Design of RNA-seq Experiments and Differential Expression Analysis

Genomic Technologies Workshop
(PLPTH885)

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Plant Pathology

6/5/2024

Schedule

- 1:00 pm **Lecture DE**

Design of RNA-Seq Experiments and Differential Expression Analysis

- 2:00 pm **Break**

- 2:10 pm **Computer Lab - R**

Introduction to R programming

- 3:10 pm **Break**

- 3:20 pm **Computer Lab - DE**

RNA-Seq data analysis using R

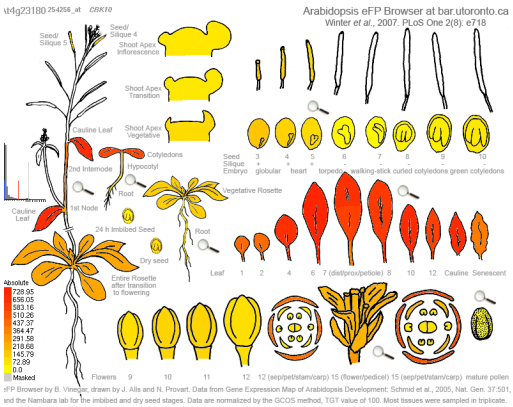
Outline

- RNA-seq procedure
- Experimental design
- Multiple testing correction
- Data visualization

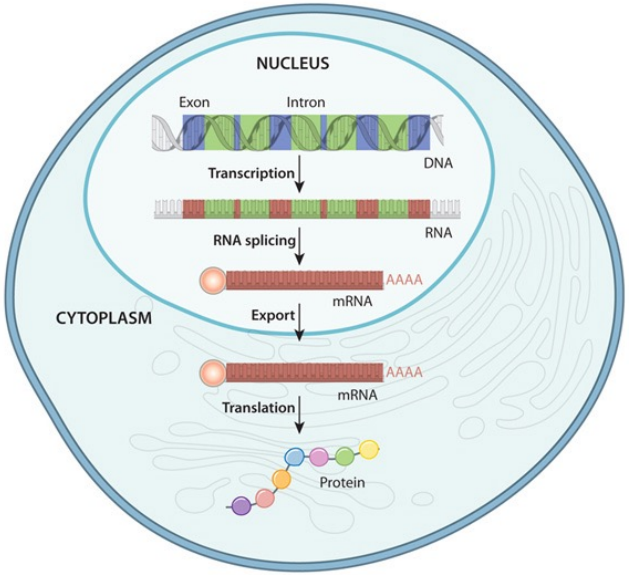
https://github.com/liu3zhenlab/teaching/tree/master/RNA-Seq-Workshop/2024/forYOU

Gene expression

What is the expression level of a gene?

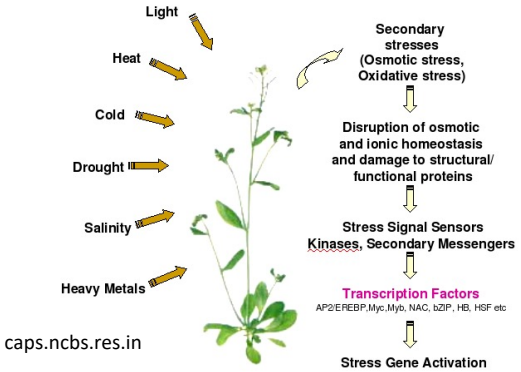


Expression profiles in different tissues



DNA to protein in eukaryote

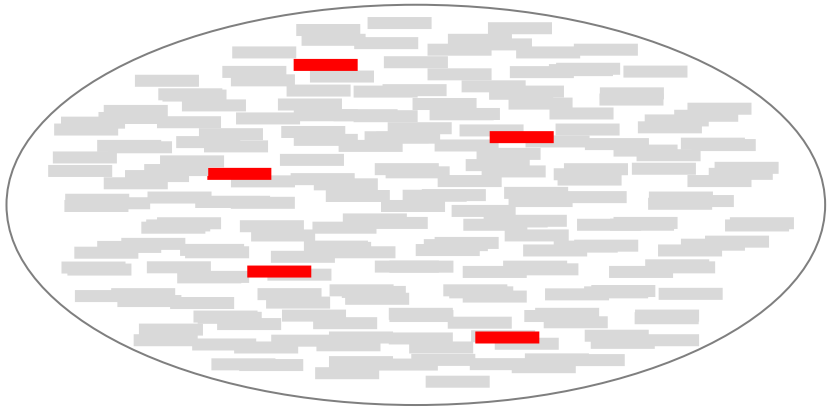
nature.com/scitable/topicpage/gene-expression-14121669



Adaptation to environmental change

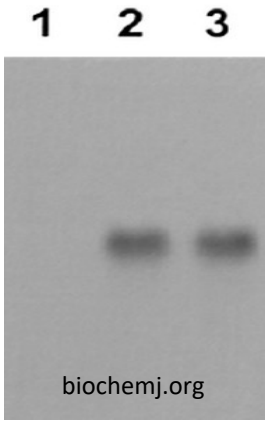
Response to biotic stress

Approaches for quantification of gene expression

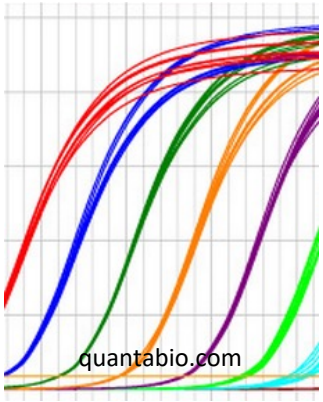


How can we measure the accumulative level of transcripts of **a given gene** in millions/billions of transcripts?

Northern blot



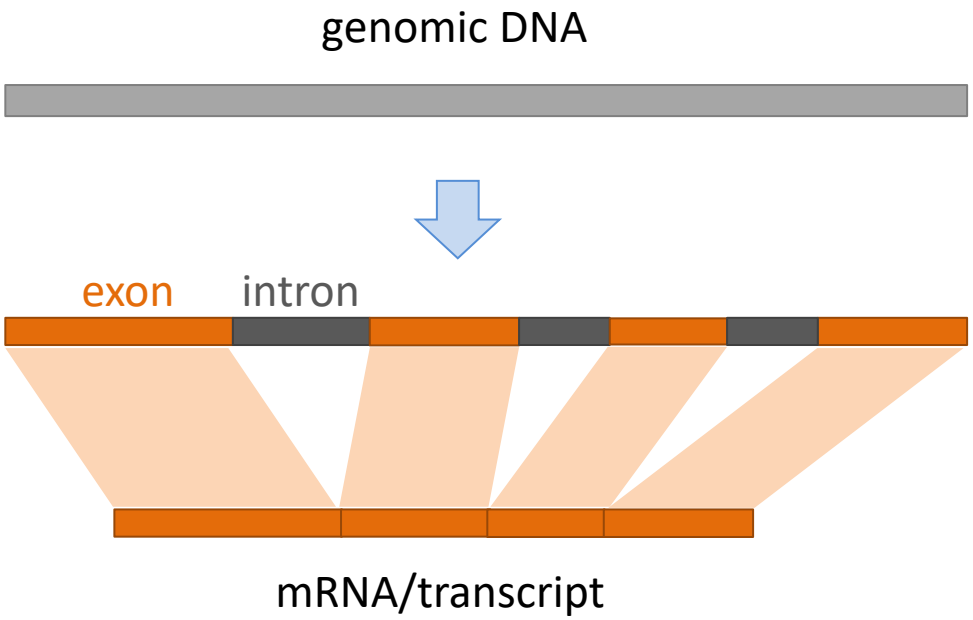
qRT-PCR



microarray

RNA-seq

Rationale of RNA-seq (mRNA sequencing)



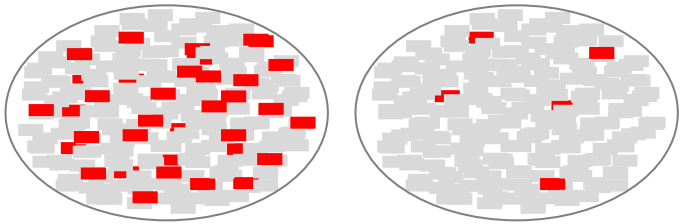
Essentially, RNA-seq is designed to measure mRNA accumulation levels of genes by

1) recognizing transcripts based on sequences

2) and quantifying transcripts of each gene

10 millions of transcripts in each sample

Including transcripts from a gene of interest



100 5

sequence 1,000 transcripts

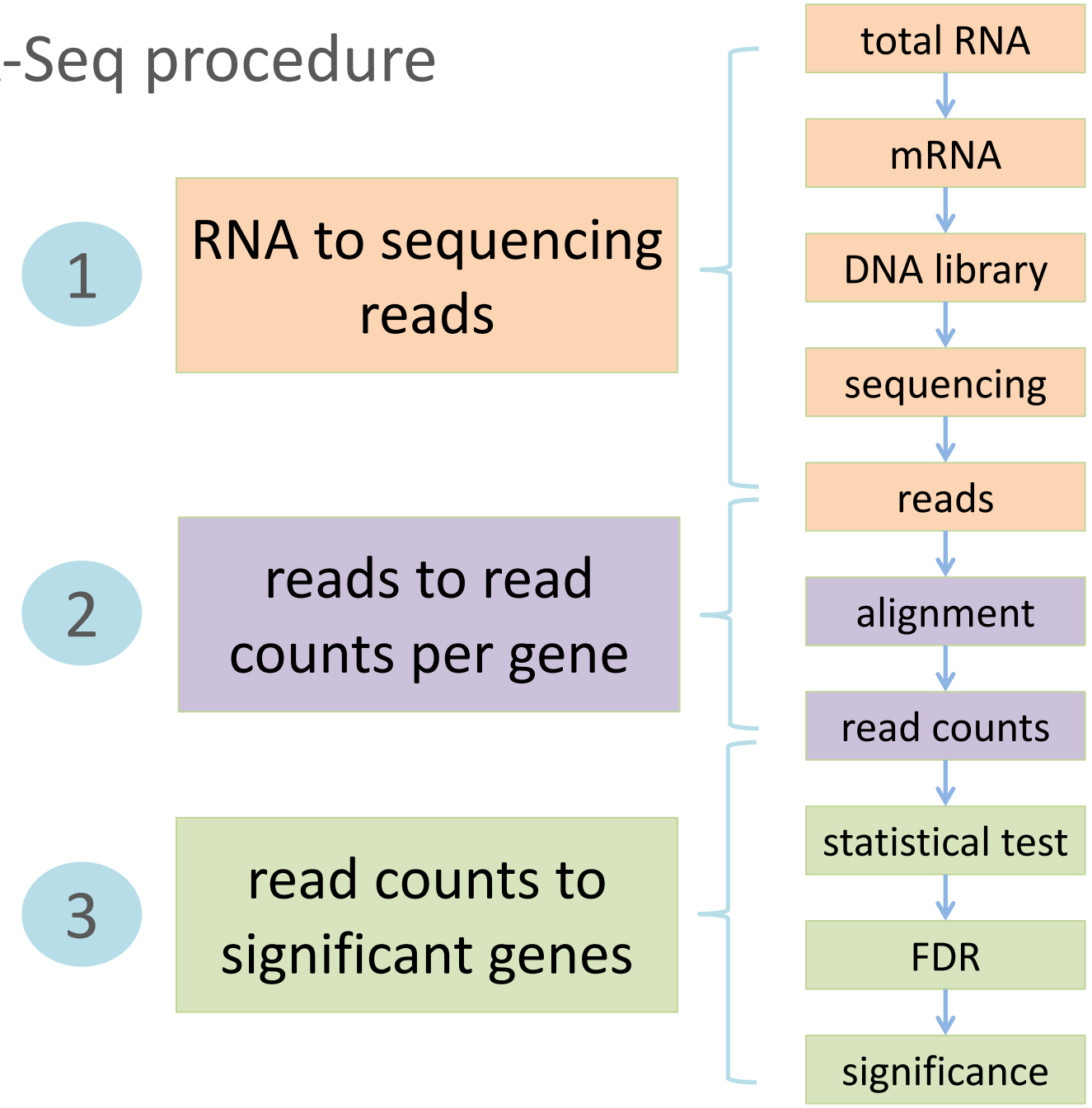
0 0

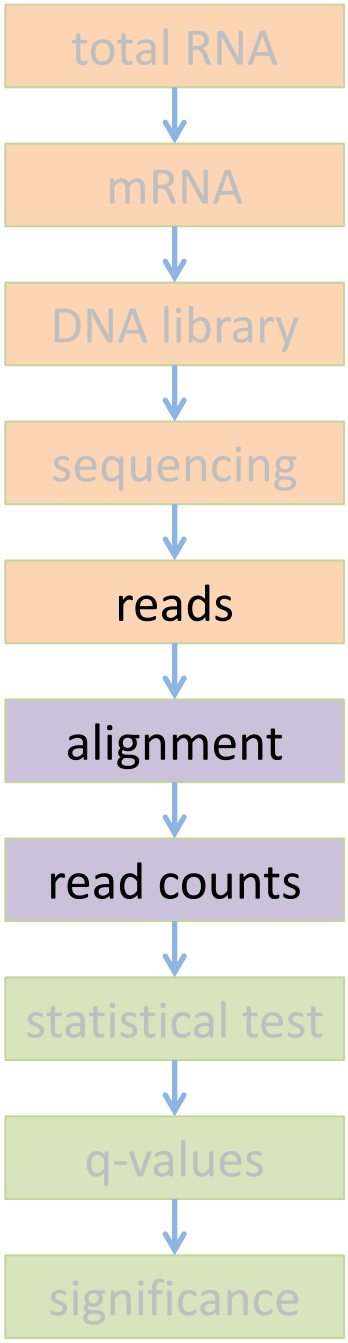
sequence **1 million transcripts**

10 1

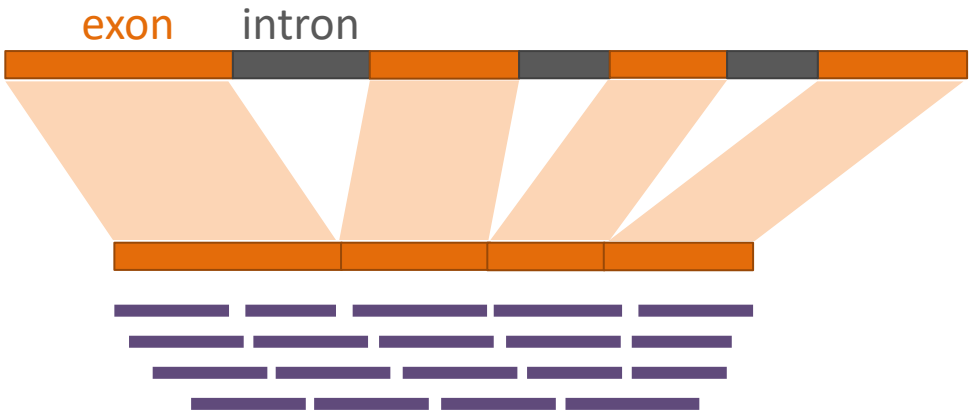
Differential expression (DE)?

RNA-Seq procedure



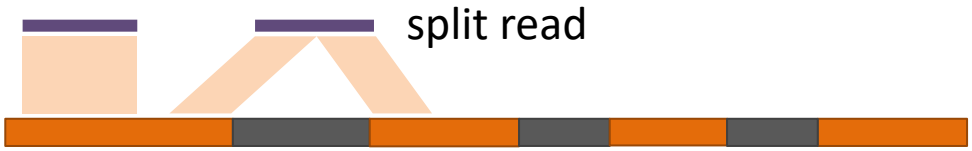


Reads to read counts per gene



1. reads

2. alignment to the reference genome (DNA sequence)



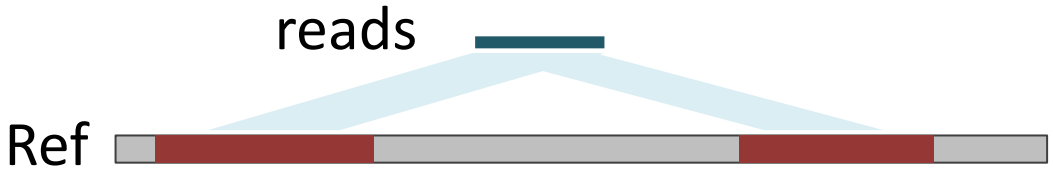
An **intron-aware** aligner is important for RNA-seq reads alignment e.g., STAR, HiSAT2

3. read counts

N = 19 if all reads can be confidently mapped to the reference genome

Alignment issues

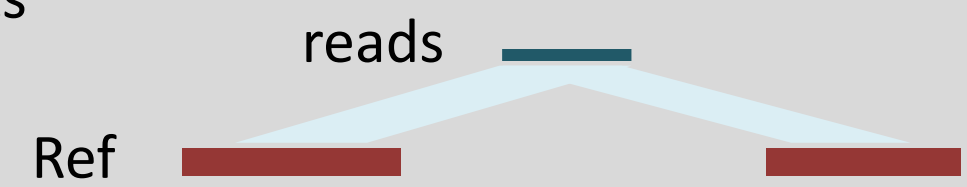
- Repeats



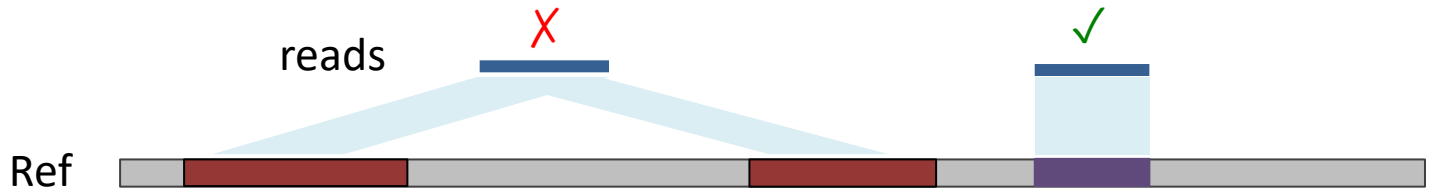
- Sequencing errors
- Polymorphisms (reference and sequenced individuals)
- Quality of reference genomes (mis-assembly and incomplete genome)

Solutions to mitigate problems - I

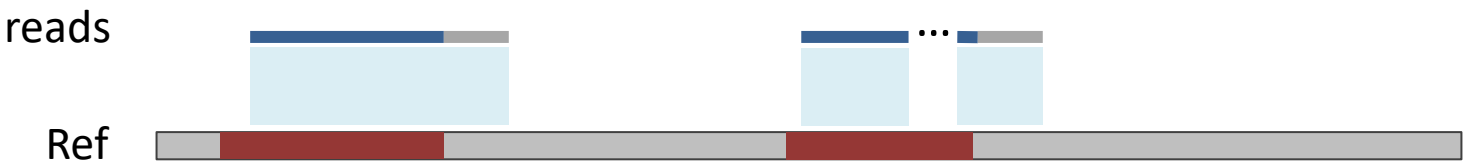
- Repeats



- Unique mapped reads



- Longer reads or Paired-end reads



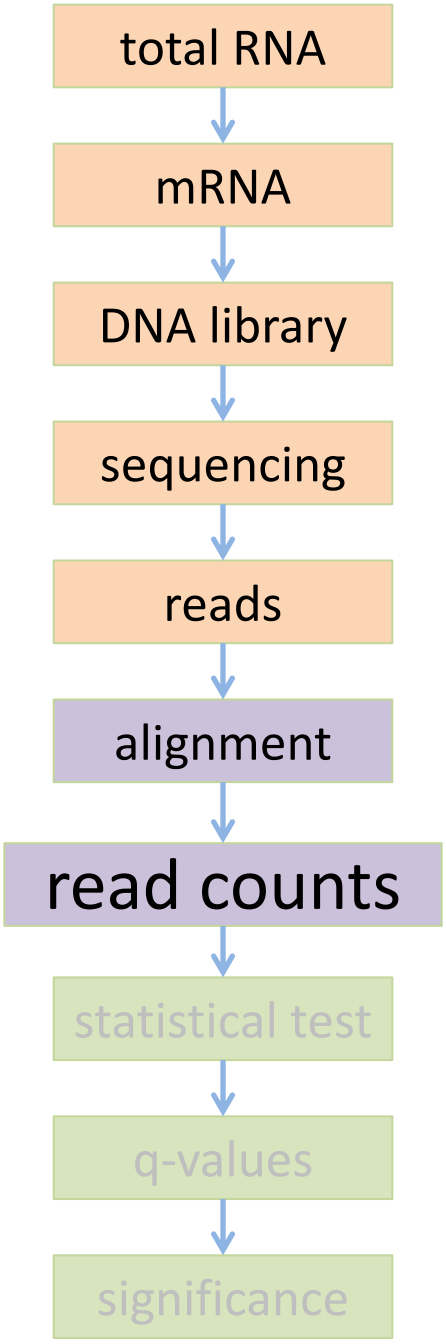
Solutions to mitigate problems

- Sequencing errors
- Polymorphisms (reference and sequenced individuals)

- Tolerance of mismatches or gaps for each alignment

- Quality of reference genomes (mis-assembly and incomplete genome)

- Better reference genome



Count matrix
Read counts (Raw) per gene

Gene	sample 1	sample 2
gene 1	6,075	5,934
gene 2	295	377
...	...	...

total RNA

mRNA

DNA library

sequencing

reads

alignment

read counts

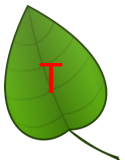
statistical test

q-values

significance

Read counts to significant genes

Control 1



TRT 1 (salt)

RNA
Library
Sequencing

N1 reads

N2 reads

Alignment
Read counting per gene

Gene	Control 1	TRT 1
1	C1	T1
2	C2	T2
…		
Sum	N1	N2

2x2 Table for Gene 1

	Gene 1	Others
Control 1	C1	N1 – C1
TRT 1	T1	N2 – T1

- Fisher's Exact Test or χ^2 test on Gene 1

A p-value for Gene 1

- Repeat on all the genes

p-values

- Multiple testing correction

q-values

- Declaration of significance

a significant gene set

Statistical test for differential expression

- Statistical test to discover differential expression (DE)
  - **Count data**: Generalized Linear Model (GLM) to deal with count data

  e.g., Poisson GLM could handle count data but overdispersion exists
  - **Overdispersion issue**: Using **negative binomial GLM** to incorporate a dispersion parameter into the model

edgeR (Robinson and Smyth, 2007), **DESeq** (Anders and Huber, 2010), NBPSeq (Di et al., 2011), and QuasiSeq (Lund 2012)


Conesa et al. Genome Biology (2016) 17:13
DOI 10.1186/s13059-016-0881-8

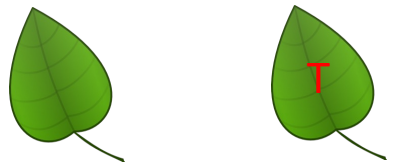
Genome Biology

REVIEW Open Access

A survey of best practices for RNA-seq data analysis

Ana Conesa[1,2*], Pedro Madrigal[3,4*], Sonia Tarazona[2,5], David Gomez-Cabrero[6,7,8,9], Alejandra Cervera[10], Andrew McPherson[11], Michał Wojciech Szcześniak[12], Daniel J. Gaffney[3], Laura L. Elo[13], Xuegong Zhang[14,15] and Ali Mortazavi[16,17*]

Source of variance in counts



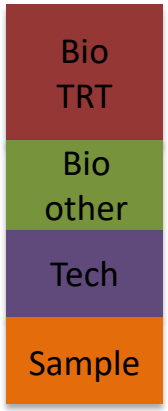
Control 1 TRT 1 (salt)

Gene 1	**C1**	**T1**
…		
Sum	N1	N2

Our interest:
the effect of the salt treatment on gene expression

Question: what could cause the difference between two values, C1 and T1?

- **Treatment effect**
- Plant difference
- RNA quality
- Library preparation
- Sequencing
- Sampling



- Sequencing depth

Sampling variance

- **Sampling variance** derived from the inherent nature of counting experiments

total molecules: 10^9

gene X: 1000 molecules

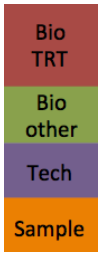
Randomly sample 10^7

First sampling	6
Second sampling	13
Third sampling	8

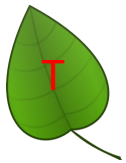
Randomly sample 10^8

First sampling	102
Second sampling	93
Third sampling	97

Sequence depth (sampling number) matters.



Technical replication



Control 1 Control 2 Control 3 TRT 1 TRT 2 TRT 3

within groups within groups

between groups

Technical replication refers to the sequencing of multiple libraries derived from **the same biological sample**.

Technical replicate

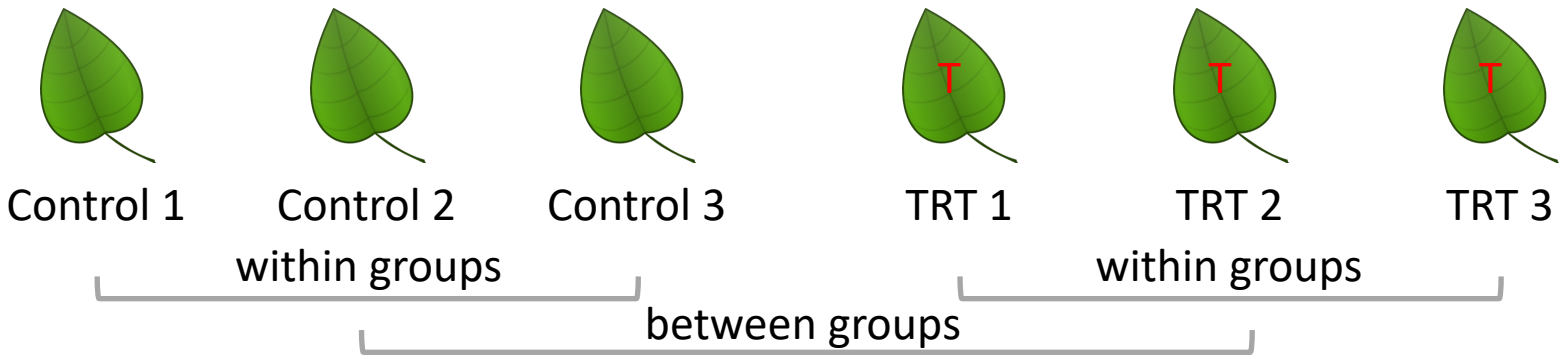
within groups

between groups

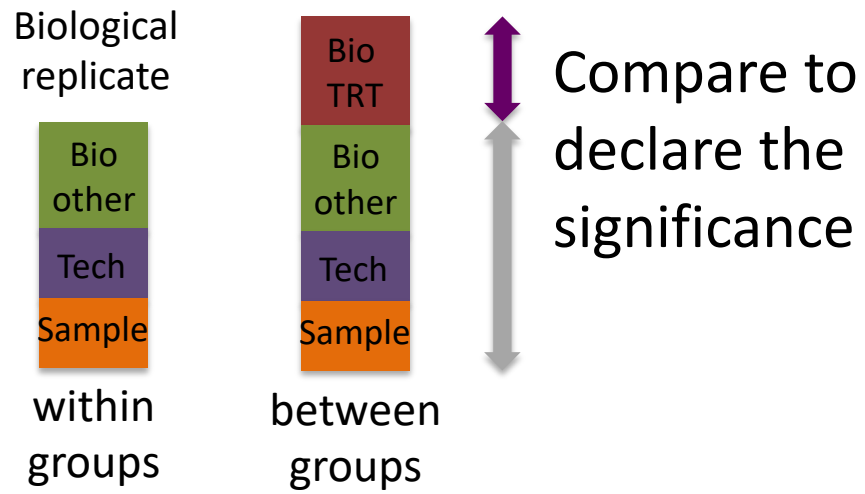
Compare to declare the significance

Spurious power

Biological replication



Biological replication refers to the sequencing of multiple libraries derived from **different biological samples**.



1. Use ***biological replication*** instead of technical replication unless you have special interests.
2. More replicates increase the power to detect small effect.

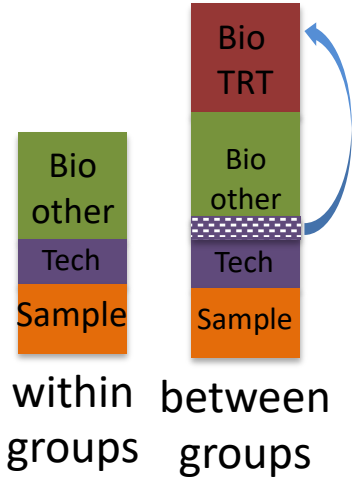
Question

Goal: to identify the DEs between two biological groups

Design: Each group has five biological replicates

To avoid messing up samples across groups, the experiment of each group was conducted separately.

Is this a sound experimental design? Why?



A **normalization** method: RPKM and FPKM

- **RPKM**: Read number per kilobase of exons per million of total reads

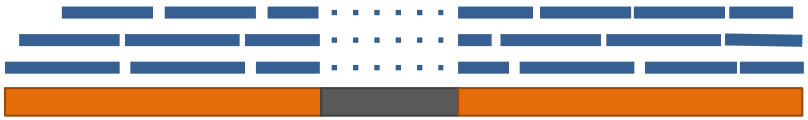
Control 1 read count = **28**

exon 1 (**220 bp**) exon 2 (**280 bp**)

total reads: **15 millions** of total reads

RPKM of X = ? = **3.7**

Treatment 1 read count = **18**



exon 1 (**220 bp**) exon 2 (**280 bp**)

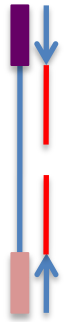
gene X

total reads: **10 millions** of total reads

RPKM of X = ? = **3.6**

- **FPKM**: **Fragment** number per kilobase per million of total reads.

Fragment = one pair of paired-end reads or one single-end read



More about RPKM

Can we say that the gene B has higher expression than the gene A?

- RPKM is not an ideal indicator to compare the expression/accumulation levels between two genes

1. amplification bias
2. alignment efficiency

Experimental Design

- **Sequencing depth**

Increasing sequencing depth decreases sampling variance relative to the mean

- **Biological replication**

A reasonable number of biological replication helps accurately estimate variances to achieve reliable statistical inference

- **Randomization and unbiasedness**

Try to avoid confounding effects

Results from DE tests

	DE Result	
GeneID	Log2FC*	p-value
1	-0.40	0.037
2	0.03	0.916
3	-0.89	2.42E-05
4	0.30	0.130
5	-0.36	0.140
6	-0.07	0.811
…		

Which genes were significantly differentially expressed?

* Log2FC: log2 of fold change (trt / control)

Outline

- RNA-seq procedure
- Experimental design
- Multiple testing correction
- Data visualization

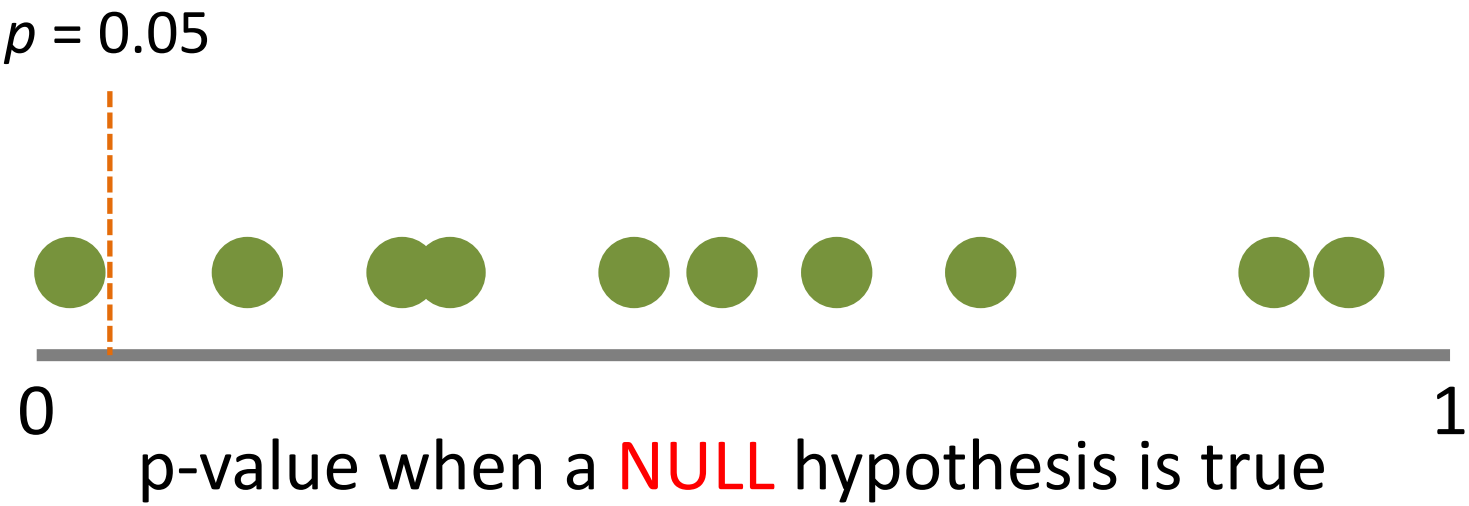
Single statistical test

H0: the null hypothesis

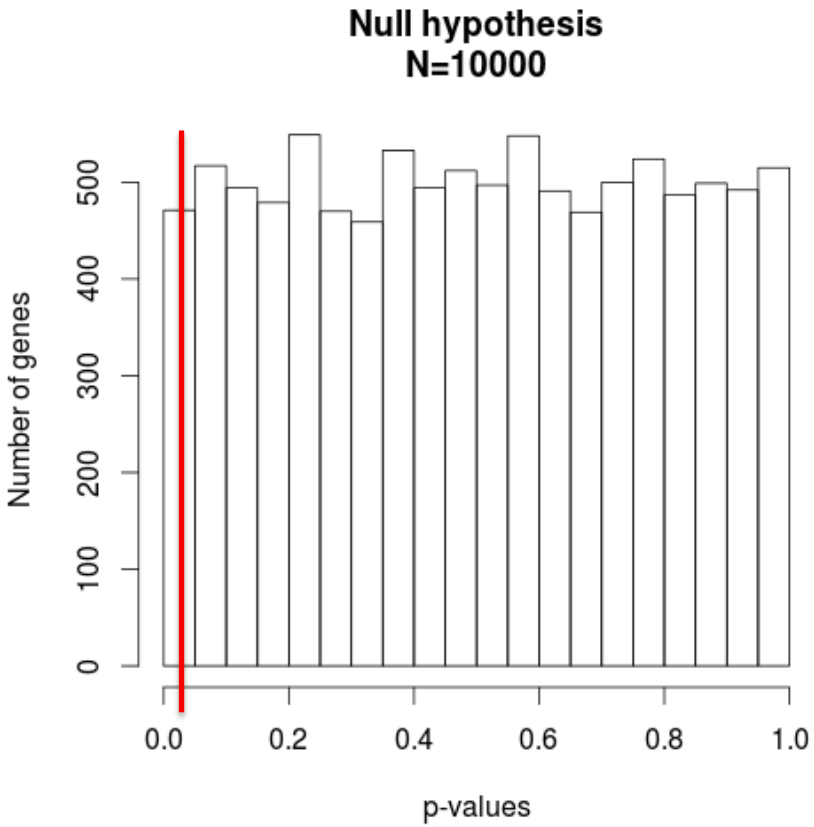
Single statistical test

H0: the null hypothesis

Multiple testing correction



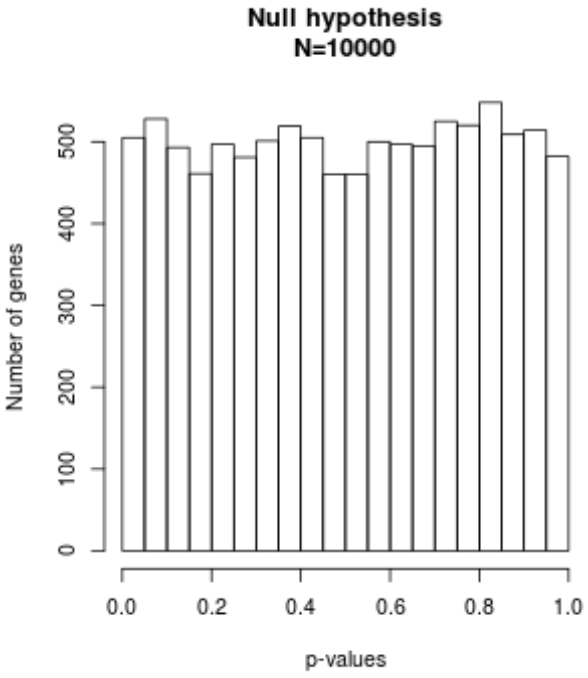
P-value distribution under the null hypothesis (e.g., no treatment effect)

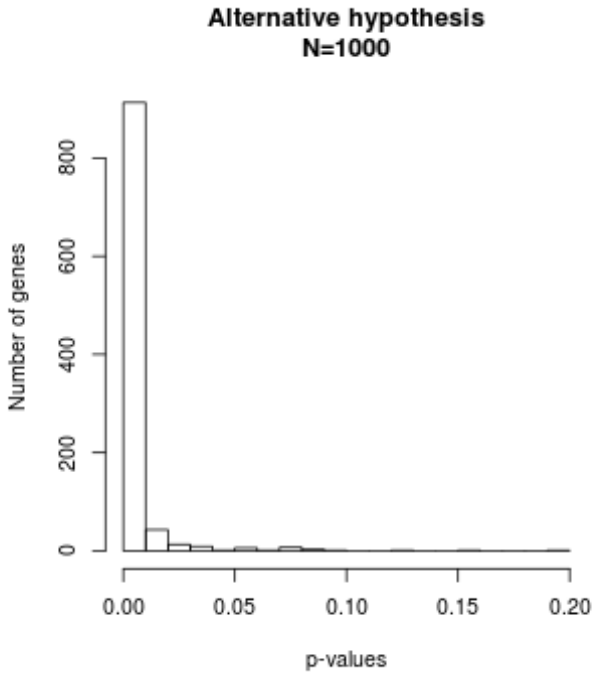


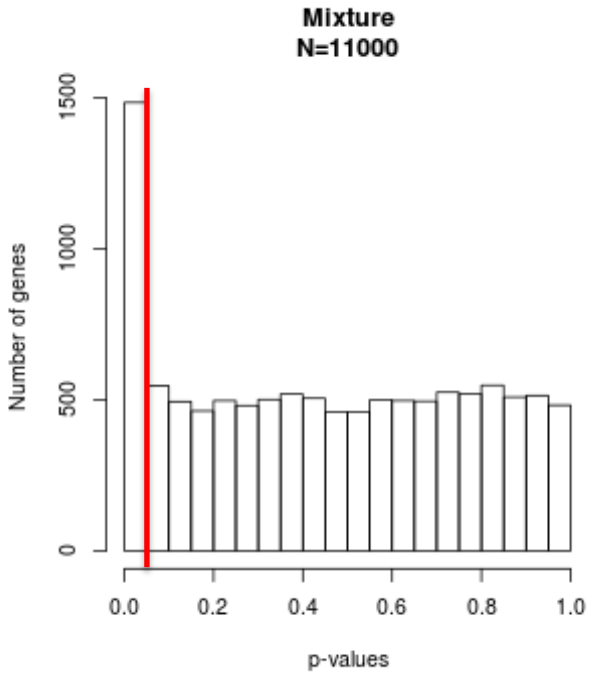
No matter how stringent the criteria are, you'll always identify genes with very small p-values and the false discovery rate (FDR) is 100%.

When the null hypothesis is true, the p-value is distributed uniformly from 0 to 1.

P-value distribution under both the null and non-null hypotheses







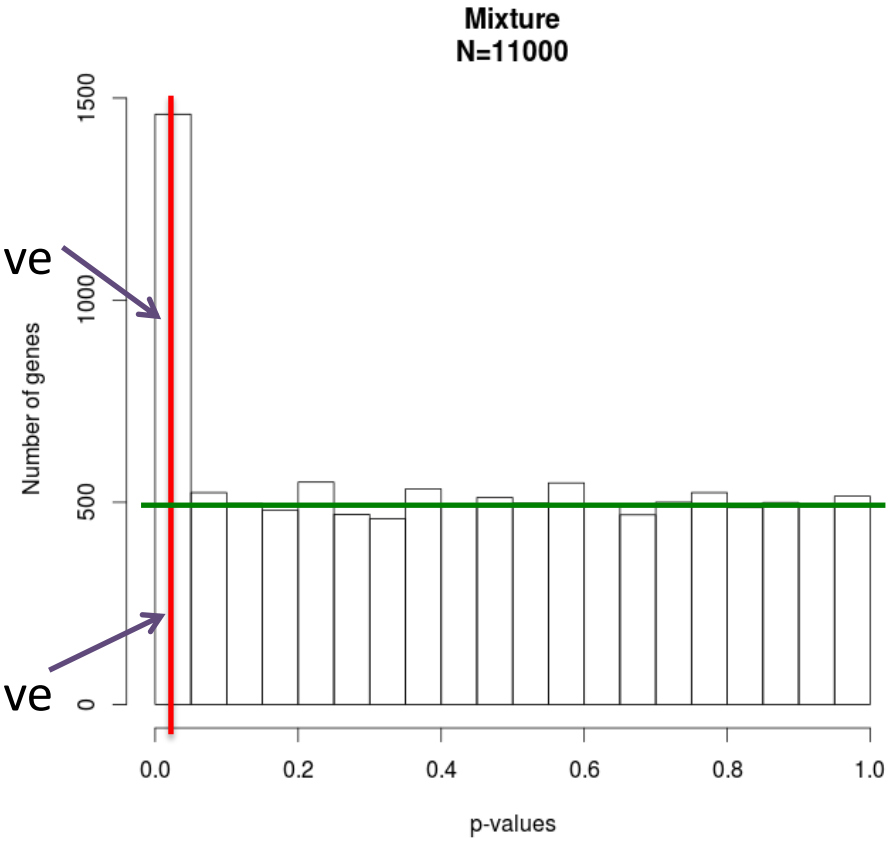
When the null hypothesis is true, the p-value is distributed uniformly.

When the null hypothesis is false, the p-value distribution is skewed toward 0.

Cutoff: p=0.05
FDR=471/(471+989)=32%

Cutoff: p=0.01
FDR=102/(102+912)=10%

Multiple test correction – FDR method



True positive

False positive

P-values < 0.00009

DE=992

False DE=99

FDR 10%

False discovery rate (concept)

For example, among 10,000 tests (10,000 genes), 100 significant genes are declared, in which 10 gene is falsely rejected. In this case, the false discovery rate is 10%.

	True null hypothesis (H_0)	False null hypothesis (H_1)	Total
Rejected (Declared significance)	**10**	90	100

q-values (adjusted p-values)

The **q-value** is **the smallest FDR** for which we can reject the null hypothesis for that one test and all others with smaller p-values.

Gene	p-values	q-values
1	0.000	0.006
2	0.002	0.015
3	0.009	0.059
4	0.013	0.063
5	0.035	0.139
6	0.051	0.171
7	0.155	0.442
8	0.197	0.492
9	0.247	0.539
10	0.269	0.539
11	0.358	0.651
12	0.396	0.656
13	0.426	0.656
14	0.493	0.702
15	0.526	0.702
16	0.622	0.777
17	0.782	0.920
18	0.862	0.958
19	0.925	0.974
20	0.992	0.992

Total number of tests: m = 20

FDR (False Discovery Rate) method (BH) is a method to calculate q-values/adjusted p-values/corrected p-values based on p-values

5% FDR, q-values < 0.05

10% FDR, q-values < 0.1

20% FDR, q-values < 0.2

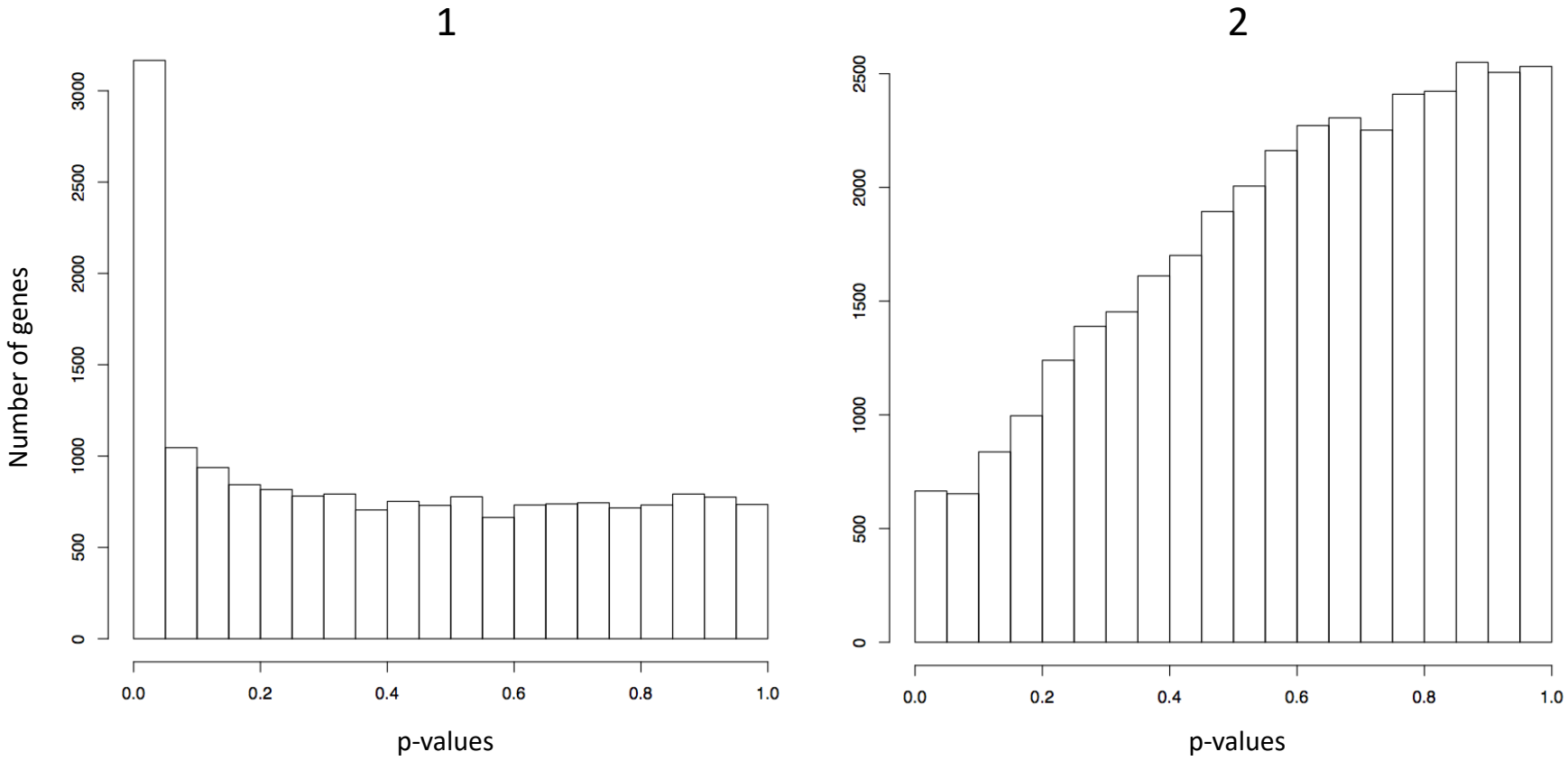
Question

If we identify 500 differential expression (DE) genes using the 5% FDR to account for multiple tests. Which one below is a better description?

1. I am 95% confident that 500 genes are DE.

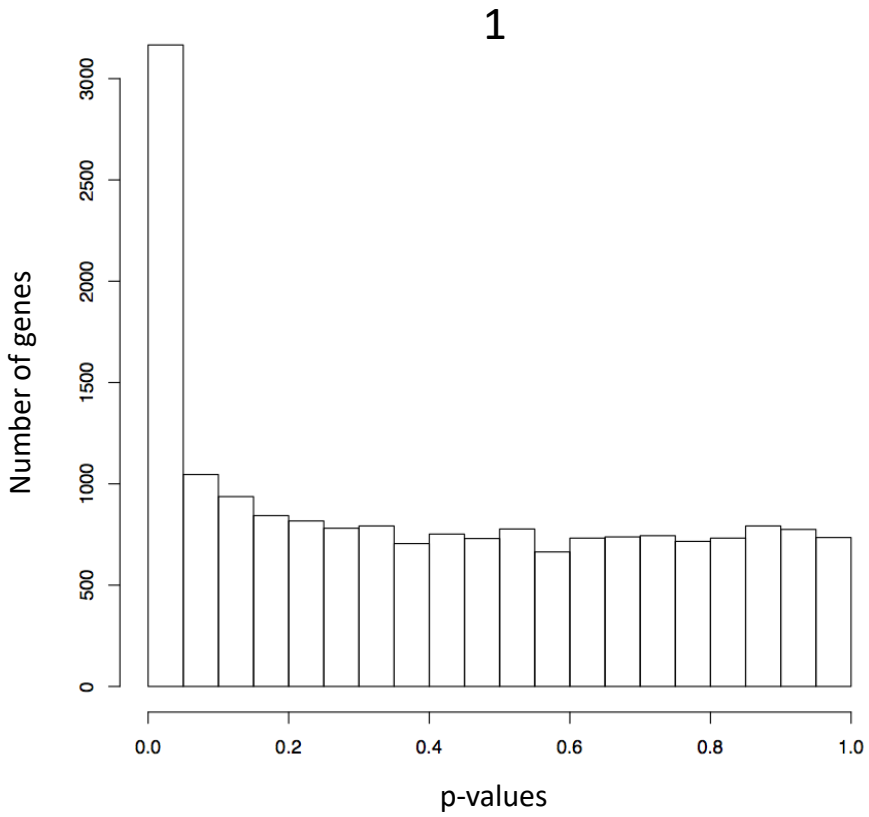
2. The 5% genes (25 genes) in the set are expected to be false DE genes.

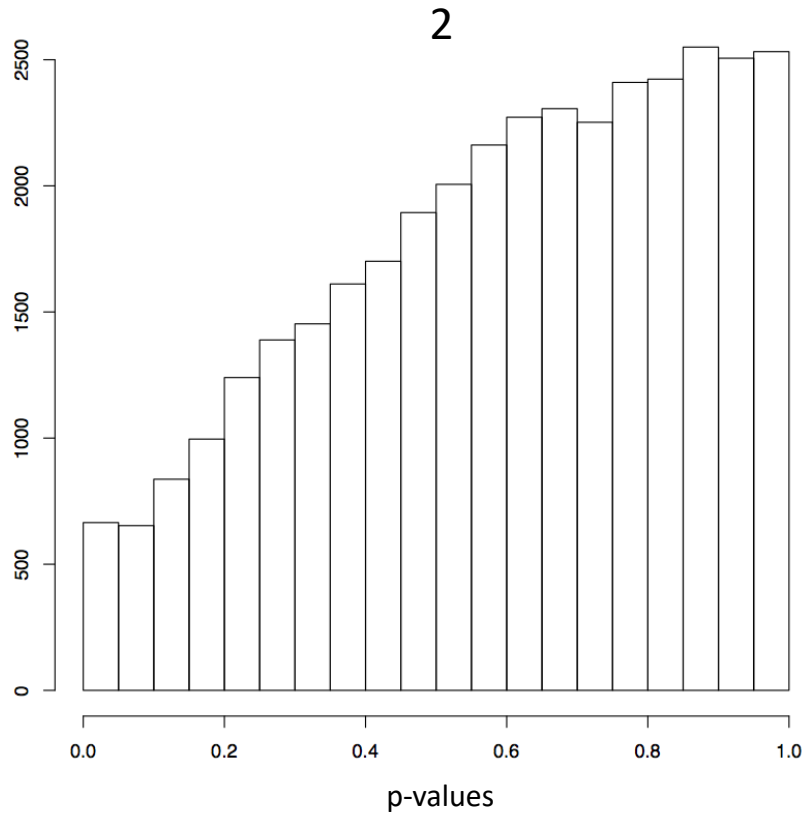
P-value histograms from real studies



If you perform an RNA-Seq experiment, which one would you hope to obtain? Why?

P-value histograms from real studies

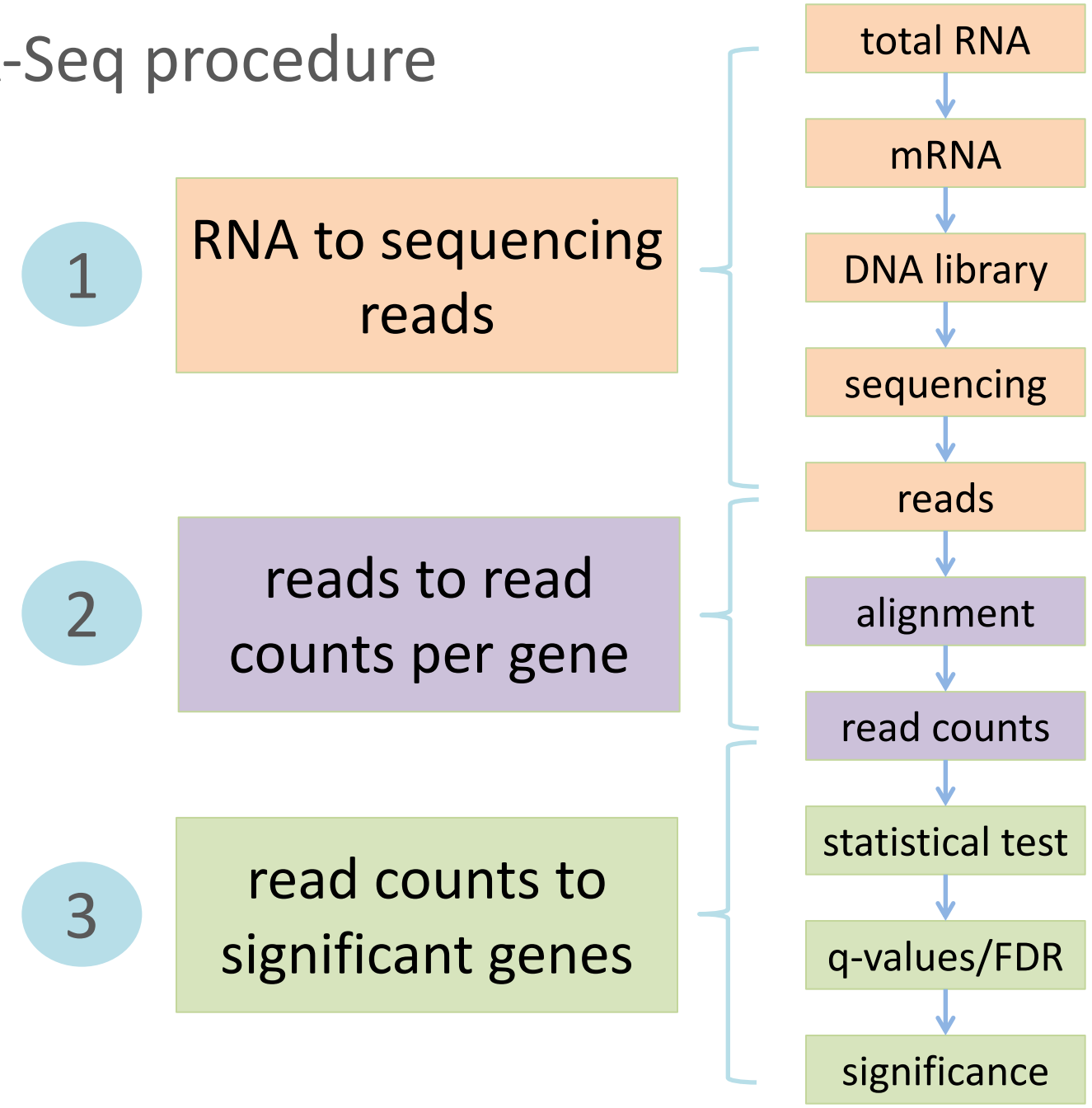




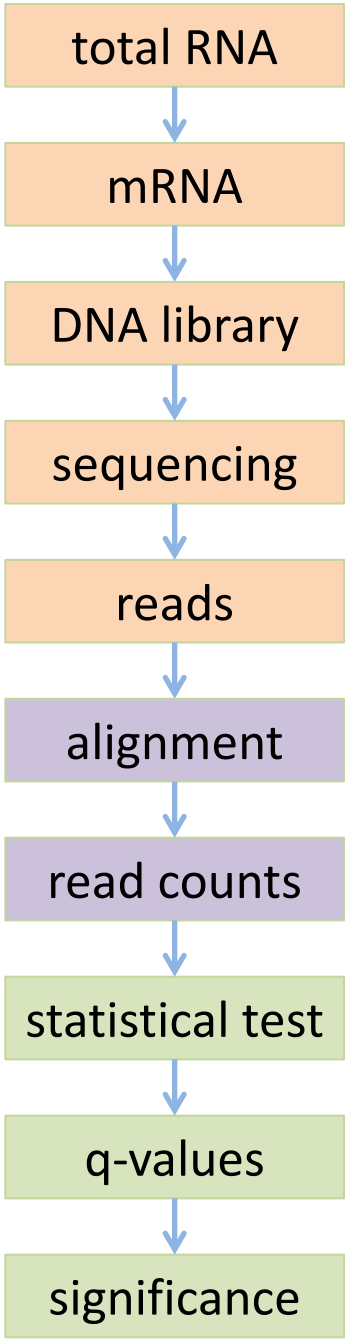
DE = 1,370, FDR=5%

DE = 0, FDR=20%

RNA-Seq procedure



Keywords



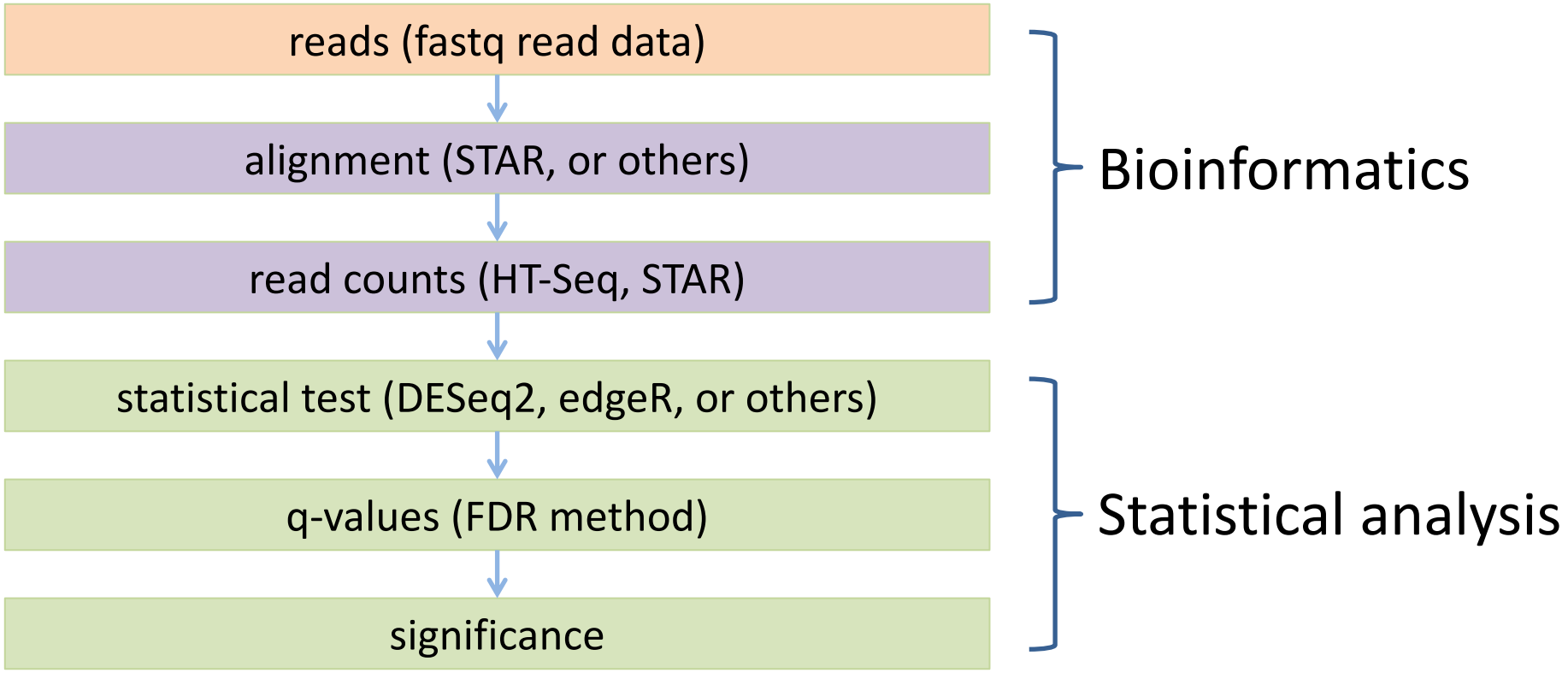
randomization, biological replication, RNA quality

short or long reads
single- or paired-end reads, read length
sequencing depths
(e.g., >20 million short reads for most experiments)

intron-spanning aligners
(e.g., STAR, HiSAT2)

count data statistical analysis (DESeq2 & edgeR)
multiple test p-value adjustment (FDR method)

Bioinformatics and Statistics (Illumina data)



STAR pipeline – from reads to counts

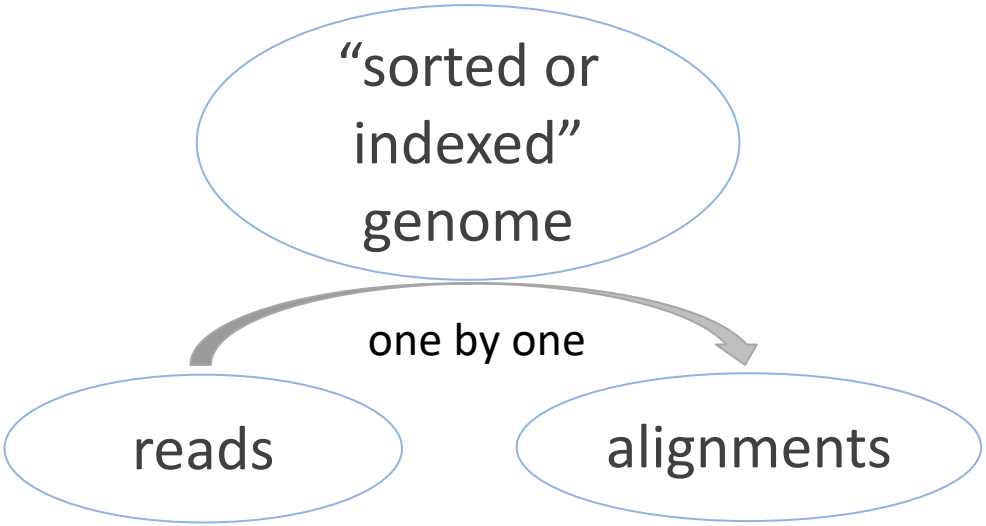
Required files:

1. Reference genome (fasta file)
2. Gene annotation (gff or gtf gene annotation)
3. Reads (fastq files) – your own data

Many reference genomes and gff/gtf files are available at:
http://ensembl.org/info/data/ftp

Species	DNA (FASTA)	cDNA (FASTA)	CDS (FASTA)	ncRNA (FASTA)	Protein sequence (FASTA)	Annotated sequence (EMBL)	Annotated sequence (GenBank)	Gene sets
Human *Homo sapiens*	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3
Mouse *Mus musculus*	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3
Zebrafish *Danio rerio*	FASTA	FASTA	FASTA	FASTA	FASTA	EMBL	GenBank	GTF GFF3

Reads to counts - **reference indexing**




```
STAR --runMode genomeGenerate \
     --genomeDir . \
     --genomeFastaFiles reference.fas \
     --sjdbGTFfile genes.gtf \
     --runThreadN 4
```

Reads to counts – **alignment and read counting**

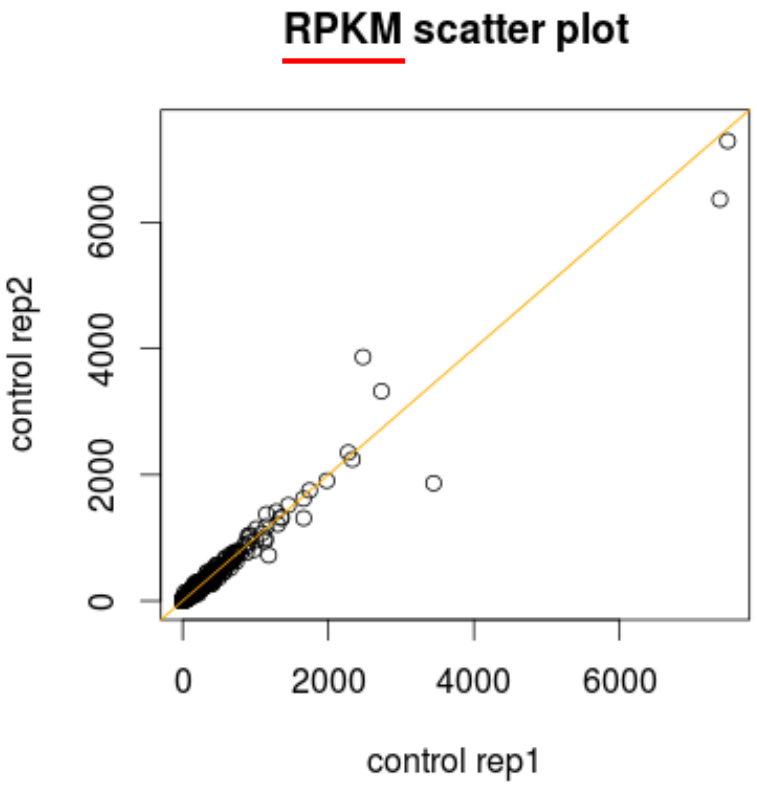
```
STAR --genomeDir reference.fas \
    --readFilesIn read1.fq read2.fq \
    --alignIntronMax 100000 \
    --alignMatesGapMax 100000 \
    --outFileNamePrefix output \
    --outSAMattrIHstart 0 \
    --outSAMmultNmax 1 \
    --outSAMstrandField intronMotif \
    --outFilterIntronMotifs RemoveNoncanonicalUnannotated \
    --outSAMtype BAM SortedByCoordinate \
    --quantMode GeneCounts \
    --outFilterMismatchNmax 5 \
    --outFilterMismatchNoverLmax 0.05 \
    --outFilterMatchNmin 50 \
    --outSJfilterReads Unique \
    --outFilterMultimapNmax 1 \
    --outSAMmapqUnique 60 \
    --outFilterMultimapScoreRange 2
```

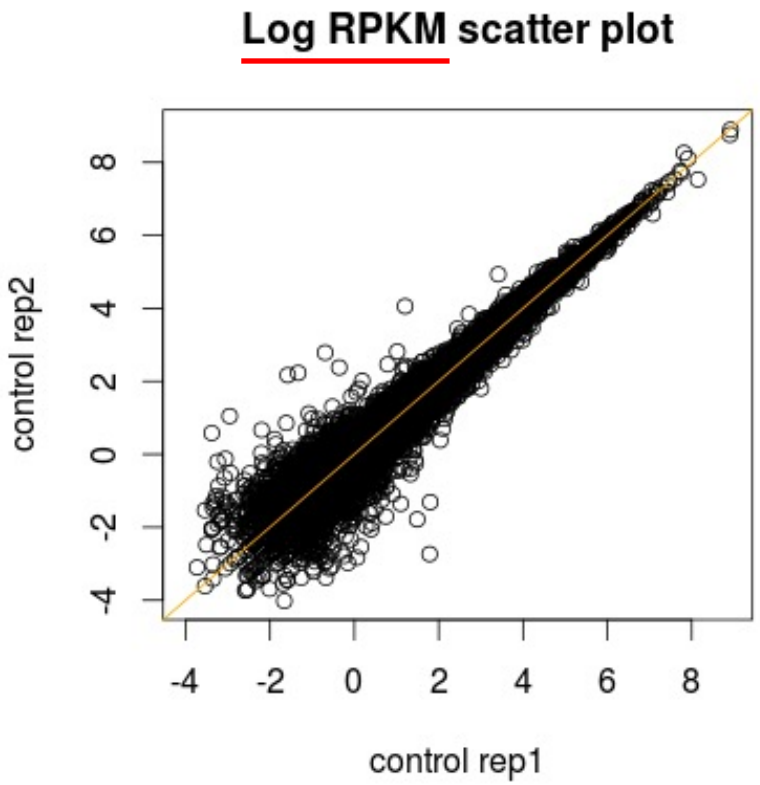
Count matrix: Read counts (Raw) per gene

Gene	sample 1	sample 2	sample 3
gene 1	6,075	5,934	3,370
gene 2	295	377	169
...	...	...	...

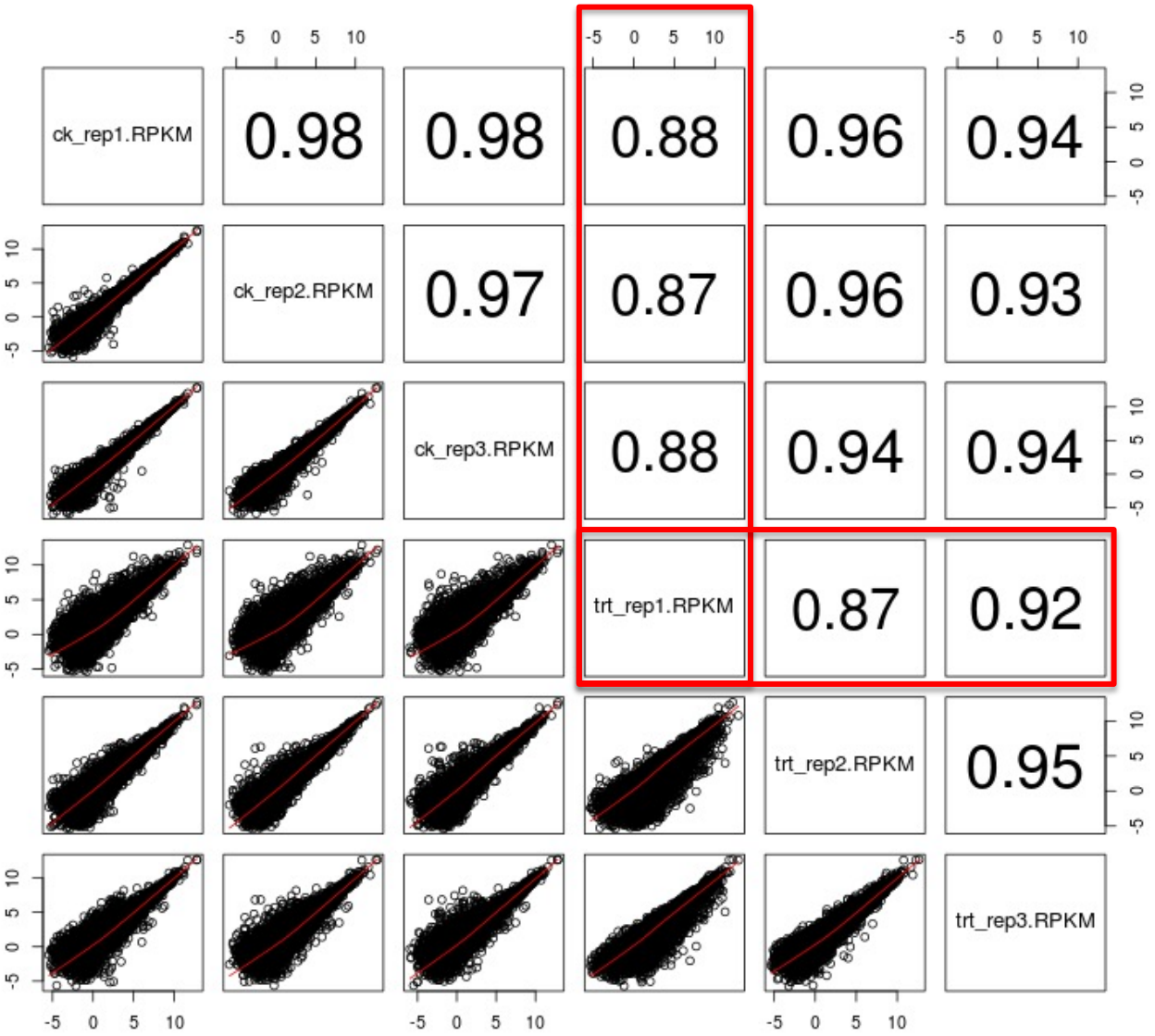
Overall comparisons of read counts among samples

Scatter plot





Pair-wise scatter plot



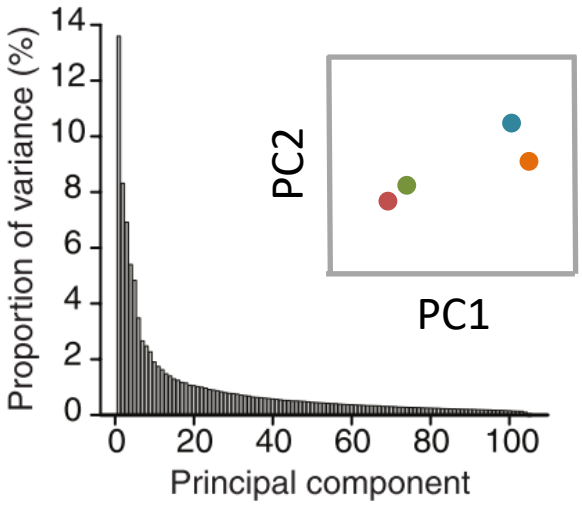
Principal Component Analysis (PCA)

PCA is a mathematical algorithm that reduces the dimensionality of the data while retaining most of the variation in the data set.

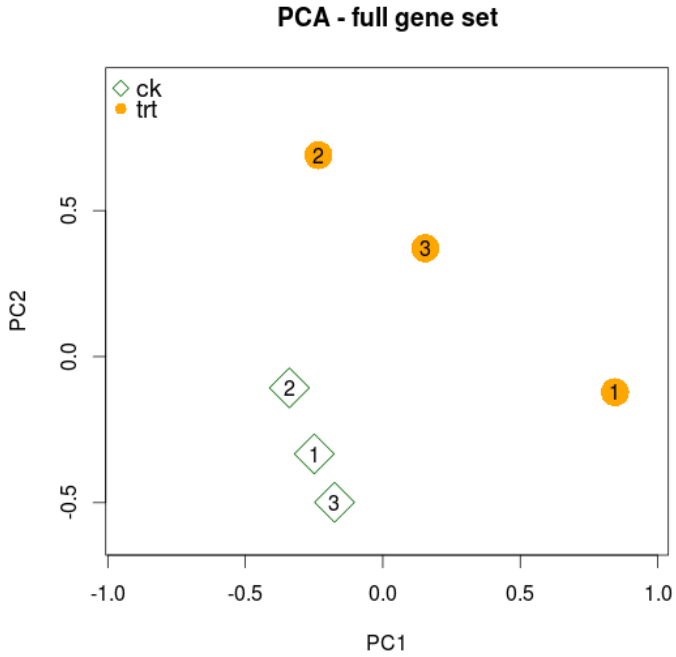
Feature/variable	John	Mike	Jack	Justin
Weight (lb)	150	243	186	128
Height (cm)	171	190	178	175
…				

	Control			Treatment		
GeneID	Rep1	Rep2	Rep3	Rep1	Rep2	Rep3
1	2679	2360	2573	2563	3398	3012
2	177	161	171	154	137	152
3	381	371	397	541	723	635
…						
30000	990	1073	1236	850	672	859

Normalized and standardized data



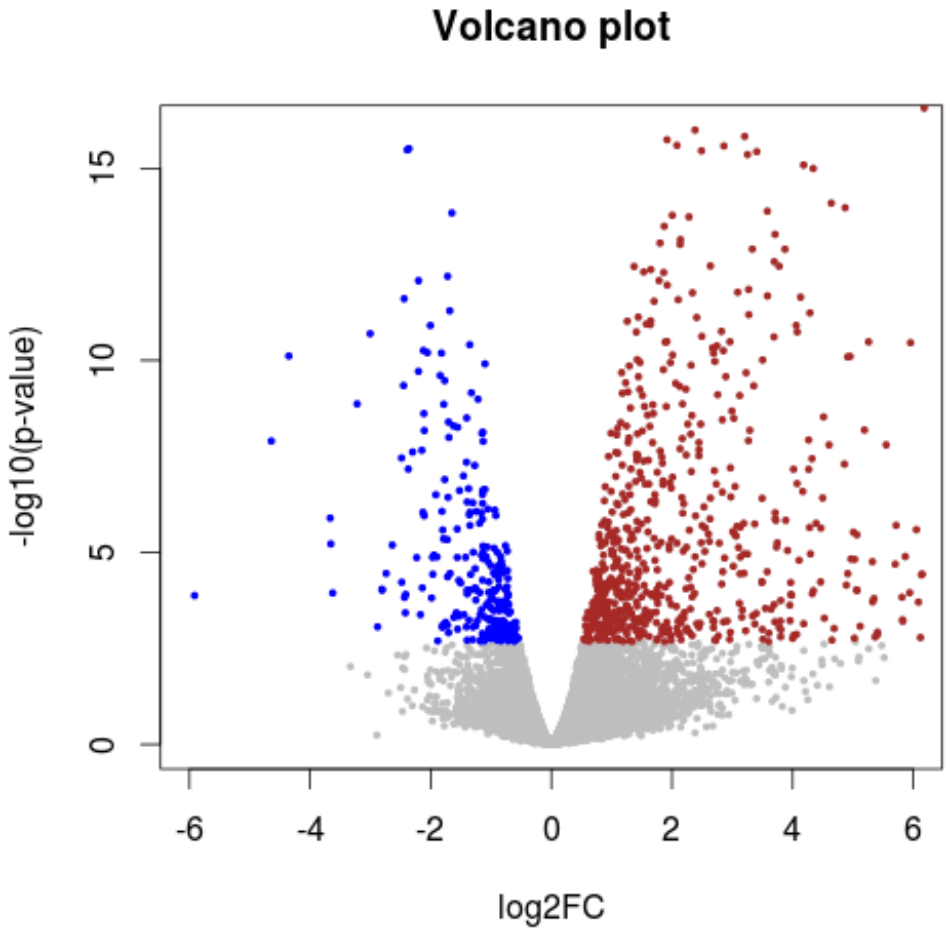
Nature Biotech, 2008, 26:303-4



Overview of differential expression

Volcano plot

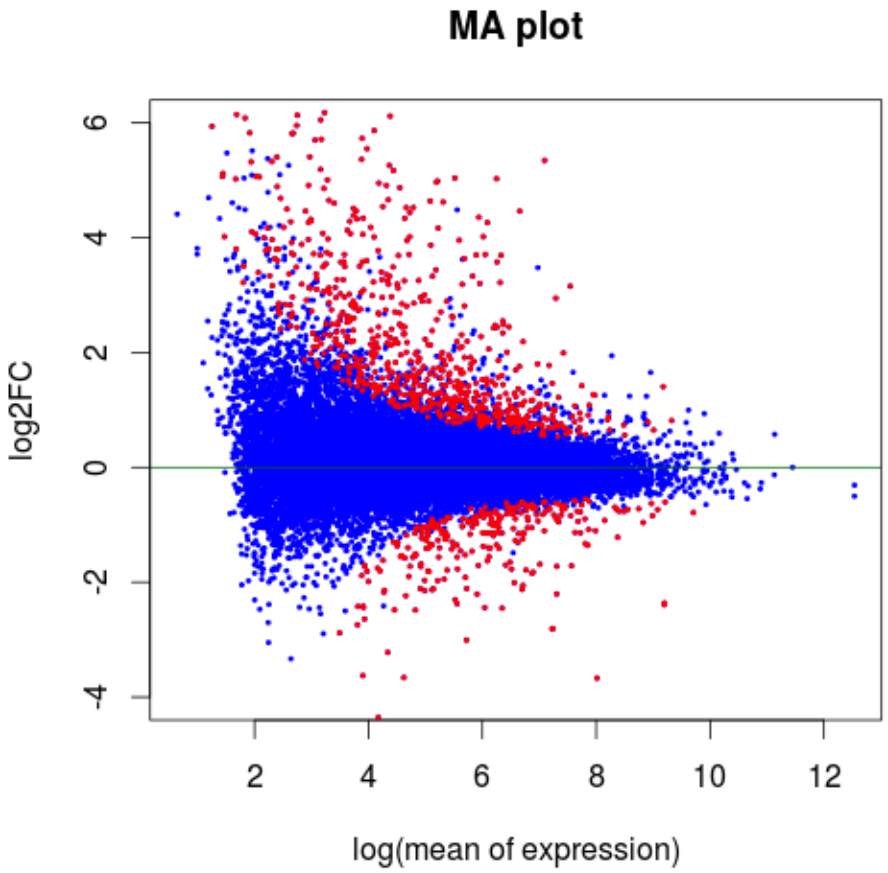
DE Result			
GeneID	Log2FC	p-value	-log10(pvalue)
1	-0.40	0.037	1.43
2	0.03	0.916	0.04
3	-0.89	2.42E-05	4.62
4	0.30	0.130	0.89
5	-0.36	0.140	0.85
6	-0.07	0.811	0.09
…			



MA plot

M (log ratios) and A (mean average)

GeneID	Mean RPKM	log mean	log2FC
1	0.51	-0.29	-0.40
2	1.25	0.10	0.03
3	3.52	0.55	-0.89
4	0.19	-0.72	0.30
5	2.34	0.37	-0.36
6	6.14	0.79	-0.07
…			



More at: en.wikipedia.org/wiki/MA_plot

Summary

- **Biological replication** rather than technical replication are typically needed for an RNA-seq experiment.
- P-values need to be corrected to account for **multiple tests**. The FDR method is a reliable approach for the correction.
- Many bioinformatics pipelines and statistical methods have been developed. Most methods work fine but **parameters** in each method need to be carefully selected.

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1. Benjamini Y, et al. 1995. Controlling the False Discovery Rate - a Practical and Powerful Approach to Multiple Testing. Journal of the Royal Statistical Society Series B-Methodological 57:289-300.
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4. Robinson MD, et al. 2010. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. Bioinformatics 26:139-140.