# Evolution of the Galaxy tool ecosystem - *happier developers, happier users*

Martin Čech[1], Björn Grüning[2], Eric Rasche[3], Kyle Ellrott[4], John Chilton[1], and Galaxy Team

[1] Department of Biochemistry and Molecular Biology, PSU, USA marten@bx.psu.edu

[2] Bioinformatics Group, Department of Computer Science, University of Freiburg, Germany

[3] Center for Phage Technology, Texas A&M University, USA

[4] Center for Biomolecular Science & Engineering, University of California Santa Cruz, USA

Project: http://galaxyproject.org Code: https://github.com/galaxyproject License: AFL 3.0

Galaxy is a powerful open-source platform for data intensive research. The number of Galaxy tool developers and users is growing due both to its steady expansion of the number of Galaxy instances into diverse settings (e.g. GalaxyP, deepTools, CoSSci, Oqtans, Genomic Hyperbrowser, Osiris)[1] and initiatives such as the DREAM SMC-Het[2] challenge (which includes a reproducibility focused sub-challenge requiring submission of Galaxy tools and workflows). The result is a need to scale tool testing, discovery, and distribution.

Galaxy uses the Tool Shed as an App Store-like platform for tool exploration and deployment with reproducible workflow sharing support. Today the Tool Shed contains more than 3000 tools from different areas of computational research and a vibrant community is updating and improving these tools.

Driven by community feedback solicited via questionnaire[3] we identified and focused on the areas that would benefit the most from improvements:

- ➔ *Tool testing* - we built Planemo that dramatically simplifies tool creation and testing.
- ➔ *Tool discovery* - we have rewritten search from the ground up to allow Galaxy deployers to more easily identify high quality tools.
- ➔ *Tool distribution* - by providing integration with Jenkins and Github we have simplified and automated the tool testing and Tool Shed publishing process.

A community based commission (IUC) is maintaining a best practice guide to address the first issue and defines standards for high quality Galaxy tools[4].

We also present Planemo - an easy to install command-line utility that gives developers a way to bootstrap, lint, test, and explore Galaxy tools without even requiring installation and configuration of Galaxy. Planemo makes existing developers more productive, and Planemo virtual appliances are being used to introduce new SMC-Het developers to tool and workflow development - lowering the barrier to entry.

Jenkins build scripts leveraging Planemo have been developed to automate testing and deployment of tool repositories, providing vital feedback by posting results back to GitHub. The scripts can also automatically deploy tool repositories to the Tool Shed, reducing the overhead of managing large number of tools.

We firmly believe the presented work will enable the Galaxy community to scale up its already great contributions and boost collaboration.

---

[1] https://wiki.galaxyproject.org/PublicGalaxyServers

[2] https://www.synapse.org/#!Synapse:syn2813581

[3] Data available at https://wiki.galaxyproject.org/Community/GalaxyAdmins/Surveys/2014

[4] http://galaxy-iuc-standards.readthedocs.org/