

Towards a cyber Galaxy ?

The IFB working team on the Galaxy platform

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Introduction

The mission of the French Institute of Bioinformatics (IFB) is to coordinate the French bioinformatics community. Within a context where high-throughput data analysis considerably modifies the way in which analysis is carried out with the use of new infrastructures, new tools and new skills, the IFB has decided to conduct a collaborative action on data analysis workflows and more specifically on the Galaxy platform.

The Galaxy platform already benefits from a very active community of users and developers. The Galaxy platform is designed for sharing all the items implied in a biological analysis: tools, data, protocols and results. Consequently, this working environment enhance collaboration between all the actors of a project: algorithmists, scientists, bioanalysts, engineers

Galaxy

- No more need to launch command lines on a terminal
- No more need to have knowledge of programming/scripting
- Jobs submission facilities on computer cluster (HPC)
- Protected data and historical management facilities
- Data and analysis workflows sharing
- Possibility of adding tools as needed: NGS, Metabolomic, Statistic, etc ...



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Training

Pooling, Seminar, Sharing ...

Context

- High-throughput data analysis requires new storage and new computing facilities.
- Integrated solutions must be proposed to biologists and bioanalysts to exploit these facilities.

Objectives

- An ideal starting point for biologists and bio-analysts to learn good analysis practices.

Ongoing work

- Training for initiation to Galaxy (Curie, Genotoul, ABiMS, MIGALE, URGI)
- Galaxy as an environment : Transcriptomic, SNP detection, Chip-seq, etc ... (all)
- An online self-learning platform (Genotoul/Sigeneae)

Architecture

Optimisation, virtualisation ...

Context

- Galaxy components: job manager, web frontal, databases ...
- Different usages: training, developmental and exploitation prototype phases
- Methods: instances virtualisation, workstation installation, data sharing, parallelisation, etc...

Objectives

- Address operating problems in the production environment, automation capabilities of deployment tasks and Galaxy servers monitoring solutions.

Ongoing work

- Presentation: "DevOps Ignition to reach Galaxy continuous integration." GCC2013, Oslo. (URGI).

Tool integration

Good practice, Toolshed ...

Context

- High-throughput analysis tools integration can be tedious: multiplicity of sources, languages, formats ...

Objectives

- Offer solutions facilitating the tools integration within Galaxy: the tool versioning versus the Galaxy releases, tools and workflows unit testing ...
- Technological survey
- Reflection on the benefits of a high quality IFB specific Galaxy toolshed

Ongoing work

- Writing a guide to good practice

Community

Users / Platform / Projects / Research institutes

Ongoing initiative

- The Galaxy-France communities, Aviesan bioinformatics school, Galaxy Aplibio group
- A working group has been made from several IFB platforms (ABiMS, Curie, Genotoul/SIGENAE, MIGALE, URGI), and from one platform of the national infrastructure MetaboHub (PFEM).
- Plurality of local instances depending on their specific activities

Conclusion and Perspectives

- The first presented work brought together a community that had already initiated some actions on Galaxy. These actions will be linked with other national research infrastructures financed by "Future Investments" ANR program (MetaboHub, EMBRC-France, etc ...).
- This work could also be seen as a first step towards a wider community. Sharing usages and good practices regarding tools and instances could be seen as first mission for this community.
- Current scientific collaborations illustrate that the Galaxy environment can become an excellent medium and a gateway between bioinformatician and biologist communities.

Schedule

- **Summer 2013:** documentation website creation
- **17-23 November 2013:** new ITMO Aviesan courses in Roscoff (ABiMS, Migale, Institut Curie, URGI and Genotoul/Sigeneae)
- **December 2013:** IFB seminar with experience feedback on Galaxy
- **Spring 2014:** 4 days of training: basic and advanced practices (tool integration, e-learning, etc ...) in Roscoff by the IFB Galaxy group

Contact

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[1] Goecks, J, Nekrutenko, A, Taylor, J and The Galaxy Team. Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. Genome Biol. 2010 Aug 25;11(8):R86.

[2] Blankenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, Nekrutenko A, Taylor J. "Galaxy: a web-based genome analysis tool for experimentalists". Current Protocols in Molecular Biology. 2010 Jan; Chapter 19:Unit 19.10.1-21.

[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.