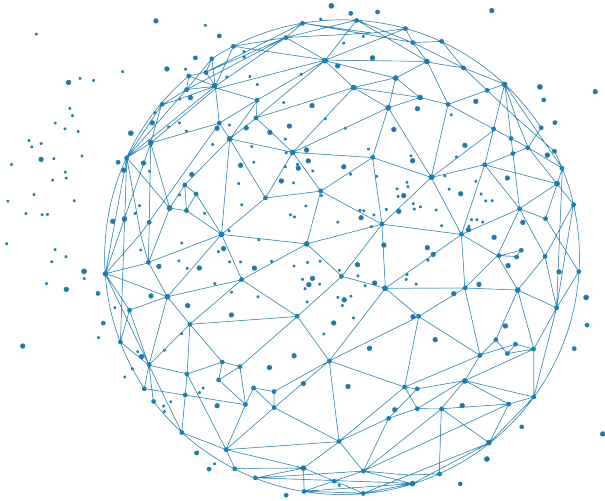


First edition 2023 in Fréjus



# Technique & tests

Lucie Khamvongsa-Charbonnier

DOI version final



## Cloud

- Virtual machine (VM)
- Biosphere nominative account
- Https, ssh, remote desktop with X2Go
  
- Network workshop (R1/R2)
- Multivariate analysis workshop (MV1/MV2)

## Cluster

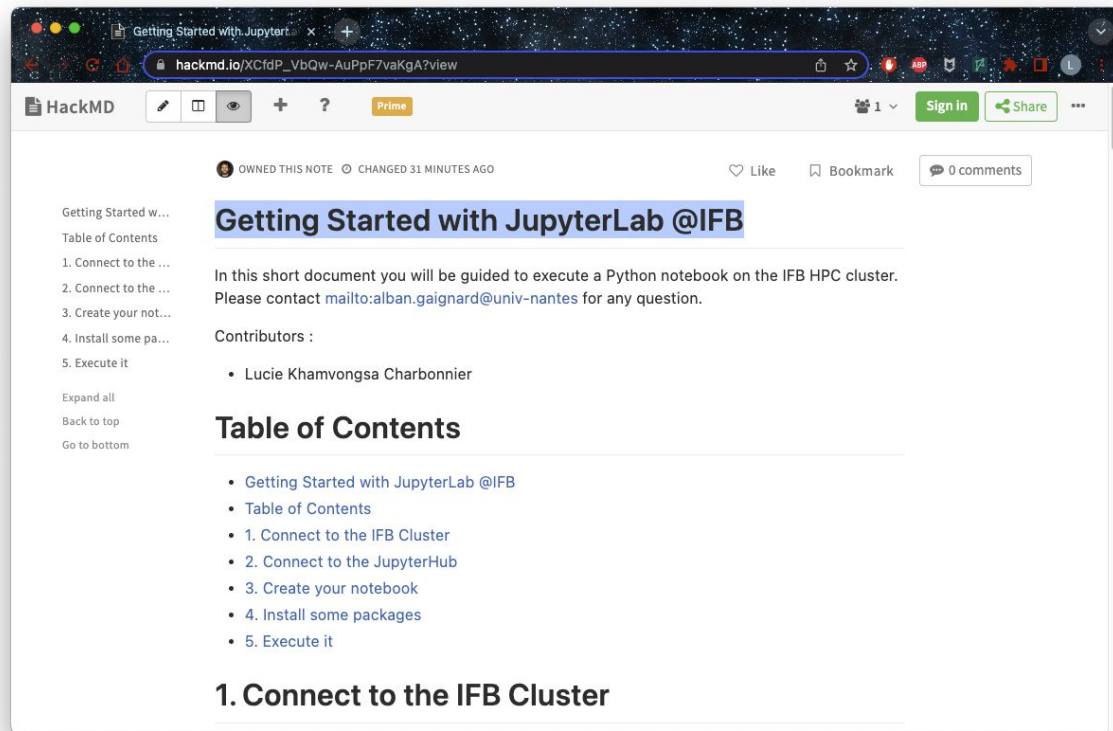
- JupyterLab
- Generic account
- Https
  
- Semantic web workshop

## Cluster

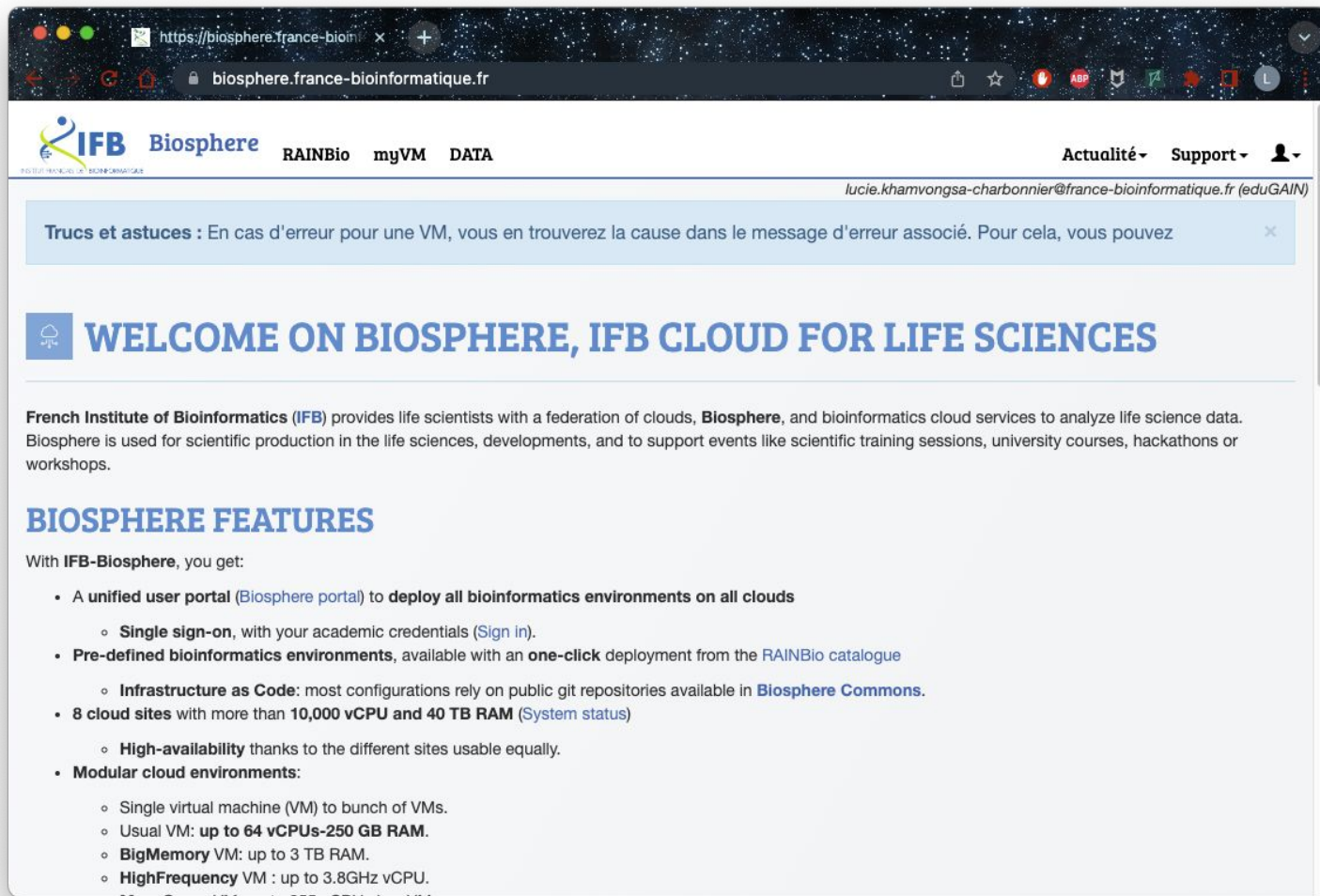
- JupyterLab
- Generic account
- Https
  
- Semantic web workshop

1. Distribution generic account
2. Go to moodle folder **Tech & tests**

### *Getting Started with JupyterLab @IFB*

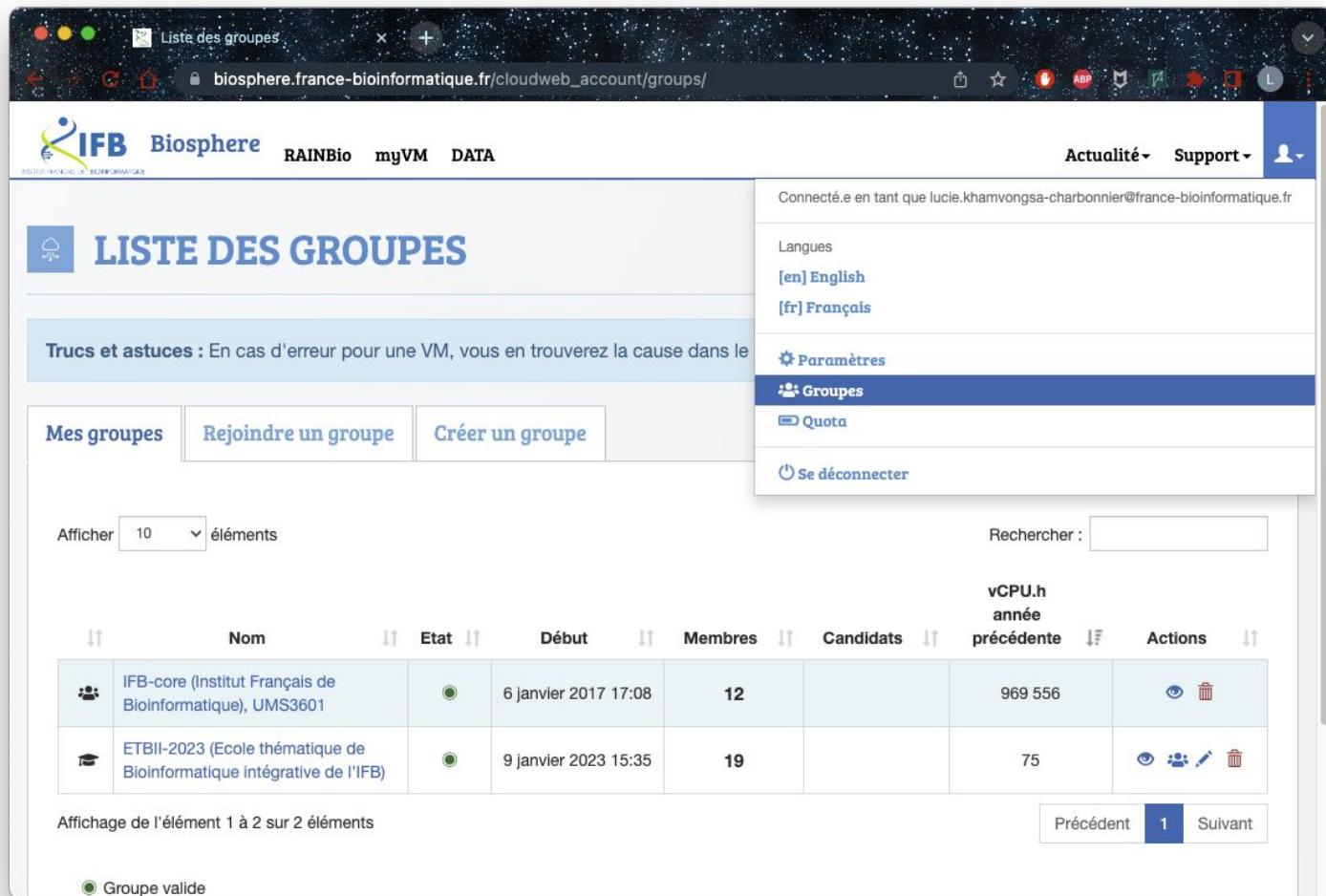


The screenshot shows a web browser displaying a HackMD document. The browser's address bar shows the URL `hackmd.io/XCfdP_VbQw-AuPpF7vaKgA?view`. The HackMD interface includes a navigation menu on the left with a 'Table of Contents' section listing five items: '1. Connect to the ...', '2. Connect to the ...', '3. Create your not...', '4. Install some pa...', and '5. Execute it'. The main content area features a title 'Getting Started with JupyterLab @IFB' in a blue box, followed by a paragraph: 'In this short document you will be guided to execute a Python notebook on the IFB HPC cluster. Please contact <mailto:alban.gaignard@univ-nantes> for any question.' Below this is a 'Contributors' section listing 'Lucie Khamvongsa Charbonnier'. A 'Table of Contents' section lists the same five items as the left menu. The first item, '1. Connect to the IFB Cluster', is highlighted in blue.



The screenshot shows the homepage of the Biosphere website. At the top, there is a navigation bar with the IFB Biosphere logo, links for RAINBio, myVM, and DATA, and user account options for 'Actualité' and 'Support'. A user email 'lucie.khamvongsa-charbonnier@france-bioinformatique.fr (eduGAIN)' is displayed. Below the navigation is a light blue banner with the text 'Trucs et astuces : En cas d'erreur pour une VM, vous en trouverez la cause dans le message d'erreur associé. Pour cela, vous pouvez'. The main heading is 'WELCOME ON BIOSPHERE, IFB CLOUD FOR LIFE SCIENCES'. The introductory paragraph states: 'French Institute of Bioinformatics (IFB) provides life scientists with a federation of clouds, Biosphere, and bioinformatics cloud services to analyze life science data. Biosphere is used for scientific production in the life sciences, developments, and to support events like scientific training sessions, university courses, hackathons or workshops.' The 'BIOSPHERE FEATURES' section lists the following:

- A unified user portal (Biosphere portal) to deploy all bioinformatics environments on all clouds
  - Single sign-on, with your academic credentials (Sign in).
- Pre-defined bioinformatics environments, available with an one-click deployment from the RAINBio catalogue
  - Infrastructure as Code: most configurations rely on public git repositories available in Biosphere Commons.
- 8 cloud sites with more than 10,000 vCPU and 40 TB RAM (System status)
  - High-availability thanks to the different sites usable equally.
- Modular cloud environments:
  - Single virtual machine (VM) to bunch of VMs.
  - Usual VM: up to 64 vCPUs-250 GB RAM.
  - BigMemory VM: up to 3 TB RAM.
  - HighFrequency VM : up to 3.8GHz vCPU.



The screenshot shows a web browser window with the URL `biosphere.france-bioinformatique.fr/cloudweb_account/groups/`. The page title is "Liste des groupes". The navigation bar includes "IFB Biosphere", "RAINBio", "myVM", "DATA", "Actualité", and "Support". A user profile dropdown menu is open, showing the user is logged in as "Lucie.Khamvongsa-charbonnier@france-bioinformatique.fr" and offering options for language (English/French), parameters, groups, quota, and disconnect.

## LISTE DES GROUPES

Trucs et astuces : En cas d'erreur pour une VM, vous en trouverez la cause dans le

Mes groupes   Rejoindre un groupe   Créer un groupe

Afficher  éléments   Rechercher :

	Nom	Etat	Début	Membres	Candidats	vCPU.h année précédente	Actions
	IFB-core (Institut Français de Bioinformatique), UMS3601		6 janvier 2017 17:08	12		969 556	
	ETBII-2023 (Ecole thématique de Bioinformatique intégrative de l'IFB)		9 janvier 2023 15:35	19		75	

Affichage de l'élément 1 à 2 sur 2 éléments   Précédent 1 Suivant

Groupe valide

The screenshot shows a web browser window with the URL `https://biosphere.france-bioinformatique.fr/cloudweb_account/settings/`. The page header includes the IFB Biosphere logo and navigation links for RAINBio, myVM, and DATA. On the right, there are links for 'Actualité' and 'Support', along with a user profile icon. The main content area is titled 'VOS PARAMÈTRES' and contains a section for 'Informations personnelles'. A dropdown menu is open, showing options for 'Langues' (English and Français), 'Paramètres', 'Groupes', 'Quota', and 'Se déconnecter'. The personal information table is as follows:

Informations personnelles	
Adresse électronique	lucie.khamvongsa-charbonnier@fr
Affiliation fournie par la fédération d'identité	
Prénom	Lucie
Nom	KHAMVONGSA-CHARBONNIER
Ville et code postal	13007
Formation initiale (optionel)	•
Pubkey	ssh-rsa AAAAB3NzaC1yc2EAAAADAQABAAQGDQCF06yW56oAHHalXiwlbec6 AH6nfvYrplP/WxWmrN4T1r39nbFbhjZ83rGl+bsl0M/CkaDpc9ktBj+ECB AvnEC9abYh2XCjBsdhpmMb//VjxRhGU0nyk6zrBwC6qcqmaD0ZeTKSr1 I5DvS/bsAZsqYqX61cxdeeRbdH6eYd2RSASRBerLcDDqfT3GxcyuEXsh wv8eb5nZ8hI7M3vqnwk5Qsr/9E4BHtidqDA5XQWgW3A5qKarlG9JhN5



RAINBio

biosphere.france-bioinformatique.fr/catalogue/

IFB Biosphere RAINBio myVM DATA

Actualité - Support - lucie.khanvongsas-charbonnier@france-bioinformatique.fr (eduGAIN)

## RAINBIO - APPLIANCES BIOINFORMATIQUES DANS LE CLOUD

Catalogue des appliances bioinformatiques dans le cloud, filtrez-les en utilisant les termes présents dans l'ontologie EDAM, ou en langage naturel.

Trucs et astuces : En cas d'erreur pour une VM, vous en trouverez la cause dans le message d'erreur associé. Pour cela, vous pouvez afficher la page de la VM en cliquant sur son ID. Dans cette page, vous trouverez le

App Store (59) Appliances Outils Topics

<b>AnalysesSV</b> <ul style="list-style-type: none"><li>bioconductor, BEDTools, BWA, Jupyter, Matplotlib, pandas, S</li><li>RNA polymorphism, Genetic variation, Genotyping experiment, GWAS site</li></ul>	<b>ANF MetaBioDiv</b> <ul style="list-style-type: none"><li>Bioconductor, DESeq2, devtools (R), ggplot2, gridExtra</li><li>Bioinformatics, Computational biology, Data management, Tra</li></ul>	<b>Askomics</b> <ul style="list-style-type: none"><li>AskOmic</li><li>Data integration and warehousing, Data visu</li></ul>	<b>BactComparativeGenomics</b> <ul style="list-style-type: none"><li>ImageJ2, Jupyter, MACS2, Matplotlib, Nextflow, pandas</li><li>Imaging, Mathematics, Statistics and probability, Chem</li></ul>	<b>Bacterial Genomics</b> <ul style="list-style-type: none"><li>HMMER, InSight, SGE - GridEngine, Ubuntu, Web interface</li><li>Protein folds and structural domains, Sequence comparison, Sequ</li></ul>	<b>Bioimaging</b> <ul style="list-style-type: none"><li>Bureau virtuel, Icy, ImageJ-Fiji, X2Go, XFCE</li><li>Informatics, Data visualisation, Imaging</li></ul>
<b>BioPipes</b> <ul style="list-style-type: none"><li>bioconda, cwltool, Docker, Nextflow, Snakemake</li><li>Informatics, Bioinformatics, Workflow</li></ul>	<b>bistar</b> <ul style="list-style-type: none"><li>bioconda, Bowtie2, FastQC, Snakemake</li><li>Bioinformatics, Genomics, Microarray, Transcriptome</li></ul>	<b>CentOS 7</b> <ul style="list-style-type: none"><li>Ansible, bioconda, Docker</li><li>Informatics, Bioinformatics</li></ul>	<b>CentOS 7 Desktop</b> <ul style="list-style-type: none"><li>Ansible, bioconda, Bureau virtuel, Docker</li><li>Informatics, Bioinformatics</li></ul>	<b>CoursAnalysesNanoporeSG</b> <ul style="list-style-type: none"><li>bandage, Jupyter</li><li>Data architecture, analysis and design, Mathematics, Statistics</li></ul>	<b>Cytoscape</b> <ul style="list-style-type: none"><li>Bureau virtuel, Cytoscape, X2Go, XFCE</li><li>Bioinformatics, Data visualization, Molecular Inter</li></ul>
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Appliance ETBII AnalyseMultivariée

Actualité - Support -

lucie.khamvongsa-charbonnier@france-bioinformatique.fr (eduGAIN)

EDITER LANCER

▶ LANCER  
▶ DÉPLOIEMENT AVANCÉ

**Trucs et astuces :** En cas d'erreur pour une VM, vous en trouverez la cause dans le message d'erreur associé. Pour cela, vous pouvez afficher la page d'erreur.

↓ Exporter en md

### Description

Environnement Rstudio pour l'atelier Analyse Multivariée de l'école ETBII-2023 (<https://www.france-bioinformatique.fr/formation/etbii>).

Site web	<a href="https://www.france-bioinformatique.fr/formation/etbii/">https://www.france-bioinformatique.fr/formation/etbii/</a>
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### Domaines associés

Biology ○ — Genetics ● — Molecu

### Outils

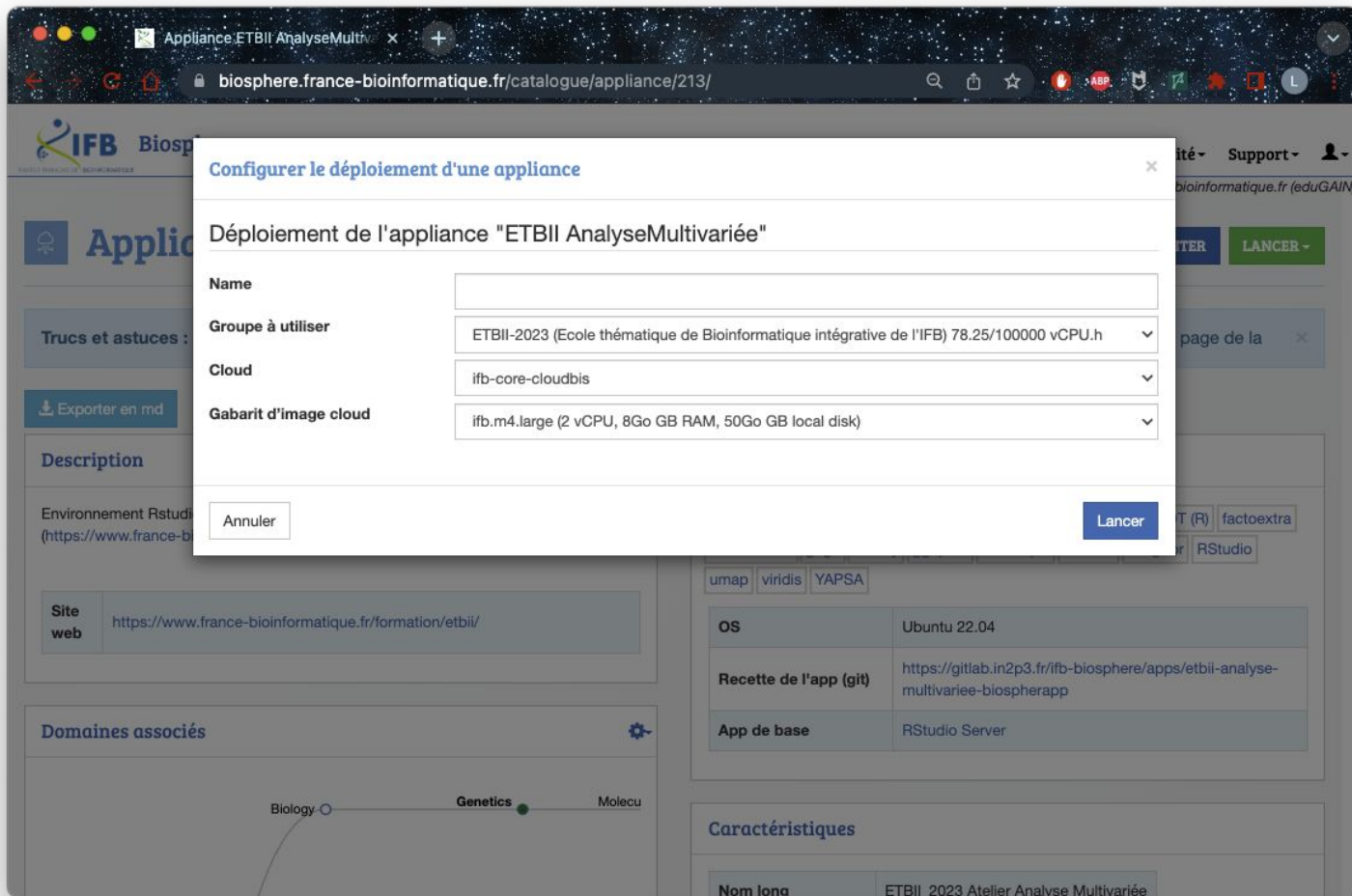
BiocStyle	ButchR	clusterProfiler	ComplexHeatmap	DESeq2	DT (R)	factoextra	
FactoMineR	gage	GGally	ggupset	MMseqs2	MOFA2	msigdb	RStudio
umap	viridis	YAPSA					

OS	Ubuntu 22.04
Recette de l'app (git)	<a href="https://gitlab.in2p3.fr/ifb-biosphere/apps/etbii-analyse-multivariée-biospherapp">https://gitlab.in2p3.fr/ifb-biosphere/apps/etbii-analyse-multivariée-biospherapp</a>
App de base	RStudio Server

### Caractéristiques

Nom long	ETBII 2023 Atelier Analyse Multivariée
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**Configurer le déploiement d'une appliance**

Déploiement de l'appliance "ETBII AnalyseMultivariée"

Name:

Groupe à utiliser: ETBII-2023 (Ecole thématique de Bioinformatique intégrative de l'IFB) 78.25/100000 vCPU.h

Cloud: ifb-core-cloudbis

Gabarit d'image cloud: ifb.m4.large (2 vCPU, 8Go GB RAM, 50Go GB local disk)

**Site web**: <https://www.france-bioinformatique.fr/formation/etbii/>

**OS**: Ubuntu 22.04

**Recette de l'app (git)**: <https://gitlab.in2p3.fr/ifb-biosphere/apps/etbii-analyse-multivariee-biospherapp>

**App de base**: RStudio Server

**Nom long**: ETBII\_2023 Atelier Analyse Multivariée

≈ 20 min

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The main content area is titled "CLOUD" and features a notification banner: "Trucs et astuces : En cas d'erreur pour une VM, vous en trouverez la cause dans le message d'erreur associé. Pour cela, [X]".

Below the banner is a "Déploiements" section with a refresh icon and a toggle switch. It contains a table of VM deployments with the following columns: ID, Nom, Début, Groupes, Spéc, Cloud, and Accès.

ID	Nom	Début	Groupes	Spéc	Cloud	Accès
23318	ETBII Reseaux (1.1)	↑ Jan 12...	IFB-core	2 8 50	ifb-core-cloudbis	ssh https https Params
23302	ETBII AnalyseMultivariée (1.0)	↑ Jan 11...	IFB-core	16 64 400	ifb-core-cloudbis	https Params
23228	Rstudio Génomique (1.0)	↑ Jan 03...	IFB-core	4 16 100	ifb-core-cloudbis	https Params



RAINBio

biosphere.france-bioinformatique.fr/catalogue/

IFB Biosphere RAINBio myVM DATA

Actualité - Support - lucie.khanvongsas-charbonnier@france-bioinformatique.fr (eduGAIN)

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<https://wiki.x2go.org/doku.php/doc:installation:x2goclient>

The screenshot shows a web browser window displaying the X2Go wiki page. The browser's address bar shows the URL `https://wiki.x2go.org/doku.php/doc:installation:x2goclient`. The page header includes the X2Go logo, the text "X2Go - everywhere@home", a search bar, and navigation links for "Admin", "Log In", "Recent Changes", "Media Manager", and "Sitemap".

The main content area is titled "Installing the Qt-based X2Go Client" and is organized into sections: "MS Windows", "Quick", and "Detailed".

- MS Windows**
  - Quick**
    - Download X2Go for MS Windows™ and install.
  - Detailed**
    - Download latest x2goclient for Windows and install. Administrator rights required for a normal install.
    - Older versions are still available.
    - Warning: Versions prior to 3.99.0.2 may have problems connecting to x2goserver if an antivirus product is installed on the client (even if it is

The left sidebar contains navigation links for "Announcements / News", "Documentation", and "Download". The right sidebar features a "Table of Contents" with expandable links for various operating systems and installation methods.



Courage !



INSTITUT FRANÇAIS DE BIOINFORMATIQUE



**Inserm**

