

UseGalaxy.fr

a Galaxy server for the French
bioinformatics community

Anthony Bretaudeau (INRAE, Rennes)

Thomas Chaussepied (CNRS, Rennes)

Lain Pavot (INRAE, Clermont-Ferrand)

Julien Seiler (CNRS, Strasbourg)

Gildas Le Corguillé (Sorbonne Université, Roscoff)

Galaxy is an open source web-based interactive data analysis platform that supports defining and executing workflows.

Jobs are executed on HPC infra.

The image displays three panels from the Galaxy web interface. The left panel, titled 'Tools List', shows a search for 'minimap2' and lists several tools with their descriptions: 'Map with minimap2', 'TB-Profiler Profile', and 'Purge overlaps'. The middle panel, titled 'Tool Forms/Result Viewer', shows the configuration options for the 'minimap2' tool, including sections for 'Indexing options', 'Mapping options', and 'Filter out top FLOAT fraction of repetitive minimizers'. The right panel, titled 'History', shows a list of recent jobs, including '4158: Preprocessing and mapping reports', '4157: MultiQC on data 4154, data 4153, and others: Plots a list', '4155: data 2165, data 2164, and others (flattened) a list with 1118 items', '2777: SnpEff eff: on collection 2 689 - HTML stats a list with 86 items', '2689: Replace Text on collection 2602 a list with 86 items', '2602: VCF-VCFintersect: on collection 2515 and collection 234 1 a list with 86 items', '2428: VCF-VCFintersect: on collection 2341 and collection 874 a list with 86 items', and '2167: Lofreq filter on collection 874 a list with 86 items'.


Tools List

Tool Forms/Result Viewer

History

UseGalaxy.fr










slurm
workload manager

Early 2023

Currently

 81 nodes	97 nodes
 4300 cpu threads	8396 cpu threads
 20 TB RAM	52 TB RAM
 2 PB storage	4 PB storage
 6 GPU cards Nvidia A100	



The IFB Core Cluster Transversal Team:
15 mutualized engineers from 7 IFB platforms ~ 4.0 FTE





1 million jobs in one year



2700 subscribers - 1351 active users in one year



1850 tools

- General Text Tools
- Genomic File Manipulation
- Common Genomics Tools
- Genomics Analysis
- Genomics Toolkits
- Metagenomics
- Workflow4Metabolomics
- ProteoRE
- Galaxy-P
- Galaxy-E
- Statistics and Visualisation
- Miscellaneous Tools



Focus on your analysis

- Personalized welcome page
- Filtered tool list

The collage displays five instances of the Galaxy France web interface, each tailored to a specific subdomain. The subdomains shown are: ecology.usegalaxy.fr, metabarcoding.usegalaxy.fr, ProteoRE Galaxy, covid19.usegalaxy.fr, and Workflow4metabolomics. Each interface features a personalized welcome message and a filtered list of tools relevant to that subdomain.

5 sub-domains | <sub-domain>.usegalaxy.fr



ecology



metabarcoding



proteome



covid19



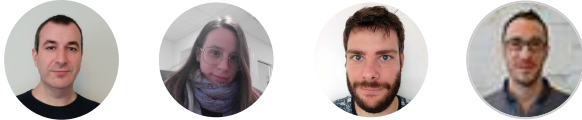
workflow4metabolomics



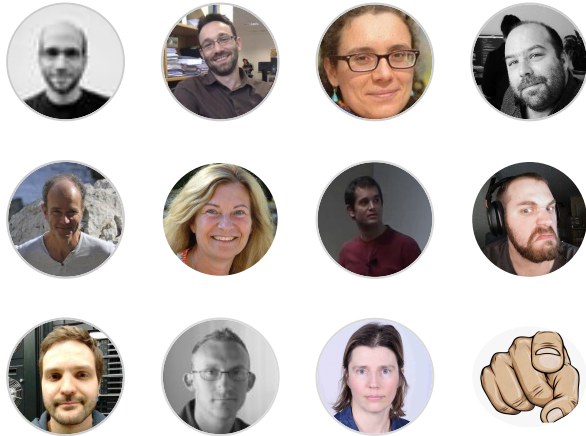
Your project



Your community



Featuring The IFB Core Cluster team



Featuring The Galaxy Community

community.france-bioinformatique.fr

IFB Community Support

Galaxy | toutes les étiquettes | tous | Récents | Non lu (1) | Top

+ Créer un sujet

Sujet	Réponses	Vues	Activité
Ajouter apps dans UseGalaxy.fr ¹	17	121	1 j
multiBamSummary Fatal error: Exit code 2 () Fatal	0	17	4 j

Need help
Give help

