

de.STAIR

Structured Analysis and Integration of RNA-Seq Experiments

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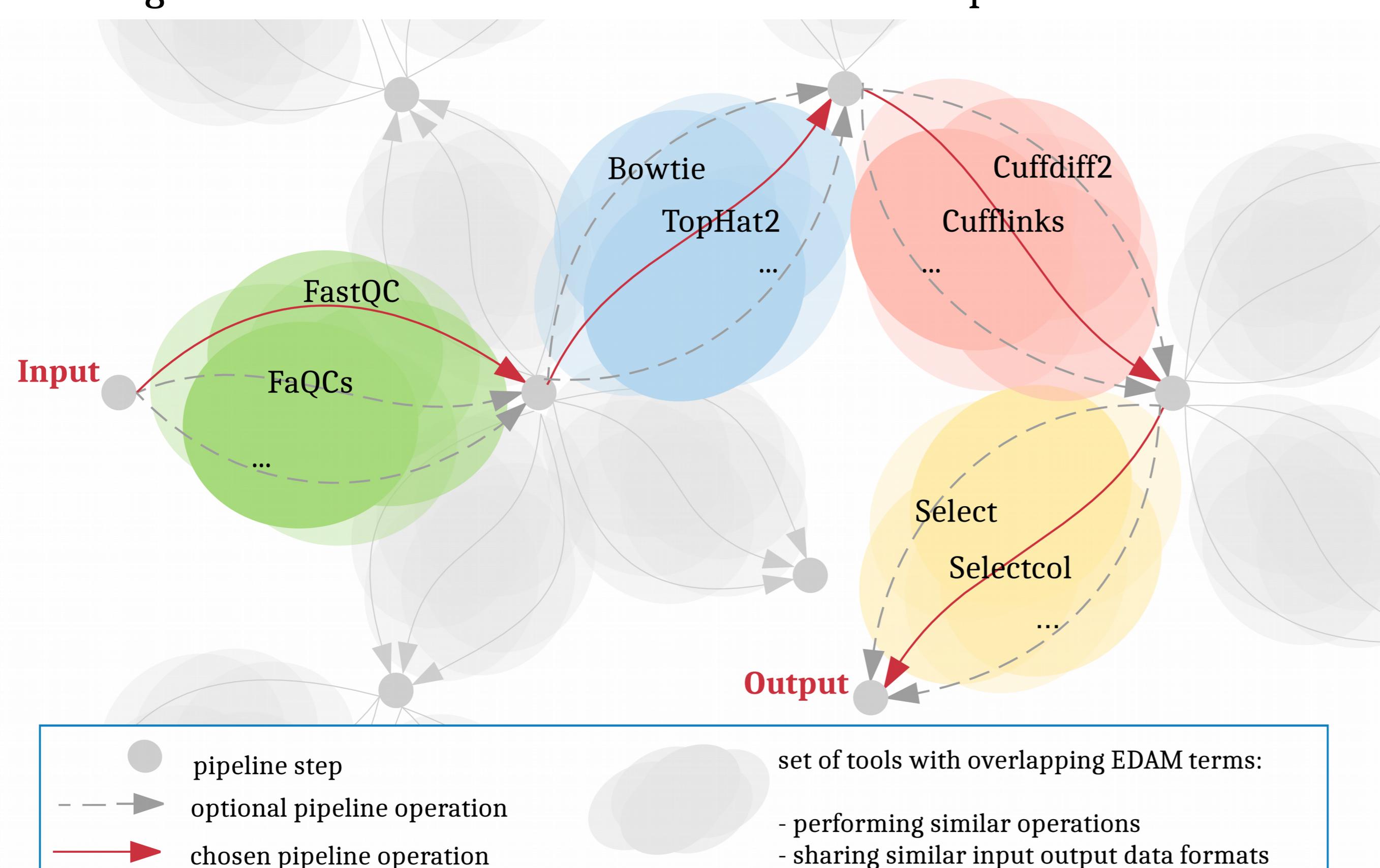
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Short description of the project

The Galaxy Community Network is promoting RNA-Seq protocols and best practices through the reuse of existing tools and the consolidation of a Training Network to provide example datasets, tutorials, and interactive tours. However, the more tools are gathered, the more complex the options for tool-chaining and parametrization become. To assist researchers in carrying out their investigations, we propose to integrate the Galaxy framework with an interactive recommendation system that leverages on community consolidated best practices as well as EDAM-annotated tools. Such a system would promote the adoption of well established pipelines, while at the same time allowing room for new and experimental tools, easing reuse, while consolidating protocols and reproducibility.

de.NBI services

- Interactive guidance on the design of RNA-Seq experiments
- Workflow design and integration within RBC's Galaxy RNA Workbench
- Dockerized Galaxy flavors
- Easing annotation and characterization of transcripts



de.STAIR's interactive recommendation system. Users can decide which path to walk towards the completion of the desired analysis by providing an input dataset and an analysis goal. Tools are recommended step by step, based on both tool's pertinence, and existing best practices within the current analysis step. Best practices are shared among the scientific community through the Galaxy platform as reusable workflows, while tool pertinence is inferred from the provided EDAM ontology terms associated to their operations and input/output data formats.

General information on the project

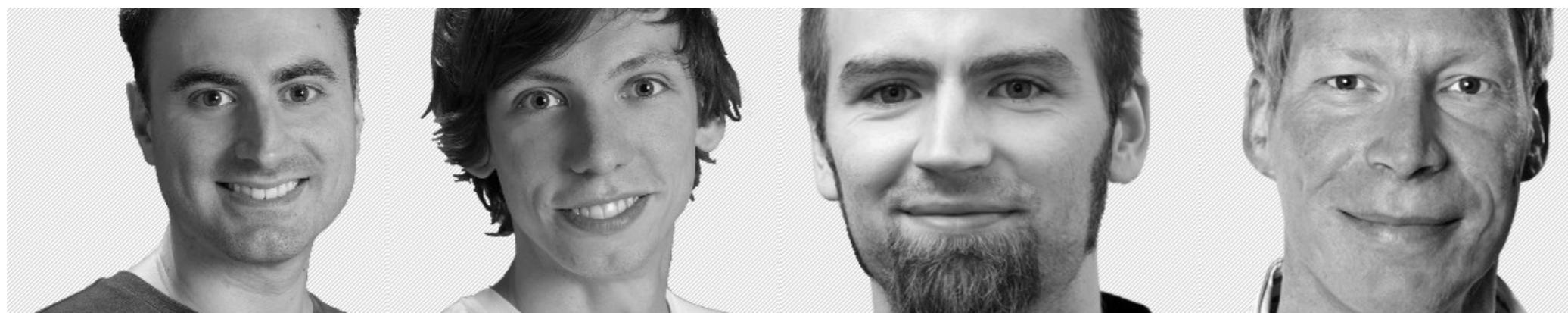
Employees paid by de.NBI funds

Scientist Andrea Bagnacani

Additional investigators within de.NBI

Scientist	Markus Wolfien
Technician	Martin Scharm
Scientist (PI)	Olaf Wolkenhauer

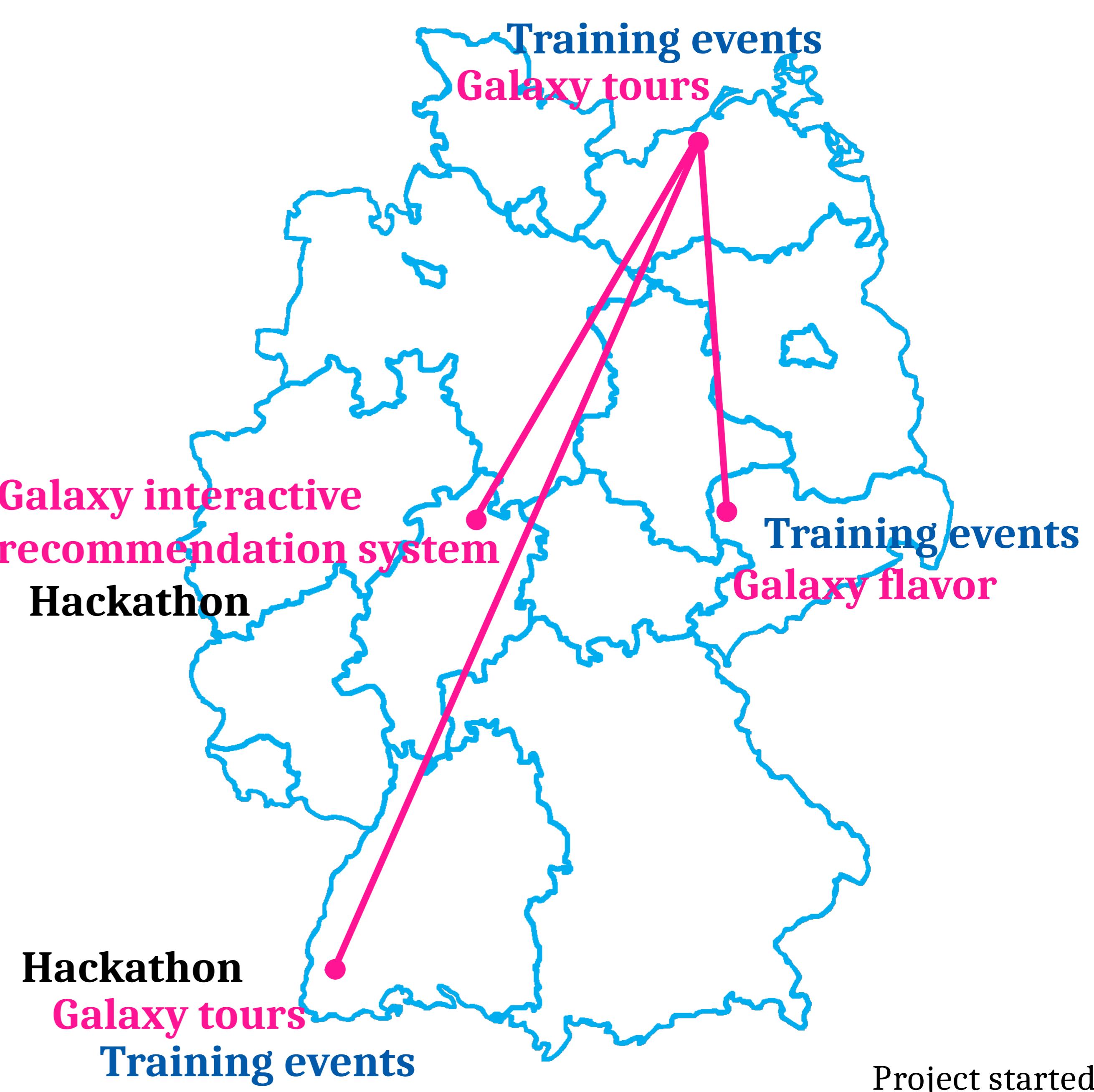
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Progress report

- Contributed to the Galaxy RNA Workbench testing and code-base
- Provided interactive Galaxy tours for best practices and training
- Took part to de.STAIR and GCC2017 hackathons
- Mined Galaxy user interactions data

<https://github.com/destairdenbi>



Project started on December 2016

de.NBI Training and education

EASyM Systems Medicine Conference	Berlin	26.10.2016 – 28.10.2016
CASyM Systems Medicine Winter School	Ljubljana	29.03.2017 – 01.04.2017
de.STAIR Training A Primer for RNA-Seq	Freiburg	04.10.2017 – 06.10.2017

Publications

- Wolfien M, Rimmbach R, Schmitz U, Jung JJ, Krebs S, Steinhoff G, David R, Wolkenhauer O.** TRAPLINE: A standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. BMC Bioinformatics, 2016. [10.1186/s12859-015-0873-9](https://doi.org/10.1186/s12859-015-0873-9)
- Schmitz U, Lai X, Winter F, **Wolkenhauer O**, Vera J, Gupta S. Cooperative gene regulation by microRNA pairs and their identification using a computational workflow. Nucleic Acid Research, 2014. [10.1093/nar/gku465](https://doi.org/10.1093/nar/gku465)
- Lott SC, **Wolfien M**, Riege K, **Bagnacani A**, **Wolkenhauer O**, Hoffmann S, Hess WR. Customized workflow development and data modularization concepts for RNA-Sequencing and metatranscriptome experiments. Journal of Biotechnology. [10.1016/j.biote.2017.06.1203](https://doi.org/10.1016/j.biote.2017.06.1203)
- Gruening BA, Fallmann J, Yusuf D, Will S, Erxleben A, Eggenhofer F, Houwaart T, Batut B, Videm P, **Bagnacani A**, **Wolfien M**, Lott SC, Hoogstrate Y, Hess WR, **Wolkenhauer O**, Hoffmann S, Akalin A, Ohler U, Stadler PF, Backofen R. The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. Nucleic Acids Research. [10.1093/nar/gkx409](https://doi.org/10.1093/nar/gkx409)

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