GEFÖRDERT VOM

Bundesministerium
für Bildung
und Forschung

Projektträger Jülich
Forschungszentrum Jülich

de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

Secure and practical computational reproducibility in the life sciences

Bioconda, BioContainers, Galaxy
& the de.NBI Galaxy-Docker-Technology

Rolf Backofen, Björn Grüning & The RBC Team

Center for RNA Bioinformatics (RBC)

RBC

Rolf Backofen

Uwe
Ohler

Nikolaus
Rajewksy

Peter Stadler

Partner Projects

de.NBI-epi

Björn
Grüning

Altuna
Akalin

de.STAIR

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Hoffmann

Olaf
Wolkenhauer

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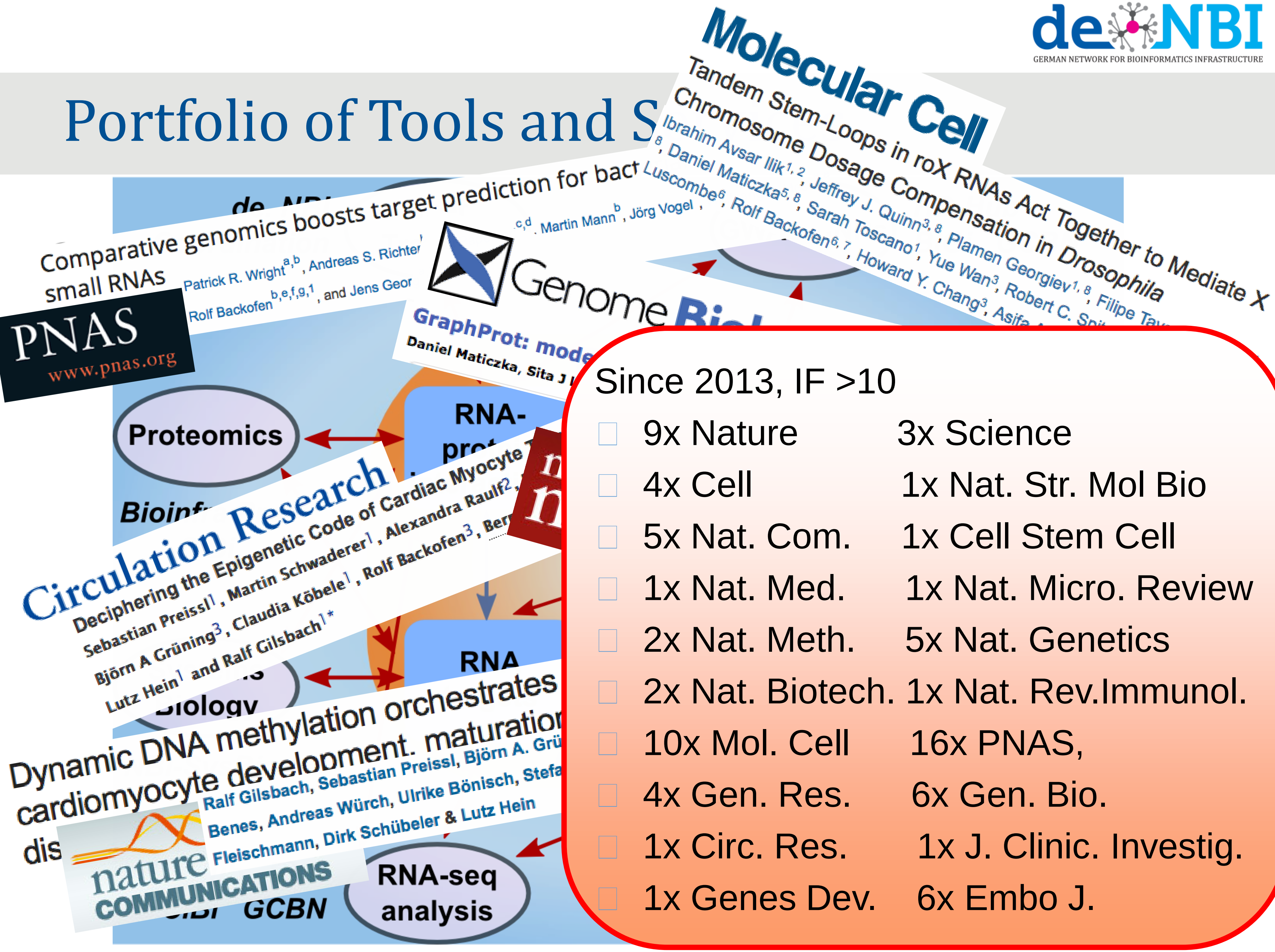
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

Portfolio of Tools and S



Molecular Cell
Tandem Stem-Loops in roX RNAs Act Together to Mediate X Chromosome Dosage Compensation in Drosophila
Ibrahim Avsar Ilik[1,2], Jeffrey J. Quinn[3,8], Plamen Georgiev[1,8], Filipe Tav [8], Daniel Maticzka[5,8], Sarah Toscano[1], Yue Wan[3], Robert C. Spi Luscombe[6], Rolf Backofen[6,7], Howard Y. Chang[3], Asifa A

Comparative genomics boosts target prediction for bact small RNAs
Patrick R. Wright[a,b], Andreas S. Richter [c,d], Martin Mann[b], Jörg Vogel, Rolf Backofen[b,e,f,g,1], and Jens Geor

PNAS
www.pnas.org

Genome Bio

GraphProt: mode
Daniel Maticzka, Sita J L

Circulation Research
Deciphering the Epigenetic Code of Cardiac Myocyte T
Sebastian Preissl[1], Martin Schwaderer[1], Alexandra Raulf[2], Björn A Grüning[3], Claudia Köbele[1], Rolf Backofen[3], Ber Lutz Hein[1] and Ralf Gilsbach[1]*

Dynamic DNA methylation orchestrates cardiomyocyte development, maturation dis
Ralf Gilsbach, Sebastian Preissl, Björn A. Grü Benes, Andreas Würch, Ulrike Bönisch, Stefa Fleischmann, Dirk Schübeler & Lutz Hein

nature COMMUNICATIONS

Since 2013, IF >10

- □ 9x Nature 3x Science
- □ 4x Cell 1x Nat. Str. Mol Bio
- □ 5x Nat. Com. 1x Cell Stem Cell
- □ 1x Nat. Med. 1x Nat. Micro. Review
- □ 2x Nat. Meth. 5x Nat. Genetics
- □ 2x Nat. Biotech. 1x Nat. Rev.Immunol.
- □ 10x Mol. Cell 16x PNAS,
- □ 4x Gen. Res. 6x Gen. Bio.
- □ 1x Circ. Res. 1x J. Clinic. Investig.
- □ 1x Genes Dev. 6x Embo J.

Service

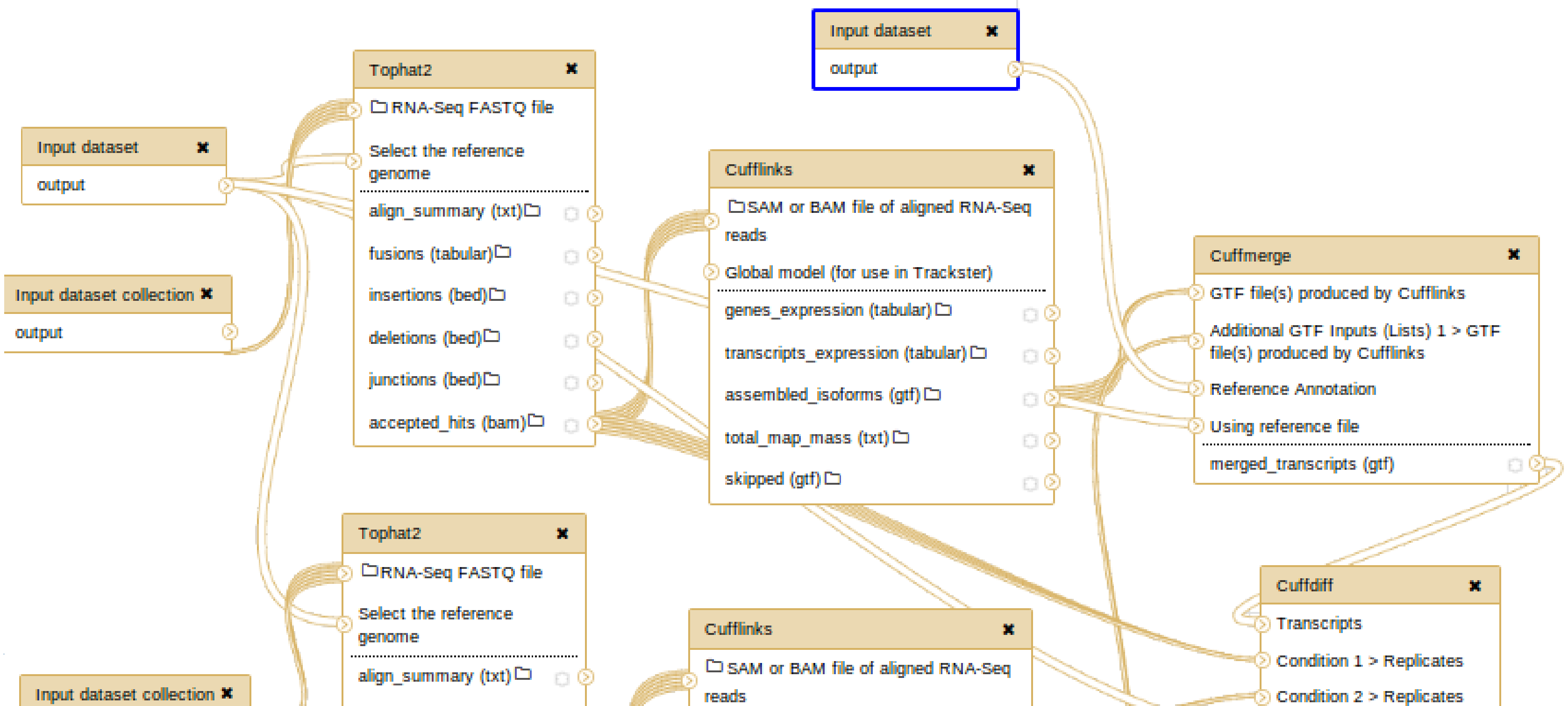
- knowledge transfer in RNA bioinformatics

- we can‘t do all analysis ourselves!
- solutions:
  - **Galaxy**
    - *standard workflows*
    - *FR server: 600+ users*
  - **virtualization**
    - *distribute computation*
  - **training, training, training**

Galaxy: Accessible Research

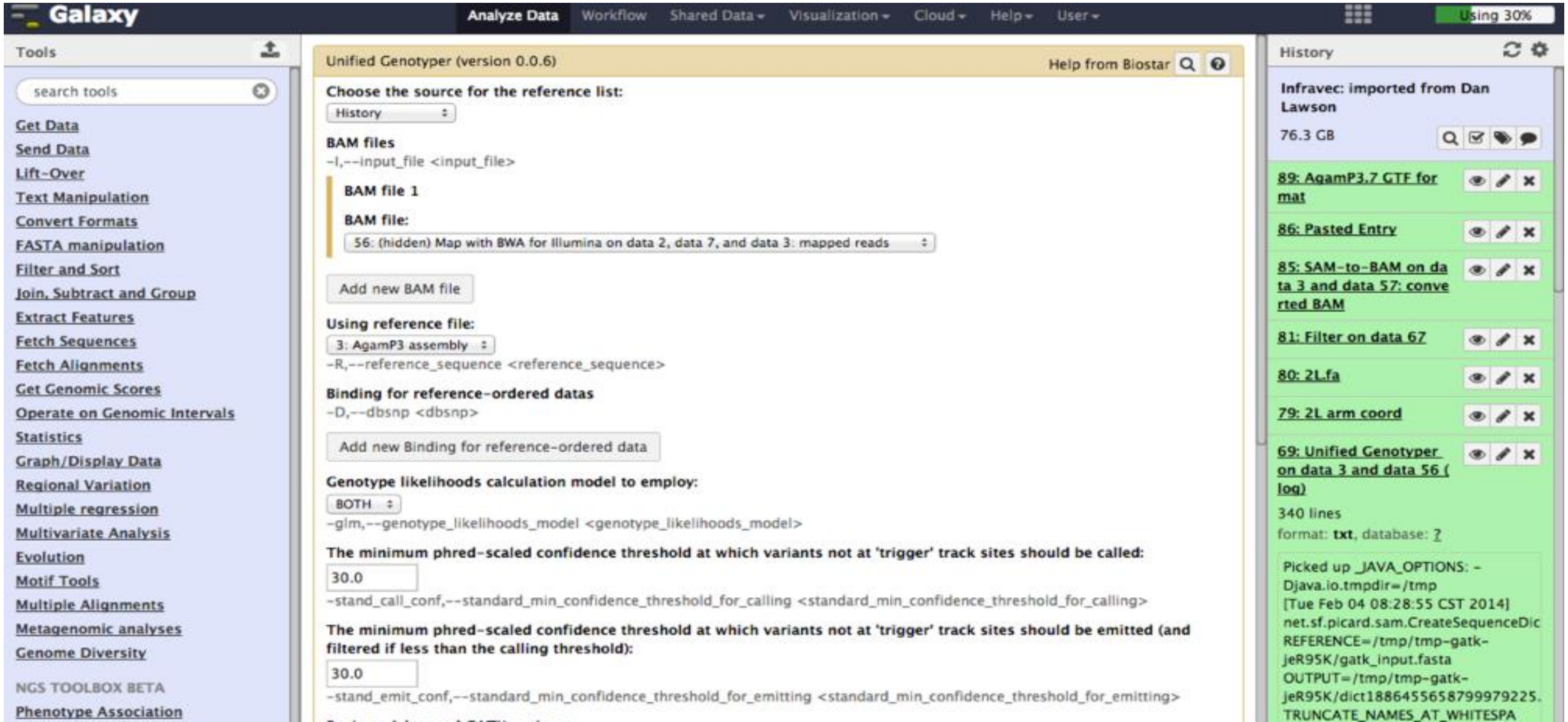
- reproducibility
  - experimental details
  - transparency
- scalable

- easy deployment
  - tools available to users
  - minimal installation overhead



What is Galaxy?

- Omics data analysis platform
- Accessible via normal web browser
- Every single step is recorded and reproducible
- 5000 citations so far
- 150.000 known user



Unified Genotyper (version 0.0.6)

Choose the source for the reference list:
History

BAM files
-I,--input_file <input_file>

BAM file 1

BAM file:
56: (hidden) Map with BWA for Illumina on data 2, data 7, and data 3: mapped reads

Using reference file:
3: AgamP3 assembly
-R,--reference_sequence <reference_sequence>

Binding for reference-ordered datas
-D,--dbsnp <dbsnp>

Genotype likelihoods calculation model to employ:
BOTH
-glm,--genotype_likelihoods_model <genotype_likelihoods_model>

The minimum phred-scaled confidence threshold at which variants not at 'trigger' track sites should be called:
30.0
-stand_call_conf,--standard_min_confidence_threshold_for_calling <standard_min_confidence_threshold_for_calling>

The minimum phred-scaled confidence threshold at which variants not at 'trigger' track sites should be emitted (and filtered if less than the calling threshold):
30.0
-stand_emit_conf,--standard_min_confidence_threshold_for_emitting <standard_min_confidence_threshold_for_emitting>

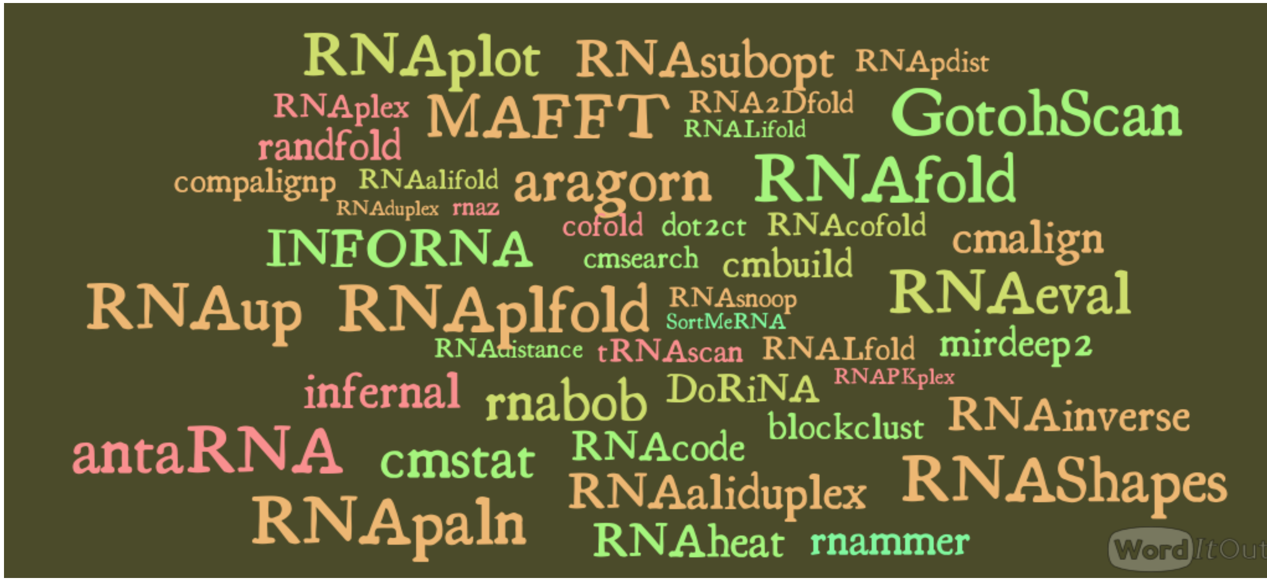
Infravec: imported from Dan Lawson
76.3 GB

89: AgamP3.7 GTF format
86: Pasted Entry
85: SAM-to-BAM on data 3 and data 57: converted BAM
81: Filter on data 67
80: 2L.fa
79: 2L arm coord
69: Unified Genotyper on data 3 and data 56 (log)
340 lines
format: txt, database: ?

```
Picked up _JAVA_OPTIONS: -
Djava.io.tmpdir=/tmp
[Tue Feb 04 08:28:55 CST 2014]
net.sf.picard.sam.CreateSequenceDic
REFERENCE=/tmp/tmp-gatk-
jeR95K/gatk_input.fasta
OUTPUT=/tmp/tmp-gatk-
jeR95K/dict1886455658799979225.
TRUNCATE_NAMES_AT_WHITESPA
```

Galaxy RNA Workbench

- already integrated: >4000 tools, ~800 by RBC
  - *We are one of 3 groups worldwide with direct Galaxy commit*
- RNA-specific tools and packages: **60+**



- RBC-specific:
  - *Vienna RNA package, doRiNA, Freiburger RNA Tools*

Services of Freiburg Galaxy Server

Workflows

General

- Build, Test, Use, Share, FAIR

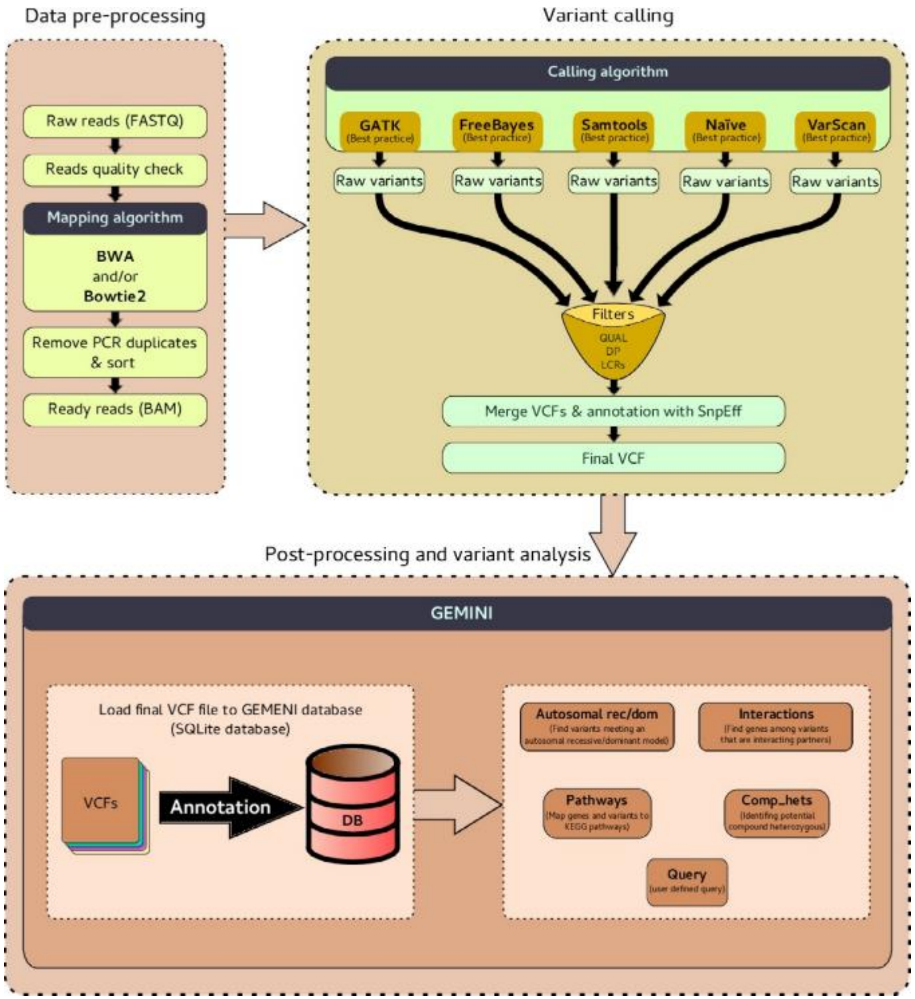
RNA-seq

- Quality Control
- Differential Expression Analysis

ChIP-seq, MethylC-seq

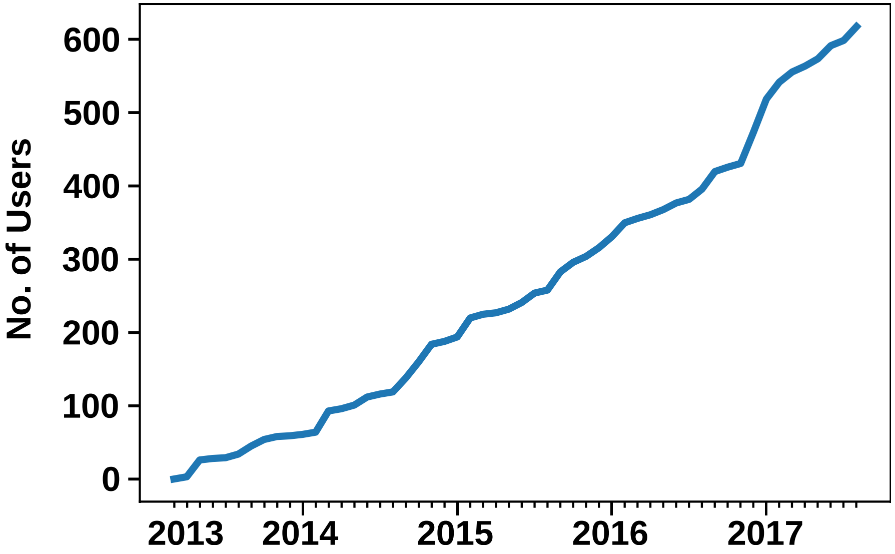
Additionally

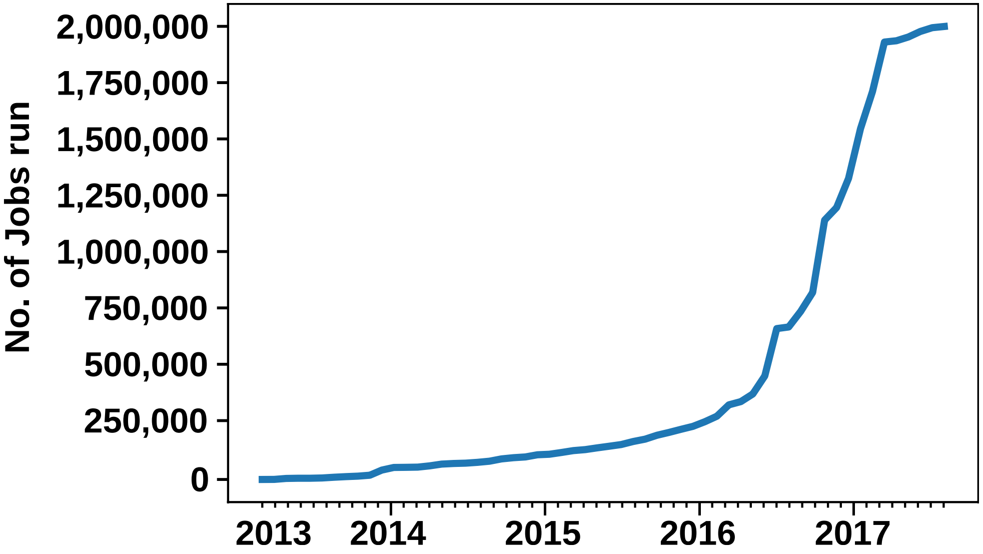
- Exome-seq
- Proteomics, Metabolomics
- Imaging, Textmining


Data pre-processing
Raw reads (FASTQ)
Reads quality check
Mapping algorithm
BWA
and/or
Bowtie2
Remove PCR duplicates & sort
Ready reads (BAM)
Variant calling
Calling algorithm
GATK (Best practice)
FreeBayes (Best practice)
Samtools (Best practice)
Naïve (Best practice)
VarScan (Best practice)
Raw variants
Raw variants
Raw variants
Raw variants
Raw variants
Filters
QUAL
DP
LCRs
Merge VCFs & annotation with SnpEff
Final VCF
Post-processing and variant analysis
GEMINI
Load final VCF file to GEMENI database (SQLite database)
VCFs
Annotation
DB
Autosomal rec/dom (Find variants meeting an autosomal recessive/dominant model)
Interactions (Find genes among variants that are interacting partners)
Pathways (Map genes and variants to KEGG pathways)
Comp_hets (Identifing potential compound heterozygous)
Query (user defined query)

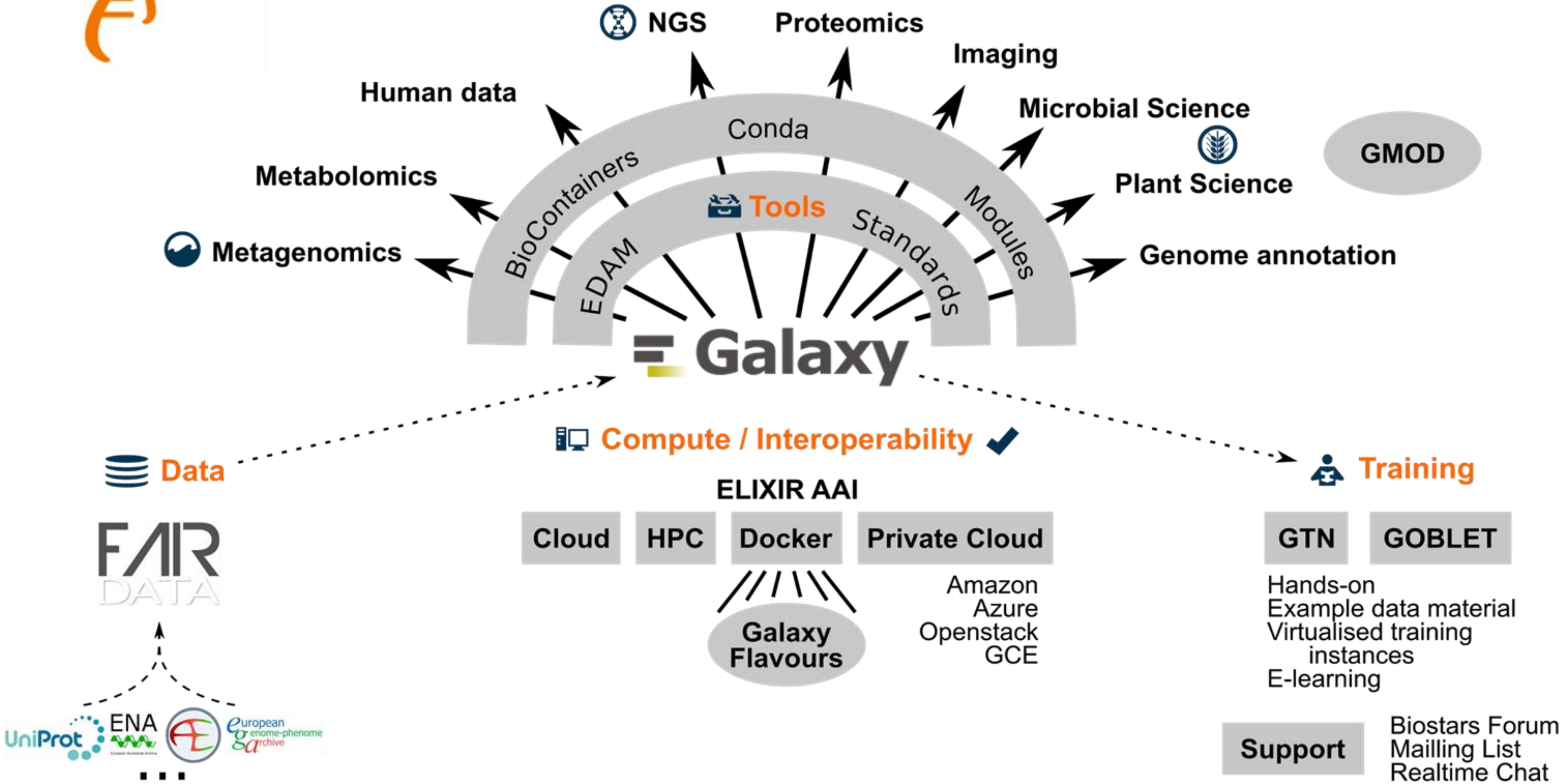
Impact Measurements

- users
- jobs run





Building a sustainable virtualized infrastructure



NGS

Proteomics

Imaging

Human data

Microbial Science

Plant Science

GMOD

Metabolomics

Genome annotation

Metagenomics

Conda

BioContainers

Modules

Tools

EDAM

Standards

Galaxy

Compute / Interoperability

ELIXIR AAI

Cloud

HPC

Docker

Private Cloud

Galaxy Flavours

Amazon
Azure
Openstack
GCE

Data

FAIR DATA

UniProt

ENA

European genome-phenome archive

...

Training

GTN

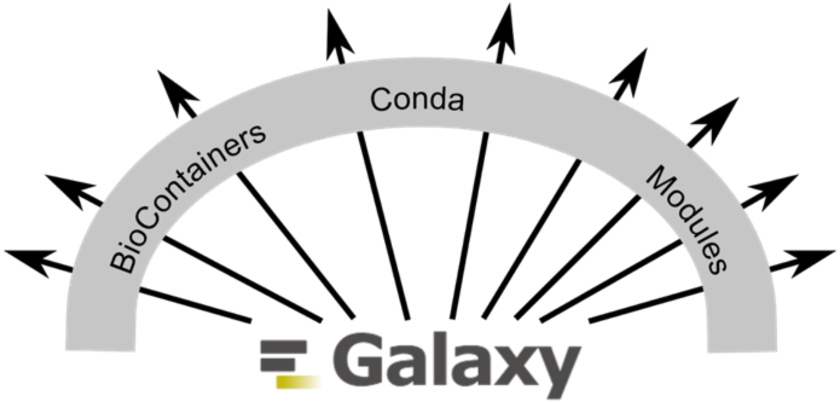
GOBLET

Hands-on
Example data material
Virtualised training instances
E-learning

Support

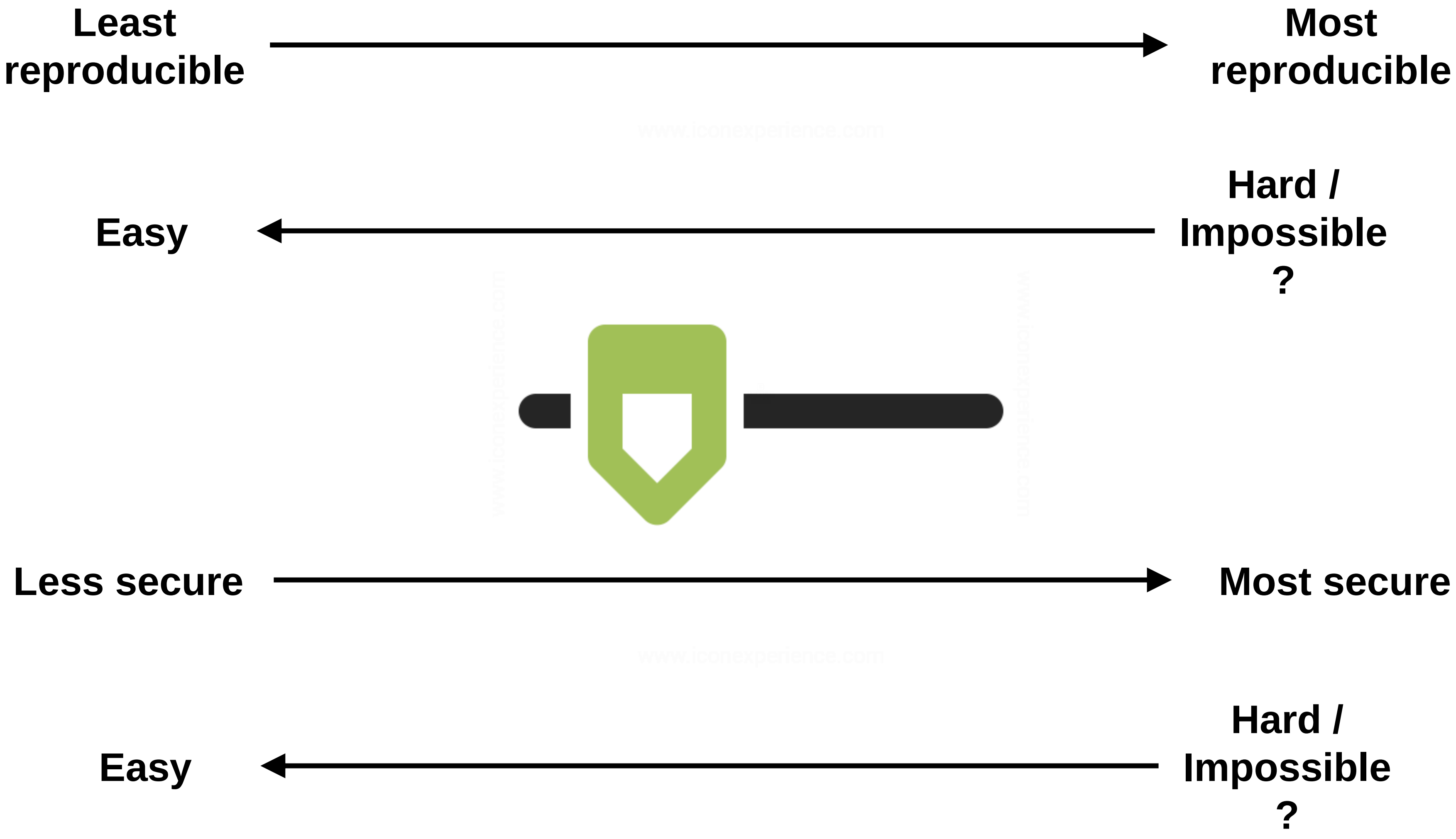
Biostars Forum
Mailling List
Realtime Chat

Building a secure virtualized infrastructure



- Isolate every single tool
  - from all other data
  - from other tools
  - from the Operating System
- Isolate the analysis workbench

adjustable reproducibility and security



Least reproducible → Most reproducible

Easy ← Hard / Impossible ?

Less secure → Most secure

Easy ← Hard / Impossible ?

Linux **Containers** for advanced isolation

If there is no standard*, embrace new technologies and make them interconvertible.

* Open Container Initiative (OCI) has released 1.0 of the container and runtime specification 3 days ago.

Sustainable community-based infrastructure

BIOCONDA

provides software for biomedical research.

- □ 14,400 commits on GitHub
- □ 287 contributors
- □ >2,700 packages

Biocontainers

provides system-agnostic executable environments for bioinformatics tools

- □ Uses Docker & rkt
- □ >2,800 Images
- □ Automatic builds from BioConda

Galaxy

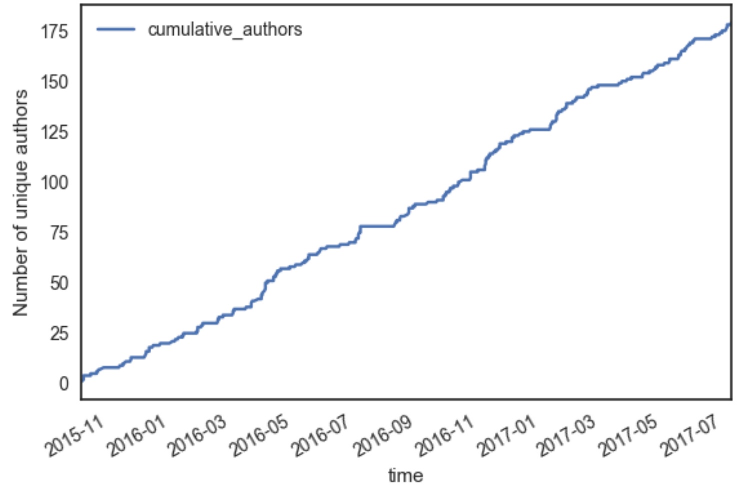
Galaxy is an open web-based platform for data intensive research

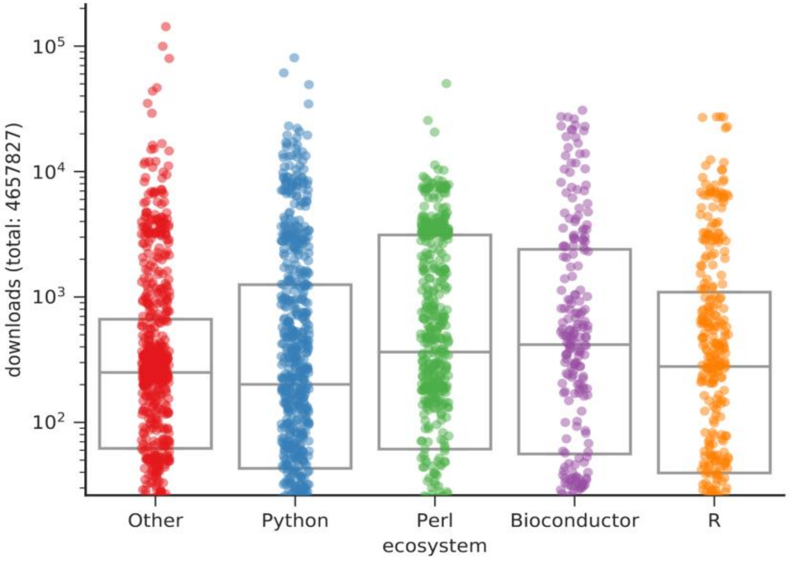
- □ 29,500 commits
- □ 163 contributors
- □ RBC is one of the biggest instances

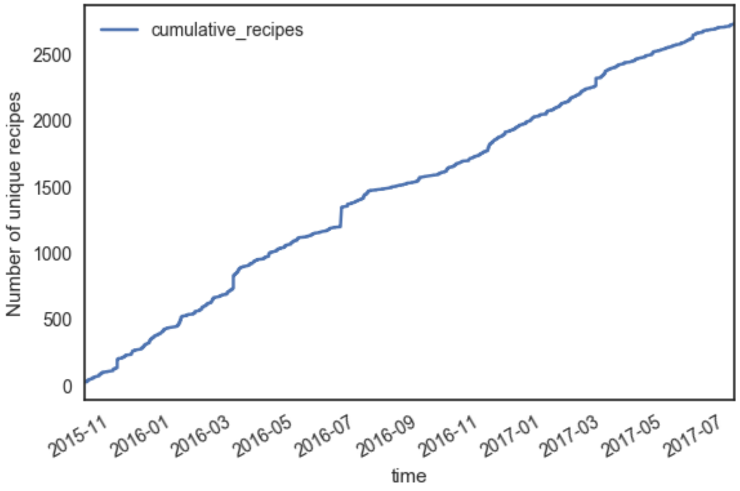
Our achievement: Cloud-Ready, all integrated into Galaxy

Biocontainers

- build out of **conda** package
- all tested automatically
- bioconda-utils / galaxy-lib







By Ryan Dale

Community

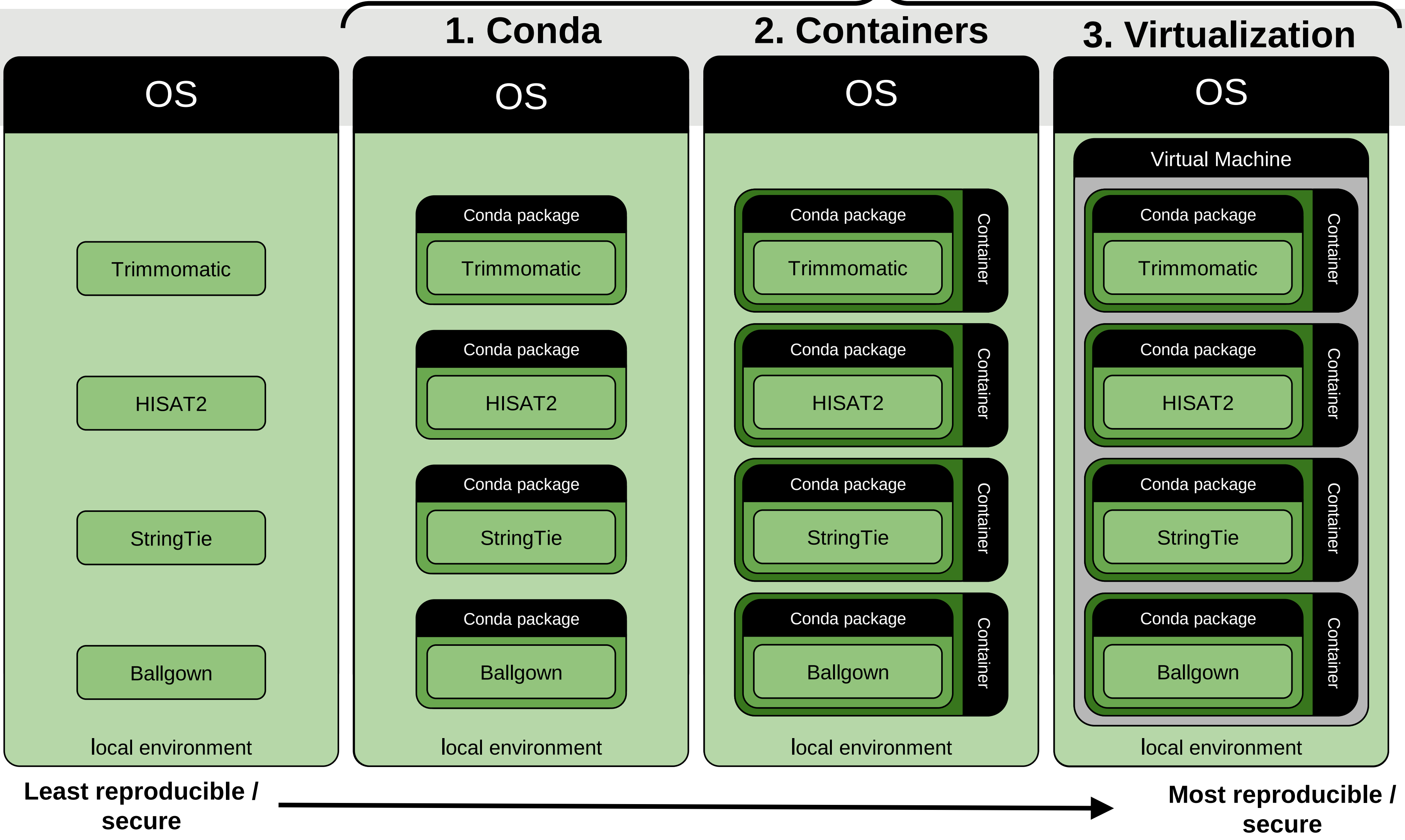
AstraZeneca
Galaxy Project, Johns Hopkins University
University Leipzig
Centre for High Performance Computing
University of Duisburg Essen
University Paris-Est
Harvard School of Public Health
ImmPort
Drexel University
University of Freiburg
Penn State
Erasmus Medical Center, Rotterdam, The Netherlands
Institute for Basic Science
University of Utah
University of Michigan
University of Oxford
Science for Life Labs
NYU Abu Dhabi Center for Genomics and Systems Biology
NIHR BRC-MH, KCL IoPPN & Farr UCL
SciLifeLab
CGAT
MDC
broadinstitute
University of Nebraska
University of Wisconsin-Madison
UCSD
PNNL
National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK), NIH
Penn State University
Lund University Cancer Center
University of Southern California
George Washington University / Goecks' Lab
NSHA
Science for Life Laboratory
Netherlands Cancer Institute (NKI-AVL)
Institute of Cancer Research and Molecular Medicine, NTNU
Massachusetts General Hospital/ Harvard Medical School
Johns Hopkins University
Rutgers University
AbVitro, Inc.
Harvard Chan Bioinformatics Core
University of California
Centrum Wiskunde & Informatica
Wolfson Wohl Cancer Research Centre
Science for Lify Laboratory
Altius Institute for Biomedical Sciences
UESC
MPI for Biophysical Chemistry
Stony Brook University
TGAC
ABiMS - UPMC-CNRS - Station Biologique de Roscoff
The McDonnell Genome Institute at Washington University
University of Birmingham
Harvard Chan School of Public Health
Institut Pasteur
University of Pennsylvania School of Medicine
UMASS Medical School
CEA
Wellcome Trust Centre for Human Genetics

by Johannes Köster

330 Contributors ***6200 merged PR***

in 2 years

Reproducibility stack



1. Conda

2. Containers

3. Virtualization

OS

Trimmomatic

HISAT2

StringTie

Ballgown

local environment

OS

Conda package
Trimmomatic

Conda package
HISAT2

Conda package
StringTie

Conda package
Ballgown

local environment

OS

Container
Conda package
Trimmomatic

Container
Conda package
HISAT2

Container
Conda package
StringTie

Container
Conda package
Ballgown

local environment

OS

Virtual Machine

Container
Conda package
Trimmomatic

Container
Conda package
HISAT2

Container
Conda package
StringTie

Container
Conda package
Ballgown

local environment

Least reproducible / secure

Most reproducible / secure

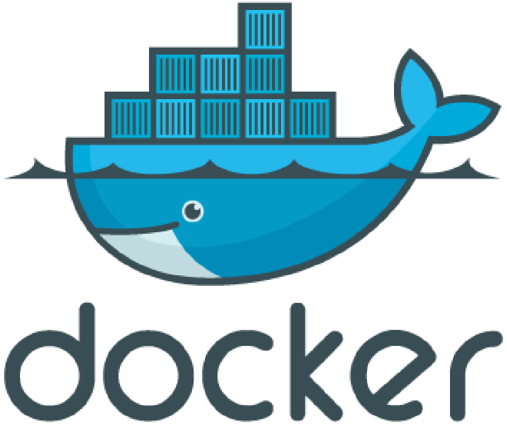
```
> git clone hisat2
> make
> sudo make install
> hisat2 --version
```

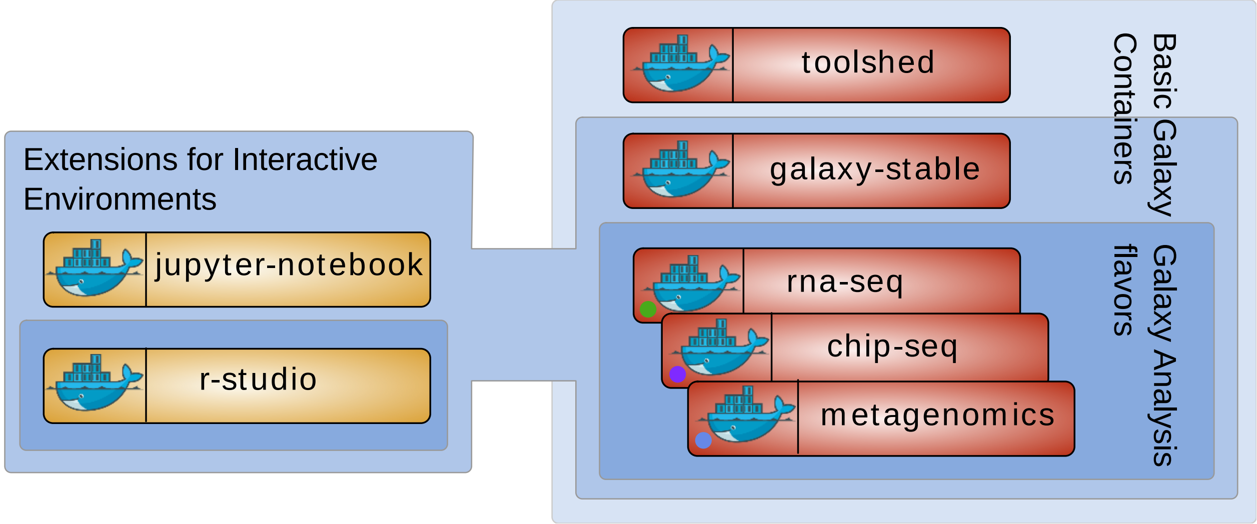
```
> conda install hisat2
> hisat2 --version
```

```
> docker run --rm
quay.io/biocontainers/
hisat2 --version
```

Galaxy in Docker

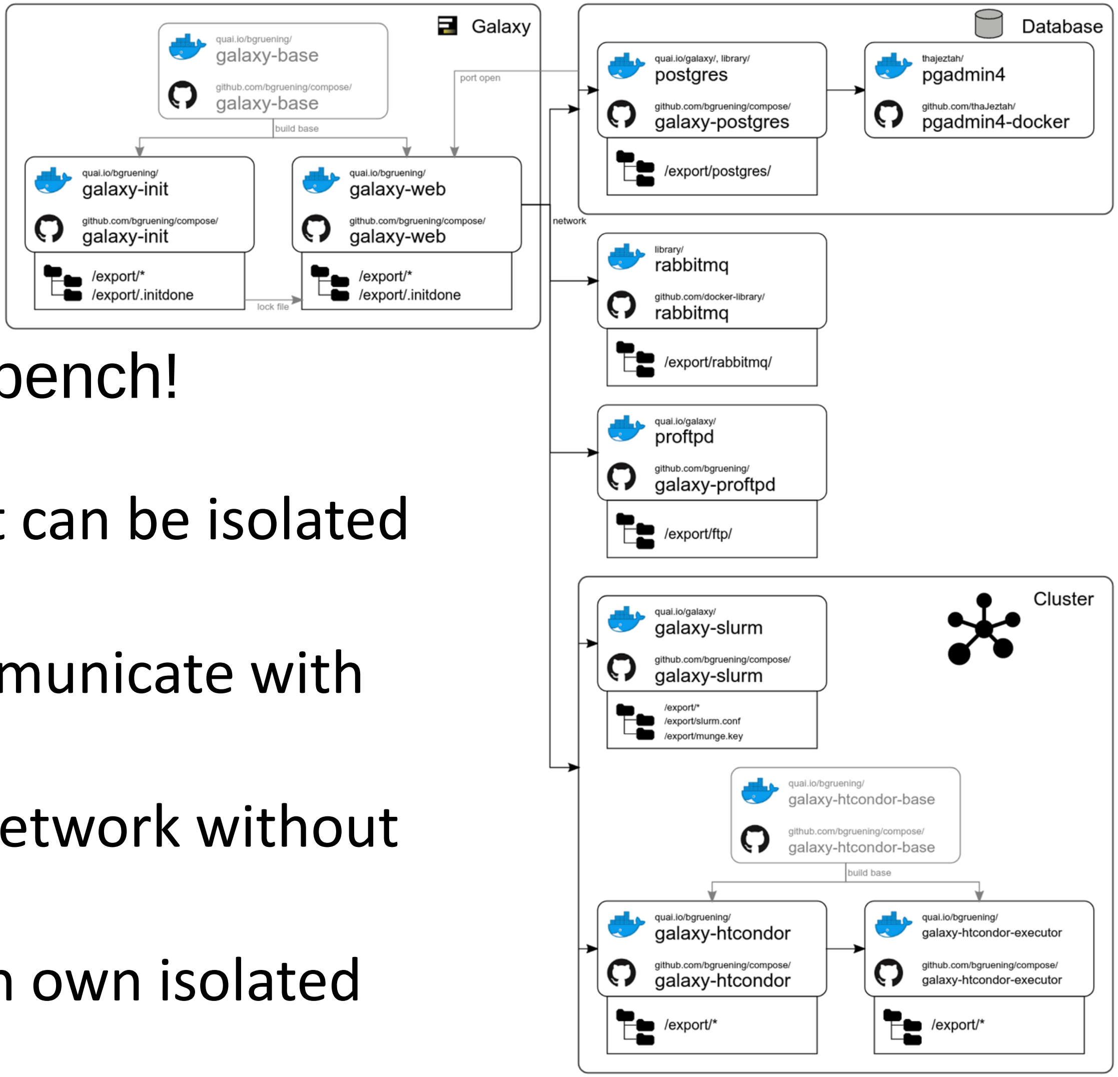
- Idea: tools to data, not data to tools -> virtualization





- drag & drop based Galaxy flavor generator
- Widely used: >28.000 downloads, ELIXIR (Tjenester for Sensitive Data 2.0 Norway), Cancer Center Amsterdam …

Galaxy in Docker: Microservices

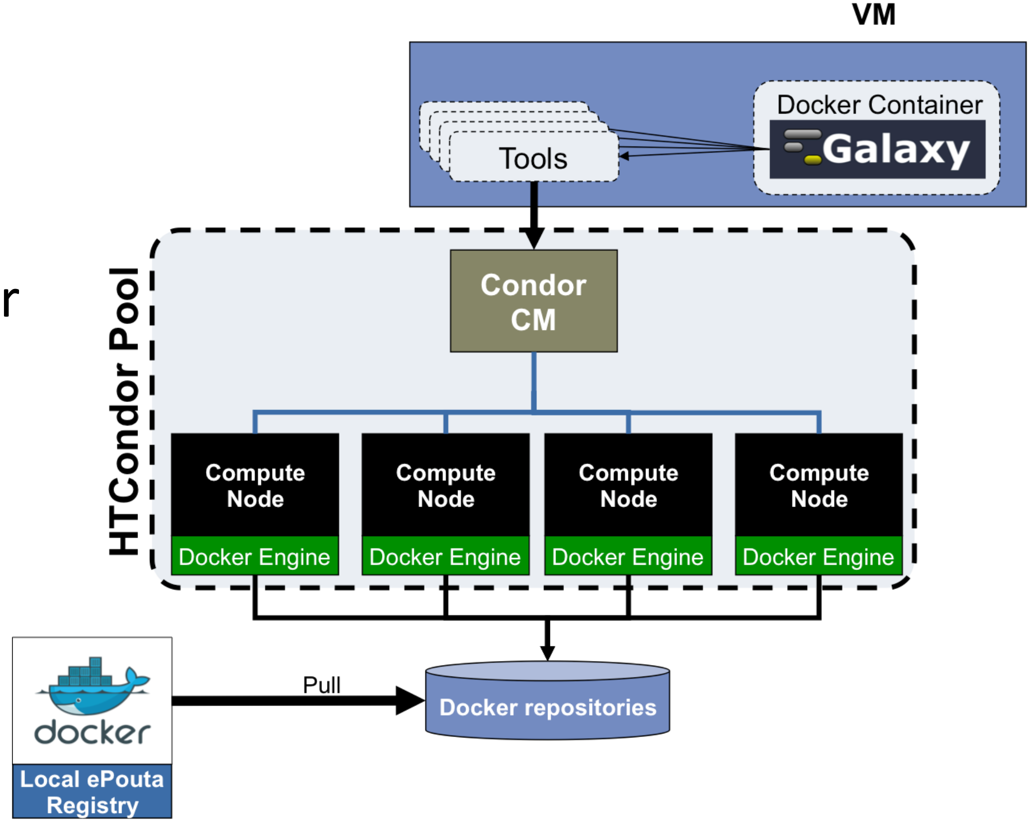


Isolate the analysis workbench!

- Every single component can be isolated and hardened
- Microservices that communicate with each other
- Can run in an isolated network without Internet
- executes analysis jobs in own isolated containers

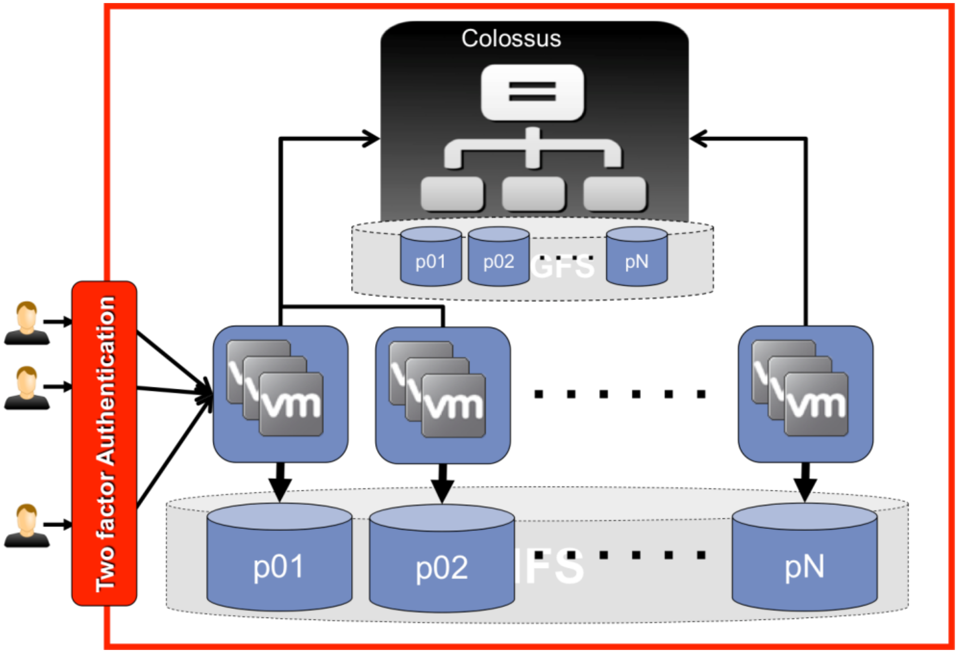
Real world deployments with sensitive data: Version 1

- central Galaxy server
- job submission to a hardened HTCondor pool
- Galaxy server runs in Docker
- every single job runs in Docker
- every job is isolated from all other data
- one job has only read access to the input data it needs
- entire stack can run in an isolated network

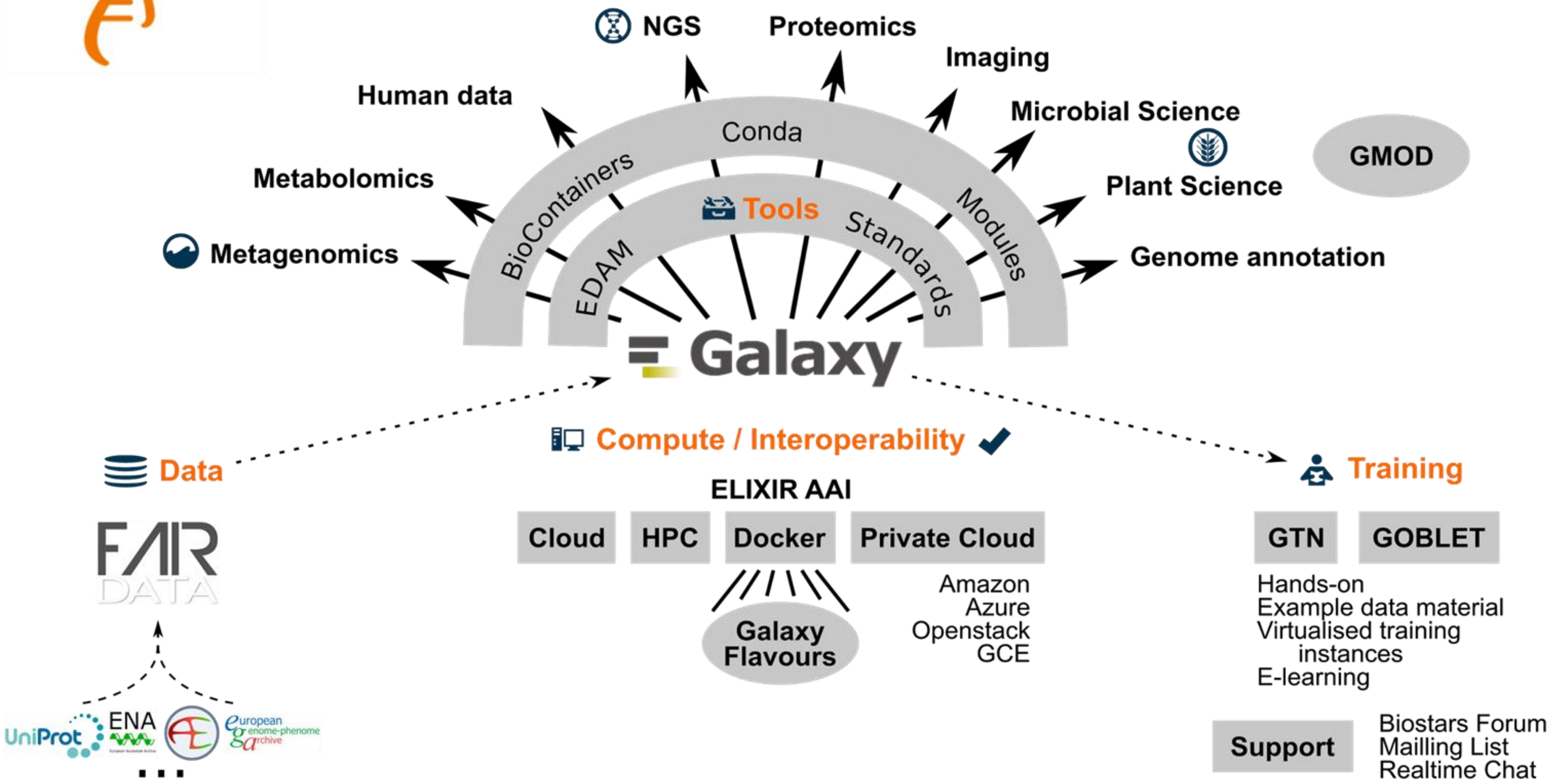


Real world deployments with sensitive data: Version 2

- 2 factor Authentication into virtual machines (VM)
- VMs are isolated
- every VM starts its own Galaxy instance
- data is saved encrypted to the local network
- Users can not interact with each other (share workflows, histories etc ...)
- every VM can run Version 1 as well



Building a sustainable infrastructure



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Human data

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FAIR DATA

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European Genome-phenome Archive

...

Compute / Interoperability ✓

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HPC

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Private Cloud

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Amazon
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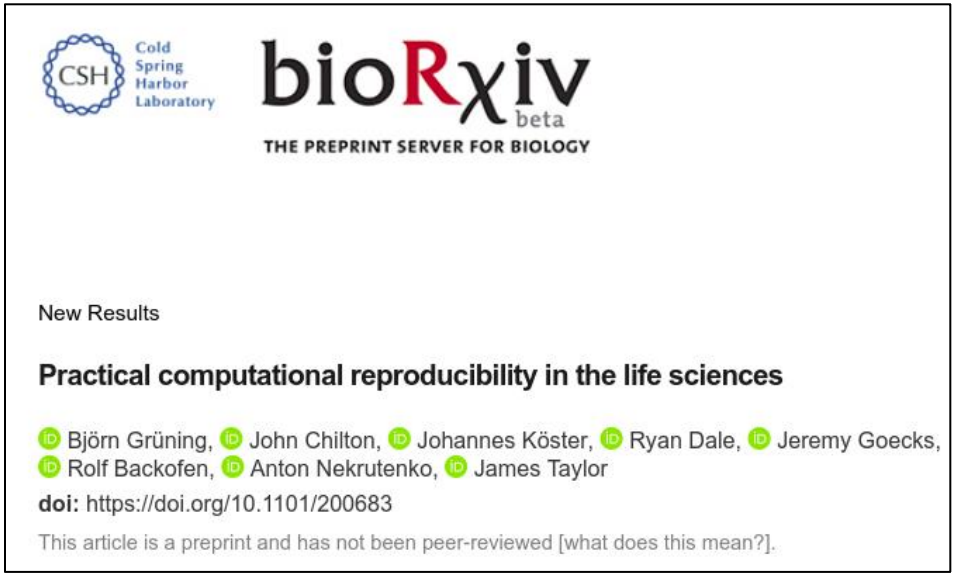


Cold Spring Harbor Laboratory
bioRχiv beta
THE PREPRINT SERVER FOR BIOLOGY

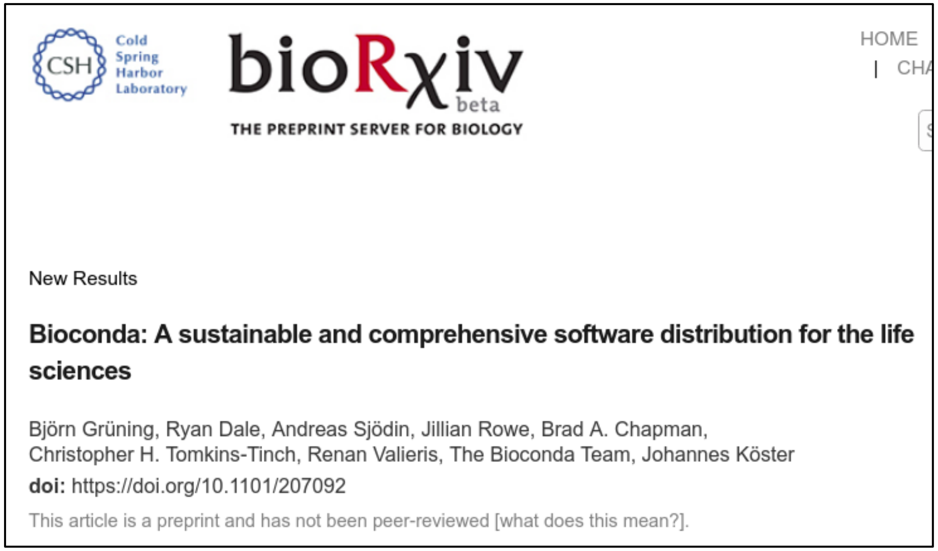
New Results

Practical computational reproducibility in the life sciences

Björn Grüning, John Chilton, Johannes Köster, Ryan Dale, Jeremy Goecks, Rolf Backofen, Anton Nekrutenko, James Taylor

doi: https://doi.org/10.1101/200683

This article is a preprint and has not been peer-reviewed [what does this mean?].



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HOME
| CHA

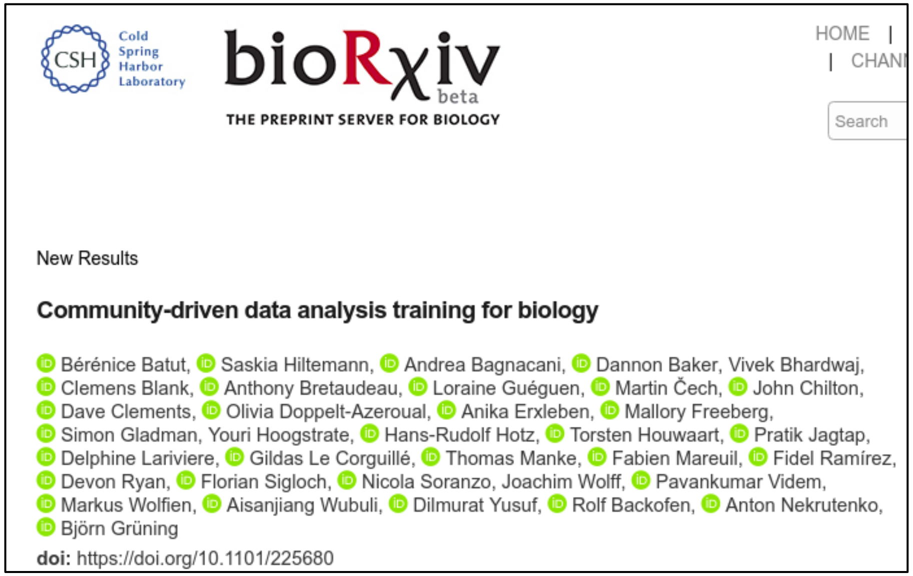
New Results

Bioconda: A sustainable and comprehensive software distribution for the life sciences

Björn Grüning, Ryan Dale, Andreas Sjödin, Jillian Rowe, Brad A. Chapman, Christopher H. Tomkins-Tinch, Renan Valieris, The Bioconda Team, Johannes Köster

doi: https://doi.org/10.1101/207092

This article is a preprint and has not been peer-reviewed [what does this mean?].



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HOME |
| CHAN
Search

New Results

Community-driven data analysis training for biology

Bérénice Batut, Saskia Hiltemann, Andrea Bagnacani, Dannon Baker, Vivek Bhardwaj, Clemens Blank, Anthony Bretaudeau, Loraine Guéguen, Martin Čech, John Chilton, Dave Clements, Olivia Doppelt-Azeroual, Anika Erxleben, Mallory Freeberg, Simon Gladman, Youri Hoogstrate, Hans-Rudolf Hotz, Torsten Houwaart, Pratik Jagtap, Delphine Lariviere, Gildas Le Corguillé, Thomas Manke, Fabien Mareuil, Fidel Ramírez, Devon Ryan, Florian Sigloch, Nicola Soranzo, Joachim Wolff, Pavankumar Videm, Markus Wolfien, Aisanjiang Wubuli, Dilmurat Yusuf, Rolf Backofen, Anton Nekrutenko, Björn Grüning

doi: https://doi.org/10.1101/225680

Conclusion

- Galaxy
  - Every single step is recorded and reproducible
  - 5000 citations so far, 150.000 known user
  - Freiburg Server: largest in Europe with 600 users.

- Deployments with Sensitive data.
  - Reproduciblity stack:

    OS -> Packages -> Containers -> VM
  - Galaxy Docker Flavour Concept
  - Community-based effort:

    Bioconda, Biocontainers & Galaxy

Thanks!

Galaxy PROJECT

de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

docker

TRAVIS

Yasset Perez-Riverol
Felipe Leprevost ...

elixir

de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

GitHub

Björn Grüning & the RBC team

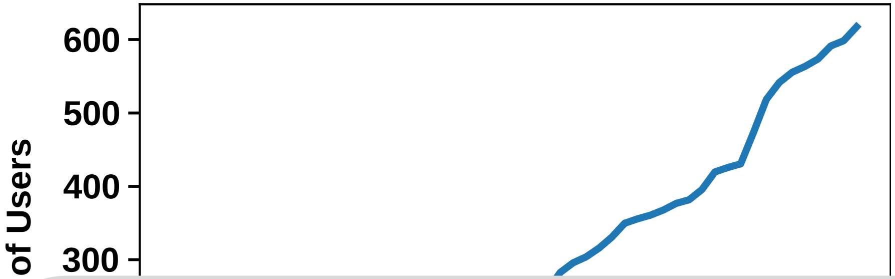
BIOCONDA®

Johannes Köster
Ryan Dale ...

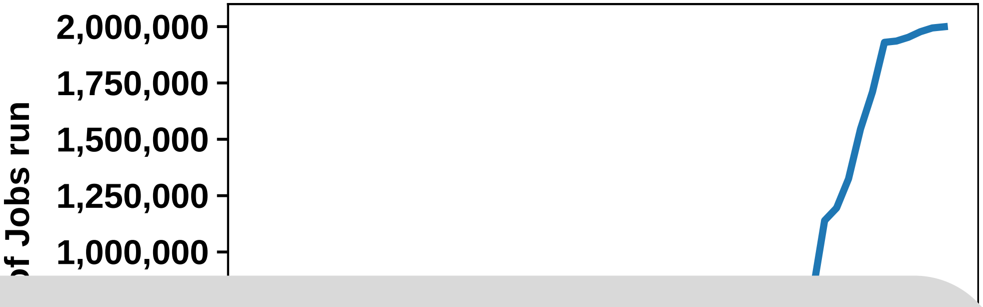
Thank you for your attention

Impact Measurements

- users



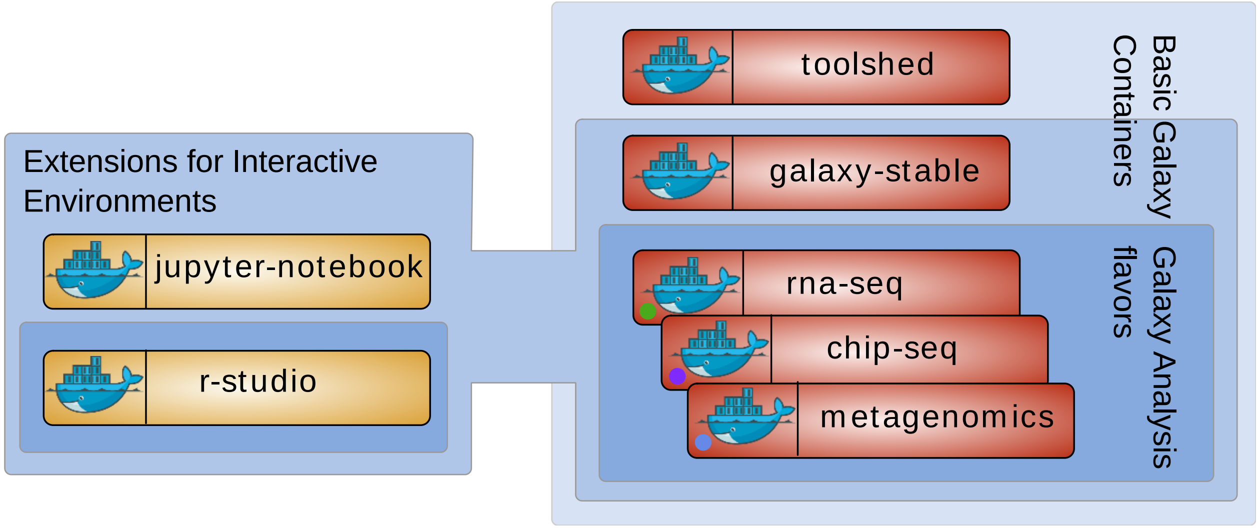
- jobs run



Measurement (from SIG2 report)	Total
Citations/links to website/acknowledgements	9,589
Supporttickets / GitHub issues	4,942
Number of downloads	3,474,974
Web app & database hits	170,411

Overcoming computational limitations

- Idea: tools to data, not data to tools -> virtualization



Extensions for Interactive Environments

jupyter-notebook

r-studio

toolshed

galaxy-stable

rna-seq

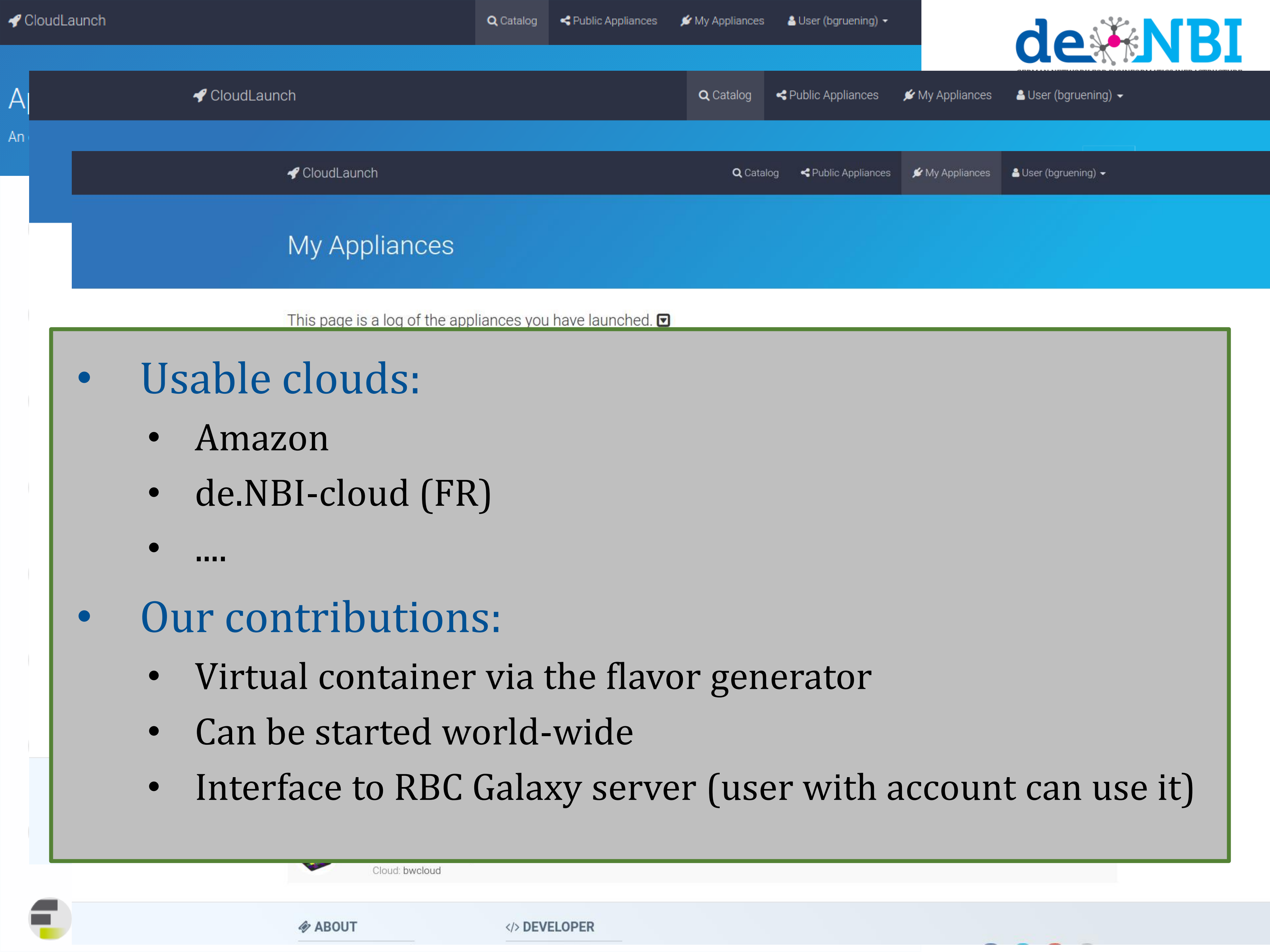
chip-seq

metagenomics

Basic Galaxy Containers

Galaxy Analysis flavors

- drag & drop based Galaxy flavor generator
- Widely used: >28.000 downloads, ELIXIR (Tjenester for Sensitive Data 2.0 Norway), Cancer Center Amsterdam …



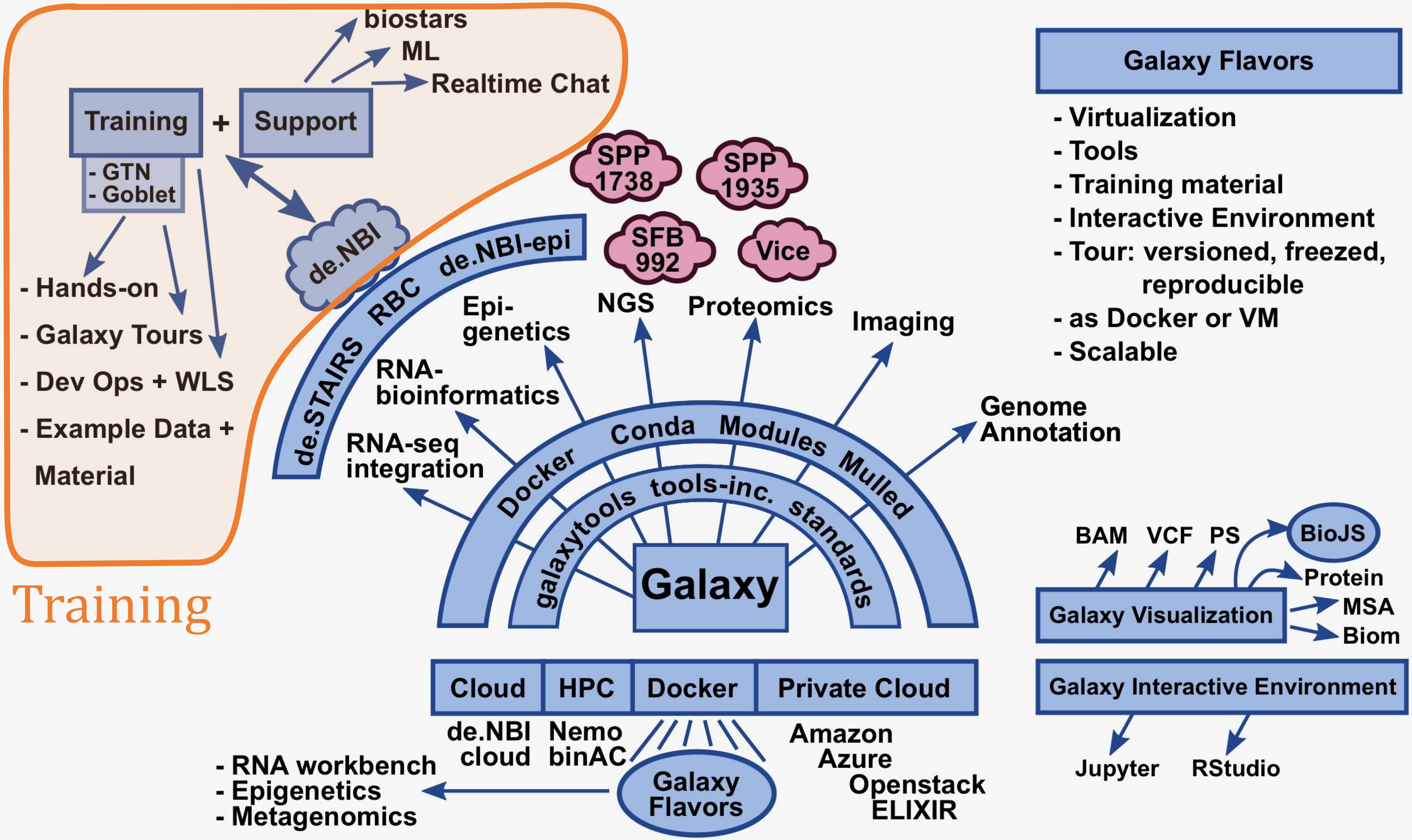
My Appliances

This page is a log of the appliances you have launched.

Cloud: bwcloud

- **Usable clouds:**
  - Amazon
  - de.NBI-cloud (FR)
  - ….
- **Our contributions:**
  - Virtual container via the flavor generator
  - Can be started world-wide
  - Interface to RBC Galaxy server (user with account can use it)

Masterplan



Training + Support

- GTN
- Goblet

biostars

ML

Realtime Chat

- Hands-on
- Galaxy Tours
- Dev Ops + WLS
- Example Data + Material

Training

de.NBI

de.STAIRS RBC de.NBI-epi

SPP 1738

SPP 1935

SFB 992

Vice

Epi-genetics

NGS

Proteomics

Imaging

RNA-bioinformatics

RNA-seq integration

Genome Annotation

Docker Conda Modules Mulled

galaxytools tools-inc. standards

Galaxy

Cloud | HPC | Docker | Private Cloud

de.NBI cloud

Nemo binAC

Amazon
Azure
Openstack
ELIXIR

Galaxy Flavors

- RNA workbench
- Epigenetics
- Metagenomics

Galaxy Flavors

- Virtualization
- Tools
- Training material
- Interactive Environment
- Tour: versioned, freezed, reproducible
- as Docker or VM
- Scalable

Galaxy Visualization

BAM VCF PS

BioJS

Protein

MSA

Biom

Galaxy Interactive Environment

Jupyter RStudio

Training by RBC

- 28 training courses, ~500 participants
- 12 locations across the world

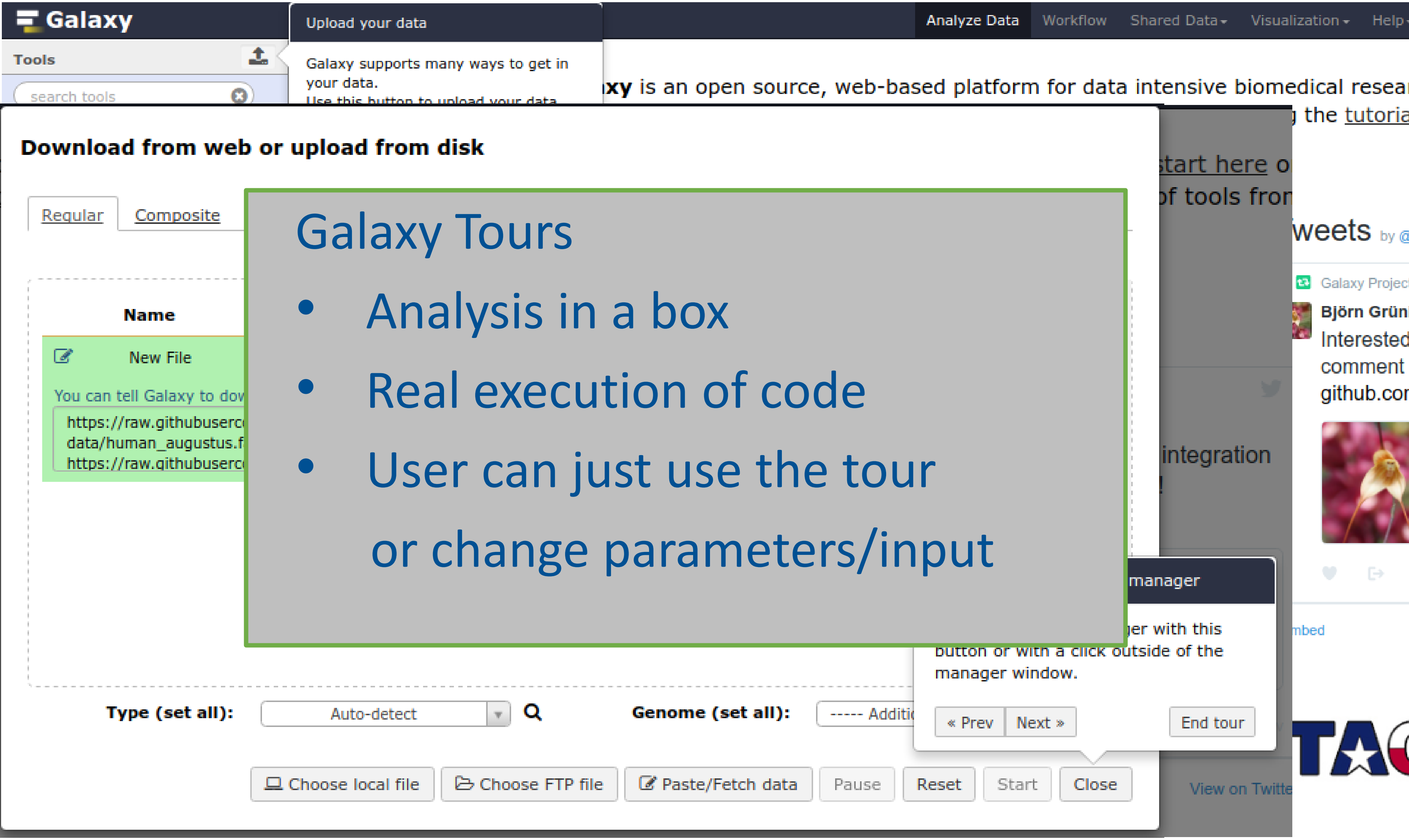
2016 events

19th – 20th Jan	ELIXIR EDAM codefest	Freiburg
22nd – 26th Feb	Galaxy HTS data analysis workshop	Freiburg
07th – 08th Mar	RAD-Seq tools and workflows codefest	Online
04th Apr	Conda codefest	Online
06th – 07th Apr	Galaxy DevOps workshop	Heidelberg
27th – 29th Apr	HPC workshop	Oslo, Norway
25th – 29th Jun	Galaxy Community Conference workshop	Indiana
27th Jul	RBC Kick-Off meeting	Freiburg
19th – 23rd Sep	Galaxy HTS data analysis workshop	Freiburg
27th – 28th Sep	GalaxyP codefest	Online
06th – 07th Oct	Galaxy training material codefest	Online
20th – 21st Oct	Swiss German Galaxy workshop	Freiburg
24th – 26th Oct	NETTAB hackathon	Rom, Italy
02nd – 03rd Nov	BioConda codefest	Online
30th Nov – 01st Dec	Galaxy Docker workshop	Barcelona, Spain
01st – 02nd Dec	FAIRDOM/de.NBI Foundry workshop	Frankfurt
15th – 16th Dec	Galaxy RNA-seq data analysis workshop	Freiburg

2017 events

09th – 10th Jan	Galaxy QIIME codefest	Online
16th – 19th Jan	European Galaxy developer workshop	Strasbourg, France

Galaxy Tours – Bioinformatics Training 2.0



Upload your data

Galaxy supports many ways to get in your data.
Use this button to upload your data.

xy is an open source, web-based platform for data intensive biomedical resea

the tutoria

start here o

of tools fron

weets by @

Galaxy Projec

Björn Grün

Interested

comment

github.cor

integration

Download from web or upload from disk

You can tell Galaxy to dow

https://raw.githubuserco
data/human_augustus.f
https://raw.githubuserco

manager

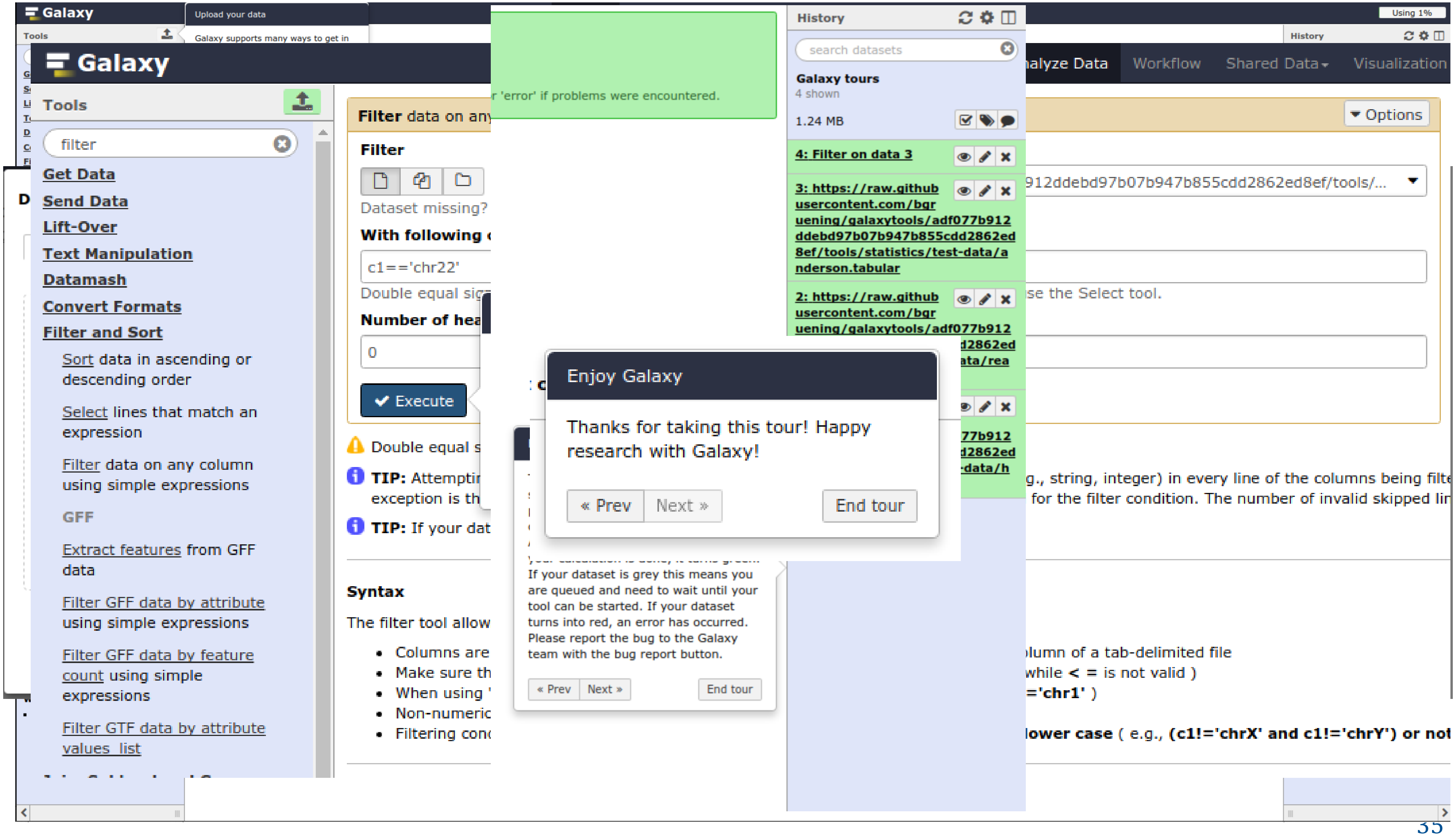
er with this button or with a click outside of the manager window.

Galaxy Tours

- Analysis in a box
- Real execution of code
- User can just use the tour or change parameters/input

Thank you for your attention

Galaxy Tours – Bioinformatics Training 2.0



'error' if problems were encountered.

Tools

filter

- Get Data
- Send Data
- Lift-Over
- Text Manipulation
- Datamash
- Convert Formats
- Filter and Sort
  - Sort data in ascending or descending order
  - Select lines that match an expression
  - Filter data on any column using simple expressions
- GFF
  - Extract features from GFF data
  - Filter GFF data by attribute using simple expressions
  - Filter GFF data by feature count using simple expressions
  - Filter GTF data by attribute values_list

Filter data on any

Filter

Dataset missing?

With following

c1=='chr22'

Double equal sig

Number of hea

0

✓ Execute

Double equal s

TIP: Attemptir exception is th

TIP: If your dat

Syntax

The filter tool allow

- Columns are
- Make sure th
- When using '
- Non-numeric
- Filtering conc

History

search datasets

Galaxy tours
4 shown

1.24 MB

4: Filter on data 3

3: https://raw.githubusercontent.com/bgruening/galaxytools/adf077b912ddebd97b07b947b855cdd2862ed8ef/tools/statistics/test-data/anderson.tabular

2: https://raw.githubusercontent.com/bgruening/galaxytools/adf077b912 ...d2862ed ...ata/rea

912ddebd97b07b947b855cdd2862ed8ef/tools/...

se the Select tool.

g., string, integer) in every line of the columns being filte for the filter condition. The number of invalid skipped lin

olumn of a tab-delimited file
while < = is not valid)
='chr1')

lower case (e.g., (c1!='chrX' and c1!='chrY') or not

Enjoy Galaxy

Thanks for taking this tour! Happy research with Galaxy!

« Prev | Next » | End tour

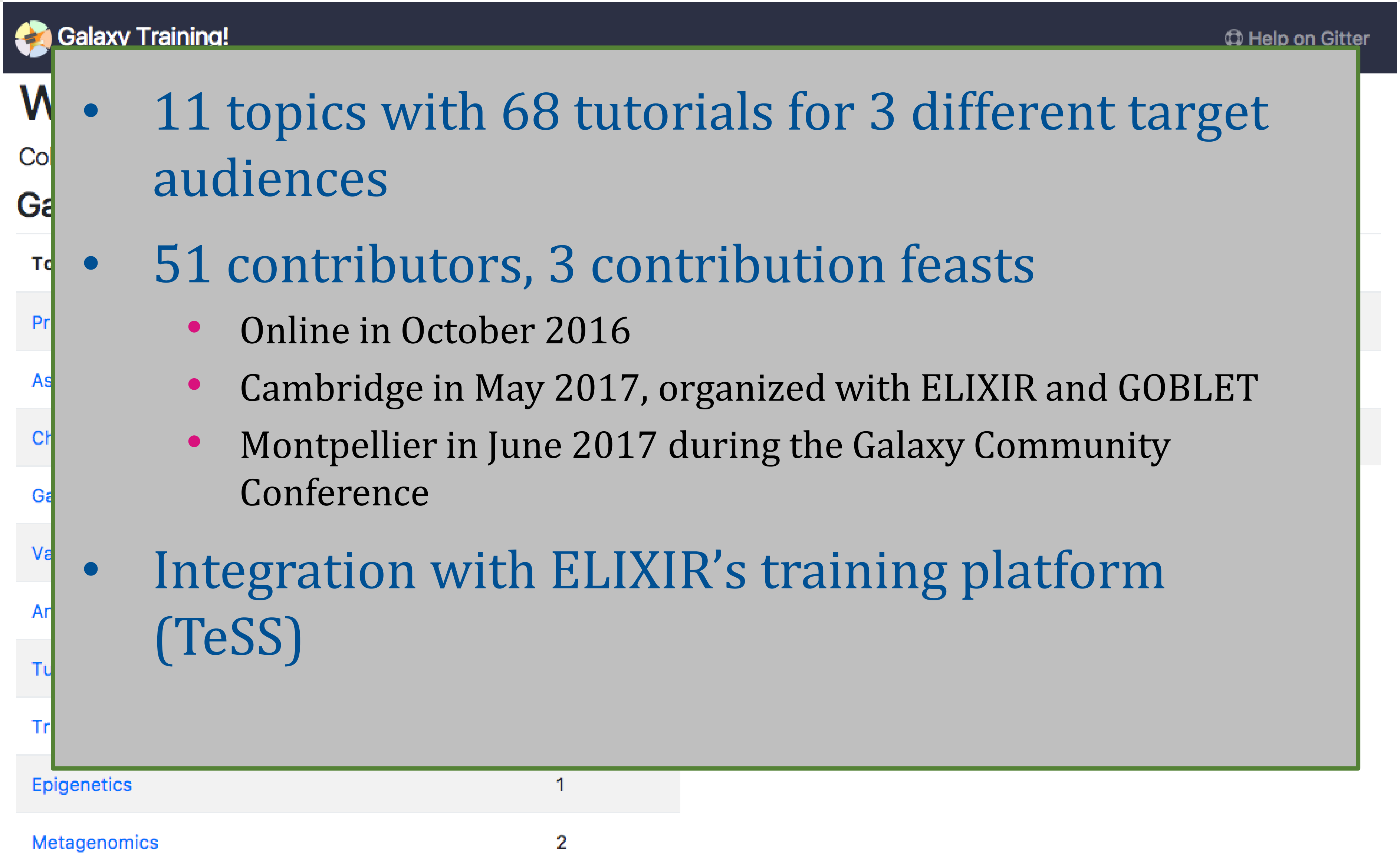
If your dataset is grey this means you are queued and need to wait until your tool can be started. If your dataset turns into red, an error has occurred. Please report the bug to the Galaxy team with the bug report button.

« Prev | Next » | End tour

De.NBI cloud

- Recently opened: Supercomputer NEMO
    - **15,000** cores, **position 214** in TOP 500
- we got
    - **1,500,000 €** hardware extension for GALAXY
    - Additionally **5% of existing NEMO resources**
    - IMPORTANT: **cloud knowledge of BW-CLOUD**

Trainings -Material



Epigenetics	1
Metagenomics	2

- 11 topics with 68 tutorials for 3 different target audiences
- 51 contributors, 3 contribution feasts
  - Online in October 2016
  - Cambridge in May 2017, organized with ELIXIR and GOBLET
  - Montpellier in June 2017 during the Galaxy Community Conference
- Integration with ELIXIR’s training platform (TeSS)

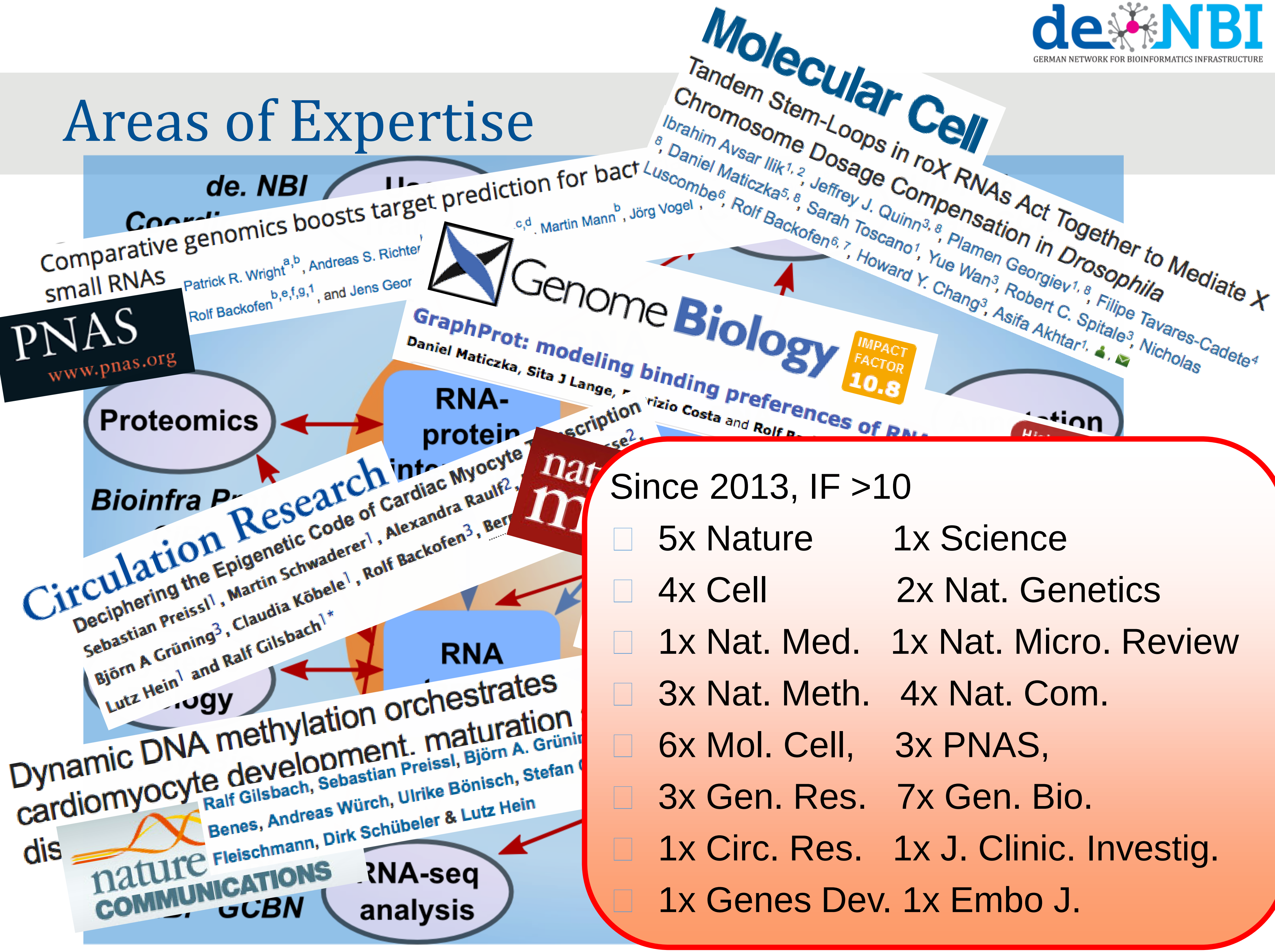
Conclusion

- RNA-Bioinformatics Center (RBC):
  - RNA-mediated post-transcriptional regulation
  - integrates all international renowned German RNA bioinformatics groups

- Important aspects of our service:
  - RNA workbench based on Galaxy
  - Virtualization for distribution of computational burden
  - Strong interaction with ELIXIR
  - training, training, training (user, user, user)

future: eLearning!!

Areas of Expertise



Molecular Cell

Tandem Stem-Loops in roX RNAs Act Together to Mediate X Chromosome Dosage Compensation in Drosophila

Ibrahim Avsar Ilik[1, 2], Jeffrey J. Quinn[3, 8], Plamen Georgiev[1, 8], Filipe Tavares-Cadete[4, 8], Daniel Maticzka[5, 8], Sarah Toscano[1], Yue Wan[3], Robert C. Spitale[3], Nicholas Luscombe[6], Rolf Backofen[6, 7], Howard Y. Chang[3], Asifa Akhtar[1],

Comparative genomics boosts target prediction for bact small RNAs

Patrick R. Wright[a,b], Andreas S. Richter, Martin Mann[b], Jörg Vogel, Rolf Backofen[b,e,f,g,1], and Jens Geor

PNAS

www.pnas.org

Genome Biology

IMPACT FACTOR 10.8

GraphProt: modeling binding preferences of RN

Daniel Maticzka, Sita J Lange, F rizio Costa and Rolf B

Circulation Research

Deciphering the Epigenetic Code of Cardiac Myocyte Transcription

Sebastian Preissl[1], Martin Schwaderer[1], Alexandra Raulf[2], Björn A Grüning[3], Claudia Köbele[1], Rolf Backofen[3], Ber Lutz Hein[1] and Ralf Gilsbach[1*]

nat m

Dynamic DNA methylation orchestrates cardiomyocyte development. maturation dis

Ralf Gilsbach, Sebastian Preissl, Björn A. Grünin Benes, Andreas Würch, Ulrike Bönisch, Stefan Fleischmann, Dirk Schübeler & Lutz Hein

nature COMMUNICATIONS

Since 2013, IF >10

- □ 5x Nature 1x Science
- □ 4x Cell 2x Nat. Genetics
- □ 1x Nat. Med. 1x Nat. Micro. Review
- □ 3x Nat. Meth. 4x Nat. Com.
- □ 6x Mol. Cell, 3x PNAS,
- □ 3x Gen. Res. 7x Gen. Bio.
- □ 1x Circ. Res. 1x J. Clinic. Investig.
- □ 1x Genes Dev. 1x Embo J.