

## de.NBI – German Network for Bioinformatics Infrastructure



# Guided workflow generation for RNA-Seq analysis as a service using Galaxy

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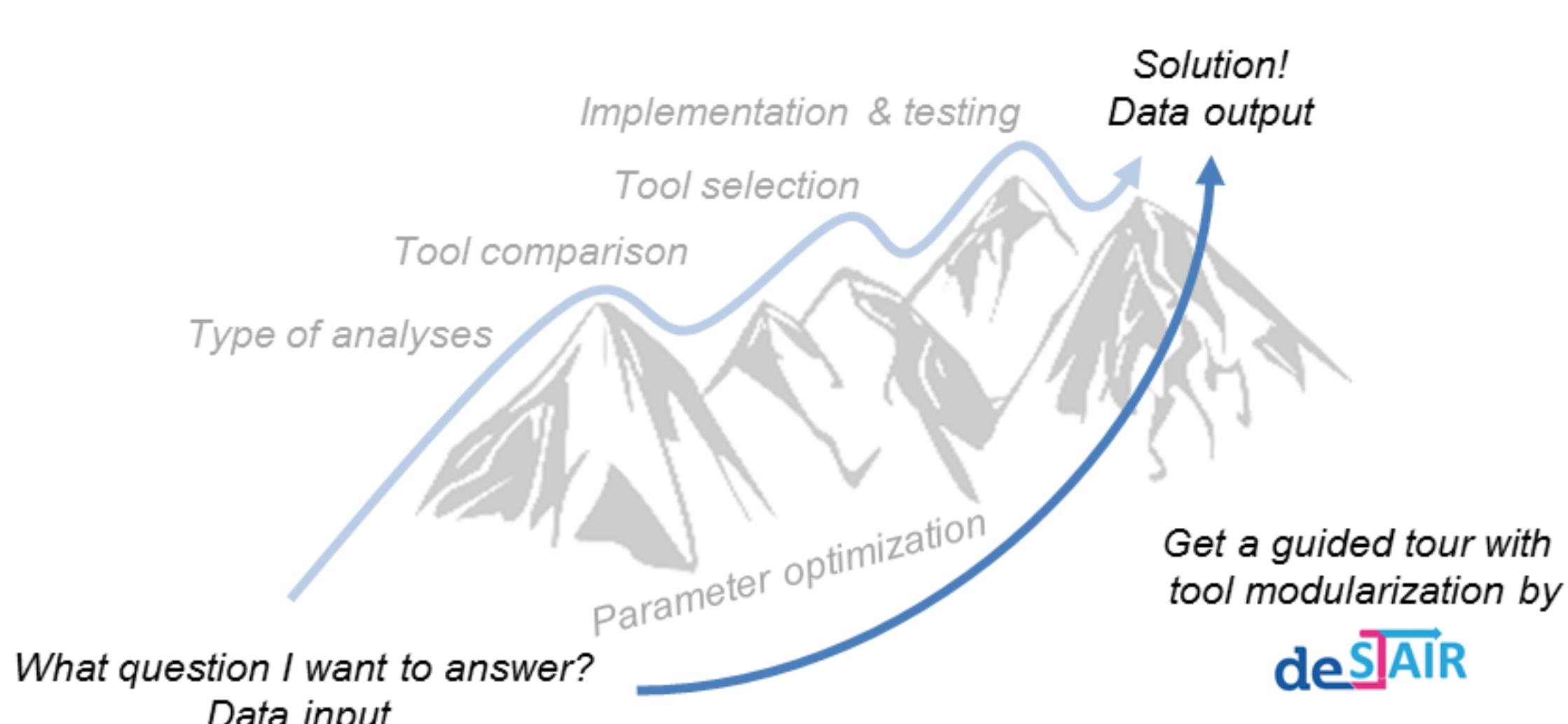
Freiburg: Steffen C. Lott and Wolfgang Hess - Genetics & Experimental Bioinformatics, University Freiburg, Germany

Rostock: Andrea Bagnacani and Olaf Wolkenhauer - Systems Biology Bioinformatics, University Rostock, Germany

## Short description of the project

The variety of RNA-Seq study designs and characteristic properties of studied organisms greatly affect bioinformatics analysis. As part of the RNA Bioinformatics center (RBC), which supports all RNA-related research within de.NBI, de.STAIR summarizes the expertise of participating laboratories to develop and maintain an flexible RNA-Seq analysis workbench for different RNA-Seq protocols, to be used locally or in a cloud environment as provided by the open source Galaxy platform for biomedical research. In addition, de.STAIR provides workshops, training programs and screencasts for experts and non-experts to lower the barriers for RNA-Seq data analysis.

Based on simulated data, personalized workflows can be created and exported using our service reachable via <http://destair.leibniz-fli.de>



## Interactive Tours and Webhooks

de.STAIR carefully chooses tools and default parameter settings to design best-practice workflows and guided tours within Galaxy. The development of webhooks enables interactive and conditional adaption by the user.

## Open Source Organization

### Guided Tours to

- Use Best-Practice Workflows
- Interactively generate Workflows
- Generate conditional Workflows

### RNA-Seq Workflows

- Preprocessing
- Taxonomic classification
- Visualization

### de.NBI Training

- Courses
- Screencasts
- Tutorials
- Software support



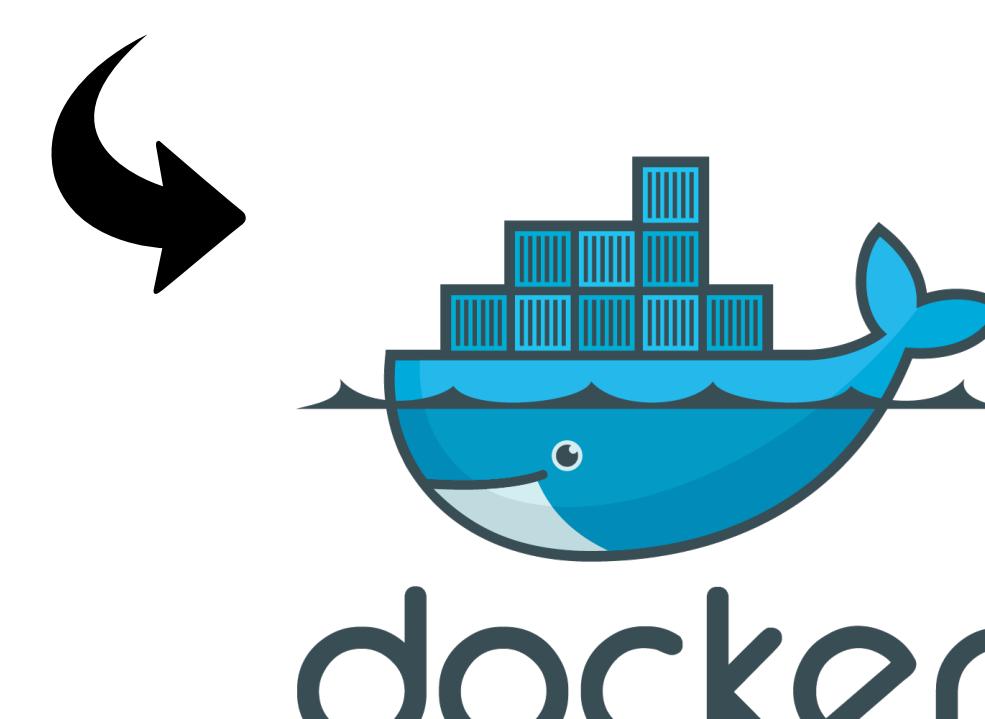
**BIOCONDA**<sup>®</sup>

**Galaxy**  
PROJECT

**Galaxy**  
ToolShed

**GitHub**  
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## Publications

S. Lott, M. Wolfien, K. Riege, A. Bagnacani et. al., J. Biotechnol. 2017

