Galaxy Project Introduction

Galaxy Demo / Training Day
September 30, 2014, Bern

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Friedrich Miescher Institute for Biomedical Research
Basel, Switzerland

the Galaxy Project

Galaxy

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the Galaxy Project

Galaxy is an open,
web-based platform for
accessible, *reproducible*, and *transparent*
computational biomedical research.

http://galaxyproject.org/

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the Galaxy Project

Galaxy

Accessible: Users without programming experience can easily specify parameters and run tools and workflows.

Reproducible: Galaxy captures information so that any user can repeat and understand a complete computational analysis.

Transparent: Users share and publish analyses via the web and create Pages, interactive, web-based documents that describe a complete analysis.

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Galaxy

Galaxy is available as

a free web server

an open source software

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These options result in several ways to use Galaxy

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Galaxy is available as

Galaxy

As a free web server integrating a wealth of tools, compute resources, terabytes of reference data and permanent storage

https://usegalaxy.org/

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a centralized solution cannot support the different analysis needs of the entire world.

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As an open source software

https://getgalaxy.org/

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As an open source software

https://getgalaxy.org/

...and it is installed in
locations around the world

FMI
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deploy Galaxy

Galaxy

install Galaxy locally

use Galaxy on the Cloud

get the SlipStream Galaxy appliance (BioTeam)

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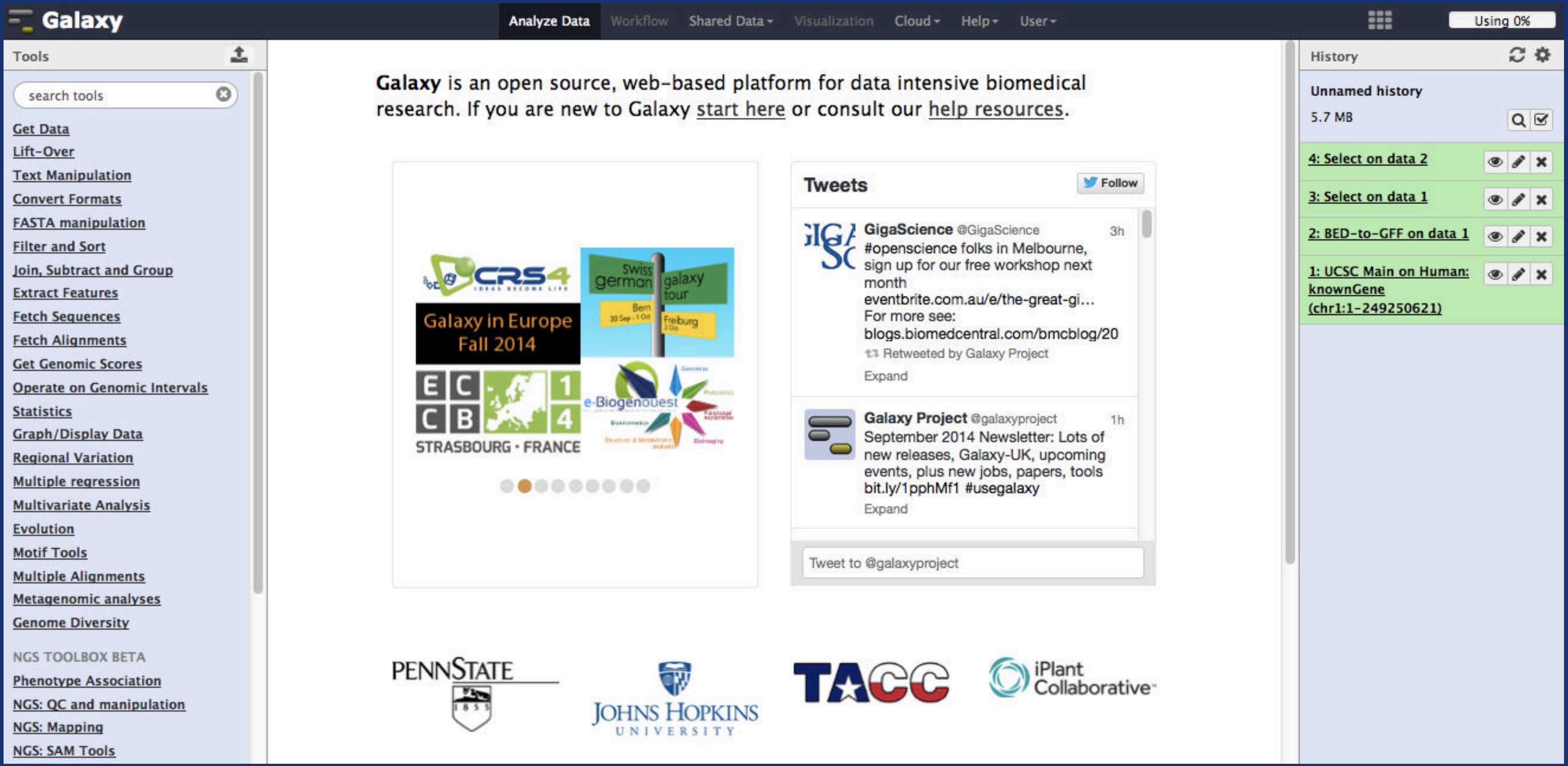
using Galaxy

Galaxy

Galaxy's public web site



Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources.

GigaScience @GigaScience 3h
#openscience folks in Melbourne, sign up for our free workshop next month eventbrite.com.au/e/the-great-gi… For more see: blogs.biomedcentral.com/bmcblog/20
Retweeted by Galaxy Project

Galaxy Project @galaxyproject 1h
September 2014 Newsletter: Lots of new releases, Galaxy-UK, upcoming events, plus new jobs, papers, tools bit.ly/1pphMf1 #usegalaxy

http://usegalaxy.org

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learning Galaxy

Galaxy

http://wiki.galaxyproject.org/Learn

tutorials
screencats
shared histories & workflows

http://wiki.galaxyproject.org/CitingGalaxy

http://wiki.galaxyproject.org/MailingLists

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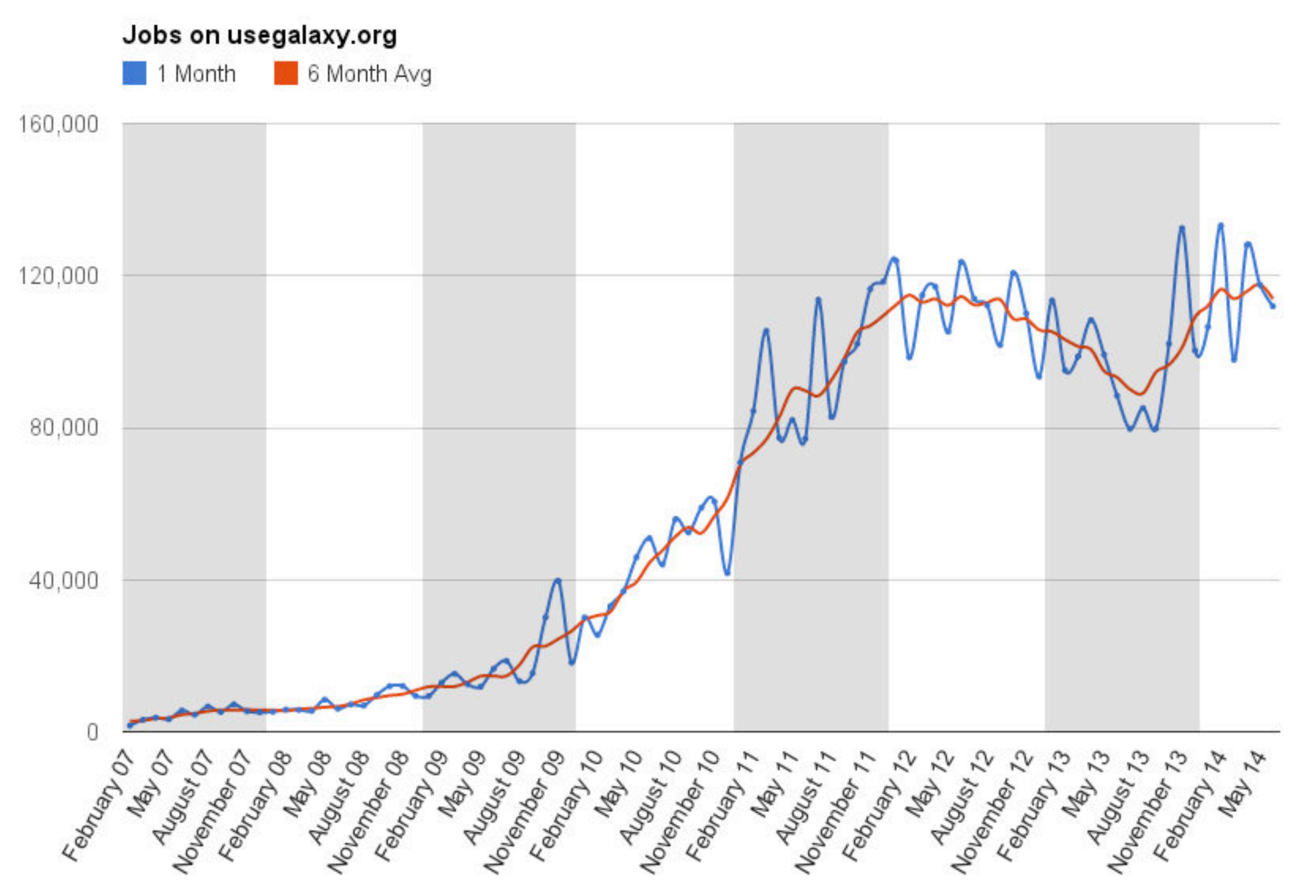
and Galaxy is used



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Galaxy is a community

Galaxy

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Galaxy is a community

Galaxy

in addition to *http://usegalaxy.org* there are 60 public instances offered by institutes from all over the world

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plus an unknown number of private Galaxy servers

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Galaxy is a community

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in addition to *http://usegalaxy.org* there are 60 public instances offered by institutes from all over the world

plus an unknown number of private Galaxy servers

~4000 code commits from over 50 people per year

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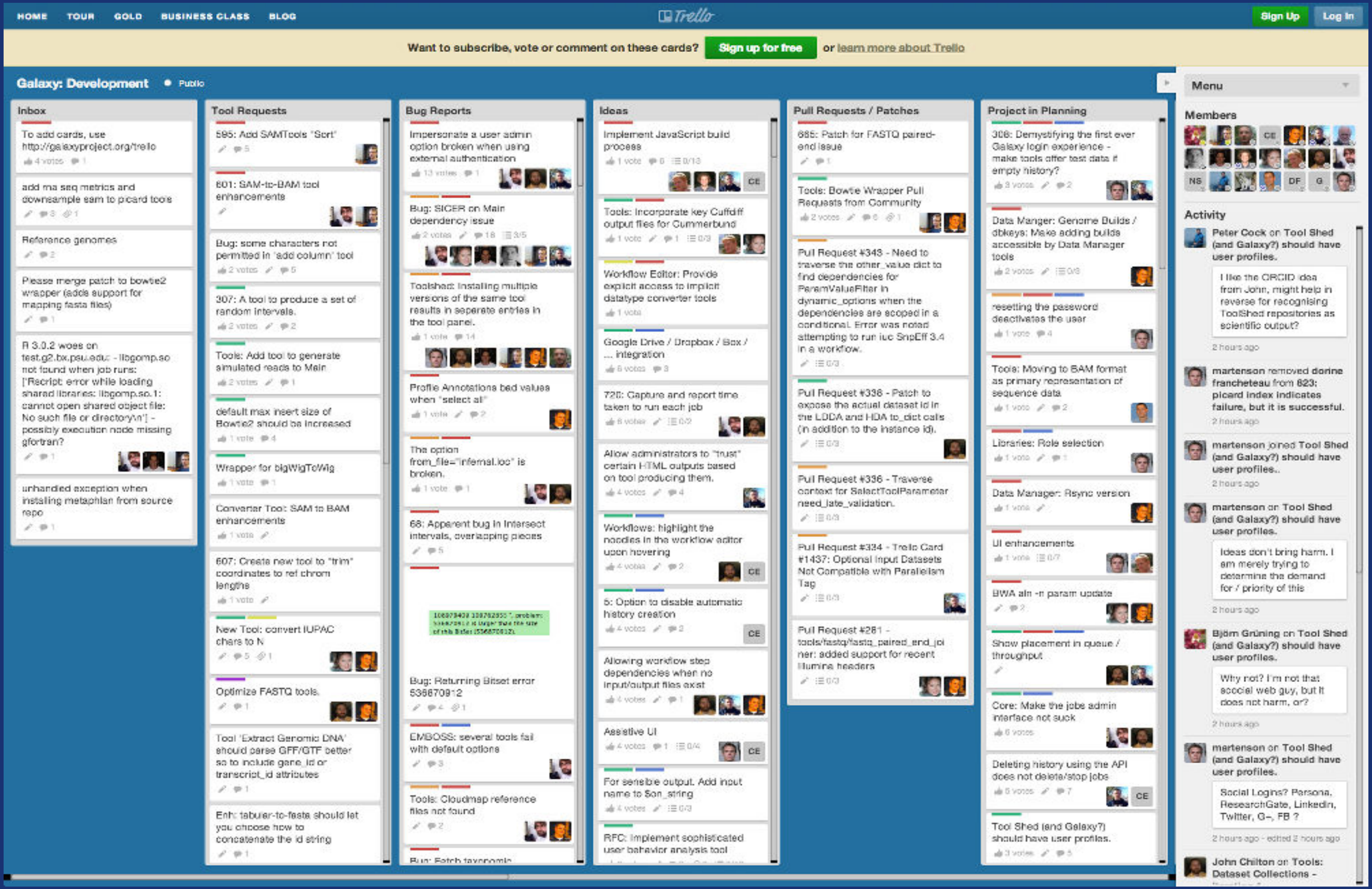
Galaxy is a community



Want to subscribe, vote or comment on these cards? Sign up for free or learn more about Trello

Galaxy: Development

Inbox
- To add cards, use http://galaxyproject.org/trello (4 votes)
- add rna seq metrics and downsample sam to picard tools
- Reference genomes
- Please merge patch to bowtie2 wrapper (adds support for mapping fasta files)
- R 3.0.2 woes on test.g2.bx.psu.edu - libgomp.so not found when job runs: ['Rscript error while loading shared libraries: libgomp.so.1: cannot open shared object file: No such file or directory\n'] - possibly execution node missing gfortran?
- unhandled exception when installing metaphlan from source repo

Tool Requests
- 595: Add SAMTools "Sort"
- 601: SAM-to-BAM tool enhancements
- Bug: some characters not permitted in 'add column' tool (2 votes)
- 307: A tool to produce a set of random intervals. (2 votes)
- Tools: Add tool to generate simulated reads to Main (2 votes)
- default max insert size of Bowtie2 should be increased (1 vote)
- Wrapper for bigWigToWig (1 vote)
- Converter Tool: SAM to BAM enhancements (1 vote)
- 607: Create new tool to "trim" coordinates to ref chrom lengths (1 vote)
- New Tool: convert IUPAC chars to N
- Optimize FASTQ tools.
- Tool 'Extract Genomic DNA' should parse GFF/GTF better so to include gene_id or transcript_id attributes
- Enh: tabular-to-fasta should let you choose how to concatenate the id string

Bug Reports
- Impersonate a user admin option broken when using external authentication (13 votes)
- Bug: SICER on Main dependency issue (2 votes)
- Toolshed: Installing multiple versions of the same tool results in seperate entries in the tool panel. (1 vote)
- Profile Annotations bad values when "select all" (1 vote)
- The option from_file="infernal.loc" is broken. (1 vote)
- 68: Apparent bug in Intersect intervals, overlapping pieces
- Bug: Returning Bitset error 536870912
- EMBOSS: several tools fail with default options
- Tools: Cloudmap reference files not found
- Bug: Fetch taxonomic

Ideas
- Implement JavaScript build process (1 vote)
- Tools: Incorporate key Cuffdiff output files for Cummerbund (1 vote)
- Workflow Editor: Provide explicit access to implicit datatype converter tools (1 vote)
- Google Drive / Dropbox / Box / ... integration (6 votes)
- 720: Capture and report time taken to run each job (6 votes)
- Allow administrators to "trust" certain HTML outputs based on tool producing them. (4 votes)
- Workflows: highlight the noodles in the workflow editor upon hovering (4 votes)
- 5: Option to disable automatic history creation (4 votes)
- Allowing workflow step dependencies when no input/output files exist (4 votes)
- Assistive UI (4 votes)
- For sensible output. Add input name to $on_string (4 votes)
- RFC: Implement sophisticated user behavior analysis tool

Pull Requests / Patches
- 685: Patch for FASTQ paired-end issue
- Tools: Bowtie Wrapper Pull Requests from Community (2 votes)
- Pull Request #343 - Need to traverse the other_value dict to find dependencies for ParamValueFilter in dynamic_options when the dependencies are scoped in a conditional. Error was noted attempting to run iuc SnpEff 3.4 in a workflow.
- Pull Request #338 - Patch to expose the actual dataset id in the LDDA and HDA to_dict calls (in addition to the instance id).
- Pull Request #336 - Traverse context for SelectToolParameter need_late_validation.
- Pull Request #334 - Trello Card #1437: Optional Input Datasets Not Compatible with Parallelism Tag
- Pull Request #281 - tools/fastq/fastq_paired_end_joiner: added support for recent Illumina headers

Project in Planning
- 308: Demystifying the first ever Galaxy login experience - make tools offer test data if empty history? (3 votes)
- Data Manger: Genome Builds / dbkeys: Make adding builds accessible by Data Manager tools (2 votes)
- resetting the password deactivates the user (1 vote)
- Tools: Moving to BAM format as primary representation of sequence data (1 vote)
- Libraries: Role selection (1 vote)
- Data Manager: Rsync version (1 vote)
- UI enhancements (1 vote)
- BWA aln -n param update
- Show placement in queue / throughput
- Core: Make the jobs admin interface not suck (6 votes)
- Deleting history using the API does not delete/stop jobs (5 votes)
- Tool Shed (and Galaxy?) should have user profiles. (3 votes)

Members

CE NS DF G

Activity

Peter Cock on **Tool Shed (and Galaxy?) should have user profiles.**

I like the ORCID idea from John, might help in reverse for recognising ToolShed repositories as scientific output?

2 hours ago

martenson removed **dorine francheteau** from **623: picard index indicates failure, but it is successful.**

2 hours ago

martenson joined **Tool Shed (and Galaxy?) should have user profiles..**

2 hours ago

martenson on **Tool Shed (and Galaxy?) should have user profiles.**

Ideas don't bring harm. I am merely trying to determine the demand for / priority of this

2 hours ago

Björn Grüning on **Tool Shed (and Galaxy?) should have user profiles.**

Why not? I'm not that soccial web guy, but it does not harm, or?

2 hours ago

martenson on **Tool Shed (and Galaxy?) should have user profiles.**

Social Logins? Persona, ResearchGate, Linkedin, Twitter, G+, FB ?

2 hours ago - edited 2 hours ago

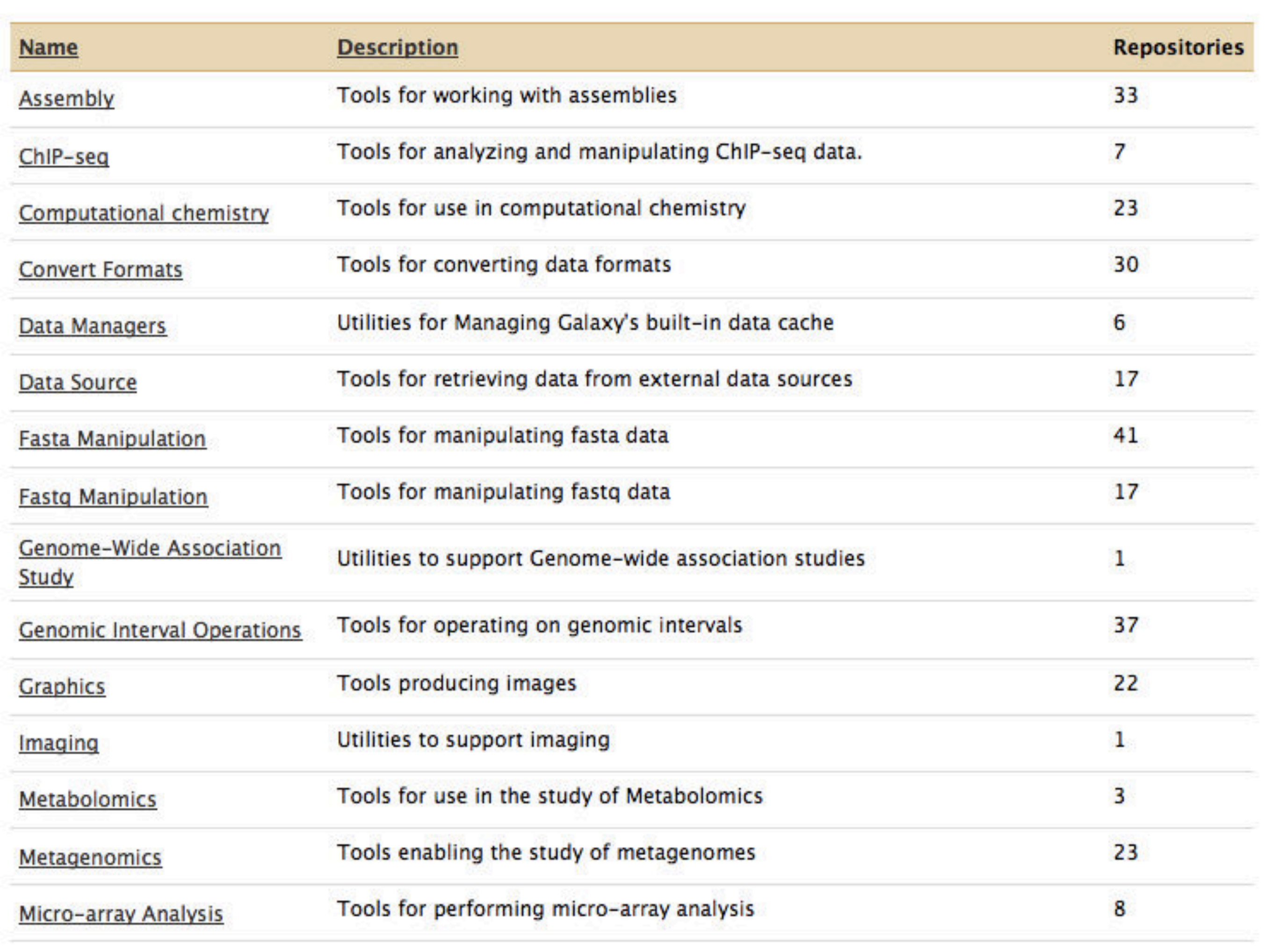
John Chilton on **Tools: Dataset Collections -**

http://bit.ly/gxytrello

Galaxy toolshed

Galaxy

2570 'tools' published from ~220 developers



Name	Description	Repositories
Assembly	Tools for working with assemblies	33
ChIP-seq	Tools for analyzing and manipulating ChIP-seq data.	7
Computational chemistry	Tools for use in computational chemistry	23
Convert Formats	Tools for converting data formats	30
Data Managers	Utilities for Managing Galaxy's built-in data cache	6
Data Source	Tools for retrieving data from external data sources	17
Fasta Manipulation	Tools for manipulating fasta data	41
Fastq Manipulation	Tools for manipulating fastq data	17
Genome-Wide Association Study	Utilities to support Genome-wide association studies	1
Genomic Interval Operations	Tools for operating on genomic intervals	37
Graphics	Tools producing images	22
Imaging	Utilities to support imaging	1
Metabolomics	Tools for use in the study of Metabolomics	3
Metagenomics	Tools enabling the study of metagenomes	23
Micro-array Analysis	Tools for performing micro-array analysis	8

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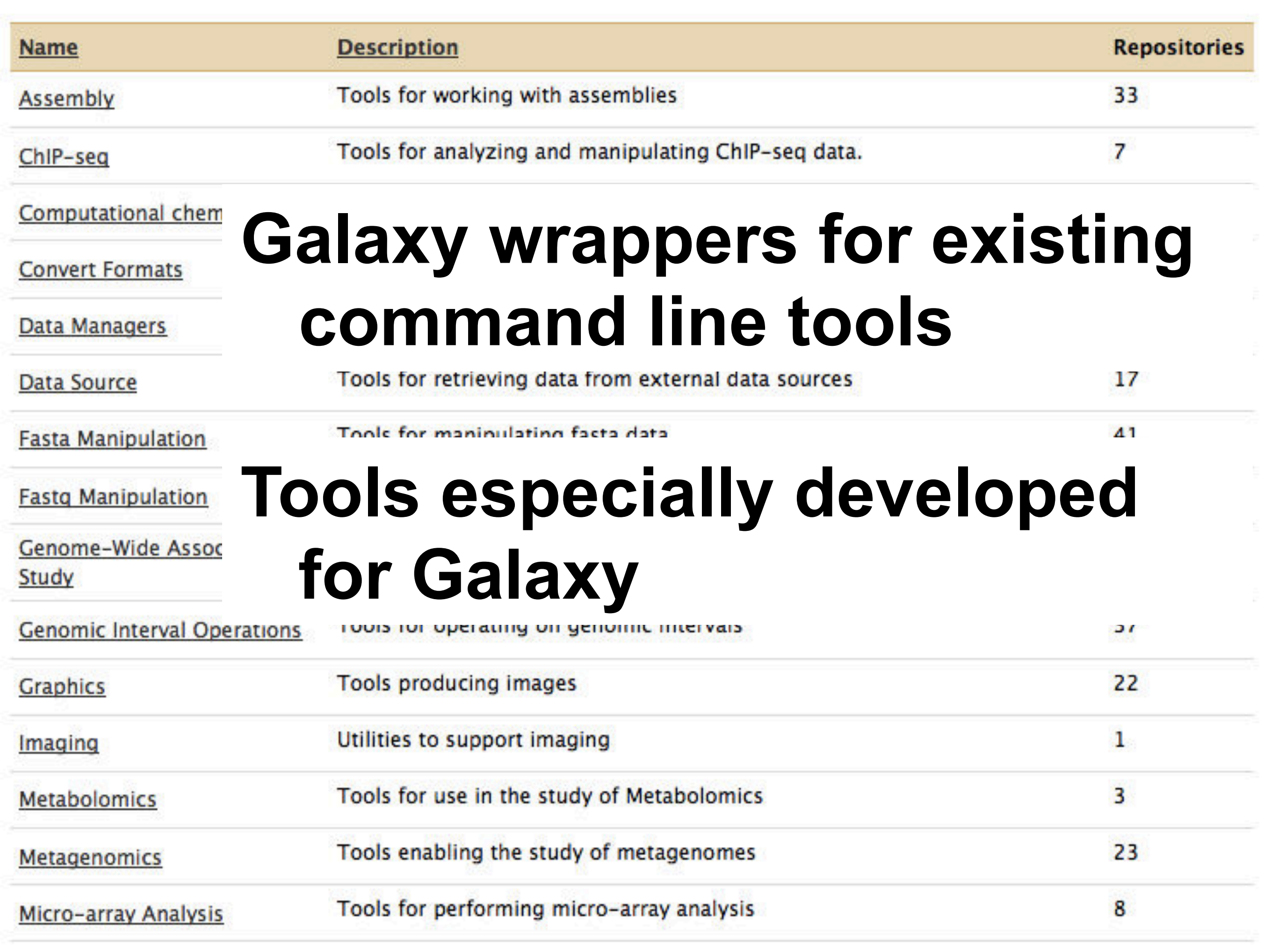

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Galaxy wrappers for existing command line tools

Tools especially developed for Galaxy

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The Galaxy Team

Galaxy

Penn State

Johns Hopkins

https://wiki.galaxyproject.org/GalaxyTeam

GCC 2015

Galaxy Community Conference

6-8th July 2015

The Sainsbury Laboratory
Norwich, UK

galaxyproject.org

let's do some work now

Galaxy

http://cloud1.galaxyproject.org

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