RNA-seq to study HIV Infection in cells

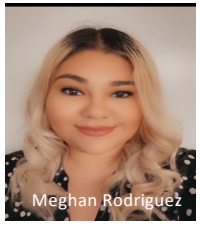
Rebecca Batorsky
Sr Data Scientist
Tufts Data Intensive Studies Center
Feb 2024

People at DISC

Tufts UNIVERSITY | Data Intensive Studies Center

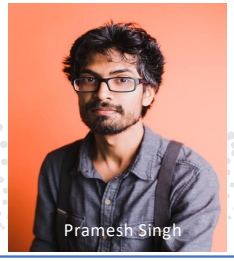
DISC Faculty

Administration



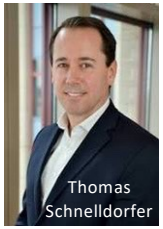
40+ faculty and **many students** across different disciplines partner with us on research, teaching and learning

DISC Data Scientists



Postdoctoral

DISC Faculty Fellows



People at DISC

Tufts UNIVERSITY | Data Intensive Studies Center

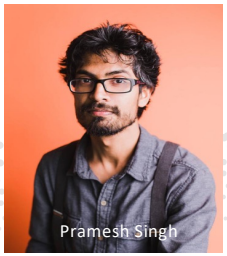
DISC Faculty

Bioinformatics & Computational Biology

DISC conducts research by developing new data science methods for bioinformatics and computational biology research, in collaboration with faculty, staff, and stakeholders within and outside Tufts University. Some of our current work focuses on:

- Single-cell Transcriptomics (Single cell profiling of Hofbauer cells and fetal brain microglia)
- Biological Networks (System-Level analysis of 'omics data)
- Proteomics (Proteomics profiling to study longevity)

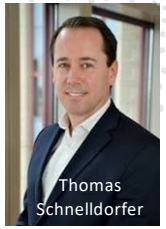
DISC Data Scientists

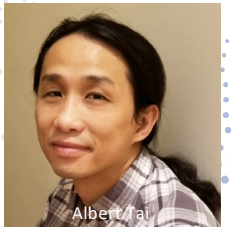


https://disc.tufts.edu/disc-research/research-projects

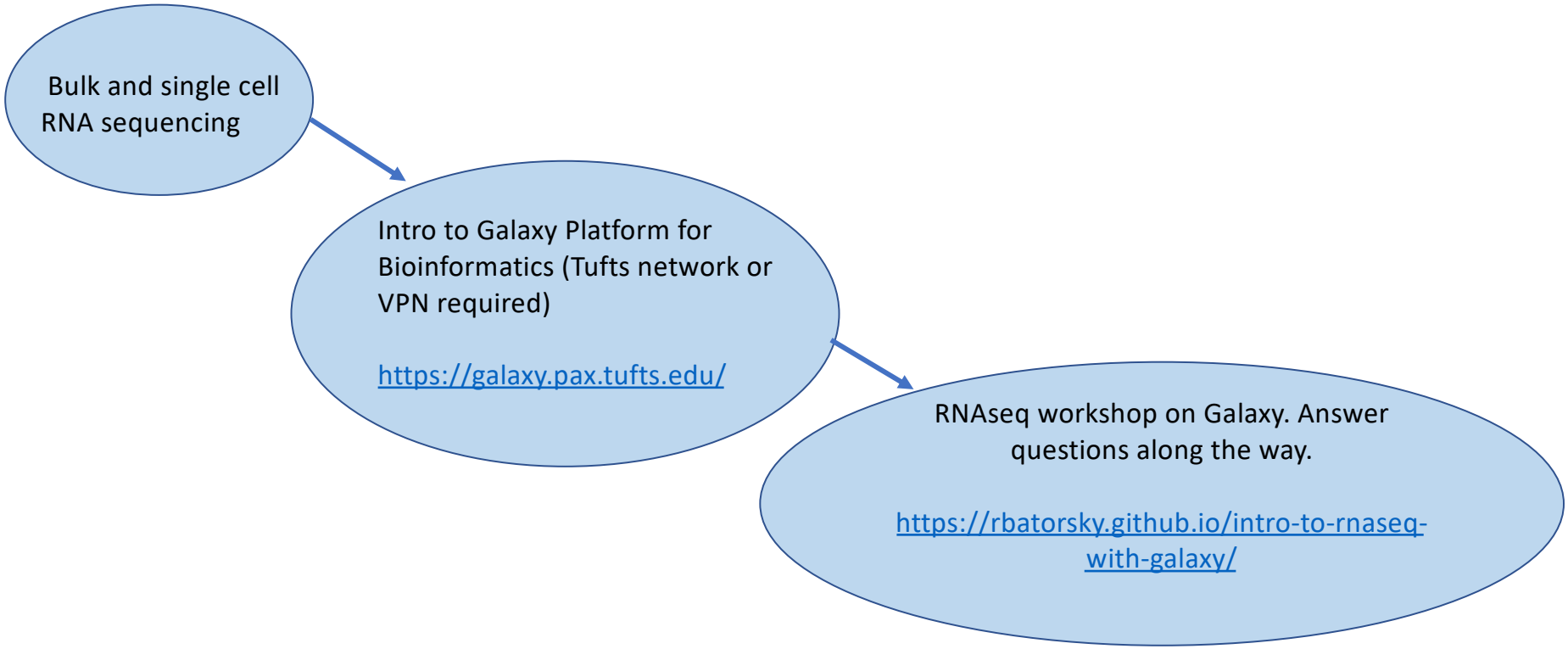
Postdoctoral

DISC Faculty Fellows

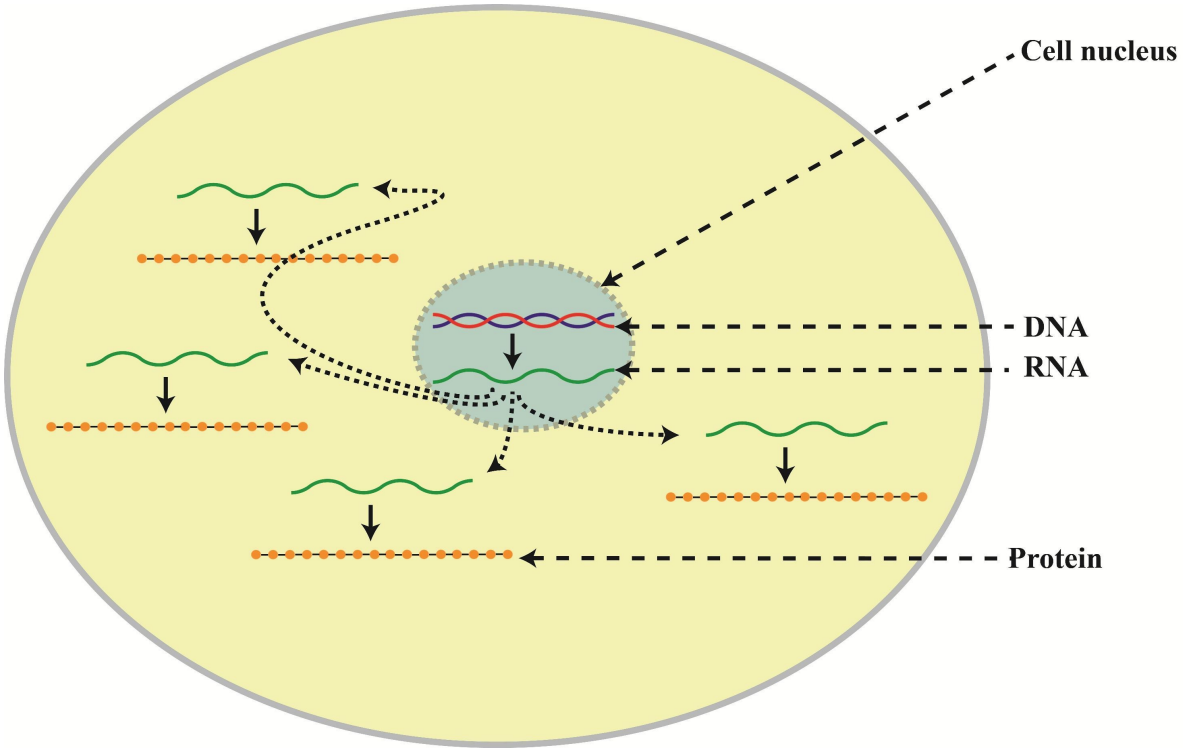




Outline


Bulk and single cell RNA sequencing
Intro to Galaxy Platform for Bioinformatics (Tufts network or VPN required)
https://galaxy.pax.tufts.edu/
RNAseq workshop on Galaxy. Answer questions along the way.
https://rbatorsky.github.io/intro-to-rnaseq-with-galaxy/

DNA and RNA in a cell

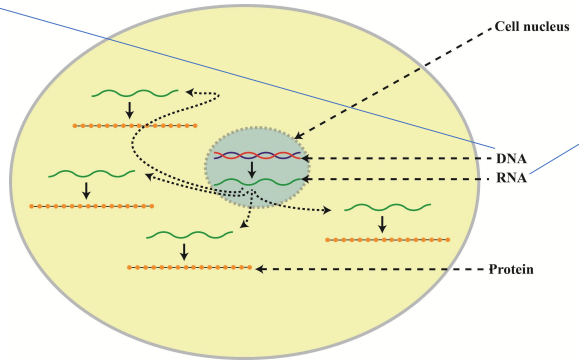


https://i0.wp.com/science-explained.com/wp-content/uploads/2013/08/Cell.jpg

Two common analyses

DNA Sequencing

- Fixed number of copies of a gene per cell
- Analysis goal:
  Variant calling and interpretation



RNA Sequencing

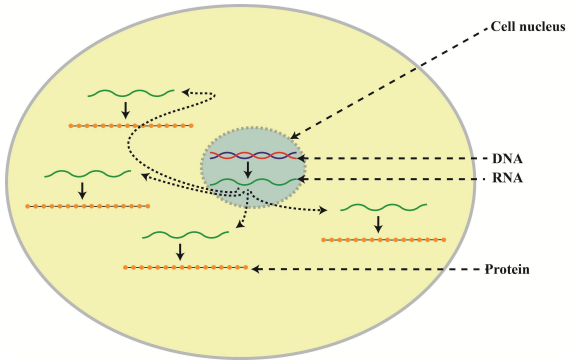
- Number of copies of a gene transcript per cell depends on gene expression
- Analysis goal:
  - Bulk : Differential expression
  - Single cell : Quantify different cell populations

https://i0.wp.com/science-explained.com/wp-content/uploads/2013/08/Cell.jpg

Today we will cover RNA sequencing

DNA Sequencing

- Fixed [illegible] of a gene per cell
- Analysis go[illegible] Variant c[illegible] interpretation



RNA Sequencing

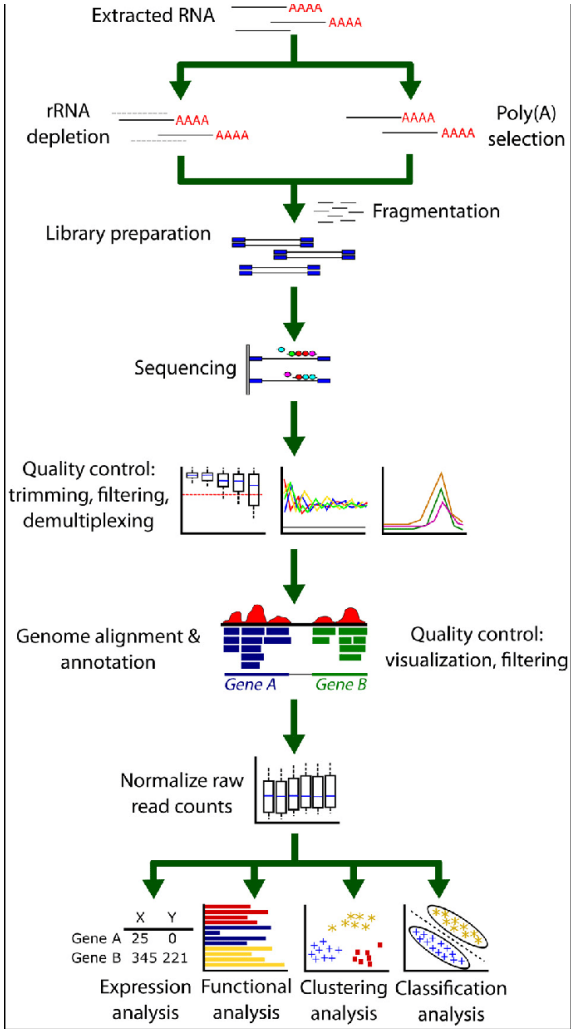
- Number of copies of a gene transcript per cell depends on gene expression
- Analysis goal:
  - Bulk : Differential expression
  - Single cell : Quantify different cell populations

https://i0.wp.com/science-explained.com/wp-content/uploads/2013/08/Cell.jpg

“Bulk” RNA seq workflow

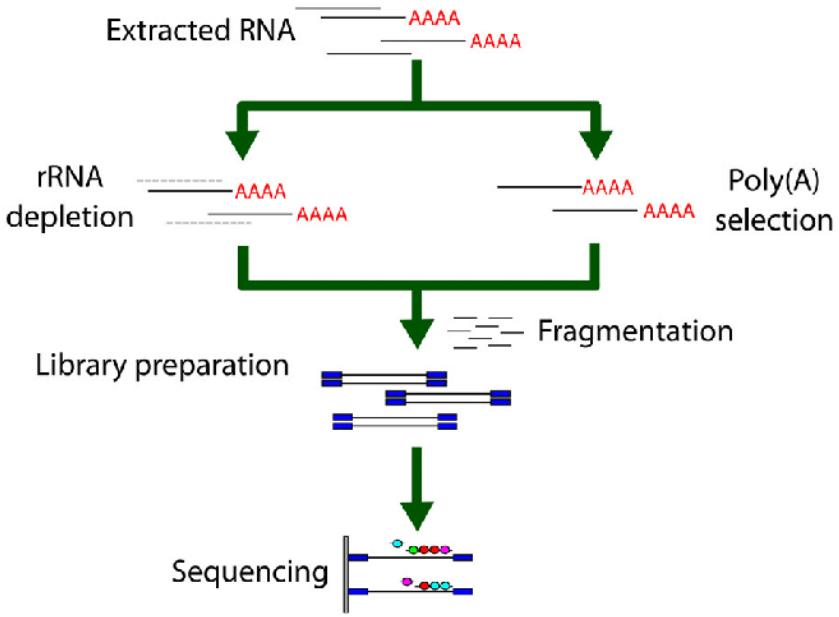
Library prep and sequencing

Bioinformatics



Good resource: [Griffiths et al Plos Comp Bio 2015]

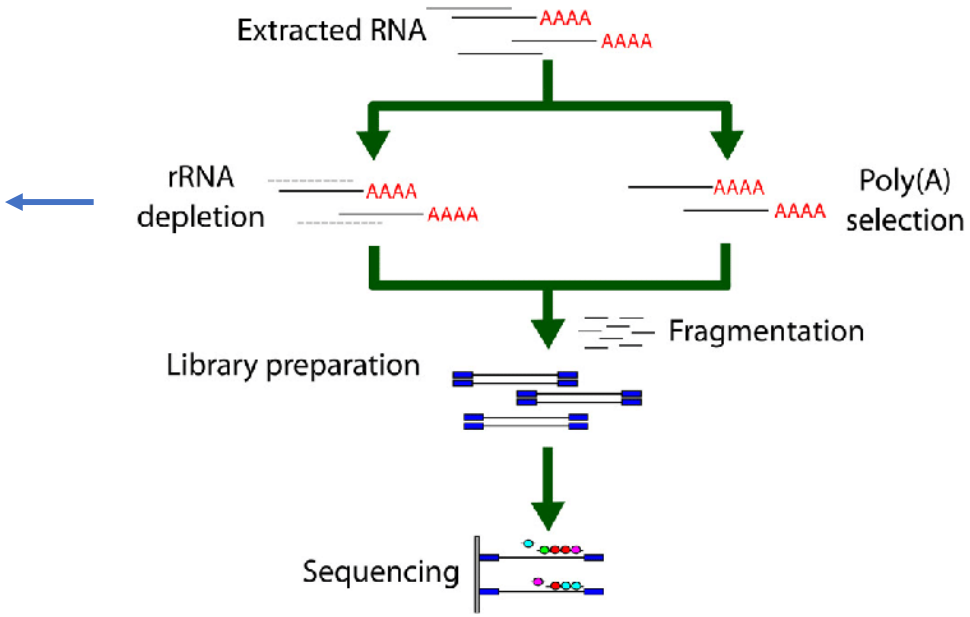
RNA seq library prep and sequencing



Good resource: [Griffiths et al Plos Comp Bio 2015]

RNA seq library prep and sequencing

- Enrichment for mRNA, two options
- In humans, ~95%–98% of all RNA molecules are rRNAs

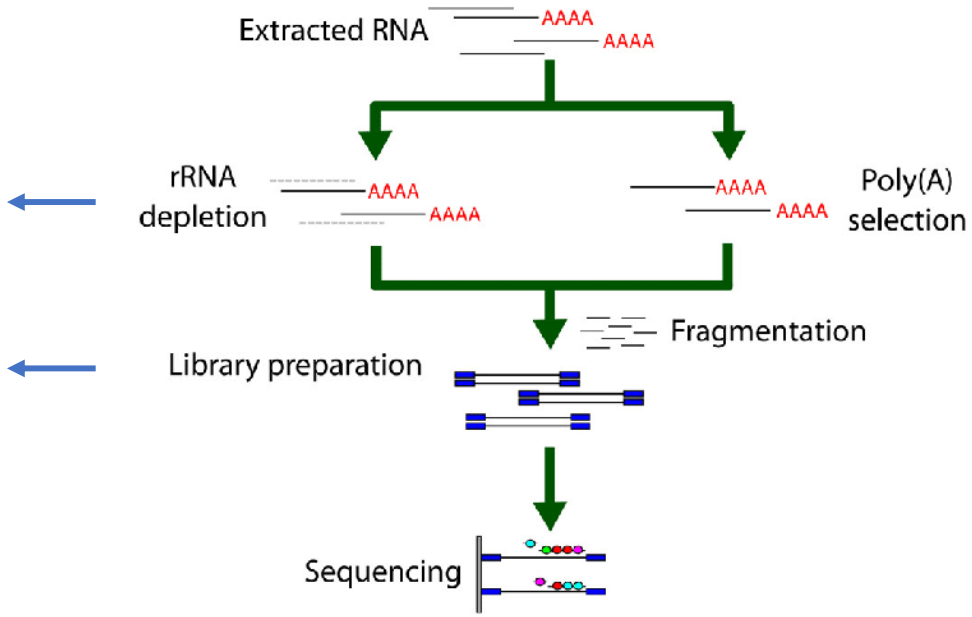


Good resource: [Griffiths et al Plos Comp Bio 2015]

RNA seq library prep and sequencing

- Enrichment for mRNA, two options
- In humans, ~95%–98% of all RNA molecules are rRNAs

- Random priming and reverse transcription
- Double stranded cDNA synthesis
- Sequencing adapter ligation

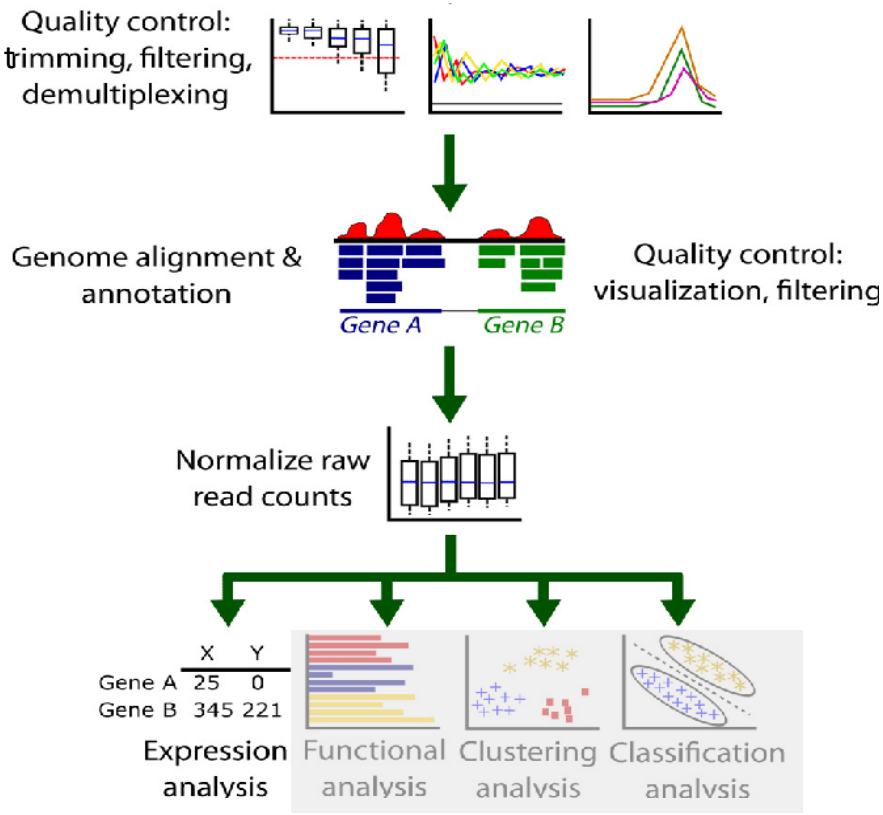


Resources:
Illumina Sequencing by Synthesis
Griffiths et al Plos Comp Bio 2015

RNA seq bioinformatics

Goal of Differential Expression

"How can we detect genes for which the counts of reads change between conditions **more systematically** than as expected by chance"

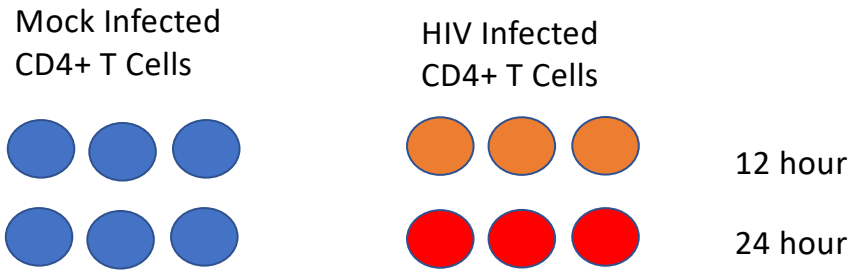


Oshlack et al. 2010. From RNA-seq reads to differential expression results. Genome Biology 2010, 11:220

Our dataset

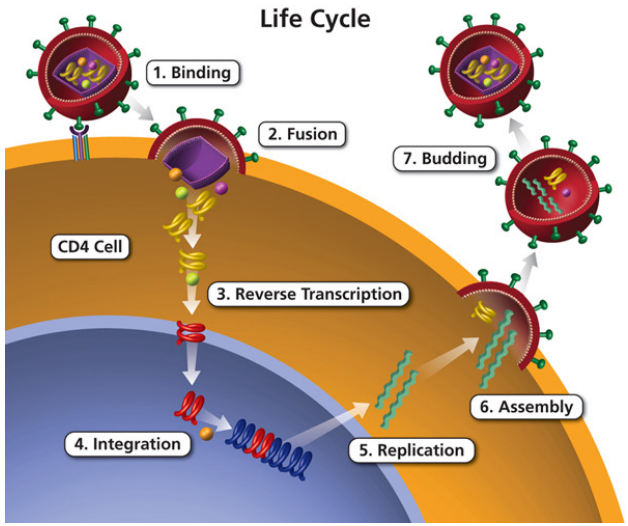
Next-Generation Sequencing Reveals HIV-1-Mediated Suppression of T Cell Activation and RNA Processing and Regulation of Noncoding RNA Expression in a CD4$^+$ T Cell Line

Stewart T. Chang, Pavel Sova, Xinxia Peng, Jeffrey Weiss, G. Lynn Law, Robert E. Palermo, Michael G. Katze



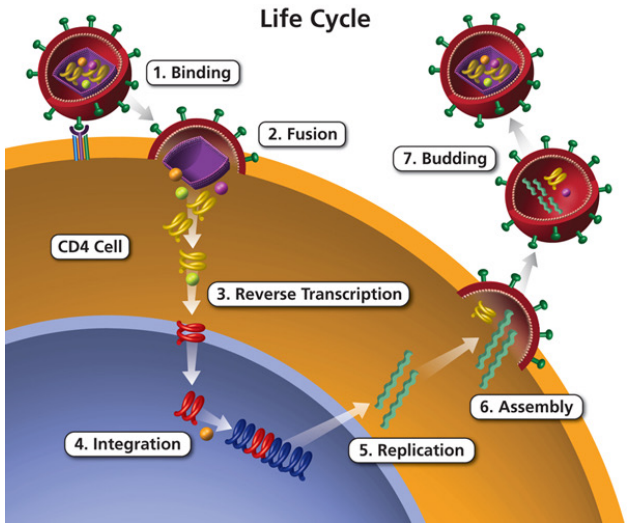
https://www.ncbi.nlm.nih.gov/pubmed/21933919

HIV lifecycle

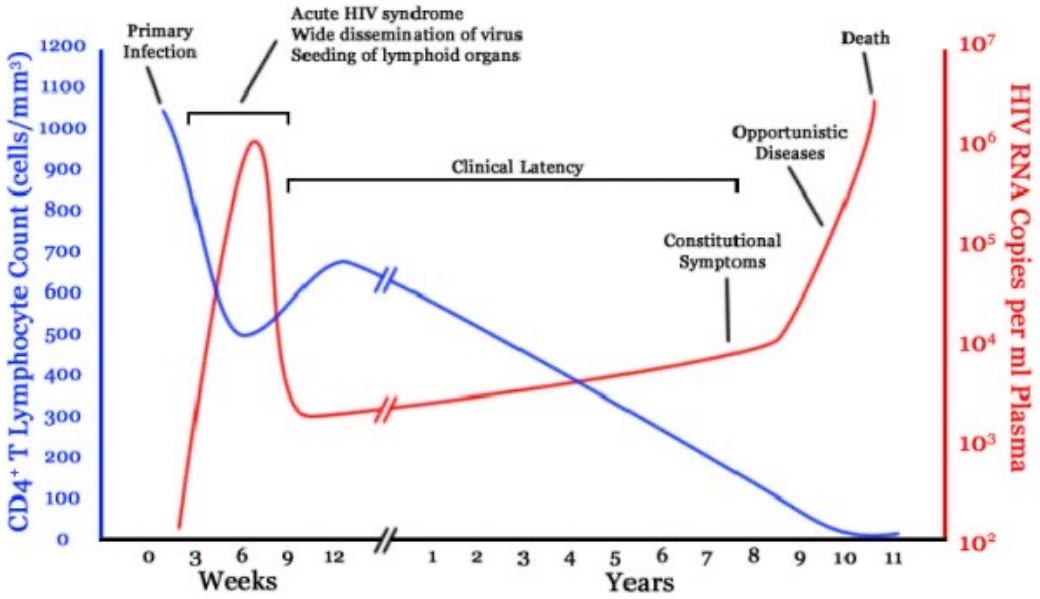


https://aidsinfo.nih.gov/understanding-hiv-aids/glossary/1596/life-cycle

HIV lifecycle



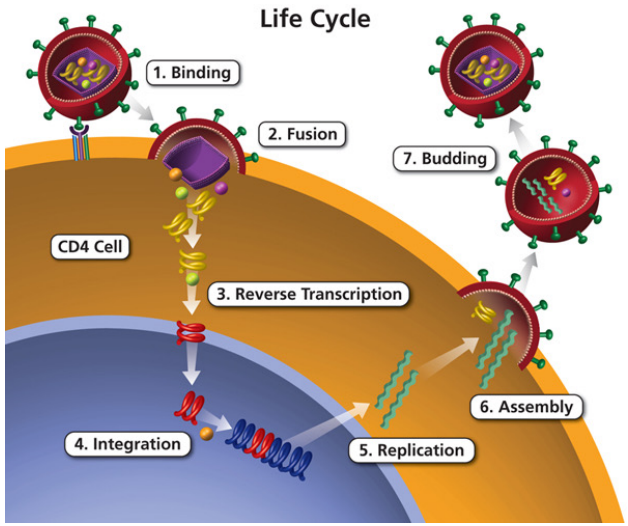
HIV infection in a human host

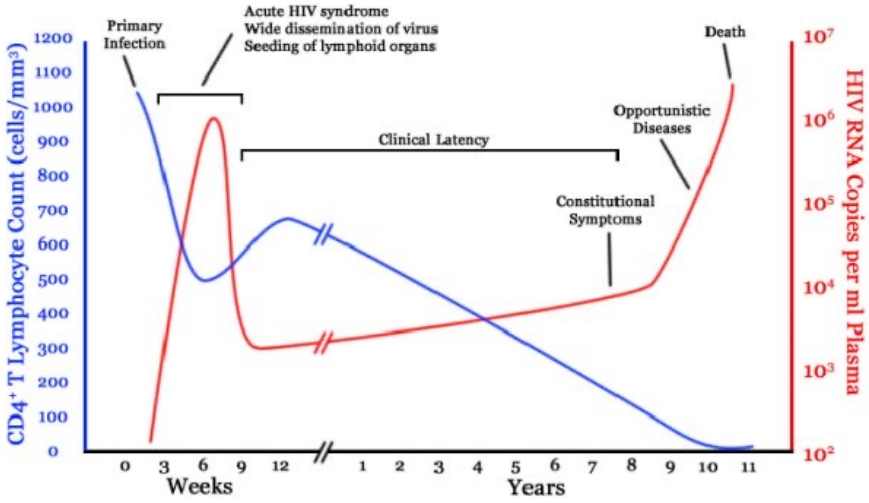


https://aidsinfo.nih.gov/understanding-hiv-aids/glossary/1596/life-cycle

The study question

What changes take place in the first 12-24 hours of HIV infection in terms of gene expression of host cell and viral replication levels?



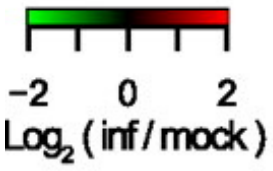


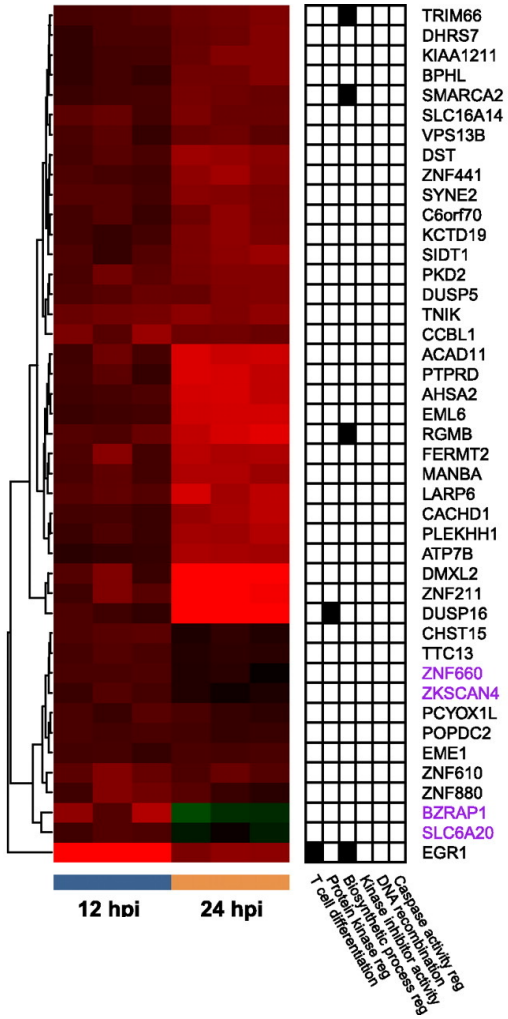
https://aidsinfo.nih.gov/understanding-hiv-aids/glossary/1596/life-cycle

Study findings

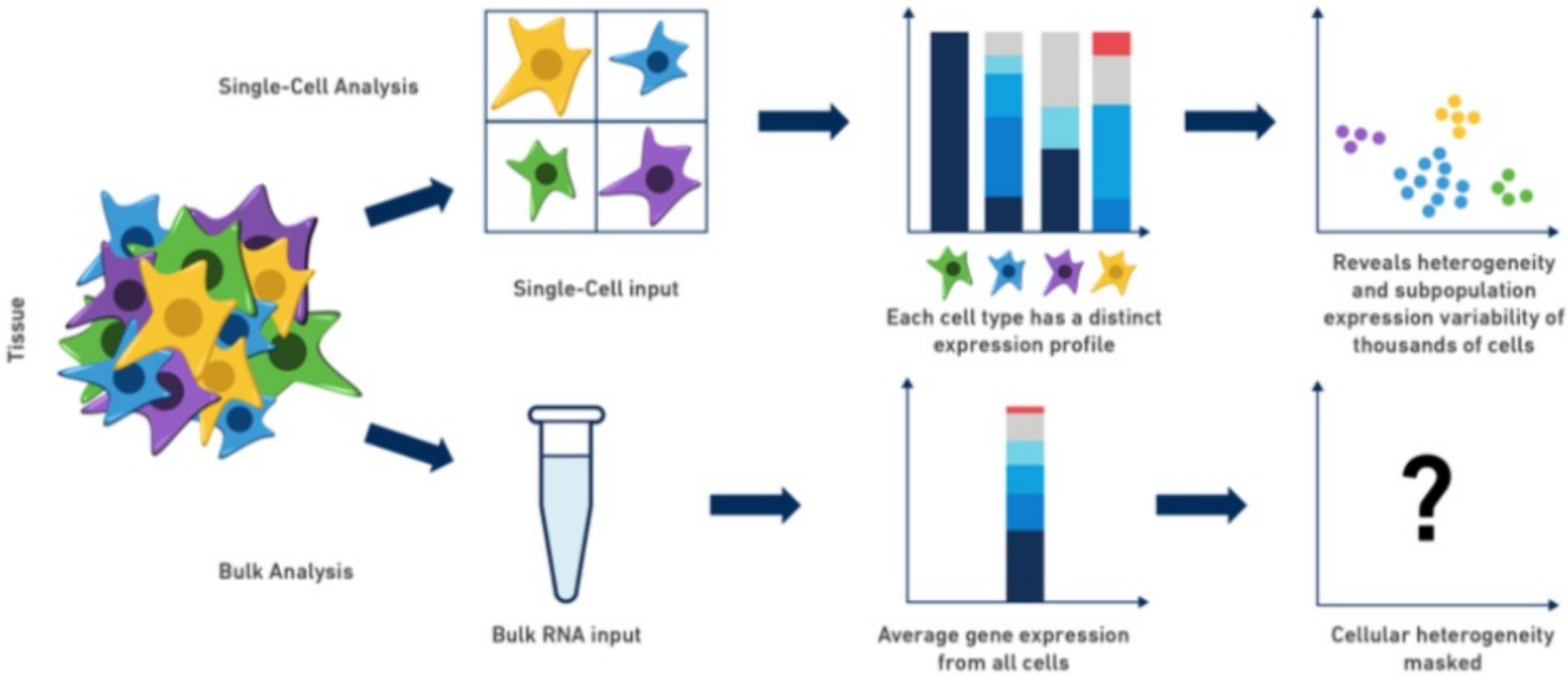
Using RNAseq, authors demonstrate:

- 20% of reads mapped to HIV at 12 hr, 40% at 24hr
- Downregulation of T cell differentiation genes at 12hr
- ‘Large-scale disruptions to host transcription’ at 24hr



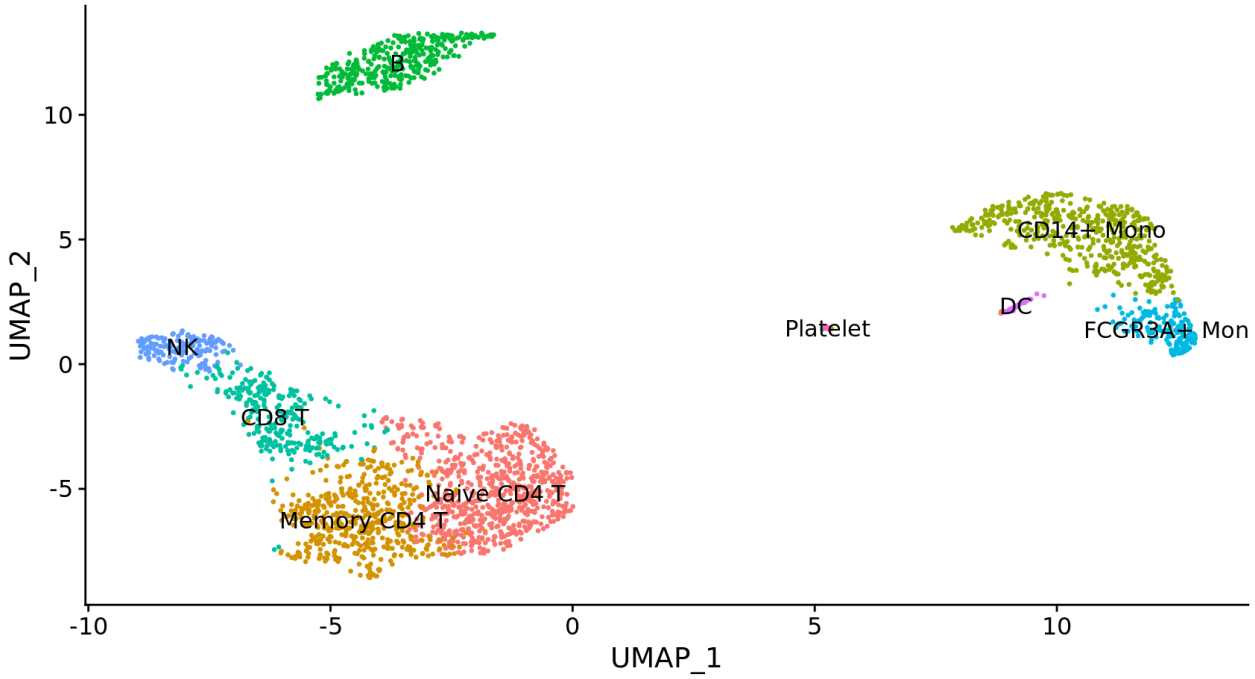


Bulk vs Single Cell RNA Sequencing



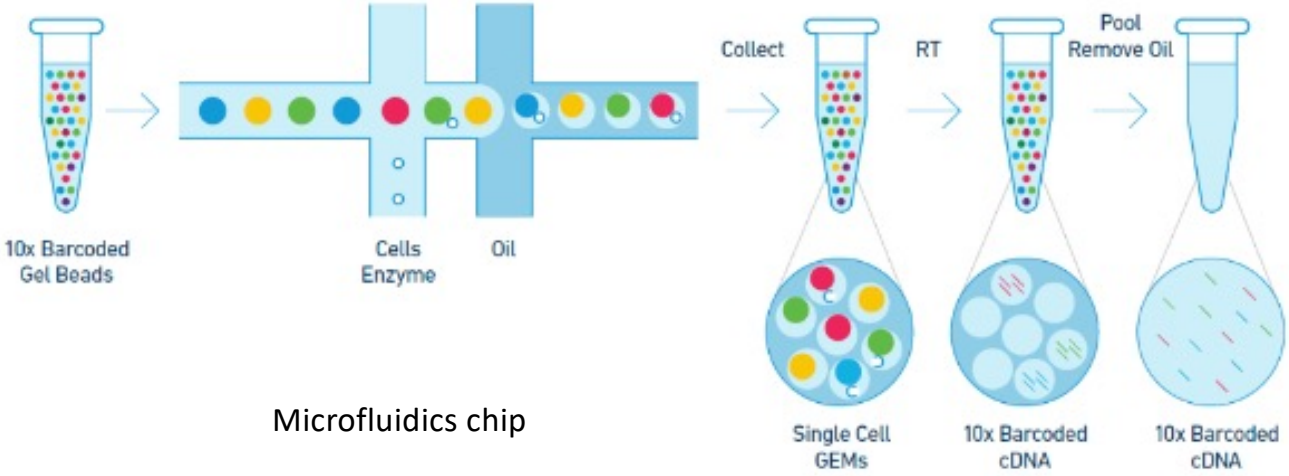
https://www.10xgenomics.com/blog/single-cell-rna-seq-an-introductory-overview-and-tools-for-getting-started

scRNA cell subsets in PBMC



https://satijalab.org/seurat/v3.2/pbmc3k_tutorial.html

10x single cell technology

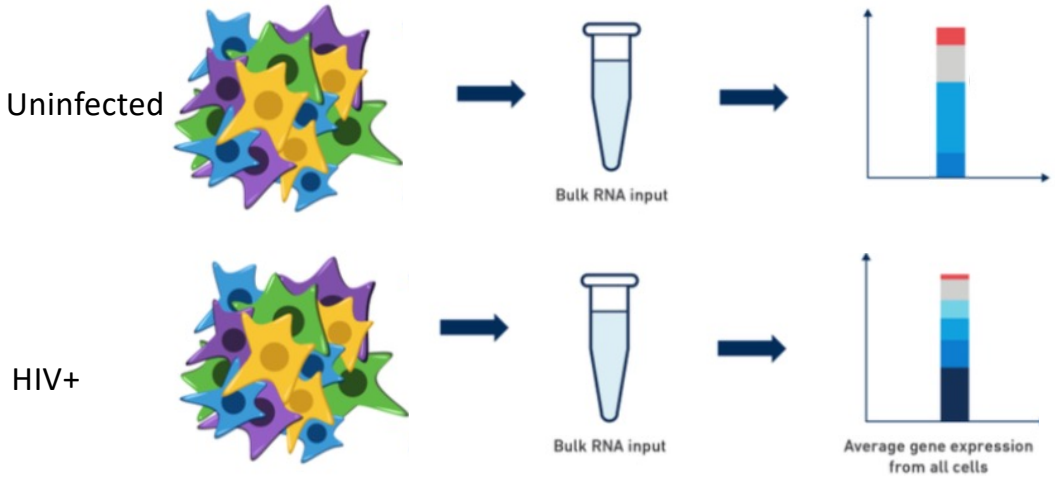


Microfluidics chip

Bulk sequencing

https://github.com/hbctraining/scRNA-seq

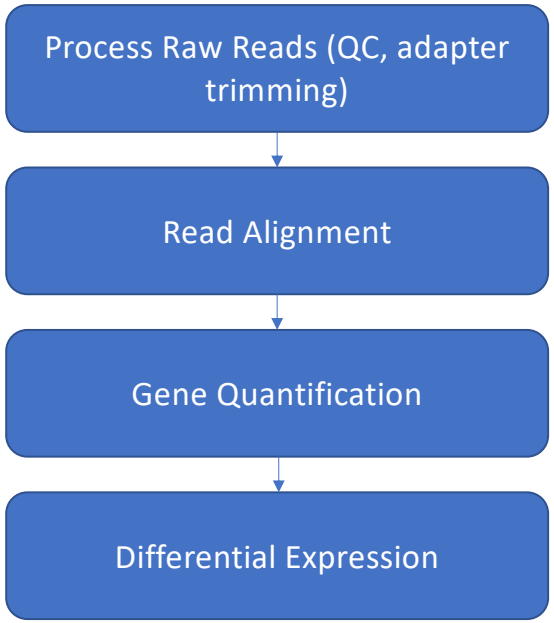
Bulk RNAseq for Differential Expression is OK!



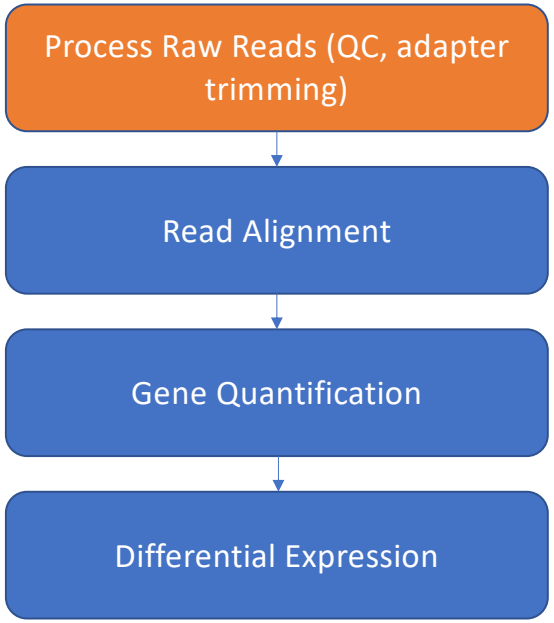
Compare relative gene expression between conditions

https://www.10xgenomics.com/blog/single-cell-rna-seq-an-introductory-overview-and-tools-for-getting-started

Our (bulk) RNAseq Workflow



Quality control on Raw Reads



Raw reads in Fastq format

```
@SRR098401.109756285
GACTCACGTAACTTTAAACTCTAACAGAAATATACTA…
+
CAEFGDG?BCGGGEEDGGHGHGDFHEIEGGDDDD…
```

1. Sequence identifier
2. Sequence
3. + (optionally lists the sequence identifier again)
4. Quality string

Base Quality Scores

The symbols we see in the read quality string are an encoding of the quality score:

```
Quality encoding: !"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHI
                  |         |         |         |         |
   Quality score: 0........10........20........30........40
```

A quality score is a prediction of the probability of an error in base calling:

Quality Score	Probability of Incorrect Base Call	Inferred Base Call Accuracy
10 (Q10)	1 in 10	90%
20 (Q20)	1 in 100	99%
30 (Q30)	1 in 1000	99.9%

https://www.illumina.com/science/education/sequencing-quality-scores.html

Base Quality Scores

The symbols we see in the read quality string are an encoding of the quality score:

```
Quality encoding: !"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHI
                  |         |         |         |         |
   Quality score: 0........10........20........30........40
```

A quality score is a prediction of the probability of an error in base calling:

Quality Score	Probability of Incorrect Base Call	Inferred Base Call Accuracy
10 (Q10)	1 in 10	90%
20 (Q20)	1 in 100	99%
30 (Q30)	1 in 1000	99.9%

Back to our read:

```
@SRR098401.109756285
GACTCACGTAACTTTAAACTCTAACAGAAATATACTA…
+
CAEFGDG?BCGGGEEDGGHGHGDFHEIEGGDDDD…
```

C –> Q = 34 -> Probability < 1/1000 of an error

https://www.illumina.com/science/education/sequencing-quality-scores.html

Raw read quality control

Fastq File

```
@SRR497699.30343179.1 HWI-EAS39X_10175_FC61MK0_4_117_4812_10346 length=75
CAGATGGCCGCAGAGGAAGCCATGAAGGCCCTGCATGGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGAC
+
IIIIGIIHFIIIIBIIDII>IIDHIIHDIIIGIFIIEIGIBDDEFIG<EIEGEEG;<DB@A8CC7<><C@BBDDB
@SRR497699.11626500.1 HWI-EAS39X_10175_FC61MK0_4_44_8384_16550 length=75
CGTACTGAACGTACAACGCTGATGCCATCCGCATATTTAAATTCGGCAGCGTTAATTAACTCCCTGACCTCGGCG
+
HHHHHHHHHHHFHHHGHHHHHHB@HHHHHHHHFHHHHHEHHHHHHHHHHHHHGEHDHHEHHHHBHHHGHHHHHHG
@SRR497699.29057557.1 HWI-EAS39X_10175_FC61MK0_4_112_12508_19308 length=75
CCGAGGCTTAGCTTTCATTATCACTGTCTCCCAGGGTGTGCTTGTCAAAGAGATAAGATCGGAAGAGCGGTTCAG
+
GGGBGGGDGBHHDHHGEGGGHHHHHGHHGHHHHHHGBGGDGGEGDHHHHHHHHHHHH@BHHGGHGHHHHHEEGHH
@SRR497699.1331889.1 HWI-EAS39X_10175_FC61MK0_4_5_4738_15920 length=75
CTTACTTTGTAGCCTTCATCAGGGTTTGCTGAAGATGGCGGTATATAGGCTGAGCAAGAGGTGGTGAGGTTGATC
+
HHHHHHHHHHGGGGGHHHGHGEBEEGGEDGGGGGGHHHHHGGEGBDGGGDDGBGGC<EADBEBE<GGGGBEEDGD
```

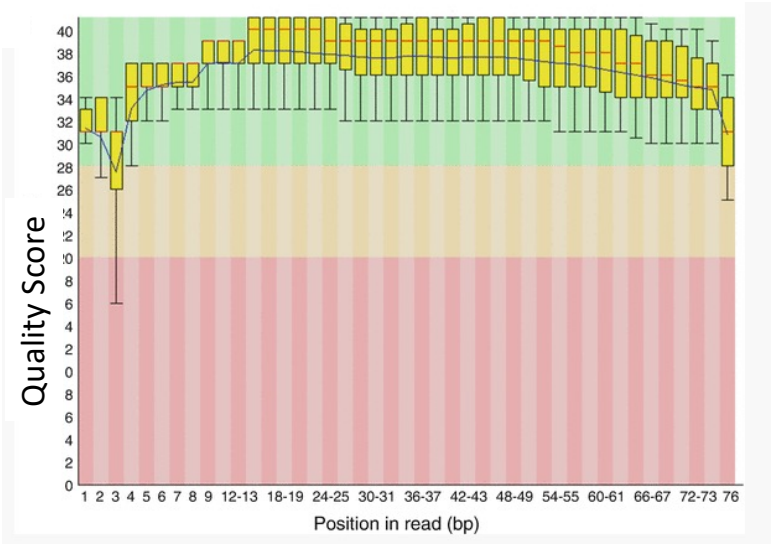
...

FastQC Tool

Metrics

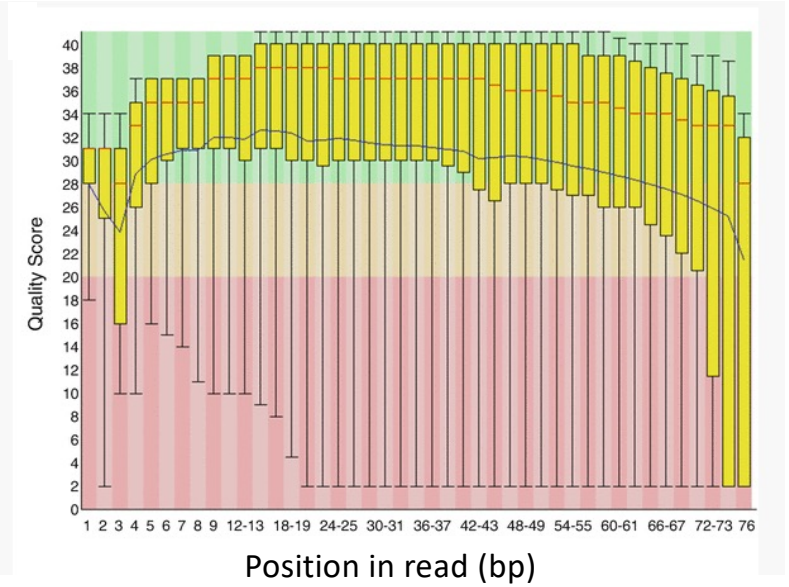
- Sequence Quality
- GC content
- Per base sequence content
- Adapters in Sequence

FastQC: Sequence Quality Histogram



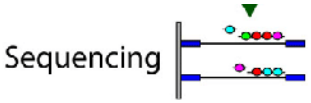
Position in read (bp)

GOOD
High quality over the length of the read

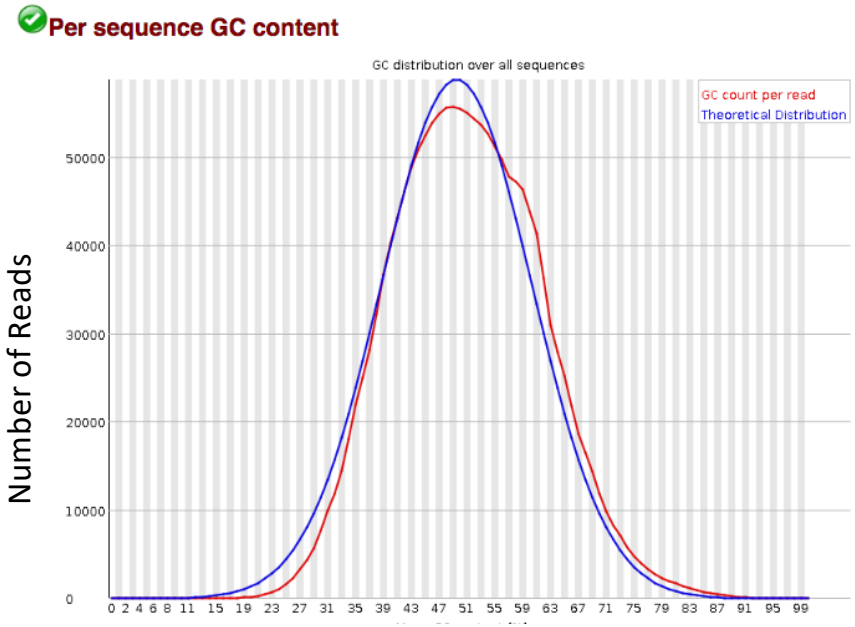


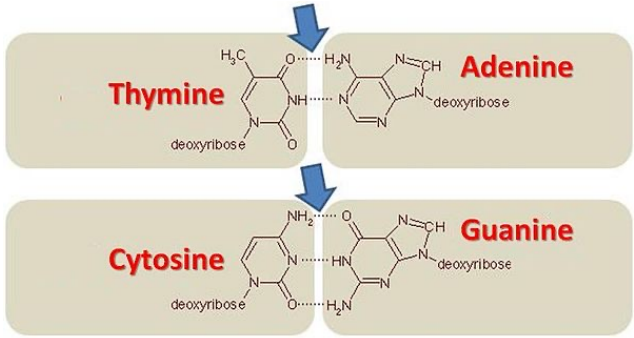
Position in read (bp)

BAD
Read quality drops at the beginning and end

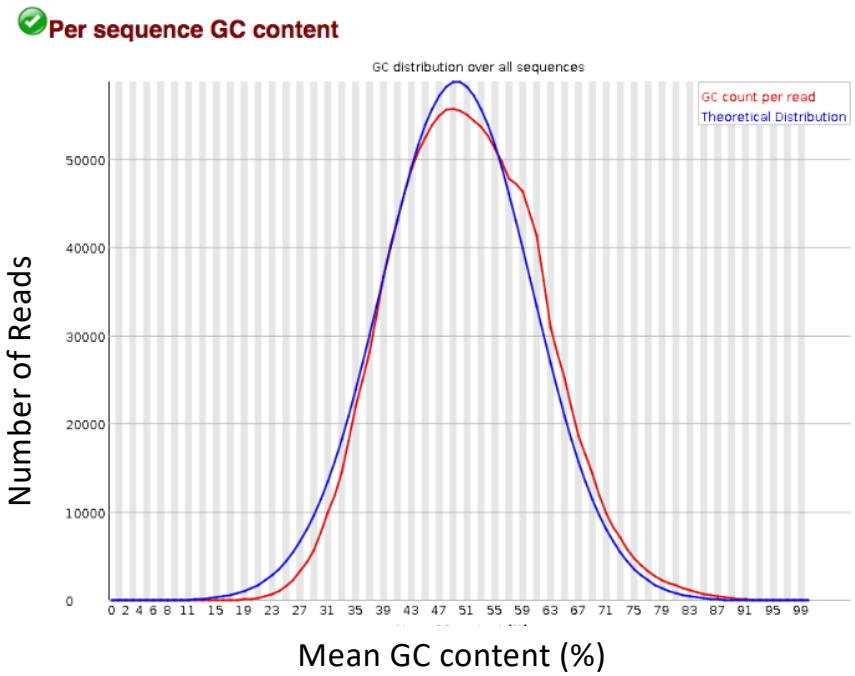


FastQC: Per sequence GC content

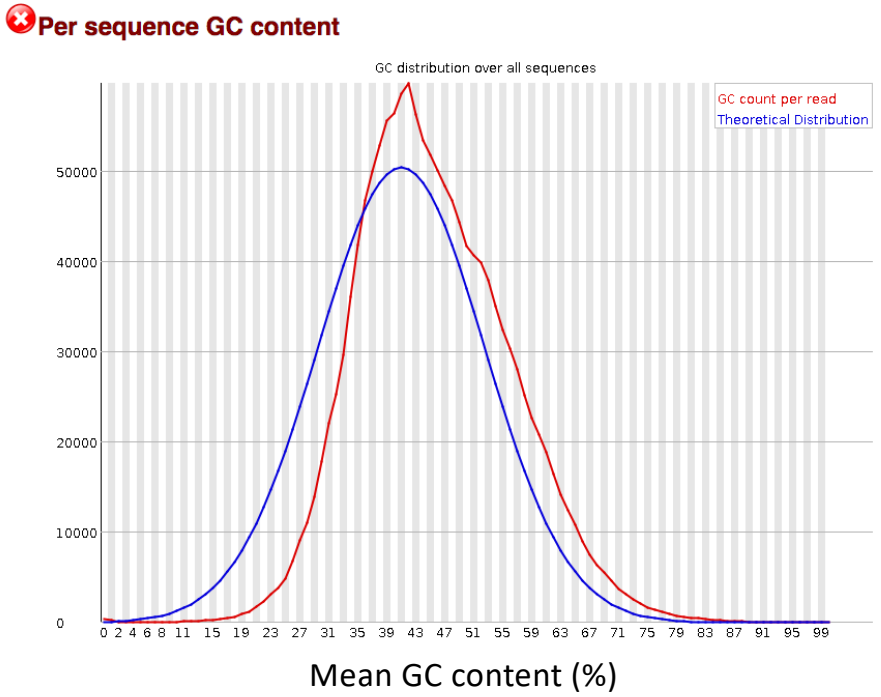




FastQC: Per sequence GC content

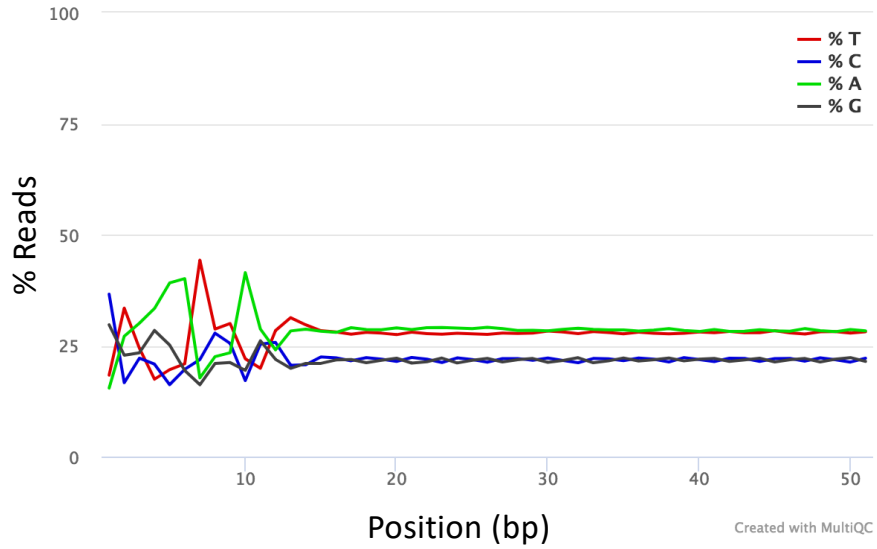


GOOD: follows normal distribution (sum of deviations is < 15% of reads)



BAD: can indicate contamination with adapter dimers, or another species

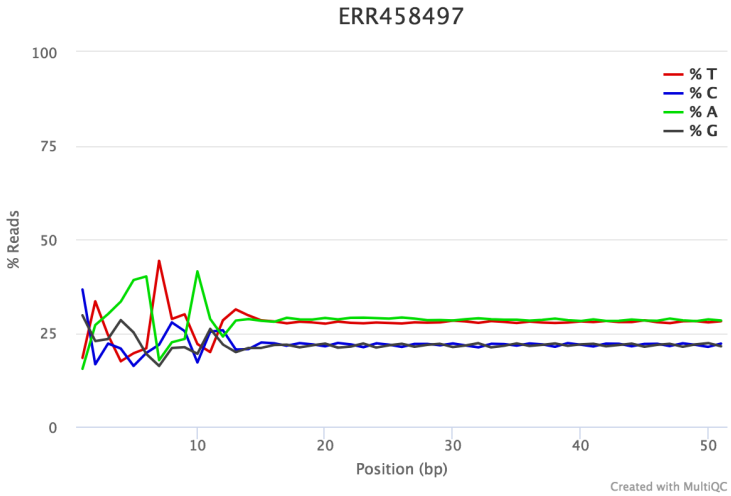
FastQC: Per Base Sequence Content



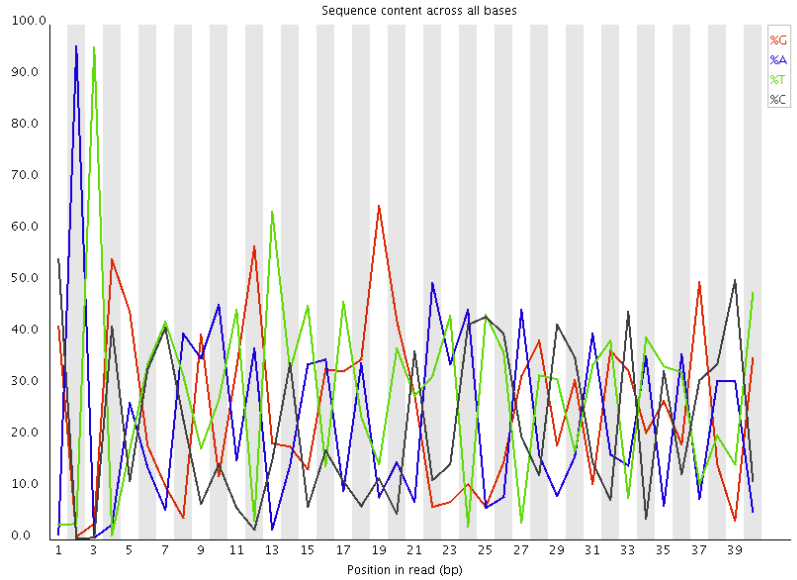
- Proportion of each position for which each DNA base has been called
- RNAseq data tends to show a positional sequence bias in the first ~12 bases
- The "random" priming step during library construction is not truly random and certain hexamers are more prevalent than others

sequencing.qcfail.com

FastQC: Per Base Sequence Content

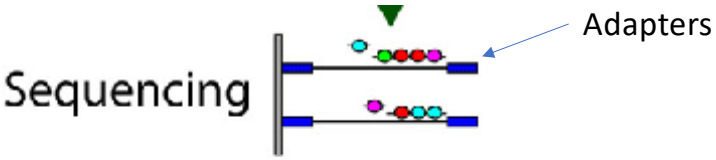


EXPECTED for RNAseq



BAD:
Shows a strong positional bias throughout the reads, which in this case is due to the library having a certain sequence that is overrepresented

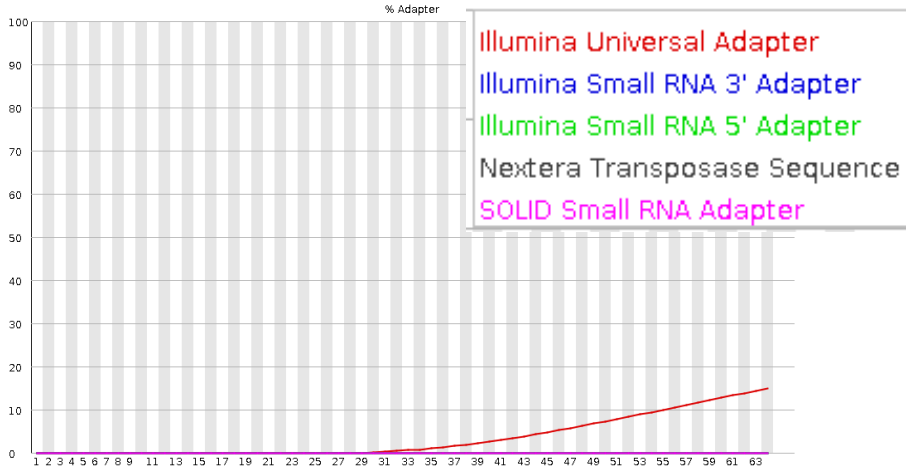
FastQC: Adapter content



FastQC will scan each read for the presence of known adapter sequences

The plot shows that the adapter content rises over the course of the read

Solution – Adapter trimming!

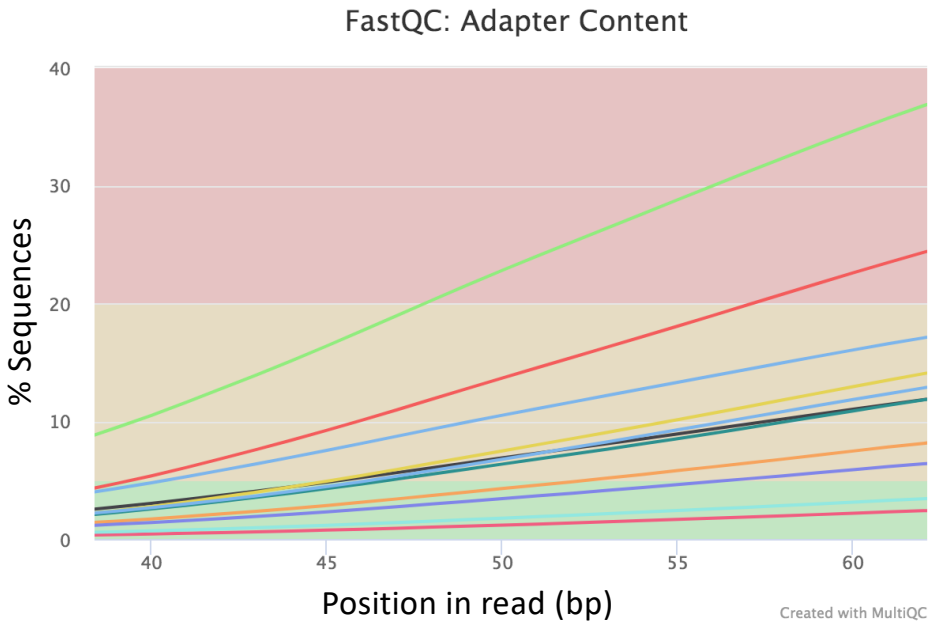


Position in read (bp)

sequencing.qcfail.com

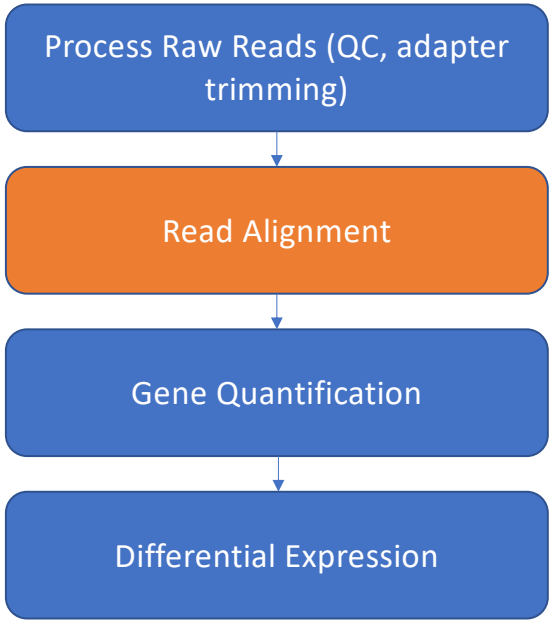
FastQC -> MultiQC

Should view all samples at once to notice abnormalities for our dataset.



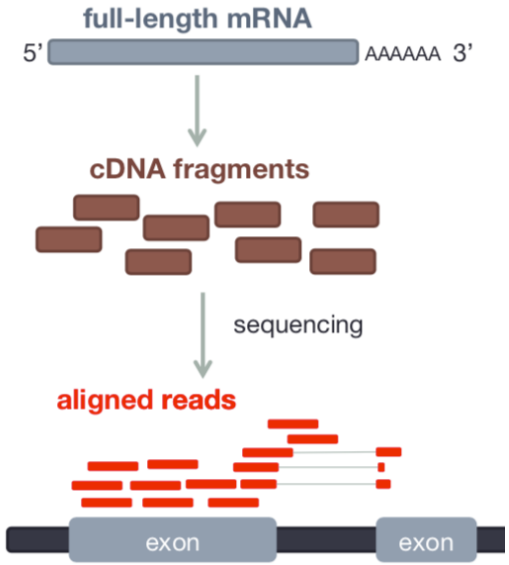
We'll use a tool called "Trim Galore!" to trim adapters and remove low quality bases/reads.

Workflow


Process Raw Reads (QC, adapter trimming)
Read Alignment
Gene Quantification
Differential Expression

Read Alignment

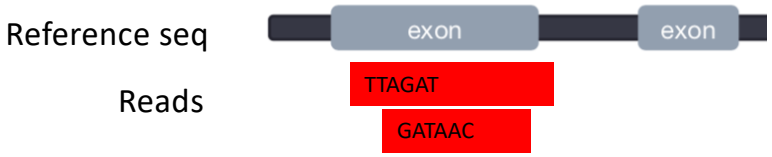
- RNAseq data originates from spliced mRNA (no introns)
- When aligning to the genome, our aligner must find a spliced alignment for reads
- We use a tool called STAR (Spliced Transcripts Alignment to a Reference) that has a exon-aware mapping algorithm.



Reference sequence

Dobin et al Bioinformatics 2013

Sequence Alignment Map (SAM)




```
@HD VN:1.5 SO:coordinate
@SQ SN:ref LN:45
r001   99 ref  7 30 8M2I4M1D3M = 37  39 TTAGATAAAGGATACTG *
r002    0 ref  9 30 3S6M1P1I4M *  0   0 AAAAGATAAGGATA    *
r003    0 ref  9 30 5S6M       *  0   0 GCCTAAGCTAA       * SA:Z:ref,29,-,6H5M,17,0;
r004    0 ref 16 30 6M14N5M    *  0   0 ATAGCTTCAGC       *
r003 2064 ref 29 17 6H5M       *  0   0 TAGGC             * SA:Z:ref,9,+,5S6M,30,1;
r001  147 ref 37 30 9M         =  7 -39 CAGCGGCAT         * NM:i:1
```

Header section

Alignment section

CIGAR: summary of alignment, e.g. match, gap, insertion, deletion

Mapping Quality

Position

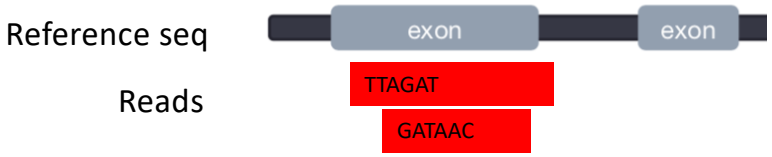
Ref Sequence name

Flag: indicates alignment information e.g. paired, aligned, etc
https://broadinstitute.github.io/picard/explain-flags.html

Read ID

www.samformat.info

Sequence Alignment Map (SAM)




```
@HD VN:1.5 SO:coordinate
@SQ SN:ref LN:45
r001   99 ref  7 30 8M2I4M1D3M = 37  39 TTAGATAAAGGATACTG *
r002    0 ref  9 30 3S6M1P1I4M *  0   0 AAAAGATAAGGATA    *
r003    0 ref  9 30 5S6M       *  0   0 GCCTAAGCTAA       * SA:Z:ref,29,-,6H5M,17,0;
r004    0 ref 16 30 6M14N5M    *  0   0 ATAGCTTCAGC       *
r003 2064 ref 29 17 6H5M       *  0   0 TAGGC             * SA:Z:ref,9,+,5S6M,30,1;
r001  147 ref 37 30 9M         =  7 -39 CAGCGGCAT         * NM:i:1
```

Header section

Alignment section

Paired end info

Sequence

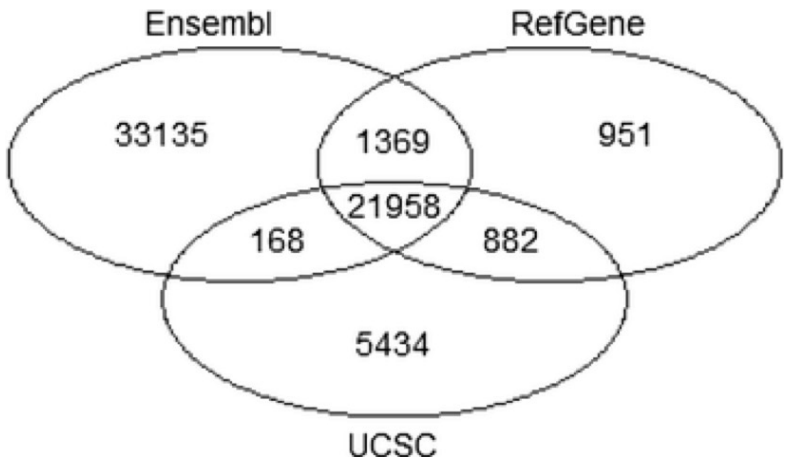
Quality Score

Optional Fields

www.samformat.info

Genome Annotation Standards

- STAR can use an annotation file gives the location and structure of genes in order to improve alignment in known splice junctions
- Annotation is dynamic and there are at least three major sources of annotation
- The intersection among RefGene, UCSC, and Ensembl annotations shows high overlap. RefGene has the fewest unique genes, while more than 50% of genes in Ensembl are unique
- Be consistent with your choice of annotation source!



Zhao et al Bioinformatics 2015

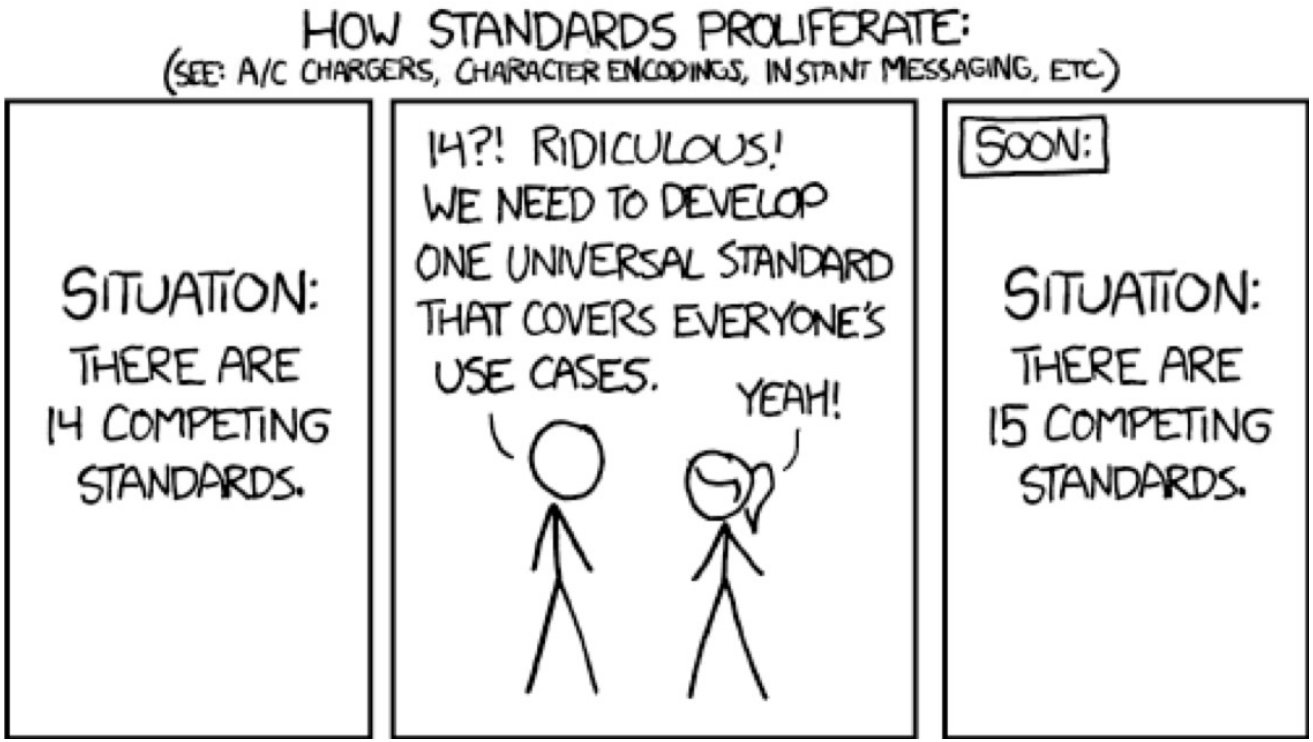
Gene Annotation Format (GTF)

In order to count genes, we need to know where they are located in the reference sequence
STAR uses a Gene Transfer Format (GTF) file for gene annotation

Chrom	Source	Feature type	Start	Stop	Score	Strand	Frame	Attribute
chr5	hg38_refGene	exon	138465492	138466068	.	+	.	gene_id "EGR1";
chr5	hg38_refGene	CDS	138465762	138466068	.	+	0	gene_id "EGR1";
chr5	hg38_refGene	start_codon	138465762	138465764	.	+	.	gene_id "EGR1";
chr5	hg38_refGene	CDS	138466757	138468078	.	+	2	gene_id "EGR1";
chr5	hg38_refGene	exon	138466757	138469315	.	+	.	gene_id "EGR1";
chr5	hg38_refGene	stop_codon	138468079	138468081	.	+	.	gene_id "EGR1";

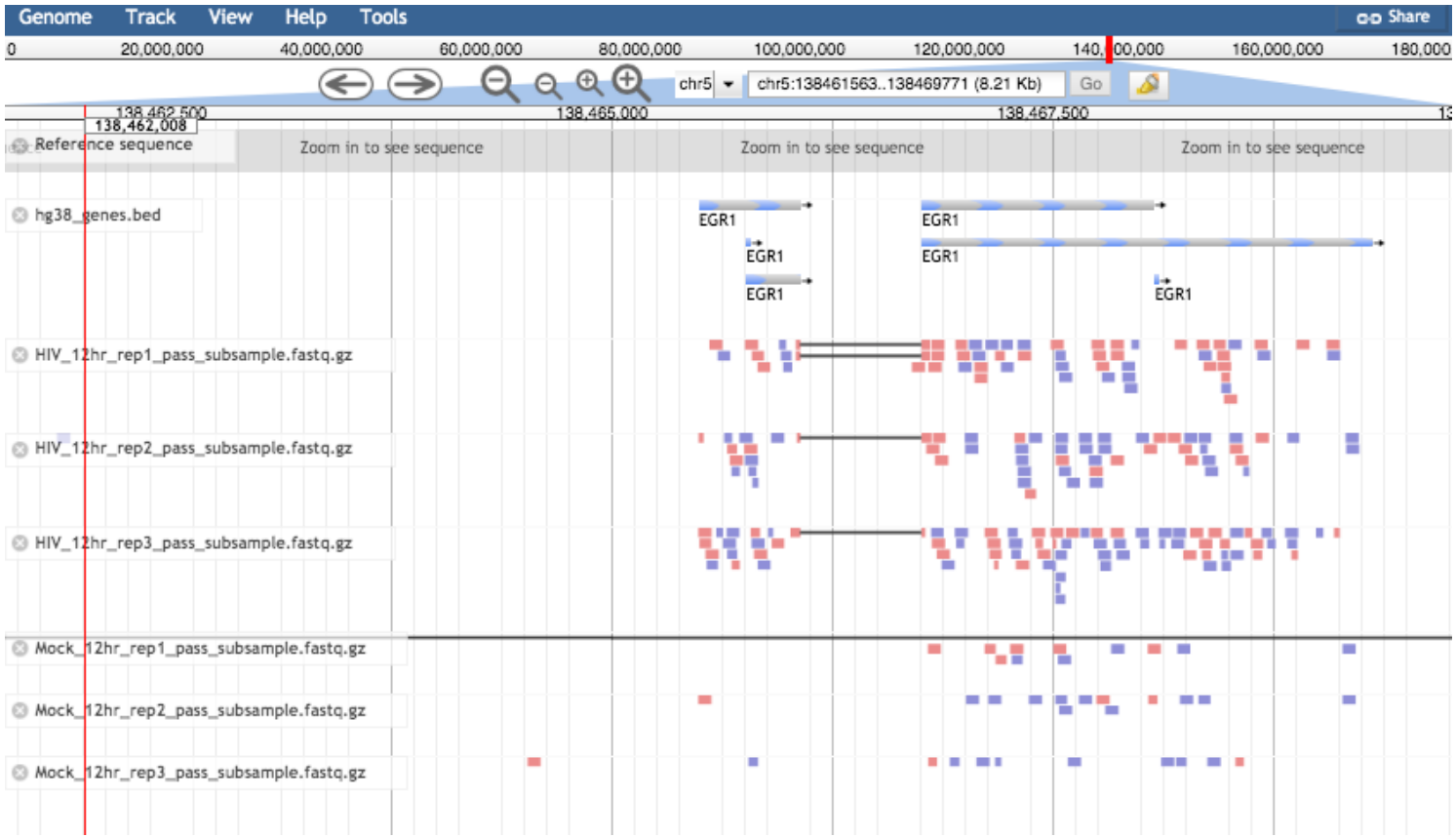
https://useast.ensembl.org/info/website/upload/gff.html

A note on standards

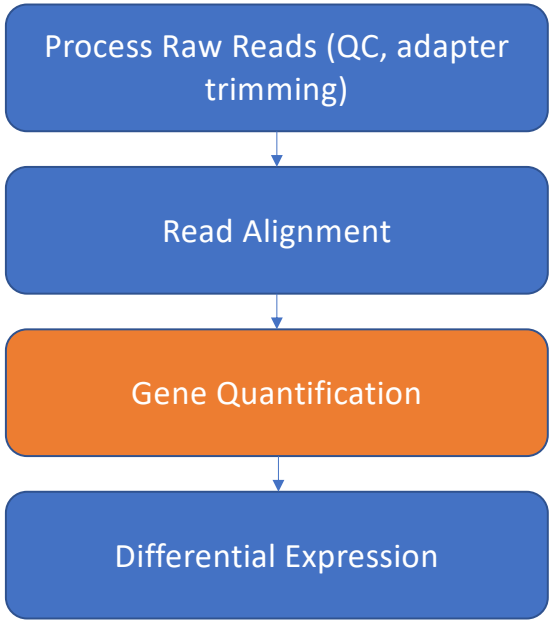


https://xkcd.com/927/

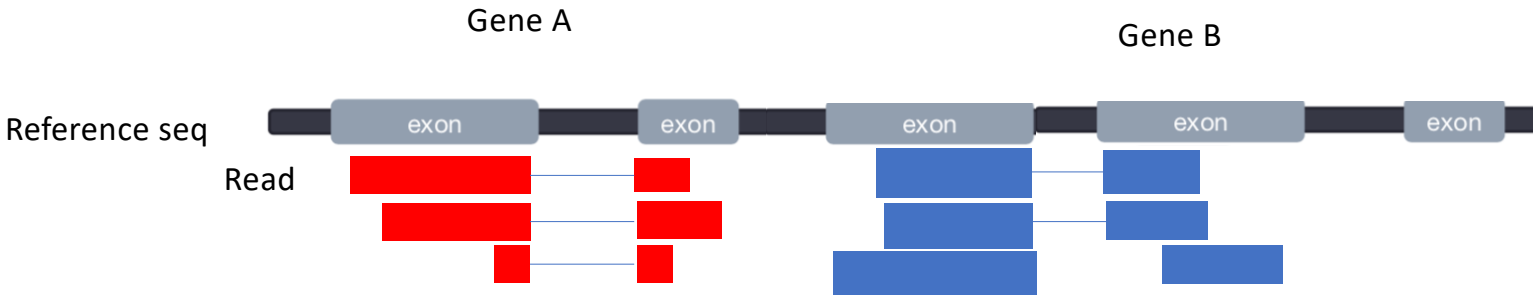
Visualizing reads with JBrowse



Workflow

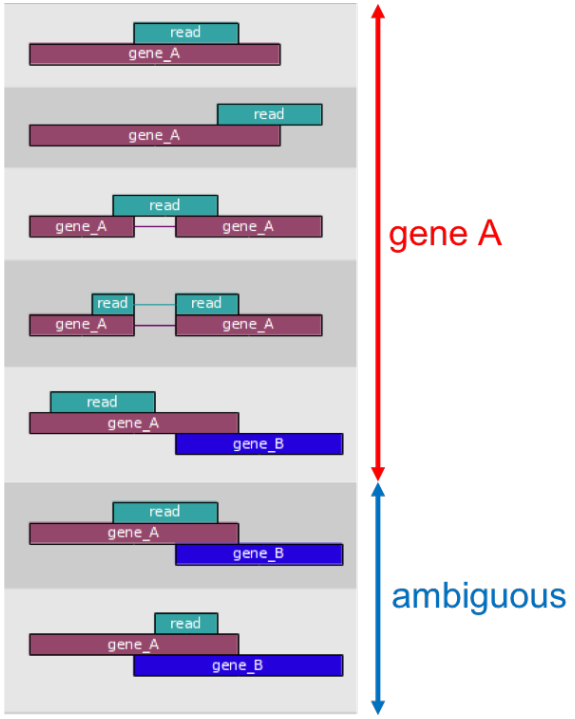

Process Raw Reads (QC, adapter trimming)
Read Alignment
Gene Quantification
Differential Expression

Counting reads for each gene



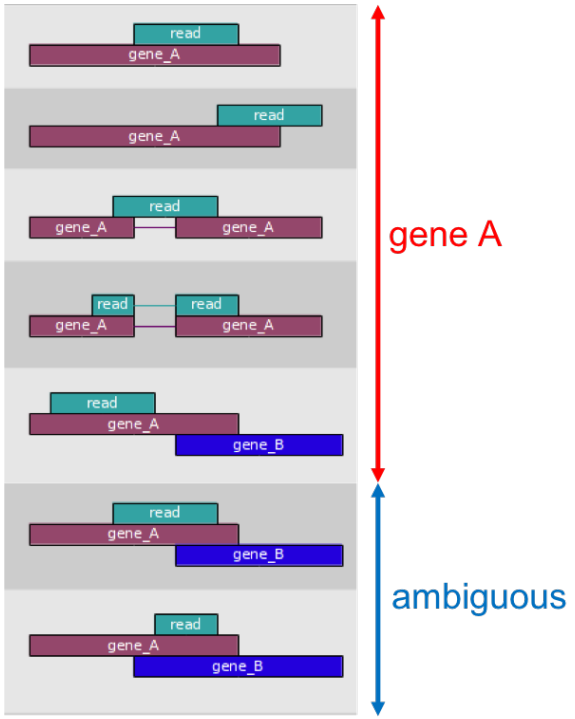
Counting reads: featurecounts

- The mapped coordinates of each read are compared with the features in the GTF file
- Reads that overlap with a gene by >=1 bp are counted as belonging to that feature
- Ambiguous reads will be discarded



Counting reads: featurecounts

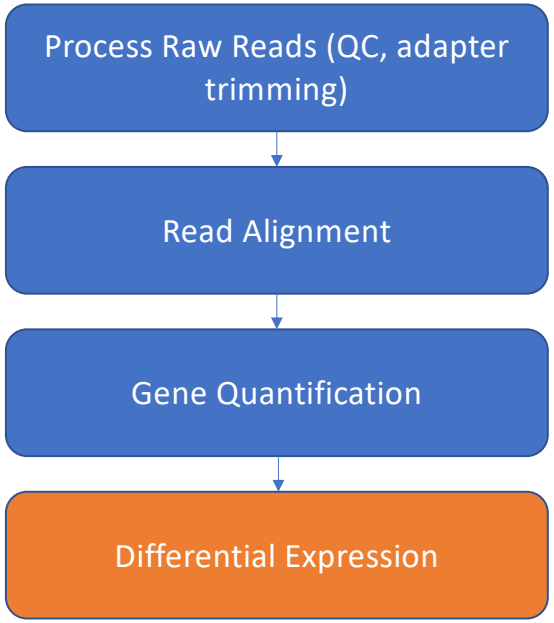
- The mapped coordinates of each read are compared with the features in the GTF file
- Reads that overlap with a gene by >=1 bp are counted as belonging to that feature
- Ambiguous reads will be discarded



Result is a gene count matrix:

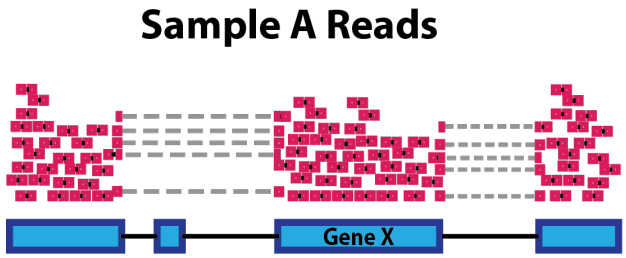
Gene	Sample 1	Sample 2	Sample 3	Sample 4
A	1000	1000	100	10
B	10	1	5	6
C	10	1	10	20

Workflow


Process Raw Reads (QC, adapter trimming)
Read Alignment
Gene Quantification
Differential Expression

Normalization

- Raw Count != Expression strength
- Normalization:
  - Eliminates factors that are not of interest for our experiment
  - Enables accurate comparison between samples or genes

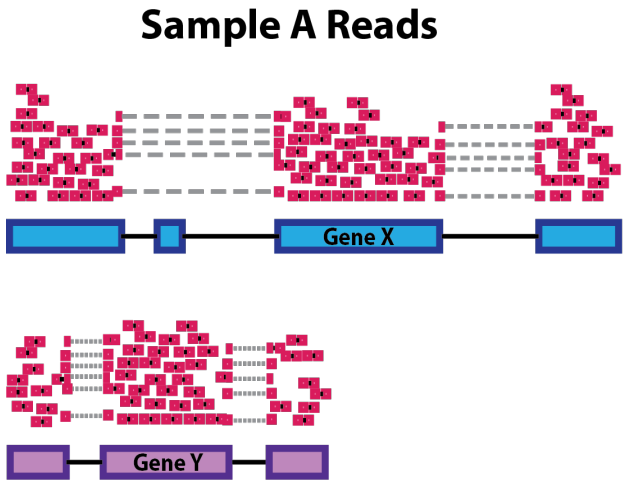


Adapted from https://hbctraining.github.io/DGE_workshop

Normalization

The number of reads mapped to a gene depends on

- **Gene Length**

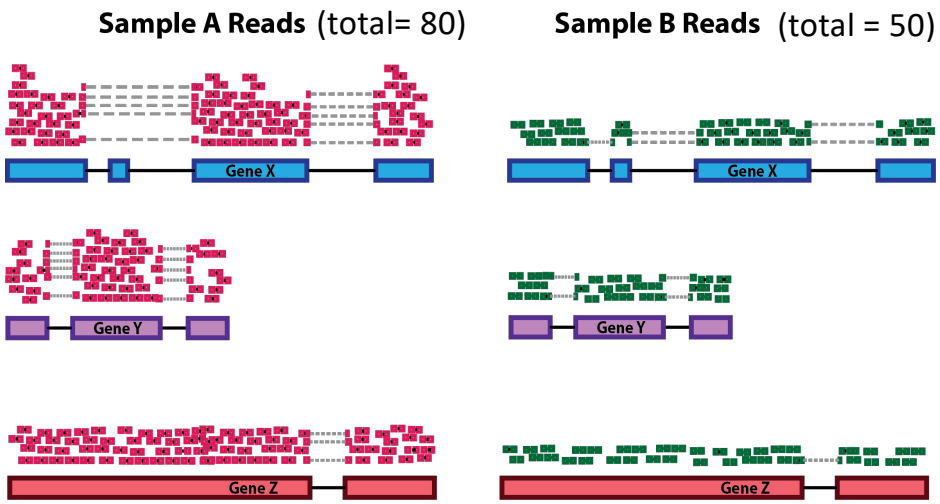


Adapted from https://hbctraining.github.io/DGE_workshop

Normalization

The number of reads mapped to a gene depends on

- Gene Length
- **Sequencing depth**

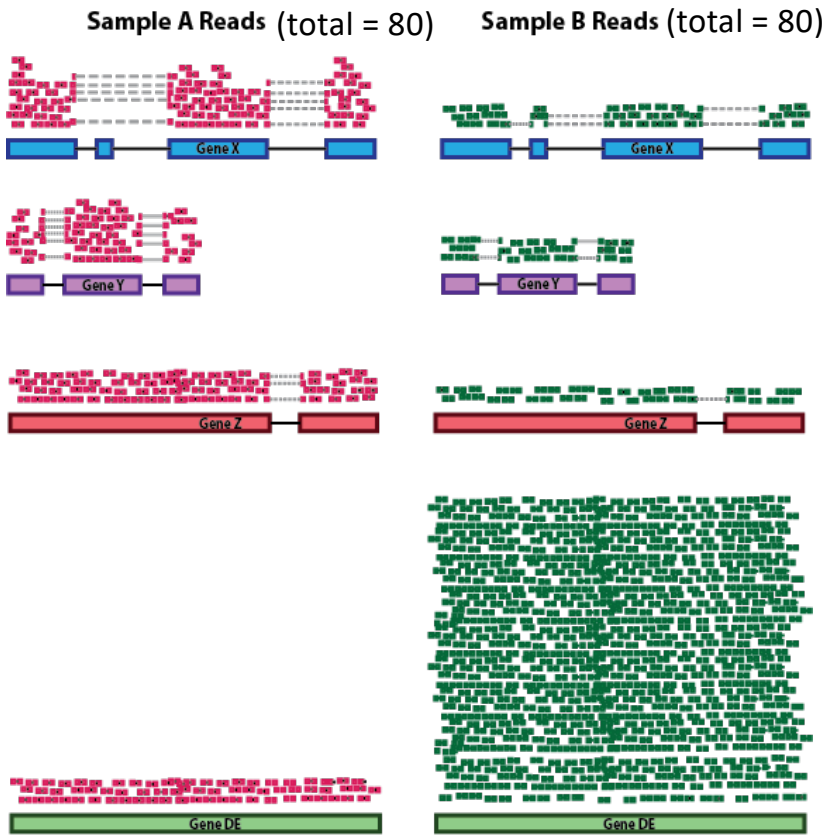


Adapted from https://hbctraining.github.io/DGE_workshop

Normalization

The number of reads mapped to a gene depends on

- Gene Length
- Sequencing depth
- **The expression level of other genes in the sample (RNA Composition)**



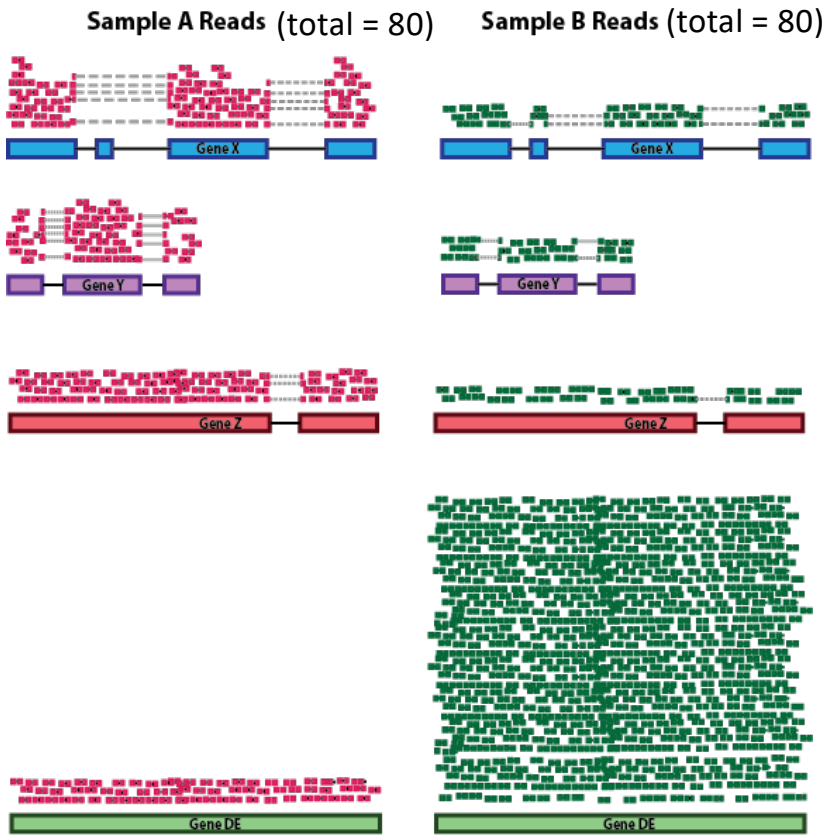
Adapted from https://hbctraining.github.io/DGE_workshop

Normalization

The number of reads mapped to a gene depends on

- Gene Length
- **Sequencing depth**
- **The expression level of other genes in the sample (RNA Composition)**

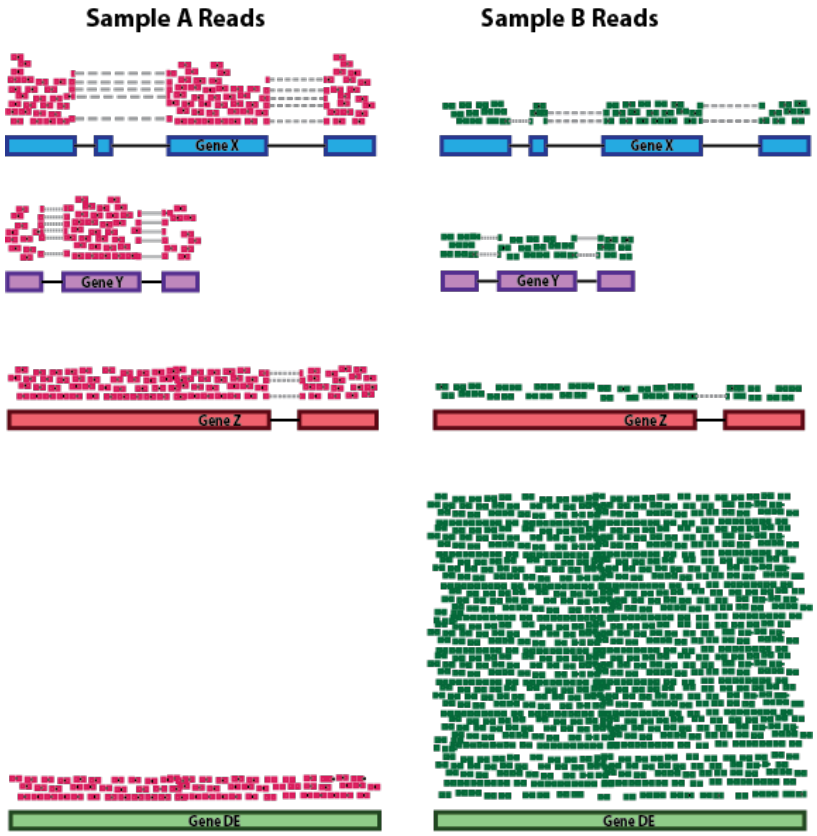
DESeq2 Median of Ratios



Adapted from https://hbctraining.github.io/DGE_workshop

Normalization: DESeq2 Median of Ratios

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50
Total =	80	80



Normalization: DESeq2 Median of Ratios

1. Take a row-wise average to produce an average sample (geometric mean) $\sqrt[n]{x_1 x_2 \cdots x_n}$

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

→

Avg. Sample
16
16
16
10

Normalization: DESeq2 Median of Ratios

1. Take a row-wise average to produce an average sample (geometric mean) $\sqrt[n]{x_1 x_2 \cdots x_n}$

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

→

Avg. Sample
16
16
16
10

2. Divide all rows by the Average Sample for that gene (**Ratio**)

Gene	Sample A/Avg.	Sample B /Avg.
X	26/16 = 1.6	10/16 = 0.6
Y	1.6	0.6
Z	1.6	0.6
DE	0.2	5

Normalization: DESeq2 Median of Ratios

1. Take a row-wise average to produce an average sample (geometric mean) $\sqrt[n]{x_1 x_2 \cdots x_n}$

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

→

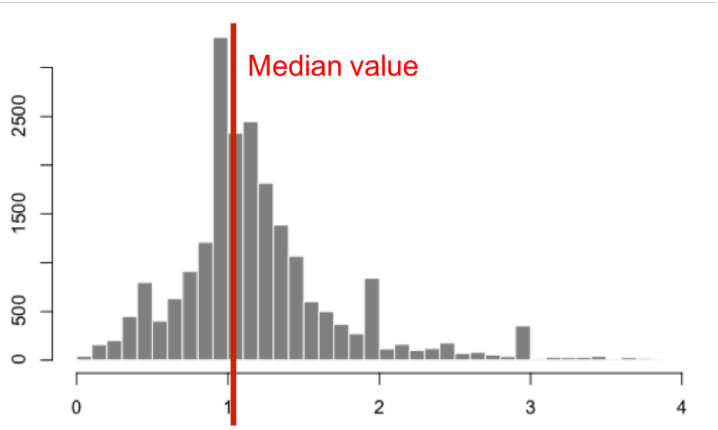
Avg. Sample
16
16
16
16

2. Divide all rows by the Average Sample for that gene (**Ratio**)

Gene	Sample A/Avg.	Sample B /Avg.
X	26/16 = 1.6	10/16 = 0.6
Y	1.6	0.6
Z	1.6	0.6
DE	0.2	5

3. Take the **median** of each column. Should be ~1 for all

Size factor	1.6	0.6



Normalization: DESeq2 Median of Ratios

1. Take a row-wise average to produce an average sample (geometric mean) $\sqrt[n]{x_1 x_2 \cdots x_n}$

Gene	Sample A	Sample B
X	26	10
Y	26	10
Z	26	10
DE	2	50

→

Avg. Sample
16
16
16
16

2. Divide all rows by the Average Sample for that gene (**Ratio**)

Gene	Sample A/Avg.	Sample B /Avg.
X	26/16 = 1.6	10/16 = 0.6
Y	1.6	0.6
Z	1.6	0.6
DE	0.2	5

3. Take the **median** of each column. Should be ~1 for all

Size factor	1.6	0.6

4. Divide all counts by sample specific size factor

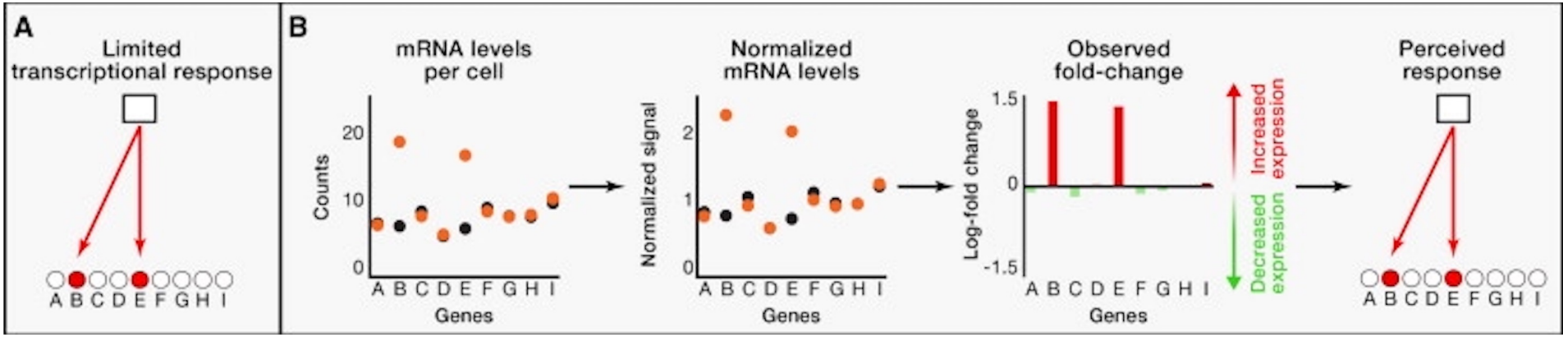
Gene	Sample A / S_A	Sample B / S_B
X	16.3	16.7
Y	16.3	16.7
Z	16.3	16.7
DE	1.3	83.3

Normalized counts for non-DE genes are similar!

```
estimateSizeFactors(dds)
```

Assumption of DESeq2 Median of Ratios

Median of Ratios method assumes that most genes are not Differentially Expressed between samples.

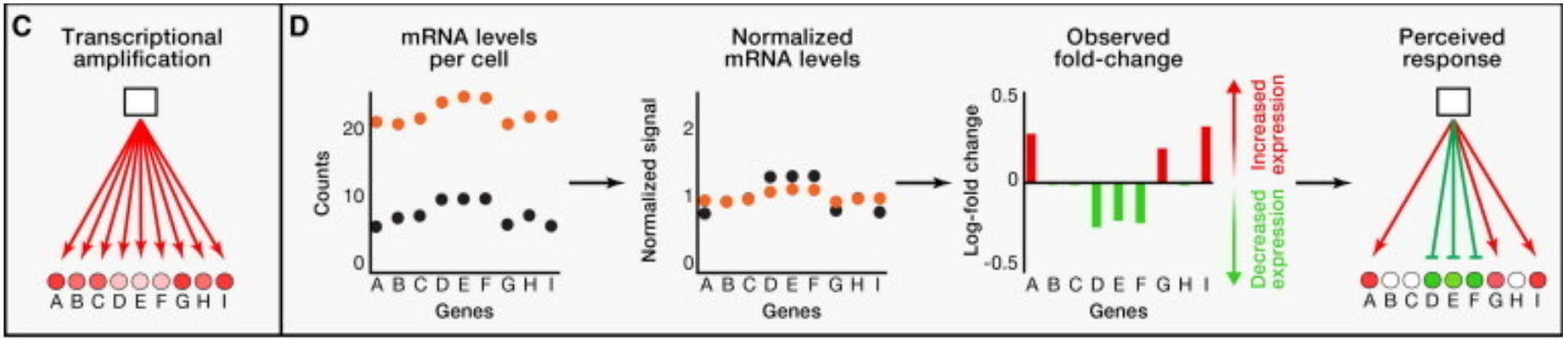


Loven et al “Revisiting Global Gene Expression Analysis” Cell 2012 https://doi.org/10.1016/j.cell.2012.10.012

Assumption of DESeq2 Median of Ratios

Median of Ratios method assumes that most genes are not Differentially Expressed between samples.

COUNTER EXAMPLE



NOTE: add back full picture or remove

- Late stage cell death (total RNA DOWN)
- High c-Myc cells (total RNA UP)

Known quantity spike-in transcripts (ERCC) can be used to normalize in these cases.

Loven et al “Revisiting Global Gene Expression Analysis” Cell 2012 https://doi.org/10.1016/j.cell.2012.10.012

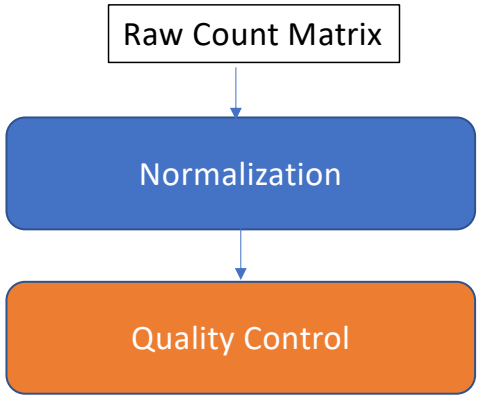
Normalization methods

Normalization method	Description	Accounted factors	Recommended use
CPM (counts per million)	$\frac{K_i}{Total\ Reads\ per\ Sample/10^6}$	sequencing depth	Comparison between replicates of the sample group
R/FPKM (reads/fragments per kilobase of exon per million reads/fragments mapped)	$\frac{K_i}{Gene\ Length/10^3 * Total\ Reads\ per\ Sample/10^6}$	sequencing depth and gene length	Comparison between genes in a sample
DESeq2's **median of ratios** [1]	K_i divided by sample-specific size factors	sequencing depth and RNA composition	**Differential Expression** between samples

Similar to DESeq2: EdgeR, limma-voom

Adapted from https://hbctraining.github.io/DGE_workshop

Quality Control Visualizations



Examine sources of variation in the data

- Principal Component Analysis
- Hierarchical Clustering

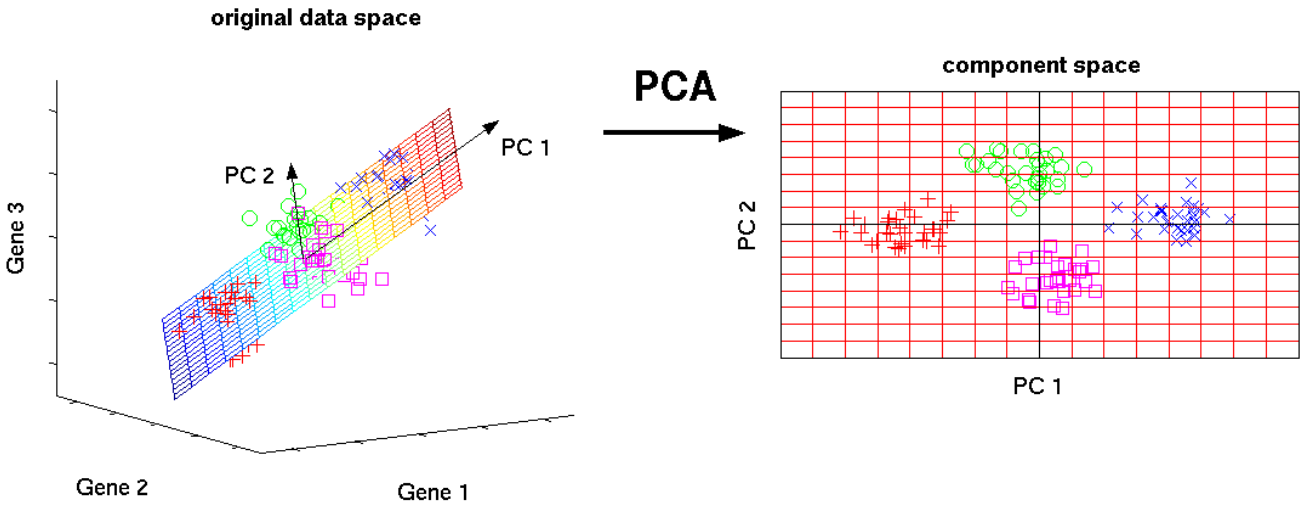
(Log2 + 1) Transformed, Normalized Count Table

Gene	Sample A	Sample B	Sample C
1	1	1.6	0.5
2	2.2	-0.2	1
3	-1	1	3.1

Principle Component Analysis

Dimension reduction technique
Example: 3 gene dimensions -> 2 PC

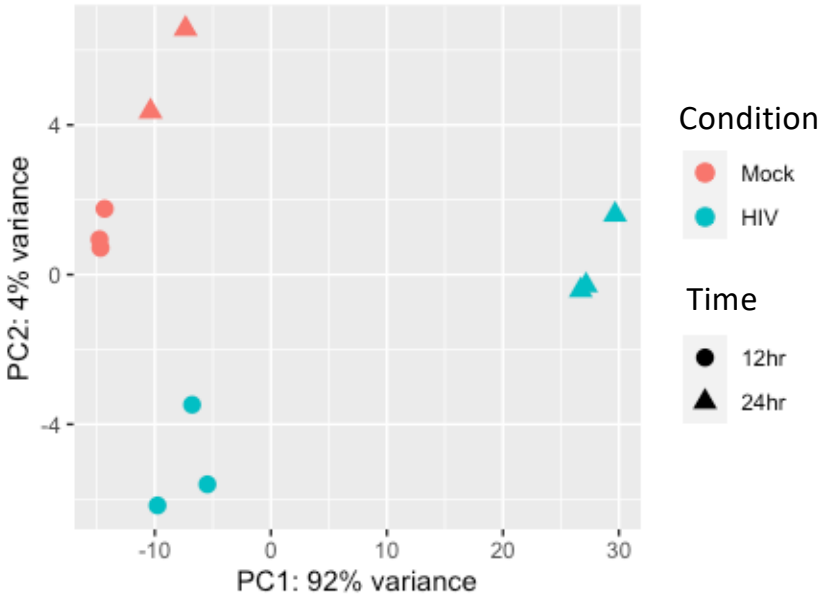
Gene	Mock_12h	Mock_12h	Mock_24h	Mock_24h	HIV_12h	HIV_12h	HIV_24h	HIV_24h
Gene 1	8.9	8.9	8.9	9.0	8.9	8.9	9.0	6.8
Gene 2	0.6	-1.0	0.6	-1.0	0.6	-1.0	0.6	3.8
Gene 3	4.1	11.9	4.1	-0.5	4.1	8.7	4.0	4.4



Do your samples cluster as expected?

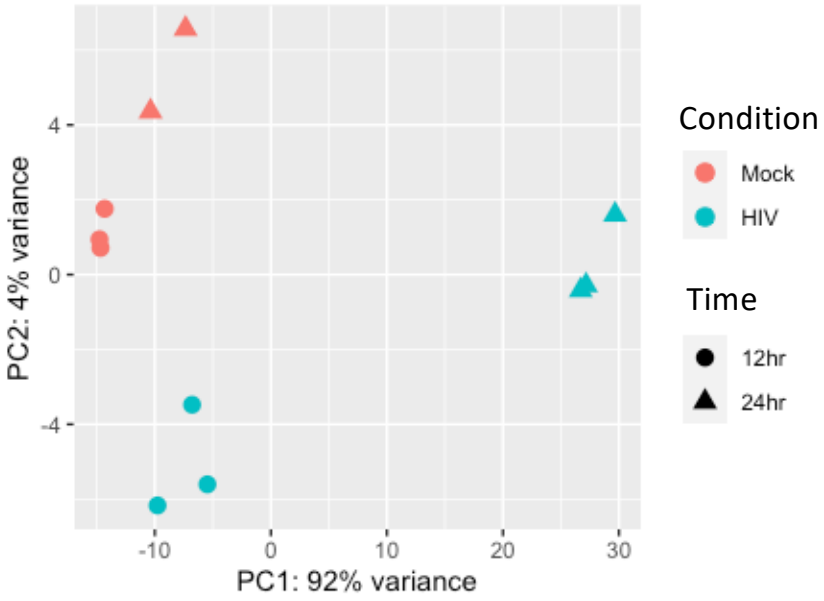
What are the major sources of variation in the data?

Principle Component Analysis



- ✓ Do your samples cluster as expected?
- ✓ What are the major sources of variation in the data?

Principle Component Analysis



- ✓ Do your samples cluster as expected?
- ✓ What are the major sources of variation in the data?
- ✓ Is there a batch effect?

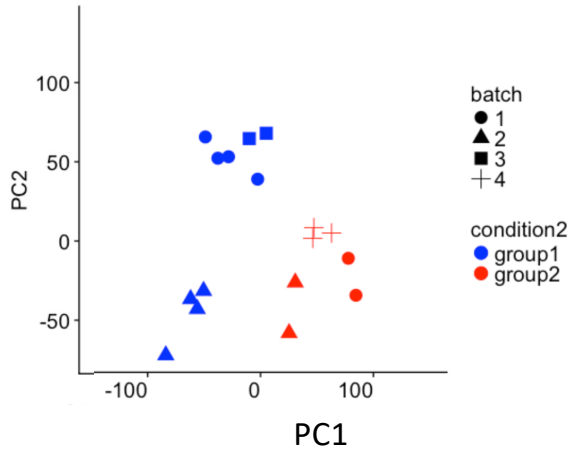
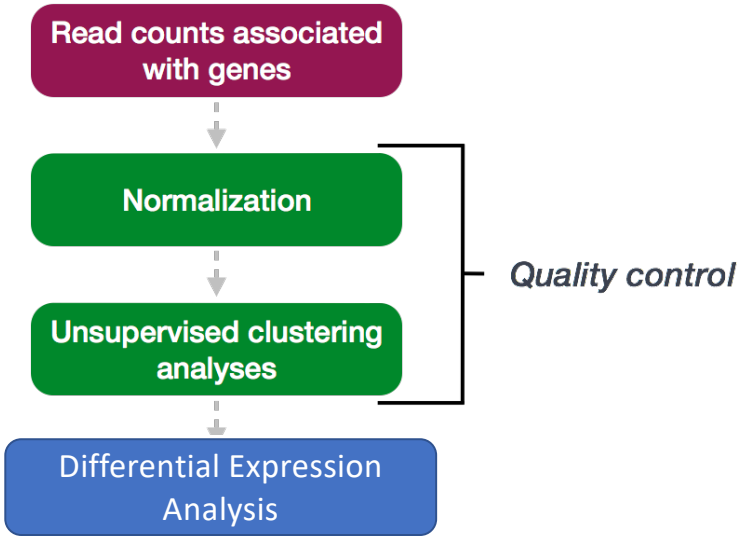


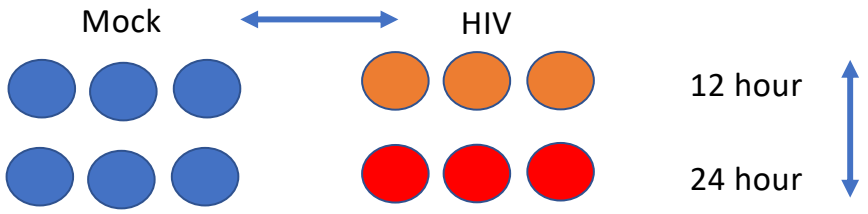
Image https://support.bioconductor.org/p/111491/

Differential Expression with DESeq2



https://hbctraining.github.io/DGE_workshop

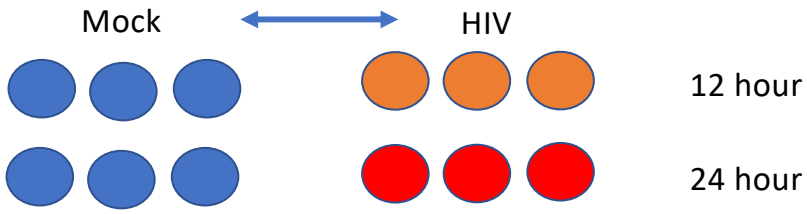
Multi-factor experiment design



Factor 1:
Infection status (Mock or HIV)

Factor 2:
Time (12 or 24 hr)

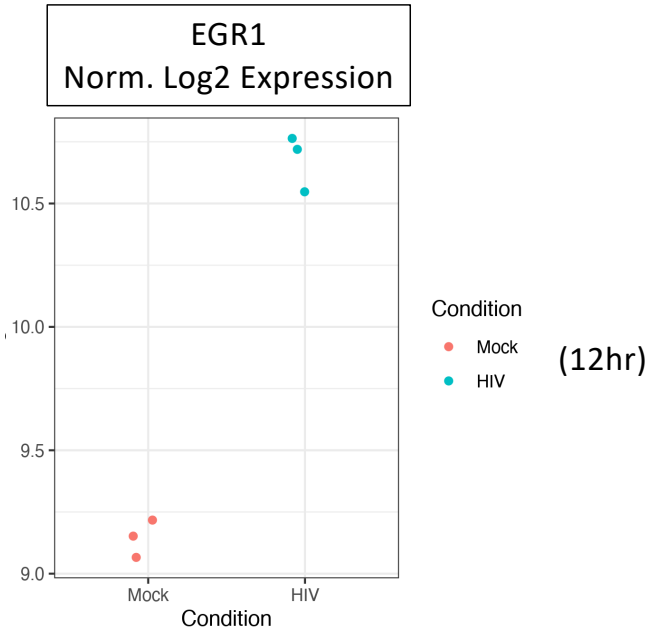
Multi-factor experiment design



- Differential Expression compares two conditions
- We'll choose Infection status at 12 hr (Mock or HIV) for comparison
- We could also choose time, or a combination of multiple factors

Step 1: Modeling gene expression values

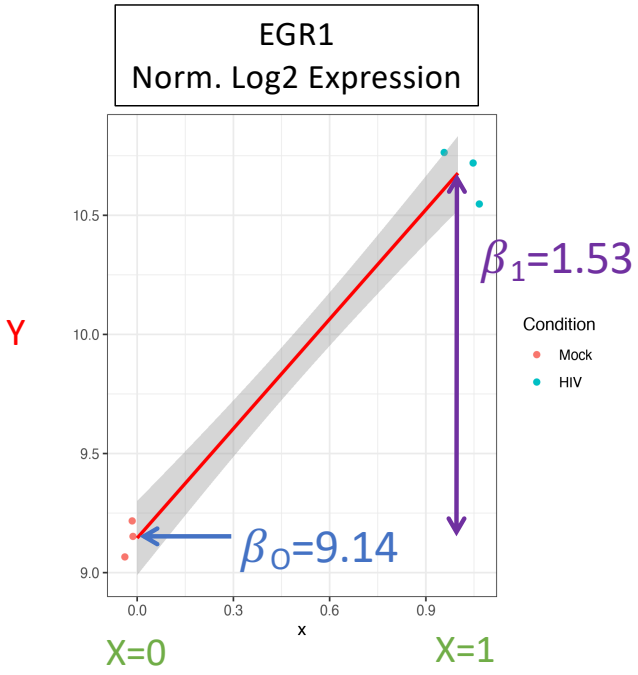
All leading DE tools use **regression models** to estimate the fold change between conditions for **each gene**



(12hr)

Step 1: Modeling gene expression values

All leading DE tools use **regression models** to estimate the fold change between conditions for **each gene**
Example, simple linear regression:



Intercept — Condition (0-Mock, 1-HIV)

$$Y = \beta_o + \beta_1 X + e$$

Log2 Expression Values

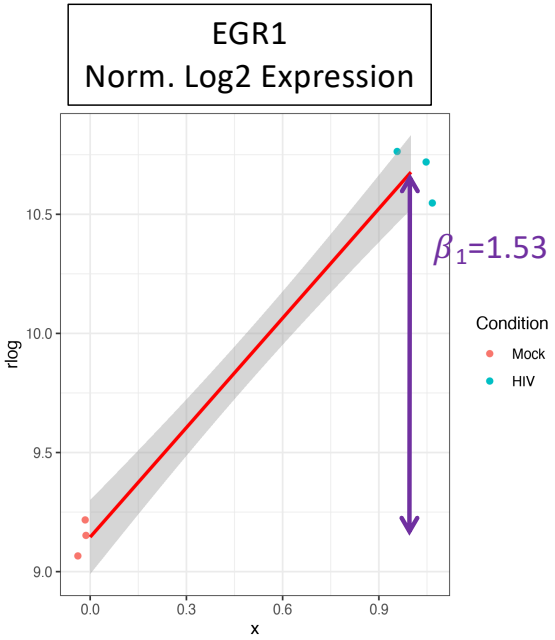
Slope: difference between Mock /HIV

Error

DESeq2 uses a Generalized Linear Model with a Negative Binomial error Distribution, which has been shown to be best fit for RNAseq data.

Love, M.I., Huber, W. & Anders, S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* **15,** 550 (2014).

Step 2: Hypothesis Testing



Is EGR1 differentially expressed?

Yes! p << 0.05

$H_O : \beta_1 = 0$ vs. $H_A : \beta_1 \neq 0$

H_o: there is no systematic difference between the average read count values for Mock vs. HIV

- Statistical test – Wald test (similar to t-test) on β_1
- $Z = \beta_1 / SE_{\beta 1}$
- Z-statistic is compared to the normal distribution and probability of getting a statistic at least as extreme is computed

DESeq2 Results table

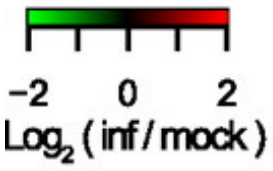
GeneID	Base mean	log2FoldChange	StdErr	P-value	P-adj
EGR1	1273	1.55	0.13	1.19e-77	1.52e-73
MYC	5226	-1.53	0.14	1.63e-36	1.03e-32

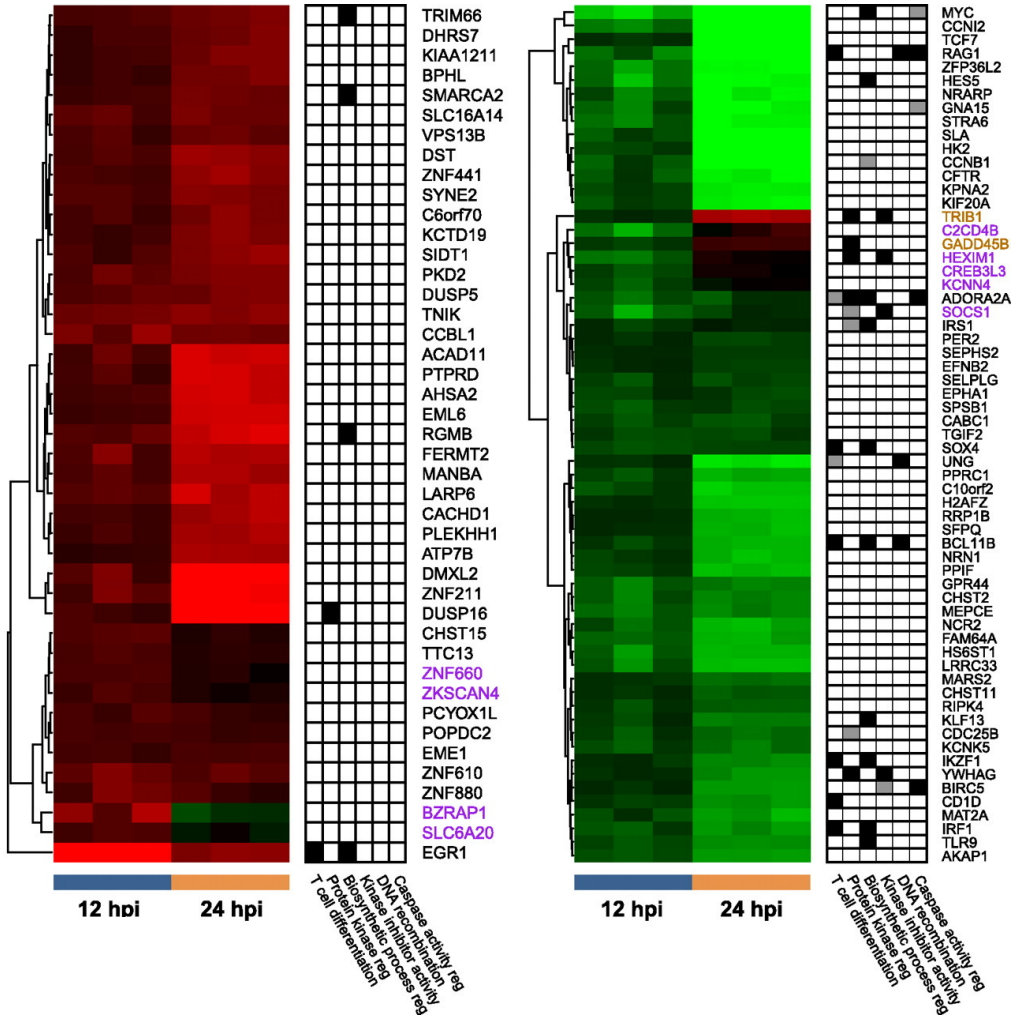
- Mean of normalized counts – averaged over all samples from two conditions (HIV, Mock)
- Log of the fold change between two conditions
- StdErr – Standard error of coefficient (e.g. b_1)
- P-value – the probability that the Wald statistic is as extreme as observed if H_O were true
- P-adj – accounting for multiple testing correction

Study findings

- T cell differentiation-related genes were overrepresented in the DEG at 24hr

- ‘Large-scale disruptions to host transcription’ at 24hr





References

DESeq2 vignette (R/Rstudio):
http://www.bioconductor.org/packages/release/bioc/vignettes/DESeq2/inst/doc/DESeq2.html#differential-expression-analysis

HBC Training (Command line/R):
https://hbctraining.github.io/DGE_workshop

Galaxy Training:
https://galaxyproject.org/tutorials/rb_rnaseq/

Review

Process Raw Reads (QC, adapter trimming)

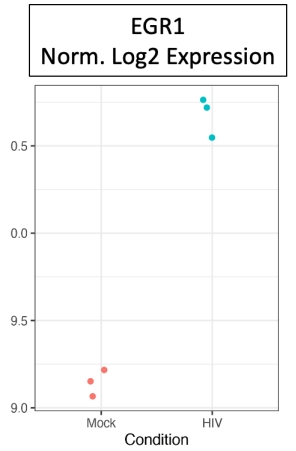
Read Alignment

Gene Quantification

Differential Expression

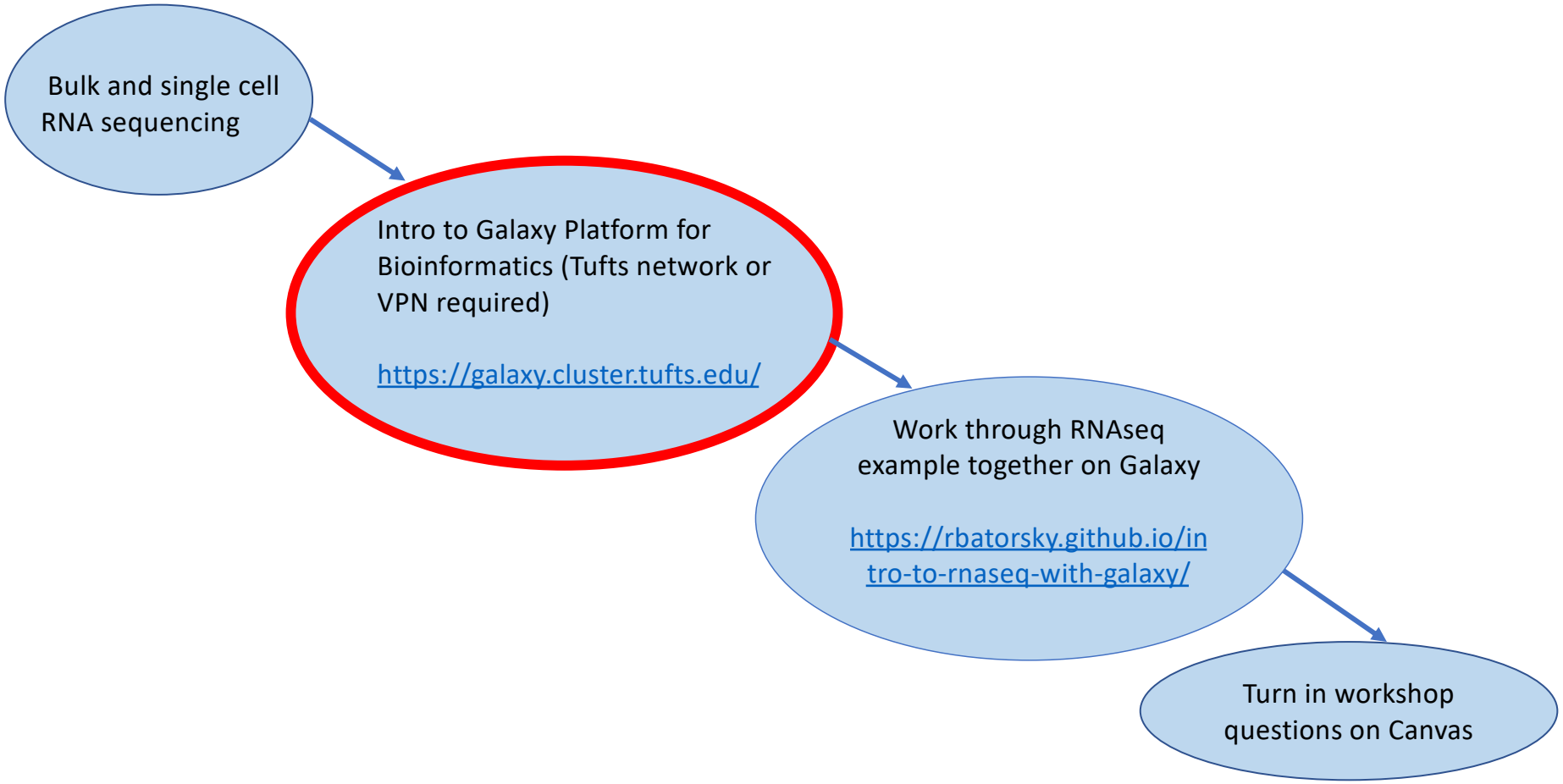
```
@SRR497699.30343179.1 HWI-EAS39X_10175_FC61MK0_4_117_4812_10346 length=75
CAGATGGCCGCAGAGGAAGCCATGAAGGCCCTGCATGGGGAGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGAC
+
IIIIGIIHFIIIIBIIDII>IIDHIIHDIIIGIFIIEIGIBDDEFIG<EIEGEEG;<DB@A8CC7<><C@BBDDB
```

Gene	Sample 1	Sample 2	Sample 3	Sample 4
A	1000	1000	100	10
B	10	1	5	6
C	10	1	10	20



log2FoldChange = 1.55
Adjusted p-val <<0.05

Outline


Bulk and single cell RNA sequencing
Intro to Galaxy Platform for Bioinformatics (Tufts network or VPN required)
https://galaxy.cluster.tufts.edu/
Work through RNAseq example together on Galaxy
https://rbatorsky.github.io/intro-to-rnaseq-with-galaxy/
Turn in workshop questions on Canvas

- **Web-based** platform for running data analysis and integration, geared towards bioinformatics
  - Open-source
  - Developed at Penn State, Johns Hopkins, OHSU and Cleveland Clinic with many more outside contributions
  - Large and extremely responsive community

Access Galaxy

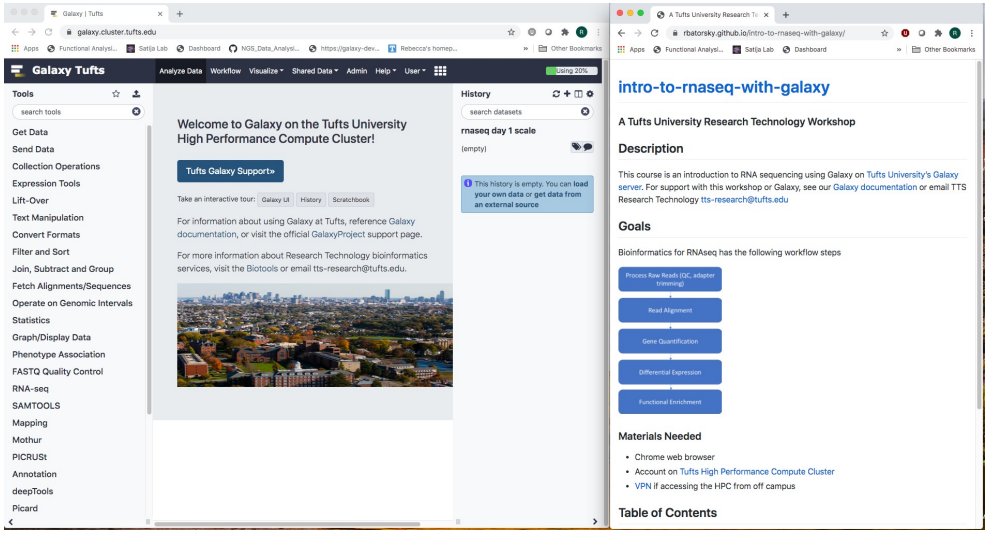
1. Connect to Tufts Network, either on campus or via VPN

2. Visit https://galaxy.cluster.tufts.edu/

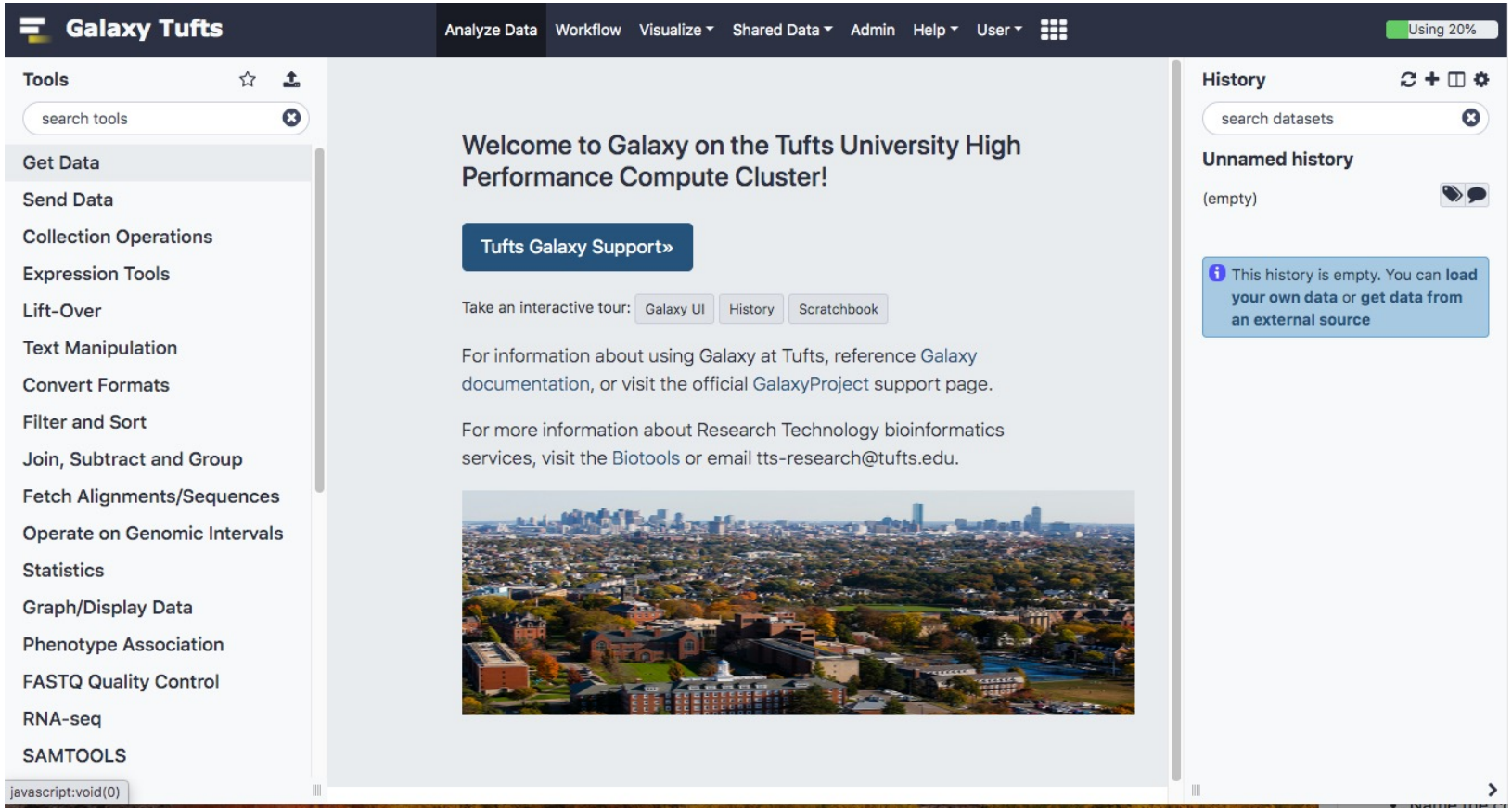
3. Log in with you cluster username and password

4. In another browser window go to course workflow: https://rbatorsky.github.io/intro-to-rnaseq-with-galaxy/

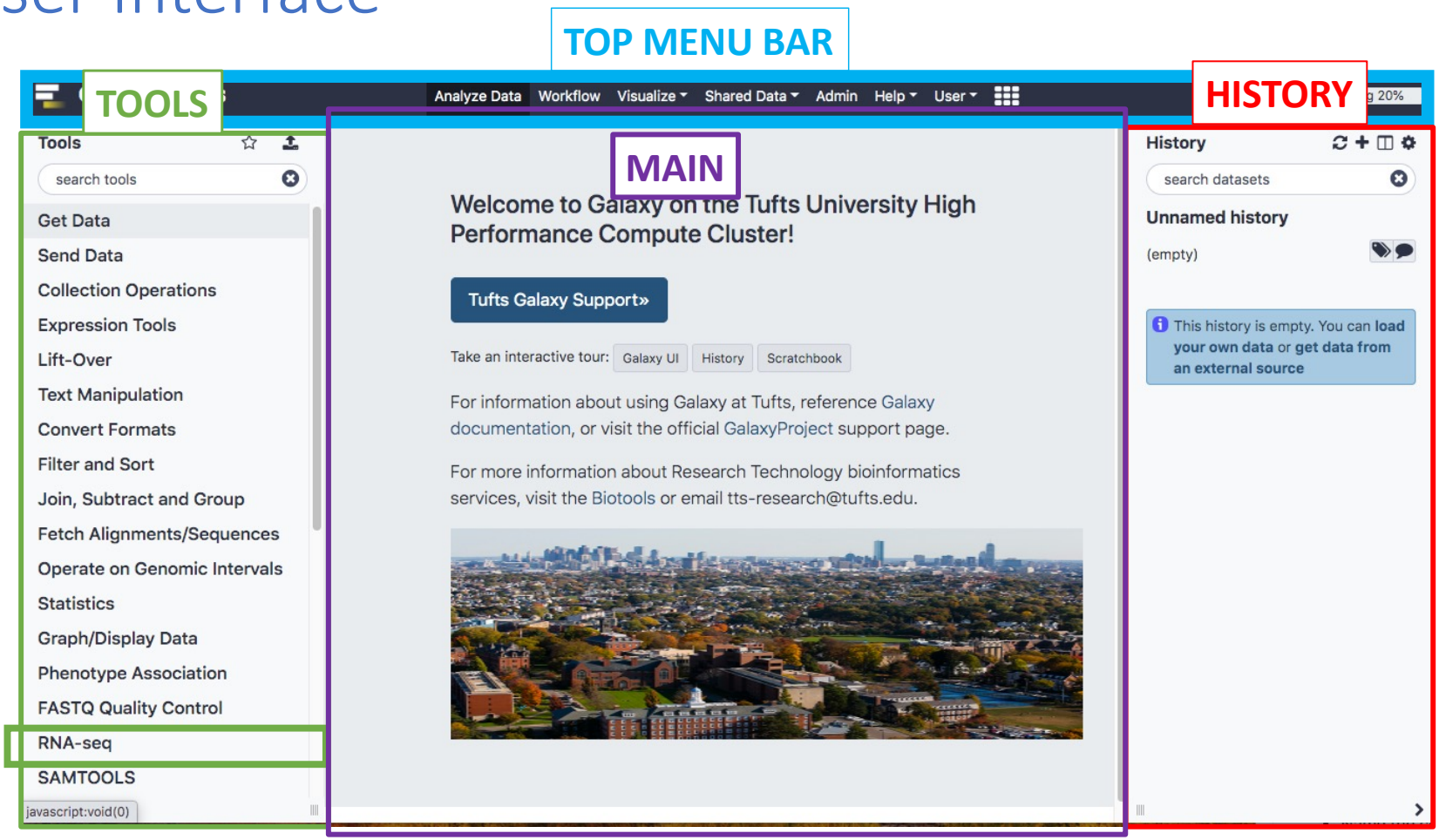
Suggested screen layout



User Interface

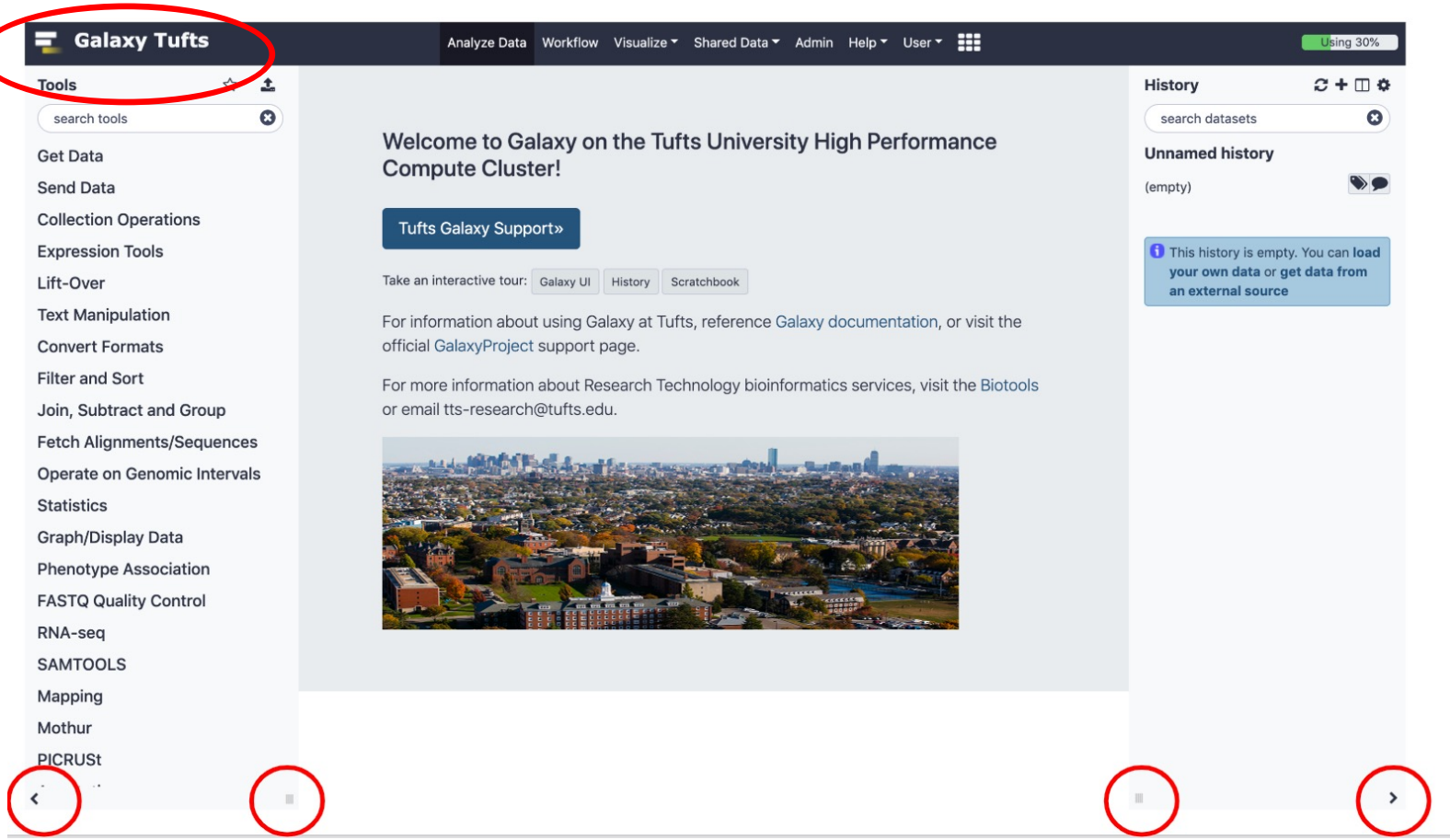


User Interface



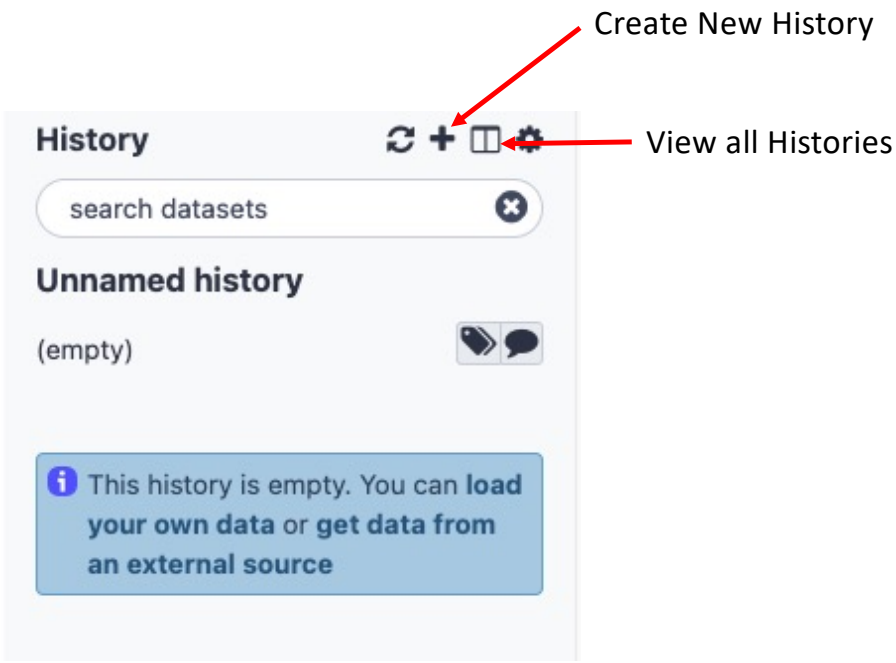
Galaxy User Interface

To return to home screen

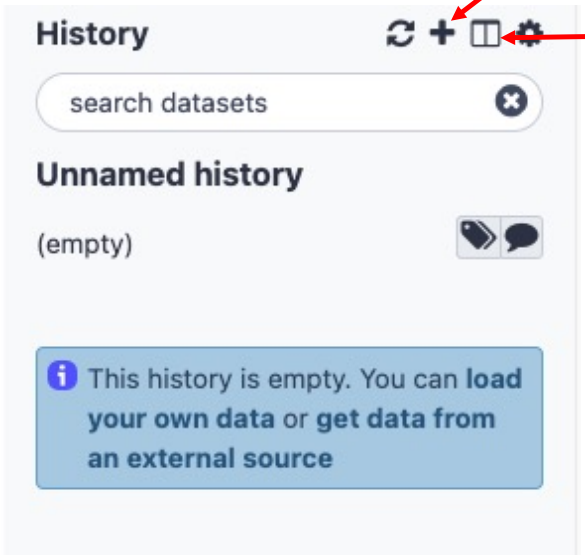


Minimize/Adjust toolbars

History

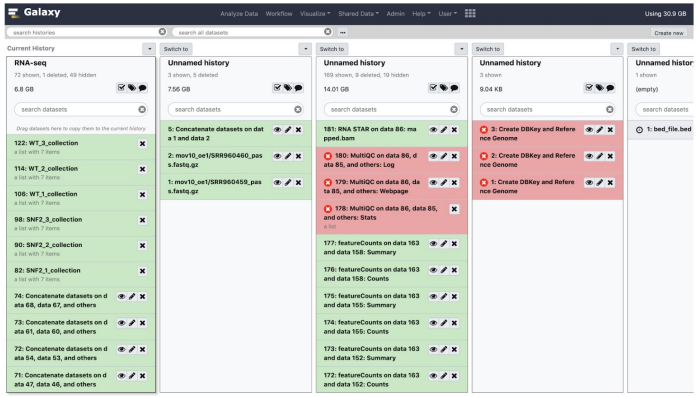

Create New History
View all Histories
History
search datasets
Unnamed history
(empty)
This history is empty. You can load your own data or get data from an external source

History

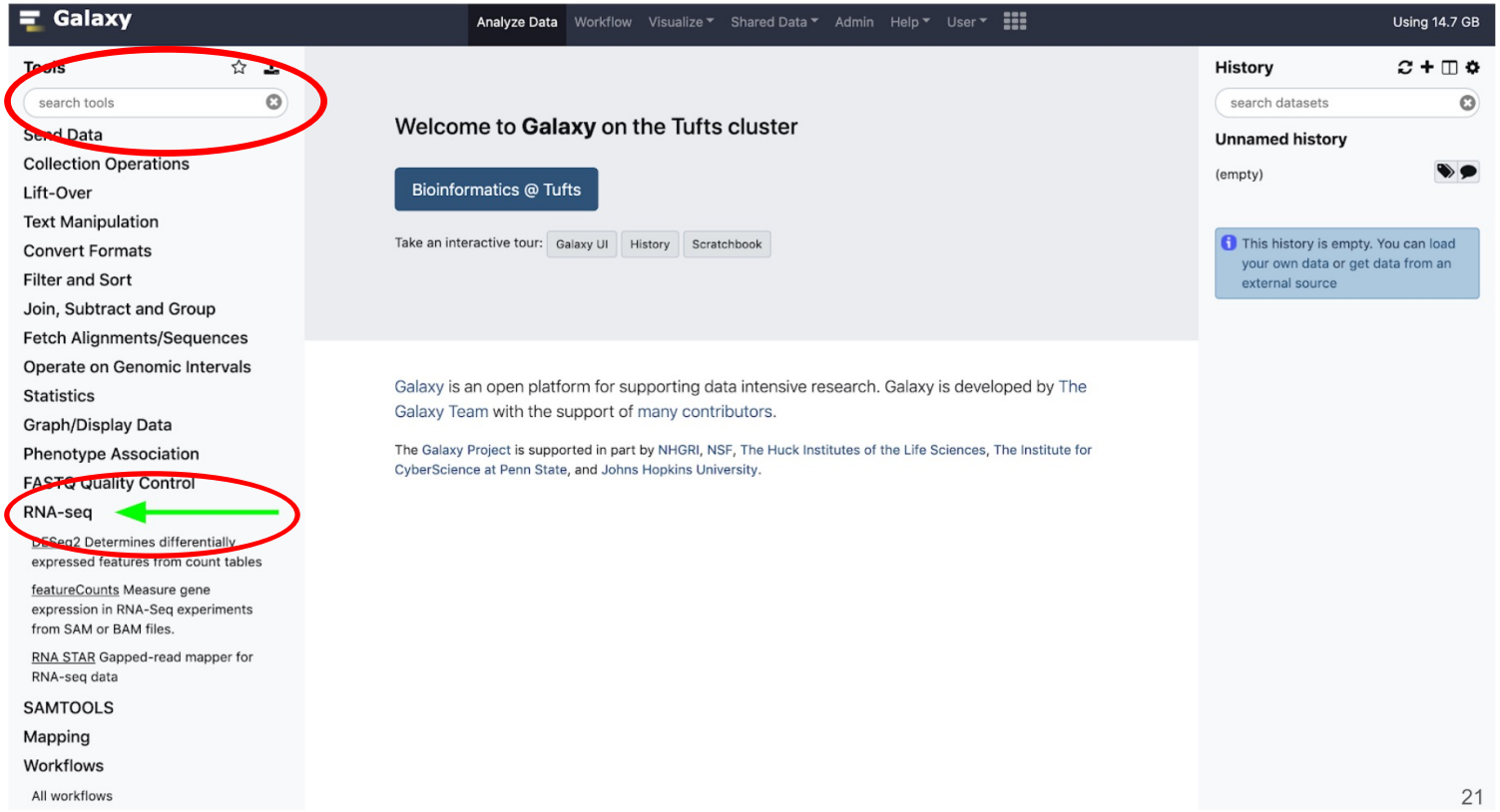


Create New History

View all Histories

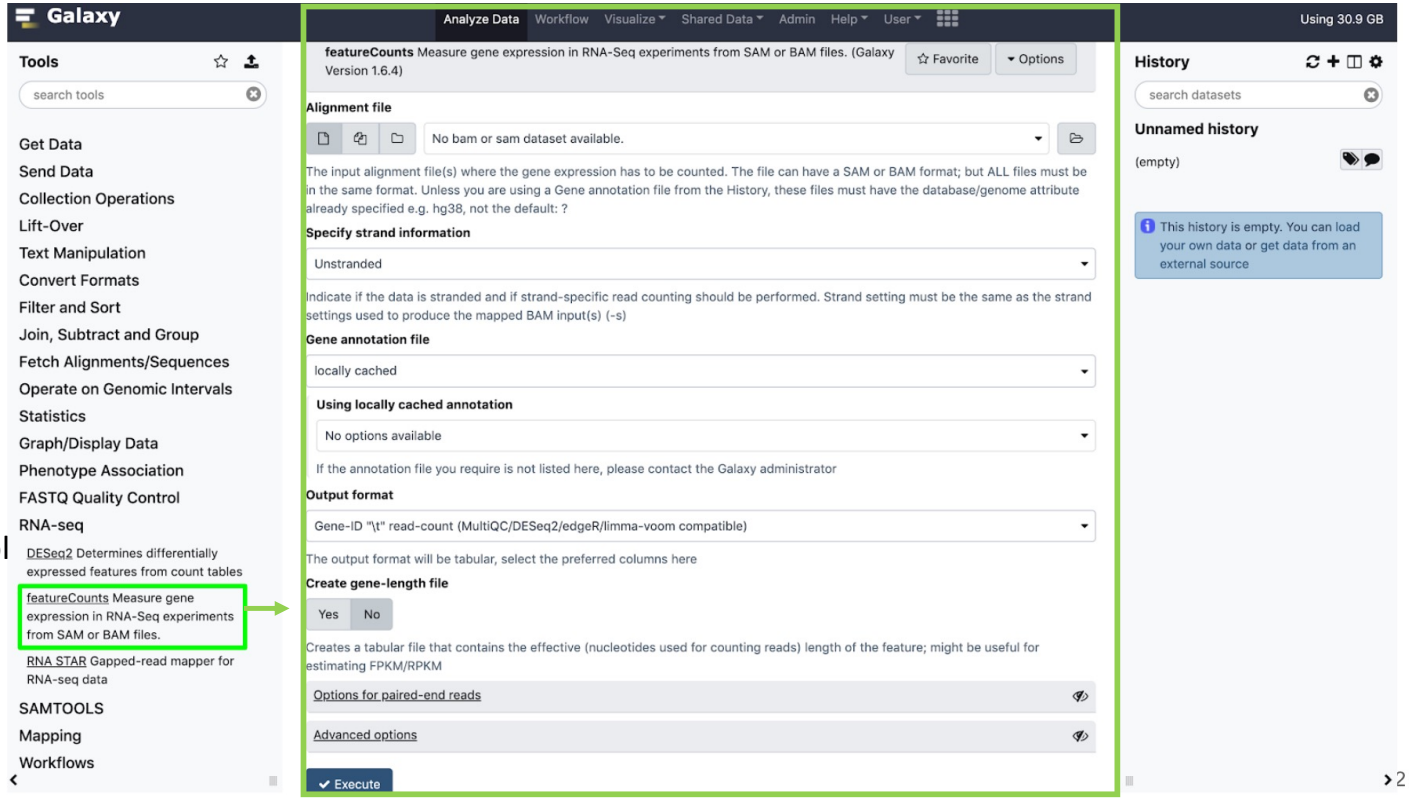


Tools

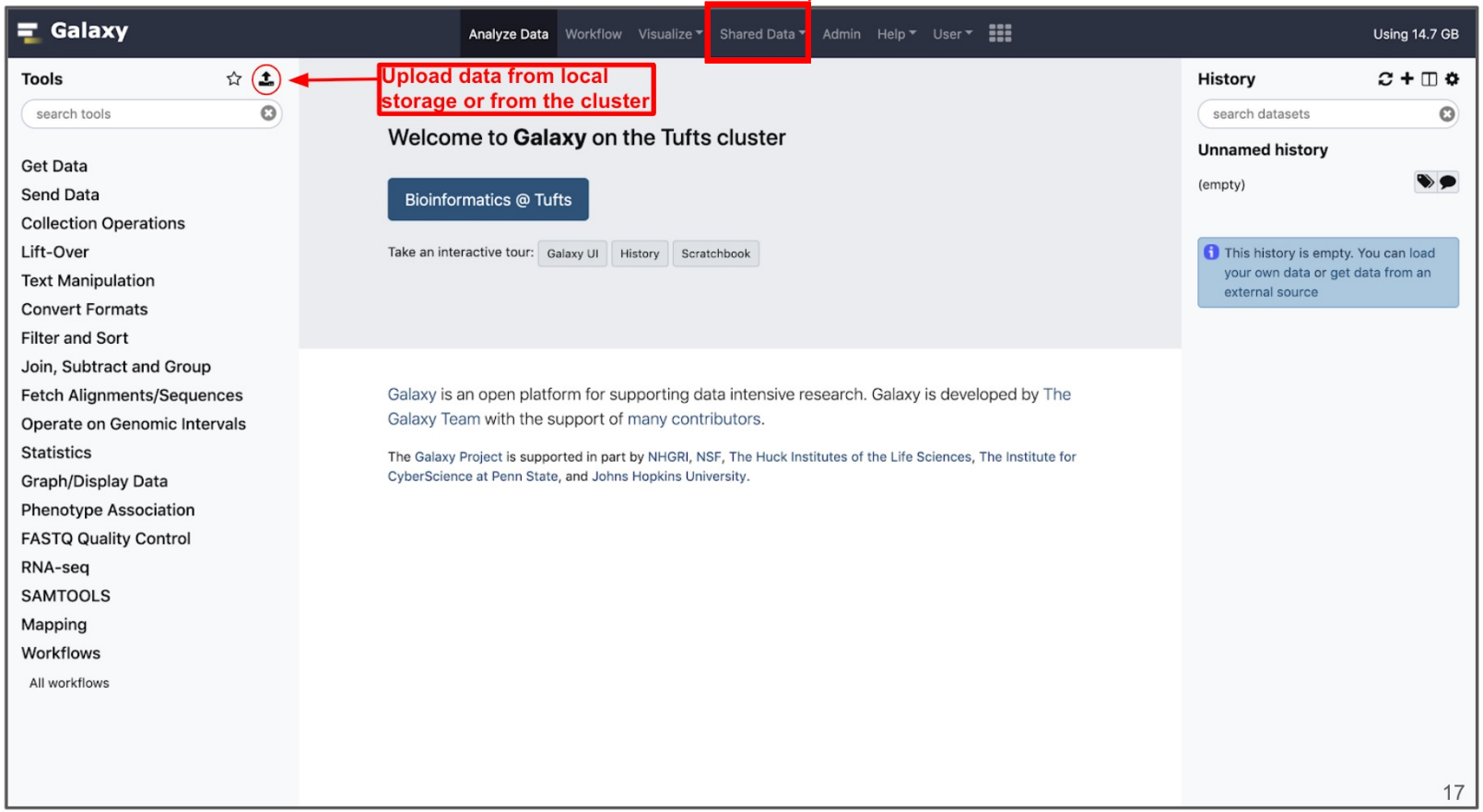

Galaxy
Analyze Data
Workflow
Visualize
Shared Data
Admin
Help
User
Using 14.7 GB
Tools
search tools
Send Data
Collection Operations
Lift-Over
Text Manipulation
Convert Formats
Filter and Sort
Join, Subtract and Group
Fetch Alignments/Sequences
Operate on Genomic Intervals
Statistics
Graph/Display Data
Phenotype Association
FASTQ Quality Control
RNA-seq
DESeq2 Determines differentially expressed features from count tables
featureCounts Measure gene expression in RNA-Seq experiments from SAM or BAM files.
RNA STAR Gapped-read mapper for RNA-seq data
SAMTOOLS
Mapping
Workflows
All workflows
Welcome to Galaxy on the Tufts cluster
Bioinformatics @ Tufts
Take an interactive tour:
Galaxy UI
History
Scratchbook
Galaxy is an open platform for supporting data intensive research. Galaxy is developed by The Galaxy Team with the support of many contributors.
The Galaxy Project is supported in part by NHGRI, NSF, The Huck Institutes of the Life Sciences, The Institute for CyberScience at Penn State, and Johns Hopkins University.
History
search datasets
Unnamed history
(empty)
This history is empty. You can load your own data or get data from an external source

Tools

Click on the name of the tool to open it in the main panel



Importing data



Access Galaxy

1. Connect to Tufts Network, either on campus or via VPN

2. Visit https://galaxy.cluster.tufts.edu/

3. Log in with you cluster username and password

4. In another browser window go to course workflow:

https://rbatorsky.github.io/intro-to-rnaseq-with-galaxy/

5. Under Table of Contents click on **"Process Raw Reads"**

Suggested screen layout