de.NBI-epi

RNA Bioinformatics Center
University of Freiburg
Chair of Bioinformatics

Fkz 031L0101C

Björn Grüning, Joachim Wolff
University of Freiburg, Germany

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

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
- > 2,900 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 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.

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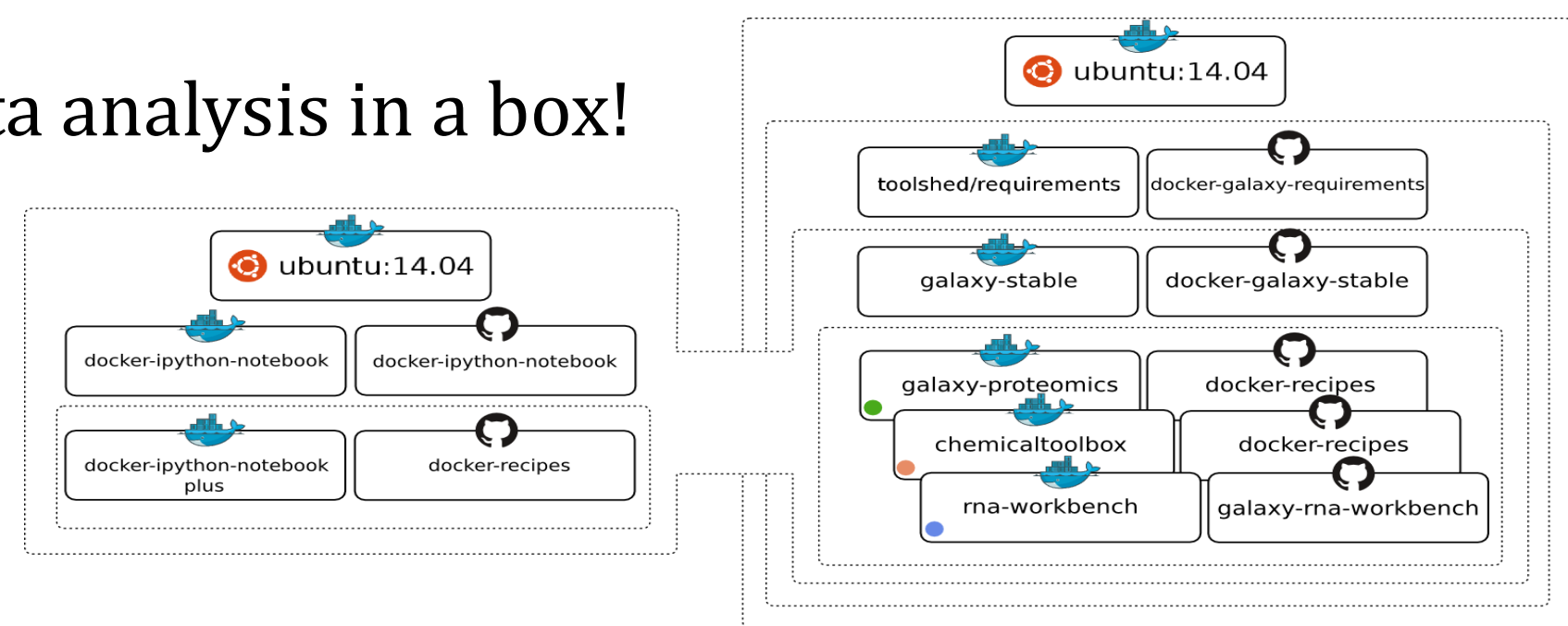
Based on the main Galaxy Docker virtualisation, a dedicated flavor for epigenetics was developed: github.com/bgruening/docker-galaxy-epigenetic

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
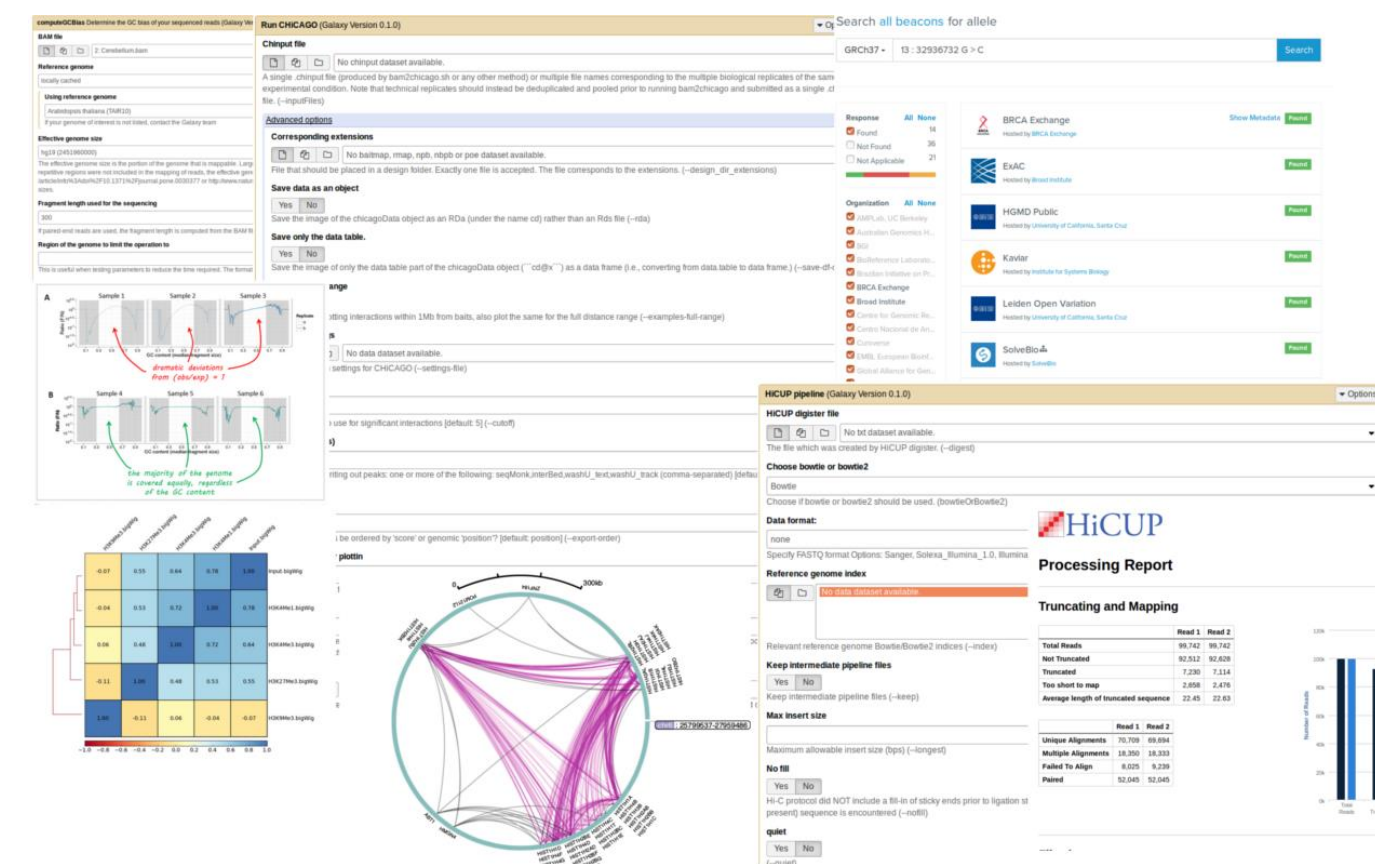
- Galaxy
- Container: Docker, rkt, Singularity

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
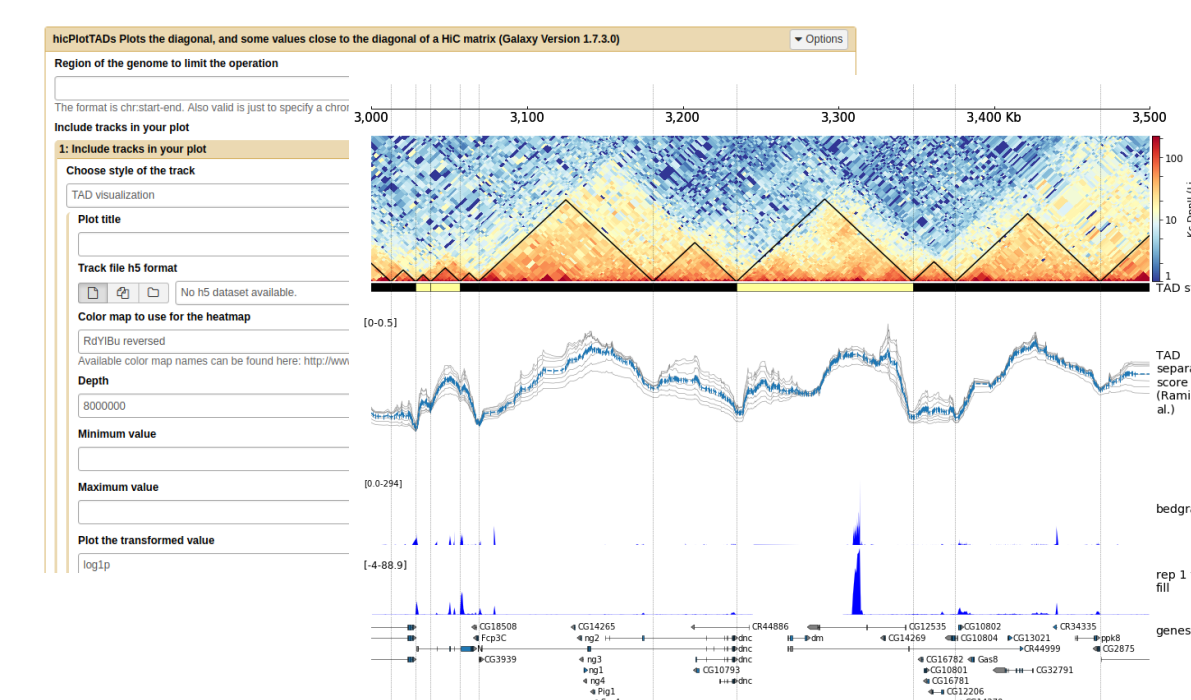
de.NBI training and education

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!
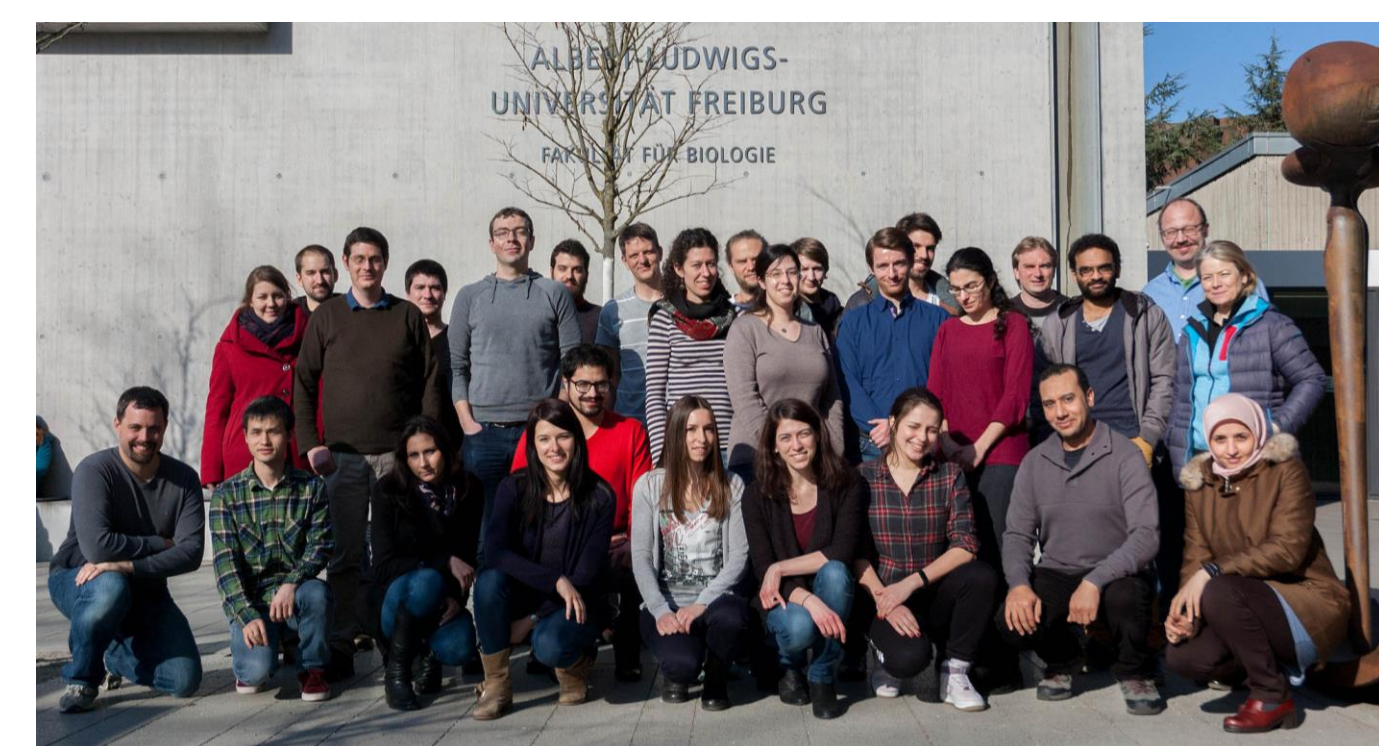
2016 / 2017 past events		
15th – 16th Dec 2016	Galaxy RNA-Seq analysis workshop	Freiburg
09th – 10th Jan 2017	Online contribution fest QIIME	
16th – 19th Jan 2017	European Galaxy Developer workshop	Strasbourg
06th – 09th Feb 2017	Galaxy Admin workshop	Melbourne
13th – 17th Feb 2017	Galaxy HTS data analysis workshop	Freiburg
04th – 05th Apr 2017	ELIXIR – de.NBI AAI workshop	Freiburg
22nd – 24th May 2017	ELIXIR – training hackathon	Cambridge
18th –22nd Sep 2017	Galaxy HTS data analysis workshop	Freiburg
2017 / 2018 planned events		
06th – 07th Nov 2017	VFU based on containers	Freiburg
08th – 12th Jan 2018	Galaxy Admin workshop	Oslo
19th – 23rd Feb 2018	Galaxy HTS data analysis workshop	Freiburg
Jan 2018	Freiburg Galaxy user meeting	Freiburg
Mid 2018	Hi-C and epigenetics workshop	Freiburg