

Introduction to Galaxy

University of Rochester

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<http://galaxyproject.org/>



#usegalaxy @galaxyproject



UNIVERSITY of
ROCHESTER



Agenda: Day 1

9:00 Welcome

9:20 Basic Analysis with Galaxy
A worked example demonstrating Galaxy Basics

10:45 Break

11:00 Integrating with other tools: BioMart & GO

12:20 Lunch (catered)

1:20 Basic Analysis into Reusable Workflows

2:50 Break

3:05 RNA-Seq Analysis, Part I

5:00 Done

http://bit.ly/UR_GXY_2016

Goals

Provide an introduction to using Galaxy for bioinformatic analysis. Demonstrate how Galaxy can help you explore and learn options, perform analysis, and then share, repeat, and reproduce your analyses.

This workshop does cover RNA-Seq but you won't be an expert at the end of the workshop. You will know enough to get started, and how to use Galaxy to learn more.

What is Galaxy?

**Data integration and analysis platform that
emphasizes accessibility, reproducibility, and
transparency**

<http://galaxyproject.org>

What is Galaxy?

Keith Bradnam's definition:

"A web-based platform that provides a simplified interface to many popular bioinformatics tools."

From

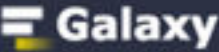
"13 Questions You May Have About Galaxy"

<http://bit.ly/13questions>

Galaxy is available several ways ...

<http://galaxyproject.org>

As a free for everyone service on the web: usegalaxy.org



Analyze DataWorkflowShared DataVisualizationHelpUser

Using 0%

Galaxy now runs some (larger, multicore) jobs on [Jetstream](#), you may encounter a few problems related to this. We are working on these, and please feel free to report any errors you encounter.


Tools


search tools

[Get Data](#)
[Lift-Over](#)
[Text Manipulation](#)
[Datamash](#)
[Convert Formats](#)
[Filter and Sort](#)
[Join, Subtract and Group](#)
[Fetch Alignments/Sequences](#)
[NGS: QC and manipulation](#)
[NGS: DeepTools](#)
[NGS: Mapping](#)
[NGS: RNA Analysis](#)
[NGS: SAMtools](#)
[NGS: BamTools](#)
[NGS: Picard](#)
[NGS: VCF Manipulation](#)
[NGS: Peak Calling](#)
[NGS: Variant Analysis](#)
[NGS: RNA Structure](#)
[NGS: Du Novo](#)
[NGS: Gemini](#)
[Operate on Genomic Intervals](#)
[Statistics](#)
[Graph/Display Data](#)
[CloudMap](#)
[Phenotype Association](#)


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](#). You can install your own Galaxy by following the [tutorial](#) and choose from thousands of tools from the [Tool Shed](#).

Want help?
Get answers.


 **Biostars**
GALAXY EXPLAINED




Tweets by @galaxyproject


 Galaxy Project @galaxyproject

Tutorial & history from today's #TAGC16 #usegalaxy workshop are at:
bit.ly/TAGC_GXY_PDF
[twitter.com/galaxyproject/...](https://twitter.com/galaxyproject/)


 16 Jul


 Galaxy Project @galaxyproject


omorrow morning 8am #TAGC16: An Introduction to Using Galaxy for Genetic Data Analysis [genetics-gsa.org/genetics/2016/...](http://genetics-gsa.org/genetics/2016/)




[Embed](#) [View on Twitter](#)

 PENNSTATE

 JOHNS HOPKINS

 TACC

 CYVERSE

A free for everyone web service:

<http://usegalaxy.org>

A free (for everyone) web server integrating a wealth of tools, compute resources, petabytes of reference data and permanent storage



CYVERSE™


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



Explore the
Galaxy with
RNA-Rocket

PATHOGENPORTAL
THE BIOINFORMATICS RESOURCE CENTERS PORTAL

Galaxy / Metabiome Portal



The Microbiome Analysis Center
Life on a Smaller Scale

Welcome to the Metabiome Portal @ GMU

We have developed the MMC Metabiome Portal, a flexible and extensible web browser, with the ability to simplify, control, integrate, compare, and analyze all microbiome data. The MMC Portal is a cloud-based database management system and also includes analytical tools and visualization tools such as interactive clustering.

香港中文大學 - 華大基因跨組學創新研究院
CUHK-BGI Innovation Institute of Trans-Omics

 (GIGA)ⁿ Galaxy
by CBIIT

Integrated publishing of workflows from GIGAⁿ SCIENCE

Cistrome



A Galaxy Server
dedicated to
ChIP-* analysis




Public Galaxy Servers
and *still* counting



The Genomic
HyperBrowser

Powered by Galaxy


SCDE
STEM CELL DISCOVERY ENGINE



**Experiments
Connected**



Whale Shark Galaxy! 

 South Green[®]
bioinformatics platform

**Genomic analysis tools
for southern and
Mediterranean plants**

bit.ly/gxyServers

Galaxy is available as Open Source Software

Galaxy is installed in locations around the world.

<http://getgalaxy.org>

Galaxy is available on the Cloud



We are using this today

<http://aws.amazon.com/education>

<http://globus.org/>

<http://wiki.galaxyproject.org/Cloud>

Galaxy on the Cloud: Galaxy CloudMan

<http://usegalaxy.org/cloud>

- Start with a **fully configured and populated** (tools and data) Galaxy instance.
- Allows you to scale up and down your compute assets as needed.
- Someone else manages the data center



CLOUDMAN

Agenda: Day 1

9:00 Welcome

9:20 **Basic Analysis with Galaxy**
A worked example demonstrating Galaxy Basics

10:45 Break

11:00 Integrating with other tools: BioMart & GO

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Quick Poll: Are you ...

1. A bioinformatics novice

2. A bioinformatics apprentice

3. A bioinformatics guru

Yes, those are your only choices.

<http://galaxyproject.org>

Basic Analysis

Which exons have most overlapping
Repeats?

Use Human, HG38, GENCODE v24,
Chromosome 22

cloud1.galaxyproject.org

cloud2.galaxyproject.org

Exons & Repeats: A General Plan

- Get some data
 - Get Data → UCSC Table Browser
- Identify which exons have Repeats
- Count Repeats per exon
- Visualize, save, download, ... exons with most Repeats

(~ <http://usegalaxy.org/galaxy101>)



Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersection of DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser presentation of the software features and usage. For more complex queries, you may want to use the [Query Builder](#). To examine the biological function of your set through annotation enrichments, send the data to [BioMart](#) for use with diverse computational tools. Refer to the [Credits](#) page for the list of contributors and the [FAQ](#) for these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Download](#) page.

clade: **genome:** **assembly:**

group: **track:**

table:

region: ☐ genome ☒ position

identifiers (names/accessions):

filter:

intersection:

correlation:

output format: Send output to ☒ [Galaxy](#) ☐ [GREAT](#) ☐

output file: (leave blank to keep output in browser)

file type returned: ☒ plain text ☐ gzip compressed



Output knownGene as BED

☐ Include [custom track](#) header:

name=

description=

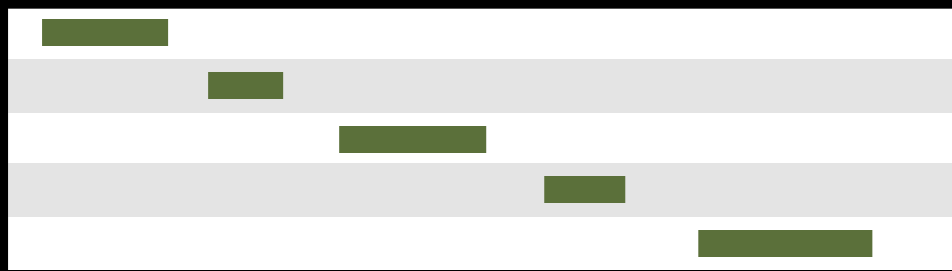
visibility=

url=

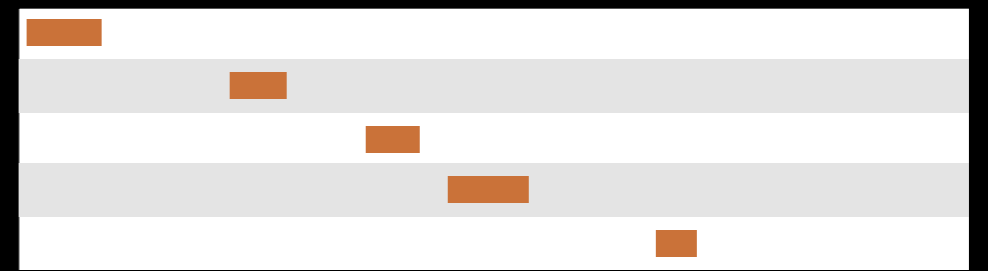
Create one BED record per:

- ☐ Whole Gene
- ☐ Upstream by bases
- ☐ Exons plus bases at each end
- ☐ Introns plus bases at each end
- ☐ 5' UTR Exons
- ☒ Coding Exons
- ☐ 3' UTR Exons
- ☐ Downstream by bases

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream in order to avoid extending past the edge of the chromosome.

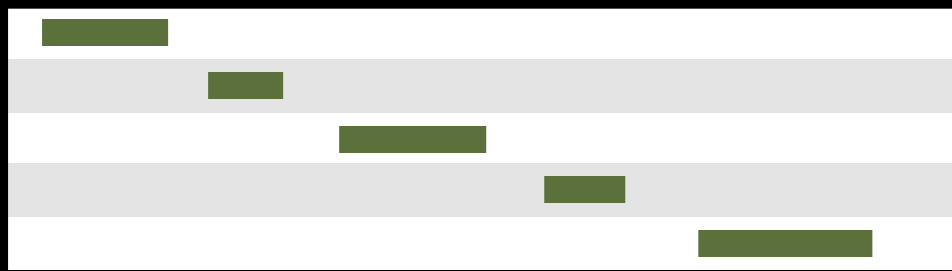


Exons

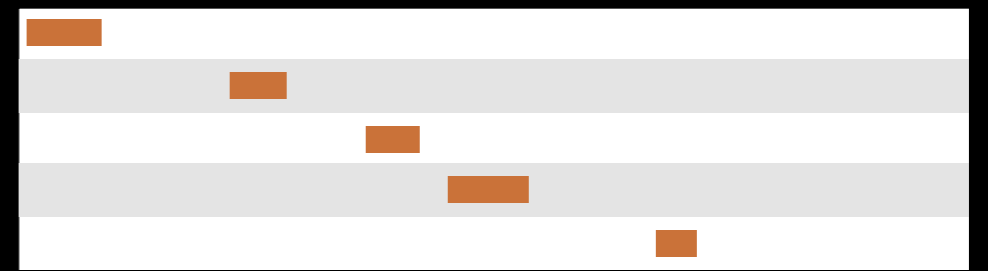


Repeats

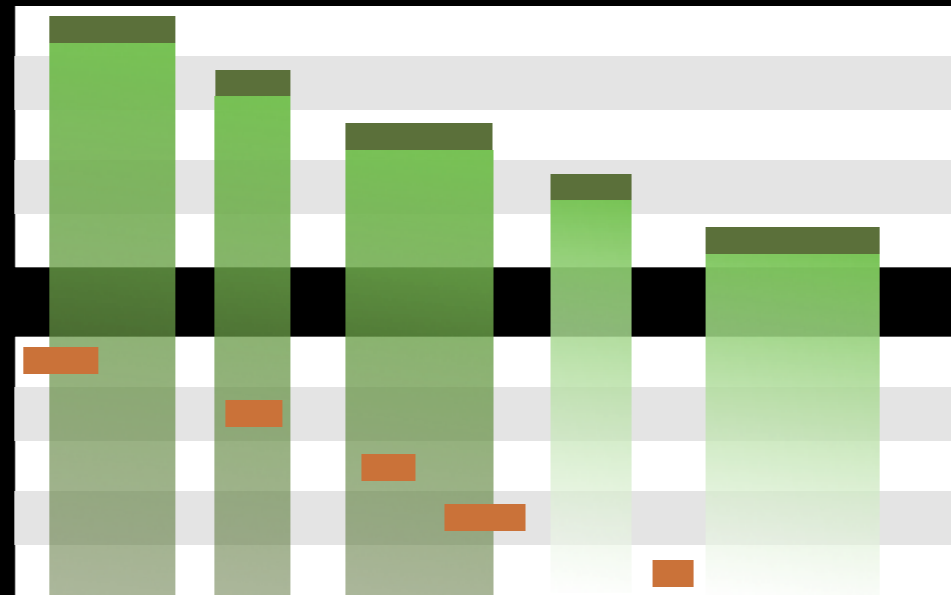
(Identify which exons have Repeats)



Exons



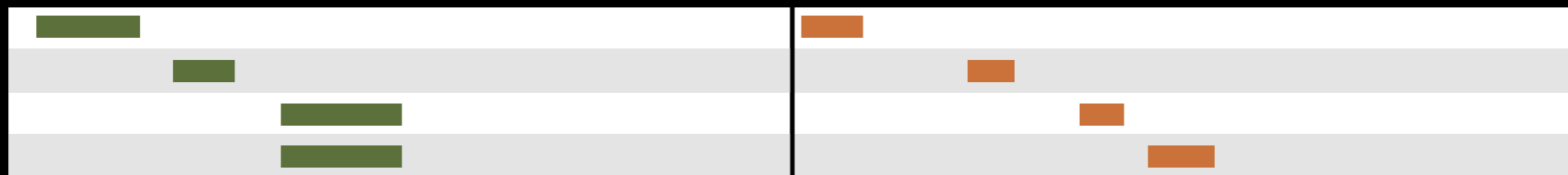
Repeats



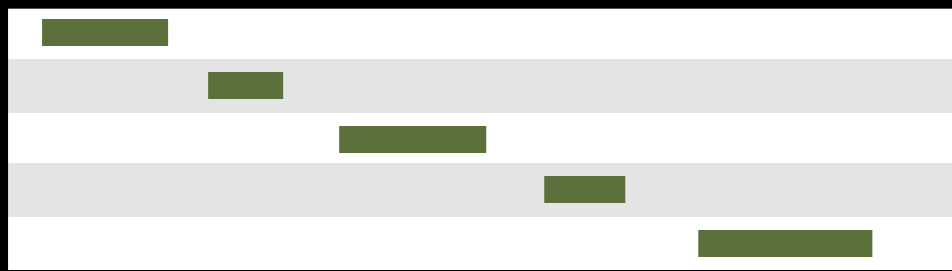
Exons

Repeats

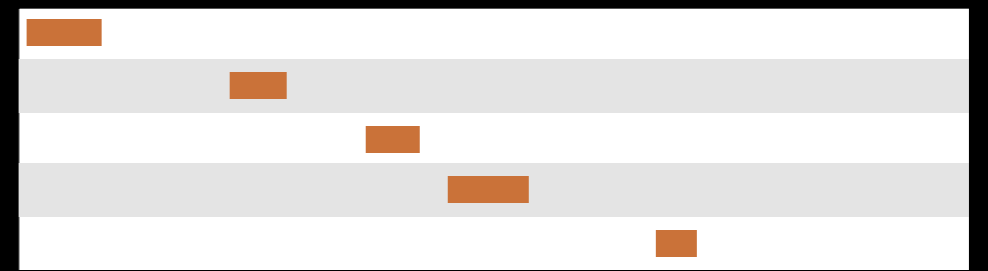
Overlap pairings



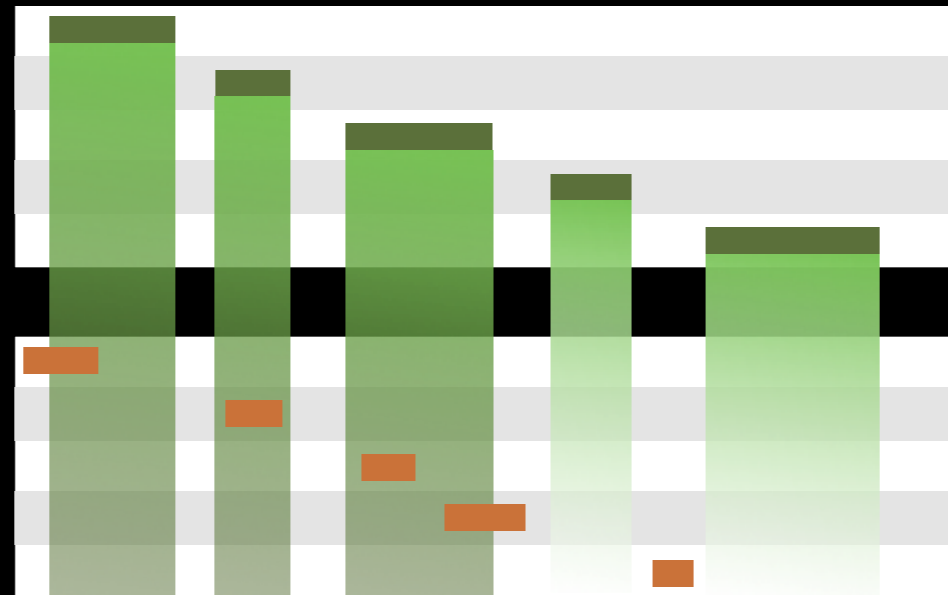
Operate on Genomic Intervals → Join
(Identify which exons have Repeats)



Exons



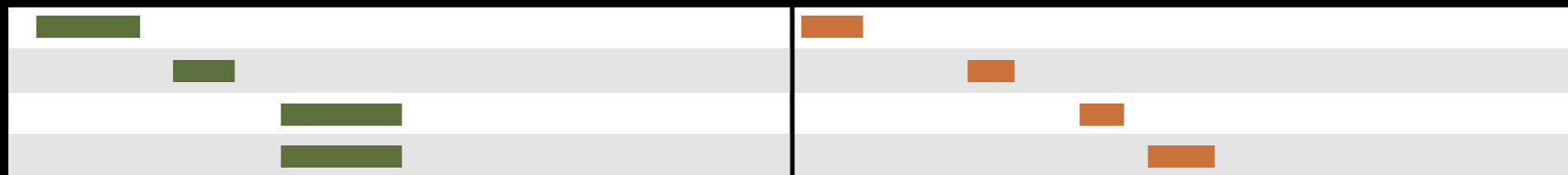
Repeats



Exons

Repeats

Overlap pairings



(Count Repeats per exon)



Exon overlap counts

Join, Subtract, and Group → Group

Published History: Exons with overlapping repeats, basic

Yay!

We have exon names and counts!

We are now going to extend that work.

Let's **create a copy** of this history that we will extend.

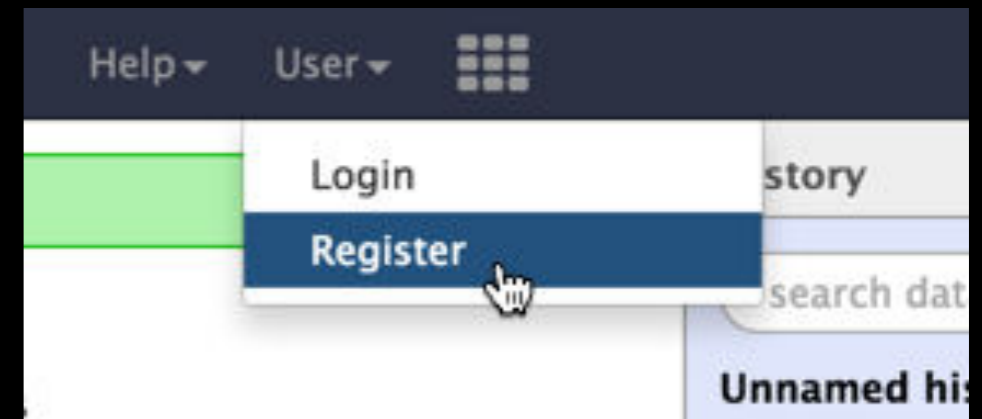
Create a login

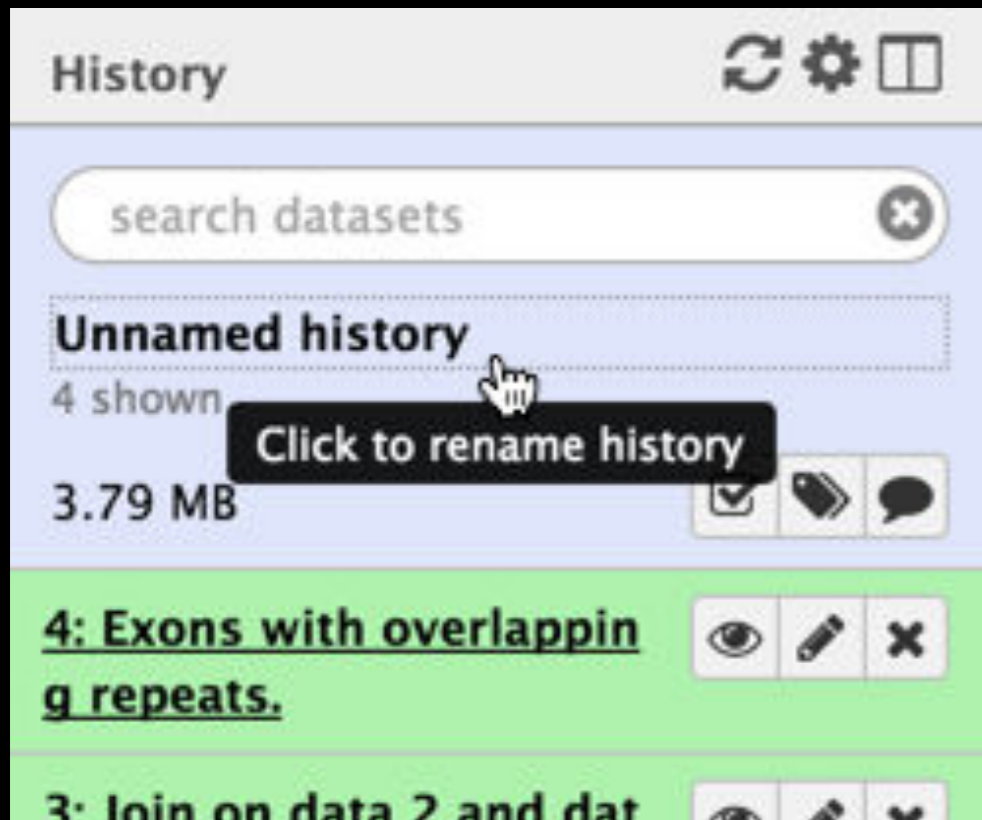
Don't need to login to use Galaxy, but do need one to use all its features

Use an email address you can remember.

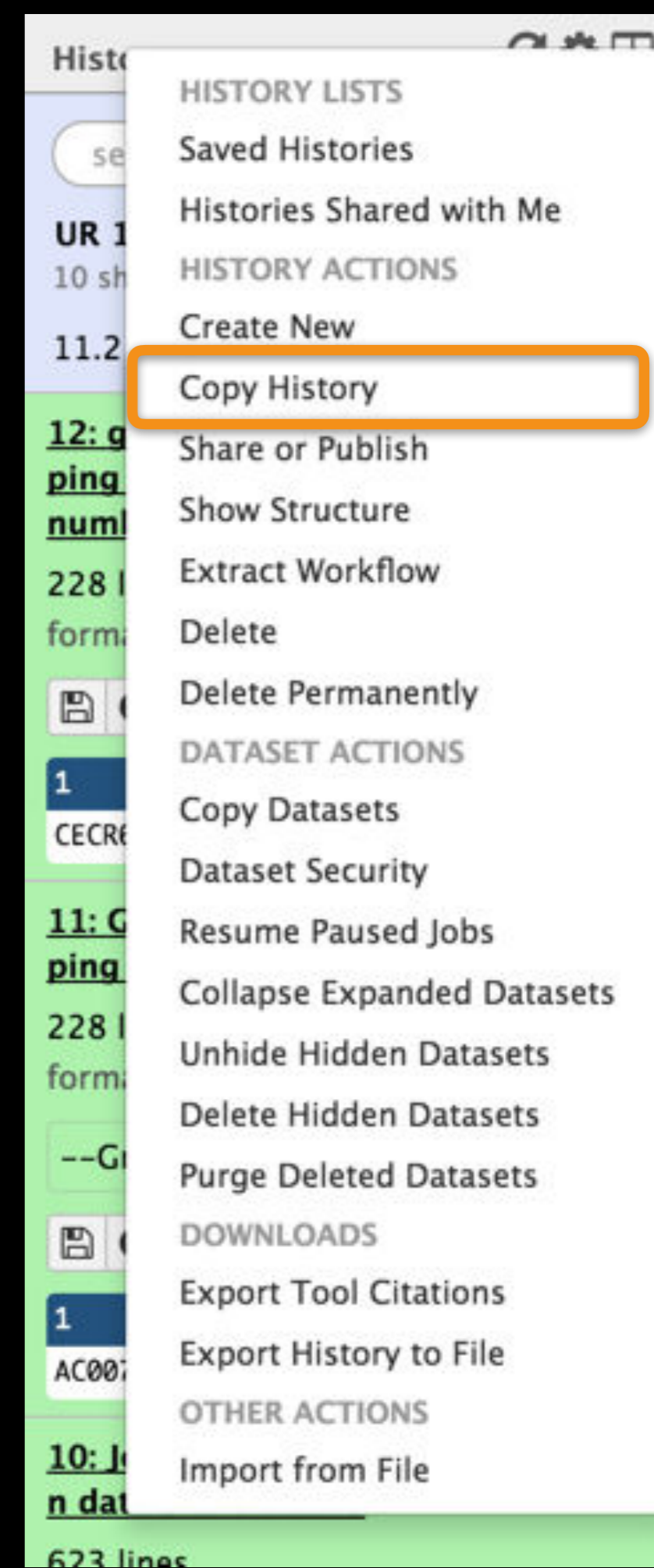
Use a low security password.

This account will go away on Wednesday night.

A screenshot of a 'Create account' form. The form has a yellow header with the title 'Create account'. It contains four input fields: 'Email address:', 'Password:', 'Confirm password:', and 'Public name:'. Below the 'Public name' field is a text explanation: 'Your public name is an identifier that will be used to generate your public profile. Public names must be at least three characters long and can only contain lower-case letters, numbers, and the '-' character.' At the bottom of the form is a 'Submit' button.



1. Give your existing history a meaningful name.



2. Create a copy of your history



(cog) → Copy History

Name the copy based on the exercise you pick from the next slide

Becomes your new current history.

Exons & Repeats: Pick an Exercise

1. Include exons with **no** overlaps in the exon name and score list. Set the score for these to 0.
2. Create a **list of exons** with overlapping repeats, **in BED format**, with the score column replaced by the number of overlapping repeats.

Everything you need will be in these toolboxes

- Text manipulation
- Operate on genomic intervals
- Join, subtract and group
- Filter and sort

All exons, even those with no overlap

Can take advantage of fact that scores are already 0.
Join, subtract and group not a bad place to start.

Published History: Exons with number of overlapping
repeats, including 0

List of exons with overlaps, in BED

Can be done in two steps, one of them a Cut,
plus an edit attributes step at the end:

The screenshot displays the Galaxy web interface. On the left, the 'Datatype' tab is selected and highlighted with an orange box. Below the tab, the 'Change data type' section shows a dropdown menu with 'bed' selected, also highlighted with an orange box. A 'Save' button is visible below the dropdown. To the right, the 'History' panel shows a list of datasets. The dataset '6: Exons with overlapping repeats, in BED' is highlighted in green, and its edit icon (a pencil) is highlighted with an orange box. The dataset description indicates it contains 792 regions in interval format using the hg38 database. Below the description, a table header is visible with columns: 1. Chrom, 2. Start, 3. End, 4. Name.

Attributes Convert Format **Datatype** Permissions

Change data type

New Type:

bed

This will change the datatype of the existing dataset but *not* modify its contents. Use this if Galaxy has incorrectly guessed the type of your dataset.

Save

History

search datasets

Exons with overlapping repeats, in BED

6 shown

3.92 MB

6: Exons with overlapping repeats, in BED

792 regions

format: interval, database: hg38

Score column is the number of repeats that overlap with this exon.

1. Chrom 2. Start 3. End 4. Name

Published History: Exons with overlapping repeats, in BED

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gmod.org

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http://bit.ly/UR_GXY_2016

Yay! But, a wee challenge

We have exon names and counts

We really want genes (or transcripts) and counts
across the whole gene (or transcript)

What we have: Computer generated Exon IDs

uc002zmb.3_cds_0_0_chr22_17119391_r

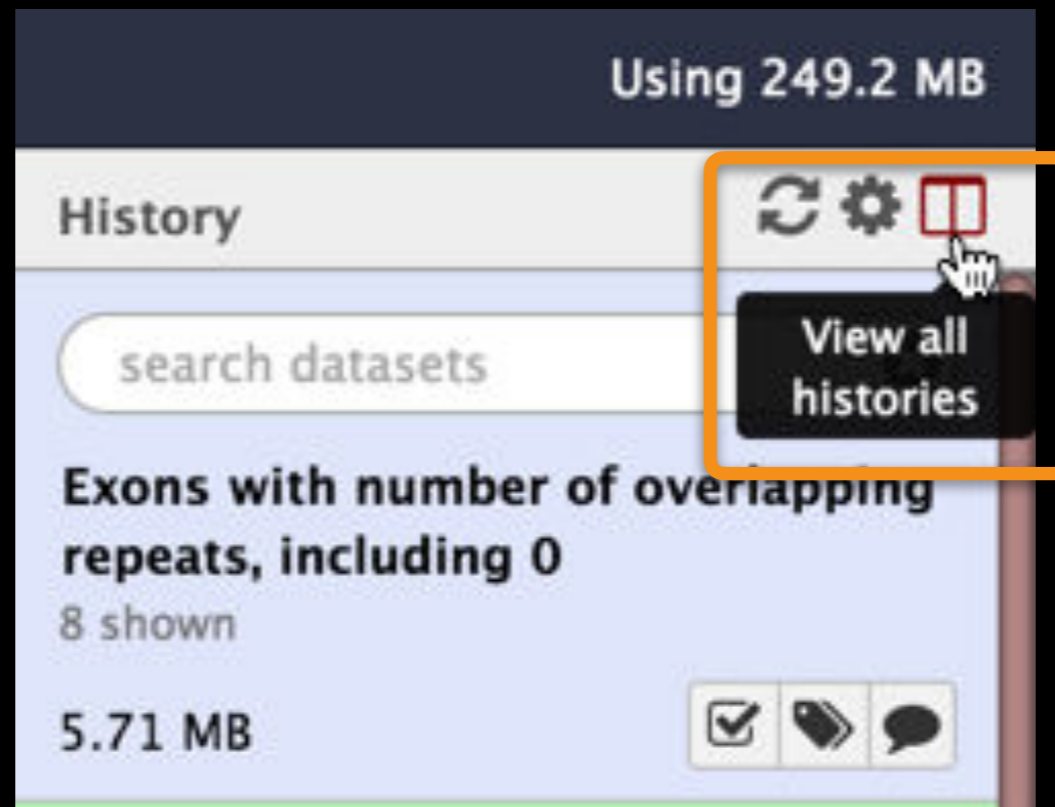
Transcript ID is embedded in Exon ID.*

How can we extract the Transcript ID from the Exon ID?

(With the transcript ID we can summarize counts for each transcript and/or get the gene ID.)

* How do we know that's a transcript ID?

Create another copy of your original history



Create another copy of your original history

The screenshot displays the UCSC Genome Browser interface with three history panels. The 'Current History' panel on the left contains a list of datasets, with the 'Done' button highlighted by an orange box. The middle panel shows a dataset named '10: Genes with # of overlapping repeats'. The right panel shows a history list with a 'Copy' button highlighted by an orange box and a mouse cursor.

Current History

- Exons with number of overlapping repeats, including 0
8 shown
5.71 MB
- 8: # of overlapping repeats per exon, distribution
- 7: Exons and number of overlapping repeats.
14,875 lines
format: **tabular**, database: hg38
- 1 uc002zly.5_cds_10_0_chr22_17105853_f 1
- 6: Cut on data 5
- 5: Compare two Datasets on data 4 and data 1
14,083 regions
format: **bed**, database: hg38

Genes with overlapping repeats
10 shown
3.91 MB

10: Genes with # of overlapping repeats
228 lines
format: **tabular**, database: hg38
--Group by c5: max[c2]

9: Join two Datasets on data 8 and data 6
623 lines
format: **tabular**, database: hg38

8: mart export.txt

Exons with overlapping repeats
4 shown
3.79 MB

4: Exons with overlapping repeats.
3: Join on data 2 and data 1
2: Repeats, chr22
1: Exons, chr22

Put the word Gene in the history name

Extract the transcript ID

Split the exon ID into its constituent parts.

uc002zmb.3_cds_0_0_chr22_17119391_r							6
uc002zmb.3	cds	0	0	chr22	17119391	r	6

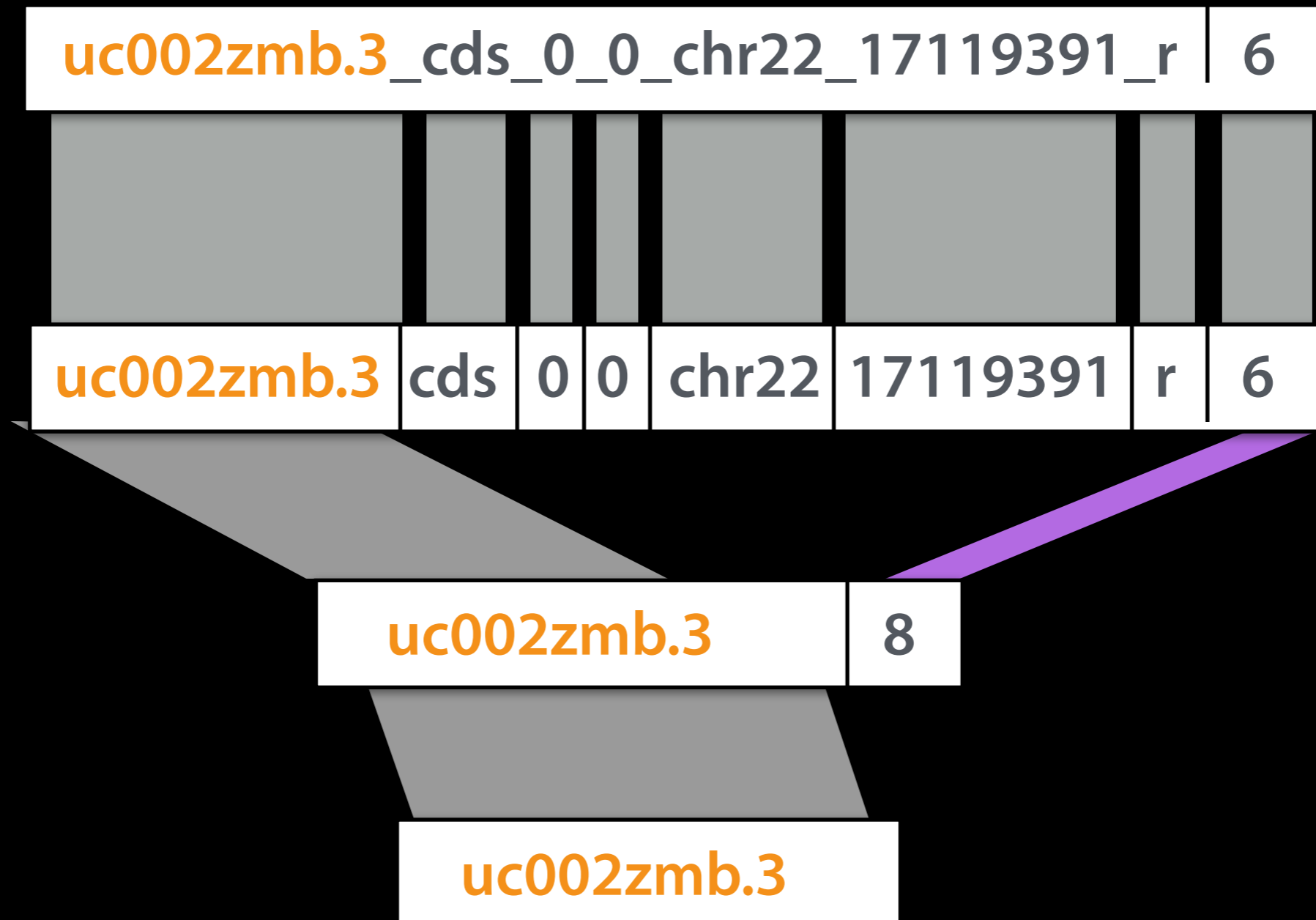
Text Manipulation → Convert delimiters to TAB
(convert underscores to tabs)

Sum the scores for all exons in each transcript



Join, Subtract and Group →
Group: by Transcript ID; Sum score

Get list of transcript IDs



Text Manipulation → Cut

Published History: Transcripts with # of overlapping repeats

Have Transcripts, now get Gene IDs

Save list of
Transcript IDs to
a file.

We'll upload it to
Ensembl BioMart

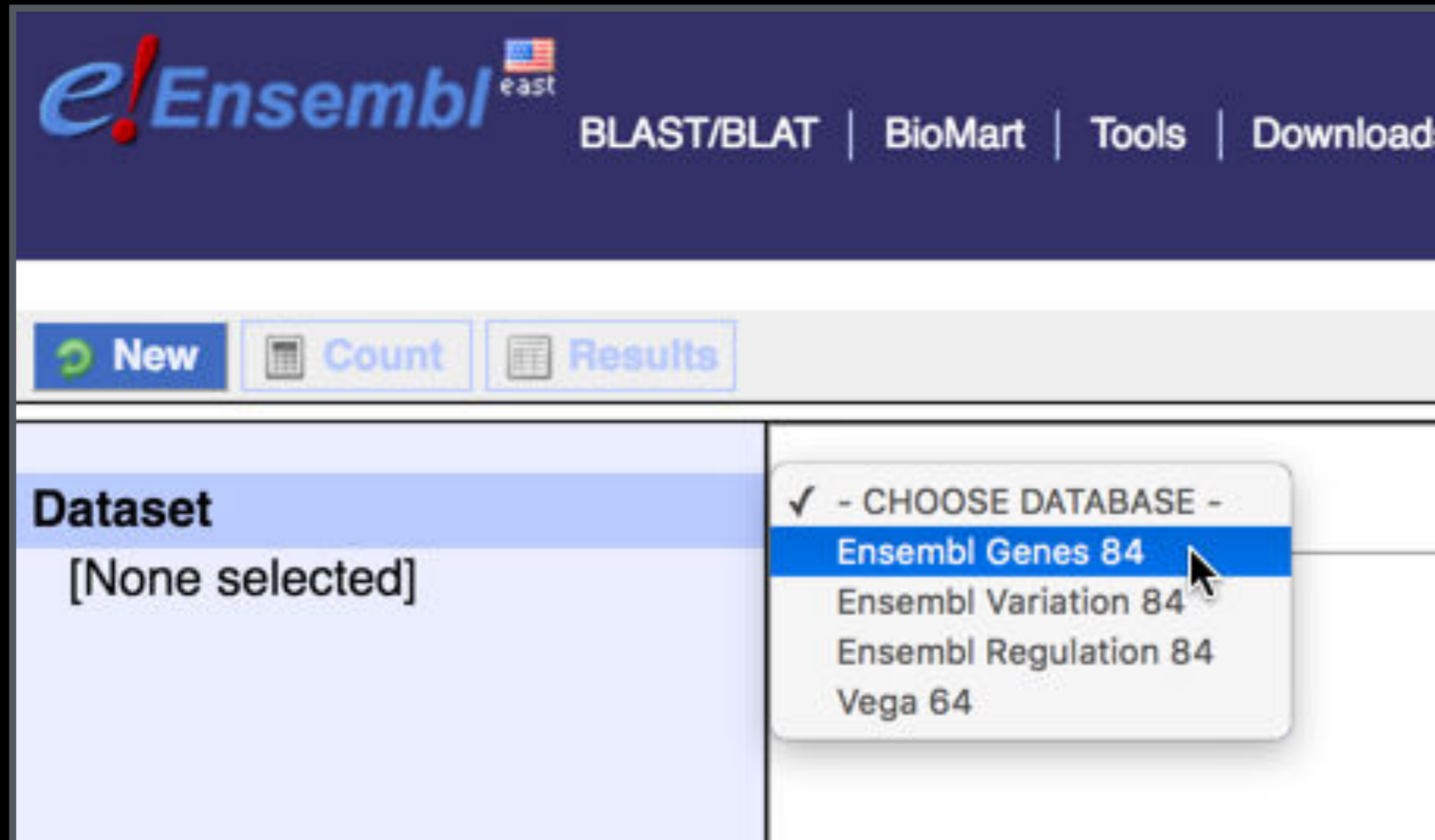
The screenshot shows the Ensembl BioMart interface. At the top, a query is titled "7: Transcripts with overlapping repeats" with a count of "628 lines". The format is set to "tabular" and the database is "hg38". Below the query title, there is a toolbar with icons for viewing, editing, deleting, and saving. The "save" icon (a floppy disk) is highlighted with an orange square. Below the toolbar, a table shows the first result: a blue bar with the number "1" and the transcript ID "uc002zly.5". At the bottom, another query is partially visible: "6: Transcripts with # of overlapping repeats".

Published History: Transcripts with # of overlapping repeats

Ensembl BioMart

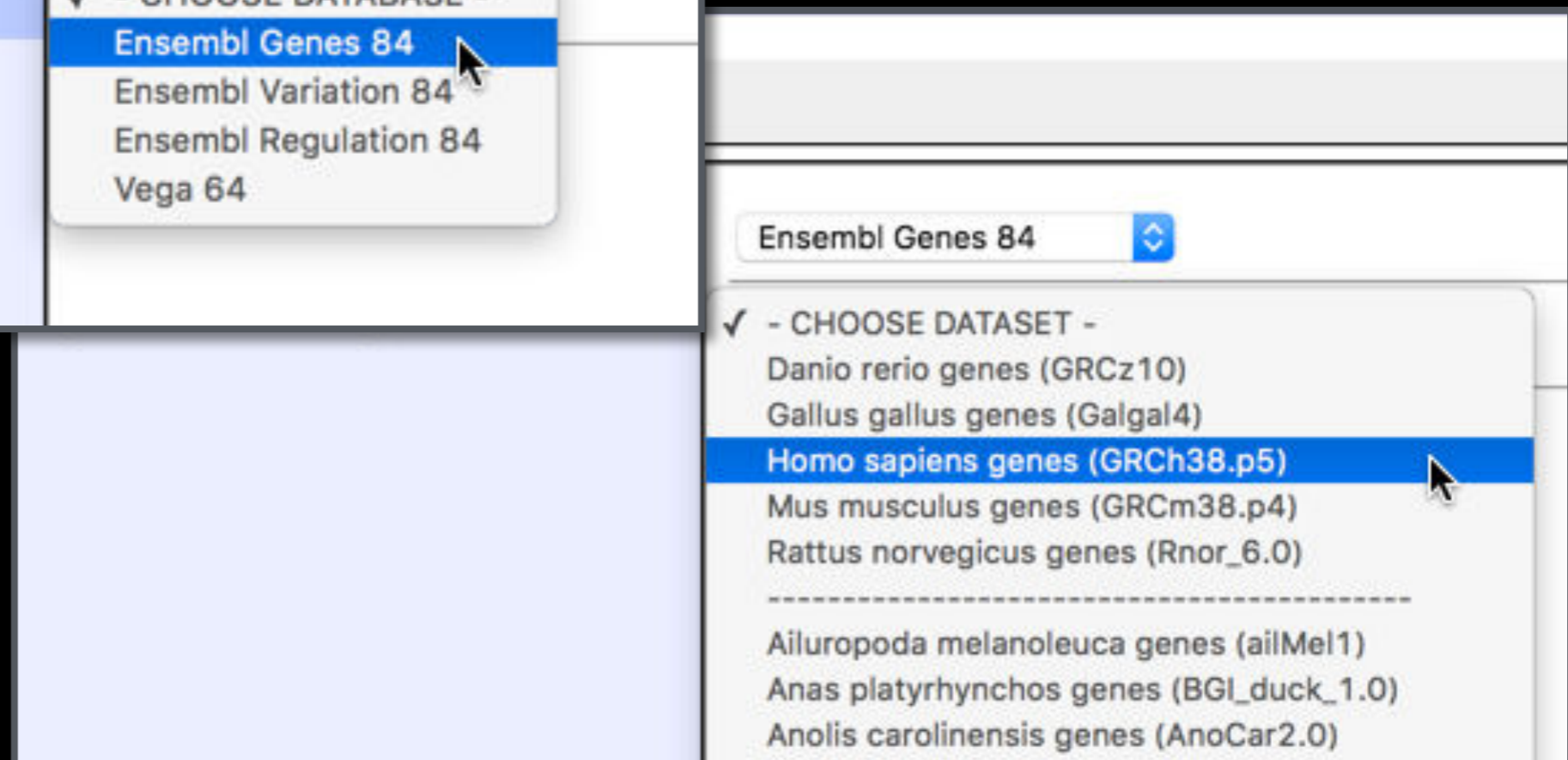
www.ensembl.org/biomart/martview

Specify Ensembl Genes 84, GRCh38.p5



The screenshot shows the Ensembl BioMart interface. At the top, the Ensembl logo is followed by navigation links: BLAST/BLAT, BioMart, Tools, and Downloads. Below this is a toolbar with 'New', 'Count', and 'Results' buttons. The 'Dataset' section is highlighted, showing '[None selected]'. A dropdown menu is open, listing the following options:

- ✓ - CHOOSE DATABASE -
- Ensembl Genes 84 (highlighted)
- Ensembl Variation 84
- Ensembl Regulation 84
- Vega 64



This screenshot shows a closer view of the 'Ensembl Genes 84' dropdown menu. The menu is open, displaying a list of species and their corresponding genome versions. The 'Homo sapiens genes (GRCh38.p5)' option is highlighted. The list includes:

- Ensembl Genes 84 (selected)
- ✓ - CHOOSE DATASET -
- Danio rerio genes (GRCz10)
- Gallus gallus genes (Galgal4)
- Homo sapiens genes (GRCh38.p5) (highlighted)
- Mus musculus genes (GRCm38.p4)
- Rattus norvegicus genes (Rnor_6.0)
-
- Ailuropoda melanoleuca genes (ailMel1)
- Anas platyrhynchos genes (BGI_duck_1.0)
- Anolis carolinensis genes (AnoCar2.0)

Ensembl BioMart:

New **Count** **Results** **★ URL** **XML** **Perl** **Help**

Dataset
Homo sapiens genes (GRCh38.p5)

Filters
[None selected]

Attributes
Ensembl Gene ID
Ensembl Transcript ID
Associated Gene Name

Dataset
[None Selected]

☒ **Features** ☐ **Variant (Germline)**
☐ **Structures** ☐ **Variant (Somatic)**
☐ **Homologues** ☐ **Sequences**

☐ **GENE:**

Ensembl

- ☒ Ensembl Gene ID
- ☒ Ensembl Transcript ID
- ☐ Ensembl Protein ID
- ☐ Ensembl Exon ID
- ☐ Description
- ☐ Chromosome Name
- ☐ Gene Start (bp)
- ☐ Gene End (bp)
- ☐ Strand
- ☐ Band
- ☐ Transcript Start (bp)
- ☐ Transcript End (bp)
- ☐ Transcription Start Site (TSS)
- ☐ Transcript length (including UTRs and CDS)
- ☐ Transcript Support Level (TSL)
- ☐ GENCODE basic annotation

Phenotype

- ☐ APPRIS annotation
- ☒ Associated Gene Name
- ☐ Associated Gene Source
- ☐ Associated Transcript Name
- ☐ Associated Transcript Source
- ☐ Transcript count
- ☐ % GC content
- ☐ Gene type
- ☐ Transcript type
- ☐ Source (gene)
- ☐ Source (transcript)
- ☐ Status (gene)
- ☐ Status (transcript)
- ☐ Version (gene)
- ☐ Version (transcript)

Specify attributes to put in output report

Ensembl BioMart:

New Count Results URL XML Perl Help

Dataset
Homo sapiens genes (GRCh38.p5)

Filters
[None selected]

Attributes
Ensembl Gene ID
Ensembl Transcript ID
Associated Gene Name
UCSC ID

Dataset
[None Selected]

☐ GOSlim GOA Accession(s) ☐ GOSlim GOA Description

External References (max 3)

☐ ArrayExpress ☐ MIM Gene Description
☐ ChEMBL ID(s) ☐ miRBase Accession(s)
☐ Clone based Ensembl gene name ☐ miRBase ID(s)
☐ Clone based Ensembl transcript name ☐ miRBase transcript name
☐ Clone based VEGA gene name ☐ PDB ID
☐ Clone based VEGA transcript name ☐ Protein (Genbank) ID [e.g. AAA0248]
☐ CCDS ID ☐ Reactome ID
☐ Database of Aberrant 3' Splice Sites (DBASS3) IDs ☐ Reactome gene ID
☐ DBASS3 Gene Name ☐ Reactome transcript ID
☐ Database of Aberrant 5' Splice Sites (DBASS5) IDs ☐ RefSeq mRNA [e.g. NM_001195597]
☐ DBASS5 Gene Name ☐ RefSeq mRNA predicted [e.g. XM_0]
☐ EMBL (Genbank) ID ☐ RefSeq ncRNA [e.g. NR_002834]
☐ Ensembl Human Transcript IDs ☐ RefSeq ncRNA predicted [e.g. XR_1]
☐ Ensembl Human Translation IDs ☐ RefSeq Protein ID [e.g. NP_001005]
☐ LRG to Ensembl link gene ☐ RefSeq Predicted Protein ID [e.g. XI]
☐ LRG to Ensembl link transcript ☐ Rfam ID
☐ EntrezGene ID ☐ Rfam transcript name
☐ EntrezGene transcript name ID ☒ UCSC ID
☐ Human Protein Atlas Antibody ID ☐ Unigene ID
☐ VEGA gene ID(s) (OTTG) ☐ UniParc
☐ VEGA transcript ID(s) (OTTT)

Specify attributes to put in output report

Ensembl BioMart:

The screenshot shows the Ensembl BioMart query interface. On the left sidebar, the 'Results' tab is highlighted with an orange box and a red number 4. Below it, the 'Filters' tab is also highlighted with an orange box and a red number 1. The main panel is titled 'Please restrict your query using criteria below' and contains several filter sections. The 'GENE' section is expanded, showing three options: 'Limit to genes (external references)...', 'Input external references ID list [Max 500 advised]', and 'Limit to genes (microarray probes/probesets)...'. The 'Input external references ID list' option is selected with a blue checkmark. To its right, there is a dropdown menu for 'with HGNC ID(s)' set to 'Only', and a text input field containing 'UCSC ID(s) [e.g. uc002cqj.3]' which is highlighted with an orange box and a red number 2. Below this, there is a 'Choose File' button and a text input field containing 'Galaxy6-[Trans...eats].tabular' which is highlighted with an orange box and a red number 3. The 'Limit to genes (microarray probes/probesets)...' option is also visible, with a dropdown menu for 'with Affymetrix Microarray huex 1 0 st v2 probeset ID(s)' set to 'Only'. At the bottom, there is an option for 'Input microarray probes/probesets ID list [Max 500 advised]' with a dropdown menu for 'Codelink probe ID(s) [e.g. GE550734]'.

New Count **Results** 4

URL XML Perl Help

Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)

Dataset
Homo sapiens genes (GRCh38.p5)

Filters 1

UCSC ID(s) [e.g. uc002cqj.3] [ID-list specified]

Attributes

Ensembl Gene ID
Ensembl Transcript ID
Associated Gene Name
UCSC ID

Dataset
[None Selected]

REGION:

GENE:

☐ Limit to genes (external references)... with HGNC ID(s) ☒ Only ☐ Excluded

☒ Input external references ID list [Max 500 advised] 2 UCSC ID(s) [e.g. uc002cqj.3]

☐ Limit to genes (microarray probes/probesets)... with Affymetrix Microarray huex 1 0 st v2 probeset ID(s) ☒ Only ☐ Excluded

☐ Input microarray probes/probesets ID list [Max 500 advised]

Codelink probe ID(s) [e.g. GE550734]

Choose File No file chosen

Choose File Galaxy6-[Trans...eats].tabular 3

Specify which genes we want this information for

Ensembl BioMart:

New

Count

Results

★ URL

XML

Perl

Help

Dataset

Homo sapiens genes (GRCh38.p5)

Filters

UCSC ID(s) [e.g. uc002cqj.3]: [ID-list specified]

Attributes

Ensembl Gene ID

Ensembl Transcript ID

Associated Gene Name

UCSC ID

Dataset

[None Selected]

Export all results to

Email notification to

View

10 rows as HTML

Unique results only

File

TSV

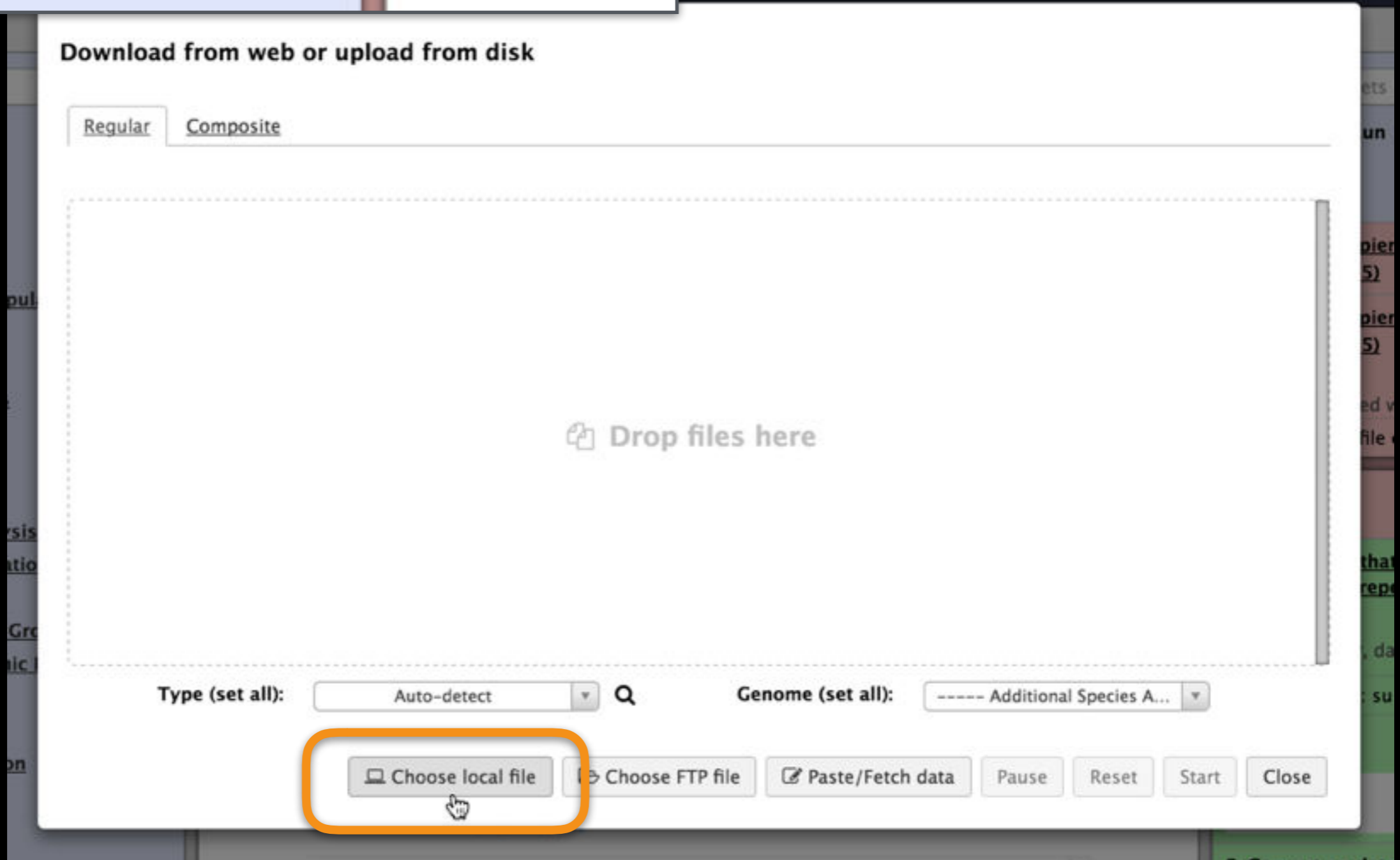
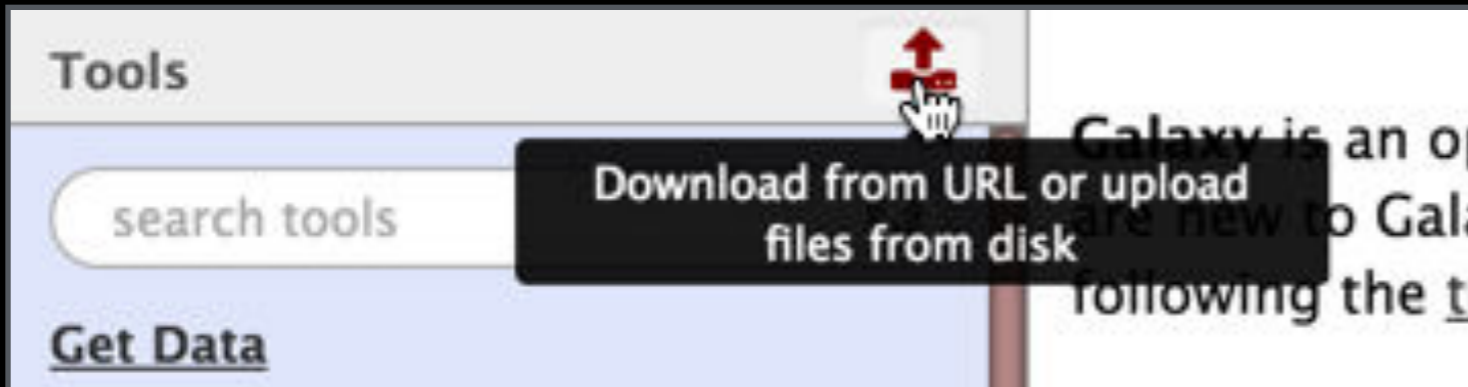
Unique results only

Go

Ensembl Gene ID	Ensembl Transcript ID	Associated Gene Name	UCSC ID
ENSG00000177663	ENST00000319363	IL17RA	uc002zly.5
ENSG00000183307	ENST00000331437	CECR6	uc002zmb.3
ENSG00000099968	ENST00000317582	BCL2L13	uc002zmw.5
ENSG00000099968	ENST00000543133	BCL2L13	uc002zmx.4
ENSG00000099968	ENST00000355028	BCL2L13	uc002zmy.5
ENSG00000099968	ENST00000418951	BCL2L13	uc002zmz.4
ENSG00000243156	ENST00000441493	MICAL3	uc002zng.5
ENSG00000184979	ENST00000215794	USP18	uc002zny.4
ENSG00000100056	ENST00000252137	DGCR14	uc002zou.4
ENSG00000100075	ENST00000451283	SLC25A1	uc002zoy.5



Save the results to a file for uploading into Galaxy

Get Genes into Galaxy



Chose local file, then Start, then Close






Get Gene IDs into Galaxy

8: mart_export.txt   




624 lines

format: **tabular**, database: ?

uploaded tabular file






    

1	2
Ensembl Gene ID	Ensembl Transcript ID

7: Transcripts with overlapping repeats   

628 lines

format: **tabular**, database: **hg38**

1
uc002zly.5

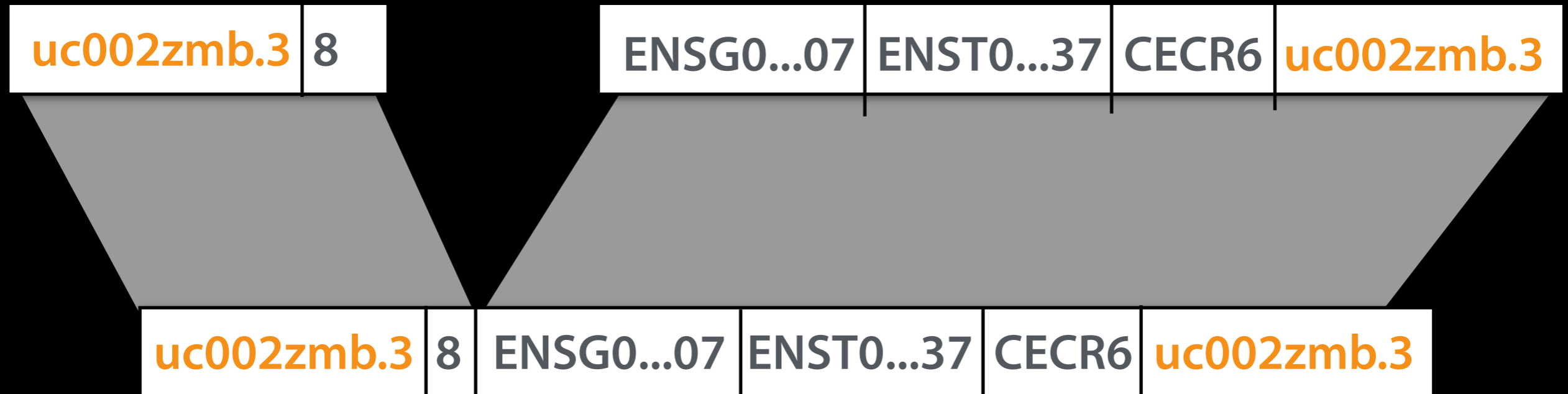
Upload file from BioMart.
Note that we lost 4-5 transcripts

Do we care?
Can we find out which were lost?

Unite our Transcript Scores with Biomart info

Transcript Scores

Biomart Info






Join, Subtract and Group →
Join: Transcripts with score and Biomart dataset;
join on UCSC transcript ID

Unite our Transcript Scores with Biomart info

Join two Datasets side by side on a specified field (Galaxy Version 2.0.2) Options




Join

   8: mart_export.txt

using column

Column: 4

with

   6: Transcripts with # overlapping repeats

and column

Column: 1

Keep lines of first input that do not join with second input


No

Keep lines of first input that are incomplete

No

Fill empty columns

No

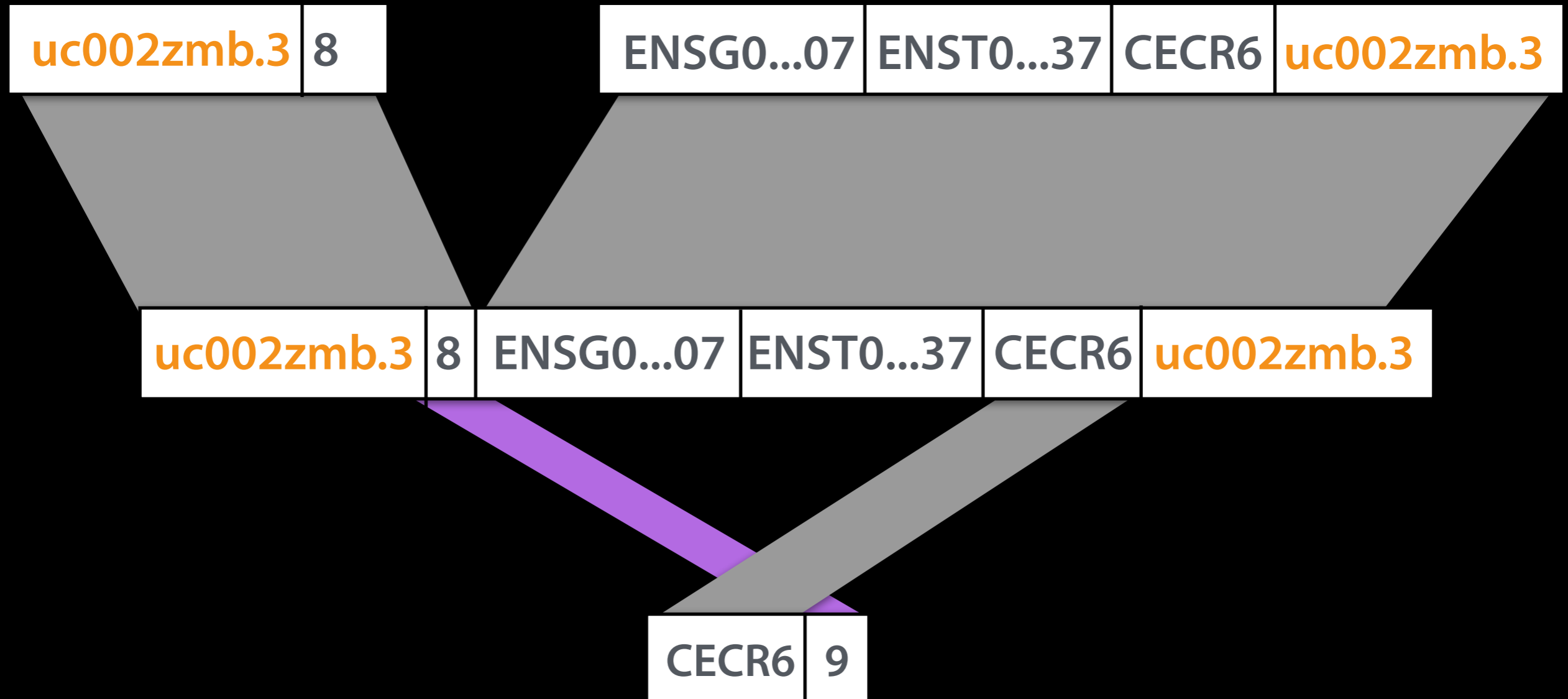
 **Execute**

Join, Subtract and Group → Join

Assign scores to genes

Transcript Scores

Biomart Info



Join, Subtract and Group →
Group: by gene symbol; Max score

Published History: Genes with overlapping repeats

Now have a list of genes with # overlapping repeats

1	2
AC007326.1	4
ACR	2
ADM2	1
ADRBK2	1
ADSL	2
ANKRD54	1
AP000349.2	1
APOBEC3B	2
APOBEC3F	1
APOBEC3H	1
APOL3	1
APOL4	2
APOL5	1
APOL6	1
ARFGAP3	1
ARHGAP8	2
ARSA	1
ASCC2	2
ASPHD2	1
ATP6V1E1	1

History

search datasets

Genes with overlapping repeats
10 shown
3.91 MB

10: Genes with # of overlapping repeats
228 lines
Format: tabular, database: hg38
--Group by c5: max[c2]

9: Join two Datasets on data 8 and data 6
623 lines
Format: tabular, database: hg38

Published History: Genes with overlapping repeats

Yay! We have a list of genes and overlap counts!*

Now, what can we do with that?

All sorts of things.

* Technically, we have a list of gene symbols, and the maximum number of overlapping repeats from any of its transcripts. We also haven't done things like normalize the scores based on gene length. Your mileage may vary. Let's not sweat the details.

GO Term Enrichment

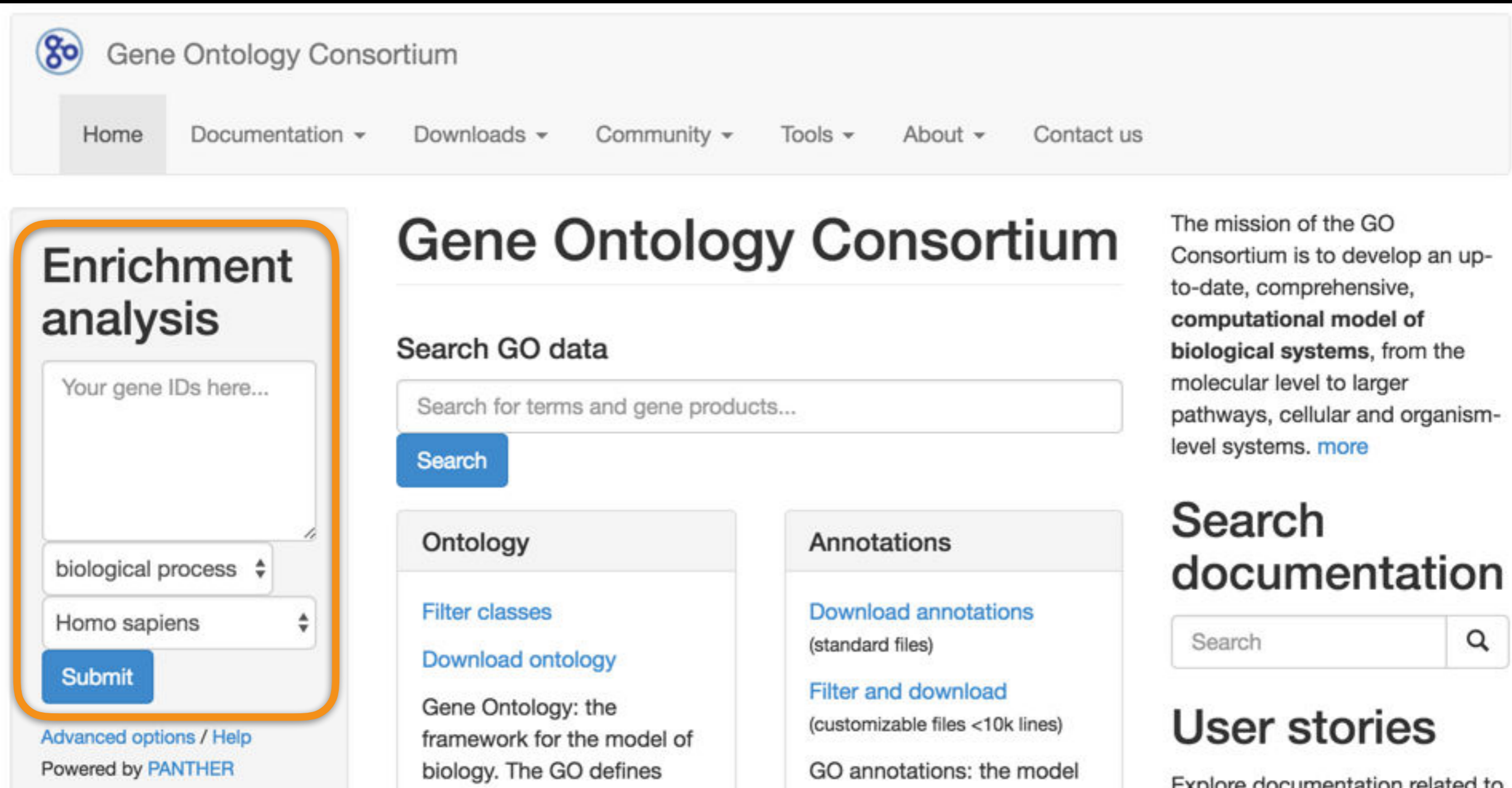
Do genes with particular functions tend to occur in this list more often than they would by random chance?



GO: Create a list of just the gene symbols

Remember how?

(Stop or) GO: Can do this step, or just watch



The screenshot shows the Gene Ontology Consortium website. The top navigation bar includes links for Home, Documentation, Downloads, Community, Tools, About, and Contact us. The main header reads "Gene Ontology Consortium". On the left, a sidebar titled "Enrichment analysis" is highlighted with an orange border. It contains a text input field for "Your gene IDs here...", two dropdown menus for "biological process" and "Homo sapiens", and a "Submit" button. Below the sidebar, there are links for "Advanced options / Help" and "Powered by PANTHER". The main content area features a "Search GO data" section with a search bar and a "Search" button. Below this are two columns: "Ontology" with links for "Filter classes" and "Download ontology", and "Annotations" with links for "Download annotations (standard files)" and "Filter and download (customizable files <10k lines)". To the right of the main content, there is a mission statement, a "Search documentation" section with a search bar, and a "User stories" section.

Gene Ontology Consortium

Home Documentation Downloads Community Tools About Contact us

Enrichment analysis

Your gene IDs here...

biological process

Homo sapiens

Submit

[Advanced options / Help](#)
Powered by [PANTHER](#)

Gene Ontology Consortium

Search GO data

Search for terms and gene products...

Search

Ontology

[Filter classes](#)
[Download ontology](#)

Gene Ontology: the framework for the model of biology. The GO defines

Annotations

[Download annotations](#)
(standard files)

[Filter and download](#)
(customizable files <10k lines)

GO annotations: the model

The mission of the GO Consortium is to develop an up-to-date, comprehensive, **computational model of biological systems**, from the molecular level to larger pathways, cellular and organism-level systems. [more](#)

Search documentation

Search

User stories

Explore documentation related to

<http://geneontology.org/>

GO: Results from whole genome, 1 or more overlapping repeats (8969 genes)

Displaying only results with P<0.05; [click here to display all results](#)

	Homo sapiens (REF)	upload 1 (▼ Hierarchy NEW! ?)				
GO biological process complete	#	#	expected	Fold Enrichment	+/-	P value
chromatin modification	289	196	123.50	1.59	+	6.66E-06
↳ chromatin organization	636	376	271.78	1.38	+	5.60E-06
↳ chromosome organization	984	555	420.49	1.32	+	6.19E-07
↳ organelle organization	3133	1636	1338.83	1.22	+	4.94E-14
↳ cellular component organization	5133	2606	2193.49	1.19	+	1.25E-19
↳ cellular process	14559	6671	6221.52	1.07	+	4.95E-22
↳ cellular component organization or biogenesis	5288	2688	2259.73	1.19	+	7.21E-21
↳ macromolecular complex subunit organization	1983	1021	847.40	1.20	+	4.89E-06
peptidyl-lysine modification	314	194	134.18	1.45	+	4.87E-03
↳ peptidyl-amino acid modification	855	456	365.37	1.25	+	1.34E-02
↳ cellular protein modification process	2836	1397	1211.91	1.15	+	9.10E-05
↳ protein modification process	2836	1397	1211.91	1.15	+	9.10E-05
↳ protein metabolic process	4036	1908	1724.71	1.11	+	5.29E-03
↳ macromolecule metabolic process	7359	3685	3144.73	1.17	+	1.39E-28
↳ organic substance metabolic process	9032	4308	3859.66	1.12	+	7.16E-18
↳ metabolic process	9443	4480	4035.29	1.11	+	2.03E-17
↳ primary metabolic process	8601	4133	3675.48	1.12	+	6.53E-19
↳ macromolecule modification	3007	1480	1284.99	1.15	+	3.58E-05

Published History: Gene-Repeat overlap, entire genome

GO: Results from whole genome, 2 or more overlapping repeats (2759 genes)

Displaying only results with P<0.05; [click here to display all results](#)

	Homo sapiens (REF)	upload 1 (▼ Hierarchy NEW! ?)				
GO biological process complete	#	#	expected	Fold Enrichment	+/-	P value
membrane depolarization during action potential	39	19	5.22	3.64	+	2.01E-02
↳ biological regulation	11384	1776	1523.15	1.17	+	2.20E-18
↳ membrane depolarization	61	24	8.16	2.94	+	3.99E-02
regulation of histone methylation	59	25	7.89	3.17	+	7.12E-03
↳ regulation of histone modification	129	43	17.26	2.49	+	9.63E-04
↳ regulation of primary metabolic process	5720	1046	765.32	1.37	+	5.02E-27
↳ regulation of metabolic process	6087	1096	814.43	1.35	+	2.49E-26
↳ regulation of biological process	10767	1708	1440.60	1.19	+	1.66E-20
↳ regulation of macromolecule metabolic process	5730	1052	766.66	1.37	+	6.06E-28
↳ regulation of cellular metabolic process	5781	1058	773.48	1.37	+	1.21E-27
↳ regulation of cellular process	10292	1651	1377.04	1.20	+	1.75E-21
↳ regulation of chromatin organization	152	50	20.34	2.46	+	1.43E-04
↳ regulation of chromosome organization	272	66	36.39	1.81	+	4.52E-02
↳ regulation of organelle organization	1097	211	146.78	1.44	+	1.37E-03
↳ regulation of cellular component organization	2246	409	300.51	1.36	+	1.22E-06
histone lysine methylation	64	27	8.56	3.15	+	2.90E-03
↳ histone methylation	84	31	11.24	2.76	+	6.88E-03
↳ histone modification	337	88	45.09	1.95	+	5.91E-05
↳ covalent chromatin modification	346	92	46.29	1.99	+	1.16E-05
↳ macromolecule metabolic process	7359	1260	984.62	1.28	+	4.66E-23
↳ organic substance metabolic process	9032	1384	1208.46	1.15	+	1.23E-07

GO: Results from whole genome, 3 or more overlapping repeats (986 genes)

Displaying only results with P<0.05; [click here to display all results](#)

	Homo sapiens (REF)	upload_1 (▼ Hierarchy NEW! ?)				
GO biological process complete	#	#	expected	Fold Enrichment	+/-	P value
histone H3-K4 methylation	32	12	1.55	7.75	+	7.35E-04
↳ histone lysine methylation	64	16	3.10	5.17	+	1.41E-03
↳ histone methylation	84	19	4.07	4.67	+	4.79E-04
↳ histone modification	337	43	16.31	2.64	+	1.67E-04
↳ covalent chromatin modification	346	44	16.75	2.63	+	1.26E-04
↳ macromolecule metabolic process	7359	496	356.16	1.39	+	1.25E-15
↳ organic substance metabolic process	9032	524	437.13	1.20	+	2.08E-04
↳ metabolic process	9443	535	457.02	1.17	+	4.42E-03
↳ chromatin organization	636	80	30.78	2.60	+	2.59E-10
↳ chromosome organization	984	93	47.62	1.95	+	1.08E-05
↳ organelle organization	3133	214	151.63	1.41	+	8.13E-04
↳ cellular component organization	5133	319	248.43	1.28	+	2.57E-03
↳ cellular process	14559	773	704.62	1.10	+	9.14E-03
↳ cellular component organization or biogenesis	5288	329	255.93	1.29	+	1.31E-03
↳ macromolecular complex subunit organization	1983	148	95.97	1.54	+	9.07E-04
↳ primary metabolic process	8601	519	416.27	1.25	+	4.01E-07
↳ cellular macromolecule metabolic process	6693	475	323.93	1.47	+	3.28E-19
↳ cellular metabolic process	8525	505	412.59	1.22	+	2.32E-05

Published History: Gene-Repeat overlap, entire genome

Agenda: Day 1

- 9:00 Welcome
- 9:20 Basic Analysis with Galaxy
A worked example demonstrating Galaxy Basics
- 10:45 Break
- 11:00 Integrating with other tools: BioMart & GO
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http://bit.ly/UR_GXY_2016

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Some Galaxy Terminology

Dataset:

Any input, output or intermediate set of data + metadata

History:

A series of inputs, analysis steps, intermediate datasets, and outputs

Workflow:

A series of analysis steps

Can be repeated with different data

Exons and Repeats *History* → Reusable *Workflow*?

- The analysis we just finished was about
 - Human chr22
 - Overlap between exons and repeats
 - And then rolling that up to genes
- But, ...
 - is there anything inherent in the analysis **about humans, exons or repeats?**

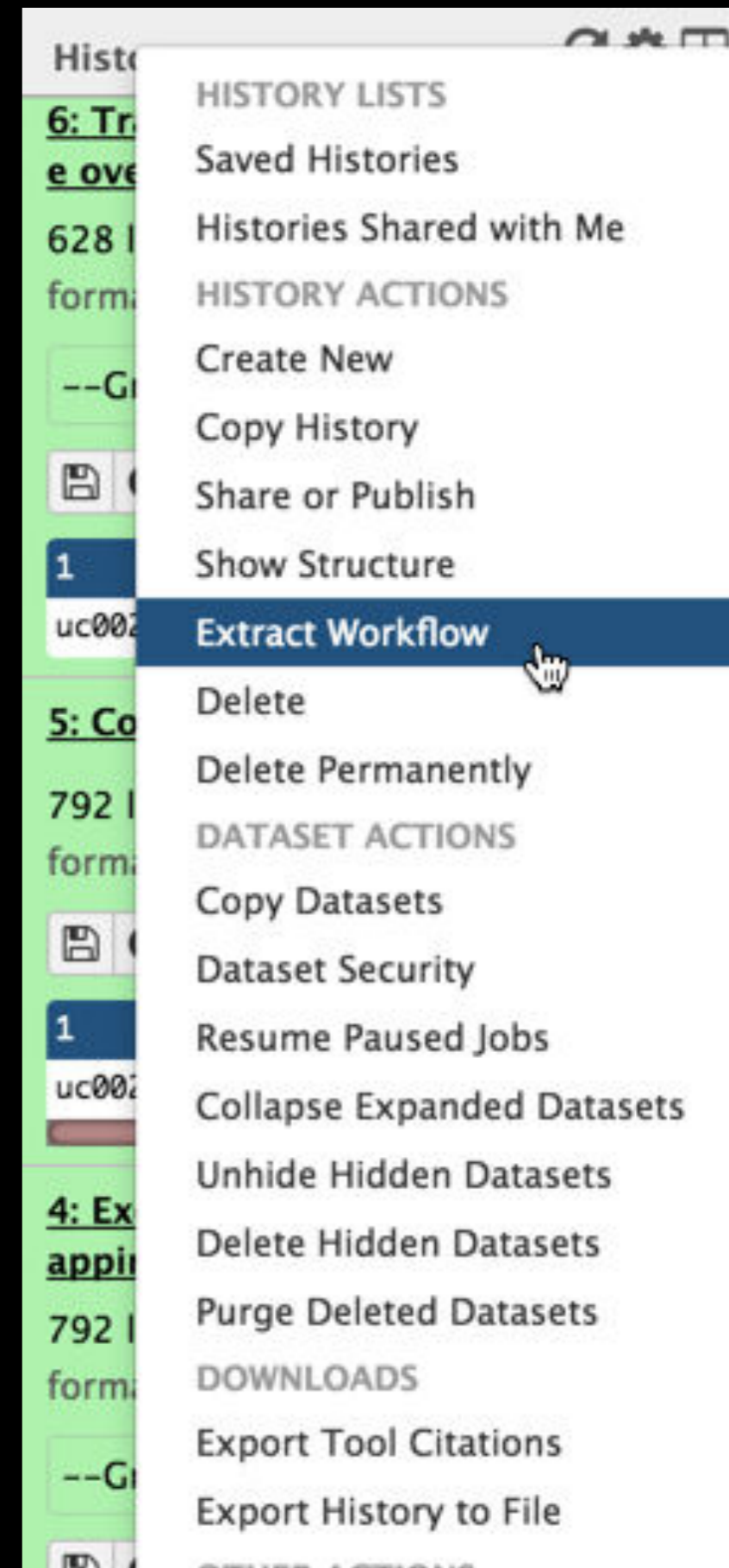
Create a Workflow from a History

Extract Workflow from history

Create a workflow from this history.
Edit it to make some things clearer.



(cog) → Extract Workflow



Create a Workflow from a History: ...

The following list contains each tool that was run to create the datasets in your current history. Please select those that you wish to include in the workflow.

Tools which cannot be run interactively and thus cannot be incorporated into a workflow will be shown in gray.

Workflow name

Workflow constructed from history 'UR 101 Test Run'

Create Workflow

Check all

Uncheck all

Tool

History items created

UCSC Main

This tool cannot be used in workflows

1: Exons, chr22

☒ Treat as input dataset

UCSC Main

This tool cannot be used in workflows

2: Repeats, chr22

☒ Treat as input dataset

Join

☒ Include "Join" in workflow

3: Join on data 2 and data 1

Group

☒ Include "Group" in workflow

4: Exons with # of overlapping repeats.

Convert

☒ Include "Convert" in workflow

5: Convert on data 4




Group

☒ Include "Group" in workflow

6: Transcripts that have overlapping repeats

History

--Group by c1: sum[c8]

1 2
uc002zly.5 2

5: Convert on data 4

792 lines
format: **tabular**, database: **hg38**

2 3 4 5 6 7 8
02zly.5 cds 10 0 chr22 17105853 f 1

4: Exons with # of overlapping repeats.

792 lines
format: **tabular**, database: **hg38**

--Group by c4: count[c1]

2
002zly.5_cds_10_0_chr22_17105853_f 1

3: Join on data 2 and data 1

911 regions
format: **interval**, database: **hg38**

Wait ...

Can this whole analysis be a useful workflow?
(No.)

Are there parts of this analysis are a good candidate for a **workflow** - something to be reused on other data?

The first 4 items count overlaps between features.
That might be useful.

Create a Workflow from a History: ...

The following list contains each tool that was run to create the datasets in your current history. Please select those that you wish to include in the workflow.

Tools which cannot be run interactively and thus cannot be incorporated into a workflow will be shown in gray.

Workflow name

count overlapping features

Create Workflow

Check all

Uncheck all

Tool

History items created

UCSC Main

This tool cannot be used in workflows

1: Exons, chr22

☒ Treat as input dataset

UCSC Main

This tool cannot be used in workflows

2: Repeats, chr22

☒ Treat as input dataset

Join

☒ Include "Join" in workflow

3: Join on data 2 and data 1

Group

☒ Include "Group" in workflow

4: Exons with # of overlapping repeats.

Convert

☐ Include "Convert" in workflow

5: Convert on data 4

Group

☐ Include "Group" in workflow

6: Transcripts that have overlapping repeats

History

--Group by c1: sum[c8]



1 2

uc002zly.5 2

5: Convert on data 4



792 lines

format: **tabular**, database: **hg38**



2 3 4 5 6 7 8

002zly.5 cds 10 0 chr22 17105853 f 1

4: Exons with # of overlapping repeats.



792 lines

format: **tabular**, database: **hg38**

--Group by c4: count[c1]



2

002zly.5_cds_10_0_chr22_17105853_f 1

3: Join on data 2 and data 1



911 regions

format: **interval**, database: **hg38**

Workflow editor

Tools

search tools

Inputs

Get Data

Send Data

Lift-Over

Text Manipulation

Filter and Sort

NGS: QC and manipulation

NGS: DeepTools

NGS: Mapping

NGS: RNA Analysis

NGS: SAM Tools

NGS: BAM Tools

NGS: Picard

NGS: Variant Analysis

NGS: VCF Manipulation

NGS: ChIP-seq

Join, Subtract and Group

Operate on Genomic Intervals

BEDtools

Convert Formats

FASTA manipulation

Extract Features

Fetch Sequences

Fetch Alignments

Workflow Canvas | count overlapping features

```
graph LR; A[Input dataset output] --> C[Join with output interval]; B[Input dataset output] --> C; C --> D[Group Select data out_file1 tabular];
```

Details

Edit Workflow Attributes

Name:
count overlapping features

Tags:

Apply tags to make it easy to search for and find items with the same tag.

Annotation / Notes:
Describe or add notes to workflow
Add an annotation or notes to a workflow; annotations are available when a workflow is viewed.

Published Workflow: Feature Overlap Counting

Workflow editor: save your changes

The screenshot displays a workflow editor interface. On the left, a 'Tools' sidebar lists various categories such as 'Inputs', 'Get Data', 'Send Data', 'Text Manipulation', 'Filter and Sort', and 'NGS: QC and manipulation'. The main 'Workflow Canvas' is titled 'count overlapping features' and shows a workflow with two 'Input dataset' blocks connected to a 'Join' block. The 'Join' block has a 'with' field set to 'output (interval)'. A context menu is open over the 'Join' block, showing options: 'Save', 'Run', 'Edit Attributes', 'Auto Re-layout', and 'Close'. The 'Save' option is highlighted. In the bottom right corner, there is a small preview window showing a grid of colored squares.

Published Workflow: Feature Overlap Counting

Workflows

Run / test it

Guided: rerun with same inputs

Workflow → Run

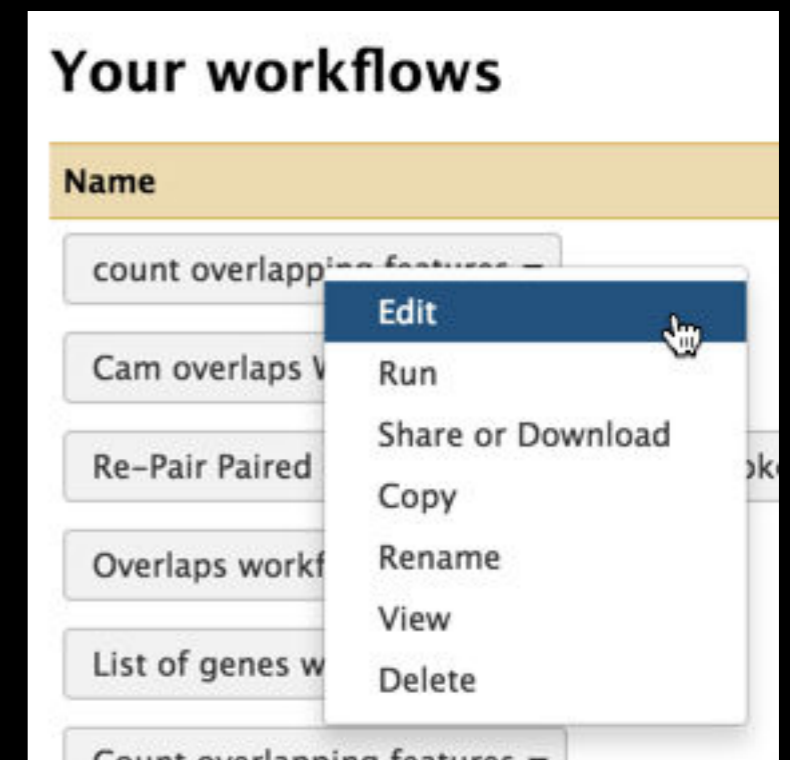
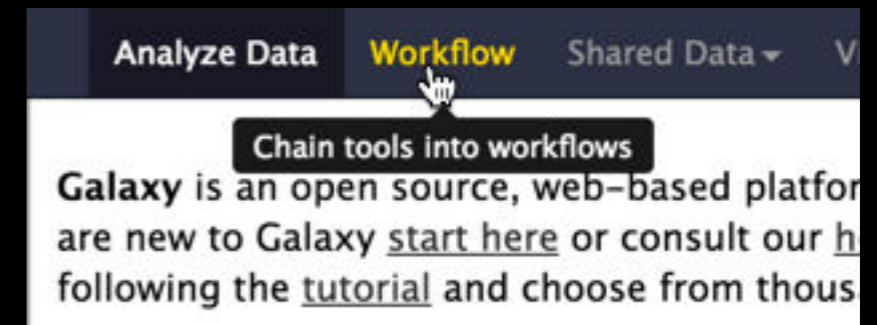
Did that work?

On your own:

Count # of exons overlapping each repeat

Did that work? *Why not?*

Edit workflow: doc assumptions



Published Workflow: Feature Overlap Counting

Workflows: Sweet spots

Short, well-defined tasks, with well-defined inputs and outputs.

Analysis pipelines for large experiments with many samples where sample and data preparation protocols are the same throughout.

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http://bit.ly/UR_GXY_2016

Quick Poll: Are you ...


1. An RNA-Seq novice
2. An RNA-Seq apprentice
3. An RNA-Seq guru

Yes, those are your only choices.

<http://galaxyproject.org>

RNA-Seq Analysis: Get the Data

Create new history

 (cog) → Create New

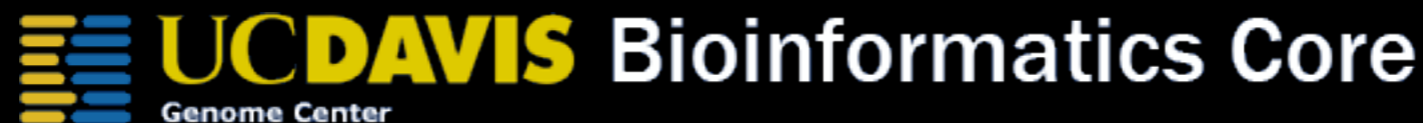
Import:

Shared Data → Data Libraries → Training → RNA-Seq*

→ UC-Davis → Raw Reads

Select first two

MeOH_REP1_R1, MeOH_REP1_R2



* RNA-Seq example datasets from the 2013 UC Davis Bioinformatics Short Course. <http://bit.ly/ucdbsc2013>

NGS Data Quality Control

- FASTQ format
- Examine quality in an RNA-Seq dataset
- Trim/filter as we see fit, hopefully without breaking anything.

Quality Control is not sexy.

But it is vital.

What is FASTQ?

- Specifies sequence (FASTA) and quality scores (PHRED)
- Text format, 4 lines per entry

```
@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
! ' ' * ( ( ( ( * * * + ) ) % % % + + ) ( % % % % ) . 1 * * * - + * ' ' ) ) * * 55CCF>>>>>CCCCCCC65
```

- FASTQ is such a cool standard, there are 3 (or 5) of them!

[illegible]

http://en.wikipedia.org/wiki/FASTQ_format

NGS Data Quality: Assessment tools

NGS QC and Manipulation → **FastQC**

Generates summary quality information.

FastQC Read Quality reports (Galaxy Version 0.63)

VersionsOptions

Short read data from your current history

1: MeOH_REP1_R1.fastq

Contaminant list

Nothing selected

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer CAAGCAGAAGACGGCATACGA

Submodule and Limit specifying file

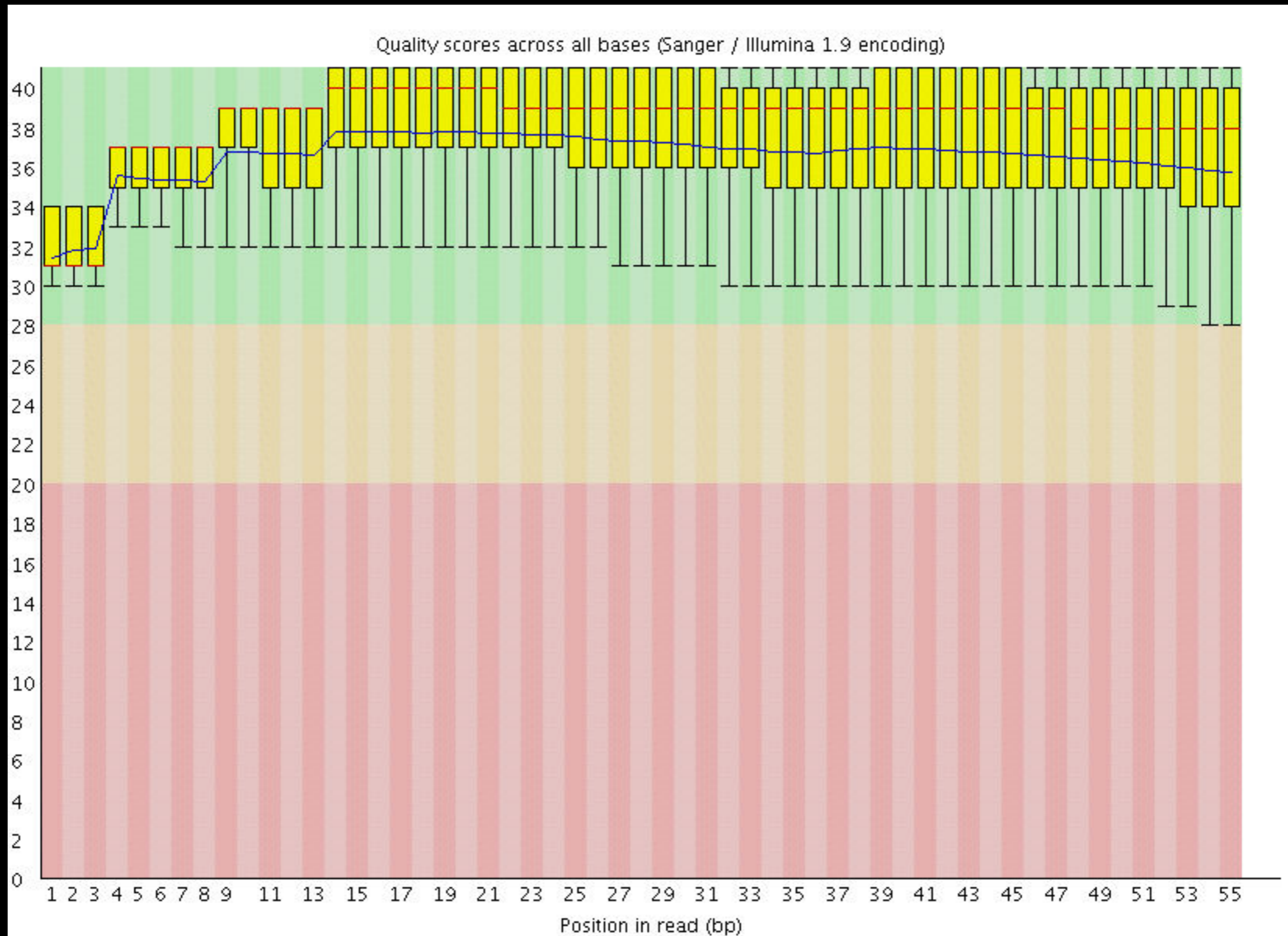
Nothing selected

a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for the each submodules warning parameter

✓ Execute

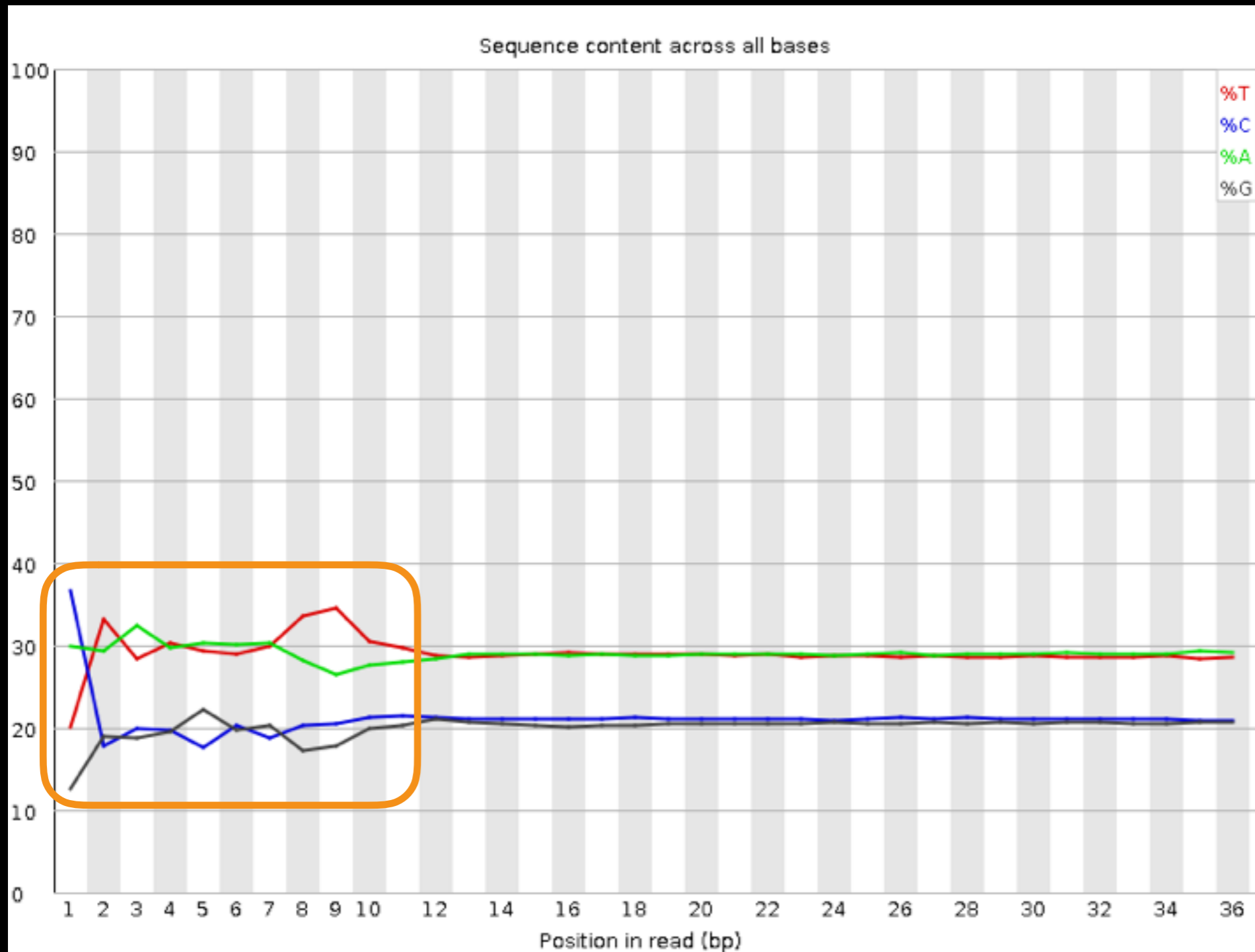
<http://bit.ly/FastQCBoxPlot>

NGS Data Quality: Assessment tools



<http://bit.ly/FastQCBoxPlot>

NGS Data Quality: Sequence bias at front of reads?



From a sequence specific bias that is caused by use of random hexamers in library preparation.

Hansen, *et al.*, "Biases in Illumina transcriptome sequencing caused by random hexamer priming" *Nucleic Acids Research*, Volume 38, Issue 12 (2010)

NGS Data Quality: Sequencing **Artifacts**

And only now we notice a problem with MeOH Rep1 R2 (the reverse reads)

Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CTGTGTATTTGTCAATTTTCTTCTCCACGTTCTTCTCGGCCTGTTTCCGTAGCCT	590	0.3541692929220167	No Hit
TT	342	0.2052981325073385	No Hit
CGGCCACAAATAAACACAGAAATAGTCCAGAATGTCACAGGTCCAGGGCAGAGGA	325	0.19509325457568719	No Hit
CTGCATTATAAAAAGGACAGCCAGATATCAACTGTTACAGAAATGAAATAAGACG	230	0.13806599554587093	No Hit
CGGCCGCAAATAAACACAGAAATAGTCCAGAATGTCACAGGTCCAGGGCAGAGGA	199	0.11945710049403614	No Hit
GTCAGCTCAACTTGTAGGCCCCAAAAGAAAACAGCGTCTTACTGGGGAGGGATAT	197	0.11825652661972422	No Hit

NGS QC and Manipulation → **Remove sequencing artifacts**

(But this will break pairings. More on that in a bit.)

Or, can rely on mapper to just not map them.

Common Trimming options

- **Drop the first n columns** from your reads
- **Drop the last n columns** from your reads
- **Sliding window** approach: only keep regions that are above a specified quality threshold
- **Keep or drop whole read** based on overall quality

Common Trimming Pitfalls

Broken Pairs

Often, one side of a pair passes QC, while the other does not.

Broken pairings can affect results in subtle or drastic ways

Short short reads.

QC may reduce reads to a length at which their mapping is no longer meaningful.

Need help with Trimming? (and anything else)

That's a **whole lotta options...**

Choices you make now have impact on downstream tools

NGS = a whole lotta options in general

What to do?

How to better understand bioinformatics & Galaxy

- **Experiment.** (You are already used to the idea and)
Galaxy makes it easy
- **Read** tool documentation and tool and method review papers
- **Get Help!**
 - <http://biostars.org/>
 - <http://seqanswers.com/>
 - <https://biostar.usegalaxy.org/>
 - <http://galaxyproject.org/search>



Trimmomatic to the rescue

Trimmomatic flexible read trimming tool for Illumina NGS data (Galaxy Tool Version 0.32.3) Options

Paired end data?

Input Type
Pair of datasets

Input FASTQ file (R1/first of pair)
 1: MeOH_REP1_R1

Input FASTQ file (R2/second of pair)
 2: MeOH_REP1_R2

Perform initial ILLUMINACLIP step?

Cut adapter and other illumina-specific sequences from the read

Trimmomatic Operation
1: Trimmomatic Operation Trash

Select Trimmomatic operation to perform
Sliding window trimming (SLIDINGWINDOW)

Bolger, A.M., Lohse, M., & Usadel, B. (2014). Trimmomatic: A flexible trimmer for Illumina Sequence Data. *Bioinformatics*, doi: 10.1093/bioinformatics/btu170

Trimmomatic Operation

1: Trimmomatic Operation

Select Trimmomatic operation to perform

Sliding window trimming (SLIDINGWINDOW)

Sliding window trimming (SLIDINGWINDOW)

Drop reads below a specified length (MINLEN)

Cut bases off the start of a read, if below a threshold quality (LEADING)

Cut bases off the end of a read, if below a threshold quality (TRAILING)

Cut the read to a specified length (CROP)

Cut the specified number of bases from the start of the read (HEADCROP)

Trimmomatic preserves read pairing

Multiple filters can be run in arbitrary order

We'll use **sliding window**, followed by **minimum length**.

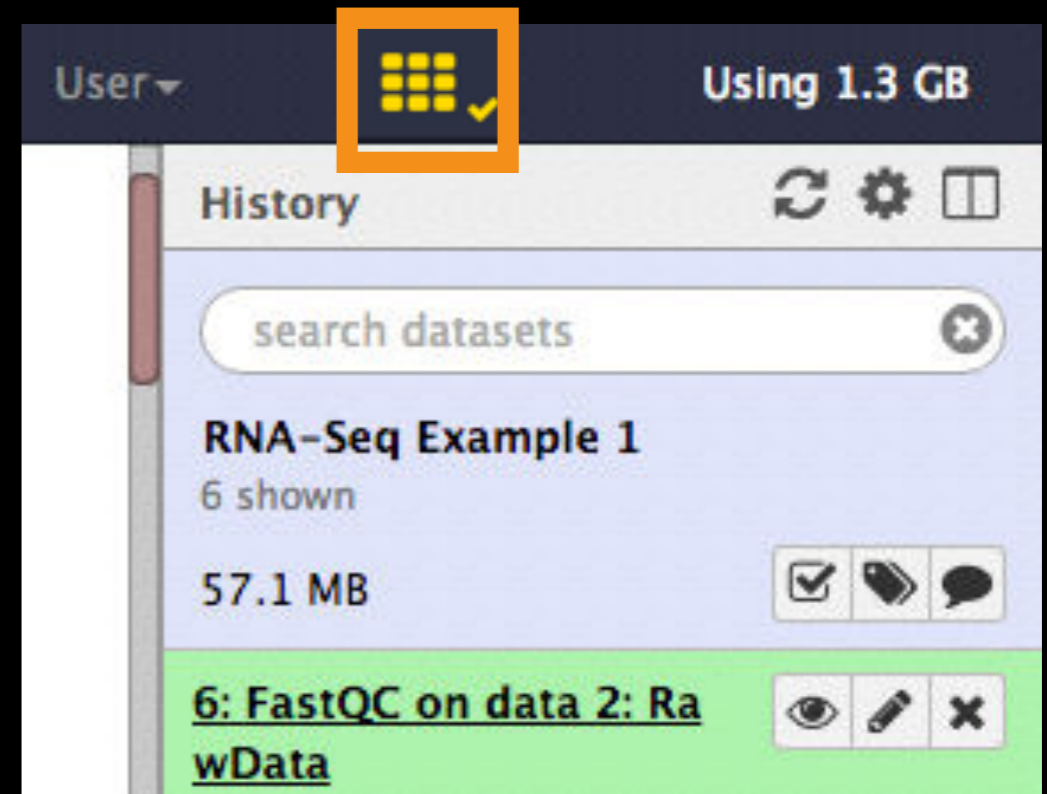
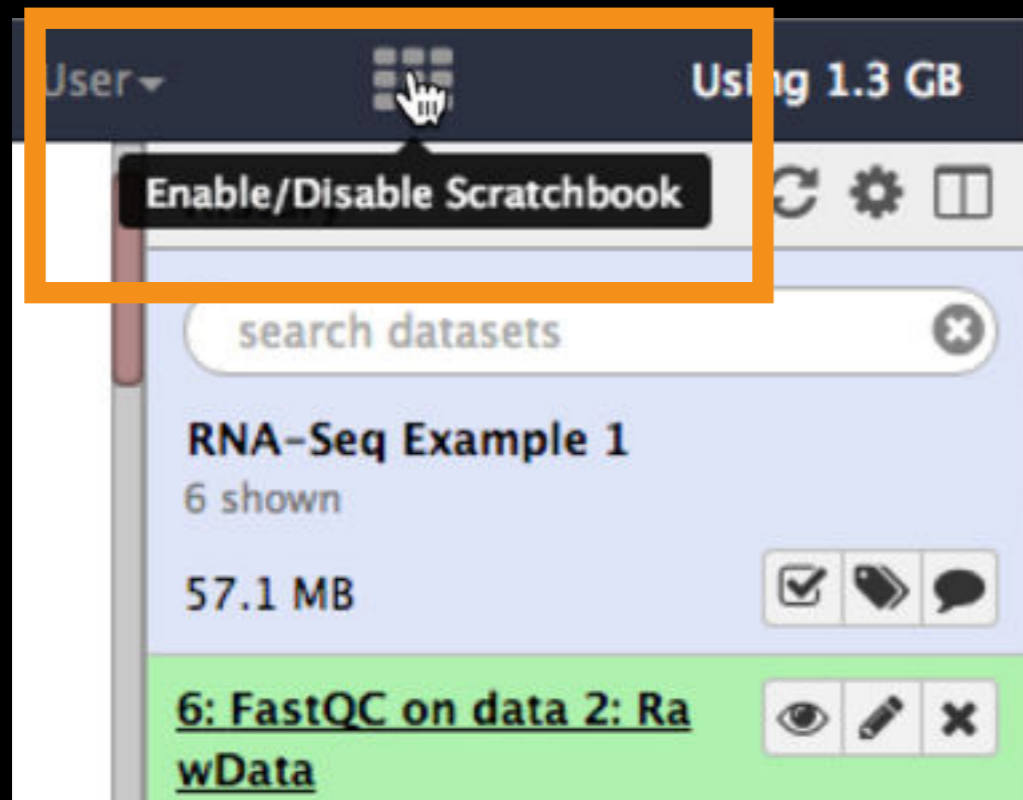
Run FastQC on post-Trimmatic Datasets

NGS QC and Manipulation → **FastQC**

Now, let's see what changed

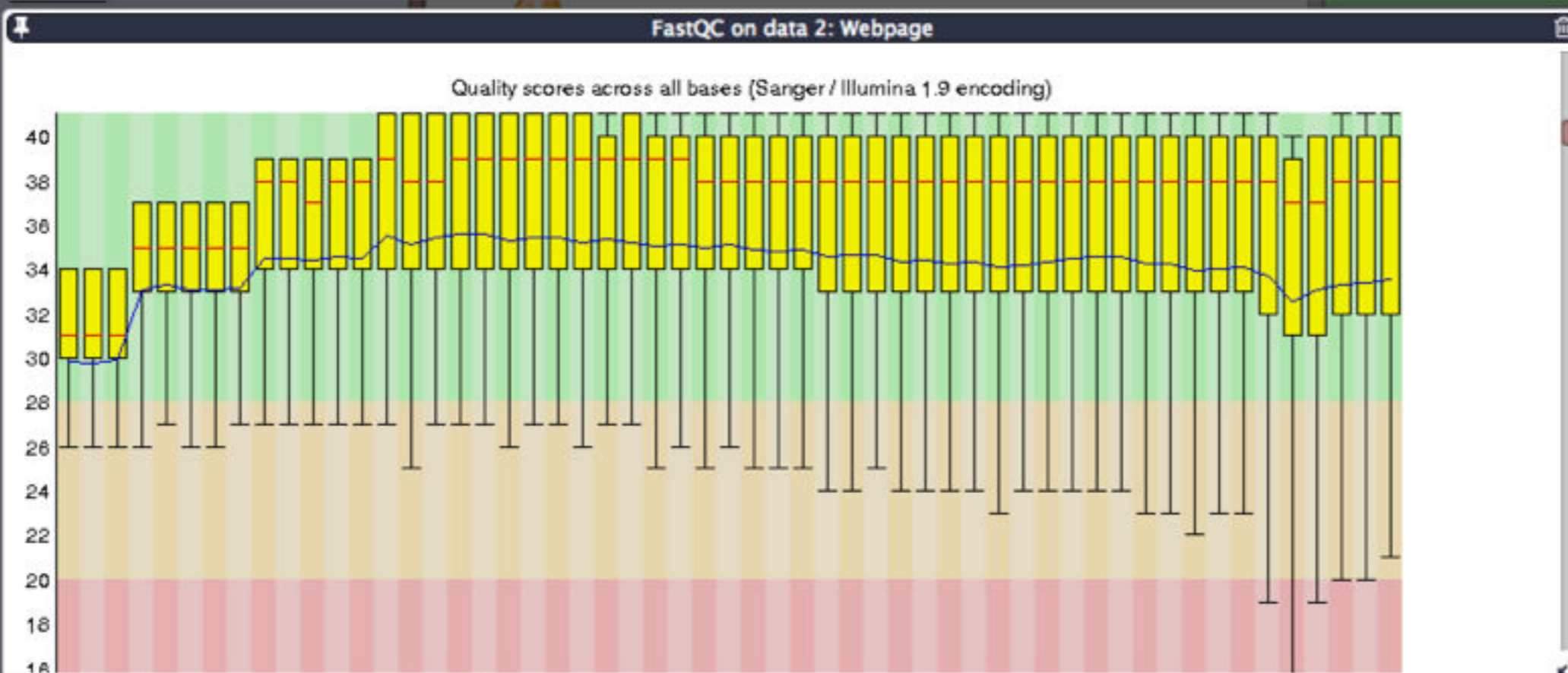
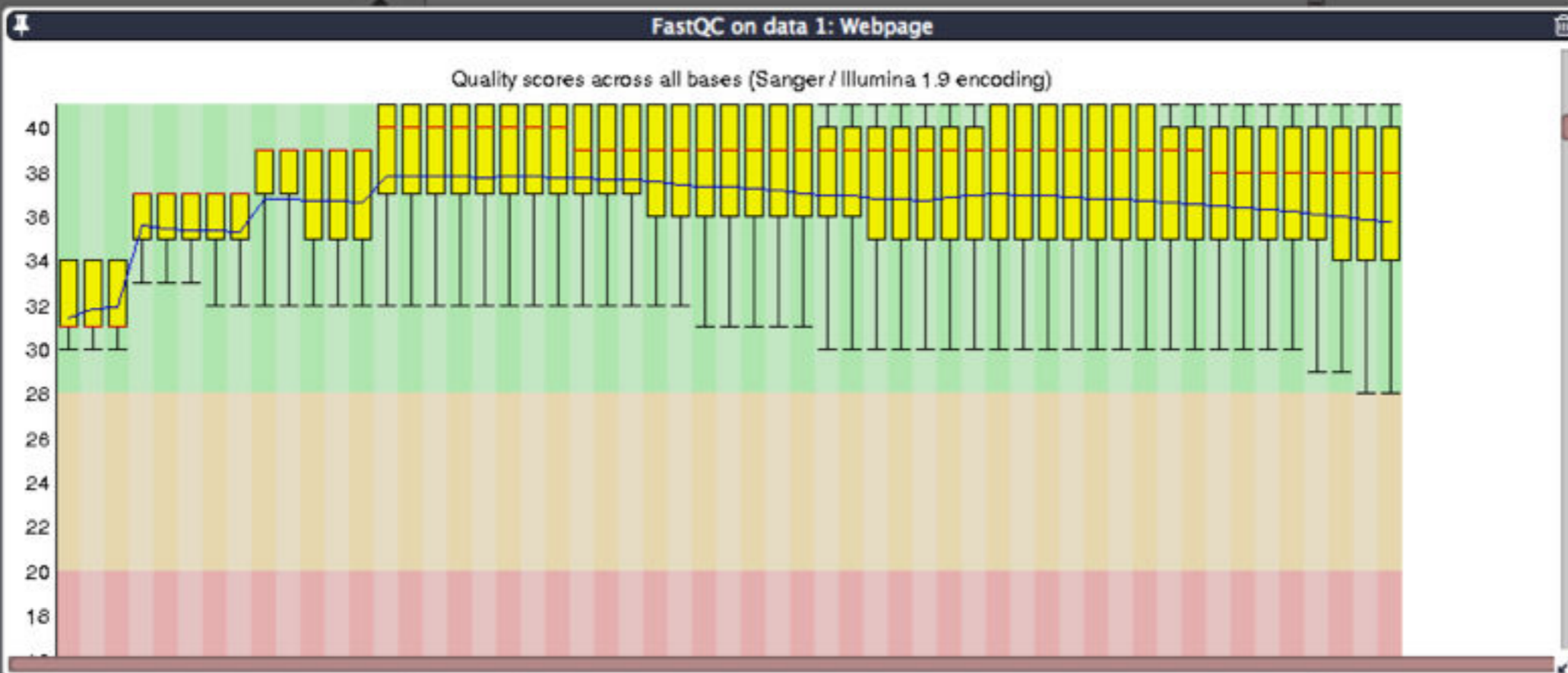
Shared History: RNA-Seq MeOH_REPI QC

Scratchbook: View multiple datasets



And the icon turns **yellow**!

Poke the **pre**-Trimmomatic reverse read FastQC report in the eye, and then poke the **post**-Trimmomatic FastQC report in the eye.



And after some resizing and scrolling you see this

NGS Data Quality Assessment

Now, just 10 more datasets to go!

Your Friend: The Multiple datasets button

Trimmomatic flexible read trimming tool for Illumina NGS data (Galaxy Version 0.32.3)

Options

Paired end data?

YesNo

Input Type

Pair of datasets

Input FASTQ file (R1/first of pair)

1: MeOH_REP1_R1.fastq

Multiple datasets

(R2/second of pair)

2: MeOH_REP1_R2.fastq

Perform initial ILLUMINACLIP step?

YesNo

Cut adapter and other illumina-specific sequences from the read

Trimmomatic Operation

1: Trimmomatic Operation

Version 0.32.3)

Paired end data?

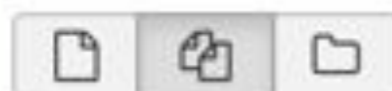
Yes

No


Input Type

Pair of datasets ▼

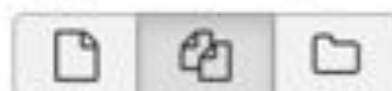
Input FASTQ file (R1/first of pair)




11: R3G_REP3_R1.fastq
10: R3G_REP2_R2.fastq
9: R3G_REP2_R1.fastq
8: R3G_REP1_R2.fastq
7: R3G_REP1_R1.fastq

 This is a batch mode input field. A separate job will be triggered for each dataset.

Input FASTQ file (R2/second of pair)



12: R3G_REP3_R2.fastq
11: R3G_REP3_R1.fastq
10: R3G_REP2_R2.fastq
9: R3G_REP2_R1.fastq
8: R3G_REP1_R2.fastq

 This is a batch mode input field. A separate job will be triggered for each dataset.

Perform initial ILLUMINACLIP step?

Yes

No

Your other friend:

Another way to avoid insanity is




Collections


Dataset collections!




Dataset Collections give Galaxy semantic knowledge about dataset relationships.

Tools can then take advantage of this knowledge.




Dataset collections




History   




search datasets 




RNA-Seq thru Mapping, w
collections
12 shown
297.73 MB   




12: R3G REP3 R2 **Operations on multiple datasets**




11: R3G REP3 R1   




10: R3G REP2 R2   




9: R3G REP2 R1   




8: R3G REP1 R2   




7: R3G REP1 R1   




6: MeOH REP3 R2   




5: MeOH REP3 R1   


4: MeOH REP2 R2   




3: MeOH REP2 R1   

2: MeOH REP1 R2   

1: MeOH REP1 R1   

History   

search datasets 

RNA-Seq thru Mapping, w
collections
12 shown
297.73 MB   

All None For all selected...

☐ Hide datasets
☐ Unhide datasets
☐ Delete datasets
☐ Undelete datasets
☐ Permanently delete datasets
☐ Build Dataset List
☐ Build Dataset Pair
☒ Build List of Dataset Pairs

☒ 6: MeOH REP3 R2

☒ 5: MeOH REP3 R1

☒ 4: MeOH REP2 R2

☒ 3: MeOH REP2 R1

☒ 2: MeOH REP1 R2

☒ 1: MeOH REP1 R1

Create a collection of paired datasets

Could not automatically create any pairs from the given dataset names

0 unpaired forward – (6 filtered out)

_1

[Choose filters](#) [Clear filters](#)

[Auto-pair](#)

Choose from the following filters to change which unpaired reads are shown in the display:

Forward: _1, Reverse: _2

Forward: _R1, Reverse: _R2

0 unpaired reverse – (6 filtered out)

_2

Analyze Data

Workflow

Shared Data

Visualization

Admin

Help

User

Create a collection of paired datasets

Could not automatically create any pairs from the given dataset names

3 unpaired forward – (3 filtered out)

_R1

[Choose filters](#) [Clear filters](#)

[Auto-pair](#)

Pair these datasets

Pair these datasets

Pair these datasets

3 unpaired reverse – (3 filtered out)

_R2

MeOH_REP1_R2

MeOH_REP2_R2

MeOH_REP3_R2

MeOH_REP1_R1

MeOH_REP2_R1

MeOH_REP3_R1

Create a collection of paired datasets

3 pairs created: all datasets have been successfully paired

0 unpaired forward – (0 filtered out) Choose filters Clear filters 0 unpaired reverse – (0 filtered out)

_R1 _R2

3 paired Unpair all




MeOH_REP1_R1 →	MeOH_REP1	← MeOH_REP1_R2	🔗
MeOH_REP2_R1 →	MeOH_REP2	← MeOH_REP2_R2	🔗
MeOH_REP3_R1 →	MeOH_REP3	← MeOH_REP3_R2	🔗


Remove file extensions from pair names? ☒




Name: MeOH

Cancel Create list

Dataset collections

History   

search datasets 

RNA-Seq thru Mapping, w
collections
14 shown
297.73 MB   

All None **Operations on multiple
datasets**

☐ **14: R3G**
a list of paired datasets

☐ **13: MeOH**
a list of paired datasets

☒ **12: R3G REP3 R2**

☒ **11: R3G REP3 R1**

☒ **10: R3G REP2 R2**

☒ **9: R3G REP2 R1**

☒ **8: R3G REP1 R2**

☒ **7: R3G REP1 R1**

☐ **6: MeOH REP3 R2**




☐ **5: MeOH REP3 R1**

☐ **4: MeOH REP2 R2**

☐ **3: MeOH REP2 R1**

☐ **2: MeOH REP1 R2**

☐ **1: MeOH REP1 R1**

History   




[← Back to RNA-Seq thru Mapping, w
collections](#)

MeOH
a list of paired datasets

MeOH REP1
a pair of datasets



MeOH REP2
a pair of datasets



MeOH REP3
a pair of datasets

History   

[← Back to MeOH](#)

MeOH_REP1
a pair of datasets

forward  

reverse  

Dataset collections Created

History

search datasets

RNA-Seq thru Mapping, w
collections
14 shown
297.73 MB

☒☐☐

AllNone

Operations on multiple
datasets

☐ 14: R3G
a list of paired datasets

☐ 13: MeOH
a list of paired datasets

☒ 12: R3G REP3 R2

☒ 11: R3G REP3 R1

☒ 10: R3G REP2 R2

☒ 9: R3G REP2 R1

☒ 8: R3G REP1 R2

☒ 7: R3G REP1 R1

☐ 6: MeOH REP3 R2

☐ 5: MeOH REP3 R1

☐ 4: MeOH REP2 R2

☐ 3: MeOH REP2 R1

☐ 2: MeOH REP1 R2

☐ 1: MeOH REP1 R1

Agenda: Day 1

- 9:00 Welcome
- 9:20 Basic Analysis with Galaxy
A worked example demonstrating Galaxy Basics
- 10:45 Break
- 11:00 Integrating with other tools: BioMart & GO
- 12:20 Lunch (catered)
- 1:20 Basic Analysis into Reusable Workflows
- 2:50 Break
- 3:05 RNA-Seq Analysis, Part I
- 5:00 Done

http://bit.ly/UR_GXY_2016



Thanks

Agenda: Day 2

- 9:00 Welcome
- 9:15 RNA-Seq Analysis Part II: Mapping
- 10:45 Break
- 11:00 RNA-Seq Analysis Part III: Differential Expression
- 12:20 Lunch (catered)
- 1:20 RNA-Seq Analysis Part IV: Novel Transcripts
- 2:50 Break
- 3:05 RNA-Seq Analysis Part V
- 5:00 Done

http://bit.ly/UR_GXY_2016

cloud5.galaxyproject.org

Just because.

Need to recreate your account

Clouds 1 and 2 are still there, but they don't work
with HISAT.

RNA-seq Exercise: Differential gene expression

Take samples under multiple conditions
(MeOH and R3G exposure in our example)

Map them

Count them

Compare them

RNA-Seq Mapping: Get the Data

Import into a new history:

Shared Data → Data Libraries → Training → RNA-Seq*

→ UC-Davis → Post QC reads → Still paired reads

Select first two

MeOH_REP1_R1 post QC

MeOH_REP1_R2 post QC

Shared Data → Data Libraries → Training → RNA-Seq*

→ UC-Davis → Reference

Select GTF for hg38, chr12 from Sanger

* RNA-Seq example datasets from the 2013 UC Davis Bioinformatics Short Course. <http://bit.ly/ucdbsc2013>

RNA-seq Exercise: **Mapping** with HISAT2

- HISAT looks for best place(s) to map reads, and best places to insert introns
- Does same thing as Tophat2, but HISAT2 is faster and more sensitive.
- Both HISAT and Tophat run on top of Bowtie

RNA-seq Exercise: Mapping with HISAT2

- *Imagine pages and pages of discussion on the intricacies and pitfalls of RNA-seq mapping here*

Mapping with HISAT2: **basics**

Single or paired: **Collection of paired reads**

Paired reads: **MeOH_REP1**

Source for reference genome: **use a built-in genome**

Select a reference genome: **hg38**

Mapping w/ HISAT2: **Primary alignments**

Some reads align to more than one place equally well.

For such reads, how many should HISAT include?

If more than the specified number, HISAT will pick those with the best mapping score.

Search for at most K distinct, primary alignments for each read. Primary alignments mean alignments whose alignment score is equal or higher than any other alignments. The search terminates when it can't find more distinct valid alignments, or when it finds K , whichever happens first. (-k)

Mapping with HISAT2: **advanced**

If you expand all parameter sections, HISAT options go from 1 screen to almost 6.

Understanding all these options is the right thing to do, but it's also daunting.

One of Galaxy's strengths is that it allows you to experiment with tools and learn them incrementally.

We are going to start with setting just a few parameters.

Mapping with HISAT2: **advanced**

Spliced alignment parameters: **Specify spliced ...**

GTF file with known splice sites:

GTF for hg38, chr12 from Sanger

becomes

`--known-splicesite-infile <path>`

With this mode, you can provide a list of known splice sites, which HISAT2 makes use of to align reads with small anchors.

<https://ccb.jhu.edu/software/hisat2/manual.shtml>

Mapping with HISAT2: **advanced**

Transcriptome assembly reporting:

Report alignments specifically tailored for Cufflinks

Click Execute

Mapping With HISAT2: What to keep?


NGS BAM
Tools → Filter

This shows
two options
for cleanup.

Condition

1: Condition

Filter

1: Filter 


Select BAM property to filter on

mapQuality ▼

Filter on read mapping quality (phred scale)

>=20

You can use >, <, =, and ! (not) in your expression. E.g., to select reads with mapping quality of at least 30 use ">=30"

2: Filter 

Select BAM property to filter on

isProperPair ▼

Select properly paired reads

☒ Yes ☐ No

Checked = Read IS in proper pair, Empty = Read is NOT in the proper pair

+ Insert Filter

+ Insert Condition

Would you like to set rules?

☒ Yes ☐ No

Allows complex logical constructs. See Example 4 below.

✓ Execute

Agenda: Day 2

- 9:00 Welcome
- 9:15 RNA-Seq Analysis Part II: Mapping
- 10:45 Break
- 11:00 RNA-Seq Analysis Part III: Differential Expression
- 12:20 Lunch (catered)
- 1:20 RNA-Seq Analysis Part IV: Novel Transcripts
- 2:50 Break
- 3:05 RNA-Seq Analysis Part V
- 5:00 Done

http://bit.ly/UR_GXY_2016

RNA-Seq Differential Expression: Get the Data

Import into a new history:

Shared Data → Data Libraries → Training → RNA-Seq*

→ UC-Davis → Mapped

Select all

Shared Data → Data Libraries → Training → RNA-Seq*

→ UC-Davis → Reference

Select GTF for hg38, chr12 from Sanger

* RNA-Seq example datasets from the 2013 UC Davis Bioinformatics Short Course. <http://bit.ly/ucdbsc2013>

Differential expression with CuffDiff

Part of the Tuxedo RNA-Seq Suite (as are Tophat, Bowtie, StringTie, Cufflinks, Cuffmerge, ...)

Identifies differential expression between multiple datasets

Widely used and widely installed on Galaxy instances

NGS: RNA Analysis → Cuffdiff

Cuffdiff

Cuffdiff previously used FPKM/RPKM as central statistic.

Total # mapped reads heavily influences FPKM/RPKM.
Can lead to challenges when you have very highly expressed genes in the mix.

Now supports geometric normalization, the same model used by DESeq (and in fact, it's now the default). Less prone to distortion from highly expressed genes.

Cuffdiff: Which transcript definitions to use?

We'll use the official genome annotations

(Same ones HISAT used for short anchors)

But there are a world of options out there for
discovering and using novel transcripts.

StringTie, Cufflinks, Cuffmerge, ...

Cuffdiff

- Running with 2 Groups: MeOH and R3G
- Each group has 3 replicates each
- Can take advantage of collections

Transcripts

13: GTF for hg38, chr12 from Sanger



A transcript GFF3 or GTF file produced by cufflinks, cuffcompare, or other source.

Omit Tabular Datasets

Yes

No

Discard the tabular output.

Generate SQLite

Yes

No

Generate a SQLite database for use with cummeRbund.

Input data type

SAM/BAM



CuffNorm supports either CXB (from cuffquant) or SAM/BAM input files. Mixing is not supported. Default: SAM/BAM

Condition**1: Condition****Name**

MeOH

Replicates

62: HISAT2 on R3G

**2: Condition****Name**

R3G

Replicates

58: HISAT2 on MeOH



Cuffdiff

Execute it

Cuffdiff

Produces many output files, all explained in doc

We'll focus on **gene differential expression testing**

test_id	gene_id	gene	locus	sample_1	sample_2	status	value_1	value_2	log2(fold_change)	test_stat	p_value	q_value	significant
A2M	A2M	A2M	chr12:9217772-9268558	MeOH	R3G	NOTEST	3.32147	3.13694	-0.0824644	0	1	1	no
A2M-AS1	A2M-AS1	A2M-AS1	chr12:9217772-9268558	MeOH	R3G	NOTEST	7.45797	13.9413	0.902515	0	1	1	no
A2ML1	A2ML1	A2ML1	chr12:8975149-9029381	MeOH	R3G	NOTEST	4.83055	7.79884	0.691072	0	1	1	no
A2MP1	A2MP1	A2MP1	chr12:9381128-9386803	MeOH	R3G	NOTEST	2.49656	0	-inf	0	1	1	no
AAAS	AAAS	AAAS	chr12:53701239-53715412	MeOH	R3G	OK	269.035	159.23	-0.756683	-2.22857	0.0005	0.00194017	yes
AACS	AACS	AACS	chr12:125549924-125627871	MeOH	R3G	NOTEST	29.2933	35.0339	0.258178	0	1	1	no
ABCB9	ABCB9	ABCB9	chr12:123405497-123451056	MeOH	R3G	NOTEST	4.68869	1.7732	-1.40283	0	1	1	no
ABCC9	ABCC9	ABCC9	chr12:21950323-22089628	MeOH	R3G	OK	553.247	487.261	-0.18323	-2.02806	0.0004	0.00162143	yes
ABCD2	ABCD2	ABCD2	chr12:39945021-40013843	MeOH	R3G	OK	86.1377	172.795	1.00435	4.3436	5e-05	0.000246739	yes
ACACB	ACACB	ACACB	chr12:109577201-109706030	MeOH	R3G	NOTEST	8.45306	15.5772	0.881885	0	1	1	no
ACAD10	ACAD10	ACAD10	chr12:112123856-112194911	MeOH	R3G	NOTEST	21.8237	27.8326	0.350882	0	1	1	no
ACADS	ACADS	ACADS	chr12:121163570-121177811	MeOH	R3G	NOTEST	38.644	16.1739	-1.25658	0	1	1	no
ACRBP	ACRBP	ACRBP	chr12:6747241-6756580	MeOH	R3G	NOTEST	2.96987	3.26939	0.138621	0	1	1	no
ACSM4	ACSM4	ACSM4	chr12:7456927-7480969	MeOH	R3G	NOTEST	0	0	0	0	1	1	no
ACSS3	ACSS3	ACSS3	chr12:81471808-81649582	MeOH	R3G	NOTEST	0	0	0	0	1	1	no
ACTR6	ACTR6	ACTR6	chr12:100593864-100618202	MeOH	R3G	OK	475.594	421.324	-0.174799	-0.797581	0.1588	0.258406	no
ACVR1B	ACVR1B	ACVR1B	chr12:52345450-52390863	MeOH	R3G	NOTEST	32.5737	38.3075	0.233922	0	1	1	no
ACVRL1	ACVRL1	ACVRL1	chr12:52301201-52317145	MeOH	R3G	NOTEST	1.27713	2.16161	0.759201	0	1	1	no
ADAM1A	ADAM1A	ADAM1A	chr12:112336866-112339706	MeOH	R3G	NOTEST	30.0162	55.2154	0.879331	0	1	1	no
ADAMTS20	ADAMTS20	ADAMTS20	chr12:43748011-43945724	MeOH	R3G	NOTEST	0.453322	0.502067	0.147346	0	1	1	no
ADCY6	ADCY6	ADCY6	chr12:49159974-49182820	MeOH	R3G	NOTEST	9.32722	17.6743	0.922135	0	1	1	no
ADIPOR2	ADIPOR2	ADIPOR2	chr12:1800246-1897845	MeOH	R3G	OK	207.468	179.333	-0.210248	-1.02392	0.09	0.158988	no
AEBP2	AEBP2	AEBP2	chr12:19592607-19675173	MeOH	R3G	OK	143.039	128.293	-0.156957	-0.688267	0.2254	0.344537	no
AGAP2	AGAP2	AGAP2	chr12:58118075-58135944	MeOH	R3G	OK	98.2385	116.302	0.243511	0.935119	0.11475	0.198086	no
AICDA	AICDA	AICDA	chr12:8754761-8765442	MeOH	R3G	NOTEST	78.1514	63.4313	-0.301077	0	1	1	no
AKAP3	AKAP3	AKAP3	chr12:4724675-4754343	MeOH	R3G	NOTEST	6.12385	7.89626	0.366731	0	1	1	no
ALDH1L2	ALDH1L2	ALDH1L2	chr12:105413561-105478341	MeOH	R3G	NOTEST	7.11374	8.11722	0.190377	0	1	1	no
ALDH2	ALDH2	ALDH2	chr12:112204690-112247789	MeOH	R3G	NOTEST	12.8033	8.05635	-0.668321	0	1	1	no
ALG10	ALG10	ALG10	chr12:34175215-34181236	MeOH	R3G	NOTEST	54.8575	59.3459	0.11346	0	1	1	no
ALG10B	ALG10B	ALG10B	chr12:38710556-38723528	MeOH	R3G	NOTEST	43.8157	63.0457	0.524952	0	1	1	no
ALKBH2	ALKBH2	ALKBH2	chr12:109525992-109531293	MeOH	R3G	OK	679.517	297.183	-1.19316	-3.34255	5e-05	0.000246739	yes
ALX1	ALX1	ALX1	chr12:85674035-85695561	MeOH	R3G	NOTEST	0	0	0	0	1	1	no

Cuffdiff: differentially expressed genes

Column	Contents
test_stat	value of the test statistic used to compute significance of the observed change
p_value	Uncorrected P value for test statistic
q_value	FDR-adjusted p-value for the test statistic
status	Was there enough data to run the test?
significant	and, was the gene differentially expressed?

Cuffdiff

- Column 7 ("status") can be FAIL, NOTEST, LOWDATA or OK
 - Filter and Sort → Filter
 - `c7 == 'OK'`
- Column 14 ("significant") can be yes or no
 - Filter and Sort → Filter
 - `c14 == 'yes'`

Returns the list of genes with

- 1) enough data to make a call, and
- 2) that are called as differentially expressed.

Cuffdiff: Next Steps

Try running Cuffdiff with different **normalization** and **dispersion estimation** methods.

Compare the differentially expressed gene lists.
Which settings have what type of impacts on the results?

Are there any patterns to the identified genes?

Shared History: RNA-Seq trimmed reads to diff gene

Agenda: Day 2

- 9:00 Welcome
- 9:15 RNA-Seq Analysis Part II: Mapping
- 10:45 Break
- 11:00 RNA-Seq Analysis Part III: Differential Expression
- 12:20 Lunch (catered)
- 1:20 RNA-Seq Analysis Part IV: Novel Transcripts
- 2:50 Break
- 3:05 RNA-Seq Analysis Part V
- 5:00 Done

http://bit.ly/UR_GXY_2016

RNA-Seq Novel Transcripts: Get the Data

Import into a new history:

Shared Data → Data Libraries → Training → RNA-Seq*

→ UC-Davis → Mapped

Select all

Shared Data → Data Libraries → Training → RNA-Seq*

→ UC-Davis → Reference




Select GTF for hg38, chr12 from Sanger

* RNA-Seq example datasets from the 2013 UC Davis Bioinformatics Short Course. <http://bit.ly/ucdbsc2013>

RNA-Seq Novel Transcripts: StringTie


StringTie transcript assembly and quantification (Galaxy Version 1.0.3) Options

Mapped reads to assemble transcripts from



58: HISAT2 on MeOH

▼




 This is a batch mode input field. A separate job will be triggered for each dataset.

Use GFF file to guide assembly

Use GFF

▼

Reference annotation to use for guiding the assembly process



13: GTF for hg38, chr12 from Sanger

▼

-G

Perform abundance estimation only of input transcripts

Yes

No

-e

Output additional files for use in Ballgown

Yes

No

-b

Options

Use defaults

▼




✓ Execute

Run it again on R3G

RNA-Seq Novel Transcripts: StringTie


StringTie transcript assembly and quantification (Galaxy Version 1.0.3) Options

Mapped reads to assemble transcripts from



58: HISAT2 on MeOH

▼




 This is a batch mode input field. A separate job will be triggered for each dataset.

Use GFF file to guide assembly

Use GFF

▼

Reference annotation to use for guiding the assembly process



13: GTF for hg38, chr12 from Sanger

▼

-G

Perform abundance estimation only of input transcripts

Yes No

-e

Output additional files for use in Ballgown


Yes No

-b

Options

Use defaults

▼

 **Execute**

Run it again on R3G

RNA-Seq Novel Transcripts: CuffMerge

Now have separately discovered transcripts for each condition.



Unify them with reference annotation using CuffMerge.


Could do this with StringTie, if the Galaxy wrapper supported it.

RNA-Seq Novel Transcripts: CuffMerge



Cuffmerge merge together several Cufflinks assemblies (Galaxy Version 2.2.1.0) Versions Options

GTF file(s) produced by Cufflinks

  210: StringTie on MeOH: Assembled transcripts

Additional GTF Inputs (Lists)
1: Additional GTF Inputs (Lists) 

GTF file(s) produced by Cufflinks




  234: StringTie on R3G: Assembled transcripts

+ Insert Additional GTF Inputs (Lists)

Use Reference Annotation

Yes

Reference Annotation

   13: GTF for hg38, chr12 from Sanger


Requires an annotation file in GFF3 or GTF format.

Use Sequence Data

No

Use sequence data for some optional classification functions, including the addition of the p_id attribute required by Cuffdiff.

Minimum isoform fraction

0.05 

Discard isoforms with abundance below this value

✓ Execute

2016 Galaxy Community Conference (GCC2016)

June 25-29, 2016

Bloomington, Indiana

galaxyproject.org/GCC2016

Slides & posters are now
online. Video will be shortly



Join us in beautiful

Bloomington, Indiana

for the 2016 Galaxy
Community Conference
and pre-conference activities!

June 25-29, 2016



Considered one of the five
prettiest campuses in the US,
Indiana University is one of
the major public research
universities in the nation, and
home to the National Center
for Genome Analysis Support.



galaxyproject.org/gcc2016



Le Corum
Conference centre

gcc2017.sciencesconf.org

November 7-11



Salt Lake City, Utah

Galaxy Community Resources: Galaxy **Biostar**

Tens of thousands of users leads to a lot of questions.

Absolutely have to **encourage community support.**

Project traditionally used mailing list

Moved the **user support list** to **Galaxy Biostar**, an online **forum**, that uses the Biostar platform








<https://biostar.usegalaxy.org/>

Scaling Training






Galaxy Training Network: Trainer Locations

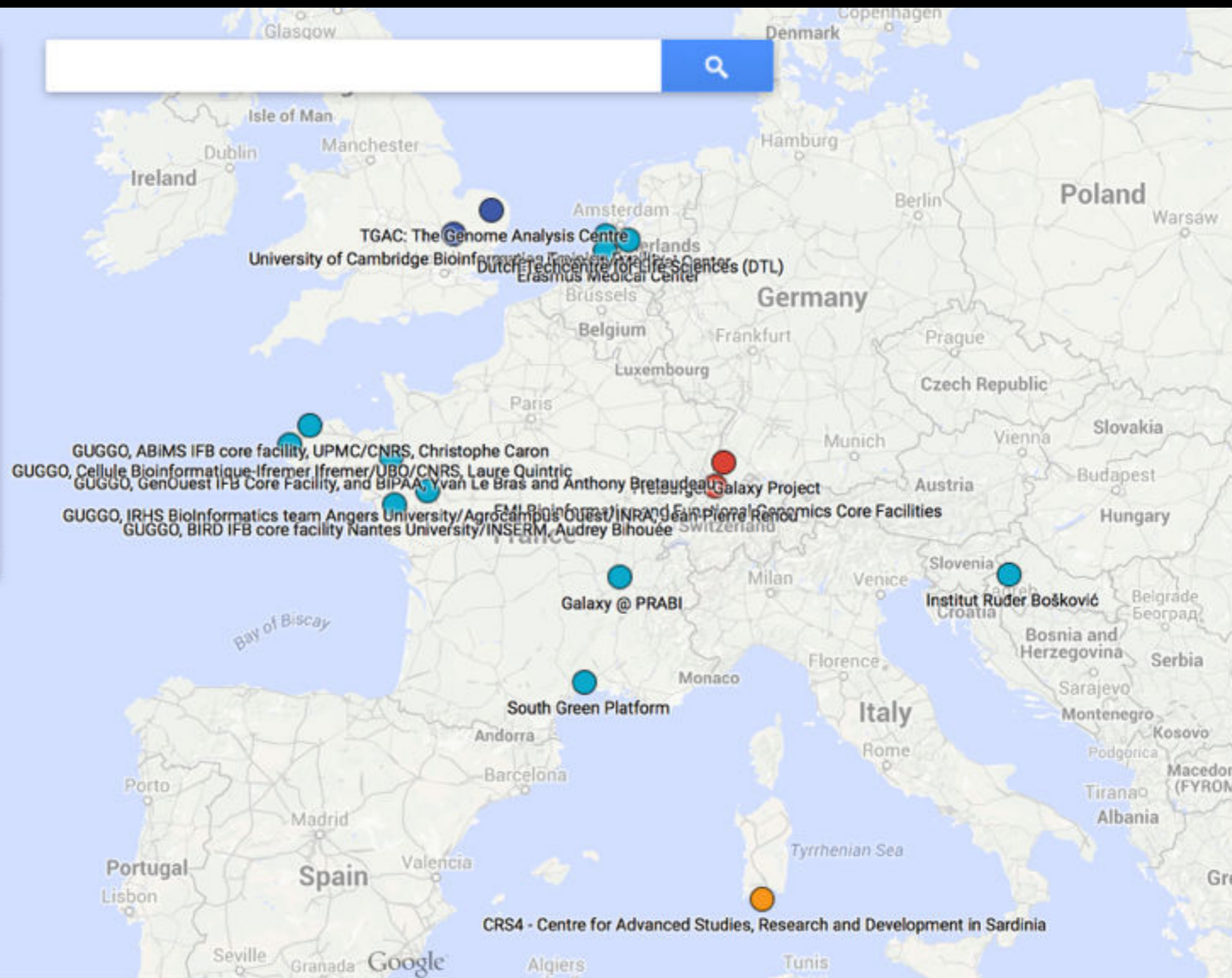
The Galaxy Training Network
(<https://wiki.galaxyproject.org/Teach/GTN>)

Made with Google My Maps

☒ **Trainers**

-  Global
-  Regional
-  Local
-  Continental
-  Institution



Galaxy Training Network

bit.ly/gxygtn

Galaxy Community Resources: Mailing Lists

<http://wiki.galaxyproject.org/MailingLists>

Galaxy-Dev

Questions about developing for and deploying Galaxy

High volume (2336 posts in 2015, 1000+ members)

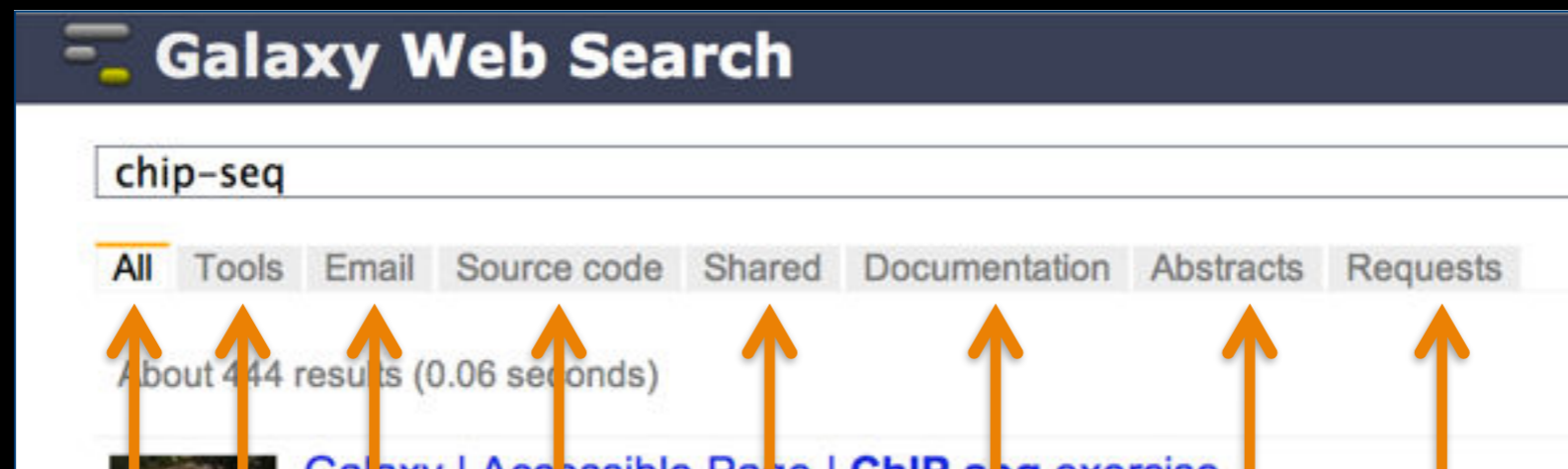
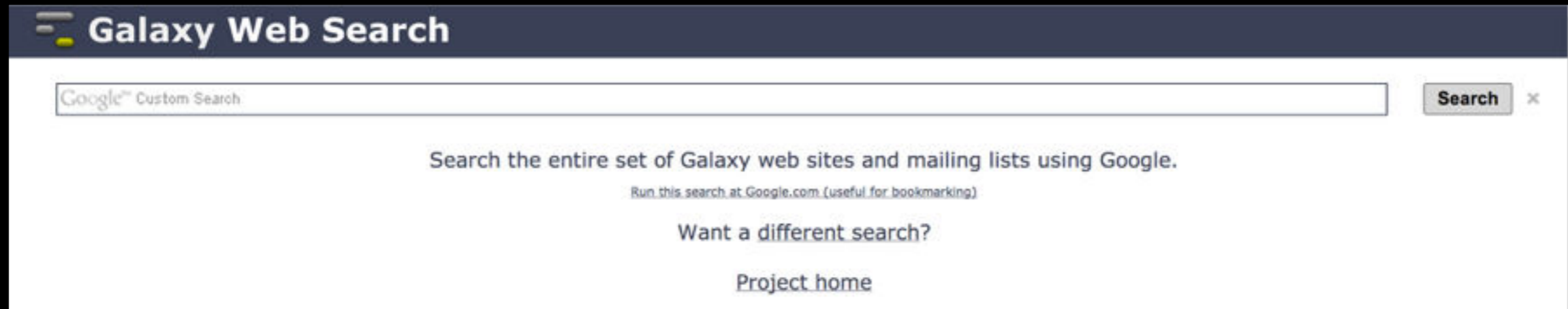
Galaxy-Announce

Project announcements, low volume, moderated

Low volume (36 posts in 2015, 6500+ members)

Also **Galaxy-UK, -France, -Proteomics, -Training, ...**

Unified Search: <http://galaxyproject.org/search>



Find

Everything on ...

Tools for ...

Email about ...

Source code for ...

Published Histories, Pages, Workflows, about ...

Documentation on ...

Papers using Galaxy for ...

Related feature requests



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

- **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.

This is the Galaxy Community Wiki. It describes all things Galaxy.

Use Galaxy

Galaxy's public web server usegalaxy.org makes analysis tools, genomic data, tutorial demonstrations, persistent workspaces, and publication services available to any scientist. Extensive [user documentation](#) applicable to any [public](#) or local Galaxy instance is available.



Community & Project

Galaxy has a large and active user community and many ways to get involved.

- [Community](#)

Deploy Galaxy

Galaxy is a free and open source project available to all. Local Galaxy servers can be set up by [downloading](#) the Galaxy application.

- [Admin](#)
- [Cloud](#)



Contribute

- **Users:** [Share](#) your histories, workflows, visualizations, data libraries, and [Galaxy Pages](#), enabling others to use and learn from them.



Use Galaxy

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Events

Galaxy Wiki

Events

Galaxy Event Horizon

Events with Galaxy-related content are listed here.

Also see the [Galaxy Events Google Calendar](#) for a listing of events and deadlines that are in the Galaxy Community. This is also available as an [RSS feed](#)

If you know of any event that should be added to this page and/or to the Galaxy Event Calendar, send it to outreach@galaxyproject.org.

For events prior to this year, see the [Events Archive](#).

Upcoming Events

Date	Topic/Event	Venue/Location
December 12	Introduction to Galaxy Workshop	Virginia State University, Petersburg, Virginia
December 16-19	RNA-Seq and ChIP-Seq Analysis with Galaxy	UC Davis, California, United States
2015		
January 10-14	Galaxy for SNP and Variant Data Analysis	Plant and Animal Genome XXIII (PAG2014), States
January 19-20	NGS pipelines with Galaxy	e-Infrastructures for Massively Parallel Sequencing, Sweden
February 9-13	Analyse bioinformatique de séquences sous Galaxy	Montpellier, France
February 16-18	Accessible and Reproducible Large-Scale Analysis with Galaxy	Genome and Transcriptome Analysis, Pacific Conference, San Francisco, California
	Large-Scale NGS data Analysis on Amazon Web Services Using Globus Genomic	Genomics & Sequencing Data Integration, of Molecular Medicine Tri-Conference, San Francisco, California

News Items

Opening at McMaster University

The [McArthur Lab](#) in the [McMaster University Department of Biochemistry & Biomedical Sciences](#) is seeking a Systems Administrator / Information Technologist to help establish a new bioinformatics laboratory at McMaster, plus develop the next generation of the [Comprehensive Antibiotic Resistance Database \(CARD\)](#).

From the [job announcement on Evoldir](#):

The candidate will configure BLADE and other hardware for general bioinformatics analysis, development of a GIT version control system, **construction of an in house Galaxy server (usegalaxy.org)**, and development of a new interface, stand-alone tools, APIs, and algorithms for the CARD (based on [Chado](#)).

See the [full announcement](#) for details.

Posted to the [Galaxy News](#) on 2014-12-05

December 2014 Galaxy Newsletter

As always there's a lot going on in the Galaxy this month. "Like what?" you say. Well, read the dang [December Galaxy Newsletter](#) we say! Highlights include:

- [Galaxy Day! In Paris! This Wednesday!](#)
- Near Richmond, Virginia? There's a [Galaxy Workshop at Virginia State U on December 12](#).
- [GCC2015 needs sponsors!](#)
- Other [upcoming events](#) on two continents
- **96 new papers**, including 6 highlighted papers, referencing, using, extending, and implementing Galaxy.
- [Job openings at 7+ organizations](#)
- A new mailing list: [Galaxy-Training](#)
- [15 new ToolShed repositories](#) from 10 contributors
- And, 10 other juicy (well maybe not *juicy*, but certainly not *crunchy*) [bits of news](#)

Dave Clements and the *crisp* Galaxy Team

Posted to the [Galaxy News](#) on 2014-12-01

Bioinformaticians, Freiburg

[Max Planck Institute of Immunobiology and Epigenetics](#) in Freiburg, Germany has an opening for a Bioinformatician for an initial period of two years. The successful candidate will work at the interface between an in-house deep-sequencing facility (HiSeq-2500) and the various research groups at the institute. Main responsibilities include

primary analysis of deep-sequencing data and quality control

Galaxy Resources & Community: Videos

The screenshot shows the Vimeo profile for the 'Galaxy Project'. The header includes the Vimeo logo and navigation links: Me, Videos, Create, Watch, Tools, Upload. A search bar is located on the right. The profile name 'Galaxy Project' is followed by a 'PLUS' badge and the text 'Joined 1 month ago'. Below this is a statistics bar showing 54 Videos, 0 Likes, 0 Following, 1 Group, 6 Channels, and 0 Albums. A 'Recently Uploaded' section displays four video thumbnails. The first three are titled 'Using Galaxy' followed by 'protocol 3', 'protocol 2', and 'protocol 1' respectively, with subtitles 'Calling Peaks For ChIP-seq Data', 'Loading Data and Understanding Datatypes', and 'Finding Human Coding Exons with Highest SNP Density'. The fourth thumbnail is titled 'FASTQ Prep' with the subtitle 'Illumina'. Each video is credited to 'CPB Using Galaxy' and has a timestamp. On the left side of the page, there is a 'Settings' button and a paragraph of text describing the Galaxy project as an open, web-based platform for data intensive biomedical research, supported by various institutions.

Galaxy Project PLUS
Joined 1 month ago

54 Videos | 0 Likes | 0 Following | 1 Group | 6 Channels | 0 Albums

Recently Uploaded + See all 54 videos

- Using Galaxy protocol 3
Calling Peaks For ChIP-seq Data
CPB Using Galaxy 3
5 days ago
- Using Galaxy protocol 2
Loading Data and Understanding Datatypes
CPB Using Galaxy 2
5 days ago
- Using Galaxy protocol 1
Finding Human Coding Exons with Highest SNP Density
CPB Using Galaxy 1
5 days ago
- usegalaxy.org
FASTQ Prep
Illumina
FASTQ Prep - Illumina
1 week ago

Settings

Galaxy is an open, web-based platform for data intensive biomedical research. Whether on this free public server or your own instance, you can perform, reproduce, and share complete analyses. The Galaxy team is a part of BX at Penn State, and the Biology and Mathematics and Computer Science departments at Emory University. The Galaxy Project is supported in part by NSF, NHGRI, The Huck Institutes of the Life Sciences, The Institute for

“How to”
screencasts on
using and
deploying
Galaxy

Talks from
previous
meetings.

<http://vimeo.com/galaxyproject>

Galaxy Resources & Community: CiteULike Group

Now
almost
3000
papers



CiteULike Group: Galaxy Search Register Log in

Group: Galaxy - library 2336 articles

Search Copy Export Sort Hide Details

✓ Adaptation of the targeted capture Methyl-Seq platform for the mouse genome identifies novel tissue-specific methylation patterns of genes involved in neurodevelopment

Epigenetics (18 May 2015), pp. 00-00, doi:10.1080/15592294.2015.1045179
by Benjamin Hing, Enrique Ramos, Patricia Braun, et al.
posted to methods by galaxyproject to the group Galaxy on 2015-05-28 21:46:38 ★★

■ Abstract

✓ Genomic and experimental evidence for multiple metabolic functions in the RidA/YjgF/YER057c/U

BMC Genomics, Vol. 16, No. 1. (15 May 2015), 382, doi:10.1186/s12864-015-1584-3
by Thomas D. Niehaus, Svetlana Gerdes, Kelsey Hodge-Hanson, et al.
posted to methods usemain by galaxyproject to the group Galaxy on 2015-05-28 21:41:14 ★★

■ Abstract

✓ NetworkAnalyst for statistical, visual and network-based meta-analysis of gene expression data

Nat. Protocols, Vol. 10, No. 6. (07 June 2015), pp. 823-844, doi:10.1038/nprot.2015.052
by Jianguo Xia, Erin E. Gill, Robert E. W. Hancock
posted to visualization by galaxyproject to the group Galaxy on 2015-05-28 21:37:43 ★★ along with 2 people and

✓ Repression by H-NS of genes required for the biosynthesis of the Vibrio cholerae biofilm matrix is mediated by the

Molecular Microbiology (1 May 2015), pp. n/a-n/a, doi:10.1111/mmi.13058
by Julio C. Ayala, Hongxia Wang, Anisia J. Silva, Jorge A. Benitez
posted to methods usemain by galaxyproject to the group Galaxy on 2015-05-28 21:30:30 ★★

■ Abstract

✓ A Sleeping Beauty forward genetic screen identifies new genes and pathways driving osteosarcoma development and

Group Tags	
All tags in the group Galaxy	
Filter:	
[Display as Cloud]	
methods	1149
workbench	702
usemain	233
tools	169
usepublic	129
isgalaxy	124
uselocal	90
cloud	89
shared	81
other	68
refpublic	57
unknown	53
reproducibility	51
howto	45
project	43
visualization	15
usecloud	4

<http://bit.ly/gxycul>

The Galaxy Team



Enis Afgan



Dannon Baker



Dan Blankenberg



Dave Bouvier



Marten Cech



John Chilton



Dave Clements



Nate Coraor



Carl Eberhard



Jeremy Goecks



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Nitesh Turaga

<http://wiki.galaxyproject.org/GalaxyTeam>

Acknowledgements

You

AWS

Anthony Corbett

Helene McMurray

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Carl Schmidtman

Harry Stern

NIH

Johns Hopkins University

Penn State University

Center for Integrated Research Computing (CIRC)

UR Genomics Research Center (GRC)

Edward G. Miner Library

UR Research Data Integration and Analytics (RDIA)

University of Rochester



Thanks

