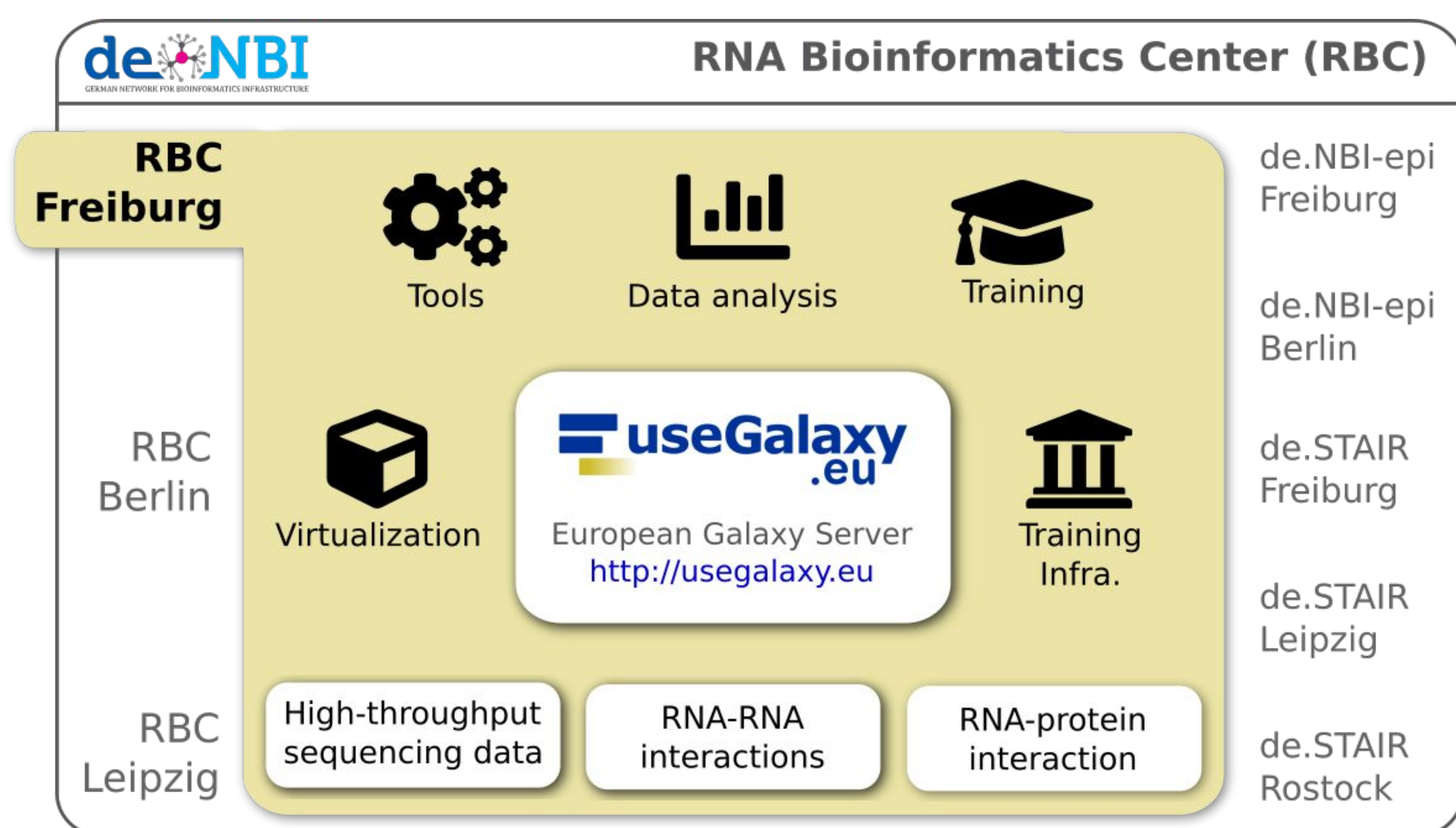


# RBC-FR RNA Bioinformatics Center Freiburg Galaxy Team

Fkz 031A538A

Bérénice Batut, Anika Erxleben, Björn Grüning, Helena Rasche, Wolfgang Maier, Rolf Backofen  
Chair of Bioinformatics, University of Freiburg, Germany

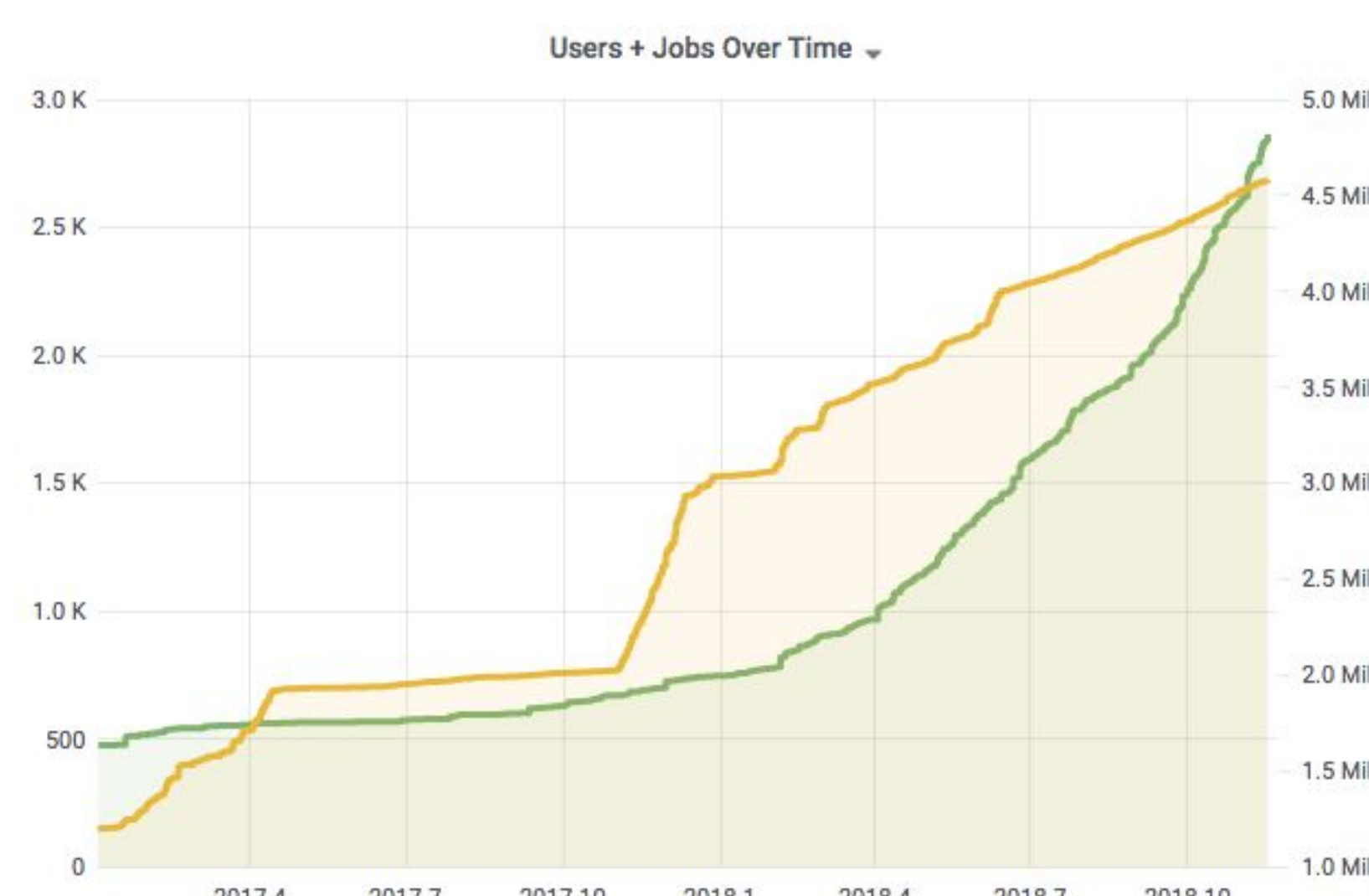
## RBC Freiburg



## Services



The European  
Galaxy Server  
3,000 users  
2,000 tools

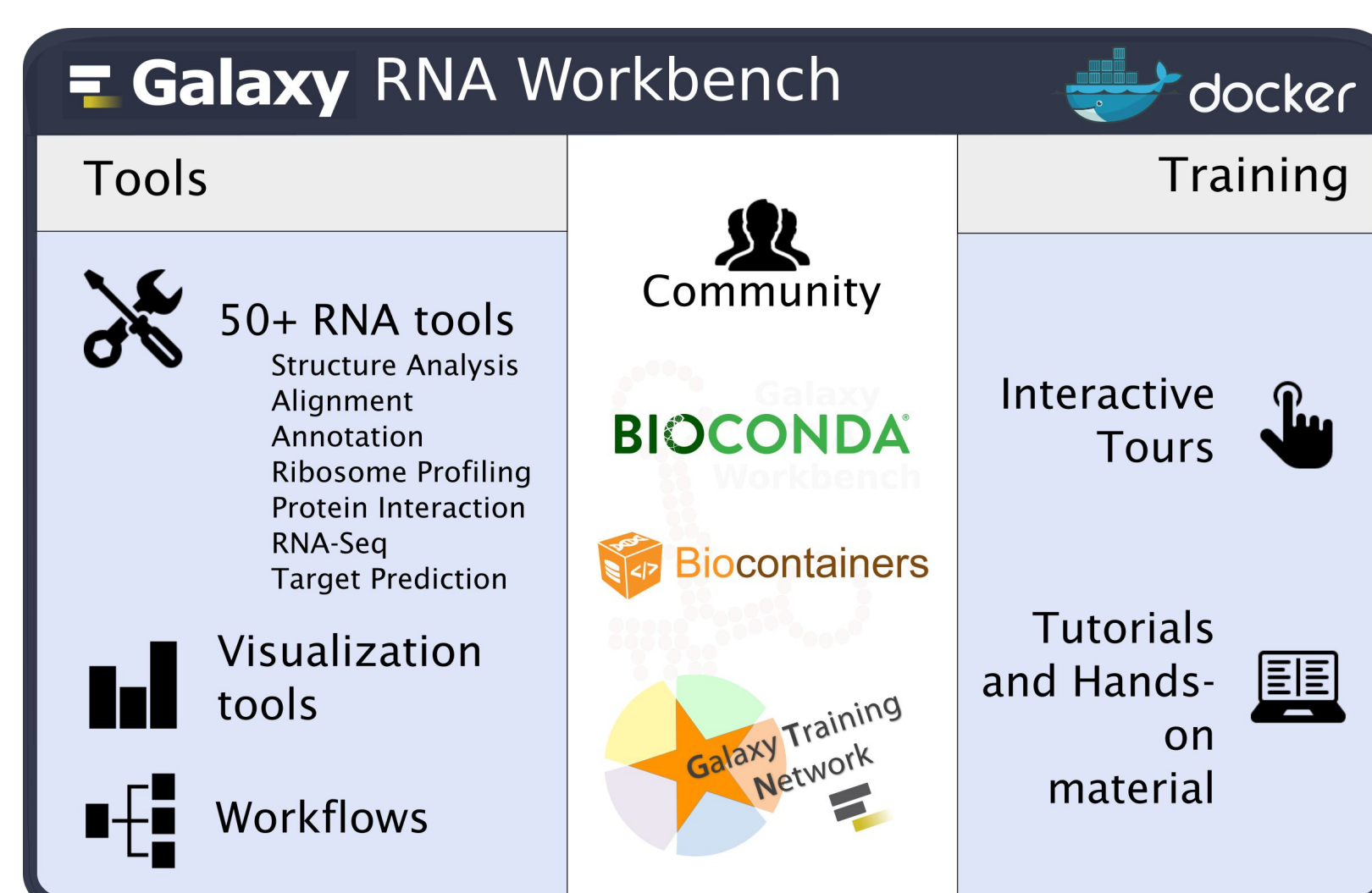


Our flagship service is our Galaxy server (<https://usegalaxy.eu>) which is the **biggest Galaxy instance in Europe**, and one of the biggest worldwide, powered by **de.NBI cloud** and GDPR compliant.

**BIOCONDA**

**Virtualization**

**Biocontainers**



RBC Freiburg is actively involved in **making software user-accessible and cloud-ready**. We joined and are leading the Bioconda and Biocontainers communities, to fix the software deployment problem once and for all.

We also developed Galaxy Docker, a **production-ready, scalable Galaxy instance** with customized tool sets. We provide the RNA-workbench flavour for all RNA related research.

## General information on the project

3.0 staff paid from de.NBI grant + 1 cloud staff  
+ 3.0 other staff involved

## Progress report

### Services

Opening of the Freiburg Galaxy Server to **all European researchers**, a huge step for open, accessible and reproducible research in Germany and Europe!  
Launch of the **ELIXIR Galaxy community**  
Publication of the Bioconda manuscript in Nature Methods  
Recognition of Biocontainers as **one pillar** of the ELIXIR tools  
**Expansion of de.NBI Cloud FR** to 3.5k cores, 15TB RAM

### Major events

Galaxy User Conference (15.-16.03.18), Freiburg  
>120 participants. 3 continents  
European Galaxy Days (19.-20.11.18), Freiburg  
>40 participants, 2 continents  
Galaxy Community Conference (1.-6.07.19), Freiburg  
>200 participants expected, 5 continents

### Training (2017-2018)

>40 training events  
>1,500 trainees

### Training

### Workshops and mentoring

Twice per year a **full-week hands-on high-throughput sequencing data analysis workshop**  
Training around the world on demand for data analysis, developers and administrators  
On-site **mentoring**  
HTS lectures and Galaxy courses for Master students

### Online training material

Main contributors of Galaxy training material  
<https://training.galaxyproject.org>  
**Freely accessible online material** designed for both **self-training** and **workshops**  
>100 tutorials with hands-on and/or slides

### Training Infrastructure-as-a-Service (TlaaS)

Dedicated compute resources for providing a Galaxy training  
In past 6 months: >500 trainees, 21 events, 4 continents

## Publications

- Afgan, E. *et al.* (2018) The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. *Nucleic Acids Research*, 46.
- Batut, B. *et al.* (2018) Community-Driven Data Analysis Training for Biology. *Cell Systems*, 6, 752–758.e1.
- Grüning, B. *et al.* (2018) Bioconda: sustainable and comprehensive software distribution for the life sciences. *Nature Methods*, 15, 475–476.
- Grüning, B. *et al.* (2018) Practical Computational Reproducibility in the Life Sciences. *Cell Systems*, 6, 631–635.
- Backofen, R. *et al.* (2017) RNA-bioinformatics: tools, services and databases for the analysis of RNA-based regulation. *Journal of Biotechnology*, 261, 76–84.
- Batut, B. and Grüning, B. (2017) ENASearch: A Python library for interacting with ENA's API. *The Journal of Open Source Software*, 2, 418.
- Grüning, B.A. *et al.* (2017) Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers. *PLoS Comput Biol*, 13, e1005425.
- Grüning, B. *et al.* (2017) The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. *Nucleic Acids Research*, 45, W560–W566.
- Veiga Leprevost, F. da *et al.* (2017) BioContainers: an open-source and community-driven framework for software standardization. *Bioinformatics*, 33, 2580–2582.