

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 and GitHub

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.

de.NBI services

Community based infrastructure

BIOCONDA

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

- 20,151 commits on GitHub
- 575 contributors
- > 4,400 packages

Biocontainers

BioContainers provides system-agnostic executable environments for bioinformatics software.

- Based on Docker & rkt
- > 2,900 Images
- Automatic builds from Bioconda

Galaxy

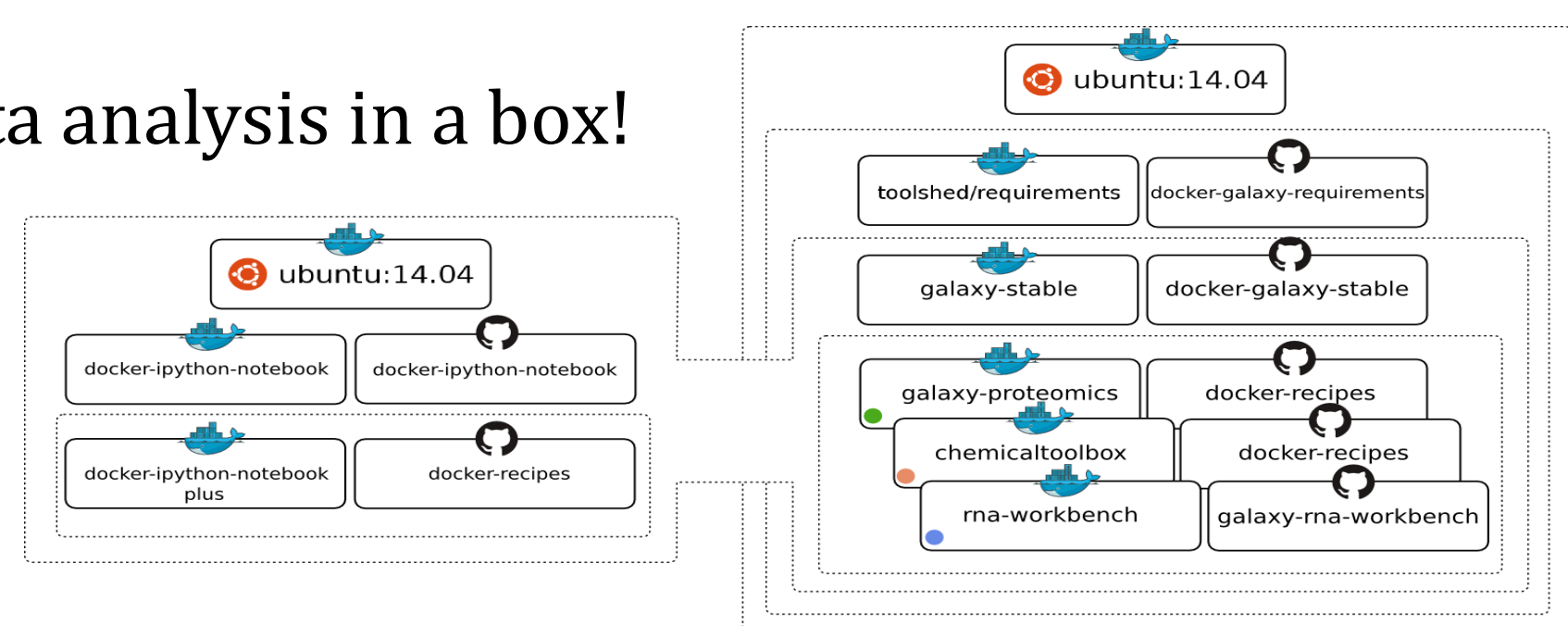
Galaxy is an open, web-based platform for data intensive research.

- 37,700 commits
- 196 contributors
- One of the biggest Galaxy instances available for de.NBI in Freiburg

The Galaxy Docker Project

The Galaxy Docker Image is an easily 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 virtualization, a dedicated flavor for epigenetics was developed: github.com/bgruening/docker-galaxy-epigenetic

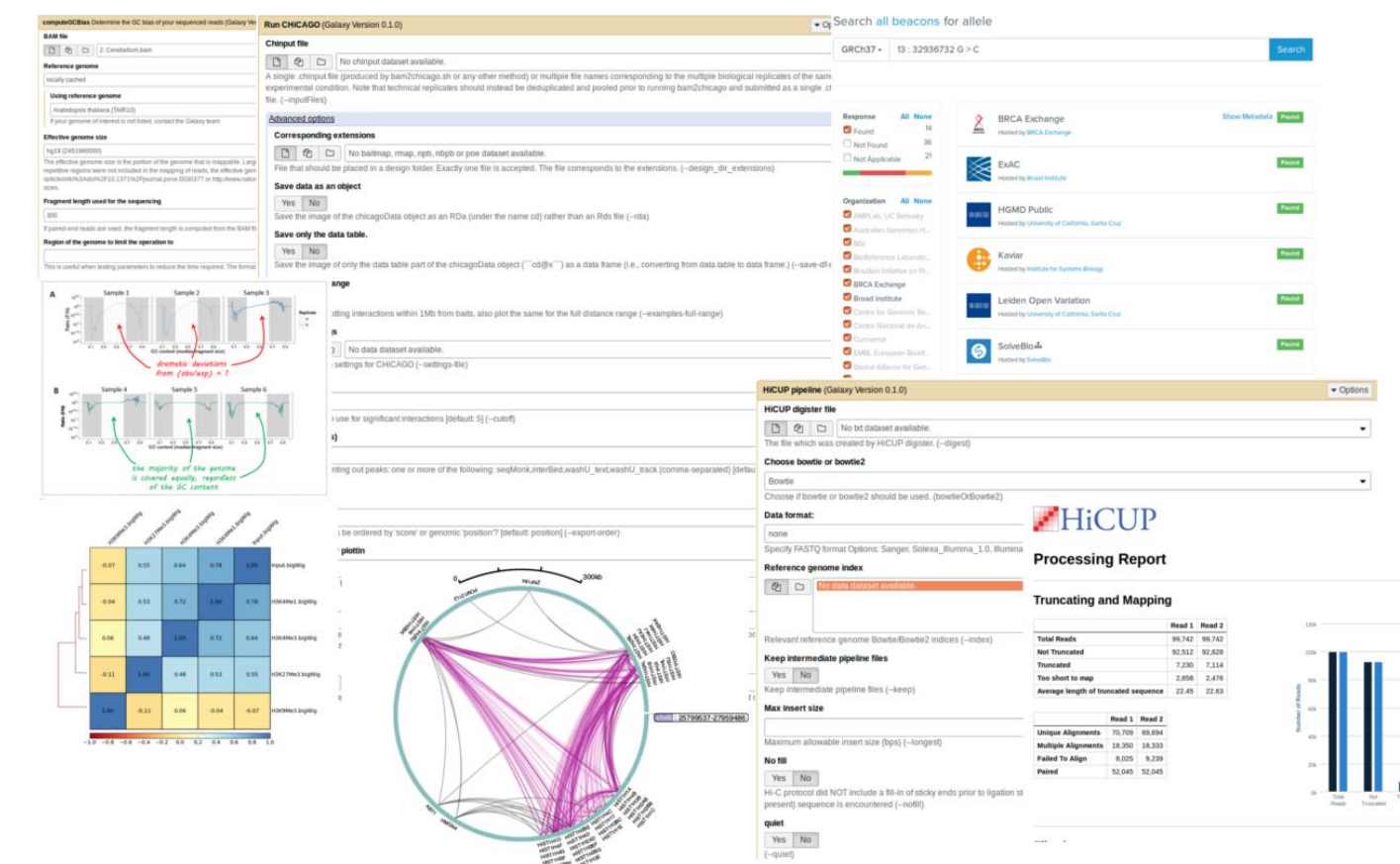
Publications

High-resolution TADs reveal DNA sequences underlying genome organization in flies.
doi: 10.1038/s41467-017-02525-w
BiocondaL sustainable and comprehensive software distribution for the life sciences.
doi: 10.1038/s41592-018-0046-7
Galaxy HiCExplorer: a web server for reproducible Hi-C data analysis, quality control and visualization.
doi: 10.1093/nar/gky504

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



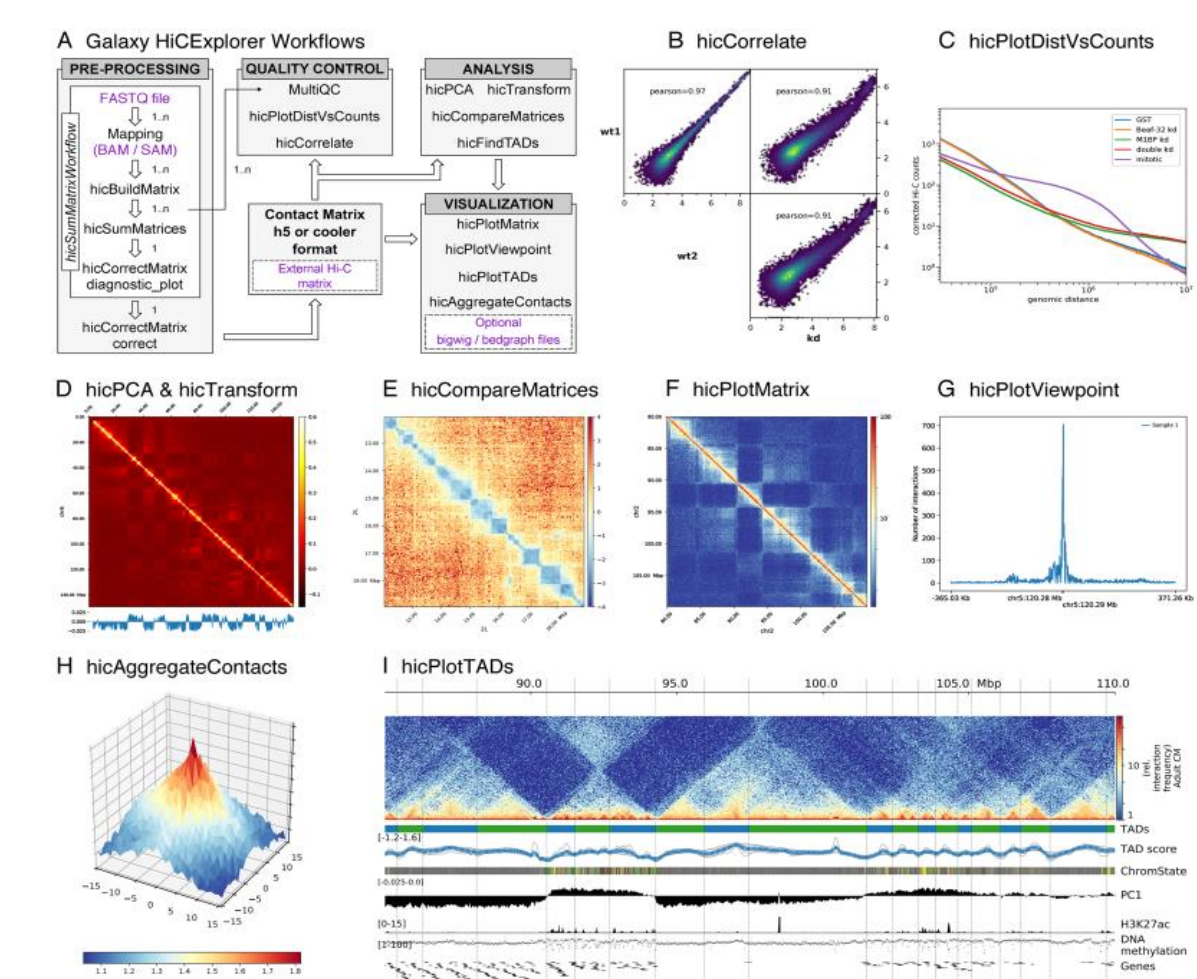
- Galaxy
- Container: Docker, rkt, Singularity

Progress report

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

HiCExplorer:

- Improved training material: hicexplorer.readthedocs.io
- Full Hi-C analysis pipeline: building an interaction matrix, QC, correction, TADs, A/B compartments
- Upcoming features:
 - Loop detection
 - cHi-C support



HiCMatrix:

- New modular structure
- Faster I/O support
- Format support: cool, hic, homer, HiCPro, h5

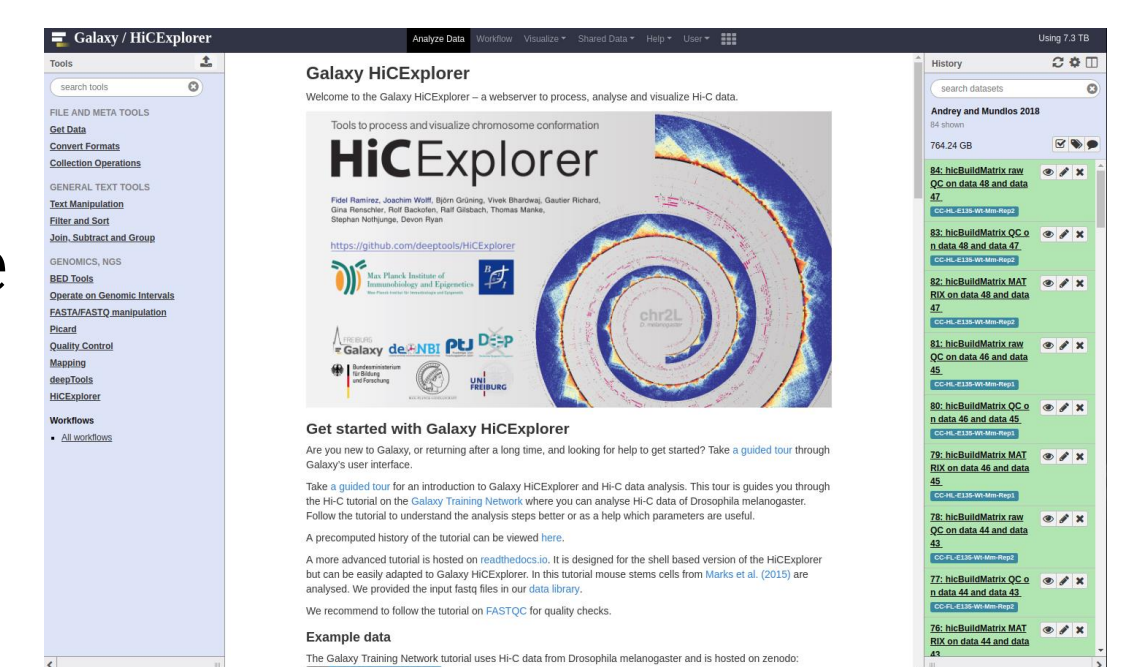
pyGenomeTracks:

- New modular structure
- Visualization of Hi-C, Bed and Bigwig tracks

Galaxy HiCExplorer:

- Webserver to make HiCExplorer accessible over the web

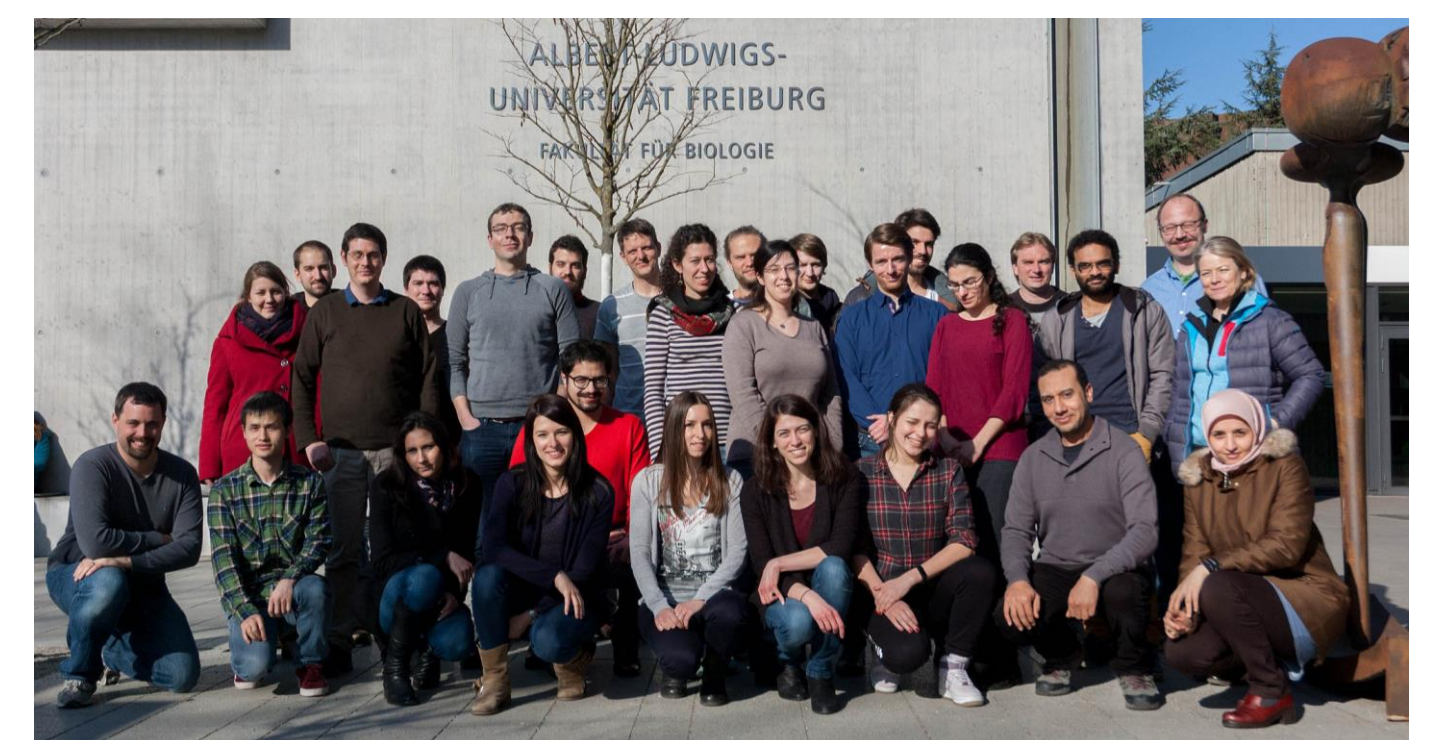
<https://hicexplorer.usegalaxy.eu>



de.NBI training and education

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

- Introduction to HTS
- RNA-Seq
- ChIP-Seq
- Hi-C
- ...and many more!



2018 past events

18.01. – 23.01.2018	Conda, Galaxy tools, Training with Galaxy	Melbourne, AUS
26.02. – 02.03.2018	Galaxy Training Course	Freiburg
15.03. – 16.03.2018	Galaxy user conference	Freiburg
24.06. – 02.07.2018	Galaxy community conference	Portland, USA
10.09.2018	ECCB Galaxy workshop	Athens, GRC
17.09. – 21.09.2018	Galaxy Training Course	Freiburg
09.10. – 10.10.2018	Hi-C workshop	Luzern, CH

This is a selection of events. Please see de.NBI status report 2018 for full list.