



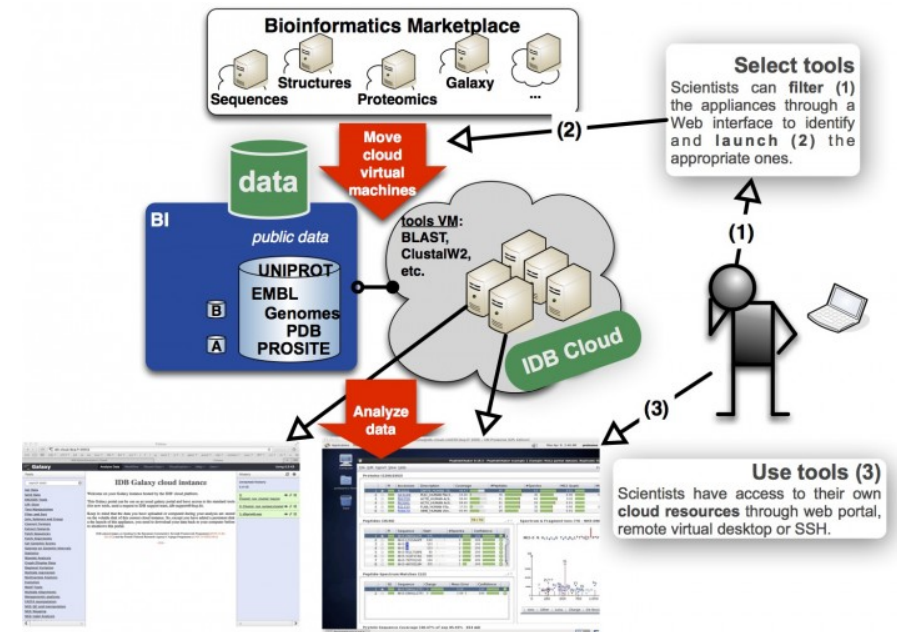
USING THE IFB CLOUD

<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."

IFB acknowledges funding by the call "Infrastructures in Biology and Health" in the framework of the French "Investments for the Future" (ANR-11-INBS-0013) initiative, and EU H2020 projects CYCLONE (644925), EXCELERATE (676559) and EGI-Engage (654142).



Inserm



IFB is the French ELIXIR node





USING THE IFB CLOUD

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



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SETTINGS

Hosted at **oris** Powered by **stratuslab**

Personal Information

Affiliation ?
City ?

Cloud Preferences

Pubkey ?

Appliance ?
Instance type ?

→ 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

<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/>





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You are signed in as **DJACOB65**


 **DASHBOARD**

Hosted at  Powered by 

Shutdown ▾ Go Get IPs Rename

New Instance New vDisk Show Instances Show vDisks

Showing 0 to 0 of 0 entries Search:

<input type="checkbox"/>	ID	Name	Appliance	CPU%	CPU	Mem.	#Storage	Access	
No instances available.									
<input type="checkbox"/>	0		0		0	0	0		

Show entries

[First](#) [Previous](#) [Next](#) [Last](#)



USING THE IFB CLOUD



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

IFB BIOINFORMATICS CLOUD

News | Dashboard | Monitor | Settings | Help | Sign out

You are signed in as DJACOB65

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Shutdown Go Get IPs Rename

Showing 0 to 0 of 0 entries

0 entries

New Instance New vDisk Show Instances Show vDisks

Launch a virtual machine

Choose The Appliance

Appliance ? **Docker (17.06)**

Filter by ? --- THEMATIC FIELDS ---

--- TOOLS ---

Configure Your Virtual Machine

Name ? bsflow

Unique ? ☒

Type ? **c2.small (1 CPU, 2GB RAM)**

Number ?

Plug Your Additional Storage

Persistent disk ?

c2.small (1 CPU, 2GB RAM)
c3.medium (2 CPU, 8GB RAM)
m1.medium (2 CPU, 32GB RAM)
c2.large (4 CPU, 8GB RAM)
c3.large (4 CPU, 16GB RAM)
c2.xlarge (8 CPU, 16GB RAM)
c3.xlarge (8 CPU, 32GB RAM)

Run Cancel

Appliance & VM Type



USING THE IFB CLOUD



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

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DASHBOARD

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Shutdown Go Get IPs Rename

New Instance New vDisk Show Instances Show vDisks

Showing 1 to 1 of 1 entries

	ID	Name	Appliance	CPU%	CPU	Mem.	#Storage	Access	
	15121	bsflow	Docker (17.06)	0%	8	0	0		
	1		pending	1	8	0	0		

Show 25 entries

First Previous 1 Next Last

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'.



USING THE IFB CLOUD



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

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DASHBOARD

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Shutdown Go Get IPs Rename Status must be 'running' New Instance New vDisk Show Instances Show vDisks

Showing 1 to 1 of 1 entries

ID	Name	Status	Appliance	CPU%	CPU	Mem.	#Storage	Access
15118	bsflow		Docker (17.06)	1%	8	32	0	ssh

Show 25 entries

Connection Information

Parameters:
host = 192.54.201.119
port = 22
identifiant = root

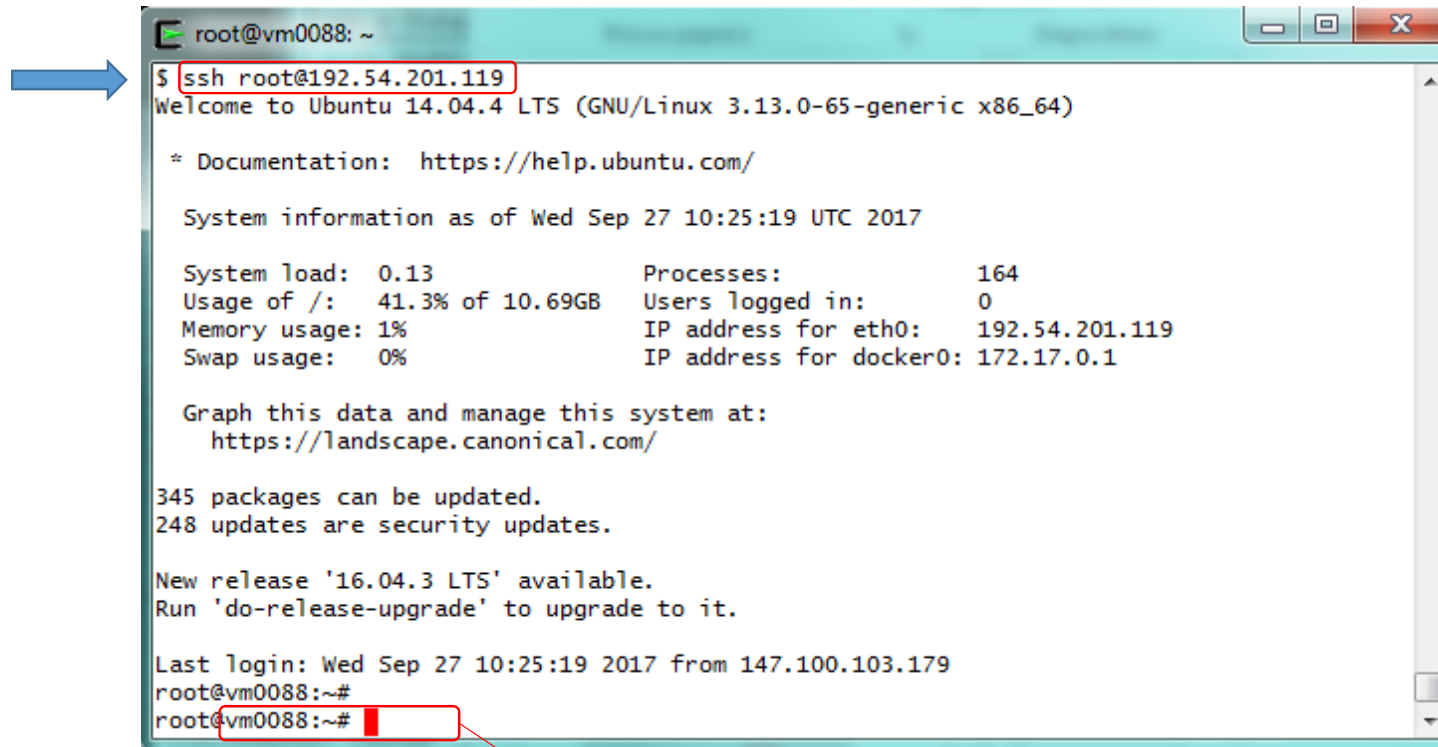
Command-line connection:
ssh -A -p 22 root@192.54.201.119

Command-line file transfers:
scp -P 22 \${localfile} root@192.54.201.119:
sftp -oPort=22 root@192.54.201.119

Close

Get the IP of the VM

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



```
root@vm0088: ~  
$ ssh root@192.54.201.119  
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 27 10:25:19 UTC 2017  
  
System load:  0.13           Processes:            164  
Usage of /:   41.3% of 10.69GB Users logged in:       0  
Memory usage: 1%           IP address for eth0:   192.54.201.119  
Swap usage:   0%           IP address for docker0: 172.17.0.1  
  
Graph this data and manage this system at:  
https://landscape.canonical.com/  
  
345 packages can be updated.  
248 updates are security updates.  
  
New release '16.04.3 LTS' available.  
Run 'do-release-upgrade' to upgrade to it.  
  
Last login: Wed Sep 27 10:25:19 2017 from 147.100.103.179  
root@vm0088:~#  
root@vm0088:~#
```

Get the name of the VM



USING THE IFB CLOUD



Install BioStatFlow 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\_bsflow\_VMcloud.sh
```

```
# Execute the script
```

```
sh ./install_bsflow_VMcloud.sh
```

```
# Launch the application
```

```
cd /opt/bsflow
```

```
./bsflow start
```

Finished !! ☺

BioStatFlow

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USING THE IFB CLOUD



Get the install script

→ root@vm0088:/home# `wget http://www.nmrprocflow.org/themes/scripts/install_bsflow_VMcloud.sh`
--2017-09-27 10:46:12-- http://www.nmrprocflow.org/themes/scripts/install_bsflow_VMcloud.sh
Resolving www.nmrprocflow.org (www.nmrprocflow.org)... 147.100.164.61
Connecting to www.nmrprocflow.org (www.nmrprocflow.org)|147.100.164.61|:80... connected.
HTTP request sent, awaiting response... 200 OK
Length: 1766 (1.7K) [text/x-sh]
Saving to: 'install_bsflow_VMcloud.sh'

100%[=====]

2017-09-27 10:46:13 (265 MB/s) - 'install_bsflow_VMcloud.sh' saved [1766/1766]



USING THE IFB CLOUD



Execute the script

→ root@vm0088:/home# `sh ./install_bsflow_VMcloud.sh`
MY IP = 194.54.201.119
latest: Pulling from bmplatform/biostatflow
7b6bb4652a1b: Pull complete
1ba9c3e0ba6a: Pull complete
b9a9a4307586: Pull complete
dbc75fb0ffce: Pull complete
4b1d6bd6cb28: Pull complete
1b36c191e15f: Pull complete
cf3b4fb4d3fd: Pull complete
626d3ef0c33d: Pull complete
5a0d0fc3ba71: Pull complete
4946d11e04fc: Pull complete
635c2cb187d8: Pull complete
4d412422801f: Pull complete
290180a23dfc: Pull complete
65d237d86ffa: Pull complete
767309a1ea12: Pull complete
f506c4e361ab: Pull complete
52eddb729eee: Pull complete
5b01f3bd4060: Pull complete
Digest: sha256:258cec328756e91a8c6cc1b92385ff5fcae36bb2d5c6356c62f26d36038d8ddd
Status: Downloaded newer image for bmplatform/biostatflow:latest
root@vm0088:/home#
→ root@vm0088:/home# `docker images`

REPOSITORY	TAG	IMAGE ID	CREATED	SIZE
bmplatform/biostatflow	latest	989e77216b2d	2 weeks ago	1.795 GB

root@vm0088:/home#

BioStatFlow

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USING THE IFB CLOUD



Launch the application

root@vm0088:/home# `cd /opt/bsflow/`

root@vm0088:/opt/bsflow# `ll`

total 16

drwxr-xr-x 3 root root 4096 Sep 27 10:47 ./

drwxr-xr-x 5 root root 4096 Sep 27 10:46 ../

-rwxr-xr-x 1 root root 1274 Sep 27 10:47 bsflow*

drwxr-xr-x 2 root root 4096 Sep 27 10:46 etc/

root@vm0088:/opt/bsflow#

root@vm0088:/opt/bsflow# `./bsflow start`

5f15eed7fd3bc55f6e24a77adf7fc87aa50924c0ee1b3930e5c8f493572c1e2e

root@vm0088:/opt/bsflow#

root@vm0088:/opt/bsflow#

root@vm0088:/opt/bsflow# `./bsflow ps`

CONTAINER ID	IMAGE	COMMAND	CREATED	STATUS	PORTS	NAMES
5f15eed7fd3b	bmlatform/biostatflow:latest	"/usr/bin/launch-serv"	6 seconds ago	Up 5 seconds	0.0.0.0:80->80/tcp	bsflow

root@vm0088:/opt/bsflow#

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USING THE IFB CLOUD



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

← → ↻

BioStatFlow
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Dataset Workflow Results

Authentication
[Register](#)
[Log in](#)

BioStatFlow: Statistical Analysis Workflow for "OMICS" Data

[Start a new session](#) ⓘ

You can work on a previous session - **Session ID:** [Load](#)


[See the Quick tutorial online.](#)


BioStatFlow facilitates access to statistical tools for biologists that are not specialists. It has been designed to execute statistical analyses sequentially, i.e. a linear chain of statistical analysis, so-called *Workflow* in BioStatFlow

BioStatFlow helps disseminate the results of statistical analyzes by saving them in a persistent session so that they can be fully restored. You can thus provide the ID of your session when publishing results.

BioStatFlow allows bioinformaticians to easily integrate a new method of statistical analysis in a workflow, or even create their own workflows.

BioStatFlow on the IFB Cloud You will find all information on how to install and launch BioStaFlow on the IFB Cloud in this [PDF](#)

**INRA**
SCIENCE & IMPACT

This application is optimized for:  chrome

Put the right name of the VM (e.g. 'vm0088' in case of our example)

Enjoy !! 😊

BioStatFlow

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USING THE IFB CLOUD



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BioStatFlow

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