







de.NBI - German Network for Bioinformatics Infrastructure

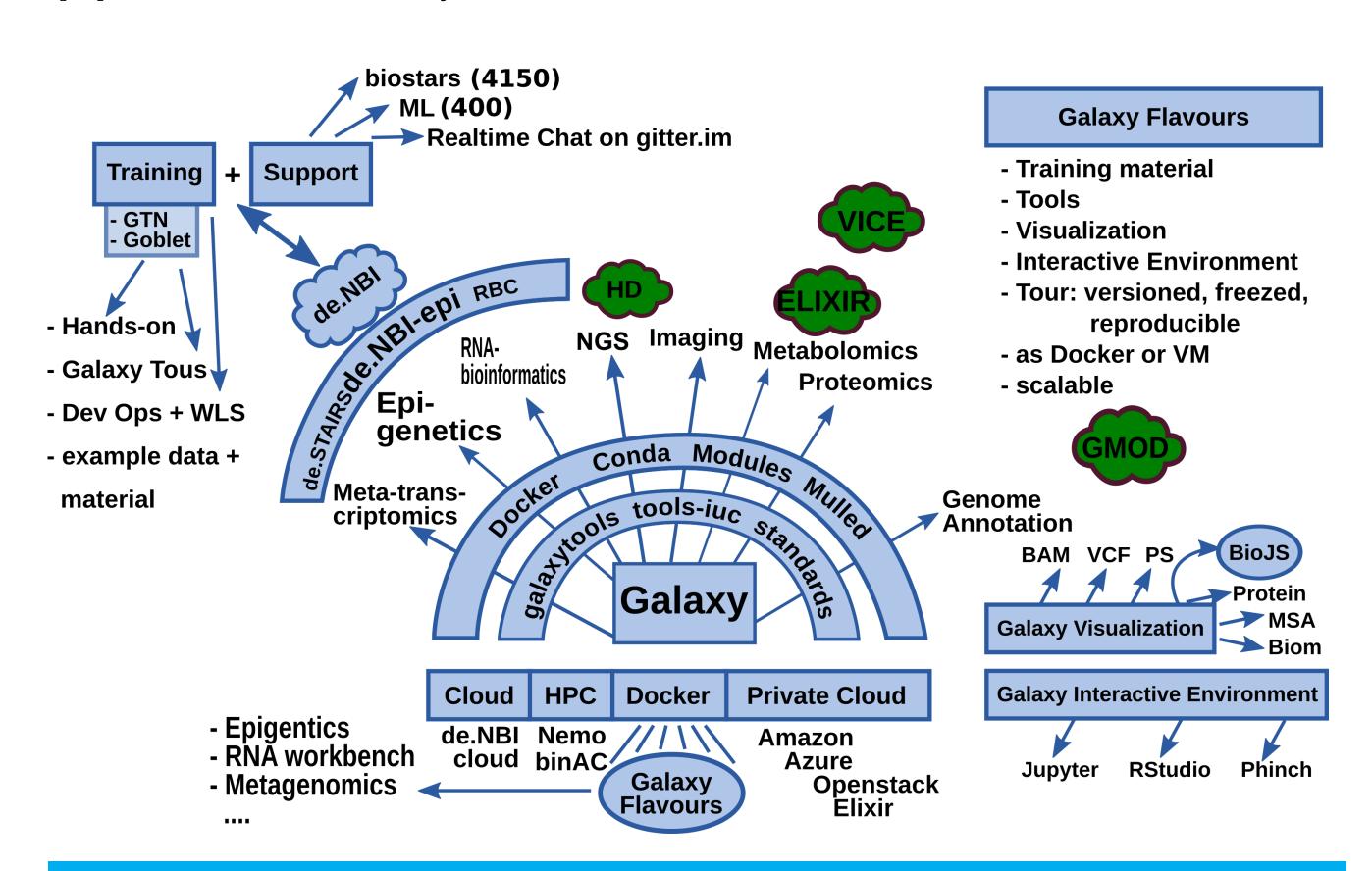
de.NBI-epi

RNA Bioinformatics Center University of Freiburg Chair of Bioinformatics

Björn Grüning, Joachim Wolff, Rolf Backofen RNA Bioinformatics Center, University of Freiburg, Germany



The de.NBI-epi project in Freiburg offers visualisation, normalisation and quality assessment of epigenetic datasets as well as integration of CHIP-seq and bisulfite sequencing analysis pipelines into Galaxy.



Community based infrastructure

BIOCONDA°

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

- 8,600 commits on GitHub
- 155 contributors
- > 1,800 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.

- 25,550 commits
- 131 contributors

ubuntu: 14.04

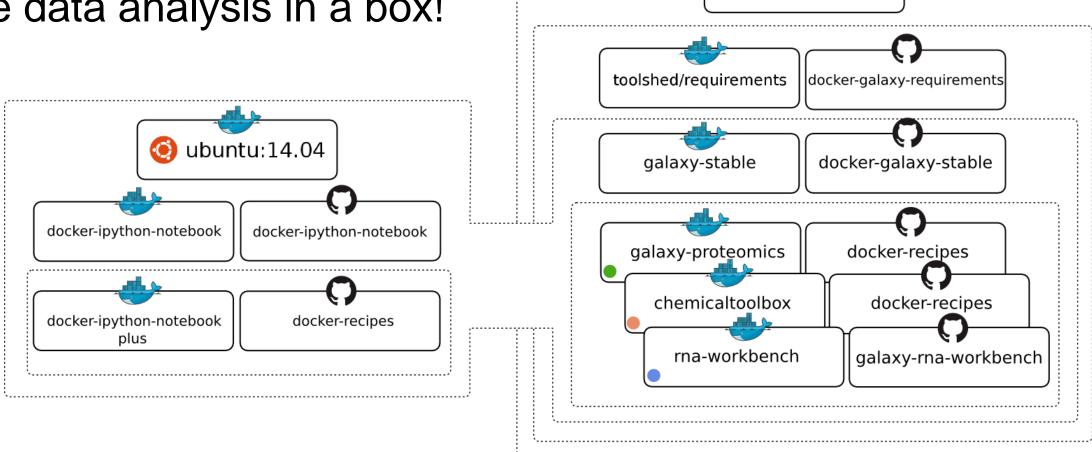
 One of the biggest Galaxy instances available for de.NBI

http://galaxy.uni-freiburg.de

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

deepTools2: a next generation web server for deep-sequencing data analysis. doi:10.1093/nar/gkw257

Tools and data services registry: a community effort to document bioinformatics resources.

doi: 10.1093/nar/gkv1116

The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. doi: 10.1093/nar/gkw343

GEFÖRDERT VOM

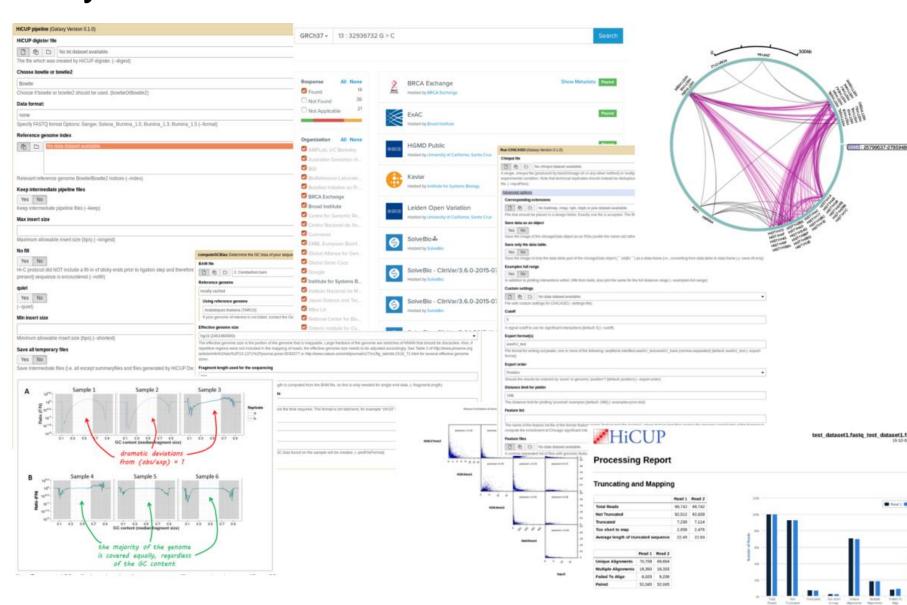
Bundesministerium

und Forschung

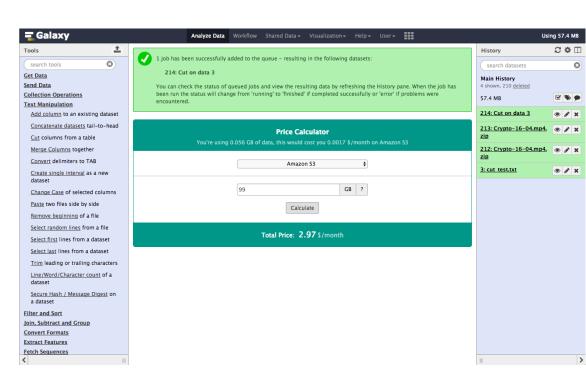
de.NBI services

Maintenance and integration of software into Galaxy to provide easy access for epigenetic analysis software:

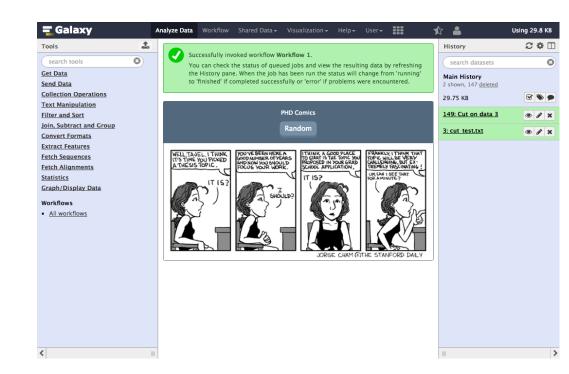
- HiCExplorer
- deepTools
- Bismark
- HiCUP
- CHiCAGO
- PileOMethMethtools
- Beacons



Galaxy WebHooks as playground for SIG-2 and SIG-4 with gamification:



Pricing system: How much would it cost to compute and store your data on Amazon EC2?



Comics: Have fun while Galaxy is computing your data.

And a lot more: RSS-Reader, PubMed recommendations, tool recommendation, runtime graphs... (leave a Post-it with your ideas!)

de.NBI training and education

Galaxy Tours – Bioinformatics Training 2.0

- For **users**: As easy as a video, but interactive as a hands-on training
- For **trainers**: Dead simple to create!



2016 past and planned events

	06 th – 7 th Oct 2016	Swiss German Galaxy workshop	Freiburg
	24 th – 26 th Oct 2016	CHARME, EMBnet and NETTAB Workshop	Rome
	02 nd – 03 rd Nov 2016	BioConda hackathon	Freiburg
	15 th – 16 th Dec 2016	Galaxy RNA-seq data analysis workshop	Freiburg
2017 planned events			
	16 th – 19 th Jan 2017	European Galaxy Developer workshop	Strasbourg
	13 th – 17 th Feb 2017	Galaxy HTS data analysis workshop	Freiburg
	4 th – 5 th Apr 2017	ELIXIR – de.NBI AAI workshop	Freiburg

Hands-on training material for self-study available:

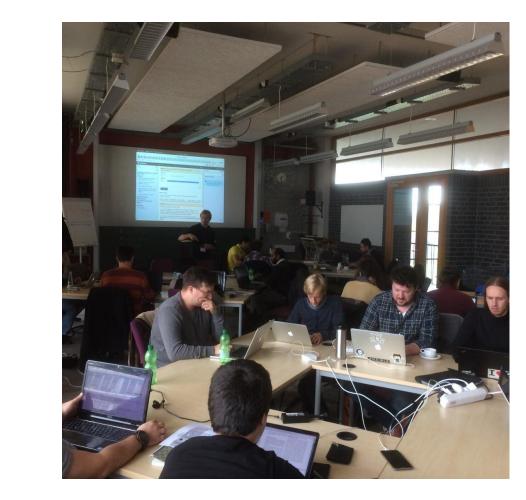
14th – 18th Sep 2017 Galaxy HTS data analysis workshop

https://bgruening.github.io/training-material



Global Organisation for Bioinformatics Learning, Education & Training





Freiburg

