



Introduction to the I2BC cluster



I2BC file system

For the
new comers



« Partages » storage system, aka. /store/

- A space designed for **storage**
- Accessible everywhere
- Regularly backed up (snapshot system)

3 subspaces:

→ **EQUIPES** (team space, 1Tb)

read/write for all team members except MEMBERS subdirectory

MEMBERS: 1 folder per team member, read-only for others

→ **USERS** (personal space, 20Gb)

→ **plateformes** (project space, 5Tb)

Useful for projects across teams or with external collaborators (ask SICS)

<https://intranet.i2bc.paris-saclay.fr/outils/informatique/#stock> => about storage @I2BC

<https://intranet.i2bc.paris-saclay.fr/procedures/info/#file> => how to access outside I2BC



S.O.S.

**For the
new comers**



Need help with your **computer, internet, some software, the cluster...?**

=> Contact the **SICS** - IT support team

support.informatique@i2bc.paris-saclay.fr

(be clear and concise in the email and email subject)

HELP!

Questions on **specific bioinformatics tools & practices?** Help on setting up an analysis pipeline? Etc.

=> Contact **BIOI2**: contact-bioi2@i2bc.paris-saclay.fr

=> Ask around you e.g. using our **FramaTeam** group: [more information](#)

=> Search through the **intranet** ([tools](#) & procedures)

=> Search & contribute to the **Wiki** on the Forge: [here](#)

Anything linked to this training session can be found on the BIOI2 website:

<https://bioi2.i2bc.paris-saclay.fr/training/i2bc-cluster/>



The screenshot shows the BIOI2 website interface. At the top, there is a navigation bar with the I2BC and BIOI2 logos, and menu items: 'About BIOI2', 'Tools & DBs', 'Tutorials & Training', and 'Publications'. The main heading is 'Getting started with the cluster of the I2BC'. Below the heading is a terminal window showing a successful SSH connection to a cluster node. The terminal output includes the command ':~\$ ssh cluster', the system response 'Linux cluster-i2bc 5.10.0-21-amd64 #1 SMP Debian 5.10.162-1 (2023-01-21) x86_64', and a colorful ASCII art logo for 'Frontale'. Below the terminal window, there is a list of links: 'About this course | Before the session | About the cluster | Course material | Exercise 1 – FastQC | Exercise 2 – MAFFT | Exercise 3 – TM-align'. The 'About this course' section is highlighted. It includes a 'Targeted audience' list with two items: 'bioinformatician newcomers who want to learn how to use the I2BC cluster' and 'biologists that are already a bit familiar with running scripts or programmes through command lines and who would like to learn how to use the I2BC cluster'. The 'Programme' section lists five topics: 'A brief introduction to the SICS and the Forge', 'What's a cluster and why should I use one?', 'How to connect to the I2BC cluster?', 'How is it organised?', and 'How do you create and submit jobs?'.

Getting started with the cluster of the I2BC

```
~$ ssh cluster
Linux cluster-i2bc 5.10.0-21-amd64 #1 SMP Debian 5.10.162-1 (2023-01-21) x86_64
Frontale
```

[About this course](#) | [Before the session](#) | [About the cluster](#) | [Course material](#) | [Exercise 1 – FastQC](#) | [Exercise 2 – MAFFT](#) | [Exercise 3 – TM-align](#)

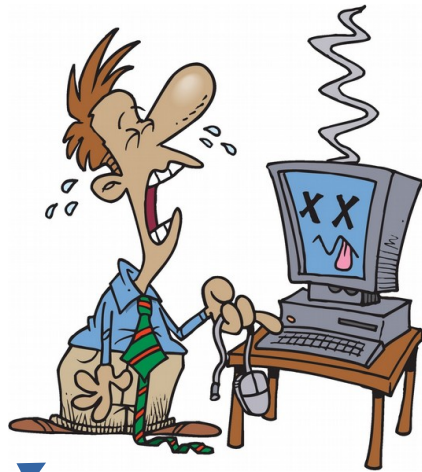
About this course

Targeted audience:

- bioinformatician newcomers who want to learn how to use the I2BC cluster
- biologists that are already a bit familiar with running scripts or programmes through command lines and who would like to learn how to use the I2BC cluster

Programme:

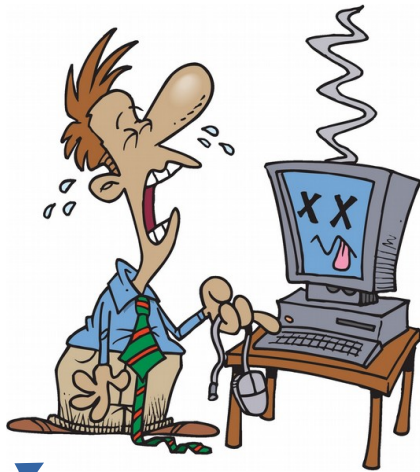
- A brief introduction to the SICS and the Forge
- What's a cluster and why should I use one?
- How to connect to the I2BC cluster?
- How is it organised?
- How do you create and submit jobs?



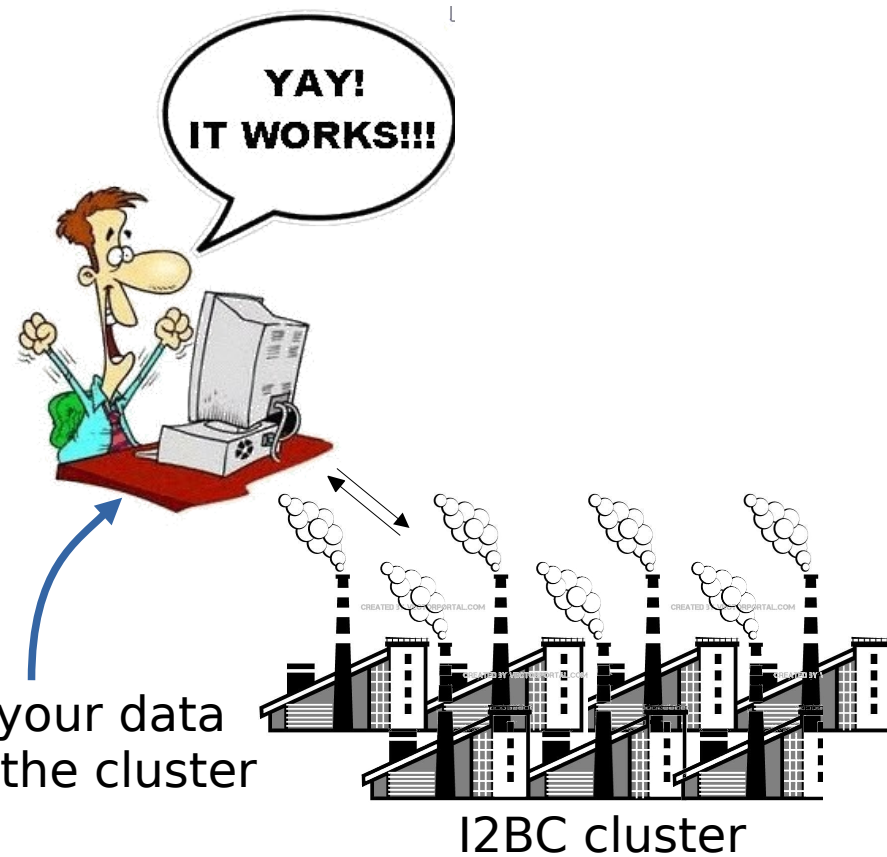
You, processing your data
with your own computer



You, processing your data
with the help of the cluster



You, processing your data
with your own computer



You, processing your data
with the help of the cluster



Goals

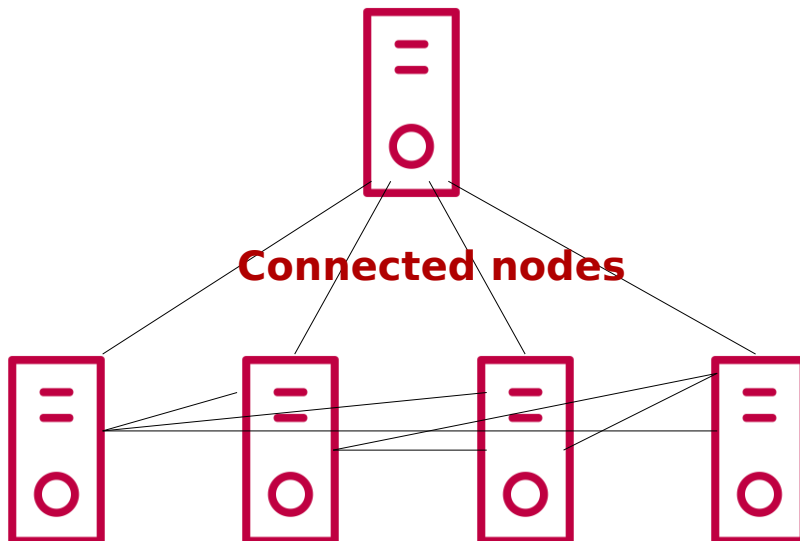


- what's a cluster?
- how to connect?
- how it is structured?
- how to use it?
- practice makes perfect!

What is a cluster?

A computer cluster:

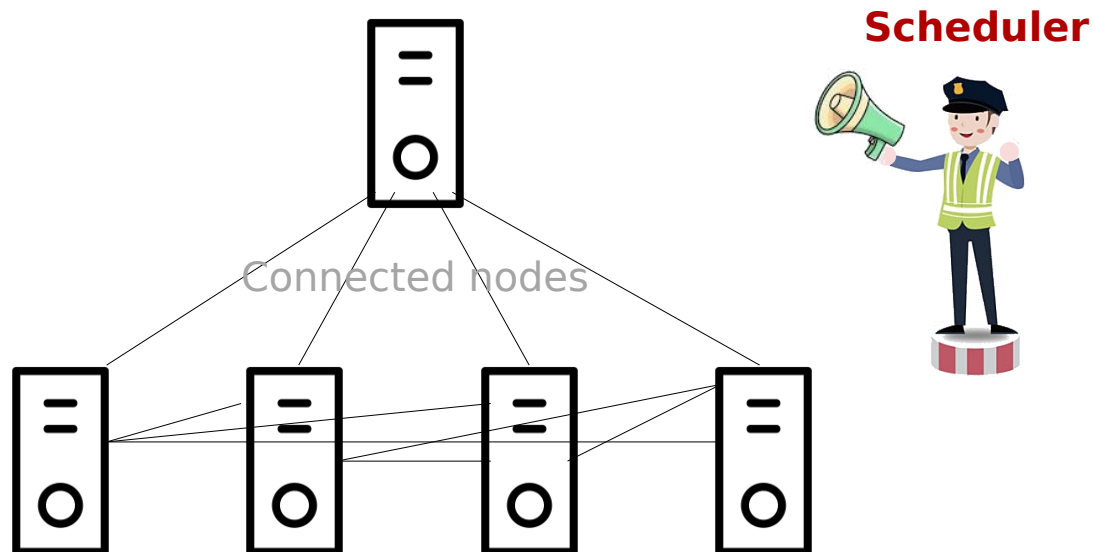
* is a set of computer servers (= **nodes**) connected together



What is a cluster?

A computer cluster:

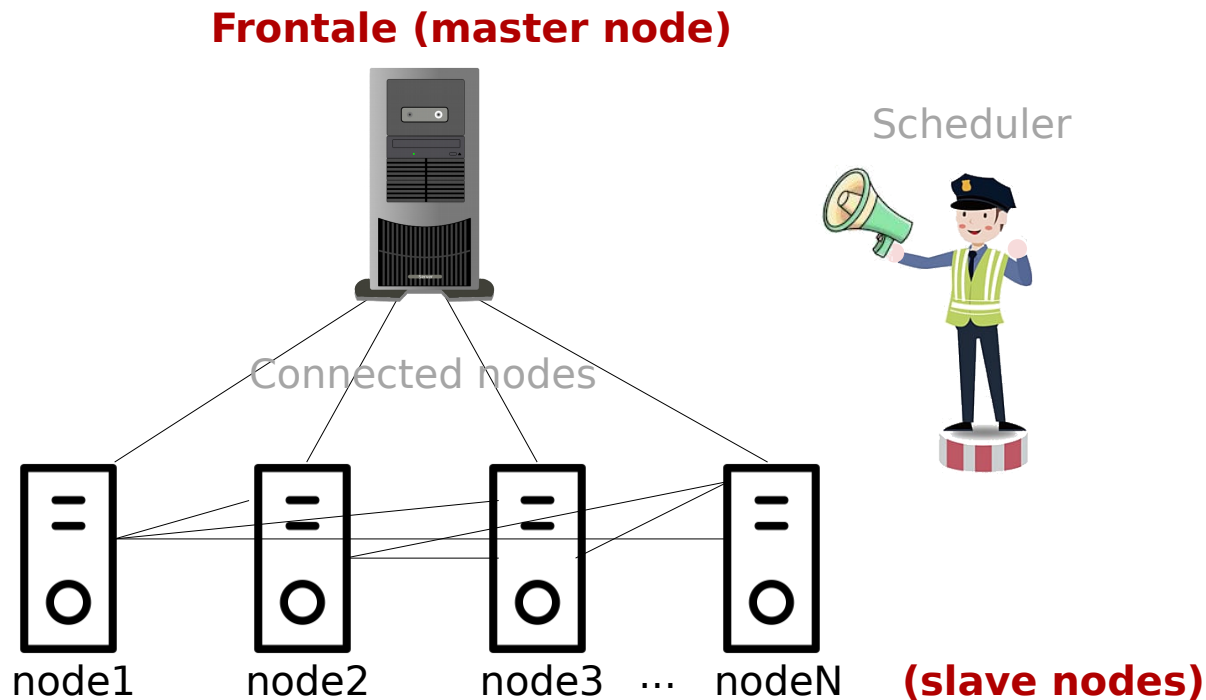
- * is a set of computer servers (= **nodes**) connected together
- * communication between nodes goes through a centralised **scheduler**



What is a cluster?

A computer cluster:

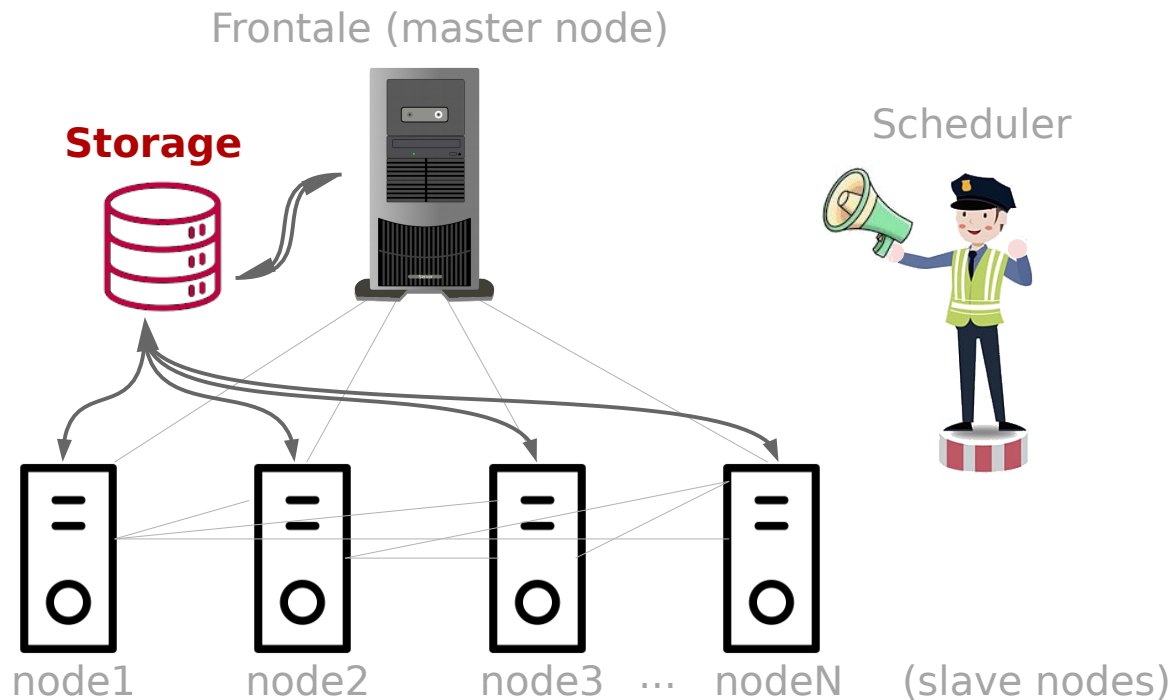
- * is a set of computer servers (= **nodes**) connected together
- * communication between nodes goes through a centralised **scheduler**
- * there are **master node(s)** (=main nodes) and **slave nodes** (=workers)



What is a cluster?

A computer cluster:

- * is a set of computer servers (= **nodes**) connected together
- * communication between nodes goes through a centralised **scheduler**
- * there are **master node(s)** (=main nodes) and **slave nodes** (=workers)
- * all nodes have **access** to the **storage** system

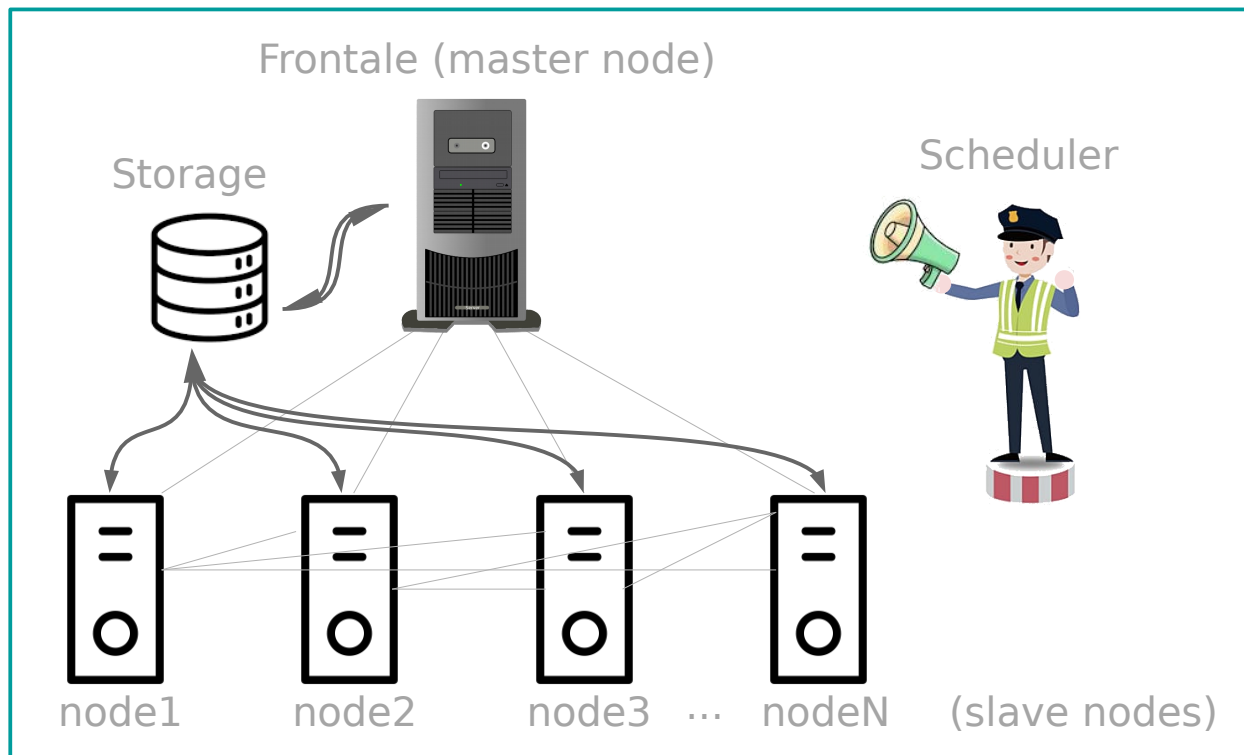


What is a cluster?

A computer cluster:

=> *The master node gives orders to the slave nodes through the scheduler*

=> *The slave nodes do all the work.*



Why use a cluster?



You, processing your data with your own computer

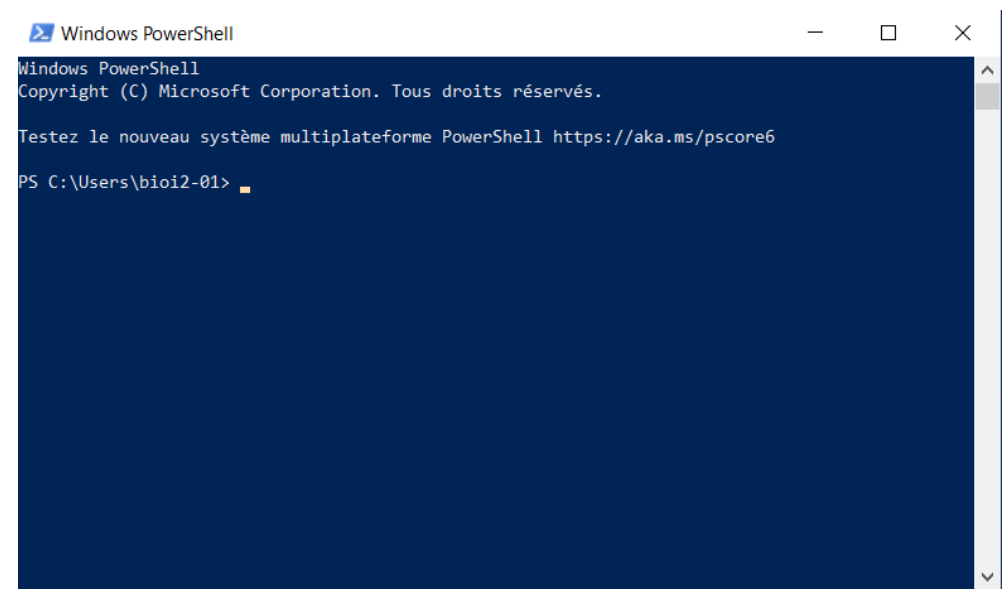
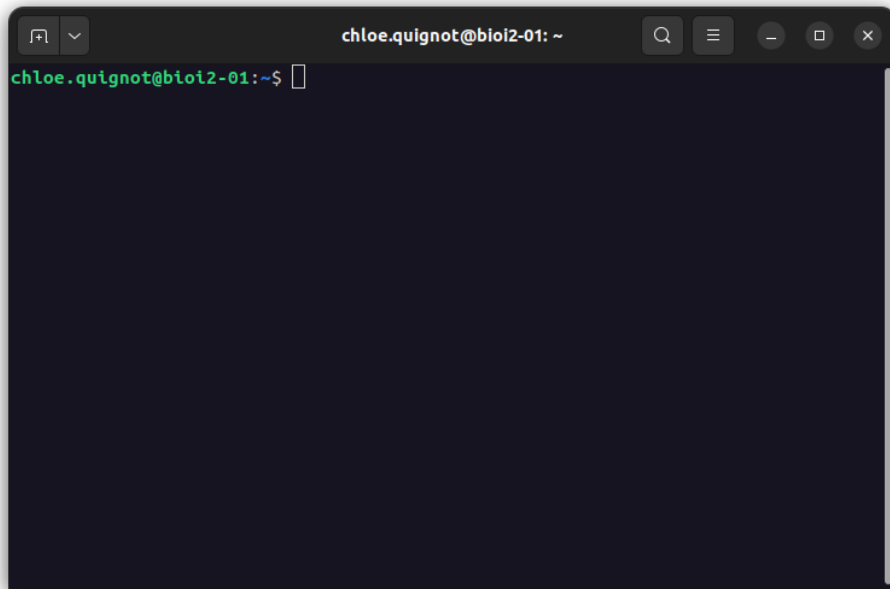


You, processing the same data with the cluster

- * A computer cluster is often **more powerful** than a personal computer.
- * You can **dispatch & parallelise the workload** onto several nodes = faster.
- * Clusters **handle heavy data better** than your own computer would.
- * When using a cluster, you save the resources of your PC for other stuff (i.e. you don't slow it down) and you also don't have to leave it on while you're waiting for computations to finish

NB: You can use a computer cluster but you don't have to. Your own PC might be good enough, it will depend on the tools and on your data.

Several ways of doing it, we'll be using the "Terminal" / "Windows Power Shell"



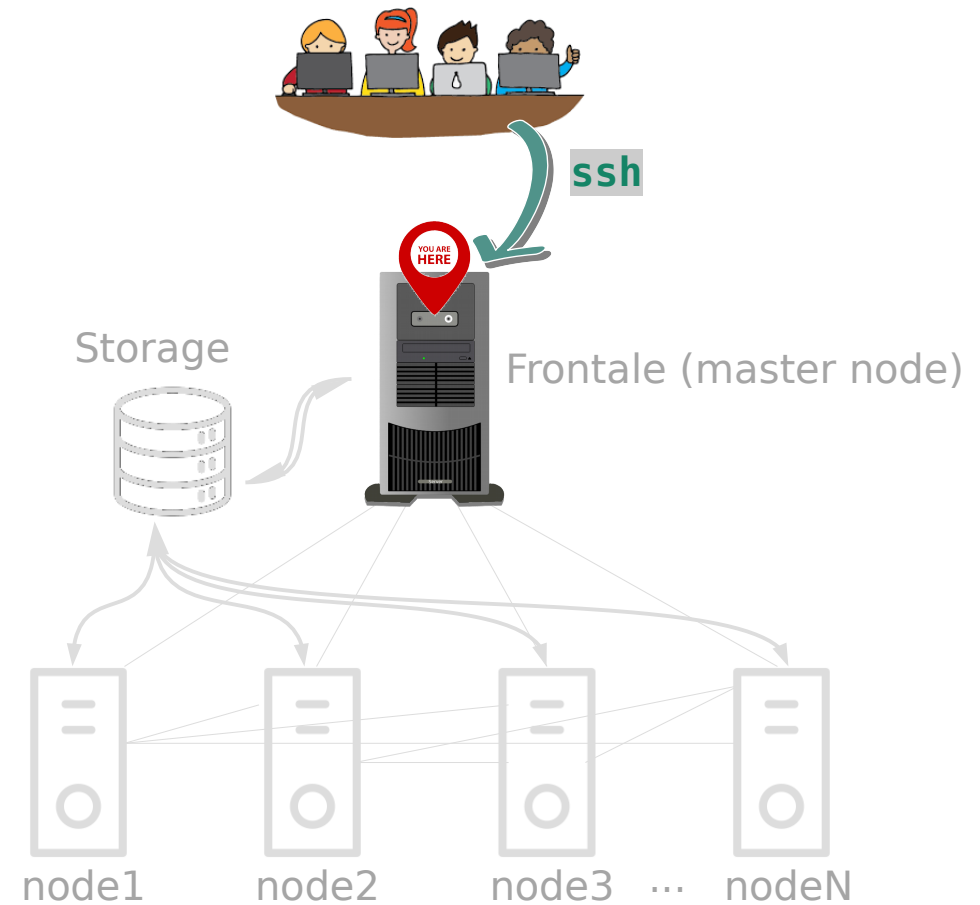
...and the SSH command line:

```
ssh john.doe@passerelle.i2bc.paris-saclay.fr
```

```
ssh john.doe@i2bc-cluster.calcul.i2bc.paris-saclay.fr
```

Then you land on the Frontale => the master node of the I2BC cluster

```
Linux cluster-i2bc 5.10.0-21-amd64 #1 SMP Debian 5.10.162-1 (2023-01-21) x86_64
The programs included with the Debian GNU/Linux system are free software;
the exact distribution terms for each program are described in the
individual files in /usr/share/doc/*/copyright.
Debian GNU/Linux comes with ABSOLUTELY NO WARRANTY, to the extent
permitted by applicable law.
Frontale
=====
Documentation: https://intranet.i2bc.paris-saclay.fr/intranet/sics/Main/Calcul
Pour voir l'état du Cluster veuillez utiliser la commande qshow ( ou qs ).
=====
```



Note the changes in your **shell prefix**! It will tell you where you are.

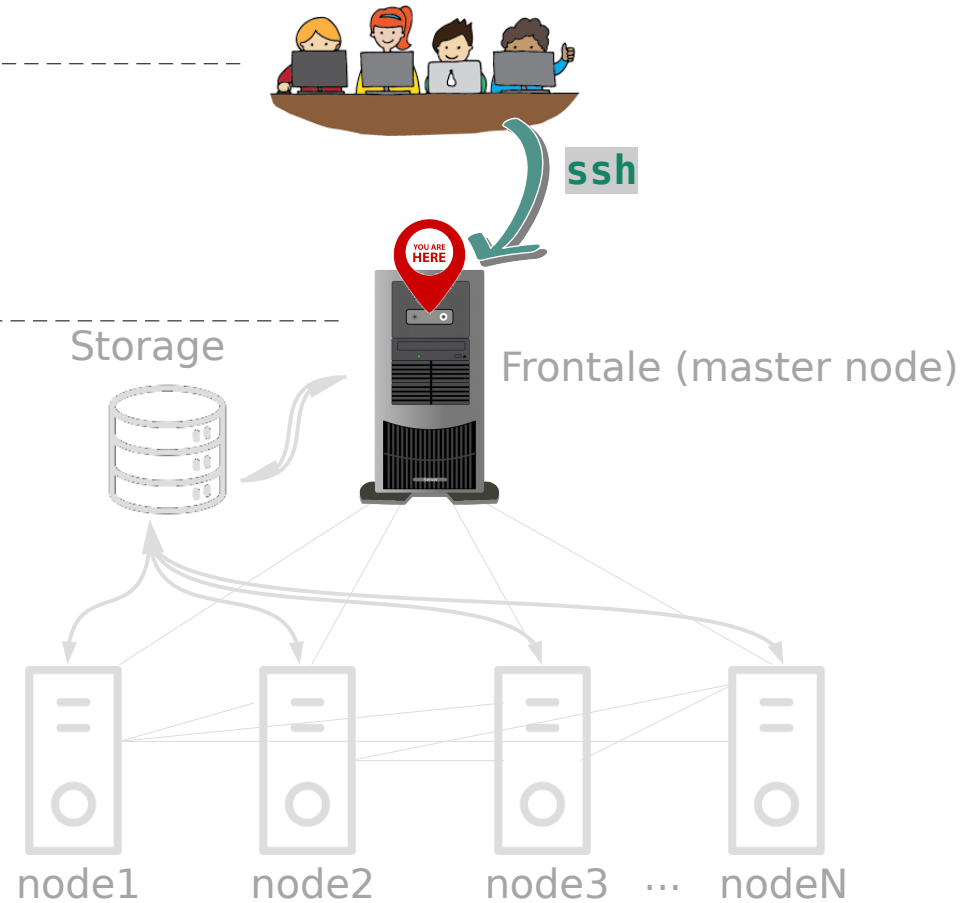
Sélection Windows PowerShell

```
PS C:\Users\bioi2-01>
```

User prefix on your PC

```
chloe.quignot@cluster-i2bc:/home/chloe.quignot$
```

User prefix on the Frontale (master node)



Note the changes in your **shell prefix**! It will tell you where you are.

Sélection Windows PowerShell

```
PS C:\Users\bioi2-01>
```

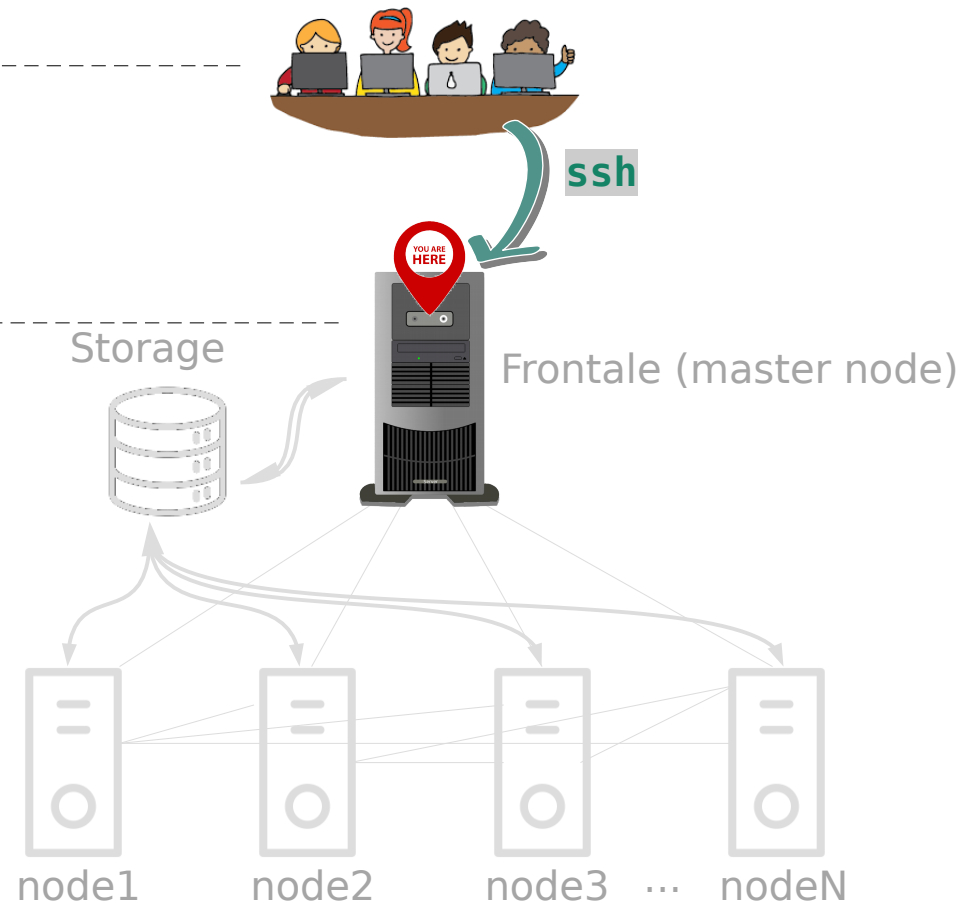
User prefix on your PC

```
chloe.quignot@cluster-i2bc:/home/chloe.quignot$
```

User prefix on the Frontale (master node)

```
chloe.quignot@node09:/home/chloe.quignot$
```

User prefix on node09 (slave node)



From here, you have access to all of the I2BC's "storage" systems:

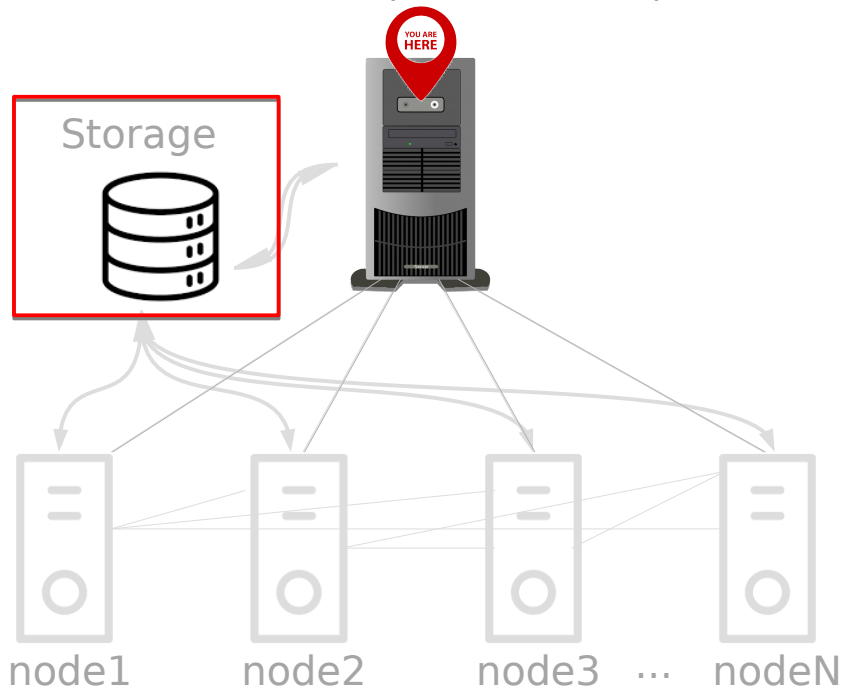
`/store/EQUIPES/<team acronym>/`

`/store/USERS/<your login>/`

`/store/plateformes/<project name>/`

} "partages" => for storage

Frontale (master node)



From here, you have access to all of the I2BC's "storage" systems:

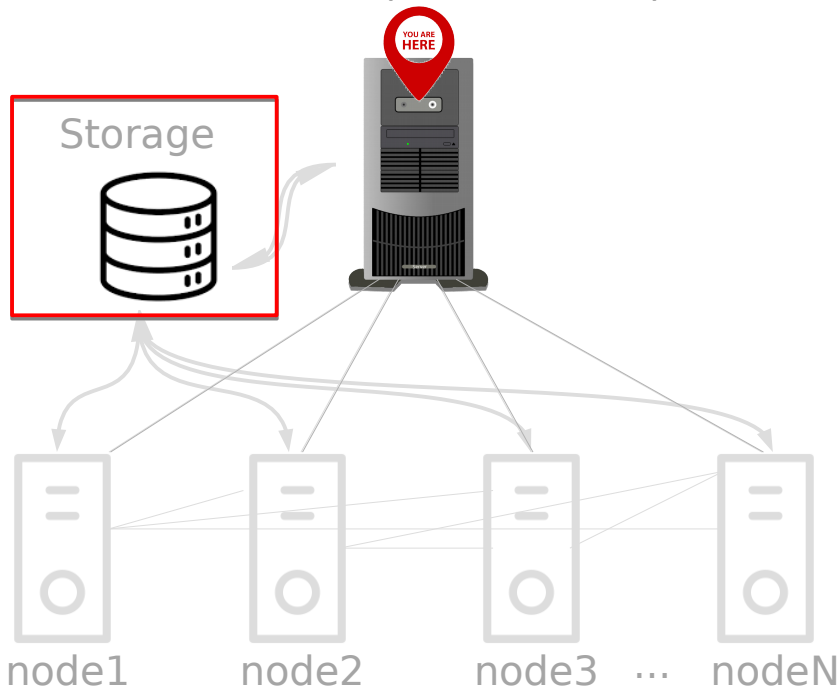
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`/store/USERS/<your login>/`

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} "partages" => for storage

Frontale (master node)



+ 3 computing spaces:

`/home/<your login>/` => your "home"

`/data/work/I2BC/` => "temporary"

`/scratchlocal/` => "temporary"

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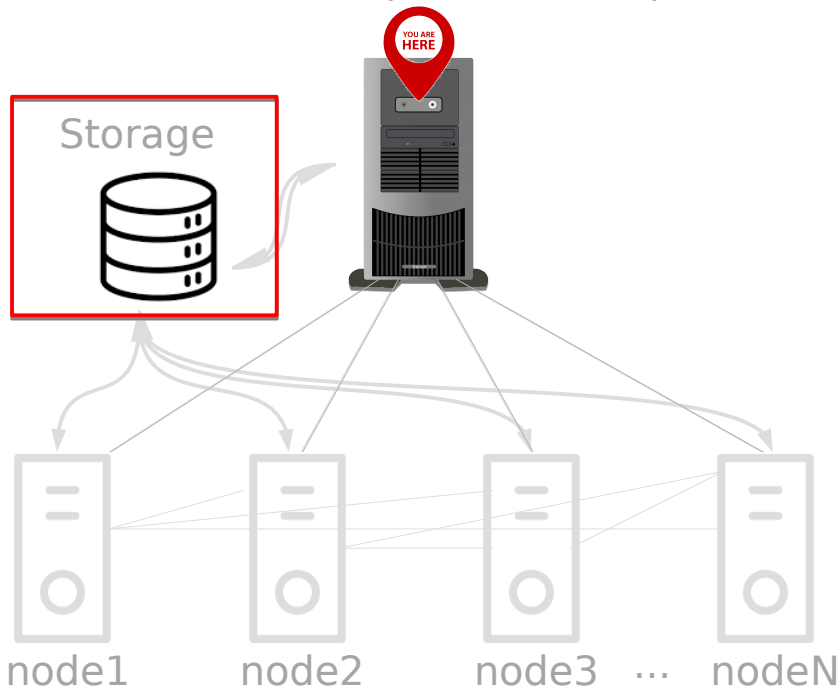
```

/store/EQUIPES/<team acronym>/
/store/USERS/<your login>/
/store/plateformes/<project name>/
    
```

STORAGE

"partages" => for storage

Frontale (master node)



+ 3 computing spaces:

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Storage system






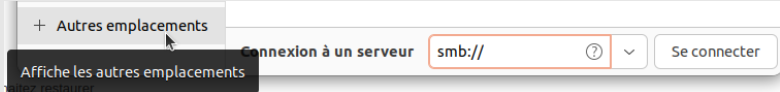


« Partages » storage system, aka. /store/

A space designed for **storage**

Folder	Quota	Usage	Accessibility
<code>/store/USERS/<your login></code>	20 GB	For personal (but professional) use	Only you (read & write)
<code>/store/EQUIPES/<team acronym></code> with a MEMBERS subdirectory	≥5 TB <1 TB	Shared team space	Team members only (read & write for everyone except MEMBERS)
<code>/store/EQUIPES/<team acronym>/MEMBERS/<your login></code>		Your dedicated space within the team space	Read for everyone in the team, write only for you
<code>/store/plateformes/<project name></code>	5 TB	For collaborations or specific projects, created on demand	People you've selected (read & write)

« Partages » storage system, aka. /store/
 A space designed for **storage**

	Within I2BC (or with VPN)	Outside I2BC
	<p><code>\\store\</code> in the navigation bar of your file explorer</p> <p>id: i2bc email address & password</p> 	<p>WinSCP: download the zip file from the intranet or use <code>\\intra.i2bc.paris-saclay.fr\partages</code></p> 
 	<p><code>smb://store/</code> in your file explorer</p>  <p>id: login, domain: <code>intra.i2bc.paris-saclay.fr</code></p> <p>Or mount from passerelle:</p> <pre>mkdir \$HOME/store sshfs chloe.quignot@passerelle:/store \$HOME/store sudo ln -s \$HOME/store /store # optional</pre> <p>Or scp from passerelle</p> <pre>scp chloe.quignot@passerelle:/path/to/file .</pre>	<p>Mount from passerelle (sshfs)</p> <p>Or scp from passerelle</p>

From here, you have access to all of the I2BC's "storage" systems:

`/store/EQUIPES/<team acronym>/`

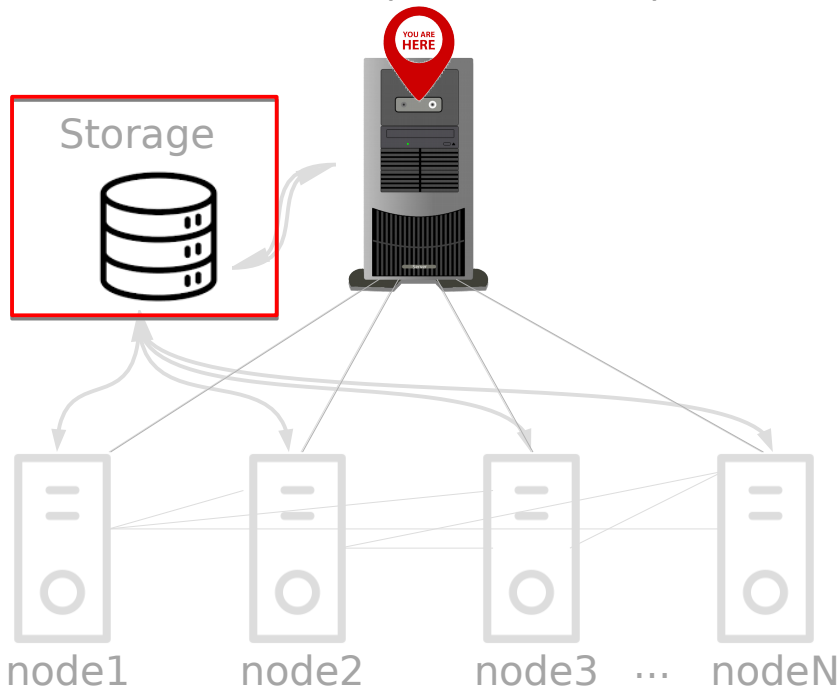
`/store/USERS/<your login>/`

`/store/plateformes/<project name>/`

STORAGE

"partages" => for storage

Frontale (master node)



+ 3 computing spaces:

`/home/<your login>/` => your "home"

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`/scratchlocal/` => "temporary"



Storage system



«Home» directory, aka. `/home/$USER`





NOT for storage but for hosting configuration and login files, locally installed packages (`.local` folder), etc.

Folder	Quota	Usage	Accessibility
<code>/home/<your login></code>	200 GB	Your home directory on the cluster, where you save e.g. config & local files	Only you (read & write)

«Home» directory, aka. /home/\$USER

NOT for storage but for hosting configuration and login files, locally installed packages (`.local` folder), etc.

Folder	Quota	Usage	Accessibility
<code>/home/<your login></code>	200 GB	Your home directory on the cluster, where you save e.g. config & local files	Only you (read & write)

	Within I2BC (or with VPN)	Outside I2BC
	Cluster home: <code>\\data\cluster-homes</code> in the navigation bar of your file explorer	 N/A
 	<code>smb://data/cluster-homes</code> in your file explorer	N/A

From here, you have access to all of the I2BC's "storage" systems:

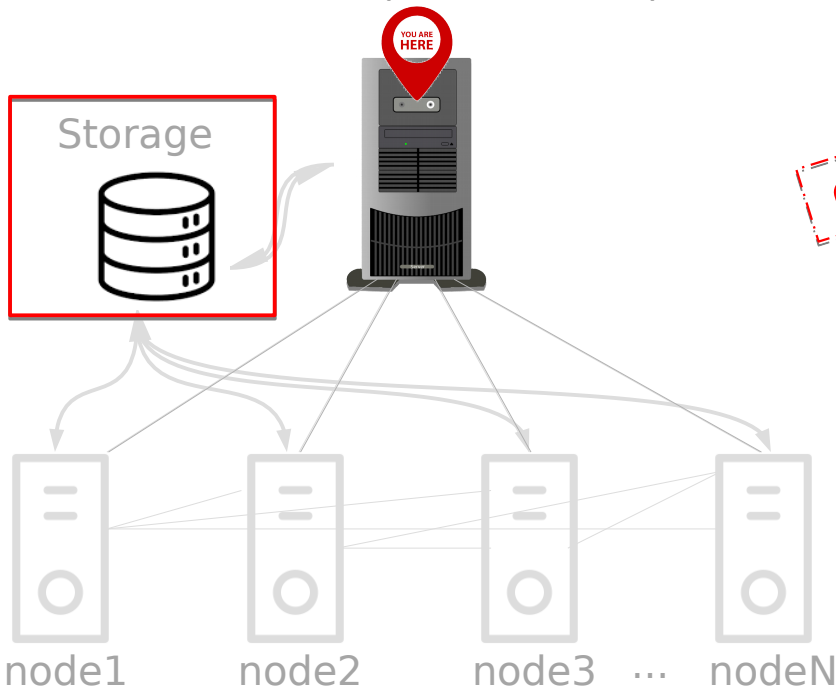
```

/store/EQUIPES/<team acronym>/
/store/USERS/<your login>/
/store/plateformes/<project name>/
    
```

STORAGE

"partages" => for storage

Frontale (master node)



+ 3 computing spaces:

CONFIG

`/home/<your login>/` => your "home"

`/data/work/I2BC/` => "temporary"

`/scratchlocal/` => "temporary"

Both `/store` & `/home/your_login` are **regularly backed-up**

In the terminal, put yourself in your folder and checkout the hidden `.snapshots/` directory (you can run a `cp` of files and directories to retrieve them “to the present”)



```

chloe.quignot@cluster-i2bc: /home/chloe.quignot
chloe.quignot@cluster-i2bc:/home/chloe.quignot$ ls .snapshots
Jour_2023_02_27__08_00  Mois_2023_02_16__01_00  Semaine_2023_02_24__06_00
Jour_2023_02_27__12_00  rep_1677513600842      Semaine_2023_02_25__06_00
Jour_2023_02_27__16_00  Semaine_2023_02_21__06_00  Semaine_2023_02_26__06_00
Jour_2023_02_27__20_00  Semaine_2023_02_22__06_00  Semaine_2023_02_27__06_00
Mois_2023_01_19__01_00  Semaine_2023_02_23__06_00
chloe.quignot@cluster-i2bc:/home/chloe.quignot$

```

`Jour_YYYY_MM_DD_HH_MM`

`Semaine_YYYY_MM_DD_HH_MM`

`Mois_YYYY_MM_DD_HH_MM`

For more information:

https://forge.i2bc.paris-saclay.fr/redmine/projects/partage-bioinfo/wiki/B_Cluster_ressources#Backups

From here, you have access to all of the I2BC's "storage" systems:

`/store/EQUIPES/<team acronym>/`

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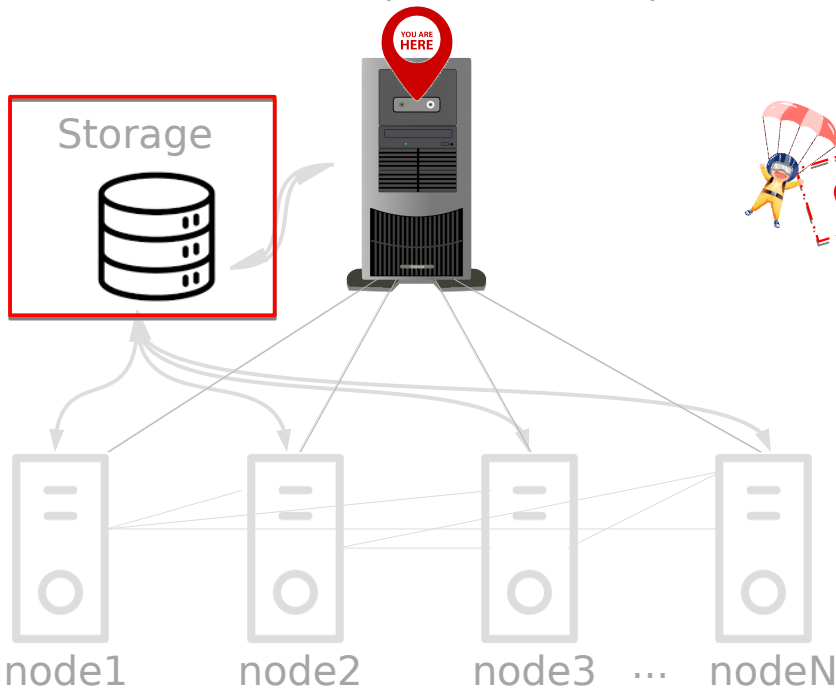
`/store/plateformes/<project name>/`

STORAGE



"partages" => for storage

Frontale (master node)



+ 3 computing spaces:

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`/scratchlocal/` => "temporary"

CONFIG



“Computing space”:

NOT for storage but for hosting temporary/intermediate files

Not backed-up, limited space, **clean up after yourselves!**

Folder	Quota	Usage	Accessibility
<code>/data/work/I2BC/</code>	20 TB	Shared between all users (for temporary files only)	Everyone (read & write)
<code>/scratchlocal/</code>	variable from node to node	For temporary files, only on the node in question, more rapid as local to the node	Read & write only for your files & directories

“Computing space”:

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Not backed-up, limited space, **clean up after yourselves!**

Folder	Quota	Usage	Accessibility
<code>/data/work/I2BC/</code>	20 TB	Shared between all users (for temporary files only)	Everyone (read & write)
<code>/scratchlocal/</code>	variable from node to node	For temporary files, only on the node in question, more rapid as local to the node	Read & write only for your files & directories





NB1: Nothing in these spaces is deleted on its own, it's up to you to clean up after yourselves when you're done!

NB2: If you're using these spaces, it's a good habit to work within a folder with your name and/or jobid

“Computing space”:

NOT for storage but for hosting temporary/intermediate files

Not backed-up, limited space, **clean up after yourselves!**

	Within I2BC (or with VPN)	Outside I2BC
	Work: <code>\\data\work</code> in the navigation bar of your file explorer 	N/A
 	<code>smb://data/work</code> in your file explorer	N/A

From here, you have access to all of the I2BC's "storage" systems:

`/store/EQUIPES/<team acronym>/`

`/store/USERS/<your login>/`

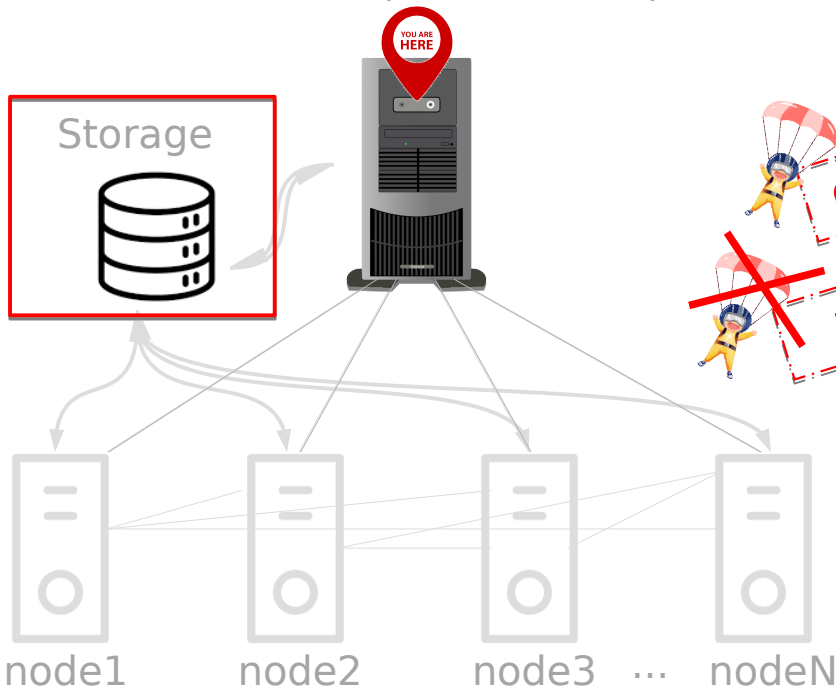
`/store/plateformes/<project name>/`

STORAGE



"partages" => for storage

Frontale (master node)



+ 3 computing spaces:

`/home/<your login>/` => your "home"

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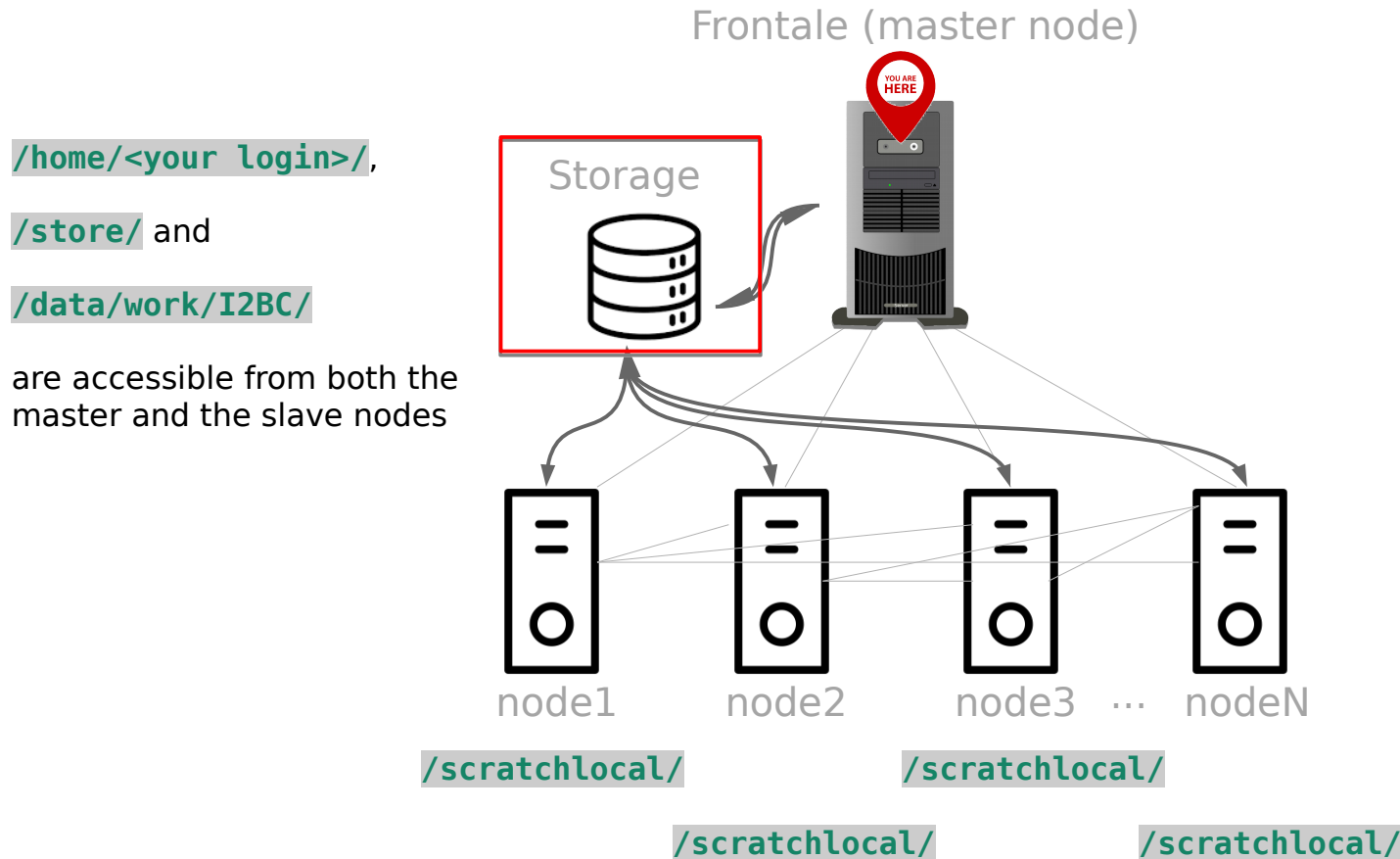
`/scratchlocal/` => "temporary"

CONFIG

TEMP



In summary: 3 spaces accessible from both the slave and the master nodes + 1 space accessible only on the nodes and specific to each node



In the terminal, you can rapidly check the quota of the disk using the in-house `i2bc_quota` command with `-a` (all) or `-u` (only your usage).

Example: total quota on `/data/work`

```

chloe.quignot@cluster-i2bc: /home/chloe.quignot
chloe.quignot@cluster-i2bc:/home/chloe.quignot$ i2bc_quota -s data -v WORK -a
Volume      Directory      Free      Used      Quota      FreeGB      UsedGB      QuotaGB
work        /I2BC          3072 GB   17.0 TB   20.0 TB    3072        17408       20480
work        /NGS           3380 GB   6.7 TB   10.0 TB    3380        6860        10240
  
```

```

chloe.quignot@cluster-i2bc: /home/chloe.quignot
chloe.quignot@cluster-i2bc:/home/chloe.quignot$ i2bc_quota
usage: i2bc_quota [-h] [-u] [-a] [-s {data,store}] [-v VOLUME]

Examples:

1) i2bc_quota -v EQUIPES /SICS
Display quota information about EQUIPES/SICS on store NAS server

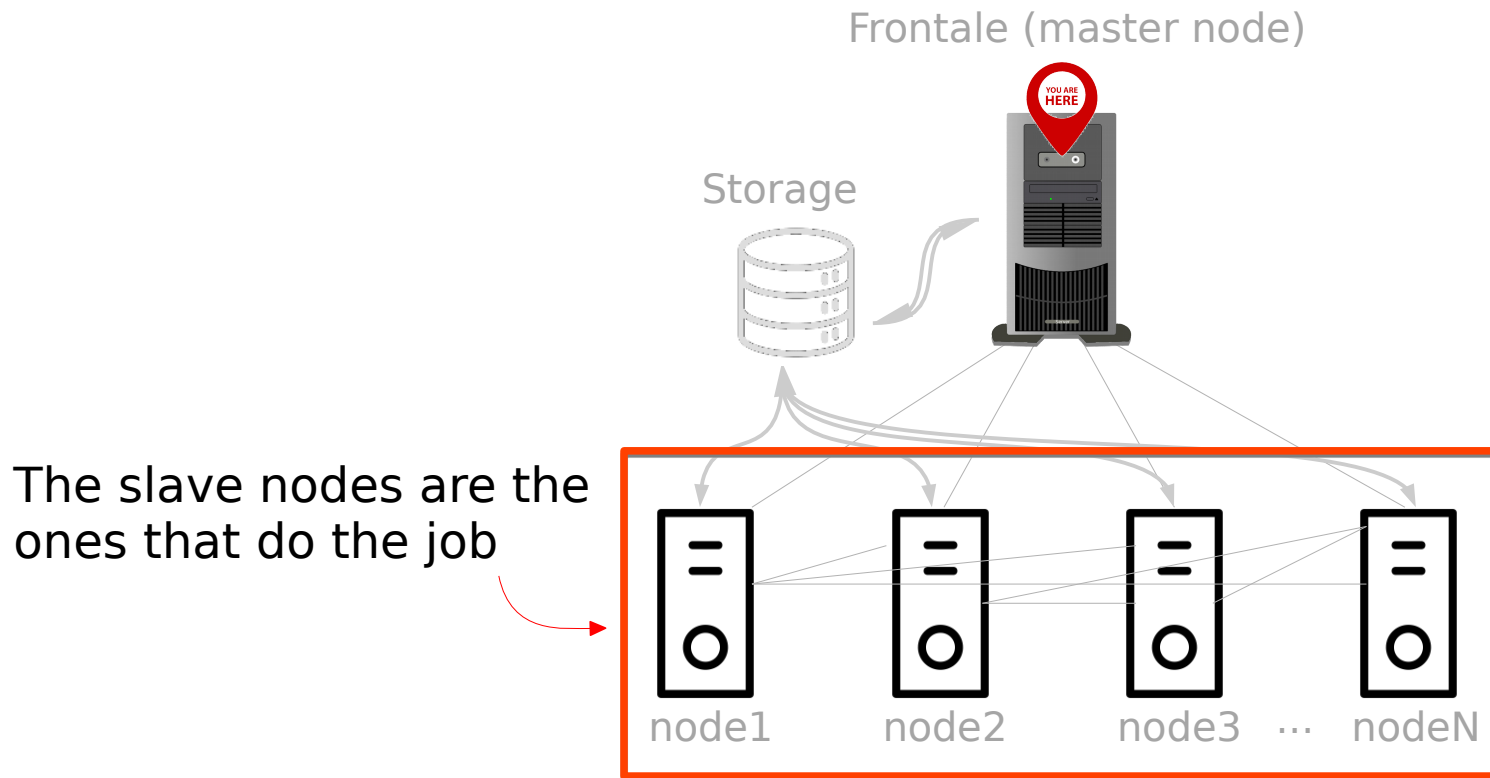
2) i2bc_quota -s data -v WORK -a
Display quota information for all directories in volume DATA on data NAS
server

3) i2bc_quota -v USERS -u
Display quota information about your own use on volume USERS (on store NA
S server)
chloe.quignot@cluster-i2bc:/home/chloe.quignot$ 
  
```

If you only type the "i2bc_quota" command, you'll get a help message to show you how to use it



Jobs are never run on the Frontale, they should always be run on the slave nodes!!!



Use `pbsnodes -avS` to list all the nodes on the cluster

```

chloe.quignot@cluster-i2bc: /home/chloe.quignot
chloe.quignot@cluster-i2bc:/home/chloe.quignot$ pbsnodes -avS
vnode      state      OS      hardware host      queue      mem      ncpus  nmics  ngpus  comment
-----
node01     state-unknown  --      --      node01     --      0kb     0      0      0      node_target: COMMON
node02     state-unknown  --      --      node02     --      0kb     0      0      0      node_target: COMMON
node03     state-unknown  --      --      node03     --      0kb     0      0      0      node_target: COMMON
node04     state-unknown  --      --      node04     --      0kb     0      0      0      node_target: COMMON
node05     free          --      --      node05     --      125gb   40     0      0      node_target: MICMAC
node06     free          --      --      node06     --      125gb   40     0      0      node_target: COMMON
node07     free          --      --      node07     --      125gb   40     0      0      node_target: COMMON
node08     free          --      --      node08     --      125gb   40     0      0      node_target: EMC2
node09     free          --      --      node09     --      125gb   40     0      0      node_target: AMIG
node10     job-busy      --      --      node10     --      125gb   40     0      0      0
node11     free          --      --      node11     --      125gb   40     0      0      0 node_target: AMIG
node12     free          --      --      node12     --      125gb   40     0      0      0 node_target: AMIG
node13     free          --      --      node13     --      125gb   40     0      0      0 node_target: COMMON
node14     job-busy      --      --      node14     --      125gb   40     0      0      0 node_target: COMMON
node15     job-busy      --      --      node15     --      125gb   40     0      0      0 node_target: COMMON
node16     job-busy      --      --      node16     --      125gb   40     0      0      0 node_target: COMMON
node17     job-busy      --      --      node17     --      377gb   40     0      0      0
node18     job-busy      --      --      node18     --      251gb   40     0      0      0 node_target: CHRODY
  
```

Each node has a name...

...we know if it's completely booked or if it has some free processors...

...we also have information on its properties: available memory, number of CPUs & GPUs and to what group it belongs

Use `pbsnodes -aSj` to list all the nodes on the cluster and the jobs that are running on them

```

chloe.quignot@cluster-i2bc: /home/chloe.quignot
chloe.quignot@cluster-i2bc:/home/chloe.quignot$ pbsnodes -aSj
vnode      state      njobs  run  susp  mem      ncpus  nmics  ngpus  jobs
-----
node01     state-unknown  0    0    0    0kb/0kb  0/0    0/0    0/0    --
node02     state-unknown  0    0    0    0kb/0kb  0/0    0/0    0/0    --
node03     state-unknown  0    0    0    0kb/0kb  0/0    0/0    0/0    --
node04     state-unknown  0    0    0    0kb/0kb  0/0    0/0    0/0    --
node05     job-busy      5    5    0    115gb/125gb 0/40   0/0    0/0    224148,224149,224150,224151,224622
node06     job-busy      5    5    0    115gb/125gb 0/40   0/0    0/0    224152,224153,224154,224155,224156
node07     job-busy      5    5    0    115gb/125gb 0/40   0/0    0/0    224157,224158,224159,224160,224161
node08     free          1    1    0    125gb/125gb 20/40  0/0    0/0    226811
node09     job-busy      5    5    0    115gb/125gb 0/40   0/0    0/0    224162,224163,224164,224165,224166
node10     job-busy      5    5    0    115gb/125gb 0/40   0/0    0/0    224167,224168,224169,224170,224171
node11     job-busy      5    5    0    115gb/125gb 0/40   0/0    0/0    224172,224173,224174,224175,224176
node12     job-busy      5    5    0    115gb/125gb 0/40   0/0    0/0    224177,224603,224604,224605,224606
  
```

Number of jobs that are running

Amount of free memory left

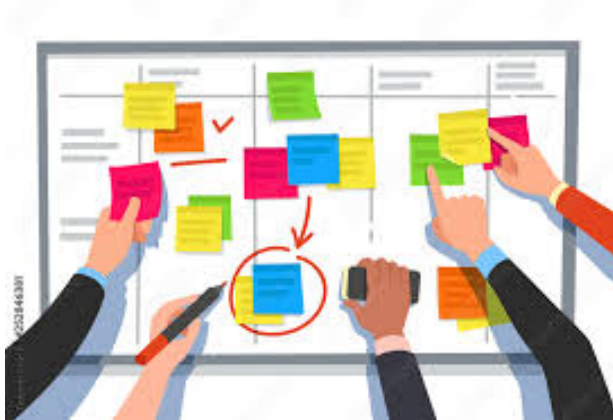
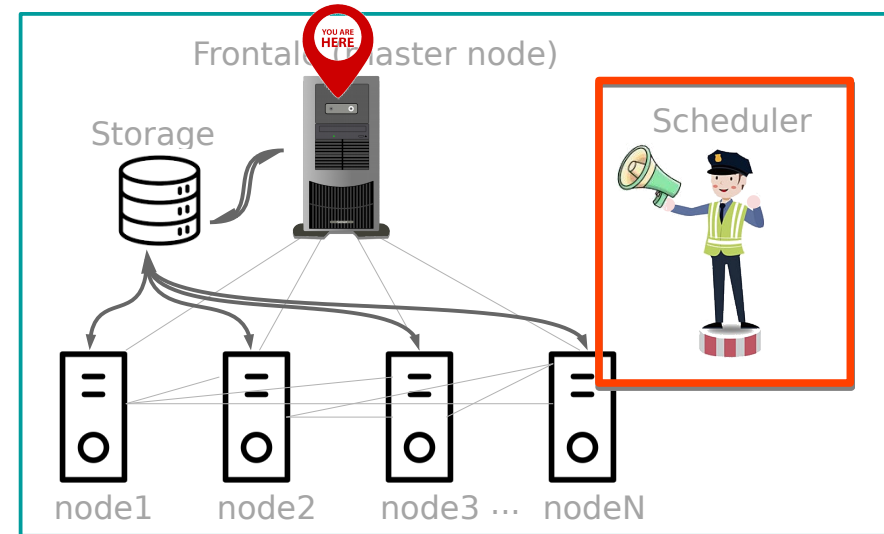
Number of CPUs that are free

Job ids of jobs that are running on that node

Communication between the nodes is done through the OpenPBS system (version 20.0)

Portable **B**atch **S**ystem (PBS) is a software scheduler that:

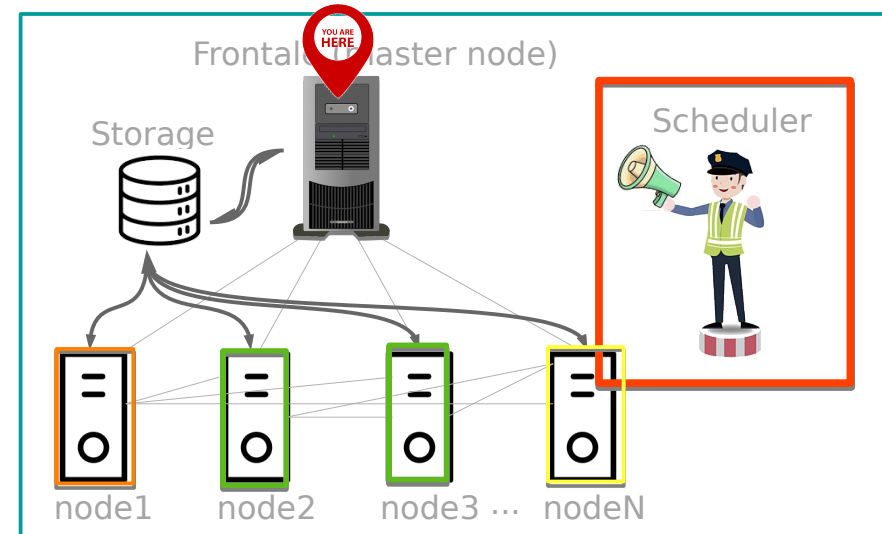
- **manages** jobs, ressources & quotas
- creates a job queue to organise **job priorities**



When you submit a job on the cluster, you submit it to a **queue**.

different queues = different properties

- **common** ← gives access to all shared nodes ("COMMON" nodes)
- **RunXX** (2,4,8,16,32) ← when several jobs, auto management to limit to XX jobs running at a time
- **<group-specific>** ← priority (or exclusive usage) for group members who financed these nodes
- **lowprio** ← access to more nodes but job could be suspended for a while (not high-priority)



`qshow` is an “in-house” script based on `qstat`, it’s only accessible on the Frontale

`qshow` can be used in many ways, it’s to help you get a general view of the cluster resources and their availability

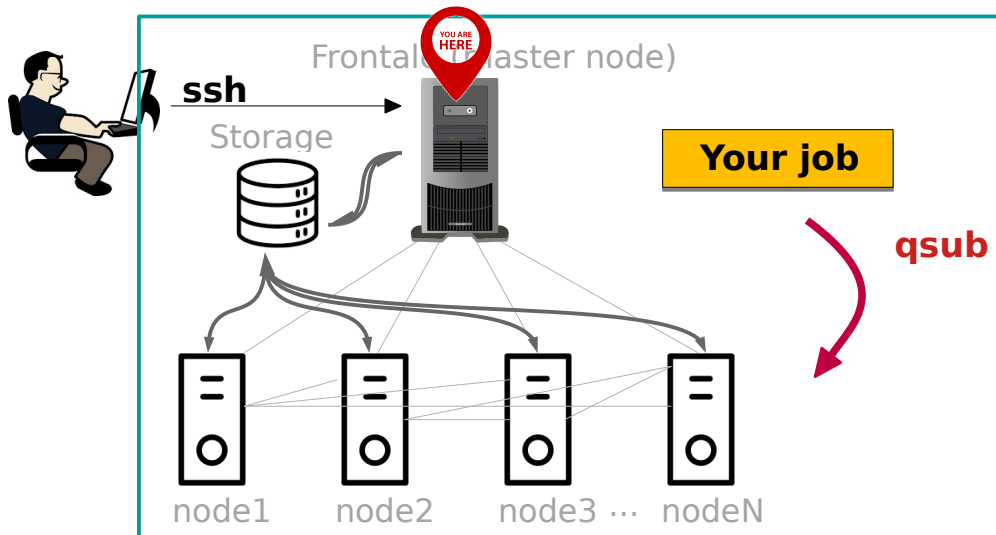
For ex: `qshow -a -q` to list all node types and their associated queues

```
chloe.quignot@cluster-i2bc:/home/chloe.quignot$ qshow -a -q
-----
Nodes AMIG : You can use these nodes by submitting yours jobs in one of the following queues: amig
6 node(s) can run new job
12 of 320 Processors used
No job blocked => Next submitted job will run immediately
No job in restricted queues (run4, run8,...)
-----
Nodes BIM : You can't use these nodes!!
2 node(s) can run new job
2 of 176 Processors used
No job blocked => Next submitted job will run immediately
No job in restricted queues (run4, run8,...)
-----
Nodes COMMON : You can use these nodes by submitting yours jobs in one of the following queues: common,run16,run2,run32,run4,run8
20 node(s) can run new job
20 of 740 Processors used
No job blocked => Next submitted job will run immediately
No job in restricted queues (run4, run8,...)
```

`qshow --help`

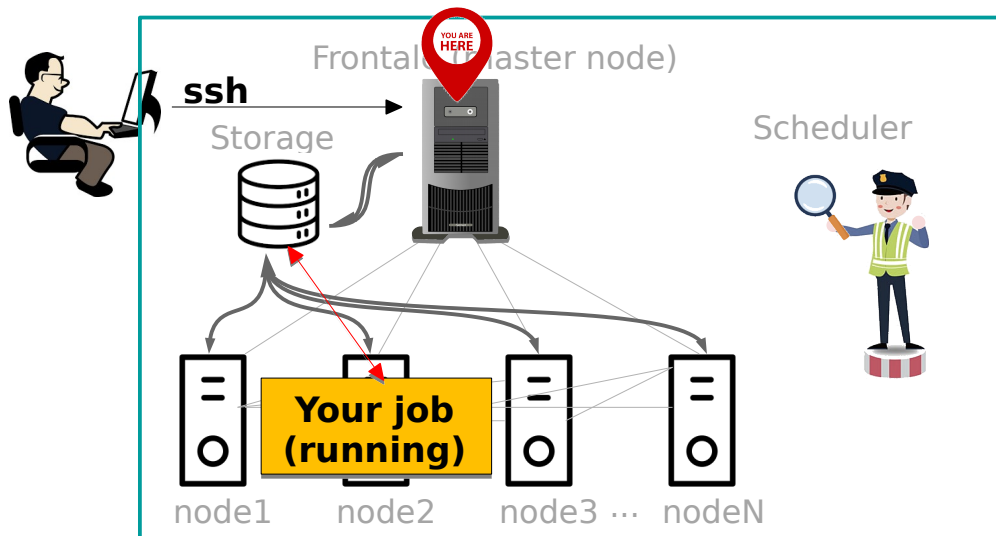
3 important commands in PBSpro:

- **qsub**: to submit the job
-
-



3 important commands in PBSpro:

- **qsub**: to submit the job
- **qstat**: to follow the job (**qshow**: more information on resource consumption)
-

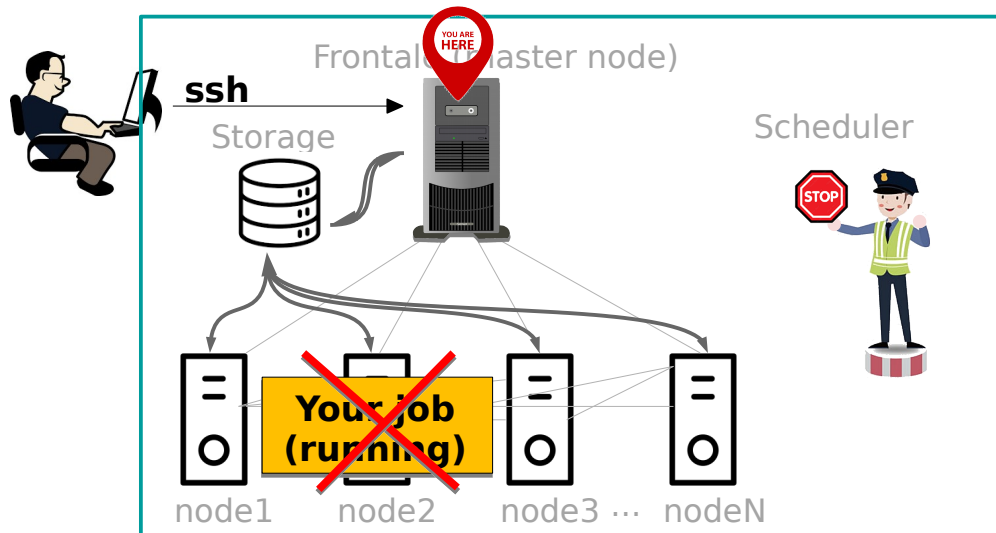


qstat *List status of submitted jobs*



3 important commands in PBSpro:

- **qsub**: to submit the job
- **qstat**: to follow the job (**qshow**: more information on resource consumption)
- **qdel**: to kill the job



qdel Kill the job that is running





Installed programmes



There is a certain number of programmes that are already installed on the nodes of the I2BC cluster (/\ not on the Frontale - only on the nodes!)

Use the module system:

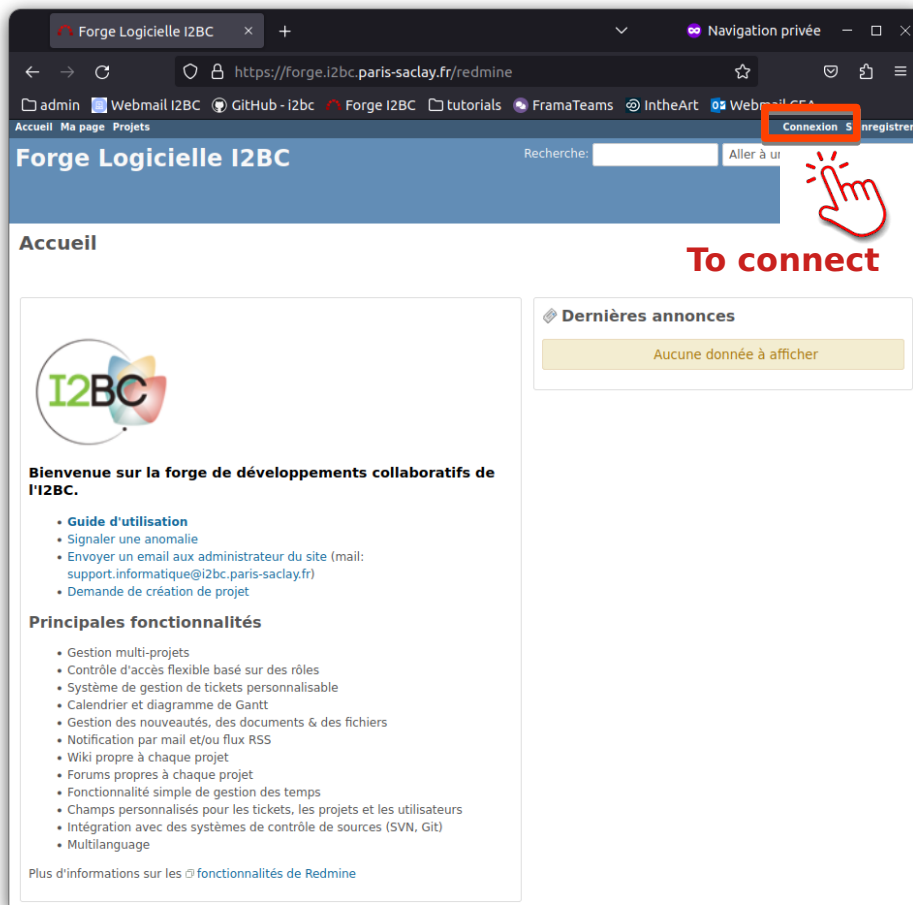
`module avail` to list all available software

`module load` to load a specific programme



Before starting the practical sessions...

We'll be using the Forge at the end of this session to download the example files. Let's just check you all have access to it.



<https://forge.i2bc.paris-saclay.fr/>

The Forge is similar to Github but files are hosted locally on the I2BC servers

Identifiant
Your multi-pass login

Mot de passe Mot de passe perdu
Your multi-pass pwd

Rester connecté

Connexion

Your multi-pass login is the one that you use to connect to your I2BC account (PC, email, etc.). It's often firstname.lastname, but not always!



Let's stay in touch



The screenshot shows a web browser window with the URL `https://framateam.org/signup_user_complete?id=y44u7h1x9jbyikh`. The page header includes the Framateam logo, navigation links for 'APPLICATIONS' and 'S'INSCRIRE', and a 'SE CONNECTER' button. The main content area is titled 'Create your account' and contains the following fields and instructions:

- Email address:** `chloe.quignot@i2bc.paris-saclay.fr`
- Spécifiez votre nom d'utilisateur:** `cquignot`
- Choose a Password:** `.....`

Instructions for the password field: « Votre mot de passe doit contenir entre 10 et 64 caractères et au moins une lettre minuscule, une majuscule, un chiffre et au moins un caractère spécial (ex. : « ~!@#\$\$%^&*() »).

At the bottom of the form is a purple button labeled 'Créer un compte' and a link: 'Créer un compte avec : Mon compte Framagit'.

https://framateam.org/signup_user_complete?id=y44u7h1x9jbyikh_zmtbb6bw3hc

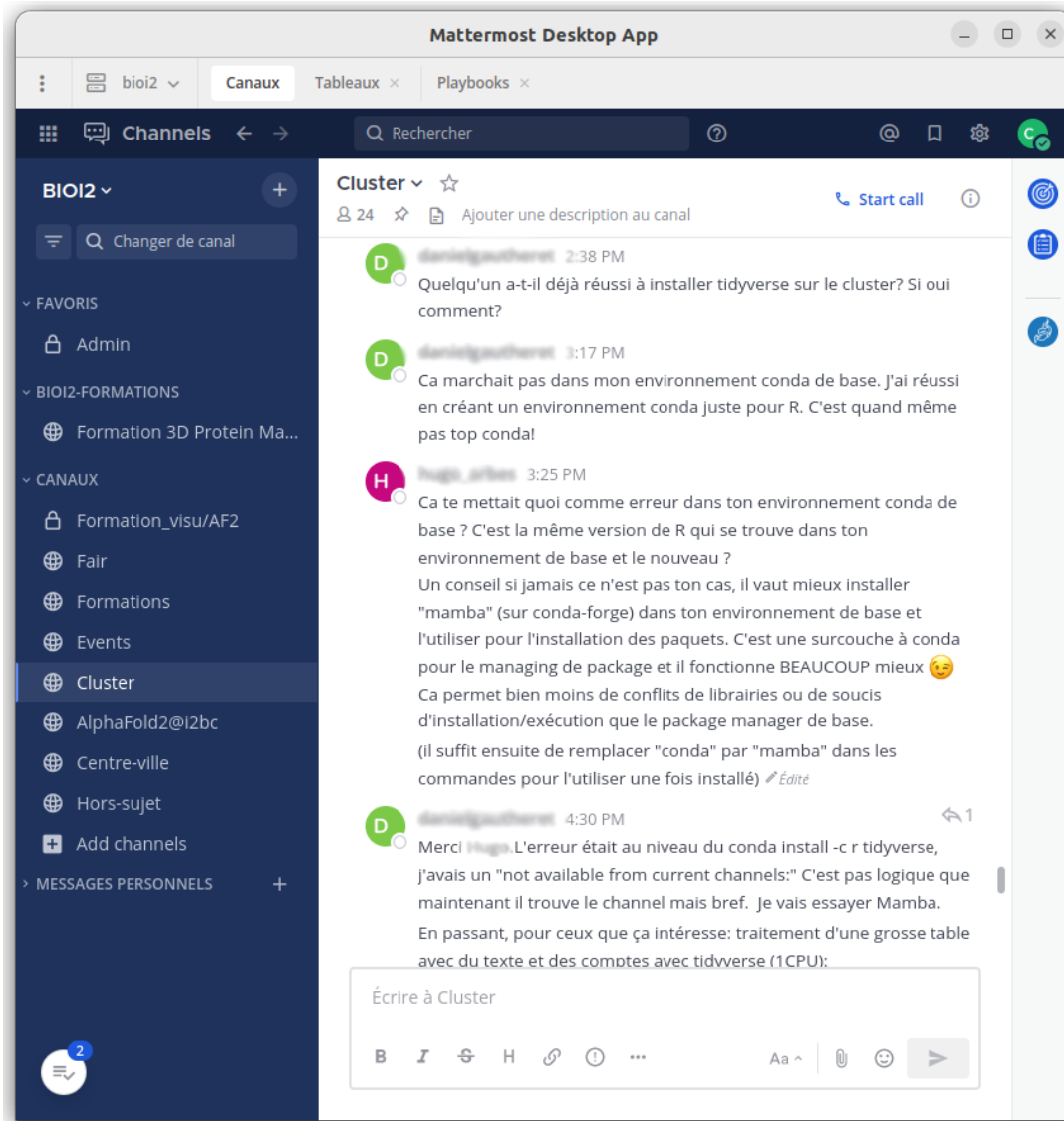
Join the Bioinformatician community of the I2BC on our FramaTeam discussion group

Just create an account with your i2bc email address and click on the link above.

You can also download the app on your computer or mobile phone (Mattermost app - specify `framateam.org` as the server URL)



Let's stay in touch



There's a channel dedicated to news and discussions about the I2BC cluster.

Don't hesitate to join us and ask your questions here.



SICS - IT support



Need help with your computer, internet, some software, the cluster...?

=> the “Support informatique” team (SICS) is there for that
Email: support.informatique@i2bc.paris-saclay.fr

Some tips for a more efficient response:

- * Be clear and concise in the email and email subject
- * Start your subject with a keyword describing the problem category (e.g. [Cluster], [Internet], [Software], etc.)



SICS - IT support



About IT resources on the intranet:

/!\ 2 pages:

- [outils/informatique](#)
- [procedures/info](#)

Information on your IT account, cluster usage, quotas, MyCore (the CNRS OneDrive), etc.



support.informatique@i2bc.paris-saclay.fr



[about & procedures](#)



Accès aux fichiers depuis Internet

[about & procedures](#)



Espaces de stockage

[about](#)



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[about & procedures](#)



Accès aux fichiers depuis Internet

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Espaces de stockage

[about](#)

Keep the FAIR practices in mind!

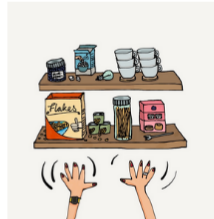
Findable



By 維基小霸王 - Own work, CC BY-SA 4.0, <https://commons.wikimedia.org/w/index.php?curid=88894774>

PID
Repository

Accessible



<https://nilsfirstworldproblems.tumblr.com/post/147555650875/i-cant-reach-the-top-shelves-of-the-kitchen>

Protocols
(free, open, auth.)

Interoperable



By Unknown author - Popular Science Monthly Volume 88, Public Domain, <https://commons.wikimedia.org/w/index.php?curid=22614407>

Standards
(format, vocabulary)

Reusable



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Metadata
License
Origin

<https://doi.org/10.1038/sdata.2016.18>

- * Write notes, keep track of what you're doing (choose the format that suits you best e.g. text files, OneNote, Forge wiki, Joplin, [eLabFTW](#) etc.)
- * Use understandable and logical filenames
- * Organise your workspace (e.g. don't mix scripts and data)
- * Keep track of versions used/downloaded
- * ...