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 https://training.galaxyproject.org
- Direct user support via gitter, GitHub or to visit as a guest researcher

Flexible availability:
- 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, ELIXIR and EOSC-life to deliver high-class services for epigenetic research.

General information on the project

Community based infrastructure

BIOCONDA

Biocontainers

Galaxy

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

- 25,649 commits on GitHub
- 856 contributors
- > 7,300 packages

BioContainers provides system-agnostic executable environments for bioinformatics software.

- Based on Docker & rkt
- > 33,000 containers
- Automatic builds from Bioconda

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

- 43,998 commits
- 223 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!
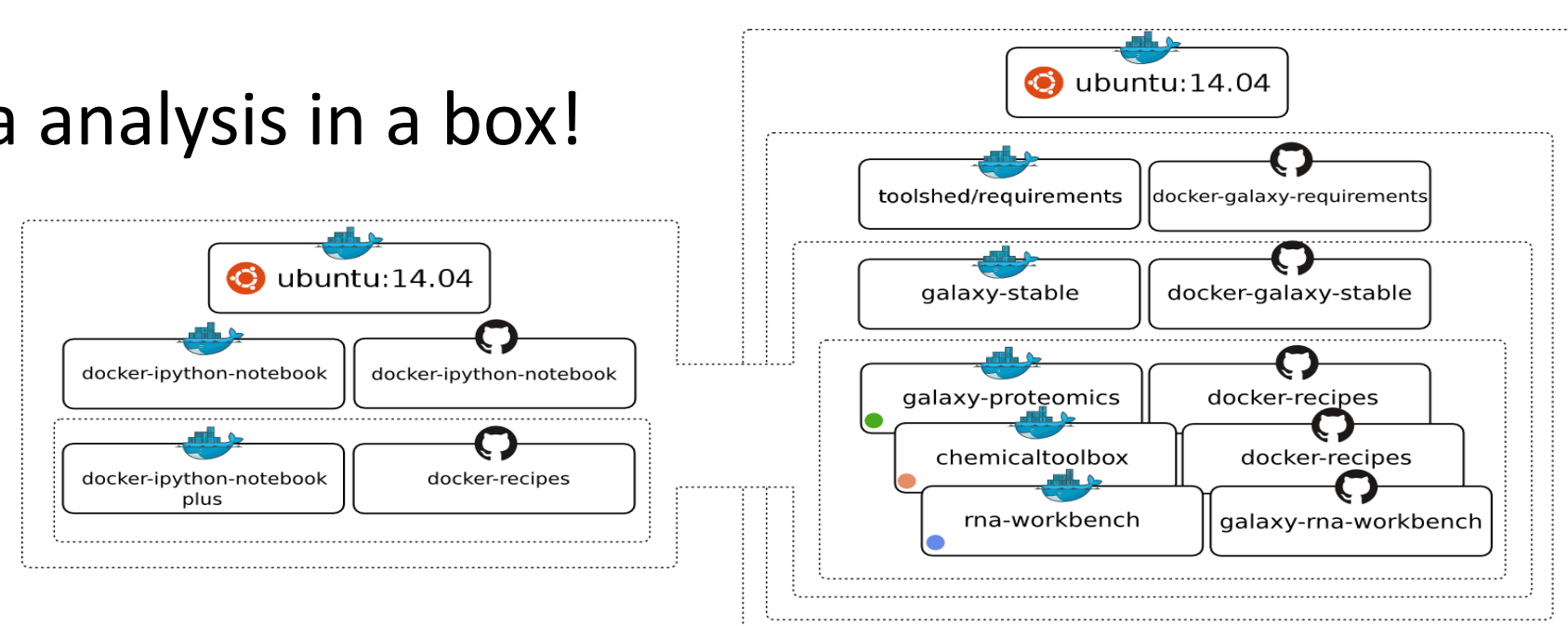
Based on the main Galaxy Docker virtualization, a dedicated flavor for epigenetics has been developed: github.com/bgruening/docker-galaxy-epigenetic

Publications

Software engineering for scientific big data analysis
    doi: 10.1093/gigascience/giz054
The de. NBI/ELIXIR-DE training platform-Bioinformatics training in Germany and across Europe within ELIXIR
    doi: 10.12688/f1000research.20244.1
The bio.tools registry of software tools and data resources for the life sciences
    doi: 10.1186/s13059-019-1772-6
Pou5f3, SoxB1, and Nanog remodel chromatin on High Nucleosome Affinity Regions at Zygotic Genome Activation
    doi: 10.1101/gr.240572.118

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
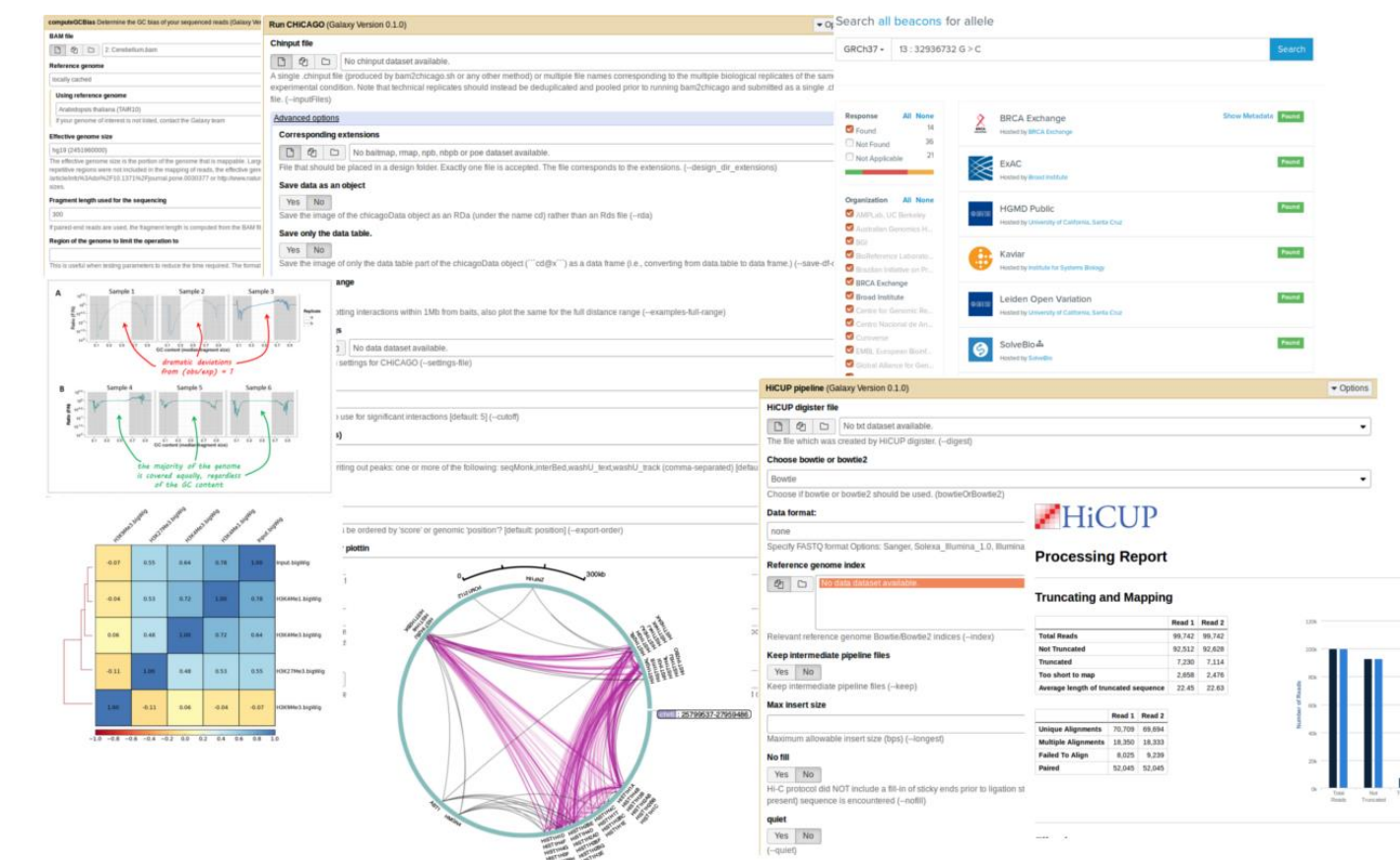
Progress report

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

HiCExplorer:
- Maintenance of HiCExplorer
  - Extending available tools with new functions
- Loop detection
- Support of more file formats
- Support of cHi-C data analysis
- Validation of loops
- Improved training material: https://hicexplorer.readthedocs.io
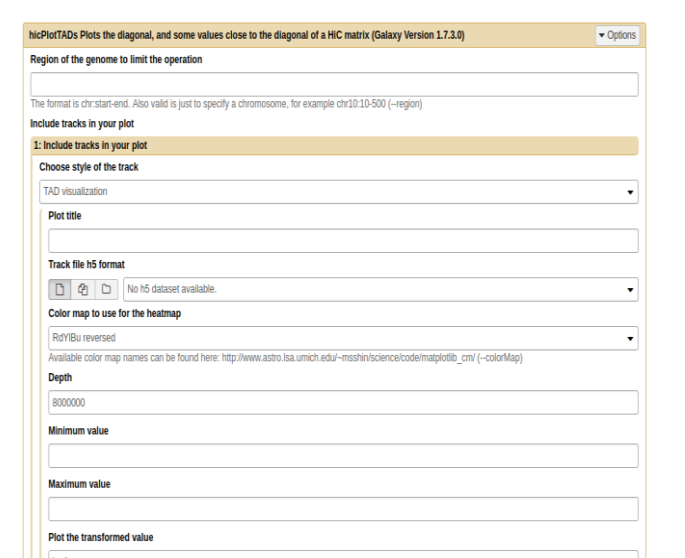
scHiCExplorer:
New software to support single-cell Hi-C data analysis:
- Tools to demultiplex raw fastq files
- Create mCool matrices and manipulation
- Methods for dimensionality reduction of scHi-C data
- Methods to cluster scHi-C data
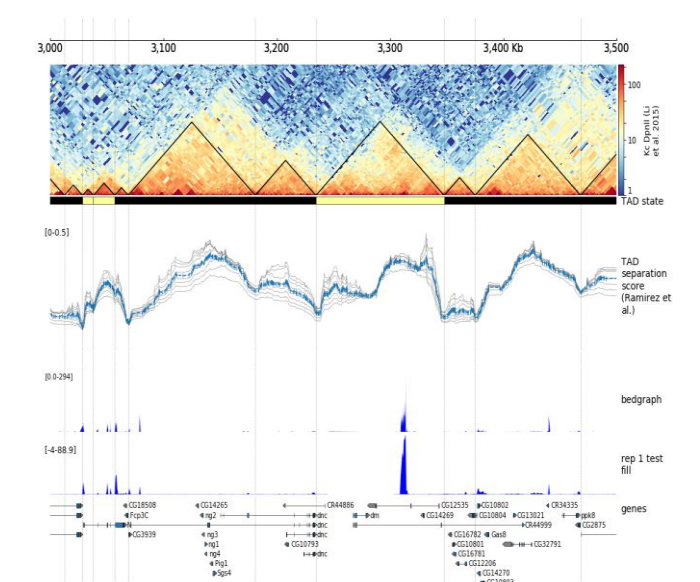
de.NBI Training and education

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!

2018 / 2019 past events

Date	Event	Location
06th – 07th Dec 2018	Galaxy RNA-Seq analysis workshop	Freiburg
17th – 18th Jan 2019	Galaxy RNA-Seq analysis workshop	Belgrad, SP
25th Feb – 01st Mar 2019	Galaxy Workshop	Freiburg
23rd – 26th Apr 2019	Elixir Galaxy Community Workshop	Roscoff, FR
1st – 6th Jul 2019	Host of Galaxy Community Conference (GCC)	Freiburg
24th Jul 2019	ISMB: Workshop for reproducible research	Basel, CH
16th Sept 2019	GCB: Workshop for Workflows, Tools and Data Management	Heidelberg
23rd – 27th Sept 2019	Galaxy Workshop	Freiburg