Multi-Cloud deployment for microbial genomes analysis

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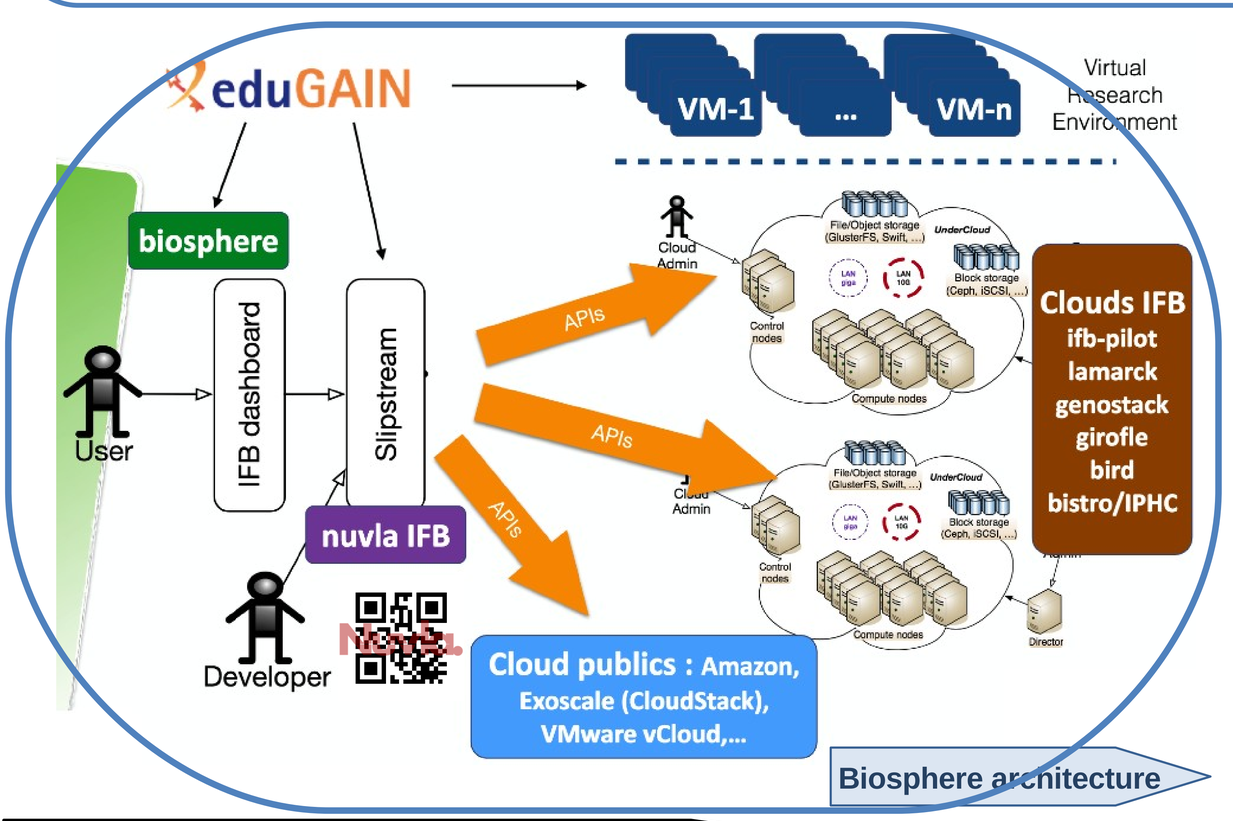
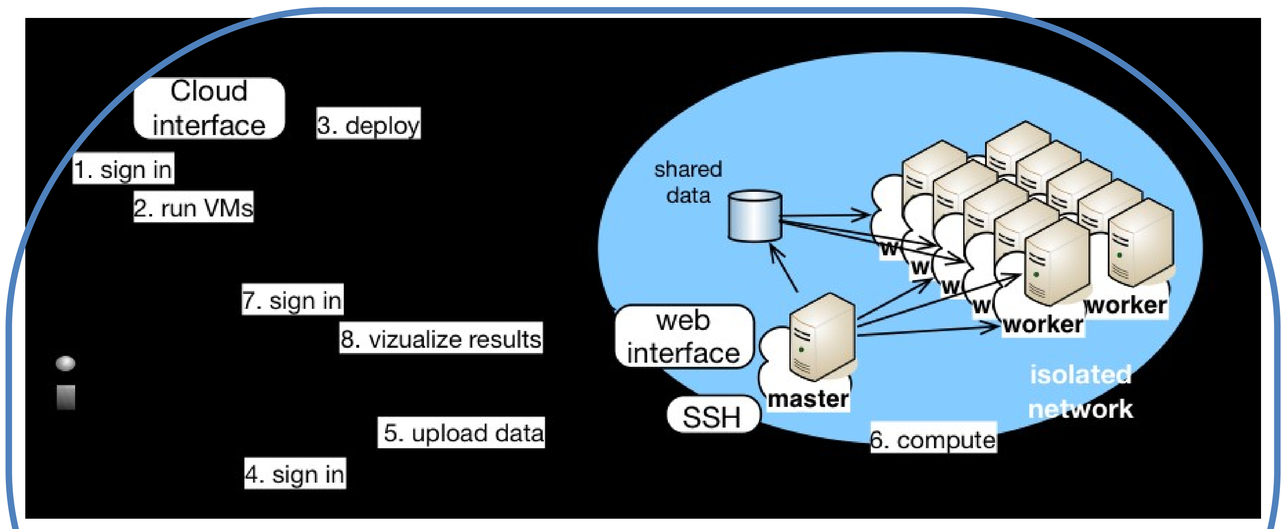
Introduction

In the post-NGS area, sequencing bacterial genomes is very cheap (few hundreds €). Most of the time, users are no longer content to analyse a single genome; they want to compare large collections of related genomes (strains). This entails that biologists have to pay too much attention and dedicate their time to sequence the genomes, instead of thoroughly analysing the genomic data. Thus, this brings light to the increasing need for automating the annotation of bacterial genomes and carrying out efficient data mining.

In that context, IFB hub and the IFB-MIGALE platform developed a virtual environment (appliance), based on virtual machines, called "bacterial genomics" that aims to provide biologists and bioinformaticians access to suitable resources via the cloud. For example, Prokka [1] is a software tool for the rapid annotation of prokaryotic genomes. Insyght [2] developed by IFB-MIGALE is a tool for the visualization of the syntenies (local conservation of the gene order along the genomes) and the exploration of the landscape of both conserved and idiosyncratic genomic regions across multiple genomes. The platform automatically launches a set of bioinformatics tools (e.g. BLAST, HMMER, Prodigal...) to analyse the data and stores the results in a relational database (PostgreSQL). These tools use several public reference data collections. A web interface allows the user to browse the results. Setting up the platform requires solid skills in system administration since many bioinformatics tools with different dependences need to be installed as well as a relational database management system, a web server and servlet container, etc. Moreover, performing the analysis of a large number of genomes requires large computing resources and the use of parallel computing.



Biosphere architecture



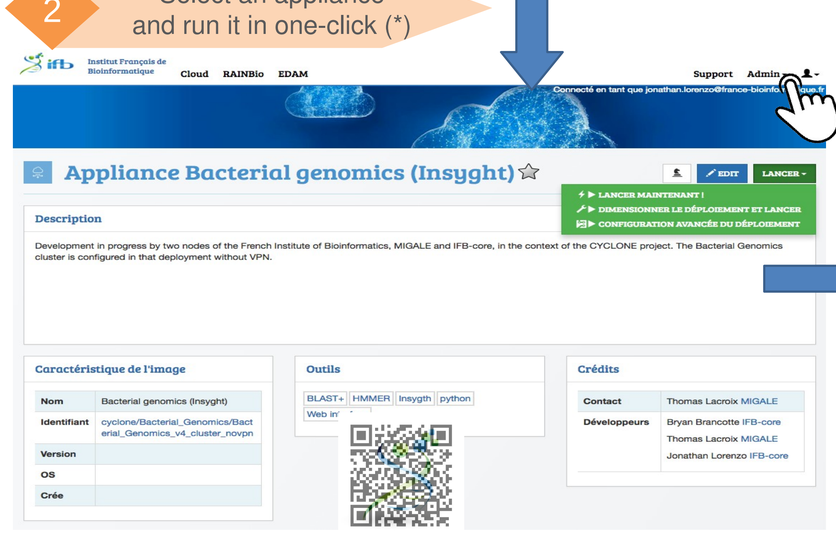
- Nuvla:
  - 1-click deployment (several VMs)
  - Multi-cloud
- Authentication Federation Provider (eduGAIN)
  - Web-access, SSH
- CNSMO-VPN: isolated network

UC2: Cloud virtual pipeline for microbial genomes analysis

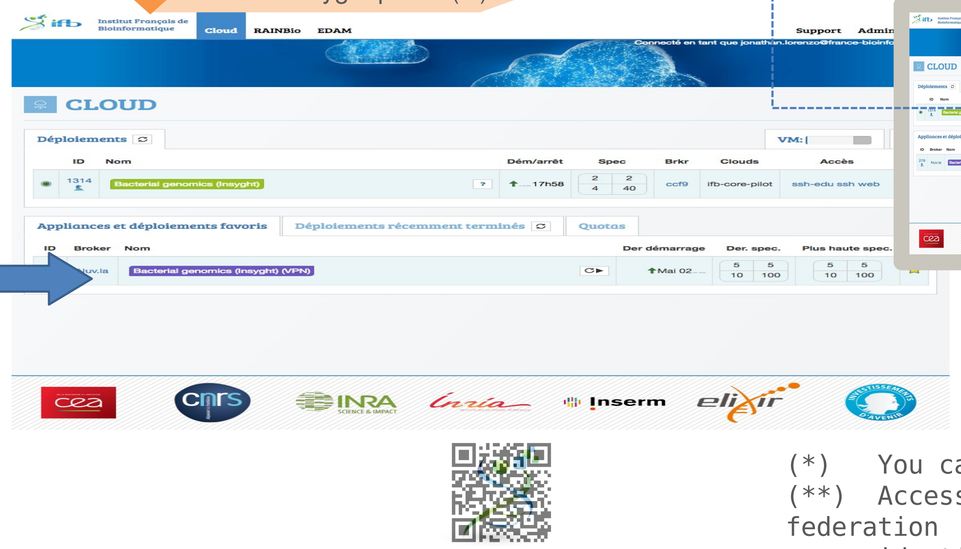
How to run Bacterial Genomics appliance for an analysis

1 Search a Bacterial Genomics appliance in RAINBio, the Biosphere catalogue

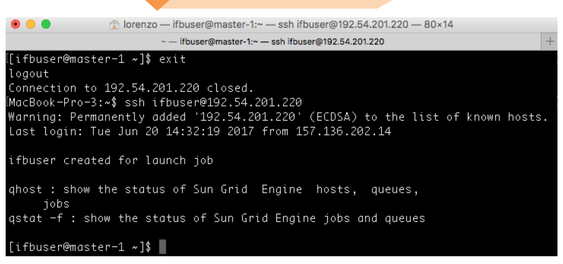
2 Select an appliance and run it in one-click (*)

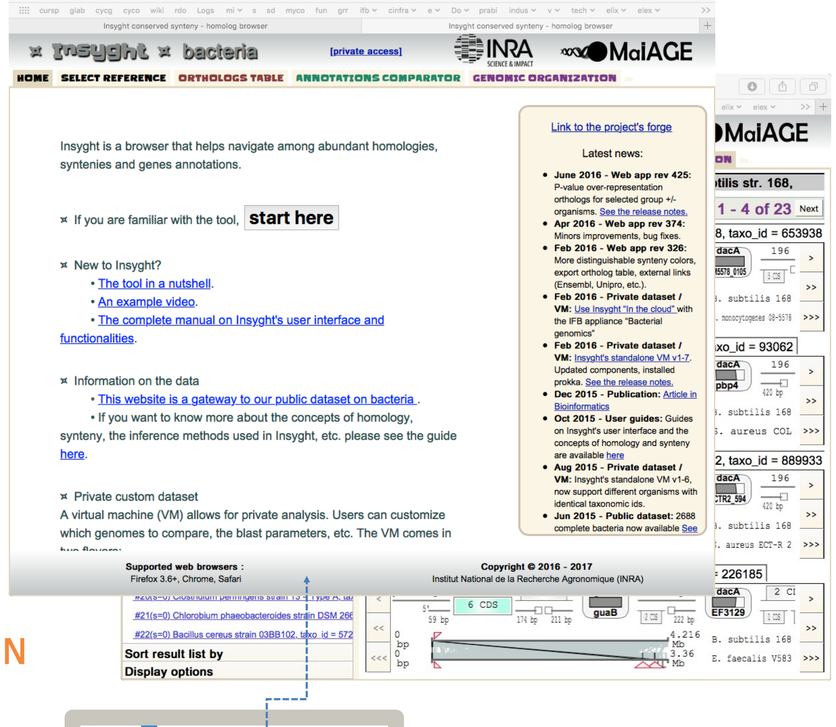


3 Direct Access on Insygth portal (**)



4 Run analysis





eduGAIN

5 Shutdown appliance at the end of analysis

(*) You can also adjust resources and target cloud

(**) Access by eduGAIN after authentication in the federation identity (no ssh-key needed) or by ssh-key for developer

Conclusion

The goal is to deploy the “appliance” in one click over one or more cloud infrastructures. To achieve this, new features to automate deployment of complex application were added to the IFB’s cloud portal through the connection to the SlipStream cloud broker. Developed by SixSq, SlipStream is a multi-cloud application management platform. It automates the full application management lifecycle, within Infrastructure as a Service (IaaS) cloud infrastructures. Such complex application deployments can be done over several cloud infrastructures and provide scientists with high-level cloud features such as the dynamic allocation of a dedicated network for the isolation of the virtual machines, with the replication of the user data and with a direct link from the cloud portal to the Insyght web portal.

[1] Seemann T. Prokka: rapid prokaryotic genome annotation. Bioinformatics. 2014 Jul 15;30(14):2068-9. PMID:24642063

[2] Lacroix T., Loux V., Gendrault A., Hoebeke M., and Gibrat J.F. Insyght: navigating amongst abundant homologues, syntenies and gene functional annotations in bacteria, it's that symbol! Nucleic Acids Res. 2014 Dec 1; 42(21): e162. doi: 10.1093/nar/gku867 : PMCID: PMC4245967

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