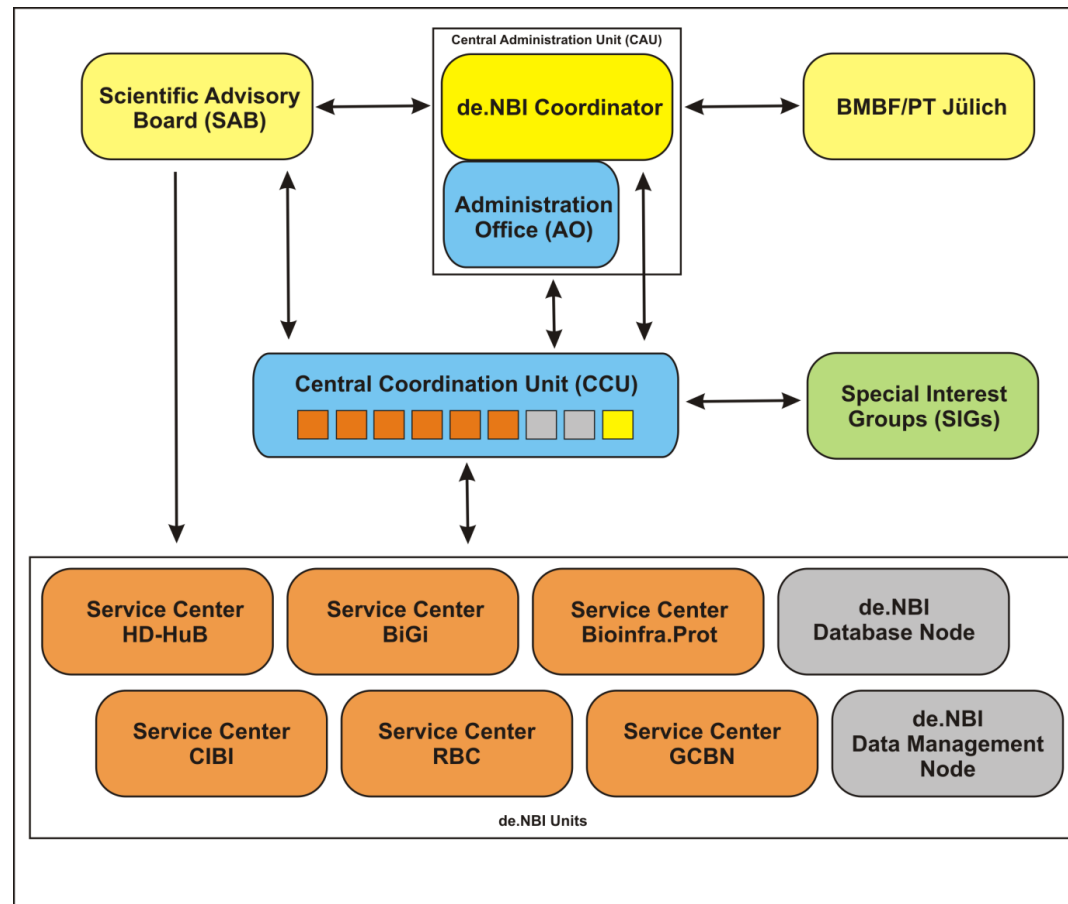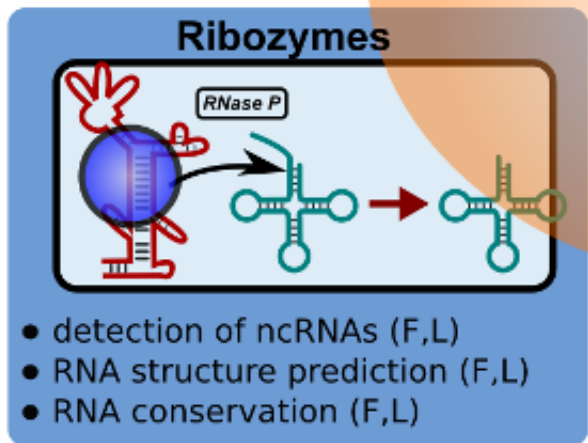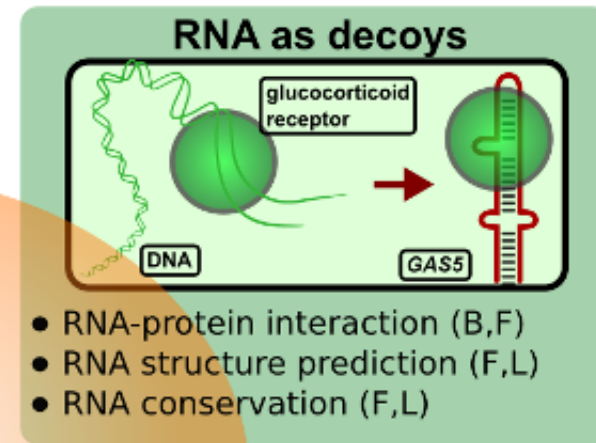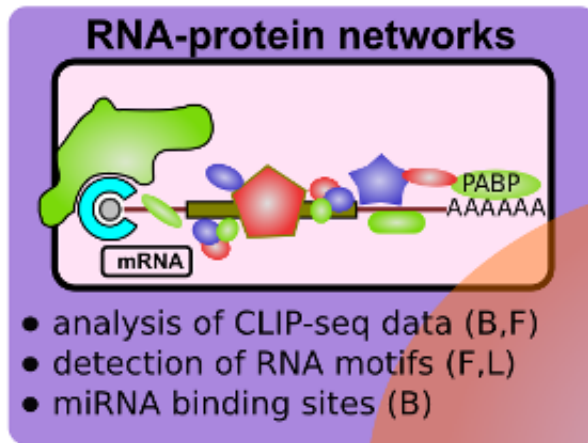Analyze more, process less:

Galaxy in Freiburg

September 2016 – Anika Erxleben – Freiburg Galaxy Team
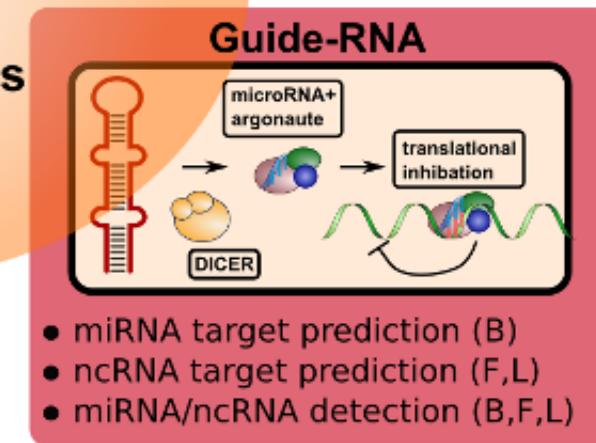
Who?

We are part of the German Network for Bioinformatics Infrastructure (de.NBI) & ELIXIR

RBC – RNA Bioinformatics Center

What do we offer

- Reproducible one-click ready-to-use pipelines

- Easy access to data, tools and protocols

- Easy deployment of tools and protocols

- Data integration and management +SRA, Genbank upload, UniProt, …

- Data visualization

- Training!

- Compute resources

What is

?

- An analysis and data integration platform
- A workflow management system
- Open source, community driven software that makes integration of your favourite tools simple

http://galaxyproject.org

Our Aim

"Enable accessible, reproducible, and transparent computational research."

accessible – web interface

accessible – get your data

"Enable accessible, reproducible, and transparent computational research."

reproducible – reload experiments

reproducible – reload experiments

reproducible – tools versioning

reproducible - workflows

reproducible - workflows

"Enable accessible, reproducible, and transparent computational research."

transparent – sharing everything

Share or Publish History 'Aspergillus NCBI Submission'

Making History Accessible via Link and Publishing It

This history is currently **accessible via link**.
Anyone can view and import this history by visiting the following URL:

http://galaxy.pharmaceutical-bioinformatics.org/u/bjoern/h/aspergillus-ncbi-submission

You can:

Disable Access to History Link
Disables history's link so that it is not accessible.

Publish History
Publishes the history to Galaxy's Published Histories section, where it is publicly listed and searchable.

Sharing History with Specific Users
The following users will see this history in their history list and will be able to view, import, and run it.

Email
wolfgang.huettel@pharmazie.uni-freiburg.de ▾
loubna.youssar@pharmazie.uni-freiburg.de ▾

Share with another user

Back to Histories List

transparent – for other researchers

Windshield splatter analysis with the Galaxy metagenomic pipeline

Sergei Kosakovsky Pond[1,2,6,9], Samir Wadhawan[3,6,7], Francesca Chiaromonte[4], Guruprasad Ananda[1,3], Wen-Yu Chung[1,3,6], James Taylor[1,5,9], Anton Nekrutenko[1,3,9] and The Galaxy Team[1]

[+] Author Affiliations

[+] Author Notes

[6] These authors contributed equally to this work.

Abstract

Footnotes

[Supplemental material is available online at http://www.genome.org. All data and tools described in this manuscript can be downloaded or used directly at http://galaxyproject.org. Exact analyses and workflows used in this paper are available at http://usegalaxy.org/u/aun1/p/windshield-splatter.]

Article published online before print. Article and publication date are at

first publication that features a live online supplement providing access to exact analyses and workflows used in the article.

Footnotes

[Supplemental material is available online at http://www.genome.org. All data and tools described in this manuscript can be downloaded or used directly at http://galaxyproject.org. Exact analyses and workflows used in this paper are available at http://usegalaxy.org/u/aun1/p/windshield-splatter.]

Article published online before print. Article and publication date are at http://www.genome.org/cgi/doi/10.1101/gr.094508.109.

"Enable accessible, reproducible, and transparent computational research."

Tools, tools, tools

Freiburg Galaxy instance

- RNA-seq

- ChIP-seq

- MethylC-seq

- Exome-seq

- Genome annotation

- Metagenomics

- Proteomics

- … and more

>2000 tools

- Text manipulation
- Format converters
- Filtering and sorting
- Join, substract, group
- Unix tools
- Alignment tools
- Mapping
- Statistics

- Plotting
- EMBOSS
- WES/WGAS
- NCBI Blast+
- Blast2GO
- DAVID
- ChemicalToolBoX
  … and many more

genVAST variant calling (SNPs)

- Pipeline for exome-seq data analysis

Uniklinikum Freiburg
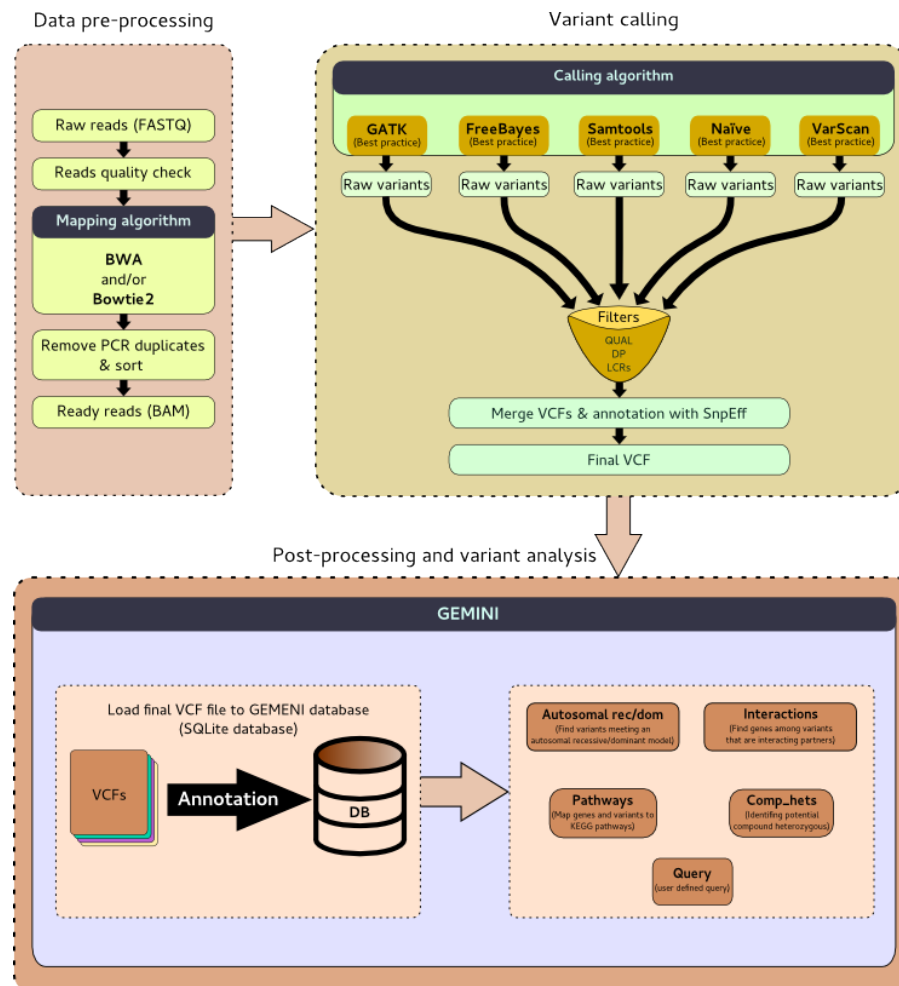
BLAST+ and genome annotation
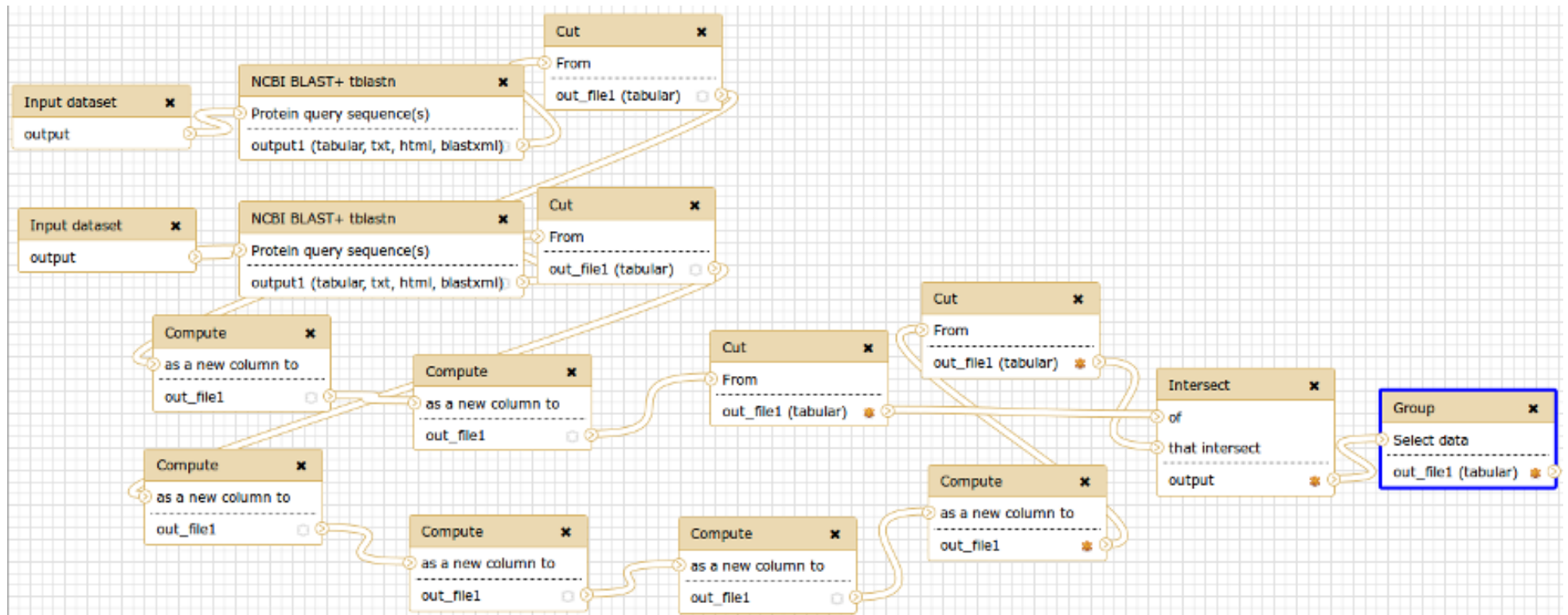
Proteomics

OpenMS workflow, Melanie Föll, AG Schilling

visualization – show your results

visualization - charts
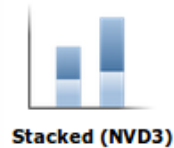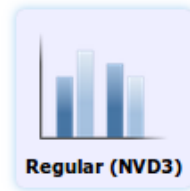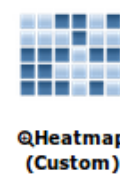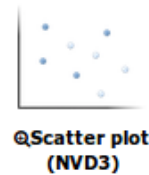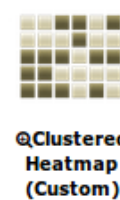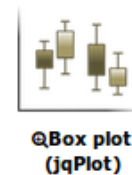
Virtualized Galaxy flavours
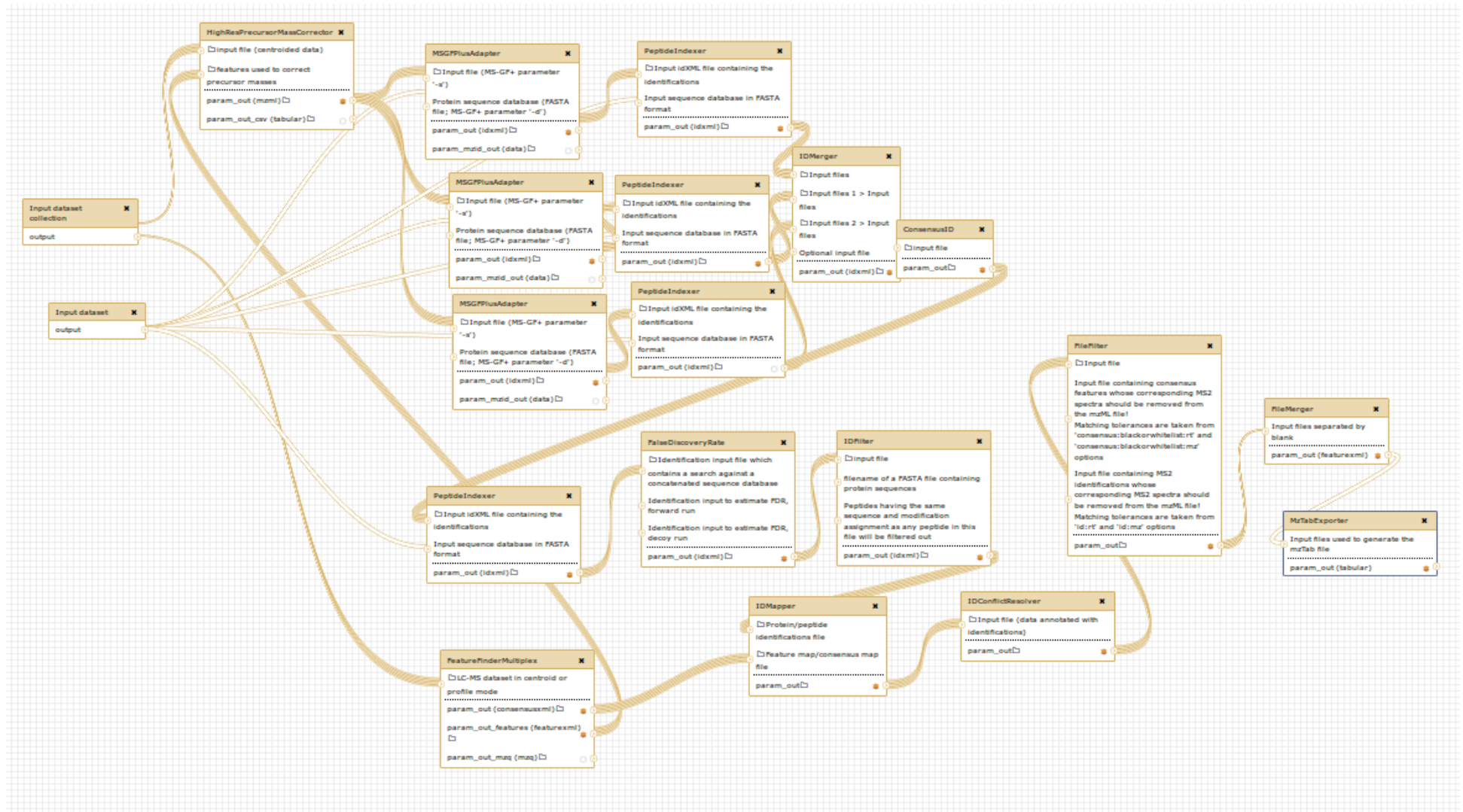

https://www.docker.io
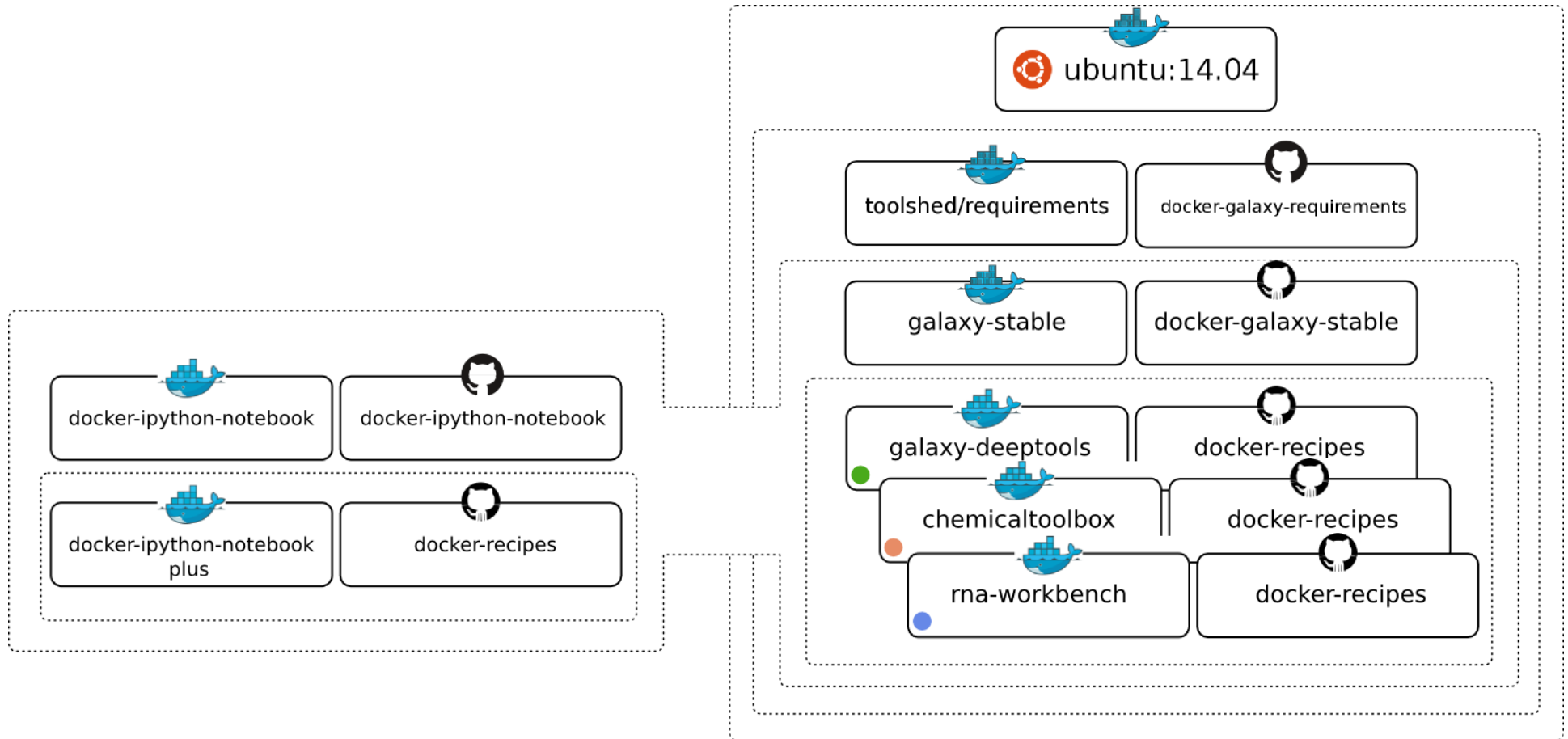
Freiburg Galaxy stats

- 360 registered users

- 48 different groups

- ~1000 different tools

- 110,000 jobs per year

- 10 workshops with ~240 participants

It's there!
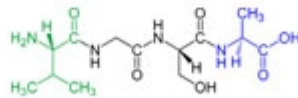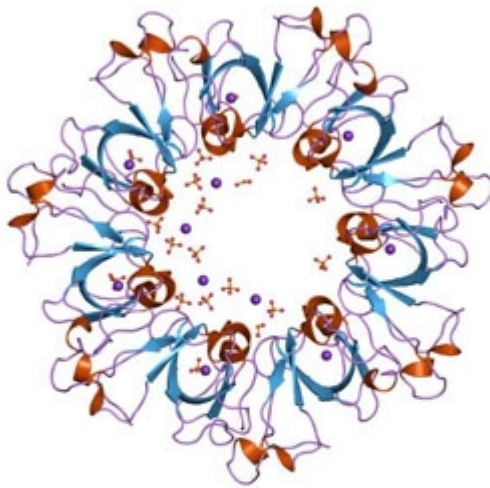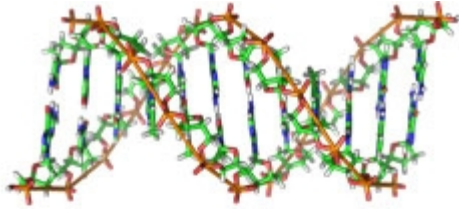
- Gen**omics**
- Prote**omics**
- Metabol**omics**
- Imaging, literature sciences, engineering, ...

Training!

- Galaxy HTS data analysis workshops

- Developers day & international workshops

- GTN (Galaxy Training Networks)

- iPython for teaching

- Galaxy for lecturing

- Training material, protocols & slides online on github! **https://github.com/bgruening/**trainings-material
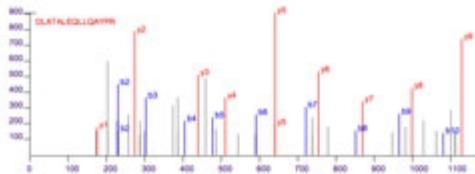
- Galaxy interactive tours

https://wiki.galaxyproject.org/Community/GalaxyAdmins

Community is the key

- ~2900 publications since 2010, 1600 articles from 2015-2016

- 75 known public instances

- https://biostar.usegalaxy.org (2016: 4600 active users)

- ~1200 registered developers (galaxy-dev mailing list

- ~400 mails per month

- Annual international community conference

- 2 positions for community-related questions

Thank you!

Freiburg Galaxy Team

Dr. Björn Grüning

- Dr. Torsten Houwaart

- Dr. Berenice Batut

- Clemens Blank

- Joachim Wolff

- Prof. Rolf Backofen

- galaxy@informatik.uni-freiburg.de

- http://www.bioinf.uni-freiburg.de