

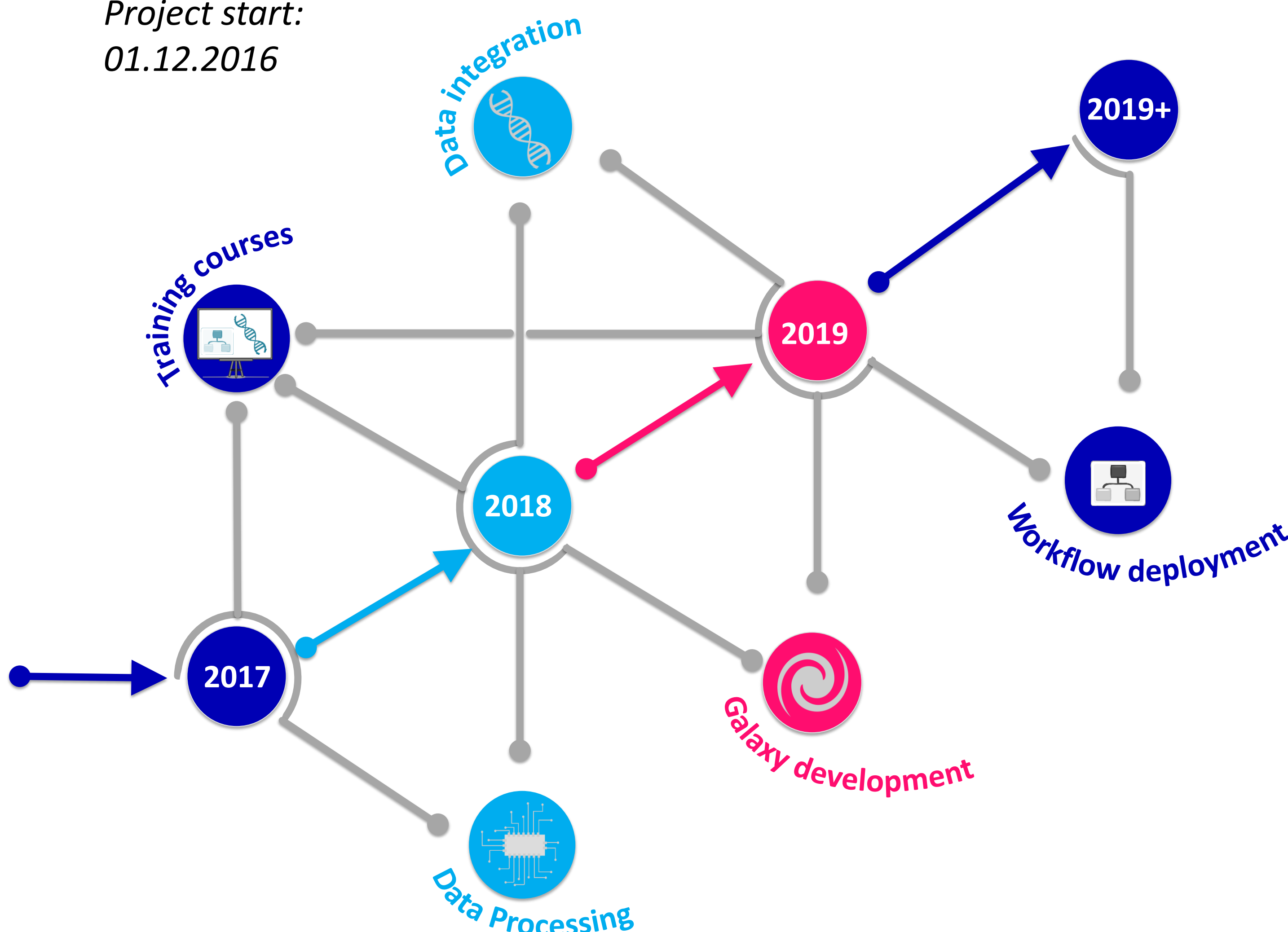
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Short description of the project

RNA sequencing (RNA-Seq) has become a widely used tool to study quantitative and qualitative aspects of the transcriptome. The variety of RNA-Seq protocols, experimental study designs and the characteristic properties of the organisms under investigation greatly affect downstream and comparative analyses. Here, we propose to complement the existing workbench of the German RNA bioinformatics center (RBC) with tools and workflows to enhance the overall integration of transcriptomic data towards additional regulative, predictive and annotation capabilities. The aim of the de.STAIR project as a whole is to enable a comprehensive analysis of RNA-Seq experiments as a service. To enable maximum usefulness, inter-connectivity, and accessibility for the developed approaches and services, we will provide dedicated workshops, training programs and screen casts for bioinformaticians and other life scientists and, ultimately, lower the barriers to RNA-Seq data analysis as a whole.

Progress report

Project start:
01.12.2016



Key concepts:

“RNA-Seq data analyses as a service”

“Workflow design and technical Integration”

Publications

Wolfien M, Rimmbach R, Schmitz U, Jung JJ, Krebs S, Steinhoff G, David R, Wolkenhauer O.

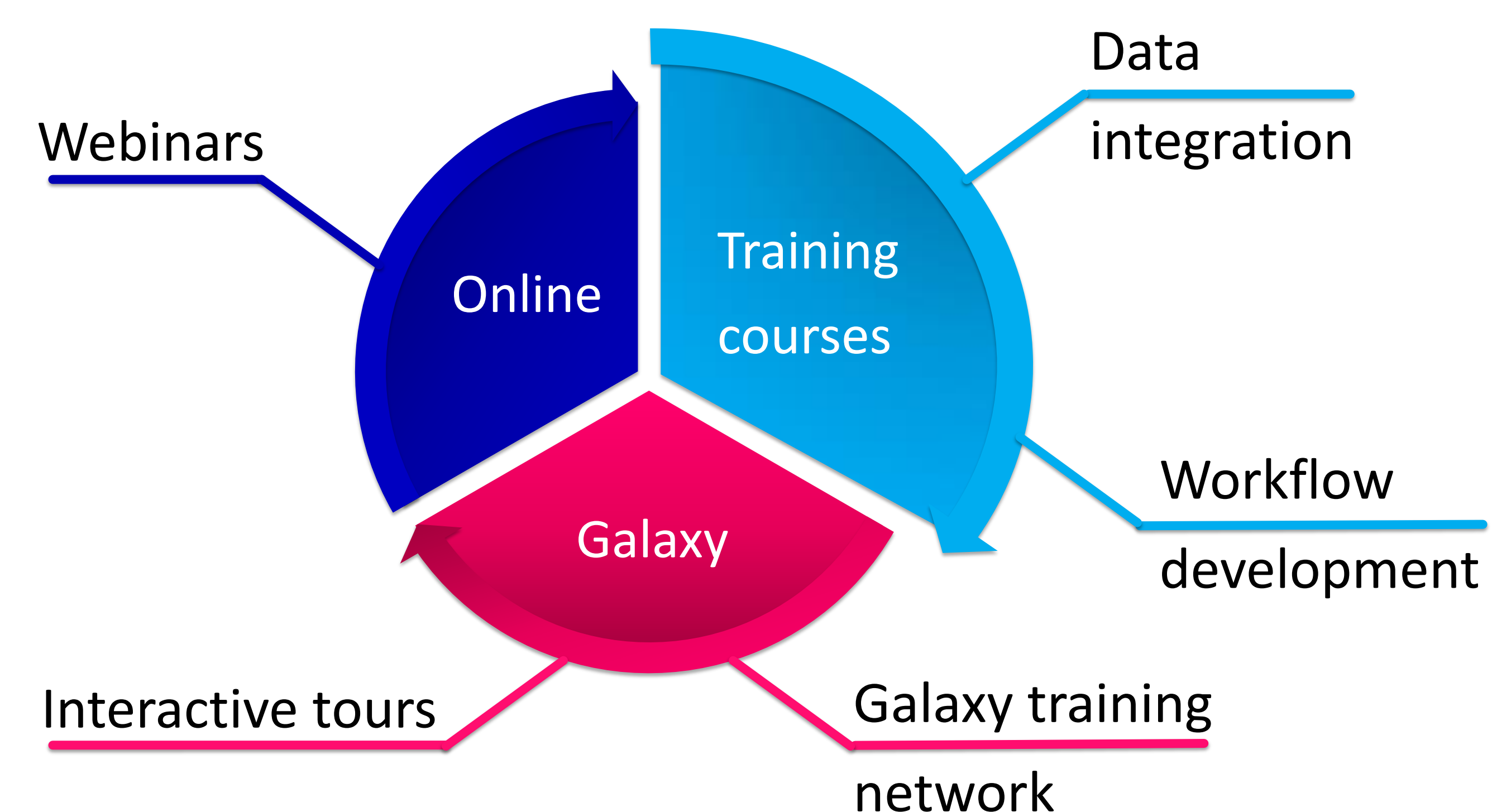
TRAPLINE: A standardized and automated pipeline for RNA sequencing data analysis, evaluation and annotation. *BMC Bioinformatics*. 2016. doi: [10.1186/s12859-015-0873-9](https://doi.org/10.1186/s12859-015-0873-9).

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

de.NBI services

- Guidance for the design of RNA-Seq experiments
- Workflow design and technical integration into the RBC workbench
- Providing alternative workflow solutions, like Docker/rkt containers
- Evaluation of preprocessing modules for sequencing data analysis
- Facilitating the annotation and characterization of transcripts
- Data retrieval interfaces for knowledge-base integration in Galaxy

de. NBI training and education



- Taking part in Galaxy online training material development – responsible curators for NGS quality control
- Workshop for NGS data analysis and data integration at the 1st European Association for Systems Medicine (EASyM) conference

de.STAIR Rostock:



www.sbi.uni-rostock.de/destair/

