de.NBI − German Network for Bioinformatics Infrastructure

RBC - BIMSB

RNA Bioinformatics Center: The Berlin Institute for Medical Systems Biology

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GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

MDC — MAX DELBRÜCK CENTER FOR MOLECULAR MEDICINE IN THE HELMHOLTZ ASSOCIATION
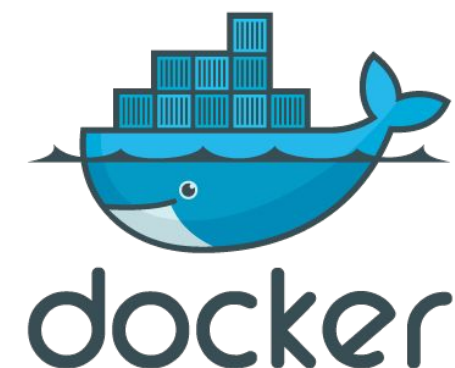BIMSB — THE BERLIN INSTITUTE FOR MEDICAL SYSTEMS BIOLOGY

Short description of the project

We offer tools, services and training for the analysis of **RNA-binding proteins** and **post-transcriptional regulation**

Progress report

Progress up to October 2016

- **Galaxy Server**
    - Offered two courses on RNA-Seq analysis
    - Integrated public/in-house tools based on user-demand
    - Developed workflows and tested tools for users
    - Switched to production server
- **RCAS (RNA Centric Annotation System)**
    - Developed an R/Bioconductor package for systematic annotation of regions of interest from RNA-based omics datasets
    - Available in Galaxy, Bioconda, Docker, Guix
    - Available as a web-service
      http://rcas.mdc-berlin.de/

Bioconductor OPEN SOURCE SOFTWARE FOR BIOINFORMATICS · WEB SERVICE · Guix · docker

Tasks planned for next year

- **Offer more training on Galaxy**
    - Chip-Seq analysis
    - Variant analysis
- **RBC summer school**
- **Integrate more tools to Galaxy server**
    - PIPmiR (Pipeline for plant miRNA identification)
    - PARalyzer (PAR-CLIP analysis pipeline)
- **Update the doRiNA database**
    - More content and functionality

Publication

Uyar B, Yusuf D, Wurmus R, Rajewsky N, Ohler U, Akalin A. *RCAS: an RNA Centric Annotation System for Transcriptome-wide Regions of Interest.* (Submitted to Nucleic Acids Research)

Acknowledgement: MDC central IT

de.NBI services

MDC Galaxy Server
- User support
- Tool/workflow development
- Server maintenance

Galaxy

Tools and Databases
- **RCAS**: RNA-centric annotation system
- **doRiNA**: Database for binding sites of RNA-binding proteins and miRNAs
- **RiboTaper**: A toolbox for analysis of Ribosome profiling data
- **microMummie**: MicroRNA target site identification tool
- **PARalyzer**: RNA binding site detection from PAR-CLIP dataset

de.NBI training and education

Offered **two workshops** for RNA-seq analysis using **Galaxy**

We have a **growing** number of **Galaxy users**

MonthlyHits
- 40000
- 80000
- 120000
- 160000

Second Galaxy Workshop

First Galaxy Workshop

TotalUserCount (y-axis: 20, 40, 60)

Date (x-axis: 2015.04, 2015.05, 2015.06, 2015.07, 2015.08, 2015.09, 2015.10, 2015.11, 2015.12, 2016.01, 2016.02, 2016.03, 2016.04, 2016.05, 2016.06, 2016.07, 2016.08, 2016.09, 2016.10, 2016.11)

➡ **http://www.denbi.de**