UNIVERSITÄT LEIPZIG
MDC BIMSB

RNA Bioinformatics Center

de.NBI − German Network for Bioinformatics Infrastructure

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Non-coding RNAs Everywhere

Genome-wide sequencing revealed that DNA is pervasively transcribed; the majority, to non-coding RNAs. Non-coding RNAs and their interaction with proteins play a fundamental role in cellular regulation. Empowered by recent advances of high-throughput technology, biologists showed that post-transcriptional regulation is as complex as the transcriptional one. For example, the human genome encodes thousands of micro RNAs and approximately 800 RNA binding proteins. Consequently, many human diseases can already be linked to post-transcriptional gene regulation.

Docker, Galaxy, and RNA: Tool Integration and Deployment

RNA Analysis Workbench
The RNA workbench is a ready-to-run Galaxy instance wrapped in a Docker container. It comes equipped with a variety of RNA analysis tools, sample data and teaching material. This image has already been proven to be useful as a platform for training users in Galaxy driven bioinformatics analysis.
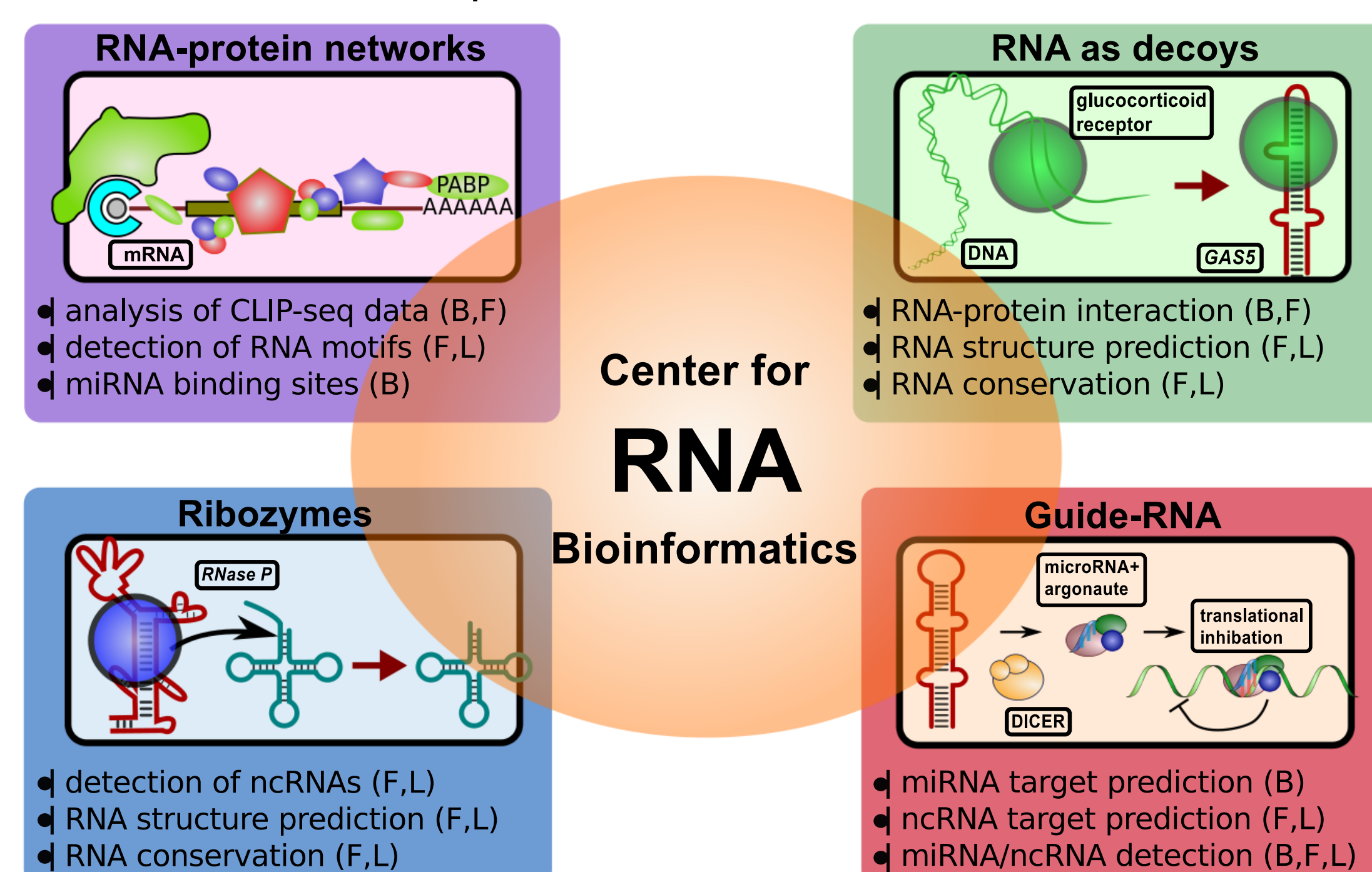
Updated and Novel RNA Tools
The RBC continually integrates and updates important RNA bioinformatics tools as well as tools and data sources of related research fields in the RNA workbench.

Extensions
Due to the modular architecture the basic RNA workbench is extensible to meet special requirements. The **rna-workbench-extra** image extends the base image with utilities to fetch and index specified reference genomes at build time, tool test and example data, and additional documentation in the form of Galaxy pages.

ubuntu:14.04

toolshed/requirements | docker-galaxy-requirements

galaxy-stable | docker-galaxy-stable

rna-workbench | galaxy-rna-workbench

Galaxy

LocARNA, IntaRNA, ExpaRNA, CopraRNA, antaRNA, INFO-RNA

DoRiNA, Mummie PicTar2, WaRSwap mirDeep2, ...

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ViennaRNA, RNAplex, RNAz, mea segemehl, RNAsnoop, RNAcode

RNA Community

DrawRNA-js, Dot2Ct, BlockClust, RNA datatypes, [your tool here]

Activities and Events

Recent Events and Activities
- Berlin Bioinformatics Hackathon (RNA tool & pipeline development)
- Data analysis course "Computational Genomics"
- Genome Annotation Workshop
- Galaxy Next Generation Sequencing Workshop
- RNA workshop for members of SPP 1738 (Emerging roles of ncRNA)
- New RNA software releases (e.g. LocARNA, Segemehl)
- New RNA-Seq SOPs & pipelines (e.g. annotation for CLIP/TAR data)
- Many RNA tools newly integrated in Galaxy

Upcoming Events
- de.NBI/ELIXIR Workshop on EDAM ontologies (Jan, 2016)
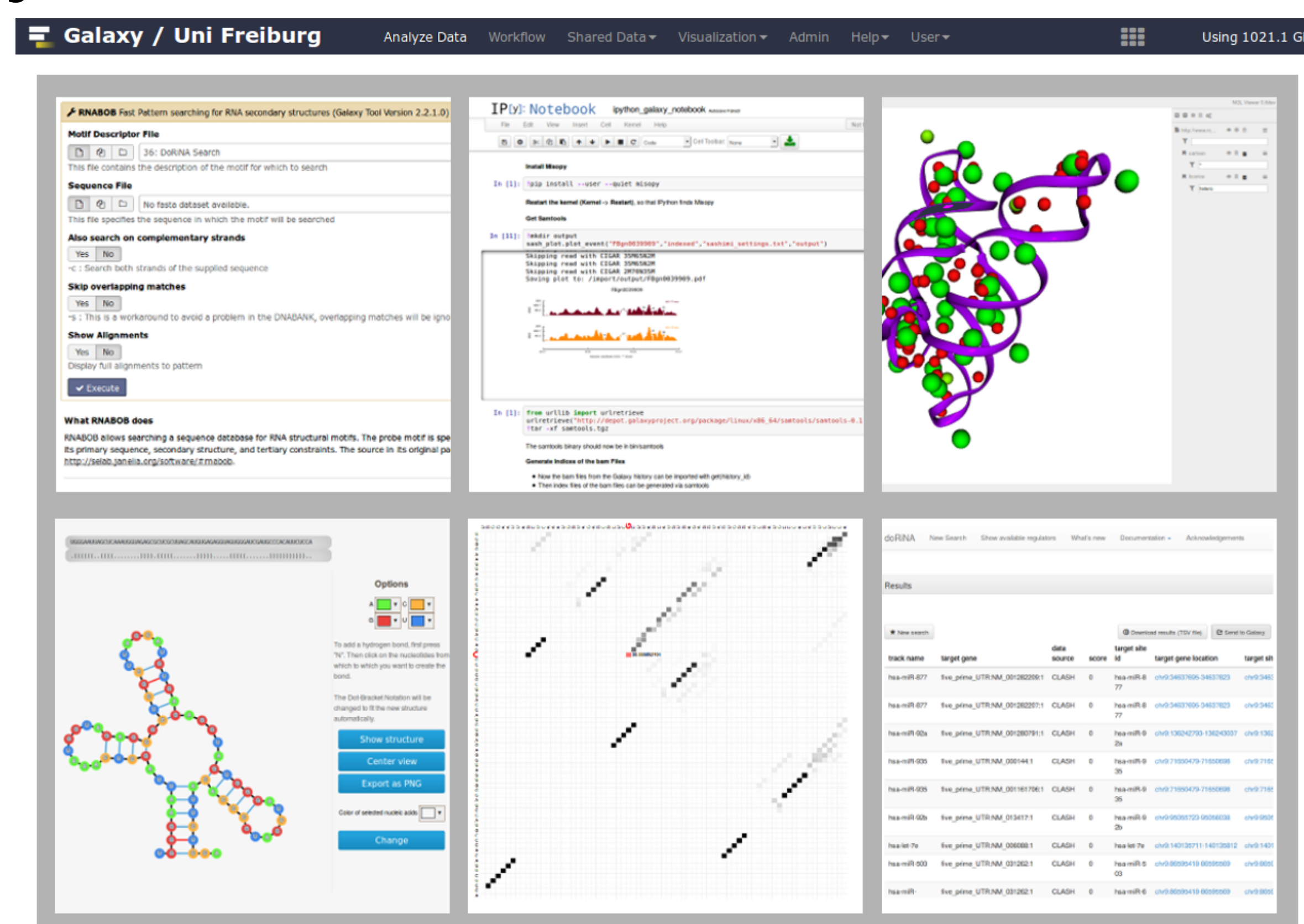- de.NBI/ELIXIR RNA Bioinformatics Summer School 2016

RBC's Mission

The RNA Bioinformatics Center's role within the de.NBI network is the support of RNA related research , such as the detection of noncoding RNAs and RNA structure prediction.

RNA-protein networks
- analysis of CLIP-seq data (B,F)
- detection of RNA motifs (F,L)
- miRNA binding sites (B)

RNA as decoys
- RNA-protein interaction (B,F)
- RNA structure prediction (F,L)
- RNA conservation (F,L)

Ribozymes
- detection of ncRNAs (F,L)
- RNA structure prediction (F,L)
- RNA conservation (F,L)

Guide-RNA
- miRNA target prediction (B)
- ncRNA target prediction (F,L)
- miRNA/ncRNA detection (B,F,L)

Center for RNA Bioinformatics

RNA bioinformatics inside the Galaxy

Tool/Database Integration: Important tools for RNA bioinformatics research are integrated in Galaxy such that they can readily be used in workflows. The RBC aims to bridge the gap between RNA research and related fields such as NGS, imaging and proteomics. The integration of databases storing RNA data is eased with the help of examples and support by the RBC.

Visualizations: RNA secondary structure can be visualized in many different ways. The RBC integrates existing and develops new visualizations that give intuitive understanding of RNA sec. structures.

Interactive Environments: Customized reproducible research in Galaxy can be achieved with the newly integrated interactive environments. Visualizations that are more flexible and interactive are integrated with this framework.

Community-Driven R & D

For sustainable impact, the research and development of of our analysis platform eventually has to be driven by the community. To foster this ideal, all tool wrappers, utilities and documentation are publically hosted on github; participation in development is encouraged; and user feedback is sought eagerly. Moreover, we hold regular Galaxy workshops for users as well as for tool developers.

www.bioinf.uni-freiburg.de   www.mdc-berlin.de   www.bioinf.uni-leipzig.de