Cloud-based automated deployment of applications and infrastructures to provide turnkey appliances for reusable bioinformatic applications

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Introduction

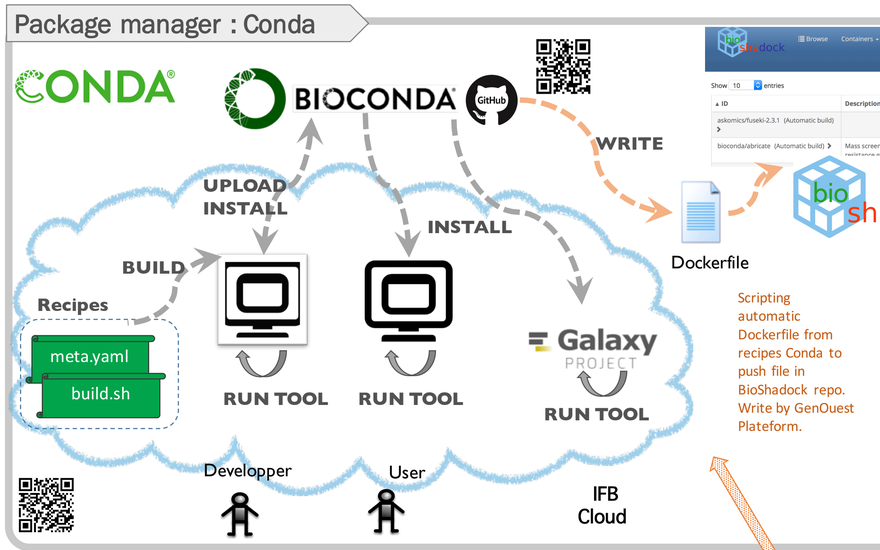
The life science community has heterogeneous needs in terms of bioinformatics resources, software and services. It needs turnkey work environments, called appliances, and will benefits from an easy maintenance of such appliances. Those needs can be addressed by cloud technologies, and are tackled since 2012 at the French Institute of Bioinformatics (IFB), which has set up a cloud to fulfil the community needs. Users can access tools and data sets through appliances, which are referenced and described in a bioinformatic-oriented marketplace. The amount of services available is rising quickly.

Packages manager

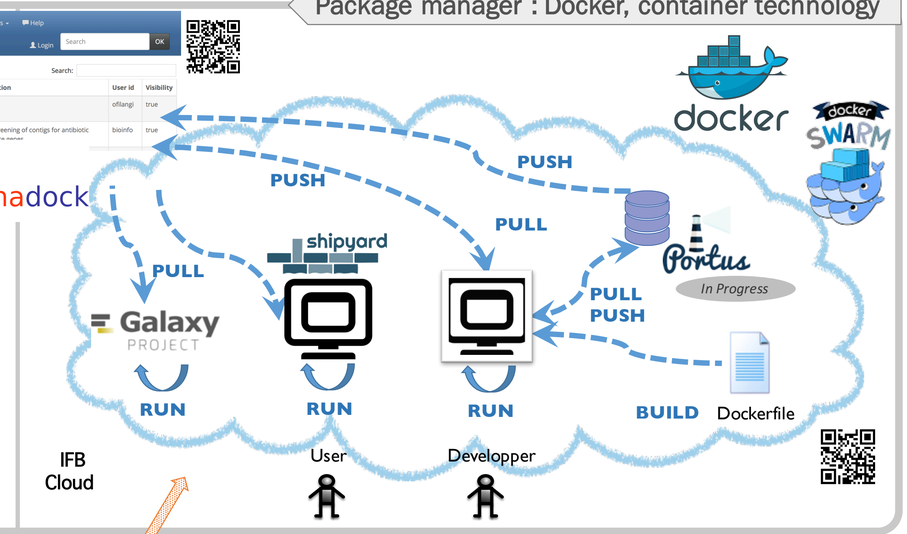
The appliance maintenance, i.e. installing or updating packages and their dependencies, can be achieved with several package managers like pip install, Debian package, **Conda** or via containers with **Docker**.

The IFB-Core uses **Puppet**, an open-source configuration management tool, to automatically deploy and configure virtual machine with a customizable list of services.

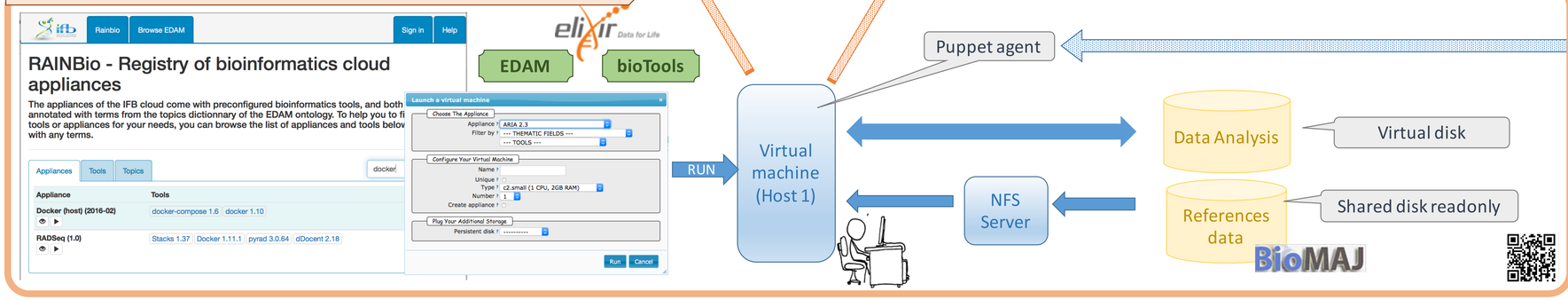
Package manager : Conda



Package manager : Docker, container technology



How to use virtual machine and virtual disk on IFB Cloud ?



Perspectives

The French Institute of Bioinformatics (IFB) is in charge of setting up a federation of Clouds that unifies a distributed network of regional infrastructures around a large national machine. This distributed infrastructure will provide an easy access to the public data collections widely used in the life sciences and allows scientists to easily use the hundreds of bioinformatics tools needed to analyse data produced by high throughput technologies. The works presented here, relying on EU H2020 projects CYCLONE and ELIXIR EXCELERATE, will be the core of such distributed deployment of life science virtual research environments adapted to the various needs of the research community.

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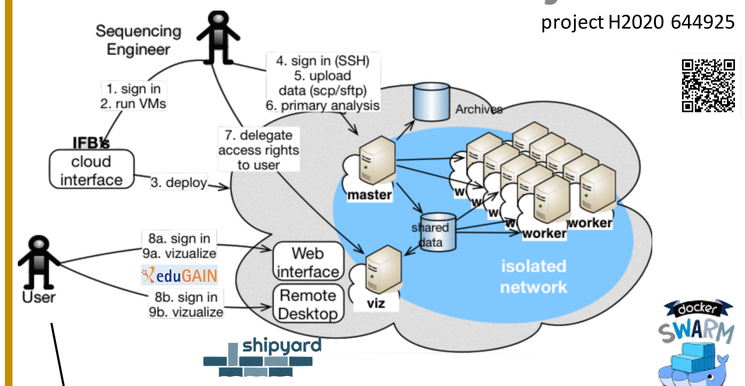
UC3 : Live remote cloud processing of sequencing data

Cyclone project H2020 644925



- Ready to use bioinformatics tools
- Cluster with Docker-Swarm
- Shipyard web Interface for docker
- Docker ready appliance
- Isolated network (CYCLONE CNSMO)
- Easy to configure Elastic virtual cluster (CYCLONE Slipstream SixSQ)
- Authentication using academics federation (CYCLONE Federation Proxy)
  - for web access and SSH (command line)

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Deployment of applications and infrastructures