An Introduction to Galaxy

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Today

- Morning session from 9:30 to 12:30
  - The Galaxy interface
    - Tutorial sections 1 & 2
  - Loading data
    - Tutorial section 3
  - Operations on Genomics intervals
    - Tutorial section 4
- Afternoon session from 13:30 to 16:30
  - Workflows
    - Tutorial section 5
  - Data visualisation
    - Tutorial section 6

Today

- What you'll gain
  - How to navigate around Galaxy
  - How to import data
  - How to run bioinformatics tools on data
  - How to create pipelines (workflow)
  - How to visualise data

- … but you won't gain
  - a PhD in Bioinformatics!

What is Galaxy?

- Web-platform for bioinformatics analysis
- Availability
  - Public servers
    - Galaxy Main http://usegalaxy.org/
    - Other Public Accessible Galaxy Servers
      - https://wiki.galaxyproject.org/PublicGalaxyServers
  - On Amazon cloud
      - https://wiki.galaxyproject.org/CloudMan
  - In VirtualBox
      - https://wiki.galaxyproject.org/Events/GCC2014/TrainingDay/VMs?highlight=%28virtualbox%29
  - As a local installation at CRUK-CI
      - http://galaxy.cruk.cam.ac.uk/

Which server to use?

- Compare and choose based on:
  - size of datasets, available storage, backup
  - data security
  - computational requirements
  - tools installed

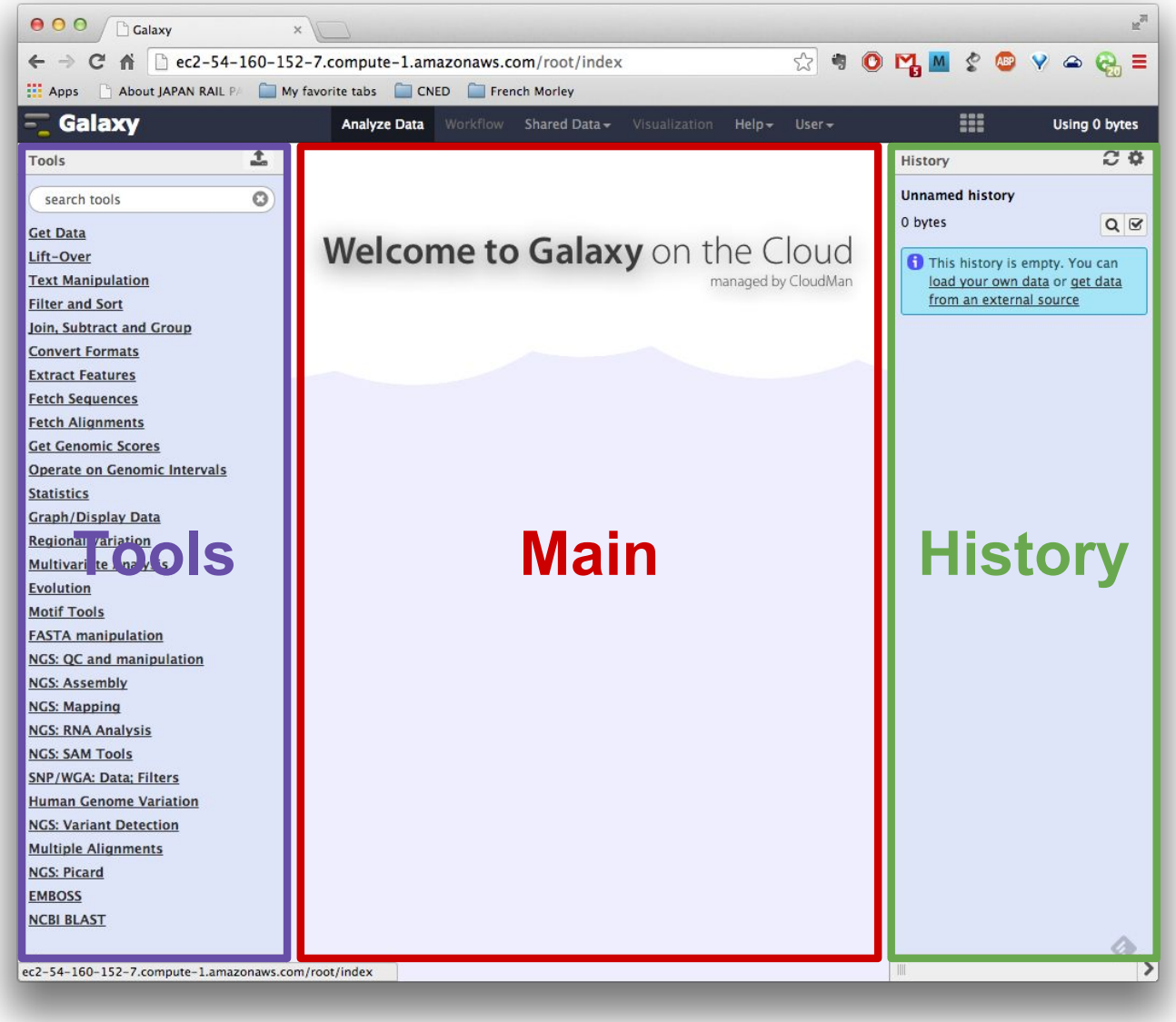
	Main	Local	Cloud	Appliance	Other
Your data sets are moderately sized	Yes	Yes	Yes	Yes	?
Your computational requirements are moderate	Yes	Yes	Yes	Yes	?
You want to share your Galaxy objects with others	Yes	Yes	Yes	Yes	?
All needed Tools are installed on Main.	Yes	?	Yes	Yes	?
Your data sets are very large	No	?	Yes	Yes	?
Your computational requirements are very large	No	?	Yes	Yes	?
You have absolute data security requirements	No	Yes	Yes	Yes	?
No network transfer of data	No	Yes	No	Yes	Yes

Why Galaxy?

- Accessible
  - Users without programming experience can easily specify parameters, run tools, workflows and parse/ filter data.
- 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 and workflows - interactive, web-based documents that describe a complete analysis.

The Galaxy interface

- Divided into 3 panels
  - Tools
  - History
  - Main



The Menu

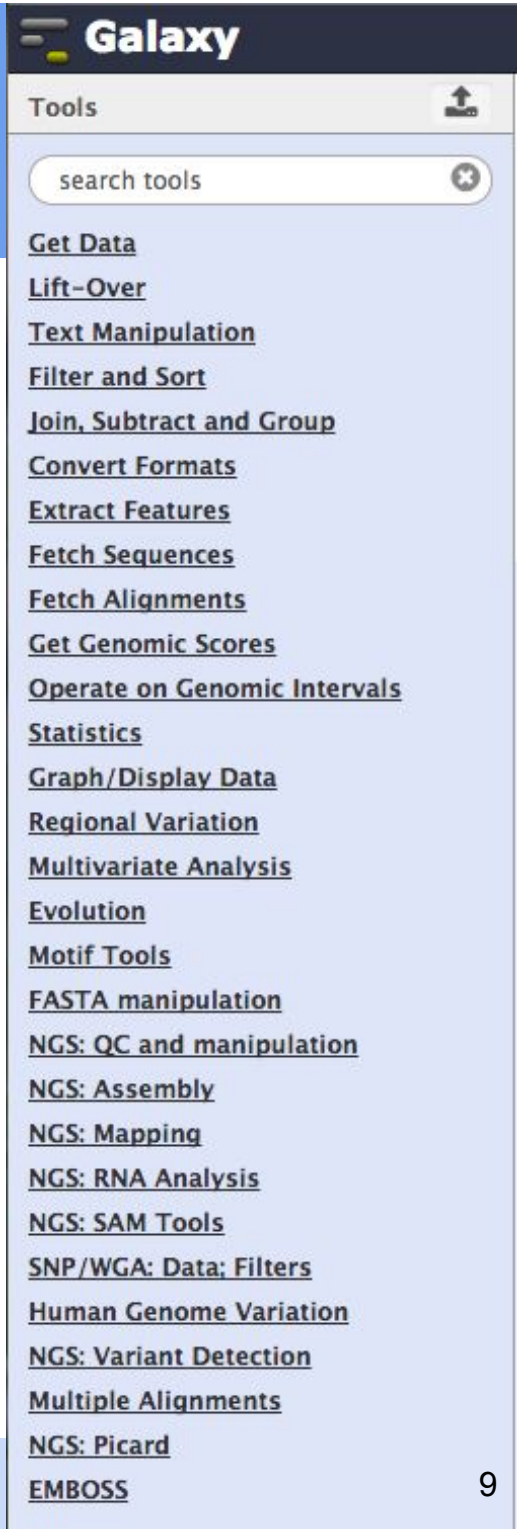
The Menu is where we look for other items in Galaxy.

- *Shared data* - your main source of data.
- *Workflow* - shows your workflows - editable diagrammatic pipeline (more later).
- *Visualization* - shows your visualisations.
- *User* – things specific to you (histories, datasets, pages, etc).

Tools

- Many tools available
- Galaxy Toolshed https://toolshed.g2.bx.psu.edu/

- Need a tool that's not in Galaxy?
  - Ask a bioinformatician! At CRUK-CI, we can install available command-line tools into Galaxy and also develop custom software for you to use.



Tutorial

- Start tutorial – Introduction to Galaxy
  - Go through Sections 1 and 2
    - The Galaxy interface
    - Getting started

http://tinyurl.com/GalaxyCamPractical

Loading data

Section 3

Importing data

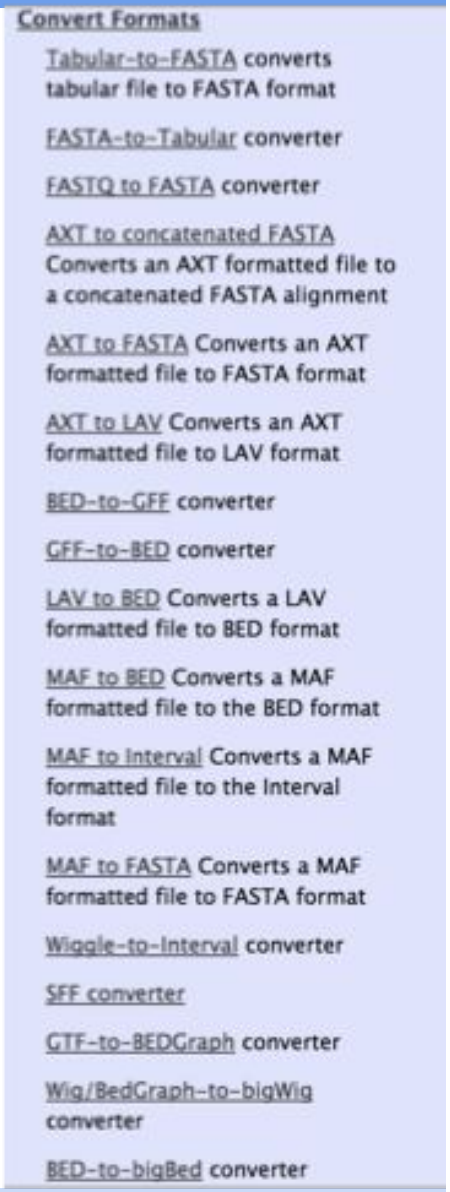
- Copy/paste from a file
- Upload data from a local Computer
- Upload data from internet
- Upload data from database queries
  - UCSC, BioMart, ENCODE, modENCODE, Flymine etc.
- Download shared data from public libraries or shared:
- Data libraries, Histories, Workflows, Visualizations, Pages
- Upload data from FTP (>2GB)

- Be aware of the data attribute: Datatype and genome assembly

Genome build and Data types

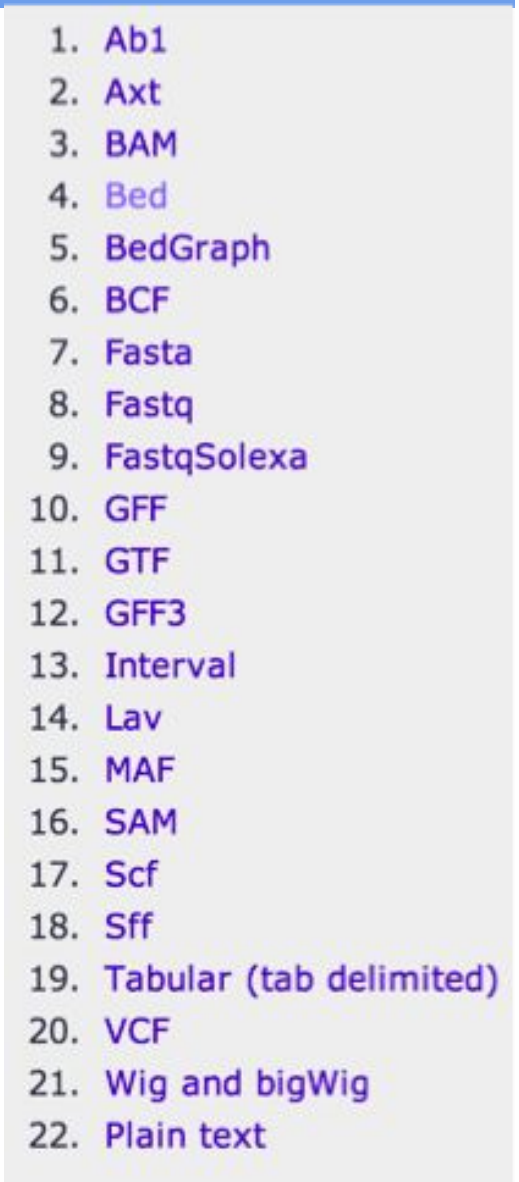
- Genome build specifies which genome assembly this dataset is associated with. e.g. mm9, hg19.
- Genome build can be detected and assigned or user specified.
- User can define their own custom genome build.
- New genome assembly can be added by the galaxy server/instance admin.

- Data type can be detected and assigned or user specified. e.g.
  - Edit Attributes
  - Convert Formats
- Data type is also assigned by tools when output is created.
- Many tools will only accept as input datasets with the appropriate data types assigned.
- New genome assembly and data type can be added by the galaxy server/instance admin.



Data types

- Sequence files:
  - Ab1, Fasta, Scf
- Sequencing files:
  - FASTQ, FastqSolexa, sff
- Alignment files:
  - Axt, SAM/BAM, MAF, LAV
- Intervals:
  - Bed (0 based), GFF, GTF(GFF2), GFF3
- Graph:
  - BedGraph, WIG/BigWIG (1 based)
- Variant files
  - VCF/BCF
- Tabular and Text



Tutorial

- Start tutorial – Introduction to Galaxy
  - Go through Section 3
    - Loading data

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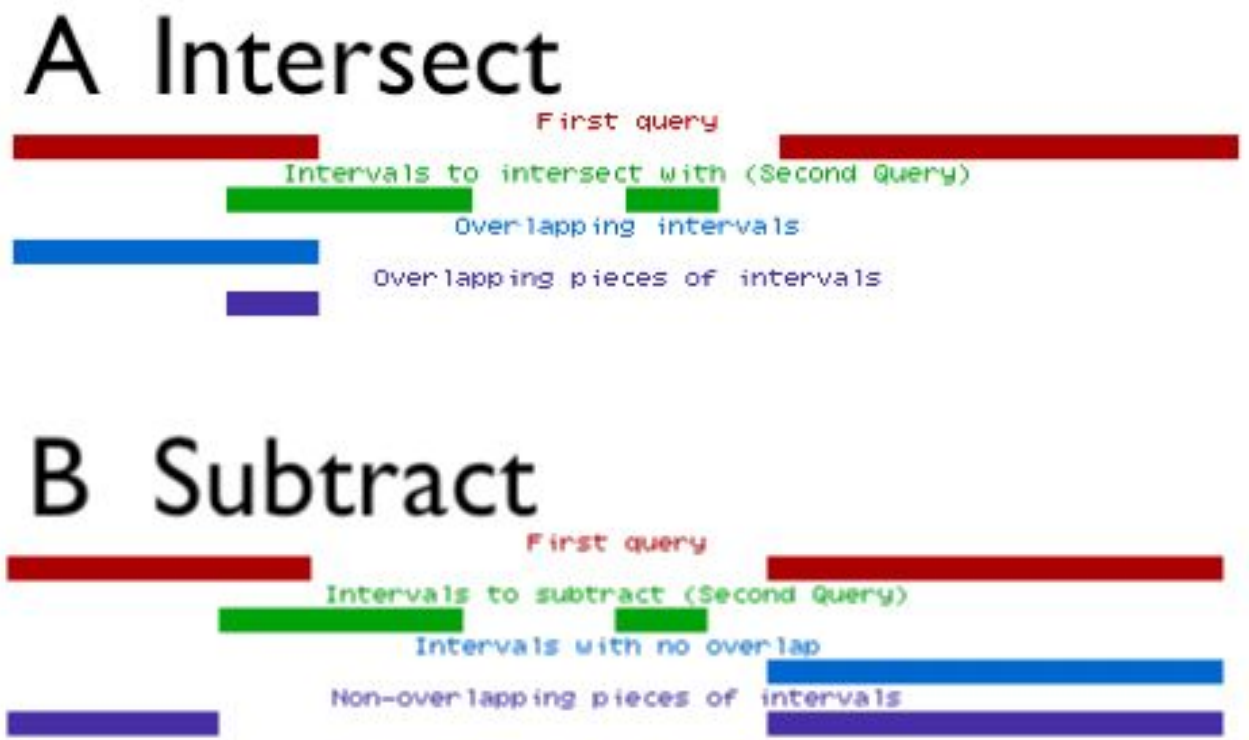
Interval Operations

Section 4

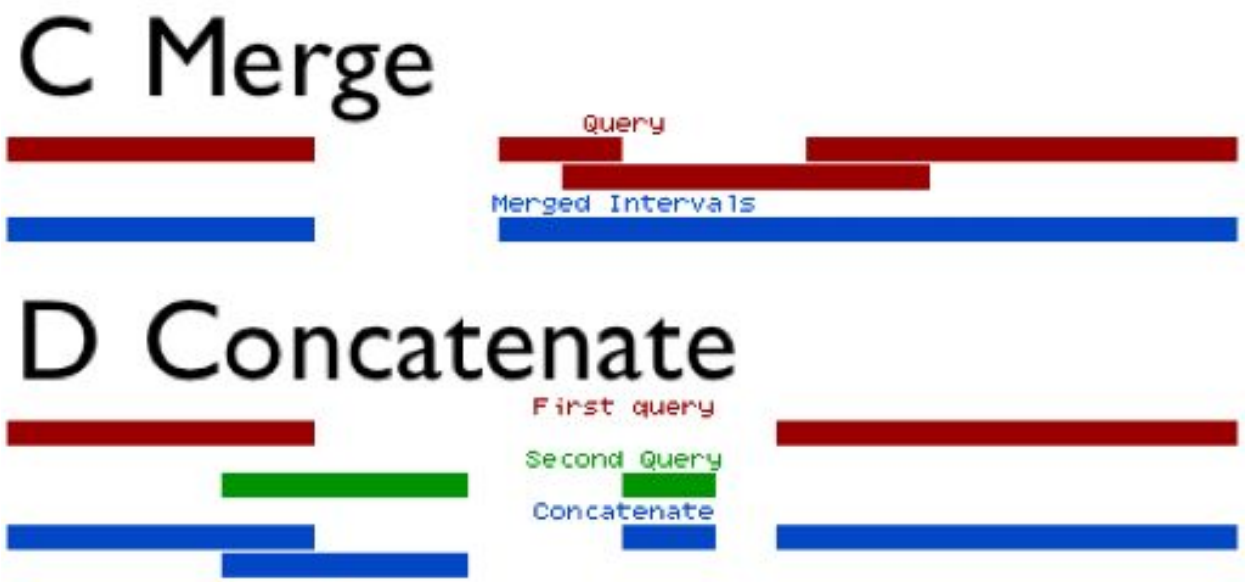
Operations on Genomic intervals

- Join
- Intersect
- Get flanks
- Coverage
- Complement
- Cluster
- Base Coverage
- Subtract
- Fetch closes non-overlapping feature
- Merge
- Arithmetic Operations on tables
- Subtract Whole Dataset
- Concatenate
- Converting into interval format

Operations on Genomic intervals



Operations on Genomic intervals



Operations on Genomic intervals

E Complement

F Cluster

Operations on Genomic intervals

- Join
- Intersect
- Get flanks
- Coverage (merge)
- Complement
- Cluster
- Base Coverage (intersect)
- Subtract
- Fetch closes non-overlapping feature
- Merge
- Arithmetic Operations on tables
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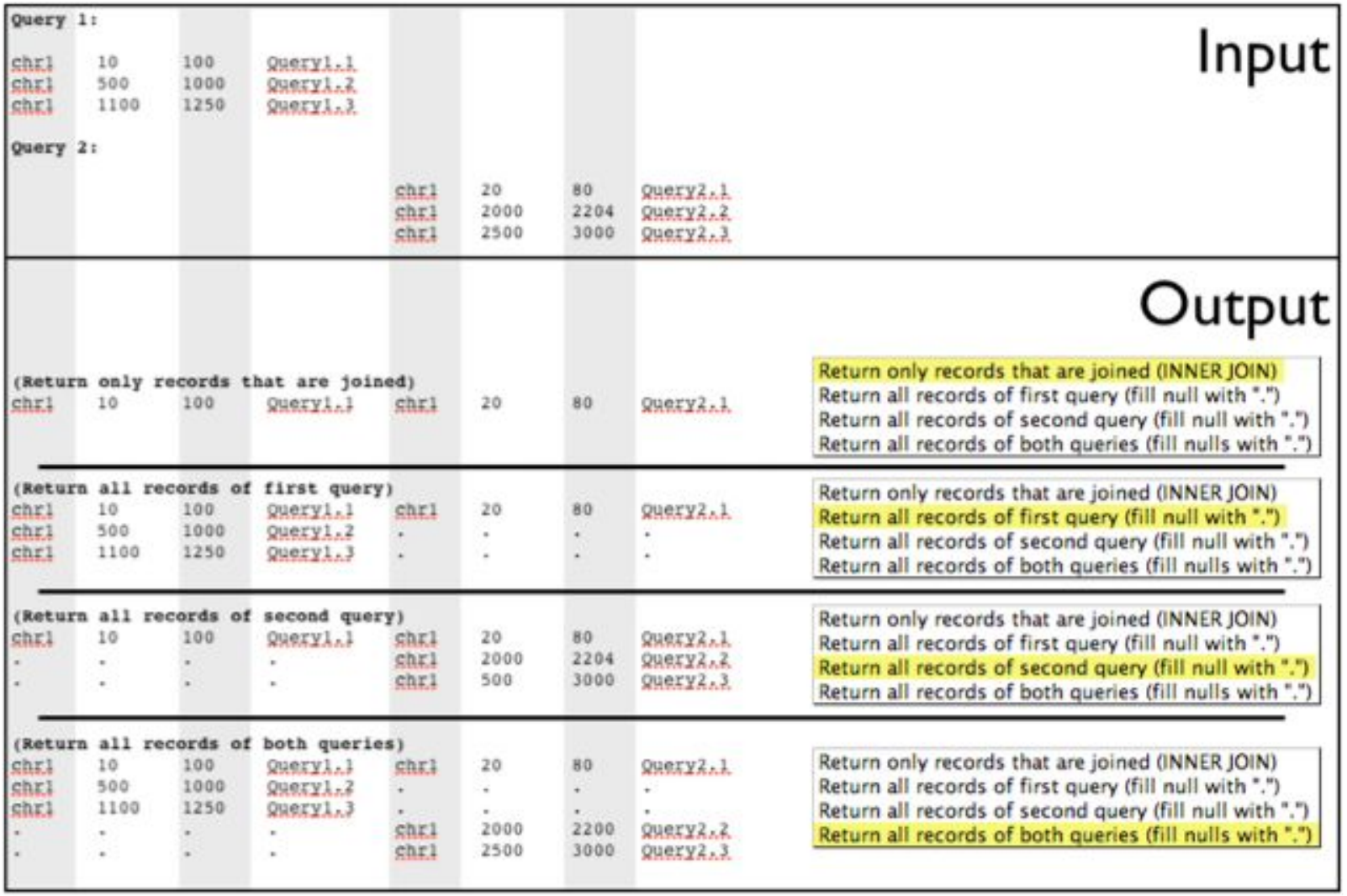
Operations on Genomic intervals



Tutorial

- Start tutorial – Introduction to Galaxy
  - Go through Section 4
    - Interval Operations
      - Basic operations
      - Identify promoter regions containing TAF1 binding sites
      - Finding coding exons with highest SNP density

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Workflows

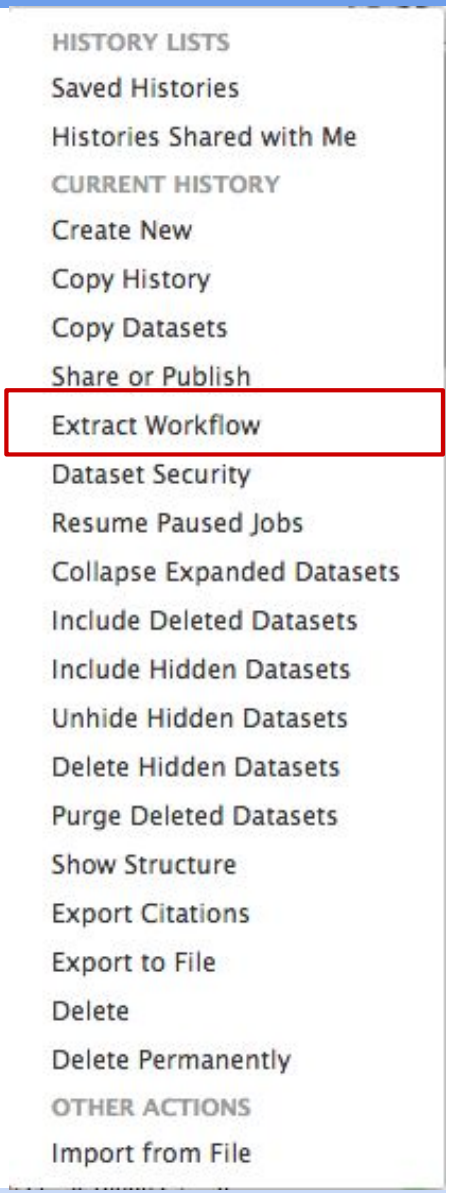
Section 5

Understanding Histories

- In Galaxy your analyses live in histories
- Histories can be very large, you can have as many histories as you want, and all history behavior is controlled by the History options on the top of the History pane
- Many of the options here are self explanatory. If you create a new history, your current history does not disappear.
- If you would like to list all of your histories just choose Saved Histories and you will see a list of all your histories in the center pane.

Workflows

- Converting histories into workflows
  - One of the history options listed is very special. It allows you to easily convert existing histories into analysis workflows.
  - Why would you want to create a workflows out of a history? To redo the analysis again with minimal clicking.

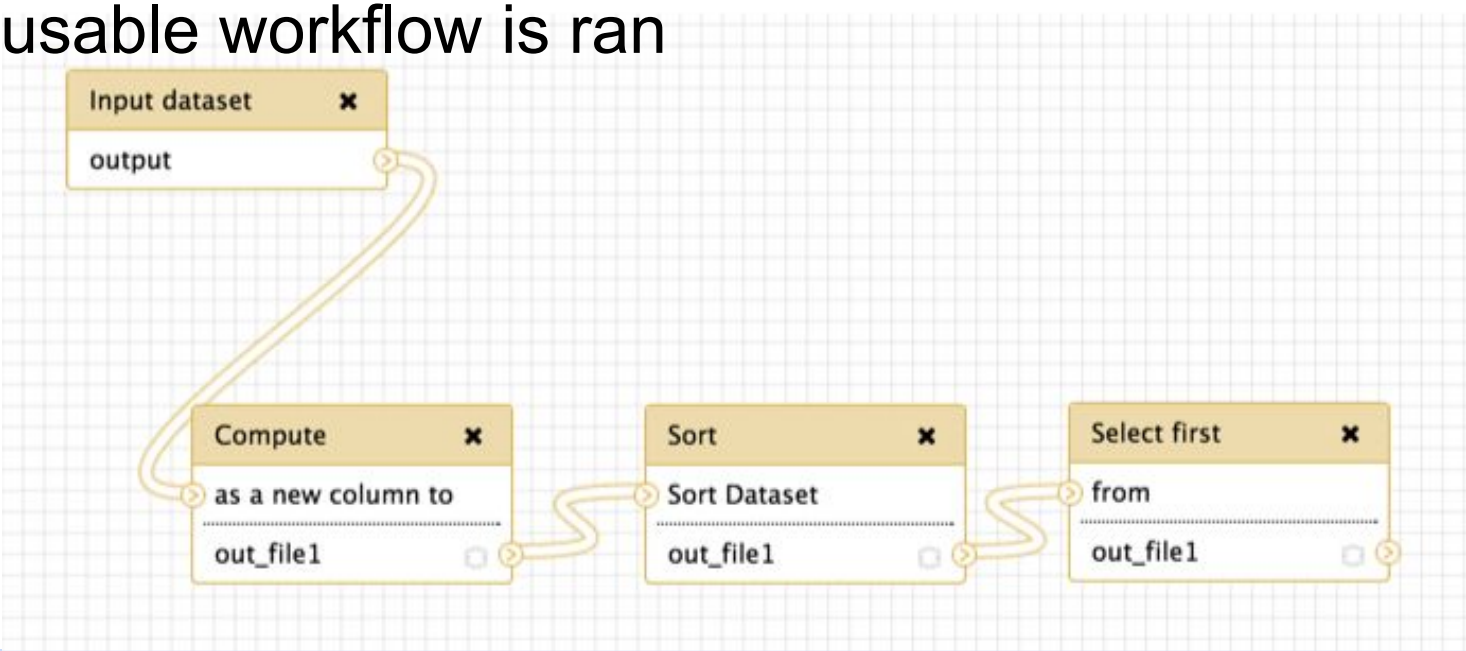


Building workflows

- Workflow allows analysis containing multiple tools to be built, run, extracted from histories, and rerun.
- Can be built
  - manually by adding tools on the workflow canvas,
  - from an existing history, or
  - by importing an existing workflow.
- Collaborations, publications, pipelines.

Building workflows

- Publish and share objects: Dataset, history, workflow, Page, visualization
- Workflow can be created: from existing project, or from scratch, or by downloading from a publicly accessible workflow
- The parameters can be modified before each time the reusable workflow is ran



Running workflows

- All the jobs are submitted to Galaxy
- Each job is run in turn
- Each job waits for output of previous tool

- Workflow can be run over and over again on any suitable datasets
- Workflow can be published, shared or downloaded from https://usegalaxy.org/workflow/list_published [menu: 'Shared Data' > 'Published Workflows']

Tutorial

- Start tutorial – Introduction to Galaxy
  - Go through Section 5
    - Workflows
      - Create workflow from history
      - Create a new workflow
      - Importing a workflow

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Visualisation

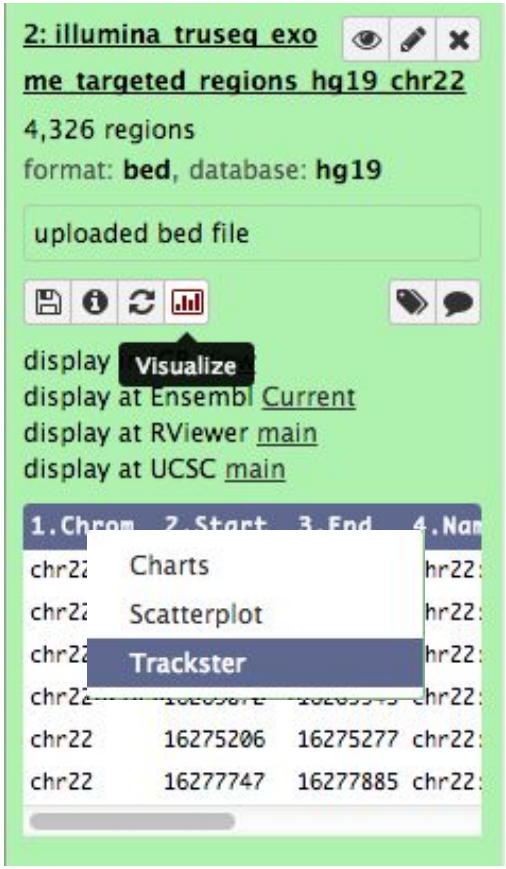
Section 6

Data sharing

- You can share your Galaxy items - histories, workflows, visualizations, and pages - with other people in three different ways:
  - Individual users: directly using a Galaxy account's email addresses on the same instance
  - One or more users: using a web link, with anyone who knows the link
  - Everyone: using a web link plus publishing into Shared Data
- Galaxy Toolshed https://toolshed.g2.bx.psu.edu/

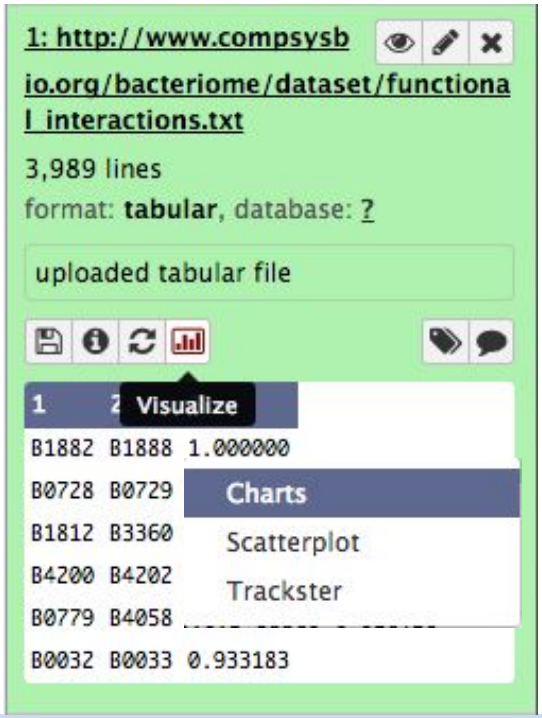
Biological visualisation

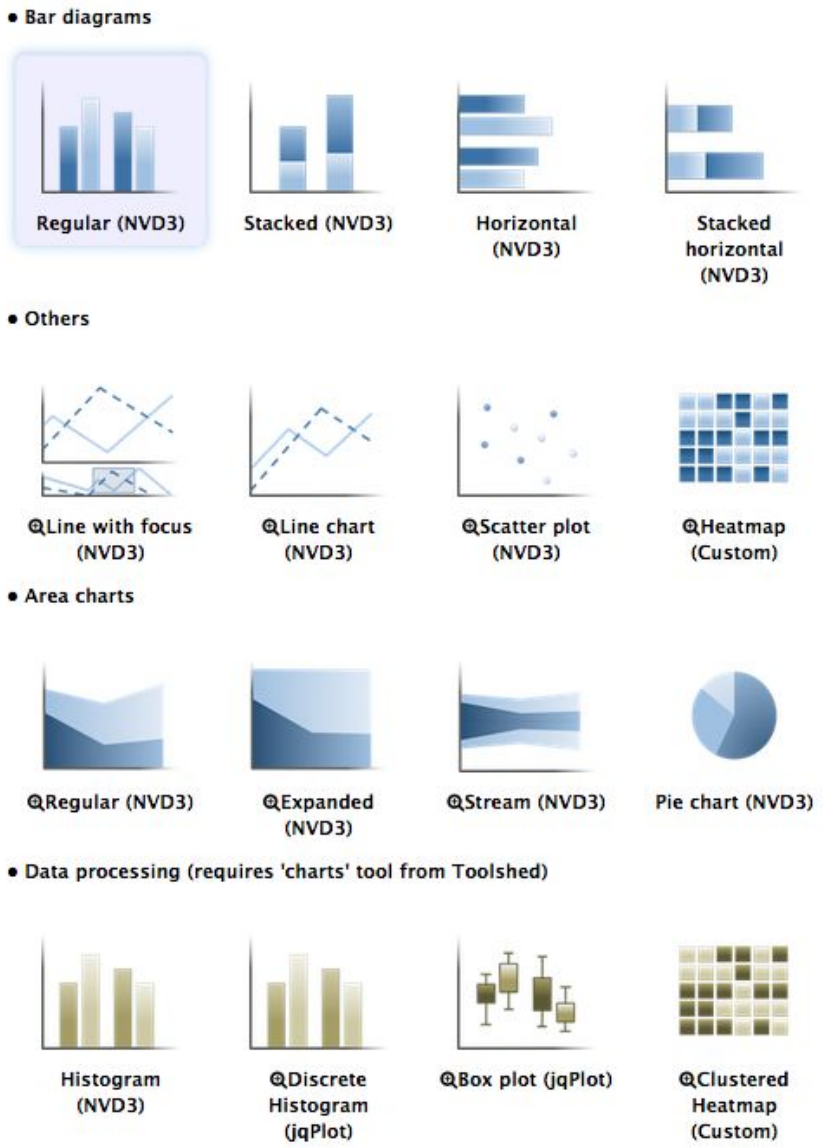
- Galaxy incorporates a track browser called Trackster.
  - This can be used to visualize genomic data within Galaxy in a tightly integrated way.
  - The browser also currently supports (and aims to support maximally) visual analytics, where visualization is used iteratively to provide feedback on analysis.



Numerical visualisation

- Additionally, Galaxy enables you to create bar diagrams, pie charts, scatter plots and other visualisations using the Charts plugin.





Tutorial

- Start tutorial – Introduction to Galaxy
  - Go through Section 6
    - Data visualisation
      - Biological visualisation
      - Numerical visualisation

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Thank you!

- Questions
- Please feel free to give us any feedback on this form http://tinyurl.com/galaxy-feedback

Acknowledgements

- Graham Etherington, Sainsbury Laboratory Norwich
  - ‘An Introduction to Galaxy’ http://tsltraining.tsl.ac.uk/
- Galaxy Team
  - ‘Galaxy 101’ https://usegalaxy.org/u/aun1/p/galaxy101
- CloudMan
  - https://wiki.galaxyproject.org/CloudMan