

de.NBI-epi

RNA Bioinformatics Center University of Freiburg Chair of Bioinformatics

Fkz 031L0101C

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Description of de.NBI-epi

The de.NBI-epi project in Freiburg offers:

Visualization, normalization and quality assessment:

- Hi-C data analysis
- MethylC-Seq data analysis
- ChIP-Seq
- Bisulfite sequencing analysis pipelines

Training and user support:

- Galaxy HTS data analysis workshops
- Self learning material on training.galaxyproject.org
- Direct user support via gitter, GitHub or guest researcher

Available on:

- All in one Gateway: https://usegalaxy.eu
- Your computer with virtualized and personalized instances

General information on the project

As part of the de.NBI-epi project in Freiburg, Joachim Wolff and Björn Grüning, are working closely with the RBC, de.NBI and ELIXIR to deliver high-class services for epigenetic research.

General information on the project

Community based infrastructure

BIOCONDA

BioContainers provides

Bioconda is a conda channel which provides system-agnostic executable software for biomedical research.

bioinformatics software.

environments for

- 25,649 commits on GitHub
- 856 contributors
- > 6,500 packages

Biocontainers Galaxy

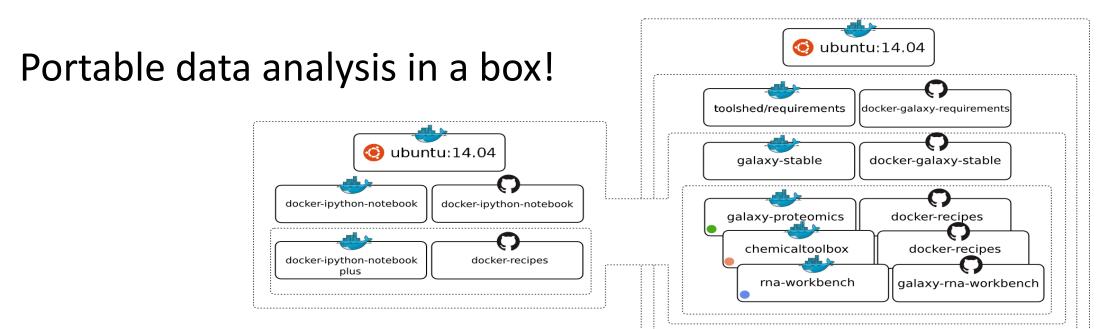
Galaxy is an open, web-based platform data intensive research.

- Based on Docker & rkt
- > 8,400 tools
- Automatic builds from Bioconda

- 43,998 commits • 223 contributors
- One of the biggest Galaxy instances available for de.NBI in Freiburg

The Galaxy Docker Project

The Galaxy Docker Image is an easy distributable full-fledged Galaxy installation, that can be used for testing, teaching and presenting new tools and features.



Based on the main Galaxy Docker virtualisation, a dedicated flavor for epigenetics was developed: github.com/bgruening/docker-galaxy-epigenetic

Publications

- High-resolution TADs reveal DNA sequences underlying genome organization in flies.
- doi: 10.1101/115063 Jupyter and Galaxy: Easing entry barriers into complex data analyses for biomedical researchers.
- doi: 10.1371/journal.pcbi.1005425 The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy
- doi: 10.1093/nar/gkx409
- BioContainers: an open-source and community-driven framework for software standardization doi: 10.1093/bioinformatics/btx192

de.NBI services

Maintenance, development and integration of software into Galaxy to provide easy access for epigenetic analysis software:

- deepTools
- Bismark
- HiCUP
- CHICAGO
- Methyldackel
- Methtools
- HiCExplorer



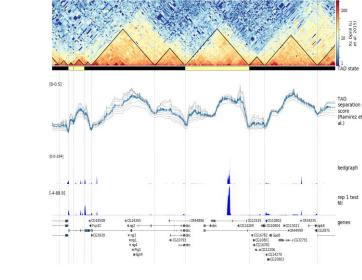
Container: Docker, rkt, Singularity

Progress report

Development and maintenance of software for Hi-C data analysis.

HiCExplorer:

- Maintenance of HiCExplorer
 - Extending available tools with new functions
- Loop detection
- Support of more file formats
- Support of cHi-C data:
- Validation of loops
- Improved training material: hicexplorer.readthedocs.io



scHiCExplorer:

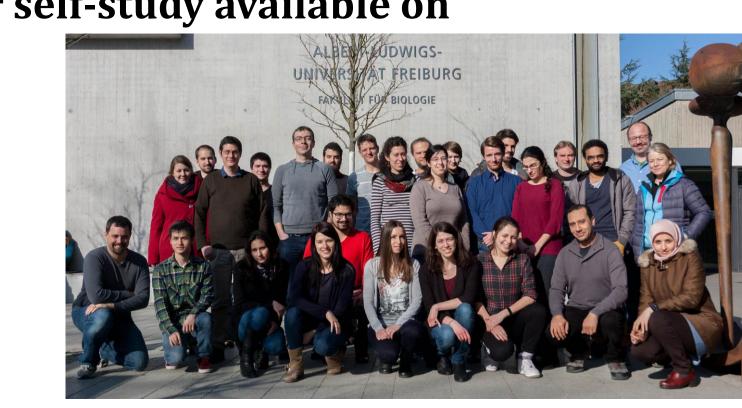
New software to support single-cell Hi-C data analysis:

- Tools to demultiplex raw fastq files
- Create mCool matrices and manipulation
- Methods to reduce dimensions of scHi-C data
- Methods to cluster scHi-C data

de.NBI Training and education

Hands-on training material for self-study available on training.galaxyproject.org

- Introduction to HTS
- RNA-Seq
- ChIP-Seq
- **Proteomics**
- MethylC-Seq ...and many more!



2018 / 2019 past events

06 th – 07 th Dec 2018	Galaxy RNA-Seq analysis workshop	Freiburg
25 th Feb – 01 st Mar 2019	Galaxy Workshop	Freiburg
1 st – 6 th Jul 2019	Host of Galaxy Community Conference	Freiburg
24 th Jul 2019	ISMB: Workshop for reproducible research	Basel
16 th Sept 2019	GCB: Workshop for Workflows, Tools and Data Management	Heidelberg
23 rd – 27 th Sept 2019	Galaxy Workshop	Freiburg





