de.NBI-epi

RNA Bioinformatics Center
University of Freiburg
Chair of Bioinformatics

Fkz 031L0101C

GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

FREIBURG Galaxy TEAM

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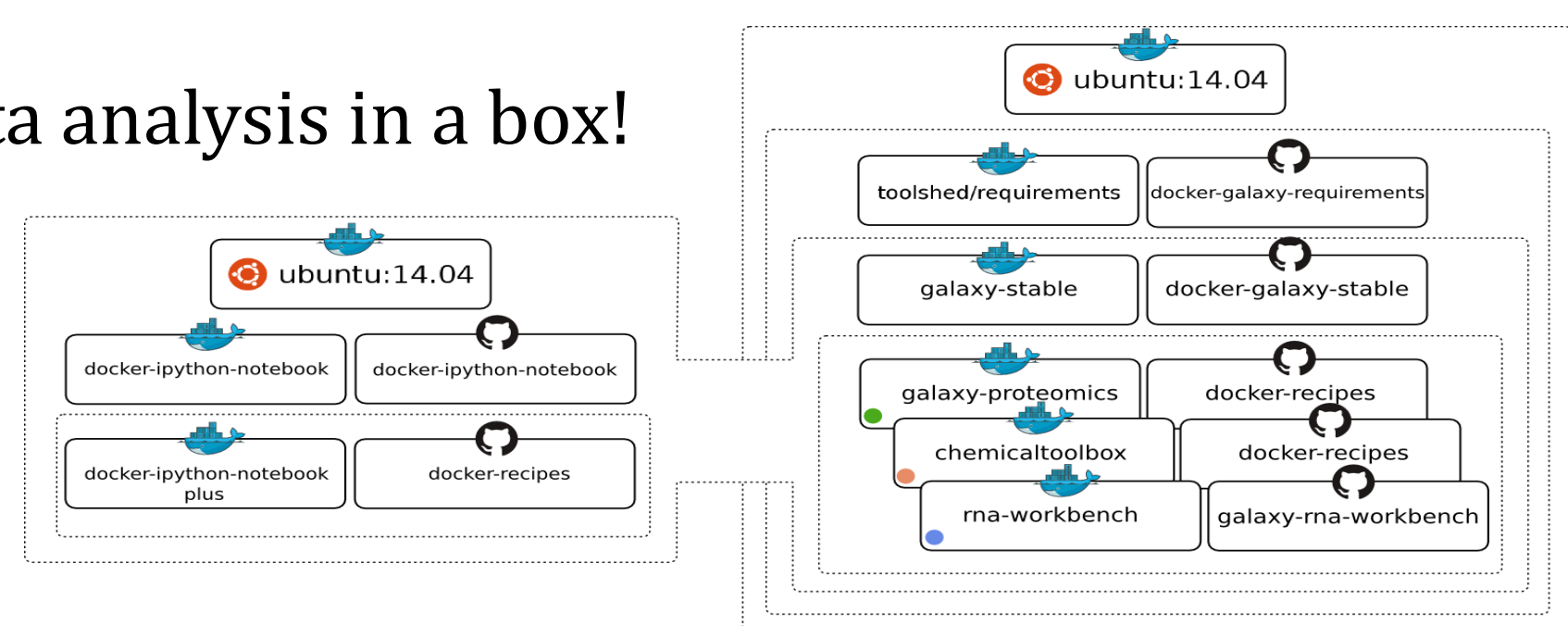
Based on the main Galaxy Docker virtualization, a dedicated flavor for epigenetics was developed: github.com/bgruening/docker-galaxy-epigenetic

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
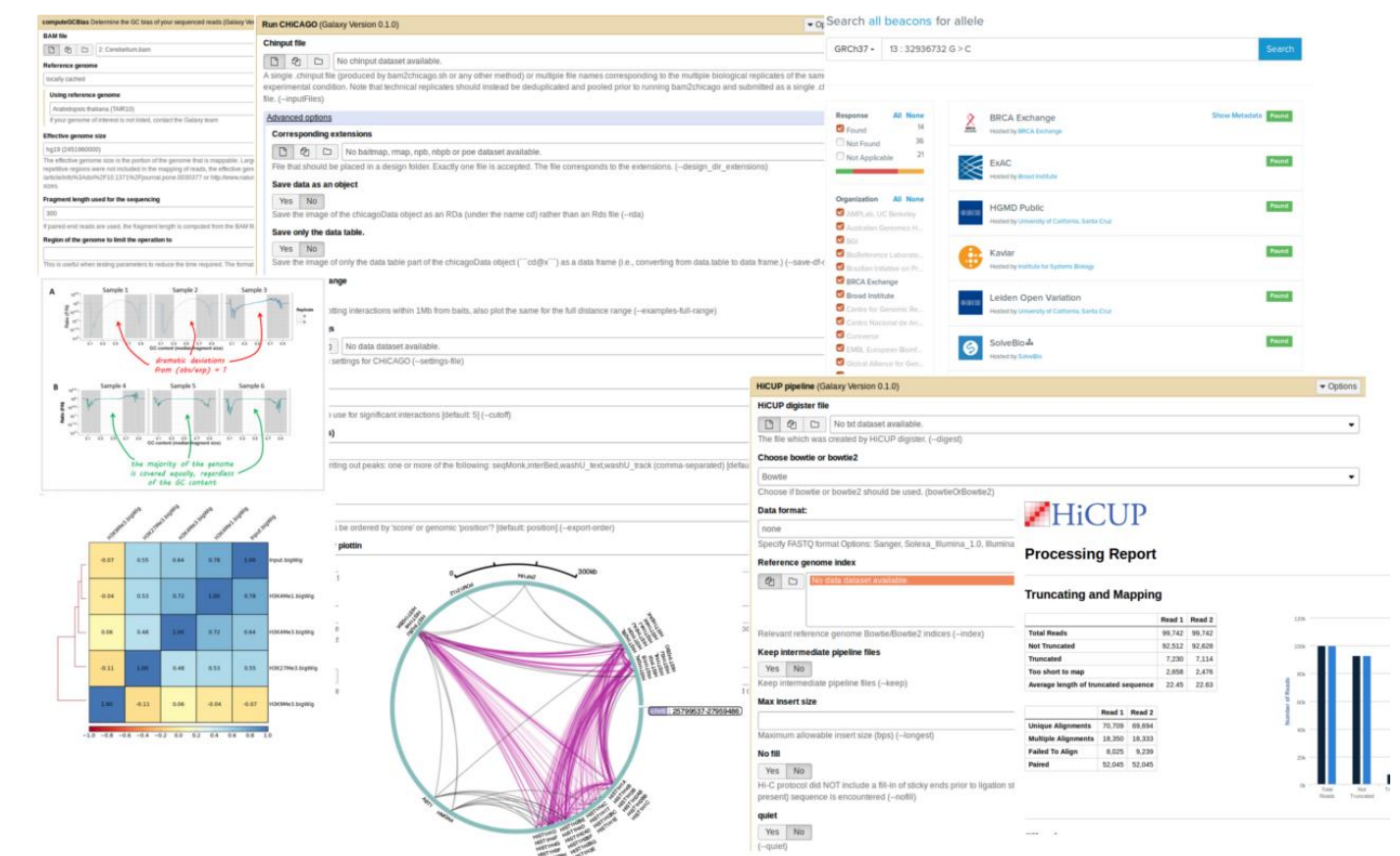
- Galaxy
- Container: Docker, rkt, Singularity

Progress report

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

HiCExplorer:
- Improved training material: hicexplorer.readthedocs.io
- Full Hi-C analysis pipeline: build of interaction matrix, QC, correction, TADs, A/B compartments
- Upcoming features:
    - Loop detection
    - cHi-C support
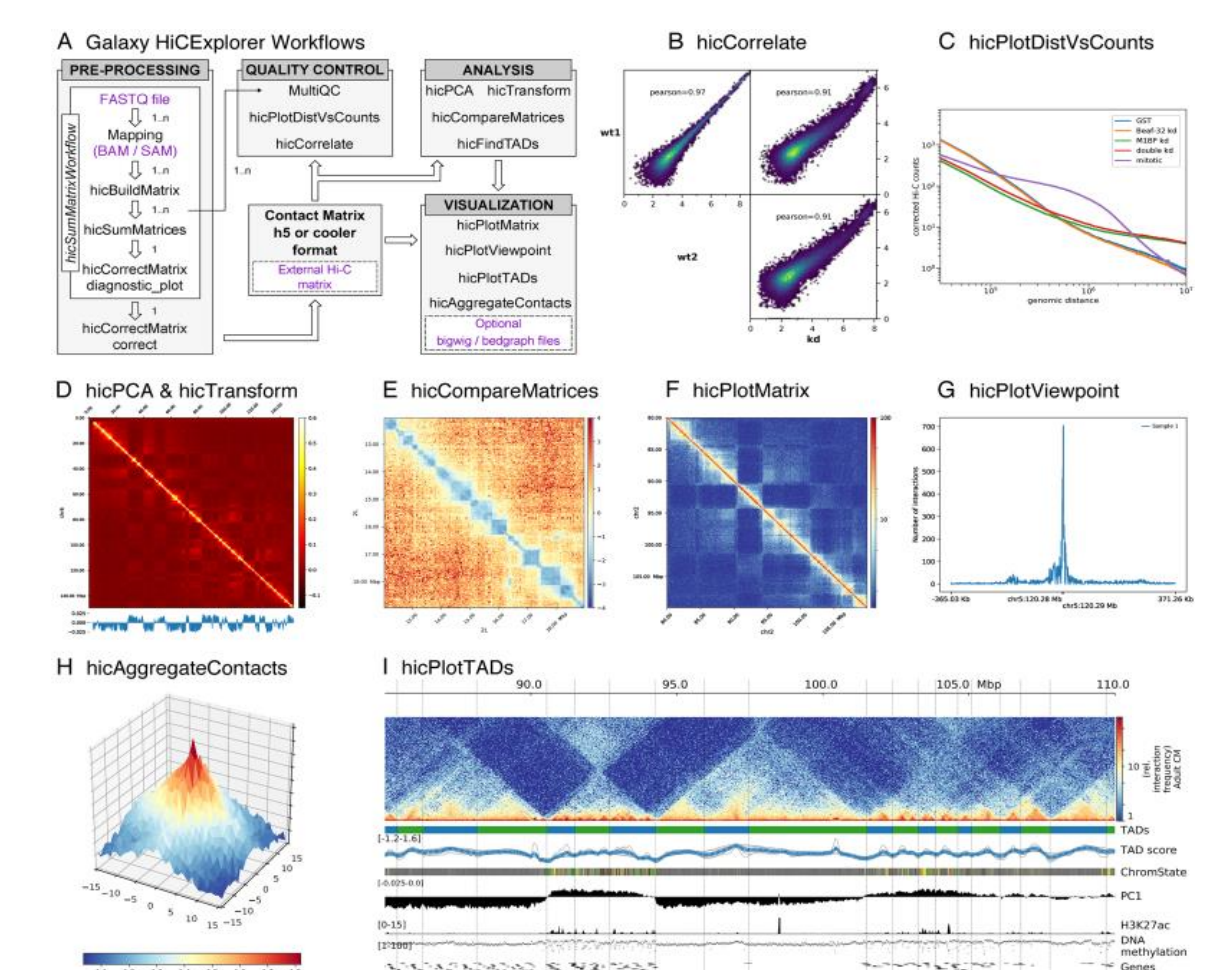
HiCMatrix:
- New modular structure
- Faster I/O support
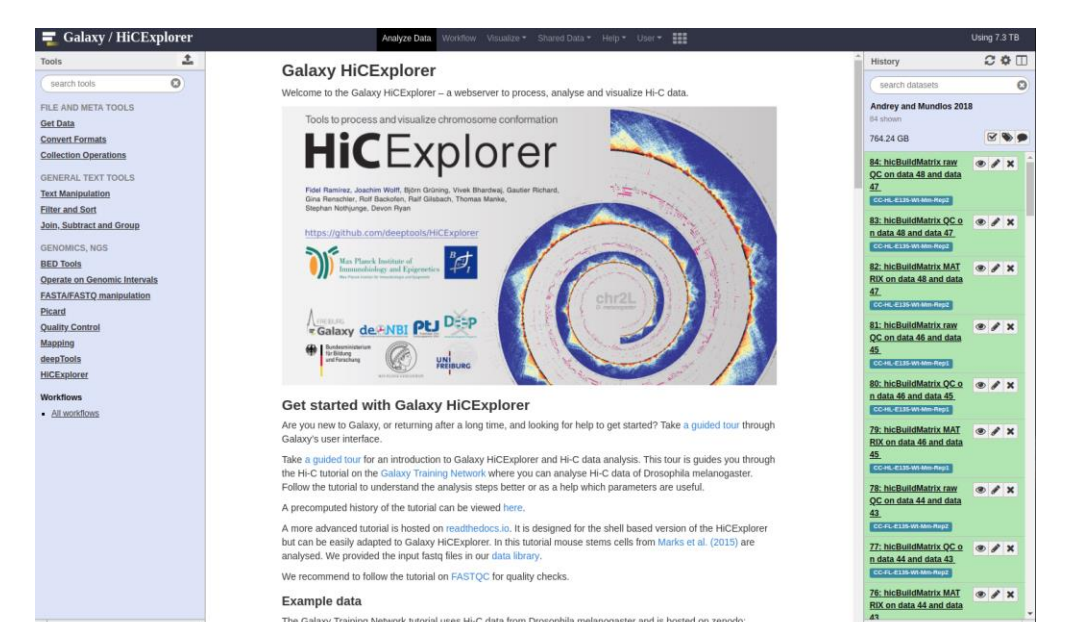- format support: cool, hic, homer, HicPro, h5

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

Galaxy HiCExplorer:
- Webserver to make HiCExplorer accessible over the web
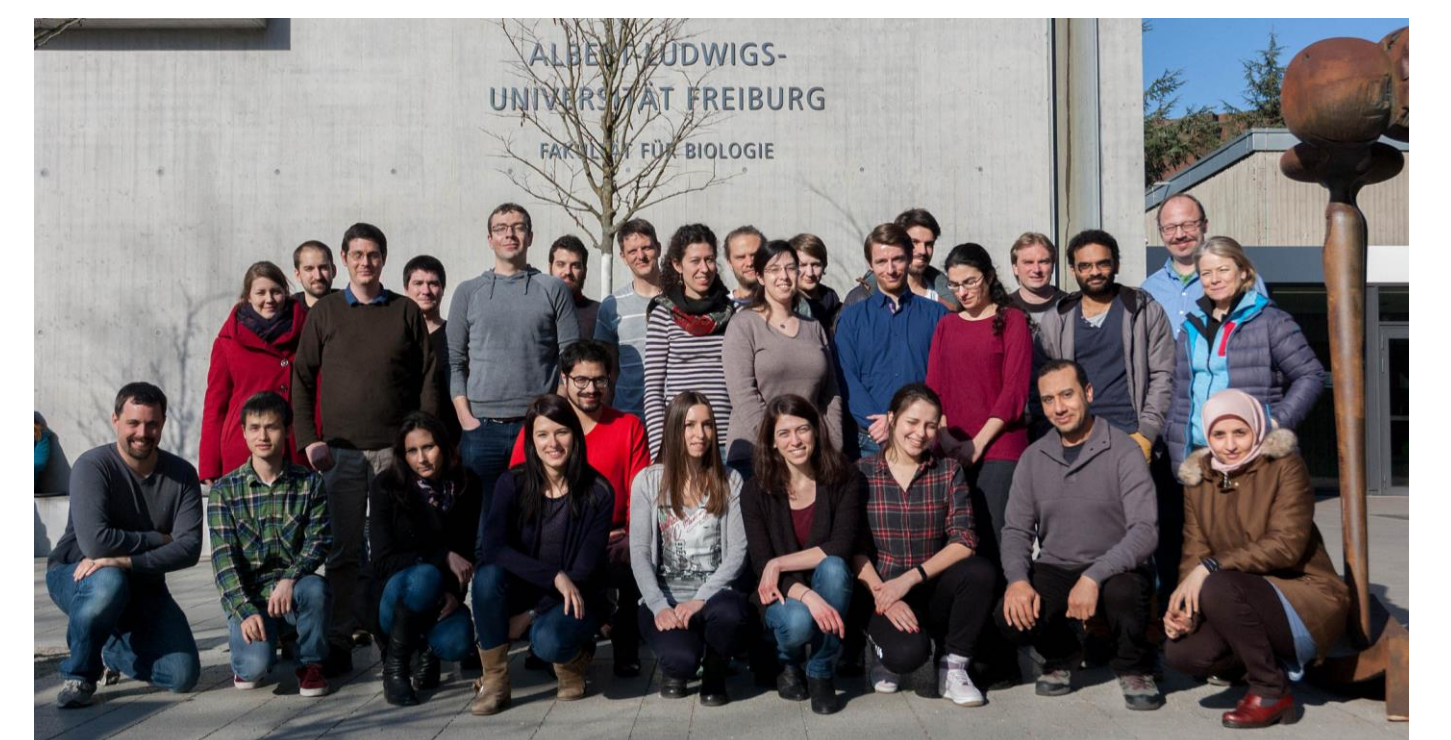https://hicexplorer.usegalaxy.eu

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

Date	Event	Location
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. – 10.10.2018	Hi-C workshop	Luzern, CH

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