

Structured Analysis and Integration of RNA-Seq experiments (de.STAIR)

Fkz 031L0106

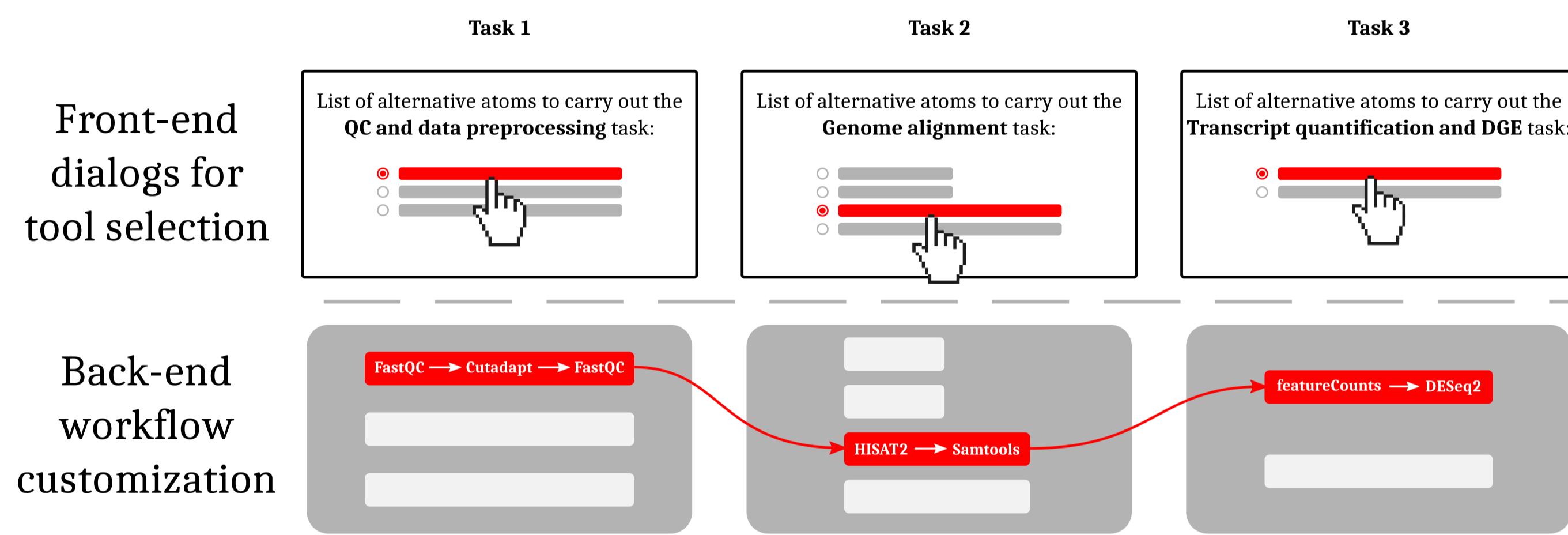
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 Steffen C. Lott and Wolfgang Hess - Genetics and Experimental Bioinformatics, University of Freiburg
 Rostock: Andrea Bagnacani and Olaf Wolkenhauer - Dept. of Systems Biology & Bioinformatics, University Rostock

Short description of the project

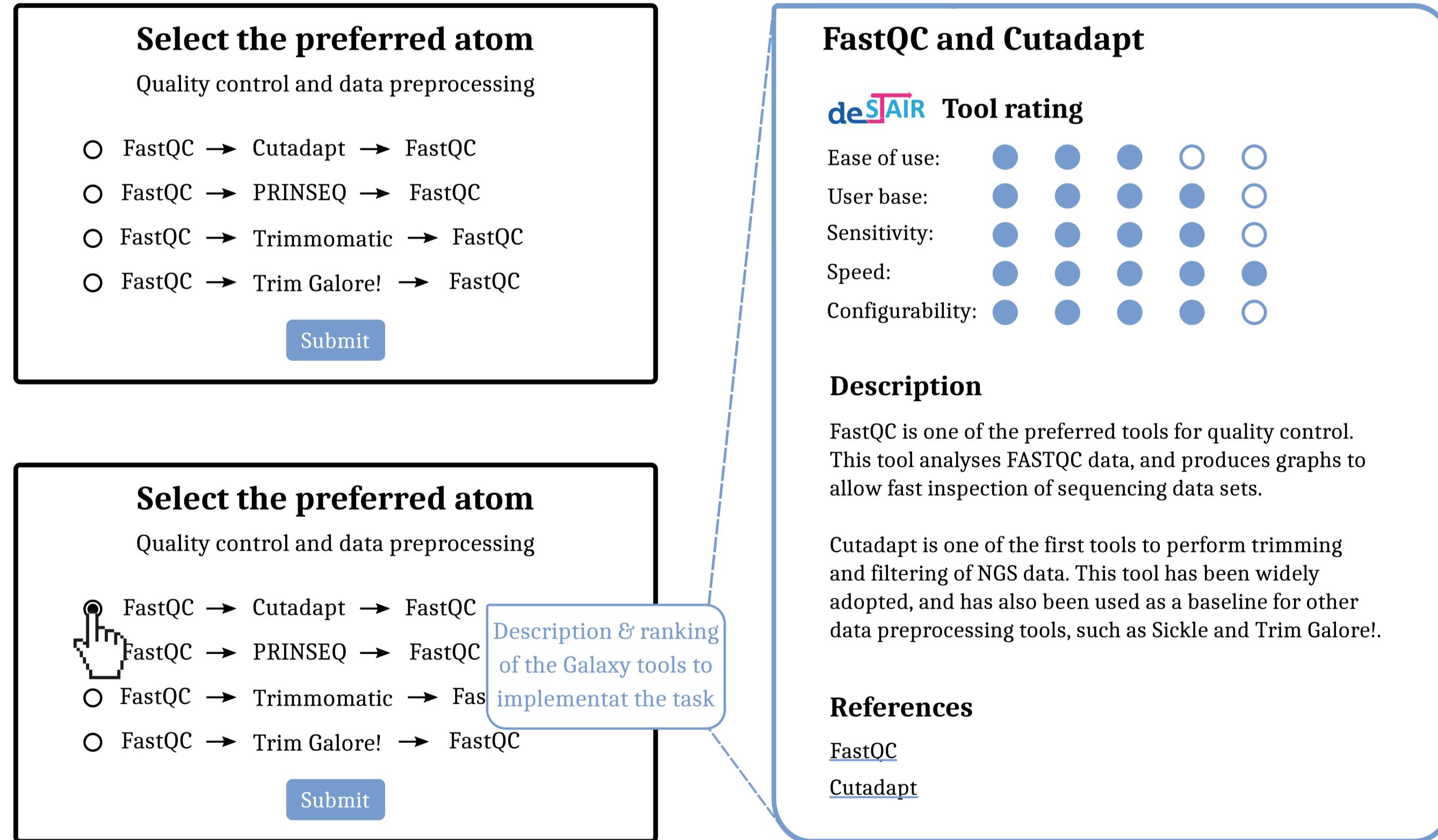
The Galaxy platform has been adopted by a growing body of Life Science communities. However, with increasing contributions, the number of Galaxy tools addressing the same or similar needs, is rising. Thus, it becomes harder for users to make informed decisions about the selection of tools and implication of their parameterizations. This is due to the lack of a systematic overview of the alternative tools of a Galaxy instance. We address this problem with the development of a **Galaxy workflow generator**, which rests on the novel concept of **Galaxy atoms**, i.e. interactive tours that illustrate individual tools (or series thereof), whose parameterization are tailored for specific experimental setups. Alternative atoms are thus presented to users via a developed plugin, which allows to compare, select, and combine tools to **customize workflows**.

Progress report

Workflow customization



Interactive comparison of the available alternative atoms



General information on the project

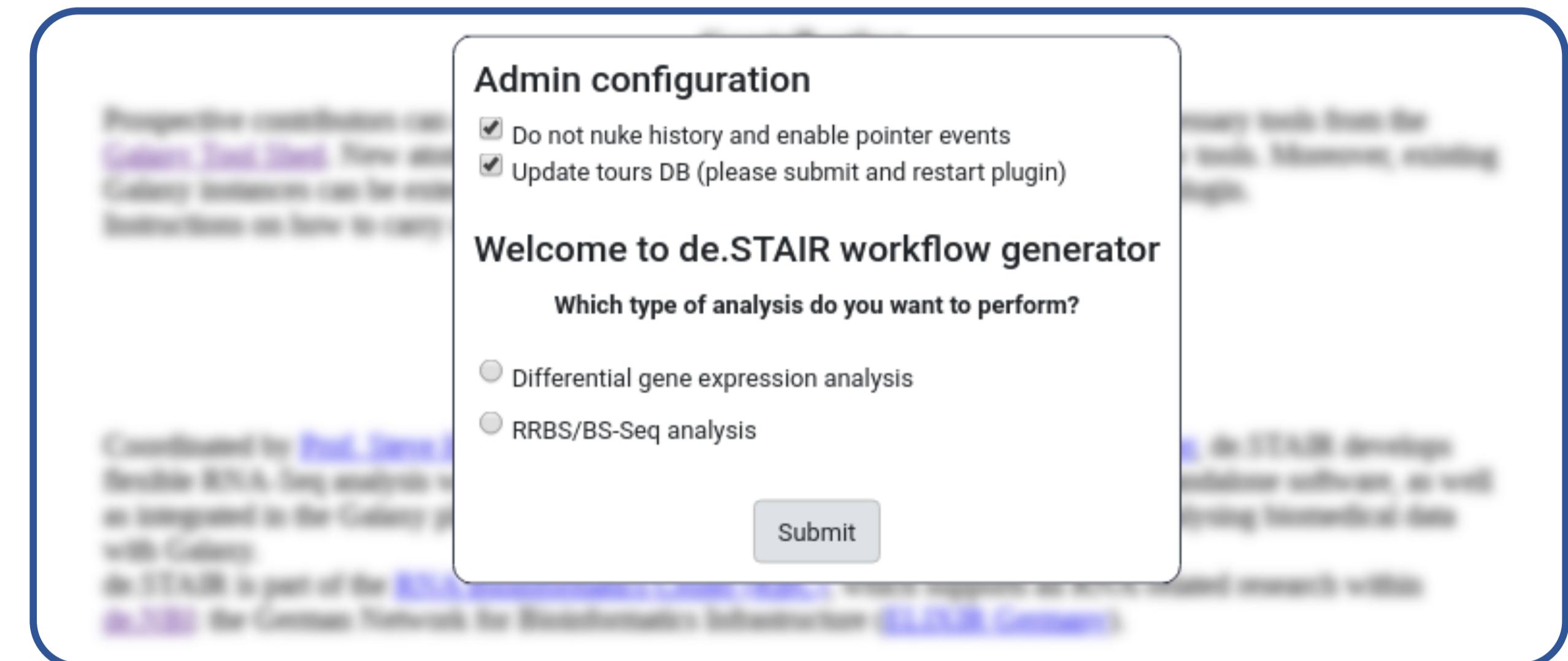
Funded by de.NBI staff

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Additional staff involved

de.NBI services

<https://destair.leibniz-fli.de>




Galaxy Atoms & Workflow generator plugin

github.com/destairdenbi

DIEGO

[10.1093/bioinformatics/btx690](https://doi.org/10.1093/bioinformatics/btx690)

GLASSgo

[10.3389/fgene.2018.00124](https://doi.org/10.3389/fgene.2018.00124)

segemehl

[10.13.71/journal.pcbi.1000502](https://doi.org/10.13.71/journal.pcbi.1000502)

Metilene

[10.1101/gr.196394.115](https://doi.org/10.1101/gr.196394.115)

TriplexRNA

[10.1093/nar/gku465](https://doi.org/10.1093/nar/gku465)

de.NBI Training and education

Introduction to RNA-Seq data analysis with Galaxy

[CASyM Ljubljana](#)
29.03.2017 - 29.03.2017

RNA-Seq data analysis with Galaxy for clinical applications

[GMDS Oldenburg](#)
18.09.2017 - 18.09.2017

A primer for RNA-Seq processing, interpretation and visualization

[Freiburg](#)
04.10.2017 - 06.10.2017

Introduction to RNA-Seq data analysis with Galaxy

[Kiel](#)
07.03.2018 - 07.03.2018

A primer for RNA-Seq processing, interpretation and visualization

[Jena](#)
27.06.2018 - 29.06.2018

RNA-Seq data analysis with Galaxy for clinical applications

[GMDS Osnabrück](#)
04.09.2018 - 04.09.2018

Galaxy for linking Bisulfite sequencing with rna sequencing

[Rostock](#)
06.03.2019 - 08.03.2019

RNA-Seq data analysis with Galaxy for clinical applications

[GMDS Dortmund](#)
08.09.2019 - 08.09.2019

Galaxy for linking Bisulfite sequencing with rna sequencing

[Freiburg](#)
09.10.2019 - 11.10.2019

Publications

- Riege et al. (2019). Dissecting the DNA binding landscape and gene regulatory network of p63 and p53. Submitted
- Bagnacani et al. (2019). Tools for understanding miRNA-mRNA interactions for reproducible data analysis
- Afgan et al. (2018). The galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. NAR
- Batut et al. (2018). Community-driven data analysis training for biology. Cell Syst.
- Lott et al. (2017). Customized workflow development and data modularization concepts for rna-sequencing and metatranscriptome experiments. J. Biotechnol.