

# A French Galaxy Tool Shed to federate the national infrastructures and offering quality assessed tools



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Abstract: The Galaxy environment, notably dedicated to bio-analyses, is finding a growing success in bioinformatics and biology communities. This project is coordinated by the IFB Galaxy Working Group. The IFB offers a reference repository to centralize and promote the bio-analyses tools of the French community. The scope of this repository, initially dedicated to "France-Génomique" NGS pipelines, is now extending to other national infrastructures and to national training actions.

# Applicants

National infrastructures

France Génomique is the national sequencing infrastructure created

## Providers

The "Institut Français de Bioinformatique" (IFB - http://www.francebioinformatique.fr) is the French node of the pan-European research

thanks to the « Investment for the future » initiative. It gathers together 9 sequencing and 6 bioinformatics platforms. The main objective of the bioinformatic part of the France Génomique project is to coordinate the necessary evaluation of these methods to avoid duplication of efforts from the bioinformatics and sequencing platforms.

**MetaboHUB** is a national infrastructure of metabolomics and fluxomics that provides tools and services to academic research teams and industrial partners in the fields of health, nutrition, agriculture, environment and biotechnology.

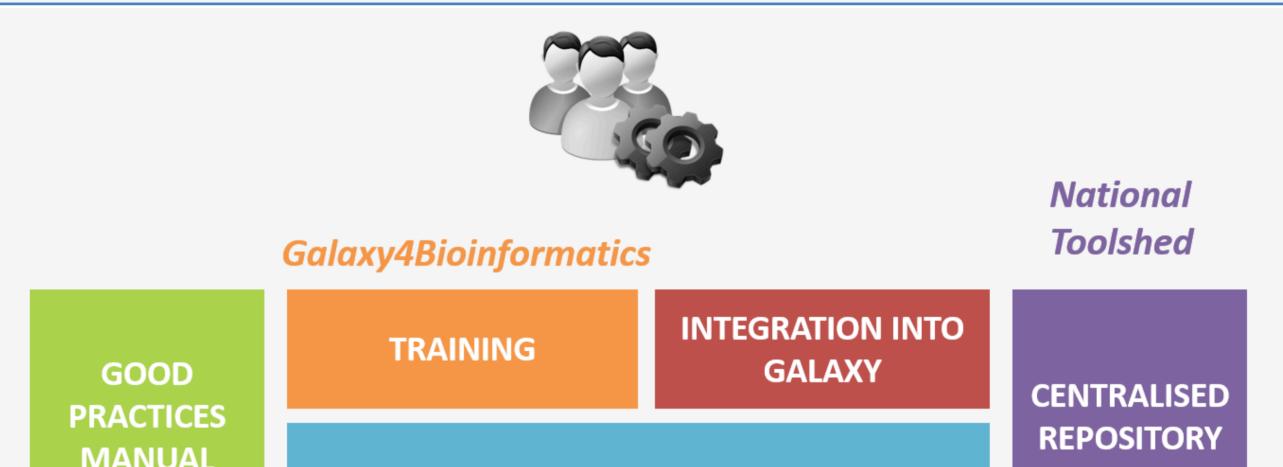
**Research team** : we also use this Tool Shed to harmonize tools installation over several Galaxy servers (Cloud, Platform...) for training session.

infrastructure ELIXIR. IFB national infrastructure provides an IT environment based on a central hub (IFB Core) and on 32 platforms distributed in 6 regional groups. This IT infrastructure is devoted to the management and analysis of biological data, in particular data generated by high-throughput technologies. IFB is also linked with others national infrastructure (MetaboHub, France Génomique...) through R&D or training activities.

IFB commissioned in 2013 a Working Group around the Galaxy platform. This group gathers several national platforms, and manages animation actions (Galaxy Day, thematic schools, etc.) and actions to structure (training, good practices guides, etc.) users and developers communities.

# Strategy to federate users communities

As a part of the bioinformatics work packages funded by the "France-Génomique" project, the community has developed or evaluated many tools and set up analysis workflows. Exploitation and diffusion of these pipelines dedicated to people unfamiliar with the command line instructions now lies on using a **common platform** (Galaxy) and on creating a **shared repository** (Tool Shed).







MANOAL	INVENTORY	
	<b>Deployment on</b>	Contacts with the
	platforms and Cloud	Galaxy Team

# Why

# **Strong focus on quality tools & validation**

- Functional tests
- Test workflows

## **Intranet access before public releases**

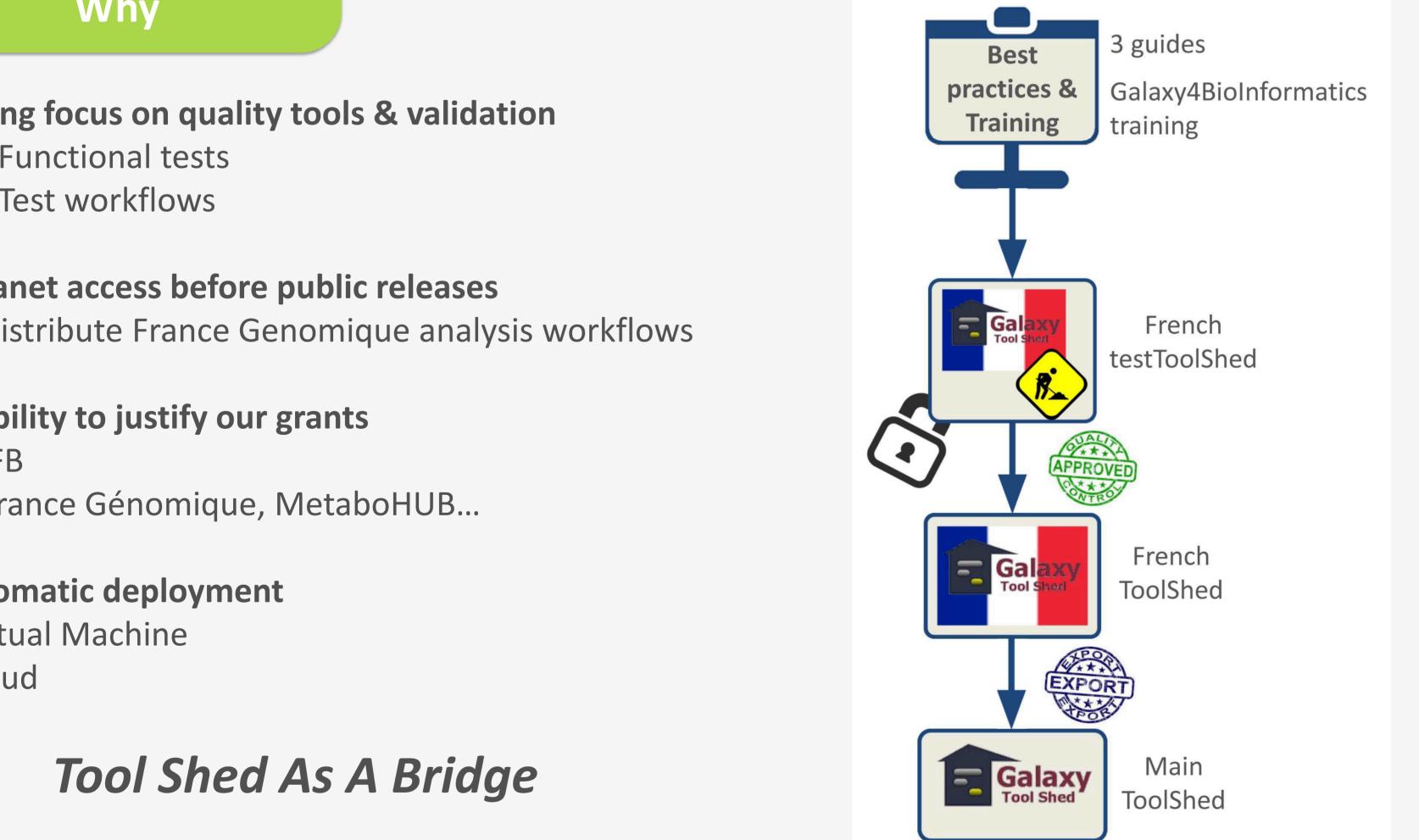
Distribute France Genomique analysis workflows

## Visibility to justify our grants

IFB France Génomique, MetaboHUB...

# Automatic deployment

Virtual Machine Cloud



# Results

### **Best practices guides**

Quick start, Advanced and Toolshed

http://www.france-bioinformatique.fr/galaxy-working-group

### Training :

### Galaxy4Bioinformatics

Roscoff (11/2014), Nantes (03/2015), Toulouse (11/2015) Used by national summer school : NGS AVIESAN (09/2015)

### **SARTools**

H, Varet, J,-Y, Copee and M,-A, Dillies, SARTools: a DESeq2 and edgeR-based R pipeline for comprehensive differential analysis of RNA-seq data, 2015 (submitted)

### W4M tools : 29 modules

# **Road Map**

# Planemo evaluation (11/2015)

Quality : automatic test specification, tools reviewing ...

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[3] Giardine B, Riemer C, Hardison RC, Burhans R, Elnitski L, Shah P, Zhang Y, Blankenberg D, Albert I, Taylor J, Miller W, Kent WJ, Nekrutenko A. "Galaxy: a platform for interactive large-scale genome analysis." Genome Research. 2005 Oct; 15(10):1451-5.

[4] Daniel Blankenberg, Gregory Von Kuster, Emil Bouvier, Dannon Baker, Enis Afgan, Nicholas Stoler, the Galaxy Team, James Taylor and Anton Nekrutenko, "Dissemination of scientific software with Galaxy ToolShed," in Genome Biology 2014, 15:403, doi:10.1186/gb4161

