

# 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](http://training.galaxyproject.org)
- Direct user support via github

Available on:

- An easy to use computing cluster: [galaxy.uni-freiburg.de](http://galaxy.uni-freiburg.de)
- Your computer with conda and docker

## General information on the project

Paid staff: 1 Joachim Wolff

Other staff: 1 Bjoern Gruening

## de.NBI services

### Community based infrastructure

#### BIOCONDA

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

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



#### Biocontainers

BioContainers provides system-agnostic executable environments for bioinformatics software.

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

#### Galaxy

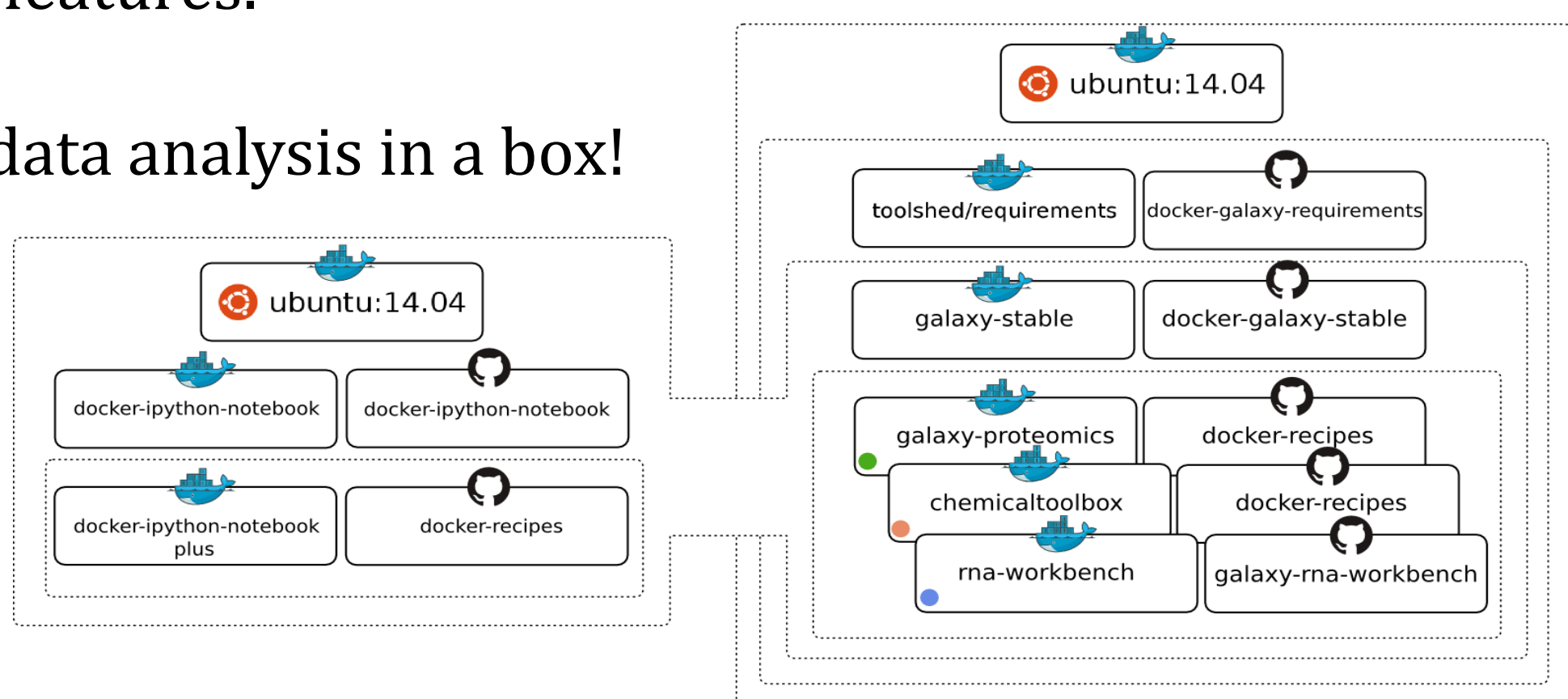
Galaxy is an open, web-based platform for data intensive research.

- 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!



<https://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

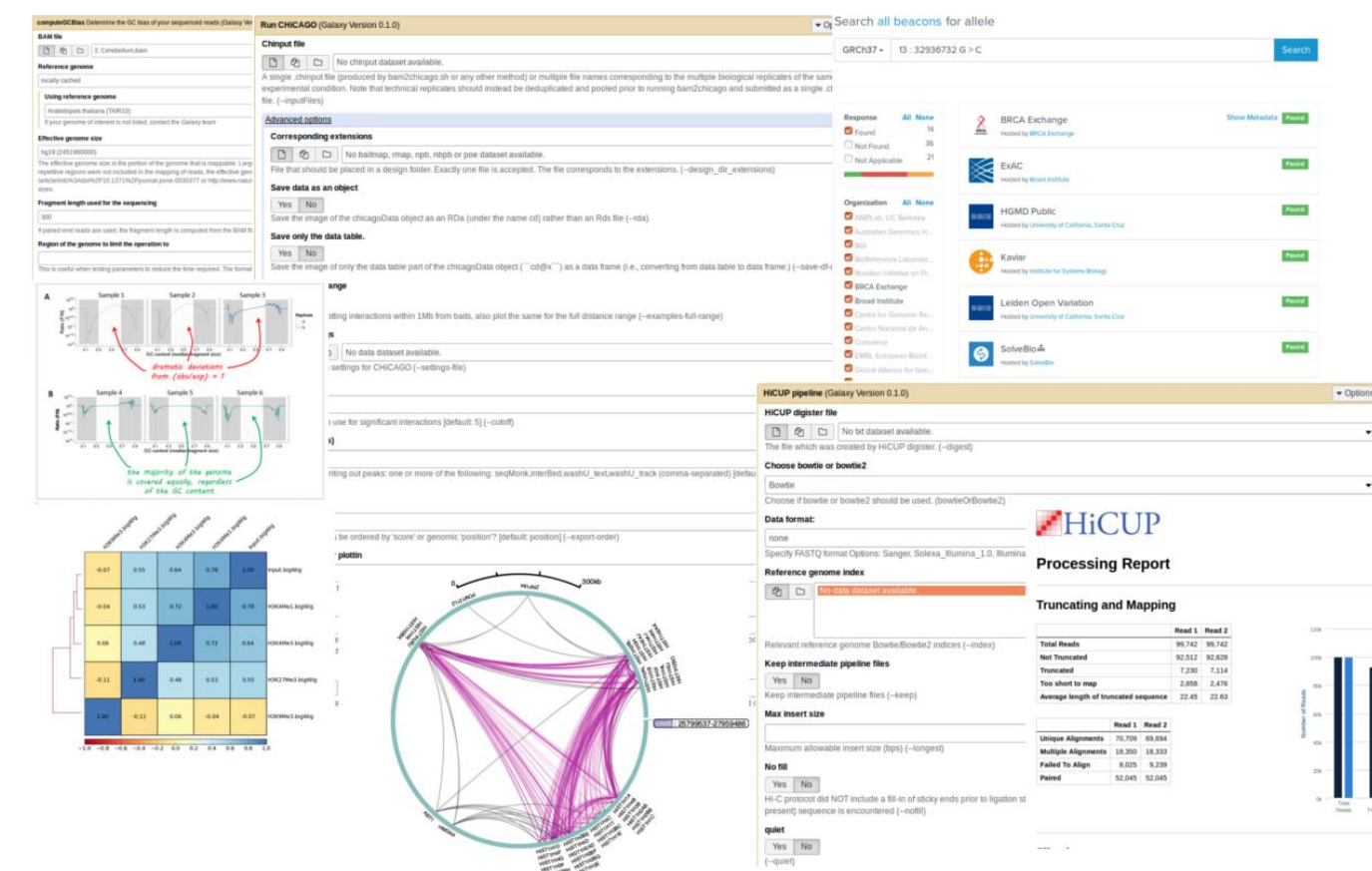
BioContainers: an open-source and community-driven framework for software standardization

doi: 10.1093/bioinformatics/btx192

## de.NBI services

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

- deepTools
- Bismark
- HiCUP
- CHICAGO
- Methyldackel
- Methtools
- HiCEXplorer



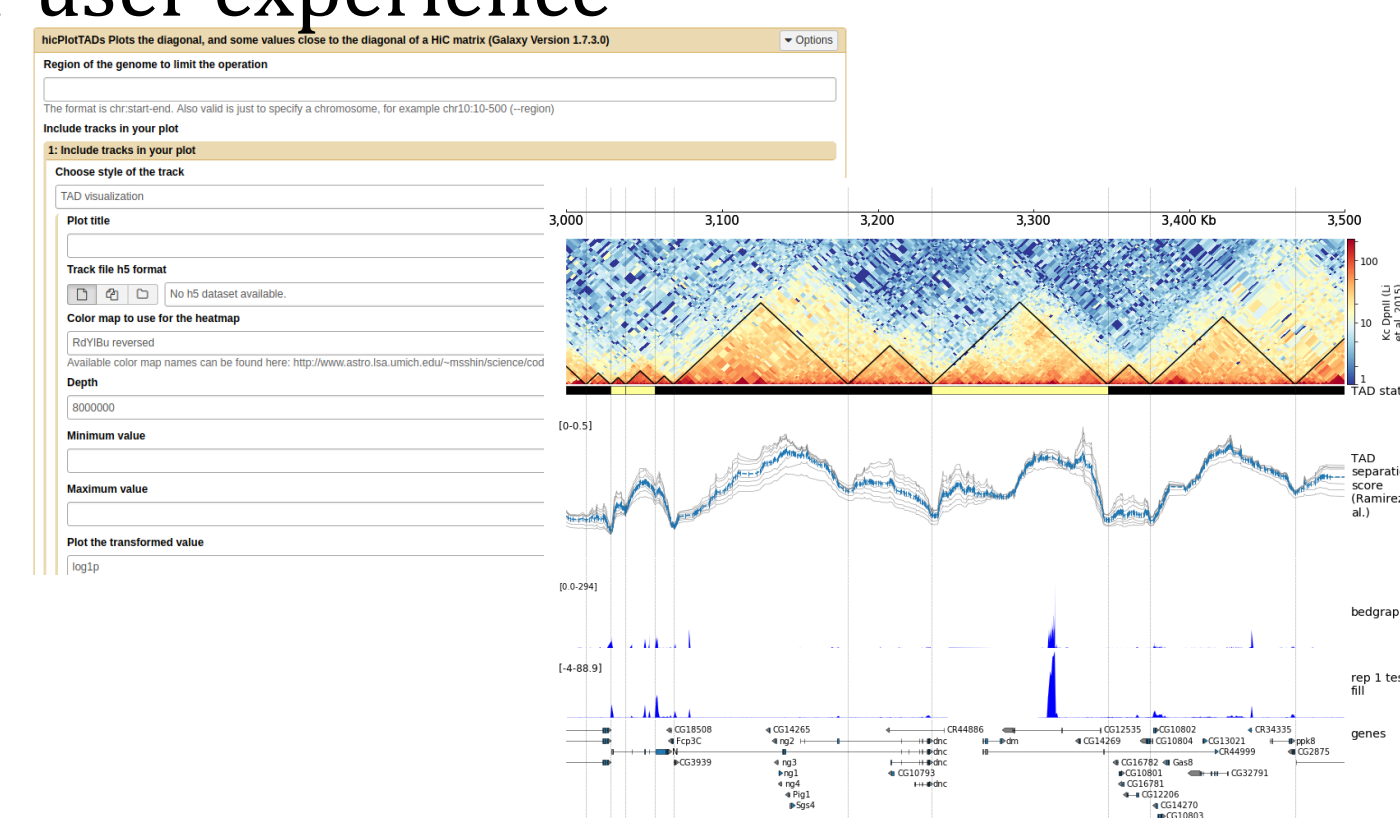
- Galaxy
- Docker

## Progress report

Development and maintenance of software for Hi-C data analysis

### HiCEXplorer:

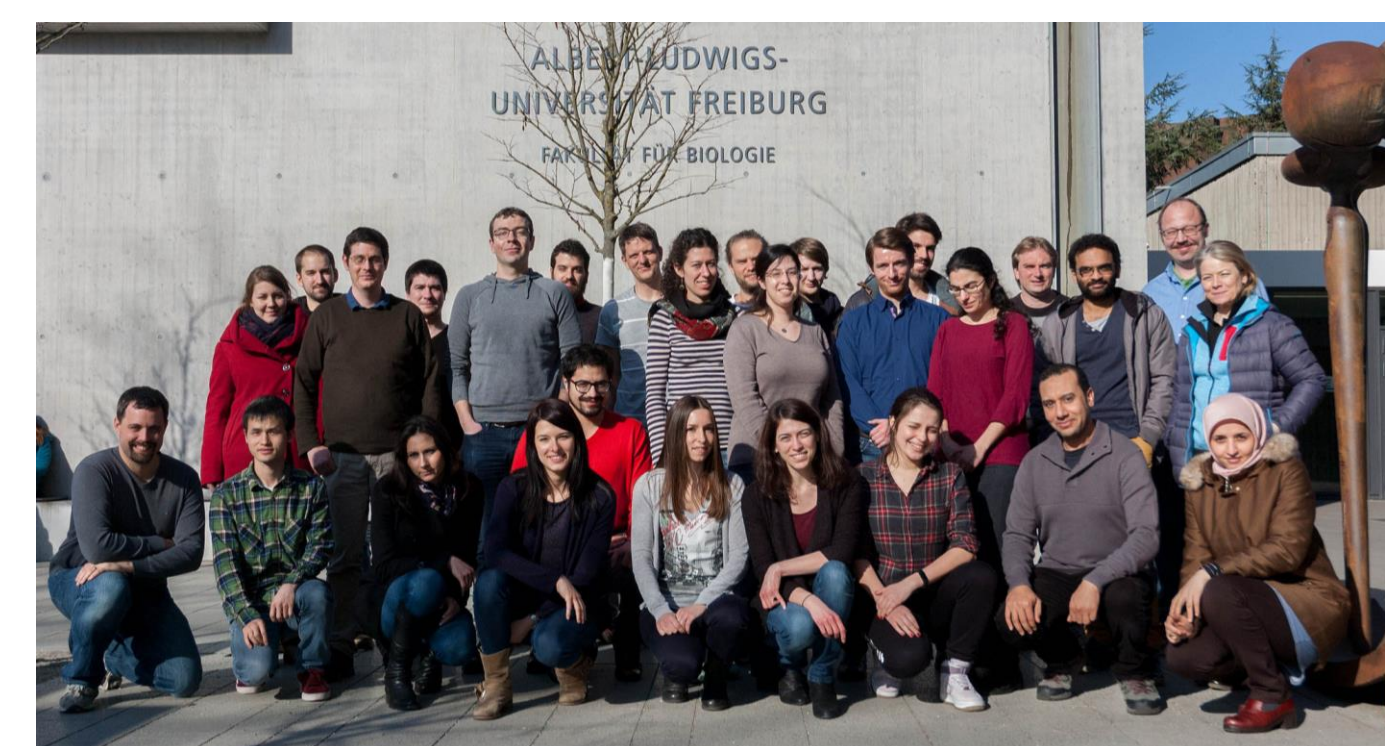
- Interaction matrix creation 3x faster
- Improved training material: [hicexplorer.readthedocs.io](http://hicexplorer.readthedocs.io)
- New Galaxy wrappers for a better user experience
- Docker integration
- Release 2.0 will have:
- Python 3 support
- 'Cool' format support
- A/B compartments
- Improved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



## de.NBI training and education

Hands-on training material for self-study available on [training.galaxyproject.org](http://training.galaxyproject.org)

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



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