



*On-demand Galaxy-based secure environments  
with Laniakea*

Donvito Giacinto (INFN)

Marco Antonio Tangaro (IBIOM-CNR)



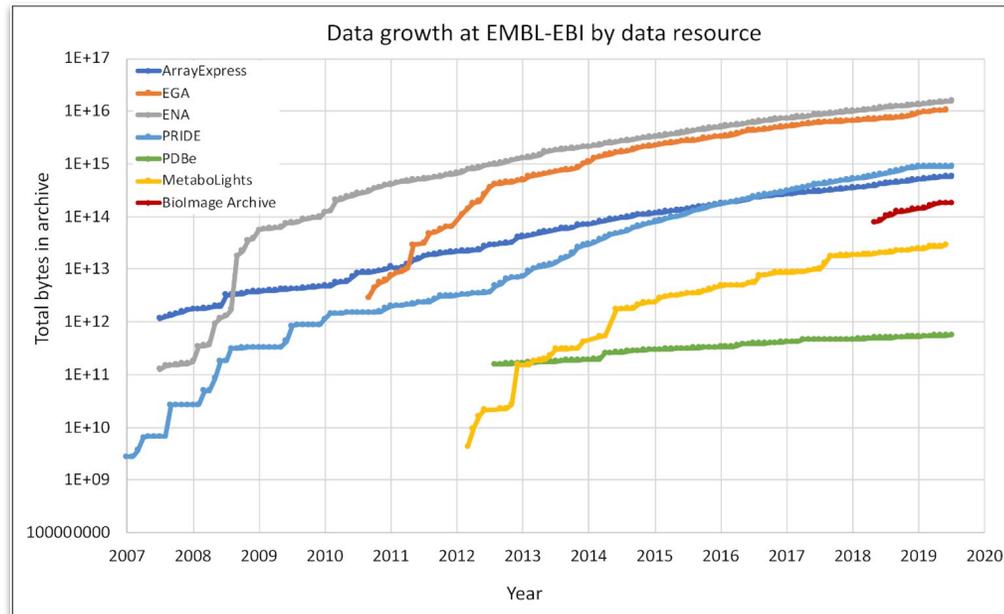
Datathon on Sensitive Data  
30th May - 1st June, 2023

# Outline



- Introduction: tools, data, compute and ... GDPR
- Galaxy
- Laniakea
- Dashboard
- Encryption
- VPN
- Demo

# Data



Genomic data are distributed across several sequencing centres and/or IT infrastructures

Data volume growing not only in quantity but also on variety!

Data growth at EMBL-EBI Source: Charles E. Cook et al. Nucl. Acids Res. 2020; Volume 48, Issue D1, Pages D17-D23

Discipline	Data size	# devices
HEP-LHC	15PB/year	1
Astronomy	15PB/year	several
Genomics	0.4TB/genome	>1000



# GDPR

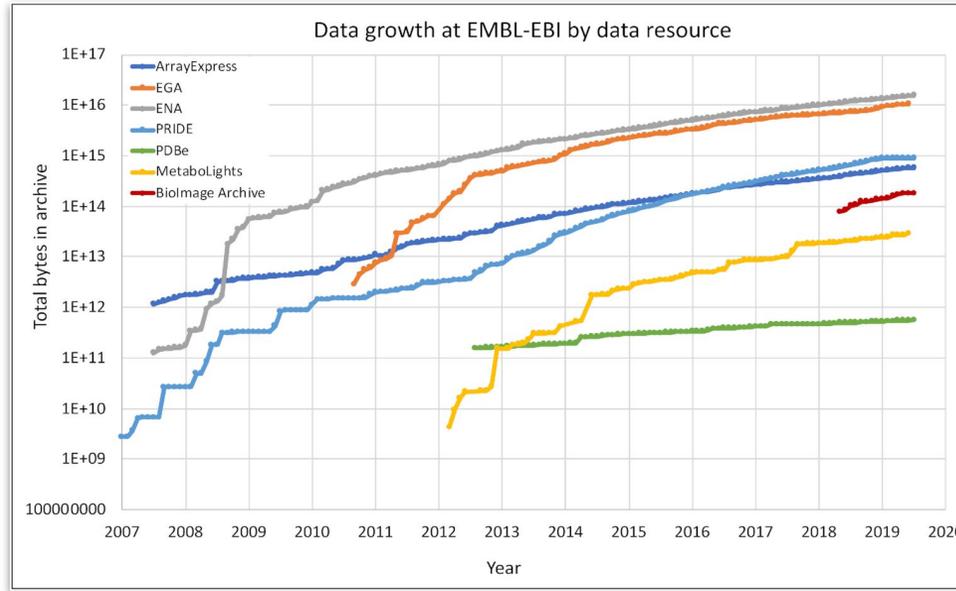
The GDPR explicitly recognizes genetic data as “Special Categories of Personal data”.

Sensitive genetic data processing for scientific research purposes is possible, provided this is allowed by EU or Member States law framework and appropriate safeguards measures are in place.



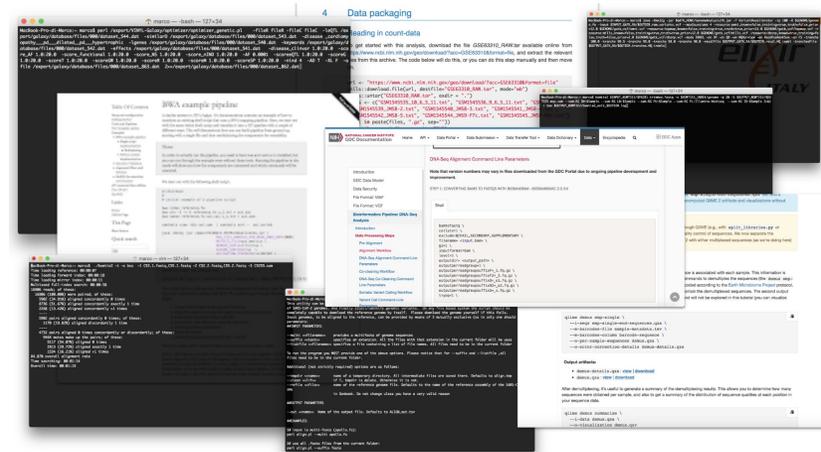
# Motivation

## DATA SOURCES



## DATA STORAGE

## DATA ANALYSIS TOOLS



## DATA PROTECTION (GDPR)



The Galaxy Project logo, consisting of a stylized icon of three horizontal bars (two dark grey, one yellow) to the left of the word "Galaxy" in a large, bold, dark grey font, with the word "PROJECT" in a smaller, spaced-out, dark grey font below it.

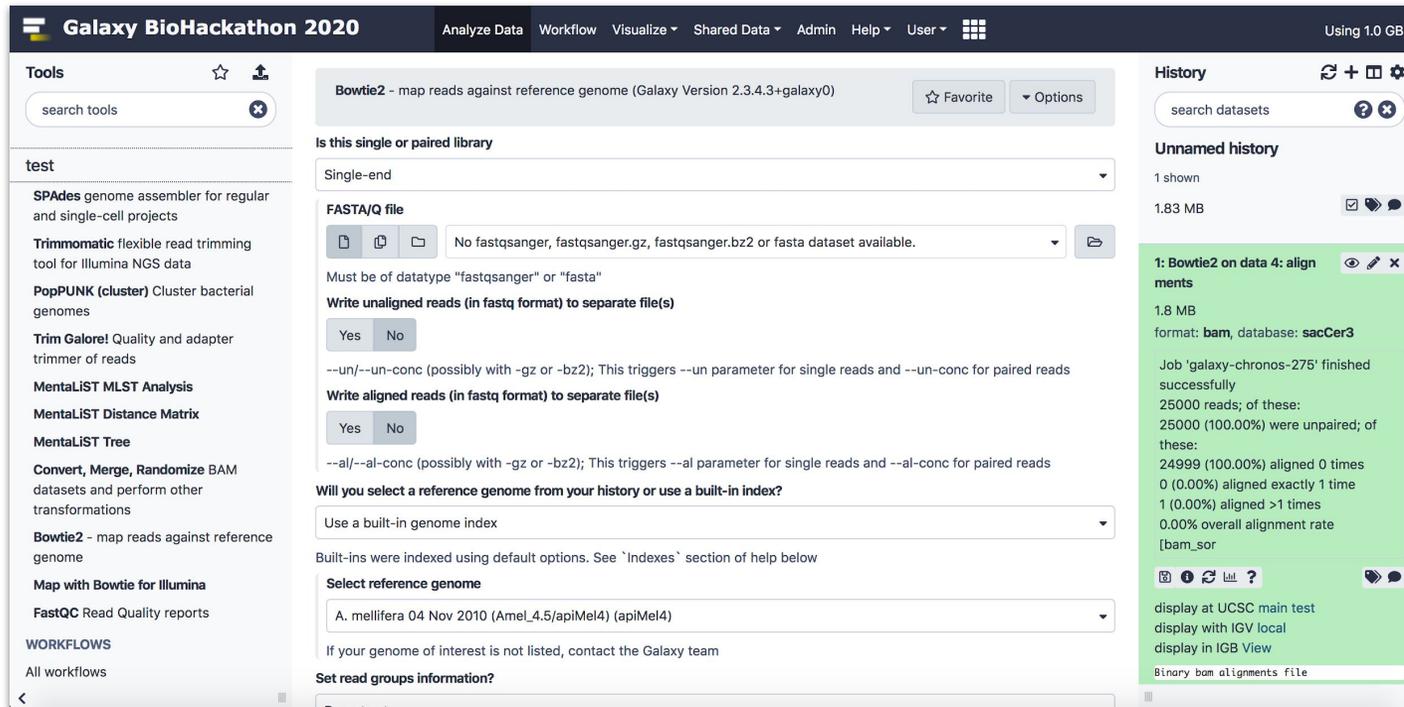
# Galaxy

## PROJECT

**Galaxy is a workflow manager** adopted in many life science research environments in order to facilitate the interaction with bioinformatics tools and the handling of large quantities of biological data.

Through a coherent work environment and an **user-friendly web interface** it organizes data, tools and workflows providing **reproducibility, transparency** and **simple data sharing** functionalities to users.

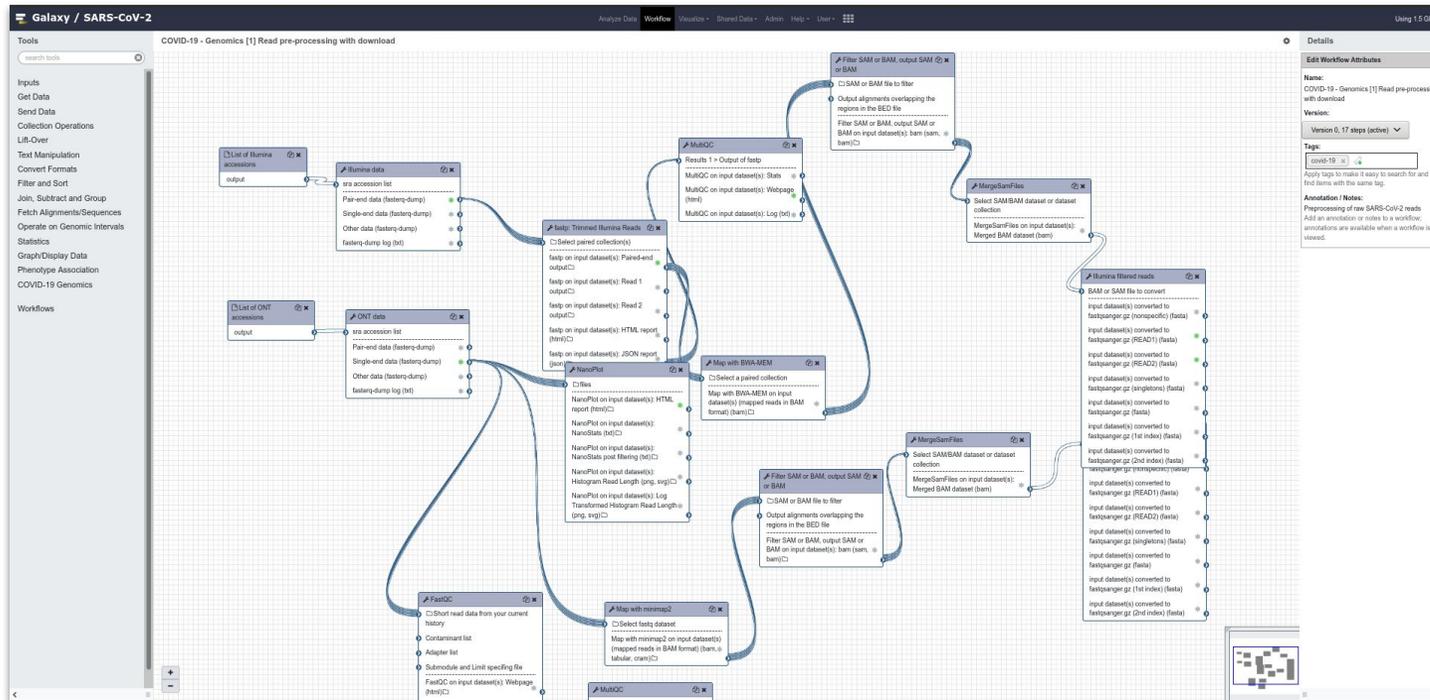
[galaxyproject.org](http://galaxyproject.org)



The screenshot shows the Galaxy BioHackathon 2020 interface. The main tool is Bowtie2, configured for a single-end library. The FASTA/Q file field is empty, with a message: "No fastqsanger, fastqsanger.gz, fastqsanger.bz2 or fasta dataset available." Below this, there are two "Write" options: "Write unaligned reads (in fastq format) to separate file(s)" and "Write aligned reads (in fastq format) to separate file(s)", both with "Yes" and "No" buttons. The "Will you select a reference genome from your history or use a built-in index?" dropdown is set to "Use a built-in genome index". The "Select reference genome" dropdown is set to "A. mellifera 04 Nov 2010 (AmeL4.5/apiMel4) (apiMel4)".

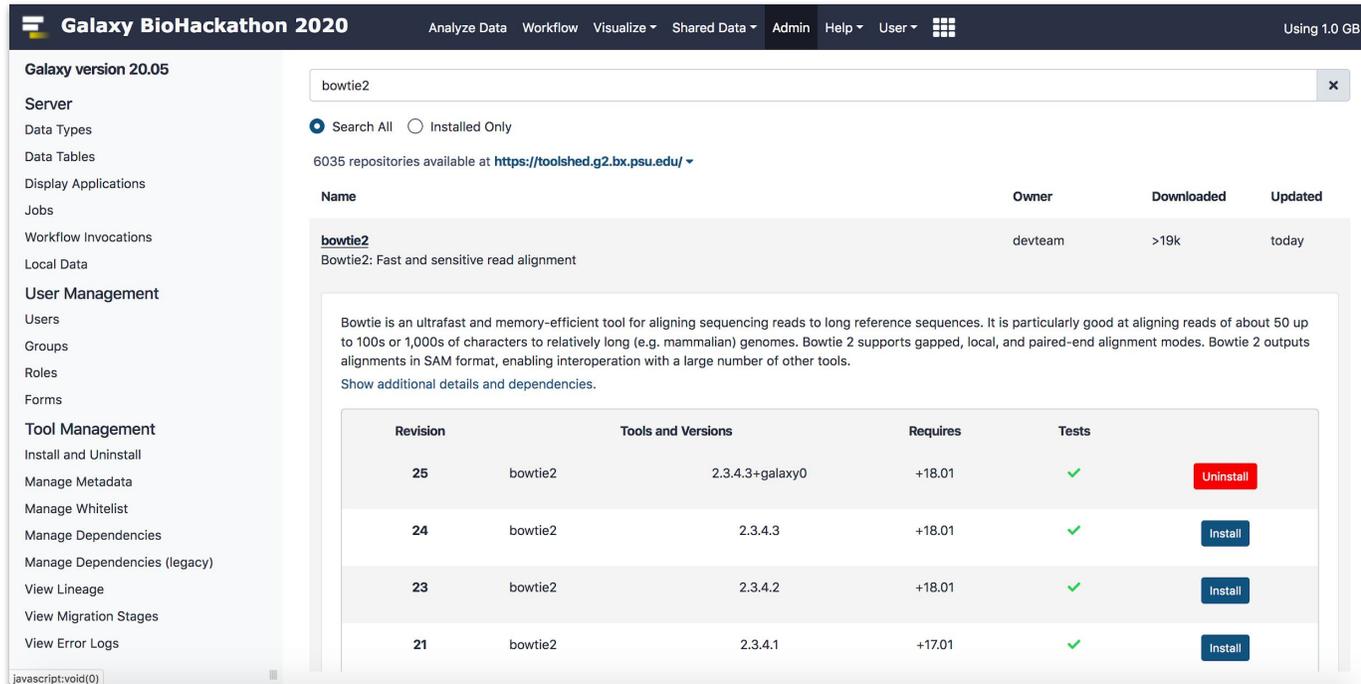
The History panel on the right shows a job titled "1: Bowtie2 on data 4: alignments" with a size of 1.8 MB. The job status is "finished successfully". The output format is "bam" and the database is "sacCer3". The job details show: "25000 reads; of these: 25000 (100.00%) were unpaired; of these: 24999 (100.00%) aligned 0 times, 0 (0.00%) aligned exactly 1 time, 1 (0.00%) aligned >1 times, 0.00% overall alignment rate [bam\_sor]". The job is displayed at UCSC main test, IGV local, and IGB View. The output is a "Binary bam alignments file".

- Tools graphical user interface.
- Input and output data management.
- Output visualization.
- Data and analysis parameters sharing.
- Used tools and parameters configuration always available -> **analysis reproducibility.**
- Reference data already available for many tools.



## Galaxy Workflow Editor

Graphical user interface to easily add, connect and configure tools for composing workflows.



Galaxy BioHackathon 2020 | Analyze Data | Workflow | Visualize | Shared Data | Admin | Help | User | Using 1.0 GB

Galaxy version 20.05

Server

Data Types

Data Tables

Display Applications

Jobs

Workflow Invocations

Local Data

User Management

Users

Groups

Roles

Forms

Tool Management

Install and Uninstall

Manage Metadata

Manage Whitelist

Manage Dependencies

Manage Dependencies (legacy)

View Lineage

View Migration Stages

View Error Logs

javascript:void(0)

Search: bowtie2

Search All  Installed Only

6035 repositories available at <https://toolshed.g2.bx.psu.edu/>

Name	Owner	Downloaded	Updated
<b>bowtie2</b> Bowtie2: Fast and sensitive read alignment	devteam	>19k	today

Bowtie is an ultrafast and memory-efficient tool for aligning sequencing reads to long reference sequences. It is particularly good at aligning reads of about 50 up to 100s or 1,000s of characters to relatively long (e.g. mammalian) genomes. Bowtie 2 supports gapped, local, and paired-end alignment modes. Bowtie 2 outputs alignments in SAM format, enabling interoperability with a large number of other tools.

Show additional details and dependencies.

Revision	Tools and Versions	Requires	Tests	
25	bowtie2 2.3.4.3+galaxy0	+18.01	✓	Uninstall
24	bowtie2 2.3.4.3	+18.01	✓	Install
23	bowtie2 2.3.4.2	+18.01	✓	Install
21	bowtie2 2.3.4.1	+17.01	✓	Install

## Galaxy ToolShed

Serves as an "app store" to all Galaxies worldwide.

It is a **free service** Galaxy developers to share tools.

Galaxy Administrator can install tools on their instances.

Tools dependencies automatically solved.

**All Galaxy users can access to the tools available on a server.**

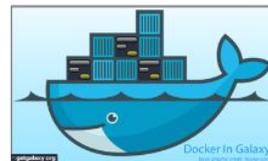
# Laniakea

LANIAKEA IS A CLOUD BASED GALAXY INSTANCE PROVIDER.

<https://laniakea-elixir-it.github.io/>

- Laniakea relies on commonly used Life Science Open Source tools, e.g. Galaxy, RStudio, Jupyter, HashiCorp Vault, LUKS and SLURM.
- Laniakea is European Open Science Cloud service provider.

Recommended for scenarios where users need full administrative control over a private Galaxy instance.



# Laniakea

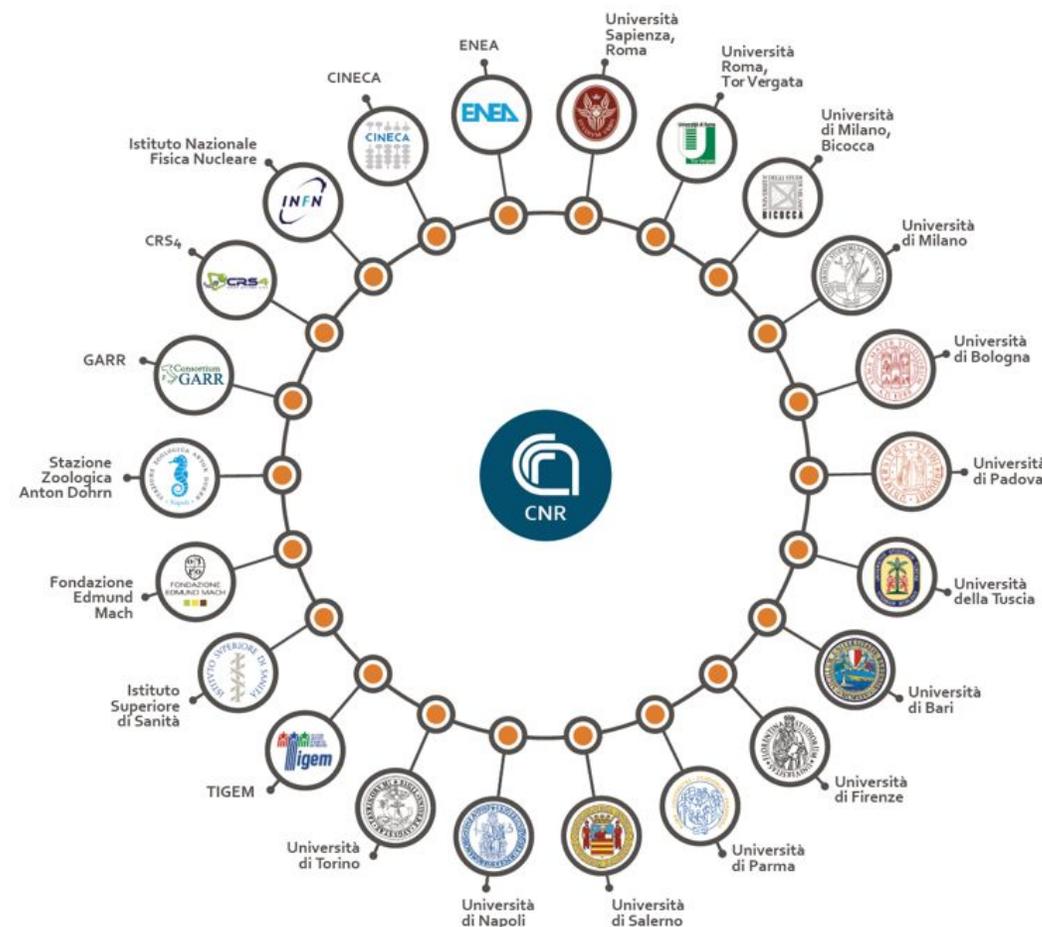


ELIXIR-Italy partners are actively involved in the service development and/or also contribute with cloud resources.

**A Laniakea service is in production for ELIXIR-ITALY partner but also for ELIXIR and external users.**

The ELIXIR-ITALY **Laniakea@ReCaS** Call offers access to Cloud resources to be used for the deployment of on-demand Galaxy instances.

[https://laniakea-elixir-it.github.io/laniakea\\_at\\_recas](https://laniakea-elixir-it.github.io/laniakea_at_recas)

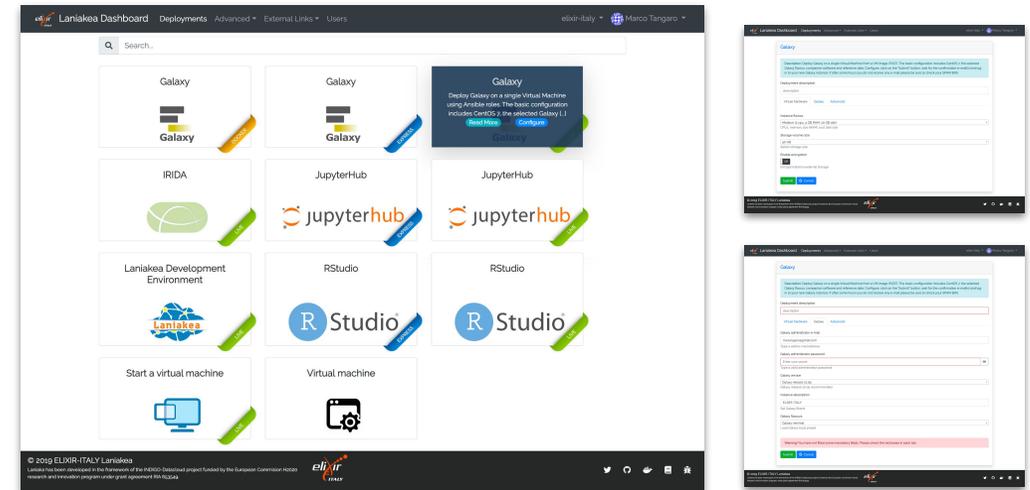


# Laniakea main features

**Dashboard** - By hiding the technical complexity behind a user-friendly web front-end, Laniakea allows its users to configure and deploy “on-demand” Galaxy instances with a handful of clicks.

No need for the end user to know the underlying infrastructure.

No need for maintenance of the hardware and software infrastructure.



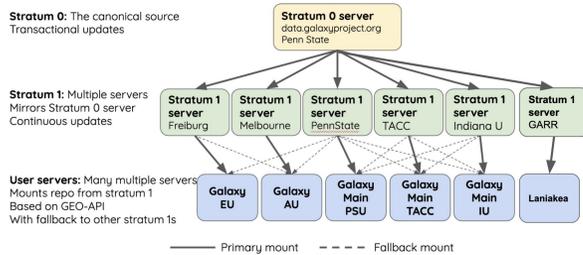
## Different deployment strategies:

**Live Build**: build Galaxy from scratch -> always up-to-date (deployment time depending by the tools number).

**Express**: pre-built Galaxy images -> fast deployment, but tools not always at the last available version.

**Docker**: fast deployment of new flavours.

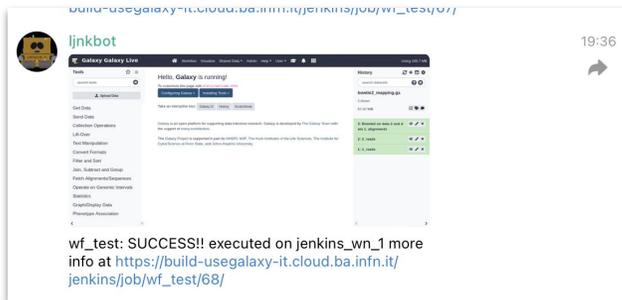
# Laniakea main features



**Shared reference data** - Each instance comes with reference data (e.g. genomic sequences) already available for many species, shared among all the instances through the CERN-VM FileSystem .



**Galaxy with cluster** - allowing to instantiate Galaxy with dedicated Resource Manager, allowing to customize the number of the virtual nodes to be created and their configuration in terms of number CPU and RAM.



**Continuous Integration** - Cloud images creation and service testing are automated using Jenkins and Github.

Cloud images automatically updated when there are changes on github  
Services are tested regularly every week.

# Laniakea main features

**Galaxy flavors** - Deploy Galaxy with sets of tested, validated and pre installed tools, named Galaxy flavors.

Current available tools presets: Galaxy Minimal, Galaxy CoVaCS, Galaxy GDC Somatic Variant, RNA Workbench, Galaxy Epigen, Covid-19.



**More Applications** - No more limited to Galaxy. Jupyter Notebooks, RStudio and IRIDA available.

Environment with NextFlow, CWLtool and other development tools available.



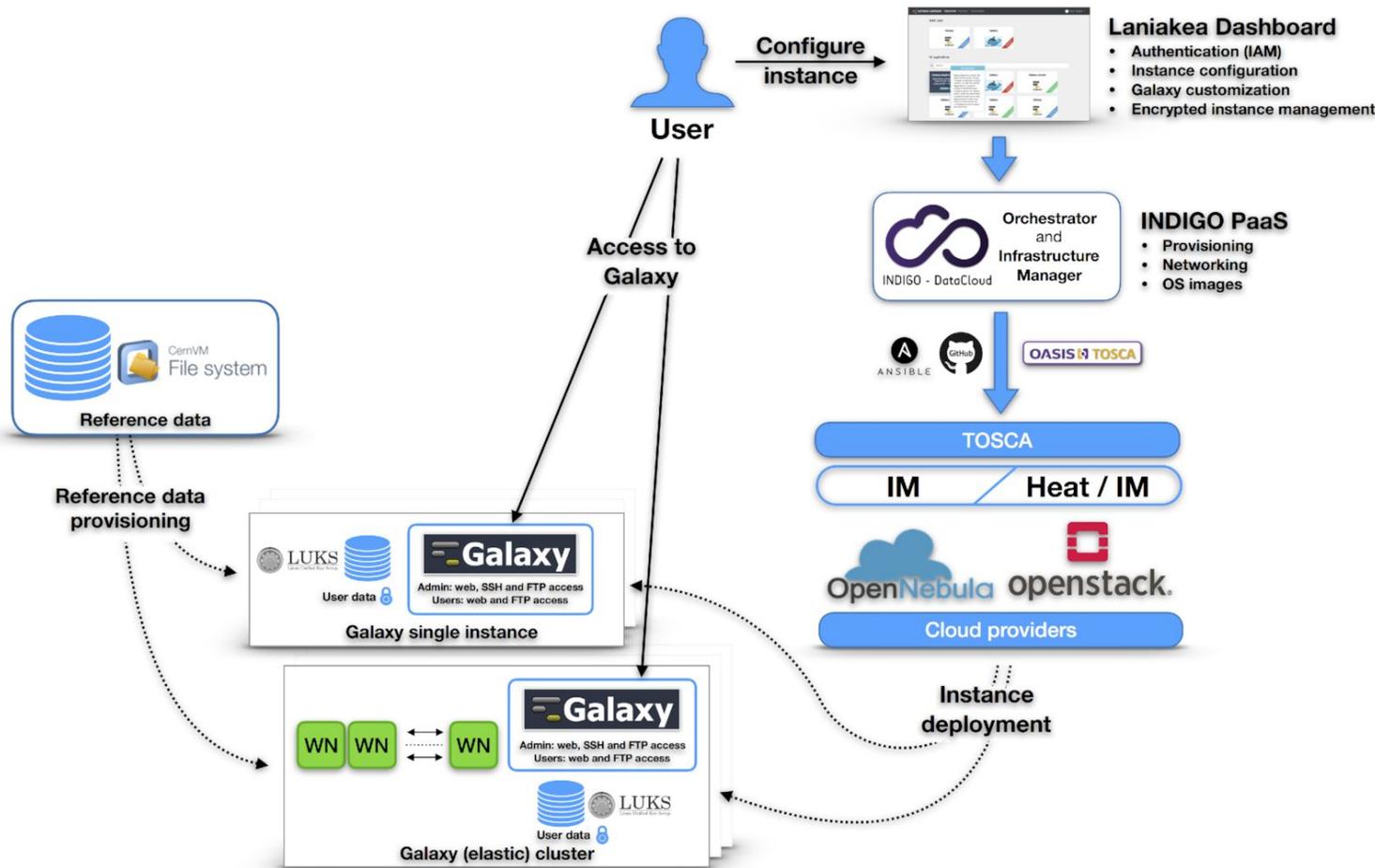
# Secured environment features

**Storage Encryption** - Data privacy is provided through encryption "on-demand".



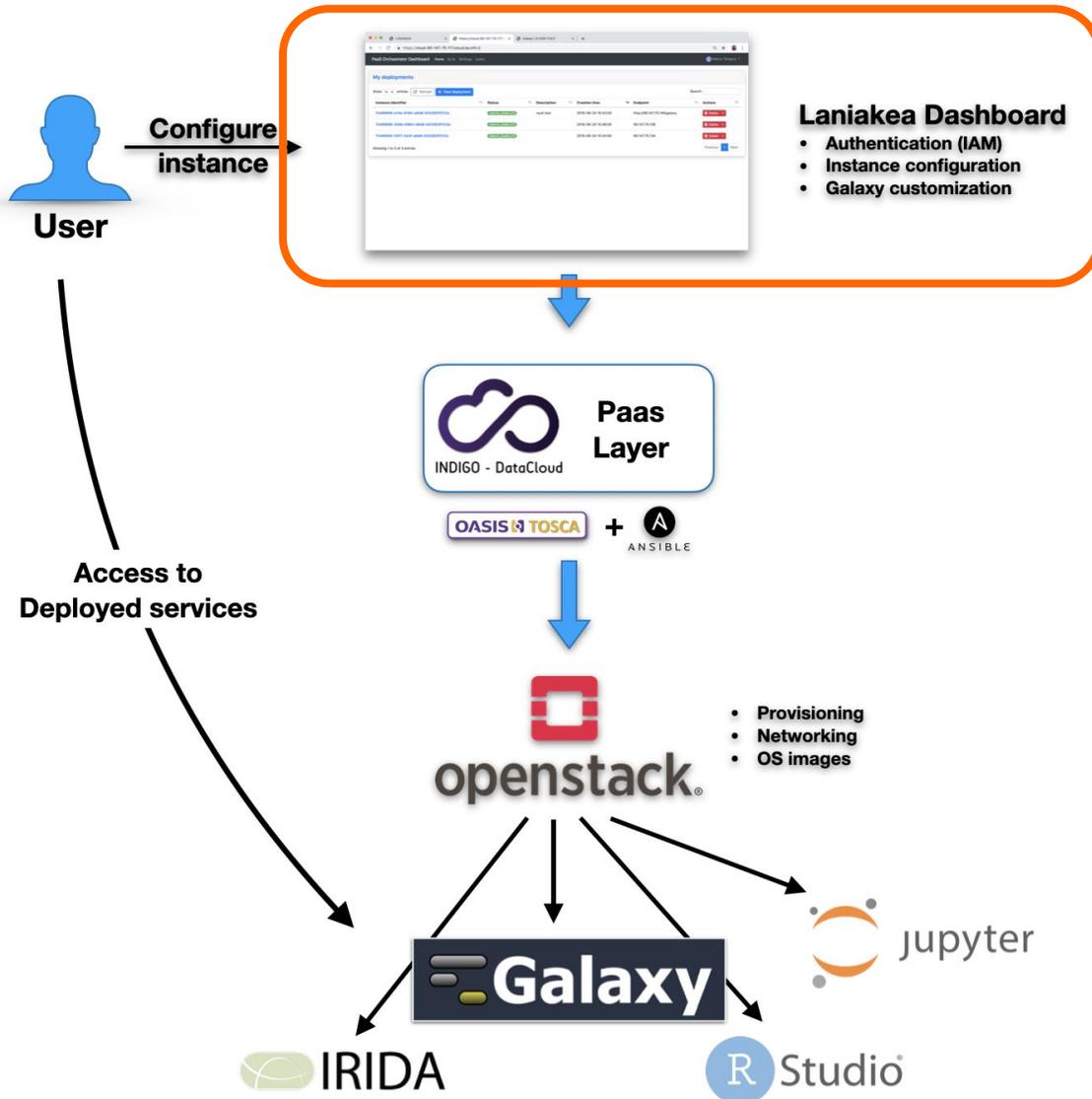
**Deployments under Private Network** - Automatic deployments of virtual environments on private networks.

# Laniakea architecture



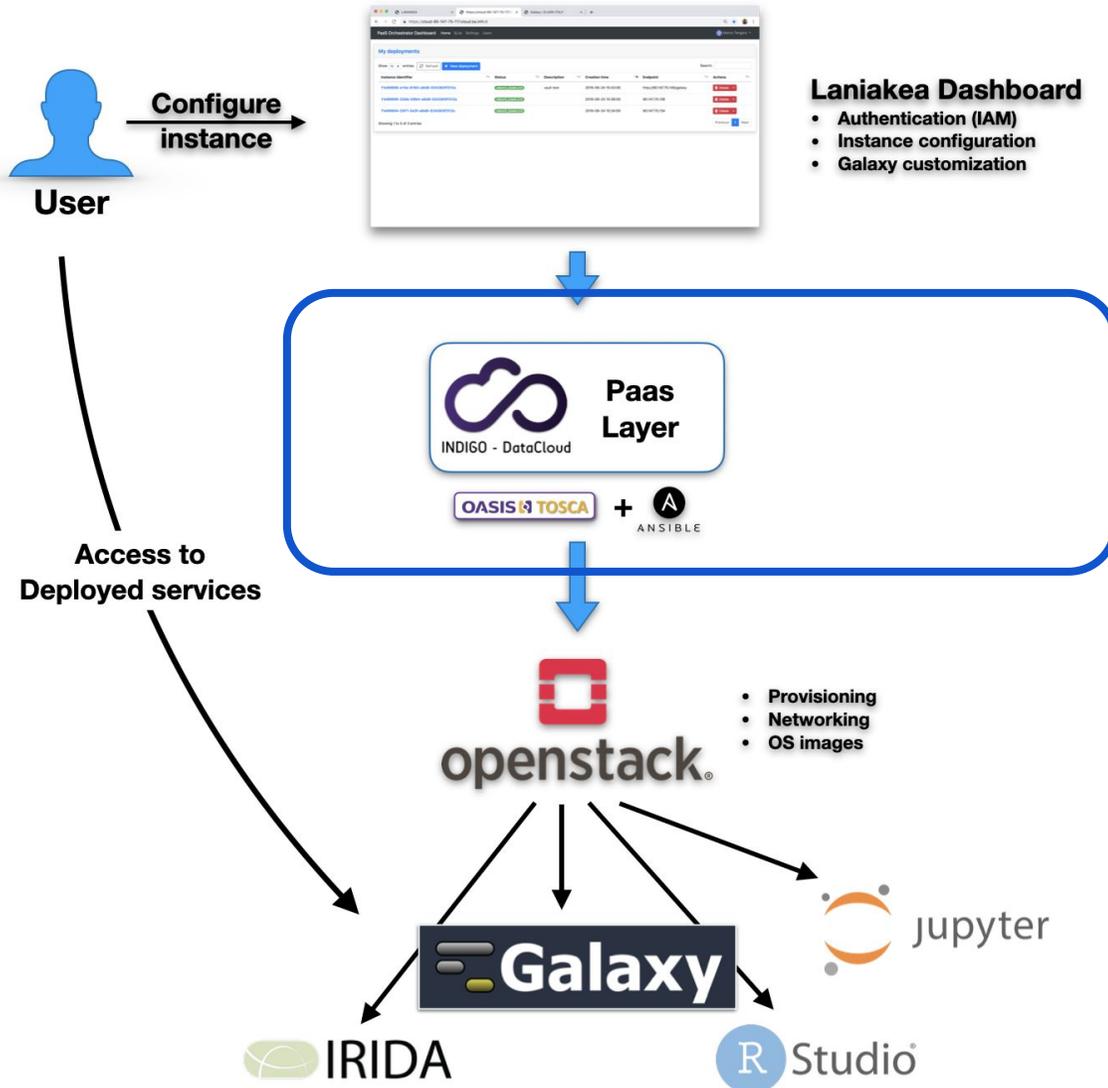
- **Dashboard** - User friendly access to configuration and launch of a Galaxy instance
- **INDIGO-IAM** - Authentication and Authorization system
- **INDIGO-PaaS** - PaaS layer for Galaxy deployment
- Cloud Provider - ReCaS Bari
- **Persistent storage** with/without encryption
- **Hashicorp Vault** - secrets management
- **Reference data** availability with CERN-VM FS

# Laniakea architecture



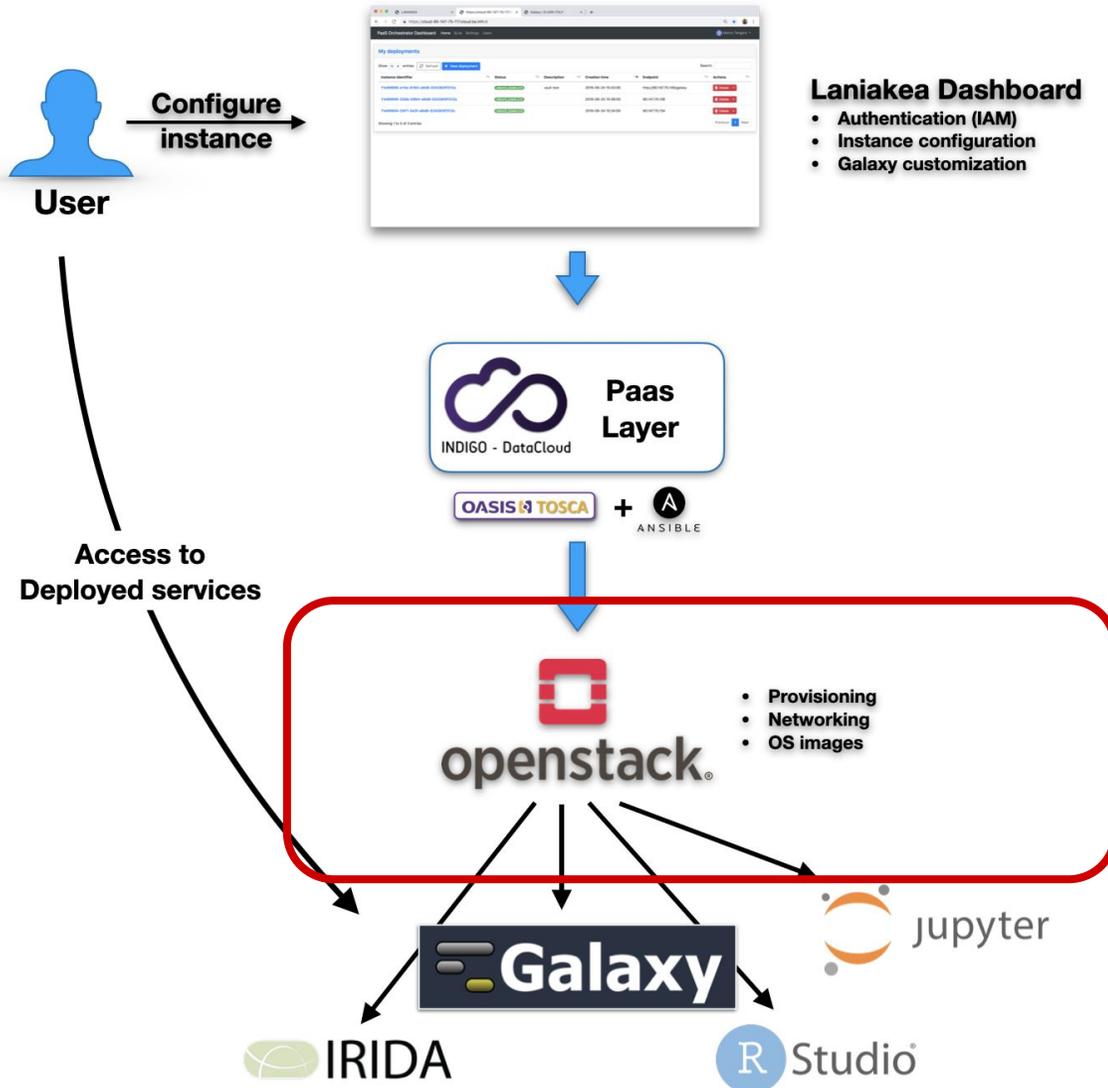
- **Dashboard** - User friendly access to configure and launch a Galaxy instance
- **INDIGO PaaS** - Galaxy automatic deployment
- **Cloud Providers** - ReCaS-Bari

# Laniakea architecture



- **Dashboard** - User friendly access to configure and launch a Galaxy instance
- **INDIGO PaaS** - Galaxy automatic deployment
- **Cloud Providers** - ReCaS-Bari

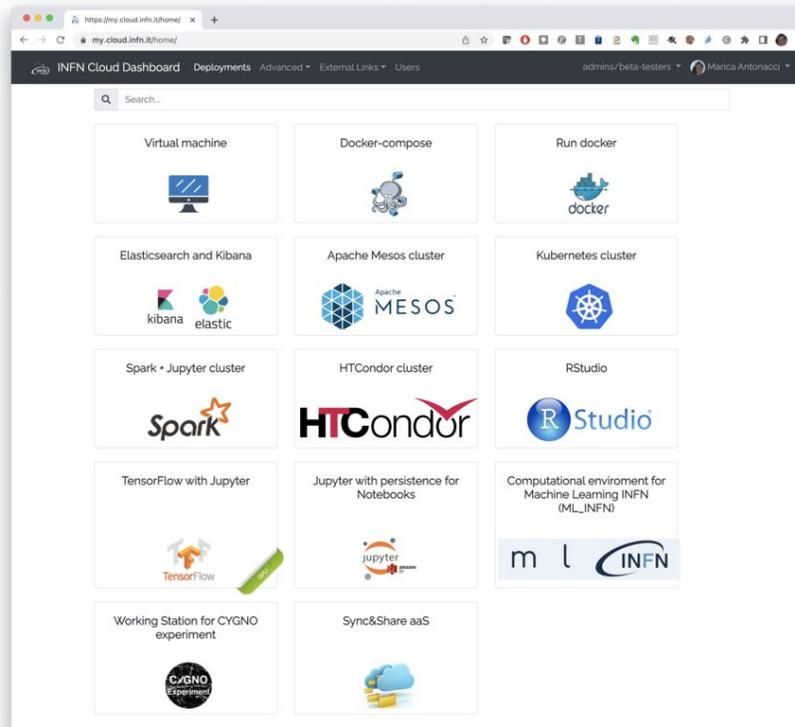
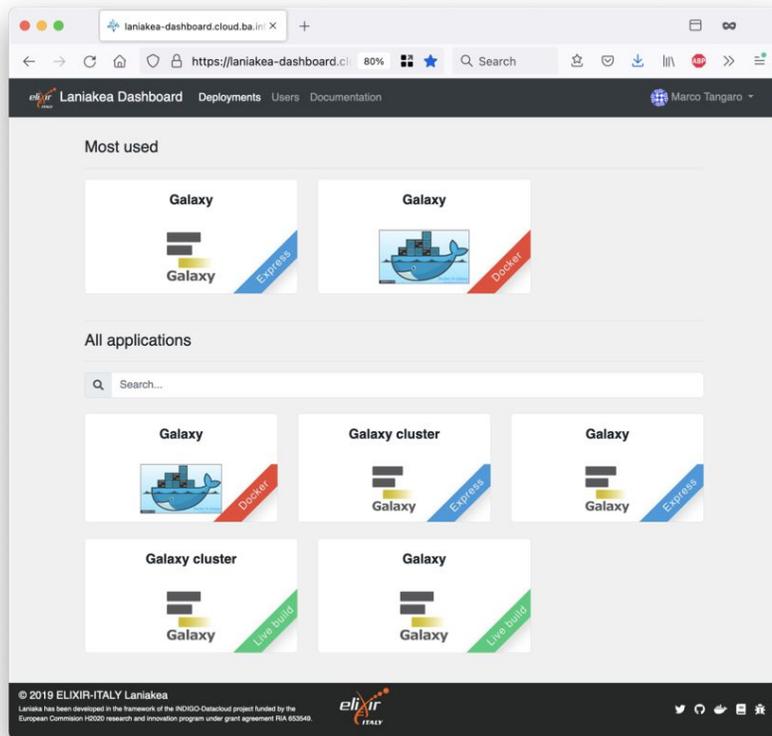
# Laniakea architecture



- **Dashboard** - User friendly access to configure and launch a Galaxy instance
- **INDIGO PaaS** - Galaxy automatic deployment
- **Cloud Providers** - ReCaS-Bari

# *Laniakea Dashboard*

# Laniakea Dashboard



Flask web micro-framework  
([flask.pocoo.org/](https://flask.pocoo.org/)),

Jinja2 template engine  
([jinja.pocoo.org/](https://jinja.pocoo.org/))

Bootstrap 4 toolkit  
([getbootstrap.com/](https://getbootstrap.com/)).

Integrated with Hashicorp  
Vault for user secrets  
management.

# *Laniakea Dashboard*



The PaaS Layer accepts deployment requests in the form of TOSCA Templates: a document (YAML syntax) describing the infrastructure to deploy, e.g. the virtual hardware and the software to be installed and configured. The Dashboard parses the TOSCA document automatically and renders the user interface with user friendly forms. This allows to extend Laniakea functionalities just adding new templates without any code modification.

**We extended the TOSCA templates inputs to create configurable forms.** This creates a flexible web interface, allowing straightforward customisation of the user experience through human readable YAML configuration files. The dashboard template is modular and can be easily adapted adding new functionalities to the user interface (e.g. adding a dropdown menu, text fields, toggles...) based on the Laniakea administrator requirements.

# Laniakea Dashboard

```
instance_flavor:  
  type: string  
  description: instance flavor (num_cpu, memory, disk)  
  default: small
```

**TOSCA template**

```
instance_flavor:  
  display_name: "Instance flavour"  
  tag_type: "select"  
  description: "CPUs, memory size (RAM), root disk size"  
  constraints:  
    - { value: "small", label: "Small (1 cpu, 2 GB RAM, 20 GB dsk)" }  
    - { value: "medium", label: "Medium (2 cpu, 4 GB RAM, 20 GB dsk)" }  
    - { value: "large", label: "Large (4 cpu, 8 GB RAM, 20 GB dsk)" }  
    - { value: "xlarge", label: "xLarge (8 cpu, 16 GB RAM, 20 GB dsk)" }  
  tab: "Virtual hardware"
```

**Parameters file**

User input field in the TOSCA template to select instance flavour in terms of vCPUs, RAM and root disk storage.

Virtual hardware **Galaxy** Advanced **Dashboard render**

Instance flavour

Small (1 cpu, 2 GB RAM, 20 GB dsk)

CPUs, memory size (RAM), root disk size

Virtual hardware **Galaxy** Advanced **Dashboard render**

Instance flavour

Small (1 cpu, 2 GB RAM, 20 GB dsk)

Small (1 cpu, 2 GB RAM, 20 GB dsk)

Medium (2 cpu, 4 GB RAM, 20 GB dsk)

Large (4 cpu, 8 GB RAM, 20 GB dsk)

xLarge (8 cpu, 16 GB RAM, 20 GB dsk)

# Laniakea Dashboard

```
users:
  type: list
  description: list of users to create on the VM
  entry_schema:
    type: toasca.datatypes.indigo.User
  default: []
  required: false

instance_flavor:
  type: string
  description: instance flavor (num_cpu, memory, disk)
  default: small
storage_size:
  type: string
  description: storage memory required for the instance
  default: 10 GB

# Storage encryption
storage_encryption:
  type: boolean
  description: Enable storage encryption.
  default: False
  required: true
vault_url:
  type: string
  description: Hashicorp Vault server url
  default: changeit
  required: false
vault_wrapping_token:
  type: string
  description: Vault Wrapping token to write secret
  default: not_a_wrapping_token
  required: false
vault_secret_path:
  type: string
  description: Vault path to store secret
  default: "subject/depuuid"
  required: false
vault_secret_key:
  type: string
  description: Vault secret key name
  default: secret
  required: false
```



### Galaxy

Description: Deploy Galaxy on a single Virtual Machine from a VM image (FAST). The basic configuration includes CentOS 7, the selected Galaxy flavour, companion software and reference data. Configure, click on the "Submit" button, wait for the confirmation e-mail(s) and log in to your new Galaxy instance. If after some hours you do not receive any e-mail please be sure to check your SPAM BOX.

Deployment description

Virtual hardware **Galaxy** Advanced

Instance flavour

  
CPUs, memory size (RAM), root disk size

Storage volume size

  
Select storage size

Enable encryption

  
Encrypt instance external storage

# Laniakea Dashboard

```
admin_email:
  type: string
  description: email of the admin user
  default: admin@admin.com
admin_api_key:
  type: string
  description: key to access the API with admin role
  default: not_very_secret_api_key
version:
  type: string
  description: galaxy version to install
  default: master
instance_description:
  type: string
  description: galaxy instance description
  default: "INDIGO Galaxy test"
export_dir:
  type: string
  description: path to store galaxy data
  default: /export

flavor:
  type: string
  description: Galaxy flavor for tools installation
  default: "galaxy-no-tools"
```



### Galaxy

Description: Deploy Galaxy on a single Virtual Machine from a VM image (FAST). The basic configuration includes CentOS 7, the selected Galaxy flavour, companion software and reference data. Configure, click on the "Submit" button, wait for the confirmation e-mail(s) and log in to your new Galaxy instance. If after some hours you do not receive any e-mail please be sure to check your SPAM BOX.

Deployment description

Virtual hardware Galaxy Advanced

Galaxy administrator e-mail

Type a valid e-mail address.

Galaxy version

Galaxy release 20.05 recommended

Instance description

Set Galaxy Brand

Galaxy flavours

Load Galaxy tools preset

# *Laniakea encryption*

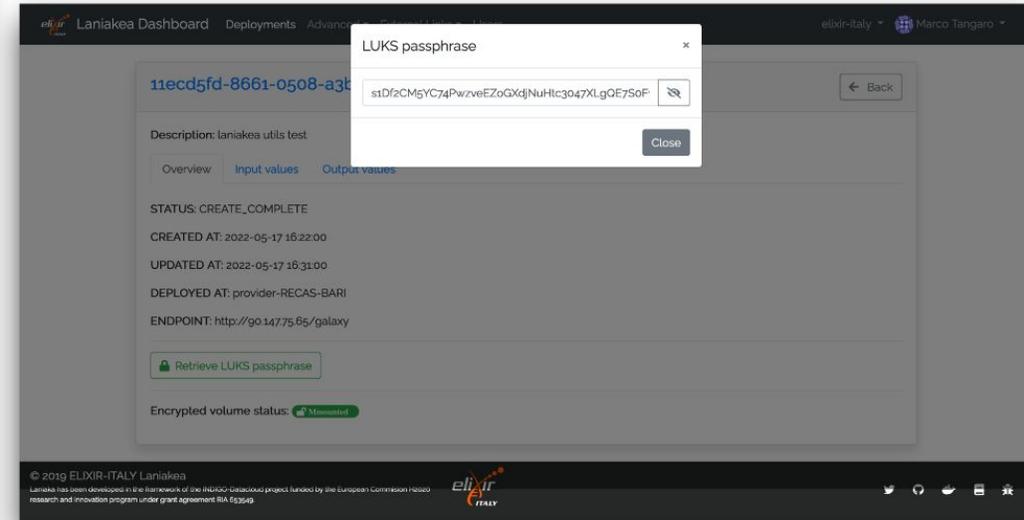
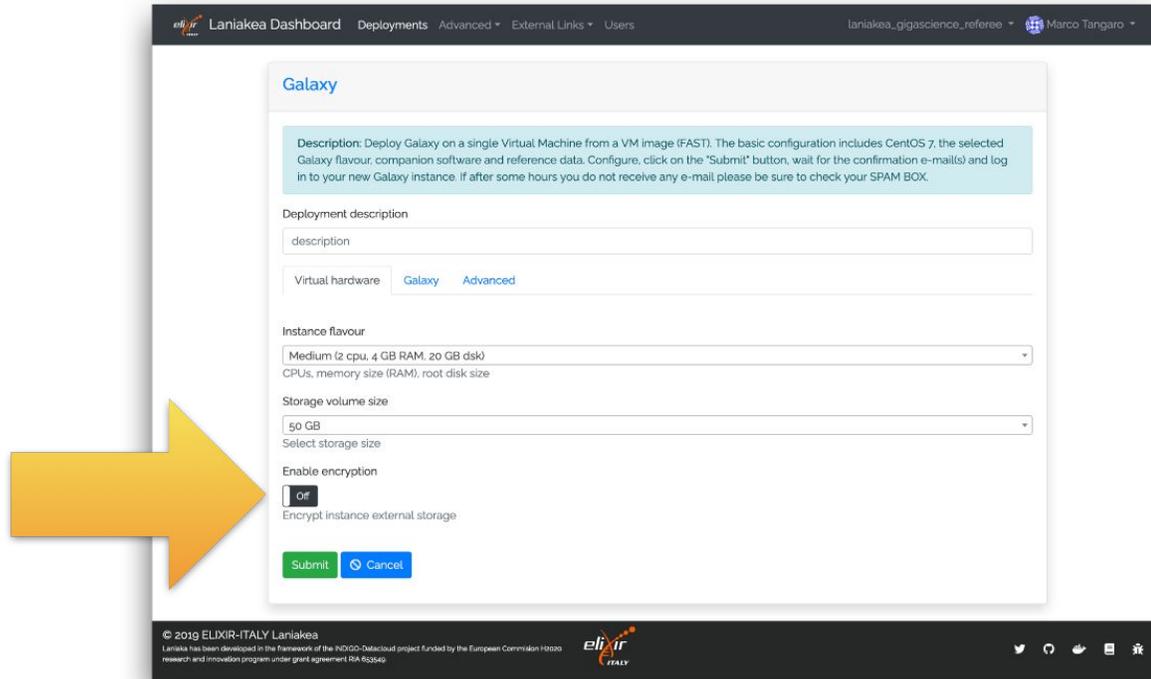
# *Laniakea encryption*



The user data privacy is granted through **LUKS** storage encryption as a service: the encryption procedure is automated in order to simplify the user experience, each user can encrypt storage on-demand, using a strong random alphanumerical passphrase.

This has been achieved integrating the Dashboard and the key management system **Hashicorp Vault** ([vaultproject.io](https://vaultproject.io)) to store encryption keys, which are shown in the Laniakea Dashboard only if explicitly requested by the user.

# Laniakea encryption: user perspective



The user can enable the storage encryption using a switch toggle in the Instance “Virtual hardware” configuration tab.

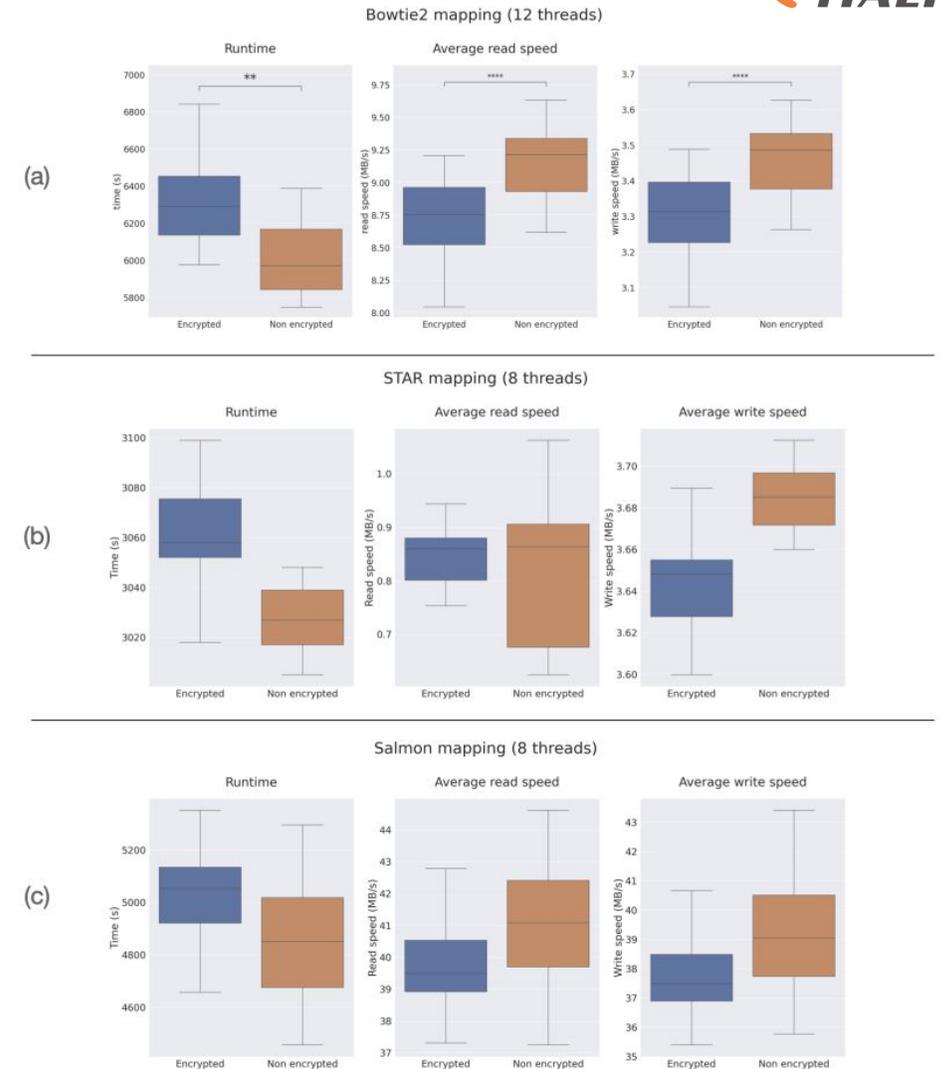
The procedure is completely automated.

The storage is encrypted and the User can retrieve his random passphrase from the Instance overview page.

# Laniakea encryption: performance

To evaluate the impact of the storage encryption layer on the performance of the main application supported by Laniakea, i.e., Galaxy, we measured jobs runtime and read/write speed on Virtual Machines generated by the Laniakea@ReCaS data center with and without storage encryption.

The impact on the performance of using the encryption layer, as measured in all our tests, is limited to ~5% or less across all the measured parameters and conditions.



# *Deployments under VPN*

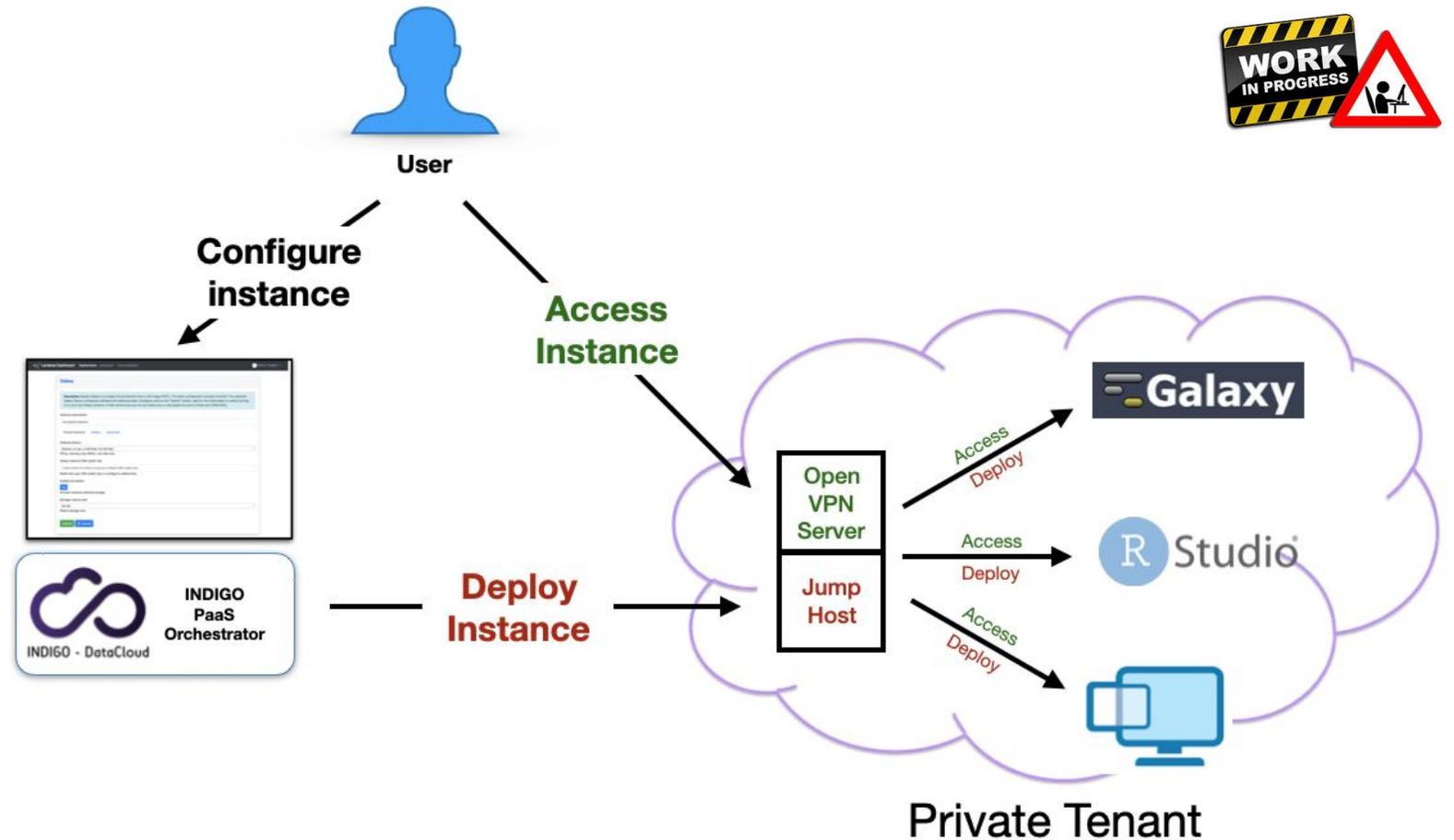
# Deployments under VPN



**VPN isolated environments** - Automatic deployments of virtual environments on private networks.

Isolation is reached using Tenant and security groups properties, granting the access only through VPN authentication.

User authentication to the VPN using the same Laniakea credentials.



# *Thanks for your attention*

## CONTACTS:

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Nadina Foggetti (Legal expert) [nadina.foggetti@ba.infn.it](mailto:nadina.foggetti@ba.infn.it)

Marica Antonacci (PaaS developer) [marica.antonacci@ba.infn.it](mailto:marica.antonacci@ba.infn.it)

Marco Antonio Tangaro (Laniakea chief developer) [ma.tangaro@ibiom.cnr.it](mailto:ma.tangaro@ibiom.cnr.it)

# *Backup*

**Galaxy BioHackathon 2020** | Analyze Data | Workflow | Visualize | Shared Data | Admin | Help | User | Using 1.0 GB

**Tools** | search tools

**test**

- SPAdes genome assembler for regular and single-cell projects
- Trimmomatic flexible read trimming tool for Illumina NGS data
- PopPUNK (cluster) Cluster bacterial genomes
- Trim Galore! Quality and adapter trimmer of reads
- MentalIST MLST Analysis
- MentalIST Distance Matrix
- MentalIST Tree
- Convert, Merge, Randomize BAM datasets and perform other transformations
- Bowtie2 - map reads against reference genome
- Map with Bowtie for Illumina
- FastQC Read Quality reports

**WORKFLOWS**

All workflows

**Bowtie2 - map reads against reference genome (Galaxy Version 2.3.4.3+galaxy0)**

☆ Favorite | Options

Is this single or paired library

Single-end

FASTA/Q file

No fastqsanger, fastqsanger.gz, fastqsanger.bz2 or fasta dataset available.

Must be of datatype "fastqsanger" or "fasta"

Write unaligned reads (in fastq format) to separate file(s)

Yes No

--un/--un-conc (possibly with -gz or -bz2); This triggers --un parameter for single reads and --un-conc for paired reads

Write aligned reads (in fastq format) to separate file(s)

Yes No

--al/--al-conc (possibly with -gz or -bz2); This triggers --al parameter for single reads and --al-conc for paired reads

Will you select a reference genome from your history or use a built-in index?

Use a built-in genome index

Built-ins were indexed using default options. See `Indexes` section of help below

Select reference genome

A. mellifera 04 Nov 2010 (AmeL4.5/apiMel4) (apiMel4)

If your genome of interest is not listed, contact the Galaxy team

Set read groups information?

**History** | search datasets

1 shown

1.83 MB

**1: Bowtie2 on data 4: alignments**

1.8 MB

format: bam, database: sacCer3

Job 'galaxy-chronos-275' finished successfully

25000 reads; of these:

- 25000 (100.00%) were unpaired; of these:
- 24999 (100.00%) aligned 0 times
- 0 (0.00%) aligned exactly 1 time
- 1 (0.00%) aligned >1 times
- 0.00% overall alignment rate

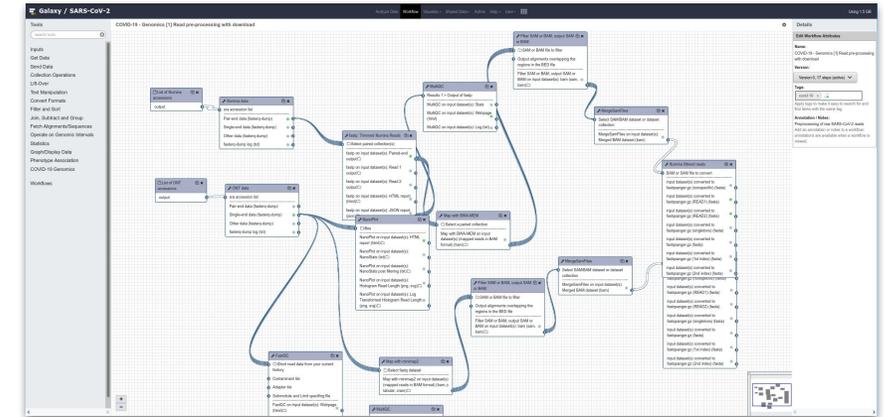
[bam\_sor]

display at UCSC main test

display with IGV local

display in IGB View

Binary bam alignments file



**Galaxy BioHackathon 2020** | Analyze Data | Workflow | Visualize | Shared Data | Admin | Help | User | Using 1.0 GB

Galaxy version 20.05

Server

Data Types

Data Tables

Display Applications

Jobs

Workflow Invocations

Local Data

User Management

Users

Groups

Roles

Forms

**Tool Management**

Install and Uninstall

Manage Metadata

Manage Whitelist

Manage Dependencies (legacy)

View Lineage

View Migration Stages

View Error Logs

6035 repositories available at <https://toolshed.g2.bx.psu.edu/>

Search All | Installed Only

Name	Owner	Downloaded	Updated
<b>bowtie2</b>	devteam	>19k	today

Bowtie2: Fast and sensitive read alignment

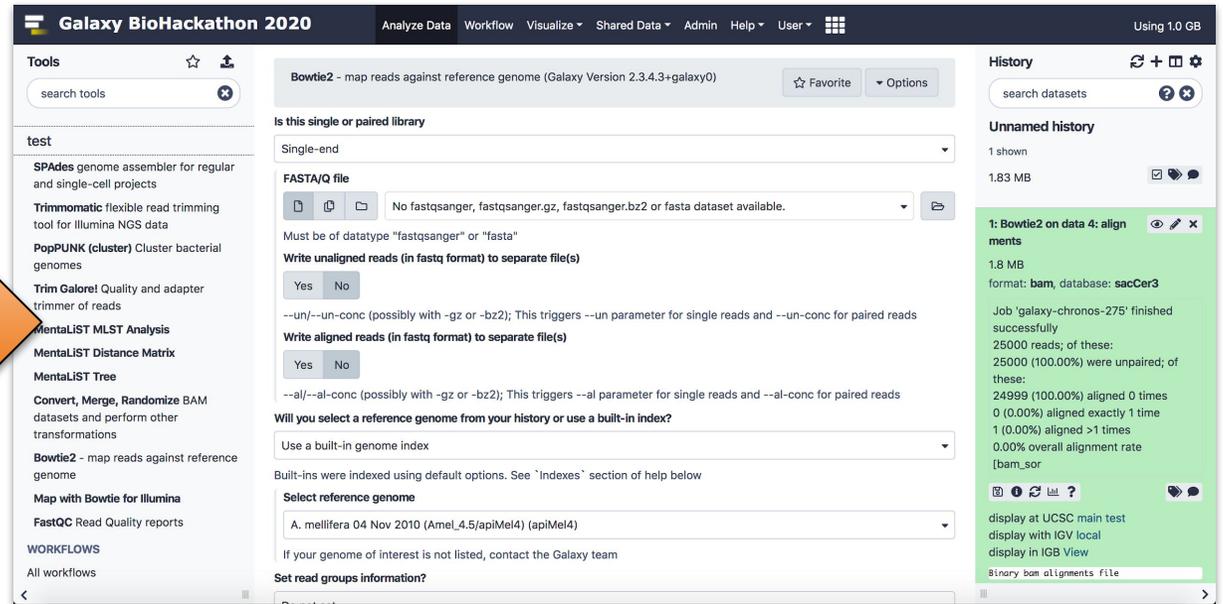
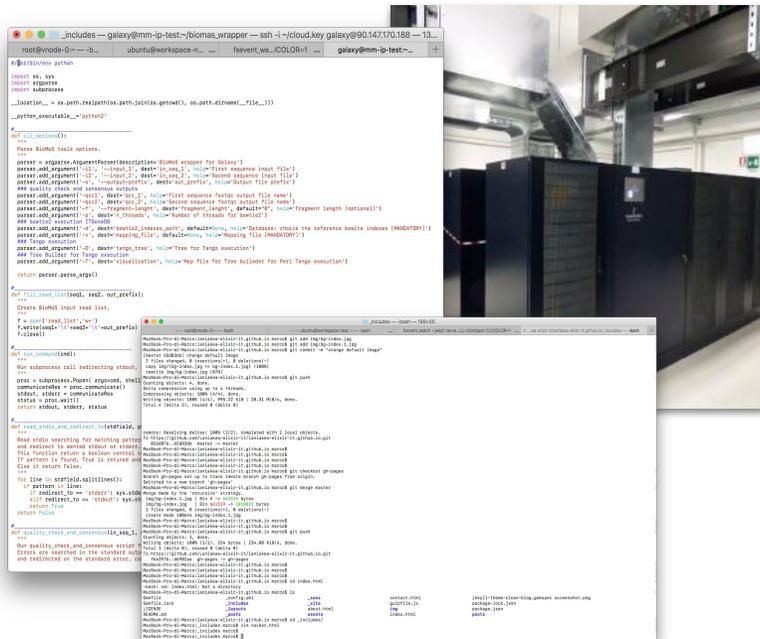
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23	bowtie2	2.3.4.2	+18.01	✓	Install
21	bowtie2	2.3.4.1	+17.01	✓	Install

- Tools graphical user interface.
- Workflow graphical user interface
- "App store" to all Galaxies worldwide
- Tools dependencies automatically solved

Allowing the community to move from command line tools to web user interfaces.



Allowing multiple users to exploit homogenous software environments, enhancing reproducibility.

# Laniakea



elixir Laniakea Dashboard Deployments Users Documentation Marco Tangaro

Most used

Galaxy Express

Galaxy Docker

All applications

Search...

Galaxy Docker

Galaxy Express

Galaxy cluster Live build

Galaxy Live build

Full description

Deploy Galaxy from a VM image with cluster support (FAST). The basic configuration includes CentOS 7, SLURM, the selected Galaxy flavour, companion software and reference data. Configure, click on the "Submit" button, wait for the confirmation e-mail(s) and log in to your new Galaxy instance. If after some hours you do not receive any e-mail please be sure to check your SPAM BOX.

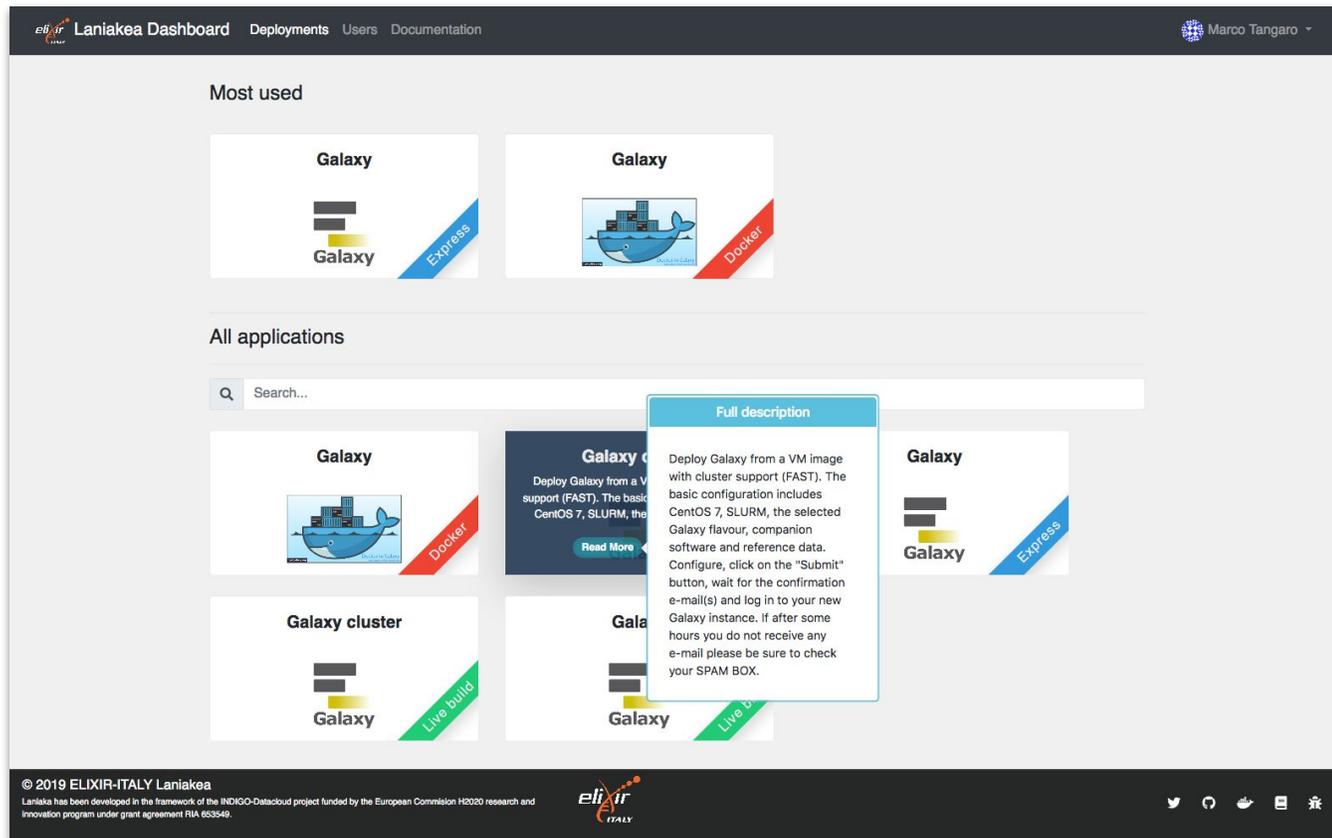
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Laniakea has been developed in the framework of the INDIGO-Datacloud project funded by the European Commission H2020 research and innovation program under grant agreement RIA 663549.

elixir ITALY

The Laniakea Dashboard home page.

Each tile provides a quick explanation of the application and links to the configuration and launch section.

Also more applications available: Jupyter, RStudio, ...



## Different deployment strategies:

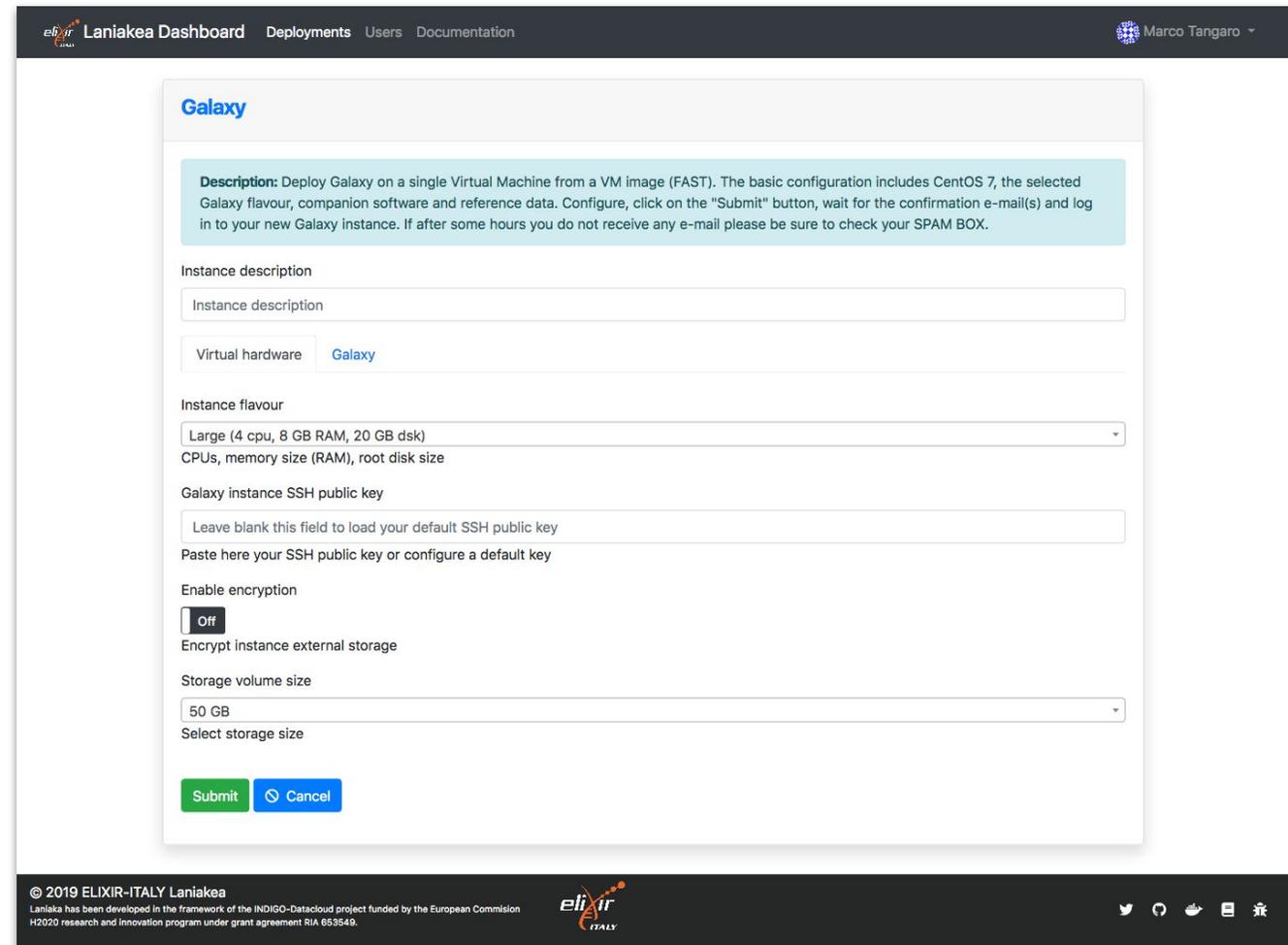
**Live Build**: build Galaxy from scratch -> always up-to-date (deployment time depending by the tools number).

**Express**: pre-built Galaxy images -> fast deployment, but tools not always at the last available version.

**Docker**: fast deployment of new flavours.

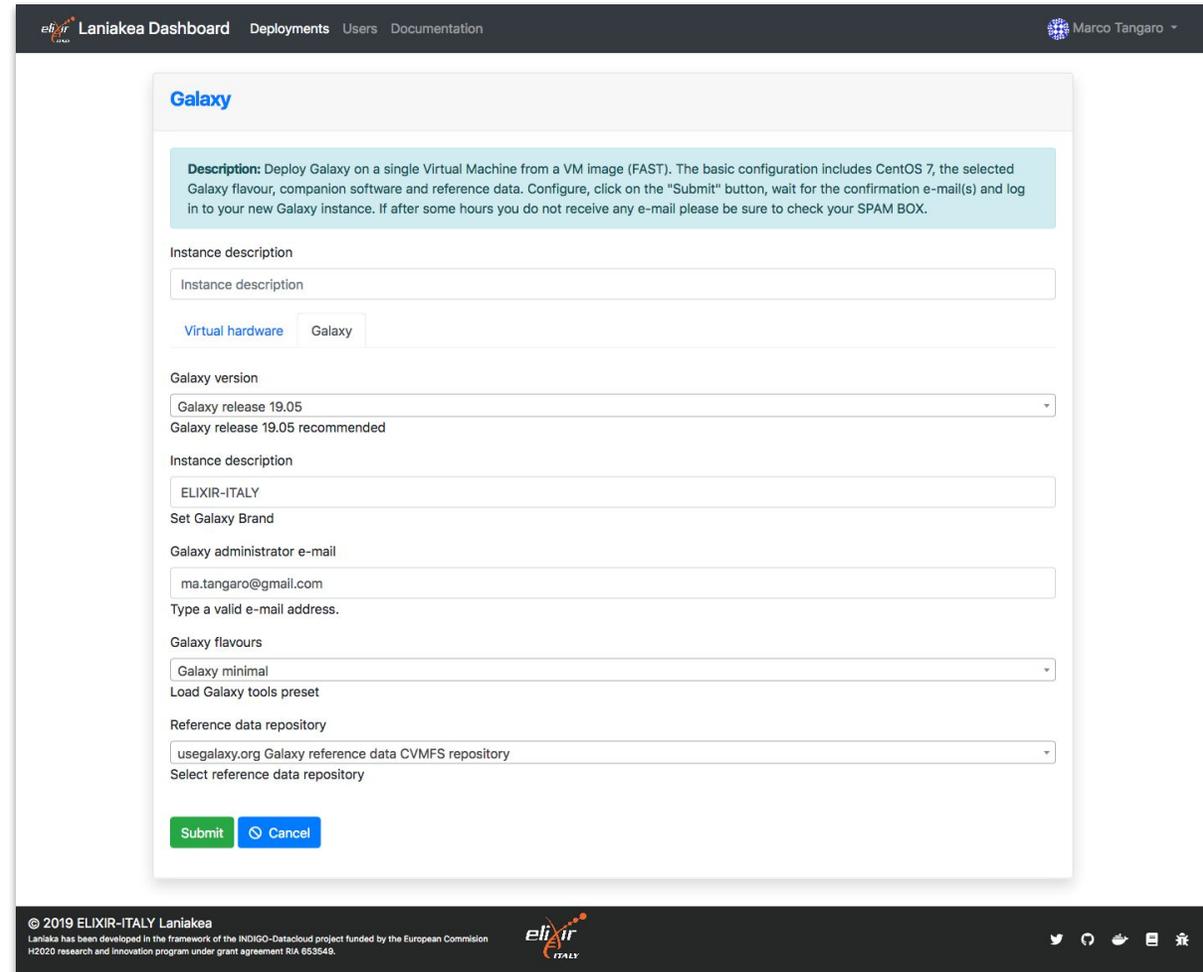
The web front-end provides different tabs to configure your Galaxy.

Virtual hardware: CPU, RAM and Storage

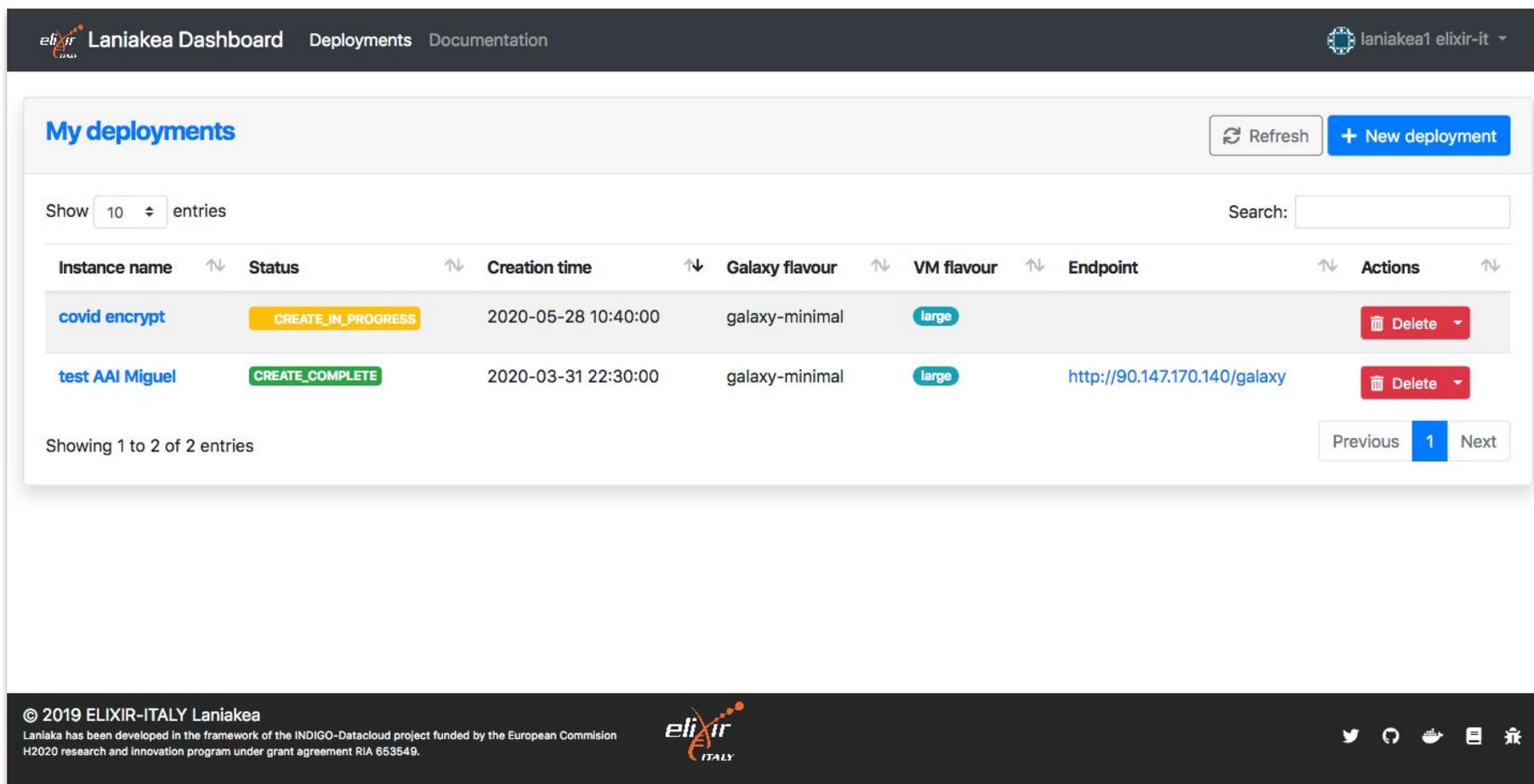
A screenshot of the Laniakea Galaxy configuration web interface. The page has a dark header with the "elixir Laniakea Dashboard" logo and navigation links for "Deployments", "Users", and "Documentation". A user profile for "Marco Tangaro" is visible in the top right. The main content area is titled "Galaxy" and contains a description box, an "Instance description" text field, a "Virtual hardware" tab (selected) and a "Galaxy" tab, an "Instance flavour" dropdown menu set to "Large (4 cpu, 8 GB RAM, 20 GB dsk)", a "Galaxy instance SSH public key" text field with a placeholder, an "Enable encryption" toggle set to "Off", and a "Storage volume size" dropdown menu set to "50 GB". At the bottom of the form are "Submit" and "Cancel" buttons. The footer contains copyright information for 2019 ELIXIR-ITALY Laniakea, a disclaimer about the project's funding, and social media icons.

The web front-end provides different tabs to configure your Galaxy.

Galaxy software: version, credentials, flavor and reference data.



The screenshot shows the 'Galaxy' configuration page in the Laniakea Dashboard. The page has a dark header with navigation links: 'Laniakea Dashboard', 'Deployments', 'Users', and 'Documentation'. A user profile 'Marco Tangaro' is visible in the top right. The main content area is titled 'Galaxy' and contains a description box with instructions on how to deploy Galaxy on a VM. Below this, there are several configuration sections: 'Instance description' with a text input field; 'Virtual hardware' and 'Galaxy' tabs; 'Galaxy version' with a dropdown menu set to 'Galaxy release 19.05' and a note that it is recommended; another 'Instance description' field containing 'ELIXIR-ITALY'; 'Set Galaxy Brand'; 'Galaxy administrator e-mail' with a text input field containing 'ma.tangaro@gmail.com' and a note to type a valid e-mail address; 'Galaxy flavours' with a dropdown menu set to 'Galaxy minimal' and a note to load Galaxy tools preset; and 'Reference data repository' with a dropdown menu set to 'usegalaxy.org Galaxy reference data CVMFS repository' and a note to select a reference data repository. At the bottom of the form are 'Submit' and 'Cancel' buttons. The footer contains copyright information for 2019 ELIXIR-ITALY Laniakea, a note about funding from the European Commission, the ELIXIR ITALY logo, and social media icons.



elixir Laniakea Dashboard Deployments Documentation laniakea1 elixir-it

### My deployments

Refresh + New deployment

Show 10 entries Search:

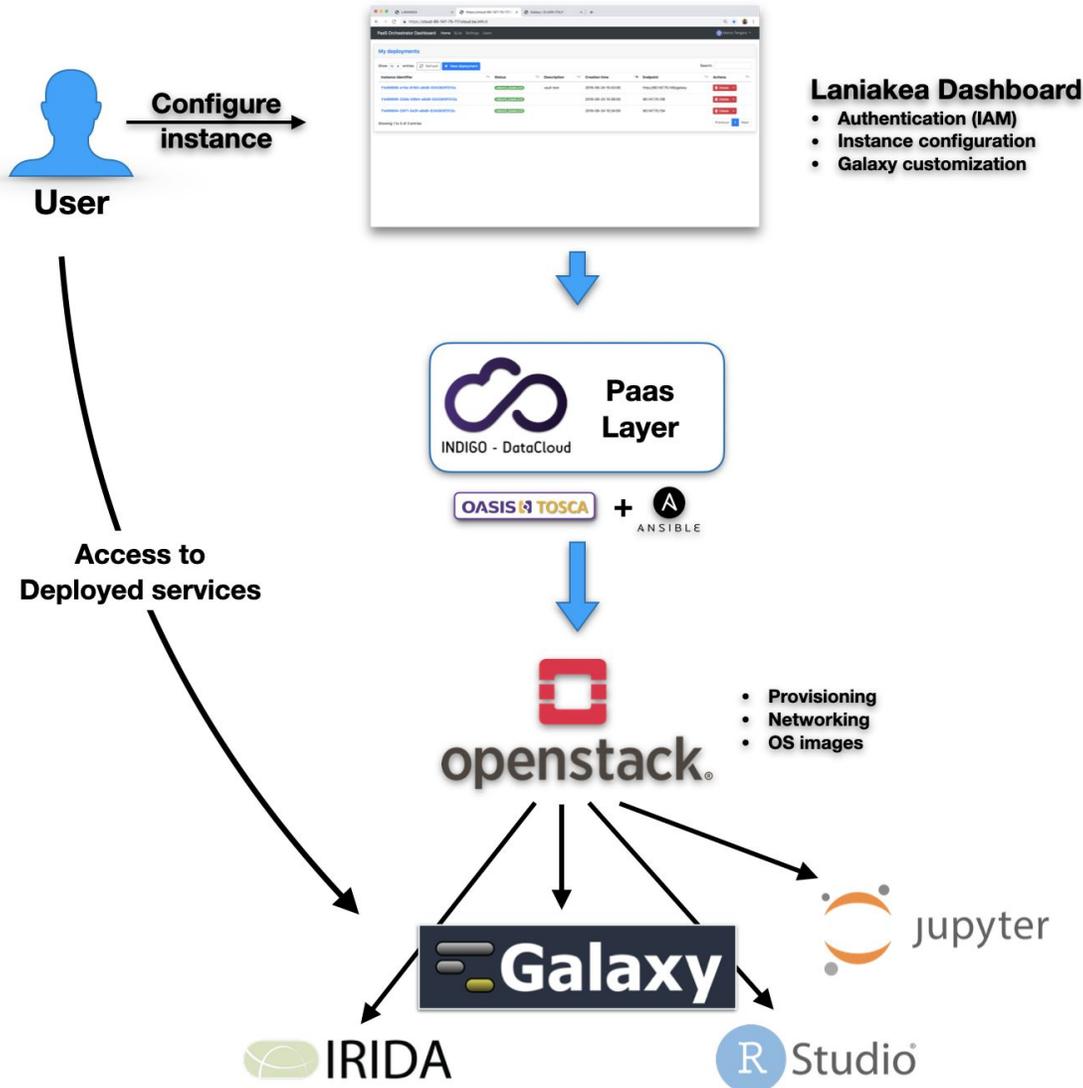
Instance name	Status	Creation time	Galaxy flavour	VM flavour	Endpoint	Actions
covid encrypt	CREATE_IN_PROGRESS	2020-05-28 10:40:00	galaxy-minimal	large		Delete
test AAI Miguel	CREATE_COMPLETE	2020-03-31 22:30:00	galaxy-minimal	large	http://90.147.170.140/galaxy	Delete

Showing 1 to 2 of 2 entries Previous 1 Next

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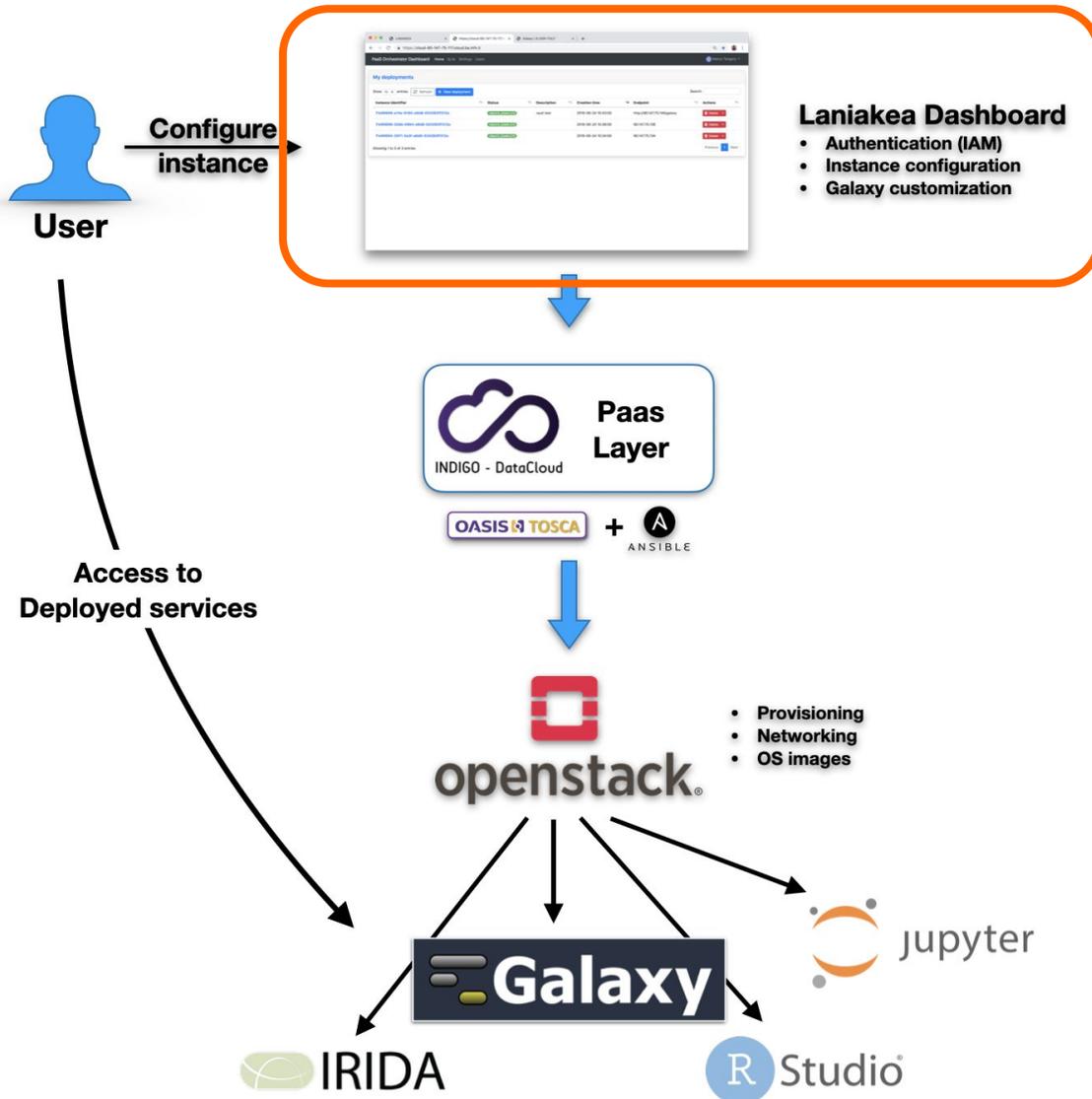


# Laniakea architecture (simplified view)



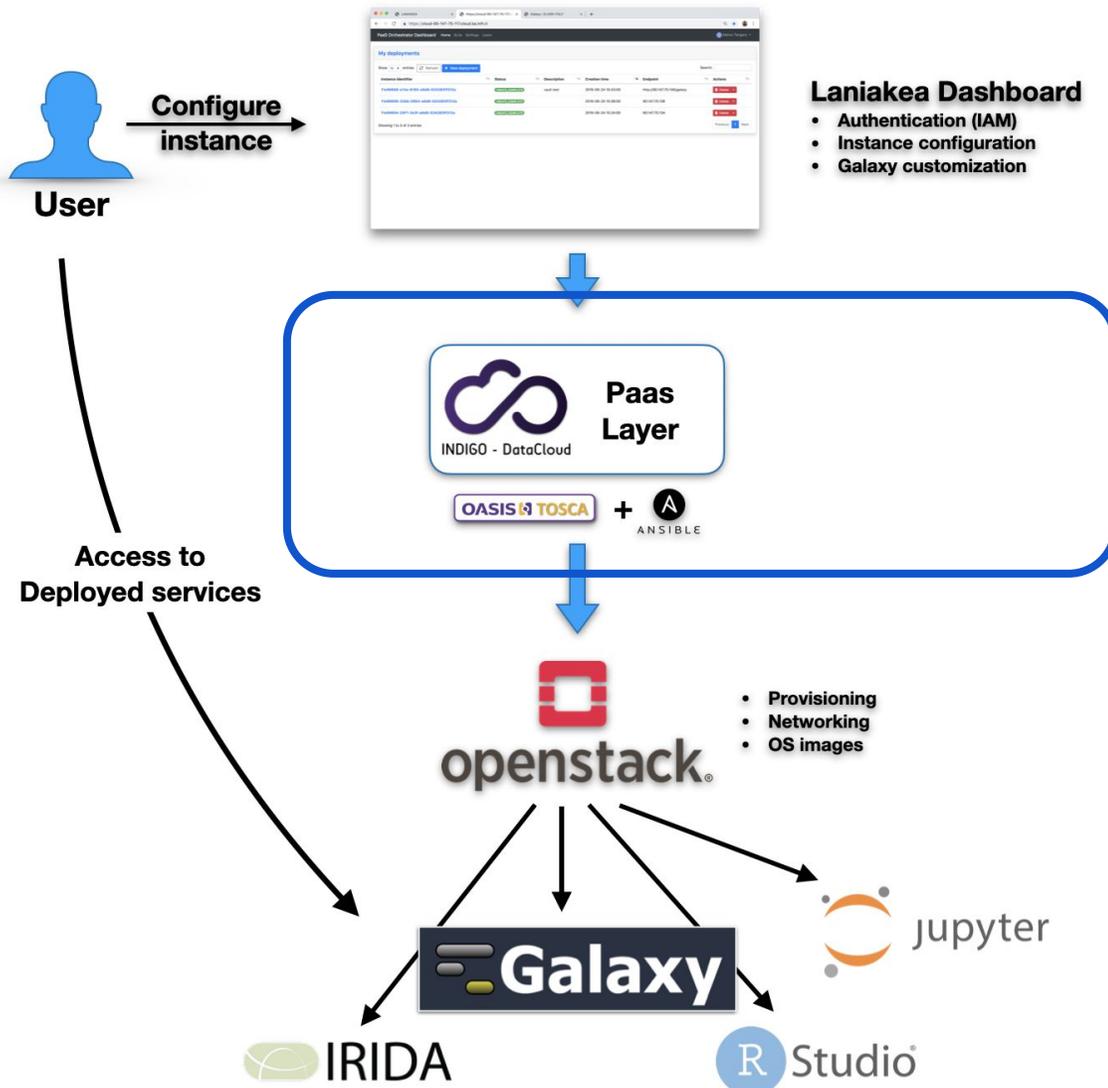
- **Dashboard** - User friendly access to configure and launch a Galaxy instance
- **INDIGO PaaS** - Galaxy automatic d
- **Cloud Providers** - ReCaS-Bari

# Laniakea architecture



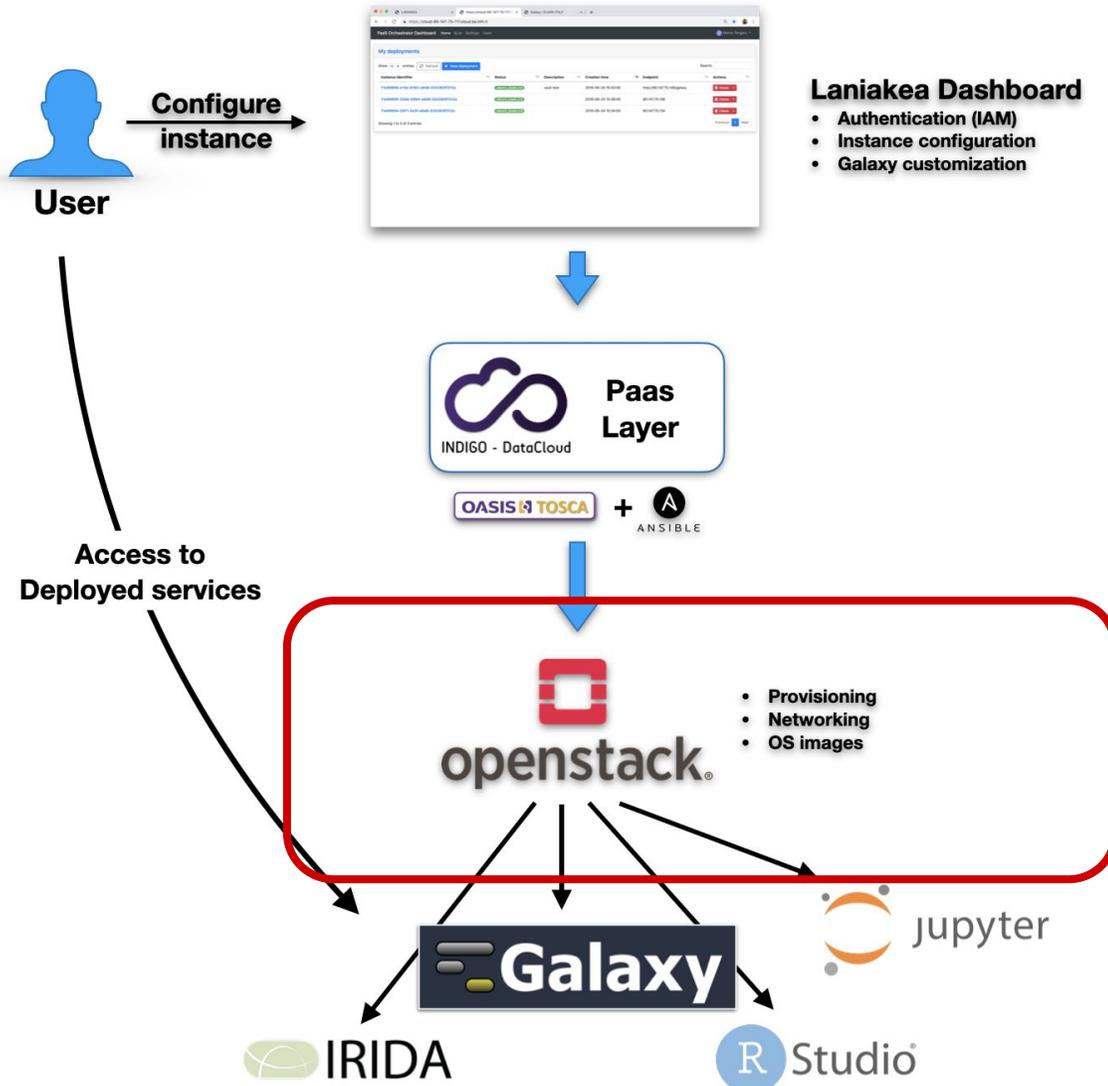
- **Dashboard** - User friendly access to configure and launch a Galaxy instance
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# Laniakea architecture



- **Dashboard** - User friendly access to configure and launch a Galaxy instance
- **INDIGO PaaS** - Galaxy automatic deployment
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# Laniakea architecture



- **Dashboard** - User friendly access to configure and launch a Galaxy instance
- **INDIGO PaaS** - Galaxy automatic deployment
- **Cloud Providers** - ReCaS-Bari

# Laniakea@ReCaS



Currently, some important Italian Institutions are using Laniakea for their daily work:

- Istituto Ortopedico Rizzoli (2 internal Galaxy servers).
- Istituto Zooprofilattico Sperimentale della Puglia e della Basilicata (2 internal Galaxy servers and 1 IRIDA instance).
- Ospedale Pediatrico Giannina Gaslini (public server).
- University of Milan (public Galaxy server and tools development).
- IBIOM-CNR (public Galaxy server and tools development).
- University of Turin (training)

... and counting.

