



New developments of IFB portal

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CYCLONE UC Hackathon, Nov 2016
Gif-sur-Yvette



IFB Portal, present



Browse to




IBF BIOINFORMATICS CLOUD

Dashboard

[New Instance](#)
[New vCores](#)
[Show Instances](#)
[Show vCores](#)
[Show Appliances](#)

[Room for VMs](#)
[CPU](#)
[Memory](#)

Room for VMs	ID	Name	Appliance	OS	CPU	Mem.	Storage	Access
6580	10	http://bioinformatics.bioinformatics.fr/ibfcloud/	Ubuntu 14.04 (IBF-1008)	CentOS 6.7	2	8	0	ssh
6924	2	UseCases	Ubuntu 14.04 (IBF-1008)	CentOS 6.7	1	2	1	ssh
7405	3	Genome Pyl-7	CentOS 6.7 (IBF-1008)	CentOS 6.7	1	2	0	ssh
7814	4	cytosine-tytthon-pair - 62-23	Ubuntu 14.04 (IBF-1008)	CentOS 6.7	1	2	0	ssh
8931	5	https://bioinformatics.bioinformatics.fr/ibfcloud/	CentOS 7.0 (IBF-1008)	CentOS 7.0	1	2	0	ssh
9975	6	https://212.54.250.101/ibfcloud/	CentOS 7.0 (IBF-1008)	CentOS 7.0	1	2	0	ssh
10080	7	Cytosine-Hydroxylation-protection	Docker (IBF-1008)	Docker	1	2	0	ssh
10110	8	KILL ME	CYCLOLINE NCA-NGS CLB 1.3	CYCLOLINE NCA-NGS CLB 1.3	1	0	0	ssh
10112	9	NCA-NGS CLB	CYCLOLINE NCA-NGS CLB 1.3	CYCLOLINE NCA-NGS CLB 1.3	1	0	0	ssh
10113	10	UCI-Strasbourg	Bacterial genomics (IBF-1008)	Bacterial genomics (IBF-1008)	1	2	0	ssh
20	11				11	24	1	ssh

[Show vCores](#)
[Show Instances](#)








[IBF bioinformatics landing page](#)
[The "Adventures in Bioinformatics" forum and "help"](#)
[The bioinformatics of the French "Excellence in Bioinformatics" Institute](#)

Run Vms
on one cloud



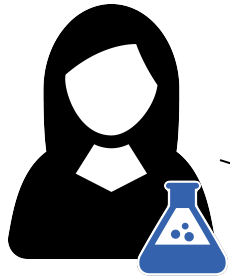
Pilot IFB

Drawback :

- Lack of appliances repository
- Only one cloud
- Start cluster « manually »
- Login/pwd to remember
- Appliance development not convenient

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

IFB Portal, present

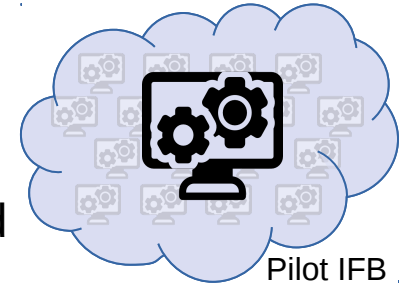


Browse to

CloudWeb



Run Vms
on one cloud



Pilot IFB

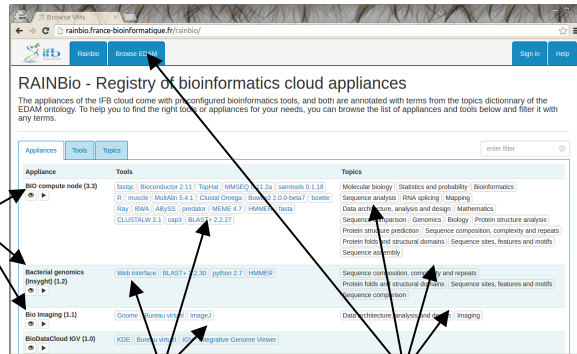
Search

Go to
RAINBio

Drawback :

- ~~Lack of appliances repository~~
- Only one cloud
- Start cluster « manually »
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- Appliance development not convenient

Appliances

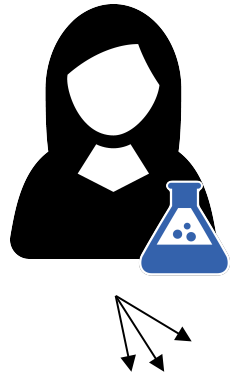


Tools

EDAM Ontology

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

IFB Portal, present and futur



CloudWeb

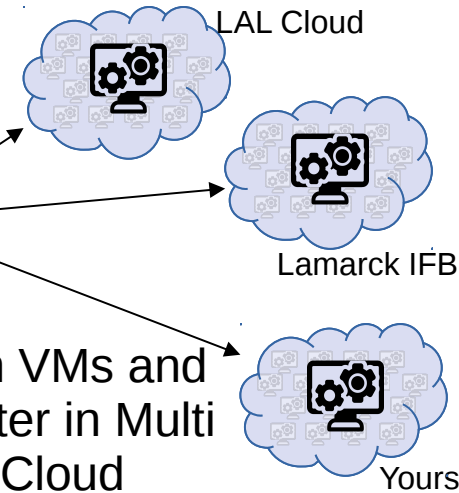
Monitor

Dashboard

Deployments Storage MEM: CPU:

ID	Name	Start/Stop	User	Spec	Access
b170ca02	centos7	↑ 22h04	br...br...te@fr...ue	0 0 0 0	ssh https
4d1d3a4c	centos7-m1.medium	↑ 22h04	br...br...te@fr...ue	0 VM 0 core 0 Go 0 Go	ssh https
080b0c52	test_2vm				

IFB acknowledges funding by the call "Infrastructures in Biology and Health" in the framework of the French National Research Agency (ANR) program Investissements d'avenir.



Run VMs and cluster in Multi Cloud

EDAM Browser

Details of the selected node

Family: Transcription factor

Label: Transcription factor

Function analysis: The mapping of conserved (typically nucleotide) sequences. Mapping (of alignment) of sequences (e.g. just alignment) has application in RNA-seq transcriptome analysis. It also covers the discovery of new genes (e.g. mapping of exome capture data).

Phylogeny: Phylogenetic trees are used to identify, map or analyse genetic markers. It also covers the discovery of new genes (e.g. mapping of exome capture data).

Sequence analysis: The mapping of conserved (typically nucleotide) sequences. Mapping (of alignment) of sequences (e.g. just alignment) has application in RNA-seq transcriptome analysis. It also covers the discovery of new genes (e.g. mapping of exome capture data).

Protein structure: The mapping of conserved (typically nucleotide) sequences. Mapping (of alignment) of sequences (e.g. just alignment) has application in RNA-seq transcriptome analysis. It also covers the discovery of new genes (e.g. mapping of exome capture data).

Sequence composition, complexity and motifs: The mapping of conserved (typically nucleotide) sequences. Mapping (of alignment) of sequences (e.g. just alignment) has application in RNA-seq transcriptome analysis. It also covers the discovery of new genes (e.g. mapping of exome capture data).

Structure analysis: The mapping of conserved (typically nucleotide) sequences. Mapping (of alignment) of sequences (e.g. just alignment) has application in RNA-seq transcriptome analysis. It also covers the discovery of new genes (e.g. mapping of exome capture data).

Related synonyms: The mapping of conserved (typically nucleotide) sequences. Mapping (of alignment) of sequences (e.g. just alignment) has application in RNA-seq transcriptome analysis. It also covers the discovery of new genes (e.g. mapping of exome capture data).

Broad synonyms: The mapping of conserved (typically nucleotide) sequences. Mapping (of alignment) of sequences (e.g. just alignment) has application in RNA-seq transcriptome analysis. It also covers the discovery of new genes (e.g. mapping of exome capture data).

URI: http://edamontology.org/topic_0502

Explore, use and contribute to EDAM

RAINBio - Registry of bioinformatics cloud appliances

The appliances of the IFB cloud come with preconfigured bioinformatics tools, and both are annotated with terms from the topics dictionary of the EDAM ontology. To help you to find the right tools or appliances for your needs, you can browse the list of appliances and tools below and filter it with any terms.

Appliances Tools Topics All appliances All tools enter filter

Appliance: BioPerl 1

Tools: HMMER HOMER-A

Topics: Biochemistry Chemistry Protein folds and structural domains Sequence composition, complexity and motifs Sequence sites, features and motifs Structure prediction

centos7

centos7-m1.medium

test_2vm

EDAM Ontology

Tools

Appliances

Search and start appliances (including clusters)

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

IFB Portal, present and futur



CloudWeb

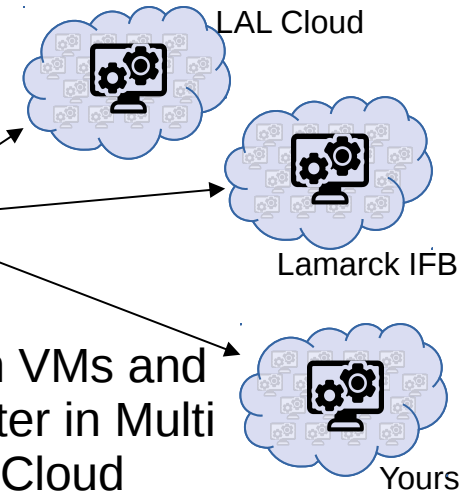
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Dashboard

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EDAM Browser

Data Format Operation Topic

start typing a term

Explore, use and contribute to EDAM

Details of the selected node

Family: Topic

Label: Topic

Abstract: The mapping of conserved (typically nucleotide) sequences. Mapping (in alignment) of regions of interest (e.g. just alignment) has application in RNA-seq transcriptome analysis and discovery (e.g. mapping of exome capture regions).

Related synonyms: The mapping of conserved (typically nucleotide) sequences. Mapping (in alignment) of regions of interest (e.g. just alignment) has application in RNA-seq transcriptome analysis and discovery (e.g. mapping of exome capture regions).

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IFB Portal, present and futur



CloudWeb

LAL Cloud

Lamarck IFB

Yours

Run VMs and cluster in Multi Cloud

Dashboard

0.0.0.0:8020/dashboard/

News Dashboard Monitor RAINBio EDAM browser Admin

Dashboard

Deployments Storage MEM: CPU:

ID	Name	Start/Stop	User	Spec	Access
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eliA INRA CNRS

RAINBio - Registry of bioinformatics resources


The at EDAM

Drawback: Improvme

Monitor

RAINBio - Registry of bioinformatics cloud appliances

Drawback: Improvements

- Lack of appliances repository
- Only one cloud Multi cloud
- Start cluster « manually » in one click
- Login/pwd to remember with  eduGAIN
- Appliance development not convenient with slipstream
- Responsive design

The screenshot displays the EDAM Browser interface. At the top, there are navigation tabs: Home, Dashboard, Monitor, R&D Hub, and EDAM browser. The main content area features a hierarchical tree on the left with 'Topic' selected, showing categories like Computational biology, Biology, Biomedical science, Chemistry, Computer science, Experimental design and studies, Informatics, Laboratory techniques, Literature and reference, Mathematics, and Medicine. The 'Genetic analysis' topic is highlighted in the tree. On the right, a panel titled 'Details of the selected node' provides information about 'Genetic analysis', including its label, parent, and a description of its purpose in mapping or analyzing genetic sequences. Below this, there are sections for 'Exact synonyms', 'Related synonyms', and 'Broad synonyms', each with a list of terms and a corresponding URI.

[illegible]

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

CYCLONE UC Hackathon

Access using eduGAIN identity and Cyclone federation provider



eduGAIN

ssh/http access based on eduGAIN



start

0.0.0.0:8020/account

ifb

Authentication

EduGain account

Use CYCLONE Federation Provider

Login

Local account

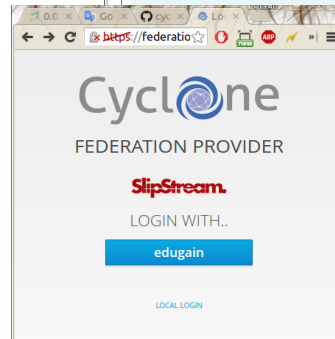
Username

Password

Login

IFB acknowledges funding by the call "Infrastructures in Biology and Health" in the framework of the French "Investments for the Future" initiative. IFB is the French ELIXIR node

elixir INRA CNRS Inserm Irstia cea



browse

New developments of IFB portal

Technical Bug ?
Graphic Bug ? (Chrome vs Mozilla vs Safari vs ...)
Suggestion ?

Fill issues on github !

<https://github.com/cyclone-project/usecases-hackathon-2016/issues>



IFB portal (alpha)
<https://cloud-dev.france-bioinformatique.fr>