Galaksio, a more user friendly interface for Galaxy using workflows
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Most researchers lack a comprehensive training in bioinformatics and prefer plain-language instructions accompanied by a comprehensive graphical user interface. These preferences are substantially different from the tools and software favoured by bioinformaticians who generally prefer command line tools and programming to control software. As a result many researchers find themselves in need of extensive support or pushed towards expensive proprietary software where an individual license for popular software such as CLC Workbench with necessary plugins can cost more than 6000 USD per year.

The Galaxy Workflows Management system is often described as a platform giving experimentalists without informatics or programming expertise the means to perform complex large-scale analysis with just a Web browser. In practice, however, our experience is that researchers with an experimentalist background find the system quite challenging to use. The Galaxy interface is designed with the idea that users should use the browser to construct workflows from the building blocks made available on public servers or through the Galaxy toolshed. To achieve this, researchers must have a solid grasp of the tools available and also correctly interpret the information passed on from the wrappers to the user interface.

To provide a more accessible interface SLU Global Bioinformatics Centre has developed the Galaksio interface which is focused on making complete workflows available to users. The interface runs on a light weight Python Web Server and passes commands directly to any available Galaxy server using the API. The user logs in via the Galaksio interface and Galaksio retrieves all workflows available to the user on the Galaxy server. The user can then browse available workflows and upload new data through Galaksio or run workflows on data already available on the server.

Galaksio is designed to make Galaxy more accessible in the B3Africa project (www.b3africa.org) but is freely available via Github and will be used by several different bioinformatics support groups. The purpose of the interface is to enable bioinformaticians to provide complete workflows to researchers working on a wide variety of subjects where it is preferable to rely on a limited number of best-practice workflows rather than inventing novel bioinformatics approaches. A small number of bioinformaticians working in a distributed network can thereby more effectively collaborate to distribute reliable workflows to improve the comparability of projects and reduce the number of potential errors caused by ad-hoc bioinformatics analysis.

Galaksio is available at: https://github.com/fikipollo/galaksio and can easily be deployed using docker from tklingstrom/galaksio on Dockerhub (for example: docker run -it -p 8081:80 tklingstrom/galaksio). All code and descriptions are available under a GNU General Public License v3.0 as described in the Github repository.