



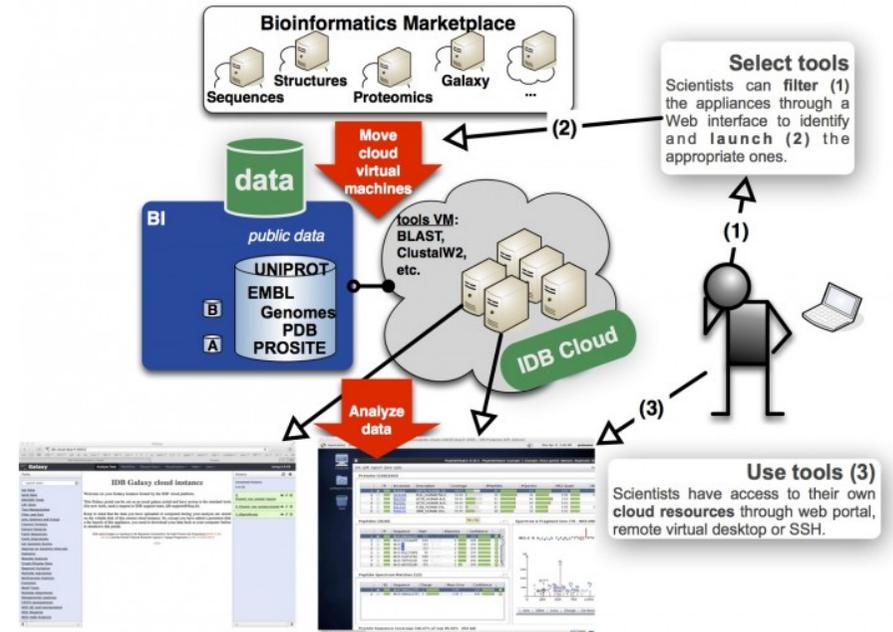
## USING THE IFB CLOUD

<https://www.france-bioinformatique.fr/en/core/cloud-usage>



## USING THE IFB CLOUD

Prior to using the IFB cloud, it is necessary to **fill out a registration application**. **Users must belong to the life science community** (whether they be an academic organization or a commercial entity) and agree to the terms and conditions. This application is **validated by the cloud administrators**. One important point to keep in mind is the personal, non-transferable and revocable nature of the cloud account provided by IFB. Users have exclusive access to the cloud resources they request. Allocation of resources for academic users beyond an initial standard allotment depends on the justification of the user's needs, the scientific excellence of the project and the level of participation of their organization in IFB. Users from commercial entities will pay a fee based on the full cost of the IFB's infrastructure operation.





# USING THE IFB CLOUD

https://cloud.france-bioinformatique.fr/accounts/login/?next=/cloud/



## IFB BIOINFORMATICS CLOUD

YOU ARE SIGNED IN AS DJACOB65

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SIGN IN



Username

Password

Login

[Lost password](#) | [Request account](#)

→ Request an account

If this resource has been useful for your work, could you acknowledge it in your publications, reports and materials by including the following sentence:  
"We would like to thank the French Institute of Bioinformatics (IFB, ANR-11-INBS-0013) for providing storage and computing resources on its national life science Cloud."

\*\*\*

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IFB is the French ELIXIR node





## USING THE IFB CLOUD

<https://cloud.france-bioinformatique.fr/cloud/profile/>



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YOU ARE LOGGED IN AS DJACOB65

Hosted at iris Powered by stratuslab

**Personal Information**

Affiliation ? INRA

City ? Bordeaux

**Cloud Preferences**

Pubkey ? ssh-rsa  
AAAAB3NzaC1yc2EAAAABIwAAAQEA+OwzWpXBLW  
ZDhj00+U4sGQjIcp3vmmCNz2ovtJDgu1kSytCo  
BPnt8BMK9LMJFS35eCorTWlGMrQAP6PE7MefZYC  
hYIK2mRj8fUeXNNmnuHho+JsmDUjq9WziICKFg  
Bca3LEoyw17suh06sLG0xm/Ra1z4NqHmnV2x7/  
mBTRnC7Fr1luCYhXFvGf3nz60SzXBfWik3kaQm  
dYIKGK/koq6rx+VAo6pf3DH4ePRZSvnow0wILH  
WCiHt/FYpQs72NSSjhMFmsSIjUeDDnsuefn5oE  
yqeQEmj0mFDhGgPKrD/pqQbbAbXkdX27TW6khi

Appliance ? Docker (17.06)

Instance type ? -----

Save changes

Your Affiliation / City  
(same as your registration form)

Your Public SSL Key

Appliance

See [http://www.france-bioinformatique.fr/sites/default/files/pages/connexion\\_cloud.pdf](http://www.france-bioinformatique.fr/sites/default/files/pages/connexion_cloud.pdf)

<https://support.automaticsync.com/hc/en-us/articles/202357135-Generating-an-SSH-Key-on-a-Mac-Linux-or-Unix-system>

<https://support.automaticsync.com/hc/en-us/articles/202357115-Generating-an-SSH-Key-on-Windows>



# USING THE IFB CLOUD

<https://cloud.france-bioinformatique.fr/cloud/instance/>



## DASHBOARD



Showing 1 to 2 of 2 entries Search:

<input type="checkbox"/>	ID	Name	<input type="checkbox"/>	Appliance	CPU%	CPU	Mem.	#Storage	Access	<input type="checkbox"/>
<input type="checkbox"/>	14922	myvm1	<input checked="" type="checkbox"/>	Docker (17.06)	2%	4	8	0	ssh	<input checked="" type="checkbox"/>
<input type="checkbox"/>	14943	myvm2	<input checked="" type="checkbox"/>	Docker (17.06)	1%	4	16	0	ssh	<input checked="" type="checkbox"/>
		2			1	8	24	0		

Show  entries



## USING THE IFB CLOUD

<https://cloud.france-bioinformatique.fr/cloud/instance/>



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DASHBOARD

Hosted at Powered by

Shutdown ▾ Go Get IPs Rename New Instance New Instance New vDisk Show Instances Show vDisks

Showing 1 to 2 of 2 entries

ID	
14922	m
14943	m

Show 25 entries

### Launch a virtual machine

**Choose The Appliance**

Appliance ? Docker (17.06) ▾

Filter by ?  
--- THEMATIC FIELDS --- ▾  
--- TOOLS --- ▾

**Configure Your Virtual Machine**

Name ?

Unique ?

Type ? c2.large (4 CPU, 8GB RAM) ▾

Number ?

**Plug Your Additional Storage**

Persistent disk ?

Run Cancel

Appliance & VM Type



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<https://cloud.france-bioinformatique.fr/cloud/instance/>

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DASHBOARD

Hosted at Powered by

Shutdown ▾ Go Get IPs Rename New Instance New vDisk Show Instances Show vDisks

Showing 1 to 2 of 2 entries Search:

<input type="checkbox"/>	ID	Name	Appliance	CPU%	CPU	Mem.	#Storage	Access	<input type="checkbox"/>
<input type="checkbox"/>	14922	myvm1	Docker (17.06)	2%	4	8	0	ssh	<input type="checkbox"/>
<input type="checkbox"/>	14943	myvm2					0	ssh	<input type="checkbox"/>

Show 25 ▾ entries First Previous 1 Next Last

**Connection Information** ✕

**Parameters:**  
host = 192.54.201.94  
port = 22  
identifiant = root

**Command-line connection:**  
ssh -A -p 22 root@192.54.201.94

**Command-line file transfers:**  
scp -P 22 *localfile* root@192.54.201.94:  
sftp -oPort=22 root@192.54.201.94

*Status must be 'running' (\*)*

*Get the IP of the VM*

*(\*) Just after creating a VM, its status is 'pending'. You have to wait a few minutes so that the VM status will be stated as 'running'.*

SSH connection to the VM using your shell terminal (Cygwin/xterm, PuTTY, ... )

```
root@vm0063: ~  
$  
DJ@DJ-PC /cygdrive/c/Workdir/Metabolomic/NMRProcFlow/dockerApps  
$ ssh root@192.54.201.94  
Welcome to Ubuntu 14.04.4 LTS (GNU/Linux 3.13.0-65-generic x86_64)  
  
* Documentation:  https://help.ubuntu.com/  
  
System information as of Wed Sep 13 10:38:50 UTC 2017  
  
System load:  0.0          Processes:            127  
Usage of /:   41.3% of 10.69GB  Users logged in:     0  
Memory usage: 1%          IP address for eth0: 192.54.201.94  
Swap usage:   0%           IP address for docker0: 172.17.0.1  
  
Graph this data and manage this system at:  
https://landscape.canonical.com/  
  
378 packages can be updated.  
282 updates are security updates.  
  
New release '16.04.3 LTS' available.  
Run 'do-release-upgrade' to upgrade to it.  
  
Last login: Wed Sep 13 10:38:52 2017 from 147.100.103.179  
root@vm0063:~#  
root@vm0063:~#  
root@vm0063:~#
```

Get the name of the VM



USING THE IFB CLOUD



## Install NMRProcFlow on the Virtual Machine

Within the shell terminal (Cygwin/xterm, PuTTY, ... ):

```
# Get the install script
```

```
cd /home
```

```
wget http://www.nmrprocflow.org/themes/scripts/install\_npflow\_VMcloud.sh
```

```
# Execute the script
```

```
sh ./install_npflow_VMcloud.sh
```

```
# Launch the application
```

```
cd /opt/npflow
```

```
./npflow start
```

Finished !! 😊





# USING THE IFB CLOUD



<http://vmXXXX.france-bioinformatique.fr/npflow/>

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## Acknowledgements

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