

de.NBI – German Network for Bioinformatics Infrastructure

RBC

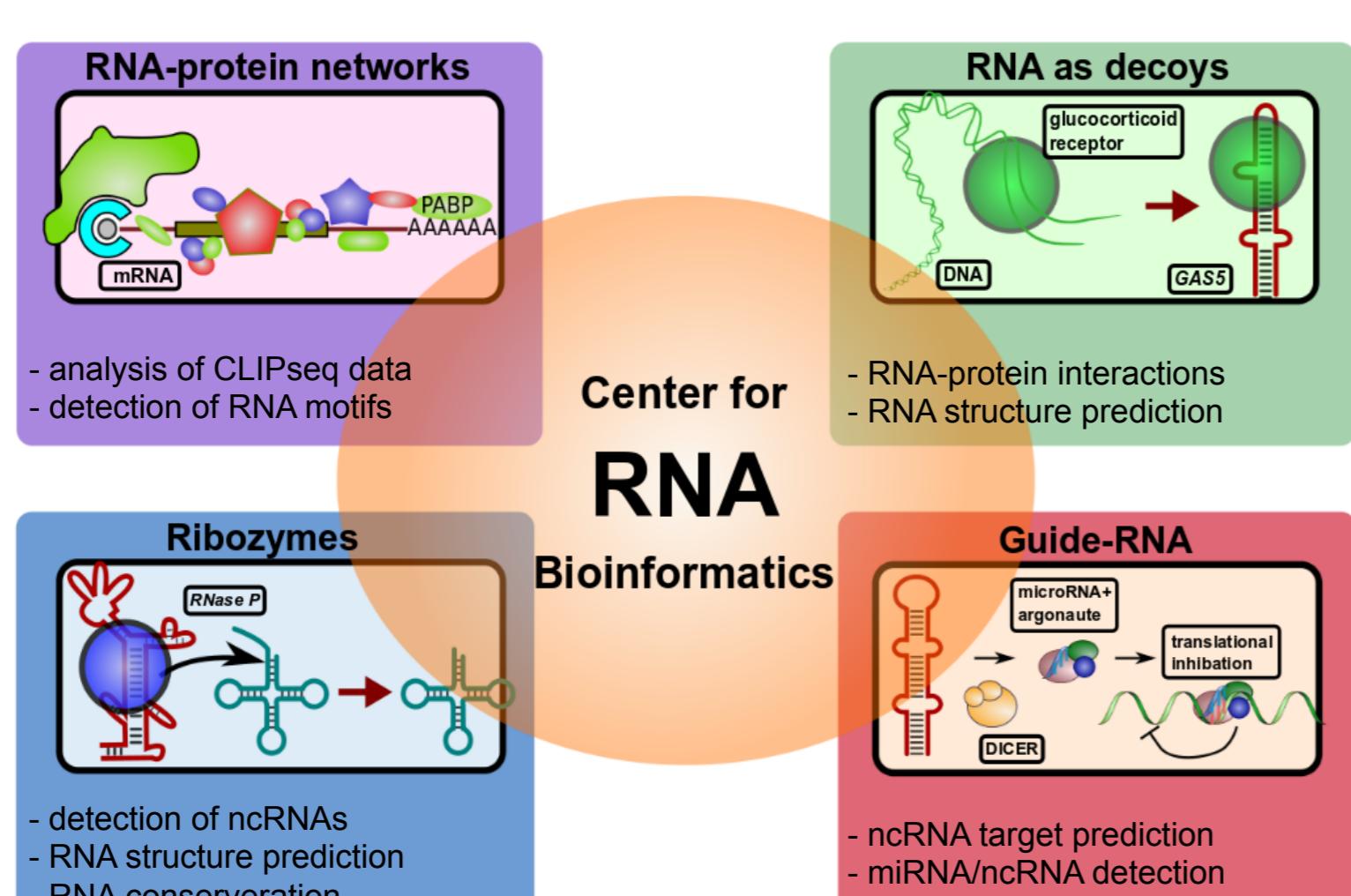
RNA Bioinformatics Center University of Freiburg Chair of Prof. Rolf Backofen

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Short description of the project

The RBC Freiburg offers tools, services and training for the analysis of:

- **high-throughput sequencing (HTS) data**
- **RNA-RNA interactions**
- **RNA-protein interactions**

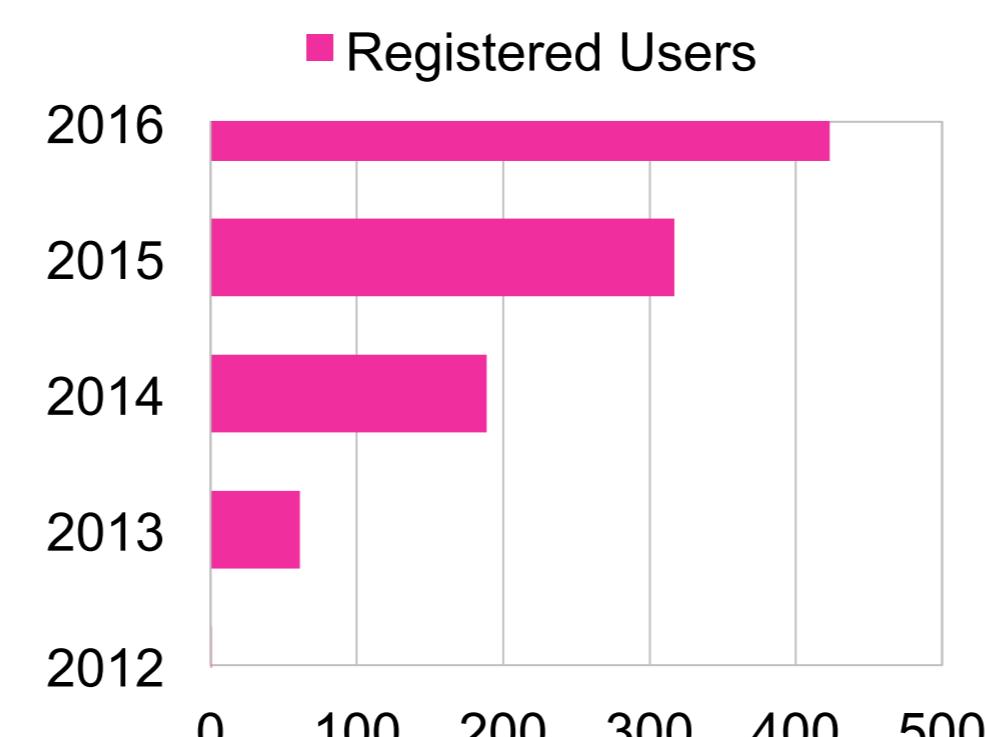


The RBC Freiburg develops and maintains the **Freiburg Galaxy server** (<http://galaxy.uni-freiburg.de>), the largest instance in Europe.

de.NBI services



The Freiburg Galaxy server (<http://galaxy.uni-freiburg.de>) enables scientists for accessible, reproducible and transparent research of biomedical data. As part of the de.NBI Cloud, the Freiburg Galaxy server will be available for all German research facilities in the beginning of 2017.



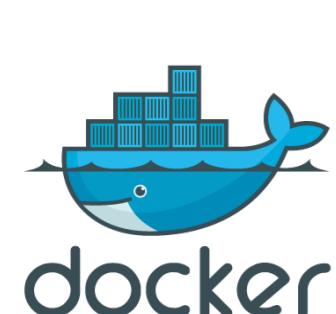
BIOCONDA[®]

The RBC Freiburg is actively involved in making software user-accessible. Tools relevant for HTS data analysis, RNA-protein interaction analysis (e.g. CLIP experiments), RNA-RNA interaction analysis are made available through distribution channels such as BioConda⁽²⁾.

Freiburg RNA Tools

The RNA workbench (<http://rna.informatik.uni-freiburg.de/>) is a server for a series of RNA research tools with for e.g.:

- Sequence-structure alignments: LocARNA, CARNA, MARNA
- Clustering: ExpaRNA
- Interaction prediction: IntaRNA, CopraRNA
- Homolog identification: GLASSgo
- Sequence design: AntaRNA, INFORNA, SECISDesign
- CRISPR repeat analyses: CRISPRmap



Analysis frameworks for specific tasks are made available as Docker images. They incorporate a Galaxy web server with seamlessly included tools, SOP analysis pipelines, training material, a Galaxy interactive tour, and help pages.

Publications

Tools and data services registry: a community effort to document bioinformatics resources.
doi: 10.1093/nar/gkv1116

The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update.
doi: 10.1093/nar/gkw343

Enhancing pre-defined workflows with ad hoc analytics using Galaxy, Docker and Jupyter.
doi: 10.1101/075457

Global RNA recognition patterns of post-transcriptional regulators Hfq and CsrA revealed by UV crosslinking *in vivo*. doi: 10.15252/embj.201593360

RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF-kappaB pathway. doi:10.1038/ncomms8367

Progress report

Training and education

- Organisation of
 - 6 training courses to teach users common HTS techniques, tool development, and Galaxy implementation
 - Contribution fests to make software more readily available
- Migration of our training material and analysis workflow documentation to online repositories for easier collaboration
- Ongoing curation and development of training material for newer versions of tools and new emerging techniques requested by users
- Active participation in the BioStars forum to answer user questions

Services

- Ongoing evaluation of new analysis techniques, methods and software for RNA-RNA and RNA-protein interactions
- Development and maintenance of standard analysis pipelines and definition of SOPs

Close cooperation and knowledge exchange with ELIXIR

de.NBI training and education

The RBC Freiburg offers biannual full-day hands-on Galaxy training week on HTS data analysis: >220 participants in the last 3 years.



Freiburg Galaxy HTS data analysis workshops February (left) and September 2016 (right)



We also offered Galaxy developers workshops in cooperation with ELIXIR

06 th – 07 th Apr 2016	Galaxy DevOps workshop	Heidelberg
20 th – 21 st Oct 2016	Swiss German Galaxy workshop	Freiburg
27 th Oct 2016	de.NBI data management workshop	Kassel

And we organized several Contribution Fest:

07 th – 08 th Mar 2016	RAD-Seq Tools and Workflows
27 th – 28 th Sep 2016	GalaxyP
06 th – 07 th Oct 2016	Galaxy Training Material
02 nd – 03 rd Nov 2016	BioConda

Upcoming events

15 th – 16 th Dec 2016	RNA-seq data analysis workshop	Freiburg
16 th – 19 th Jan 2017	European Galaxy Developer workshop	Strasbourg
13 th – 17 th Sep 2017	Galaxy HTS data analysis workshop	Freiburg

topic	features
Genome Annotation	book
RNA-seq	book
ChIP-seq	book
Exome-seq	book
MethylC-seq	book
Galaxy Introduction	book
Data Sources	book
Planemo documents	book
Galaxy Tool Dev Corner	book
Galaxy Docker Project	book

Hands-on training material for self-study available

To overcome limited capacities in our workshops, we developed free accessible training material for self-learning.

<http://bgruening.github.io/training-material/>

