

de.NBI-epi RNA Bioinformatics Center University of Freiburg Chair of Bioinformatics

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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://galaxy.uni-freiburg.de>
- Your computer with virtualised and personalised 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.

de.NBI services

Community based infrastructure

BIOCONDA



Biocontainers

Galaxy

BioConda is a conda channel which provides software for biomedical research.

- 14,475 commits on GitHub
- 287 contributors
- > 2,700 packages

BioContainers provides system-agnostic executable environments for bioinformatics software.

- Based on Docker & rkt
- > 1,800 Images
- Automatic builds from BioConda

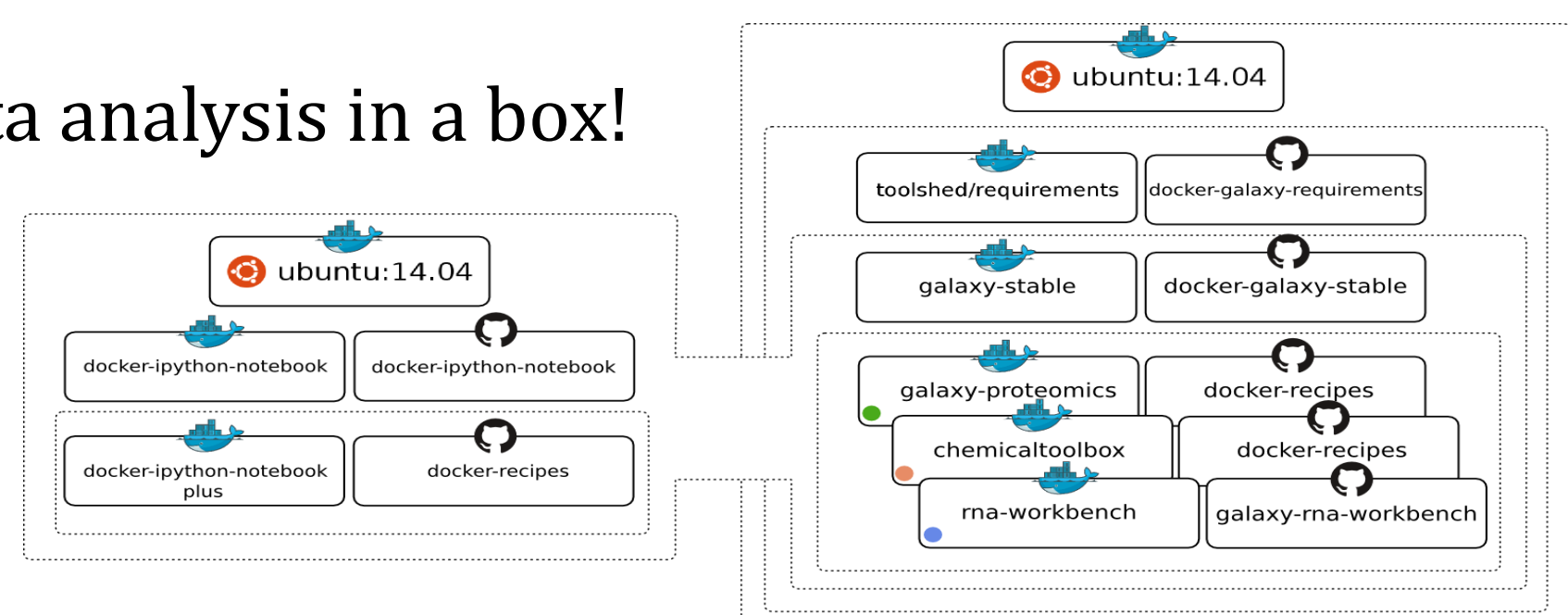
Galaxy is an open, web-based platform for data intensive research.

- 29,588 commits
- 163 contributors
- One of the biggest Galaxy instances available for de.NBI

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.

Portable data analysis in a box!



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

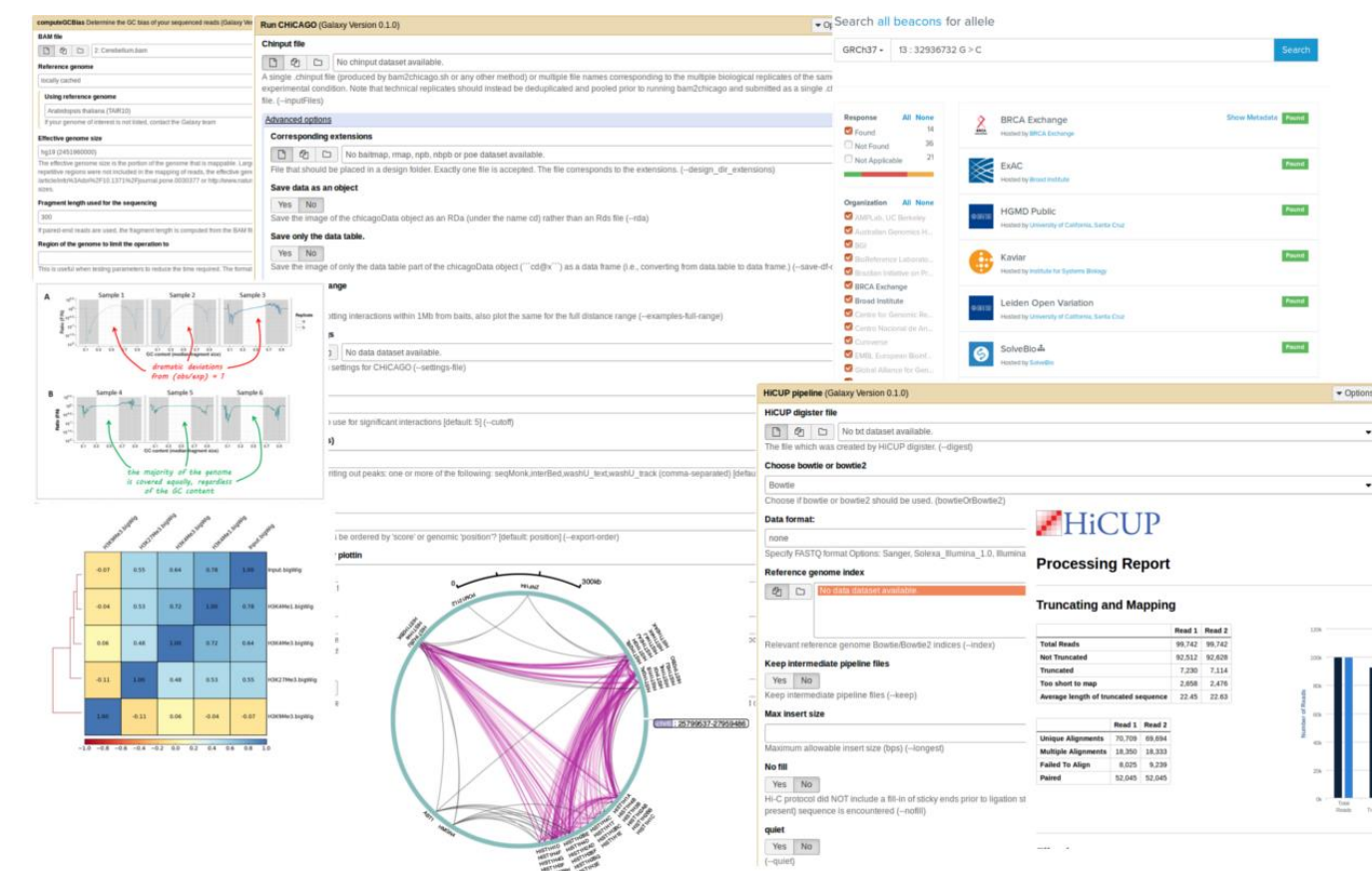
BioContainers: an open-source and community-driven framework for software standardization

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



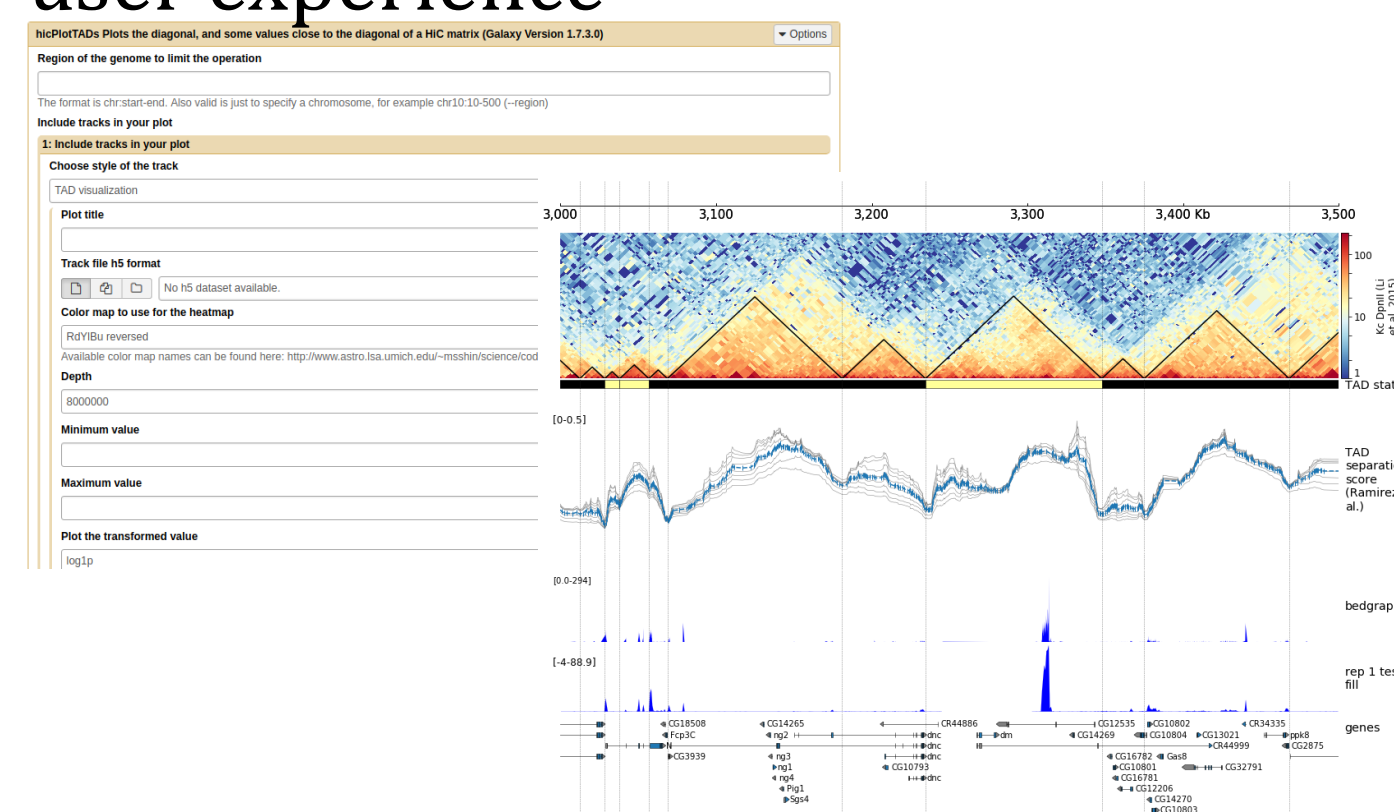
- Galaxy
- Docker

Progress report

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

HiCEXplorer:

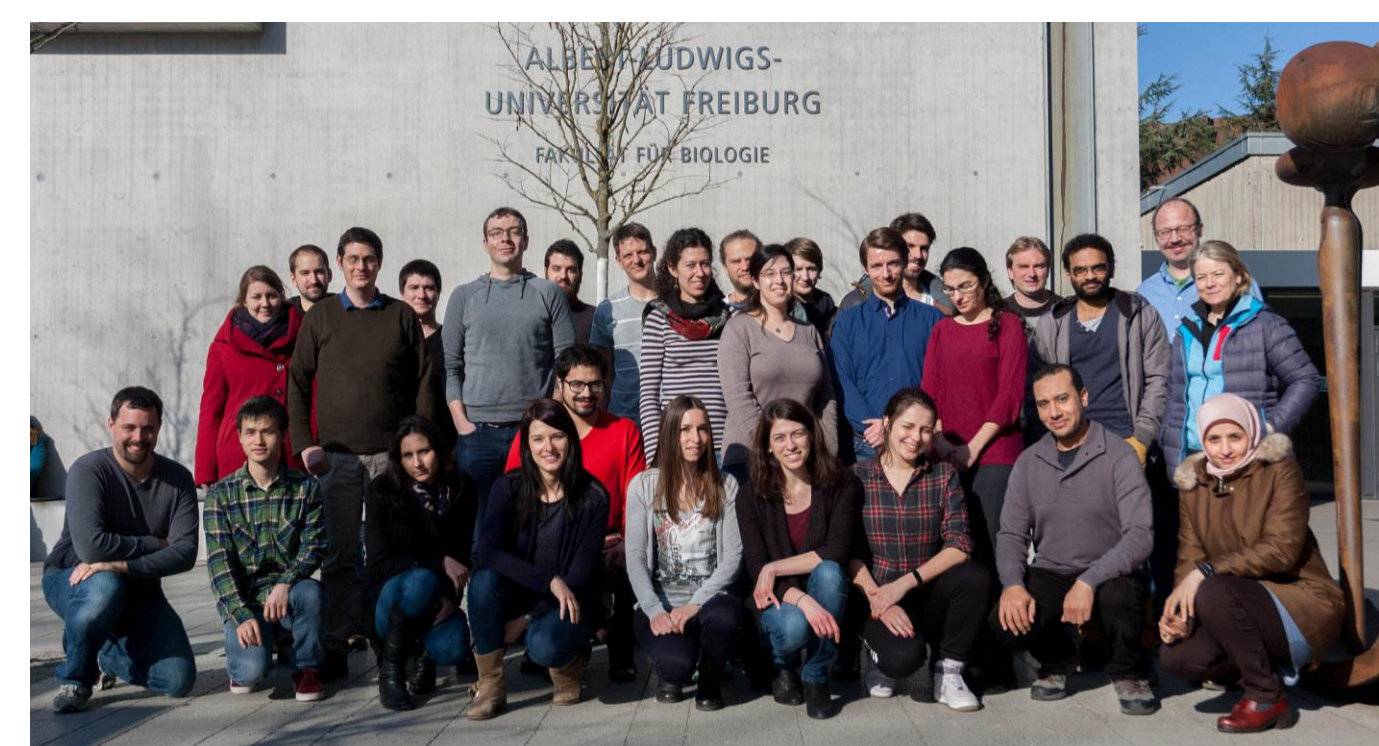
- Interaction matrix creation 3x faster
- Improved training material: hicexplorer.readthedocs.io
- New Galaxy wrappers for a better user experience
- Docker integration
- Release 2.0 will have:
- Python 3 support
- 'Cool' format support
- A/B compartments
- Improved visualization



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!



2016 / 2017 past events		
15 th – 16 th Dec 2016	Galaxy RNA-Seq analysis workshop	Freiburg
09 th – 10 th Jan 2017	Online contribution fest	
16 th – 19 th Jan 2017	European Galaxy Developer workshop	Strasbourg
06 th – 09 th Feb 2017	Galaxy Admin workshop	Melbourne
13 th – 17 th Feb 2017	Galaxy HTS data analysis workshop	Freiburg
04 th – 05 th Apr 2017	ELIXIR – de.NBI AAI workshop	Freiburg
22 nd – 24 th May 2017	ELIXIR – training hackathon	Cambridge
14 th – 18 th Sep 2017	Galaxy HTS data analysis workshop	Freiburg
2017 / 2018 planned events		
08 th – 12 th Jan 2018	Galaxy admin workshop	Oslo
19 th – 23 rd Feb 2018	Galaxy HTS data analysis workshop	Freiburg
March 2018	Freiburg Galaxy user meeting	Freiburg
Mid 2018	Hi-C and epigenetics workshop	Freiburg