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 ans user support:
- Galaxy HTS data analysis workshops
- Self learning material on training.galaxyproject.org
- Direct user support via github

Available on:
- An easy to use computing cluster: 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
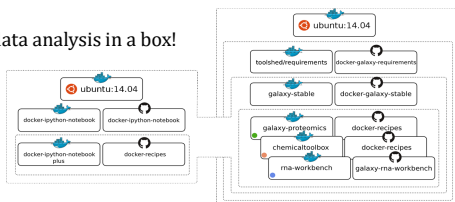
Publications

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
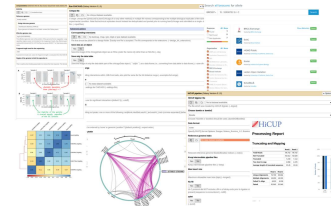
- Galaxy
- Docker

Progress report

Development and maintenance of software for Hi-C data analysis

HiCExplorer:
- Interaction matrix creation 3x faster
- Improved training material: hicexplorer.readthedocs.io
- 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
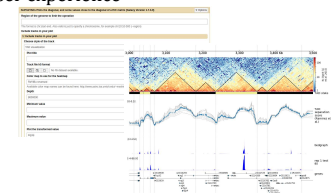
de.NBI Training and education

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

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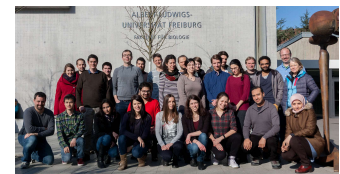
2016 / 2017 past events		
15th – 16th Dec 2016	Galaxy RNA-Seq analysis workshop	Freiburg
09th – 10th Jan 2017	Online contribution fest	
16th – 19th Jan 2017	European Galaxy Developer workshop	Strasbourg
13th – 17th Feb 2017	Galaxy HTS data analysis workshop	Freiburg
04th – 05th Apr 2017	ELIXIR – de.NBI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