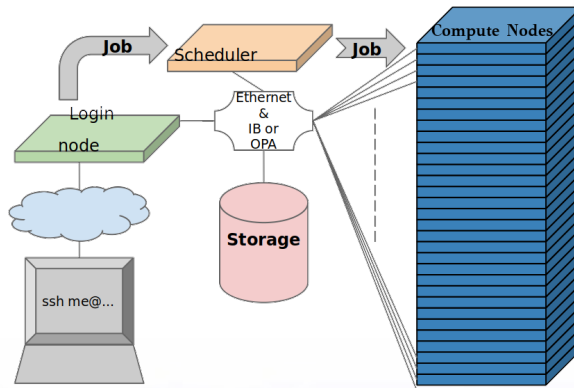


Figure: HPC for data sciences

# More details, type of HPC load



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- ▶ Parallel jobs
- ▶ Pipelines or batch jobs (That is GenPipes)

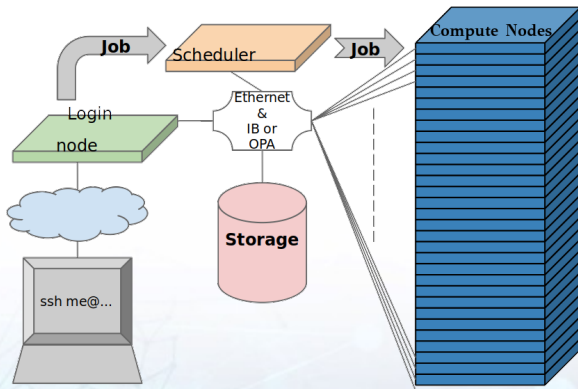
# How to make it work?

For many task, you don't have to think that the super computer is super... In fact, GenPipes is taking care of that part for you!

- ▶ You run Genpipes on a a single (simple) computer and it creates a script with supercomputer commands
- ▶ You just ask the supercomputer to execute it and then look at your data being generated.

# Scheduler

- ▶ Older sites often use or still uses PBS/TORQUE (qsub)
- ▶ On all new CC system SLURM (Simple Linux Utility for Resource Management) is the workload manager/job scheduler (Useful SLURM commands **sbatch**, **scancel**, **squeue**)





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Genome Canada



Ontario Genomics



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Thank you!



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Terry Fox

PROFYLE



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