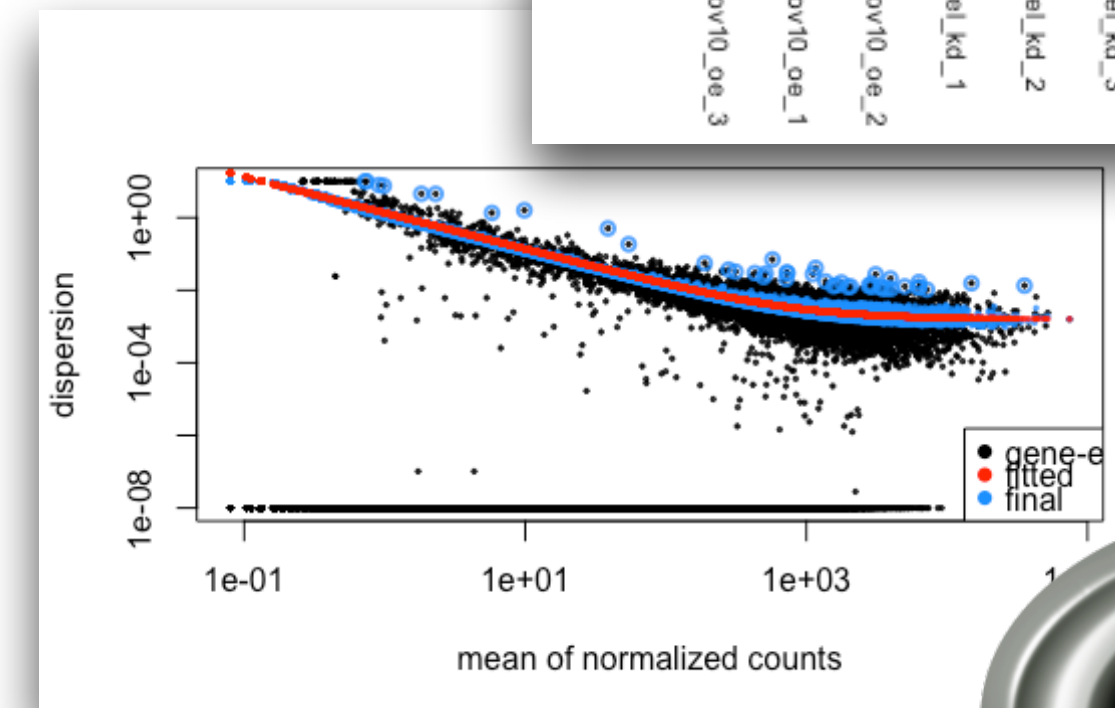
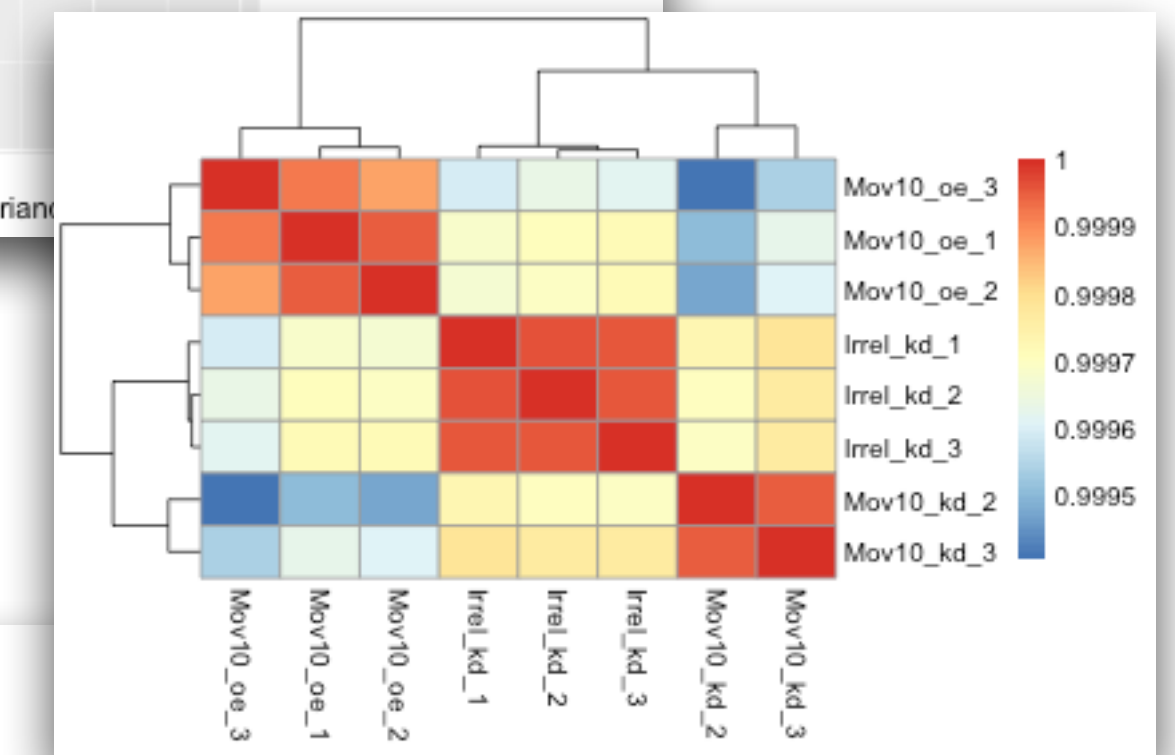
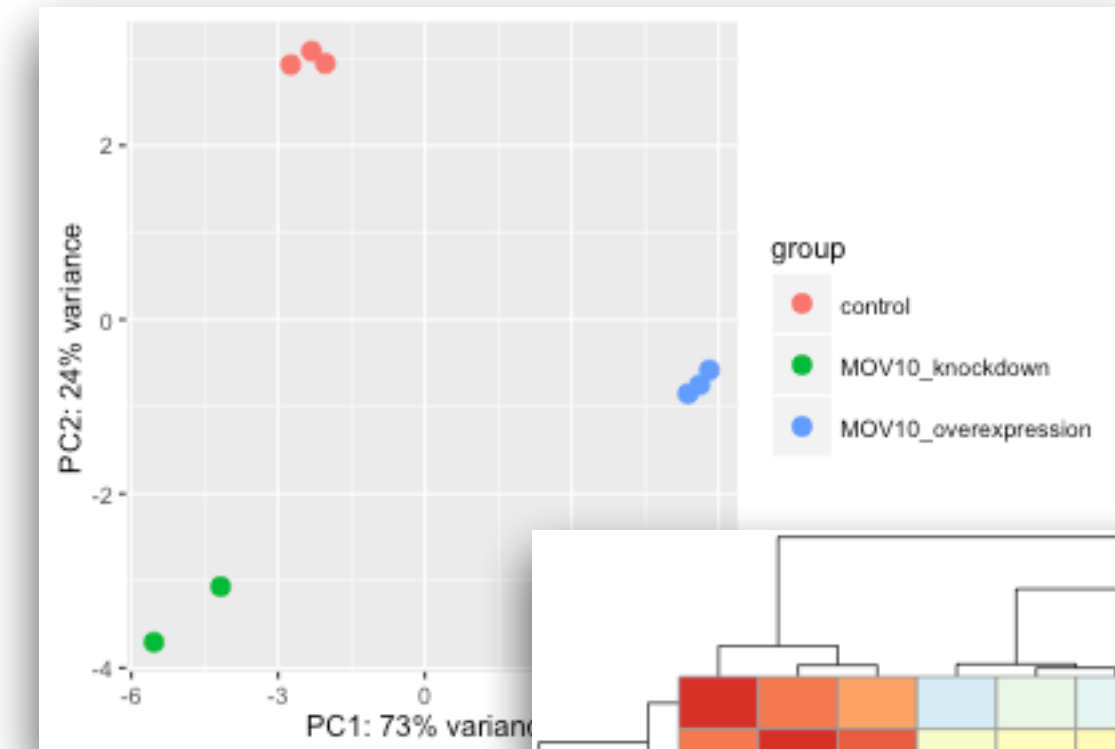


Using R for Differential Gene Expression Analysis

Harvard Chan Bioinformatics Core

October 20, 2016

<http://tinyurl.com/hbc-DGEworkshop>



Learning Objectives

- ✓ Understand the considerations for performing statistical analysis on RNA-Seq data
- ✓ Utilize R knowledge to perform a standard differential expression analysis
 - ✓ Starting with Gene Counts (after alignment and counting), perform basic QC on the count data
 - ✓ Use DESeq2 to perform differential expression (DE) analysis on the count data and obtain a list of significantly different genes
 - ✓ Visualize expression patterns of DE genes

The image shows handwritten mathematical derivations on a blackboard. The top part shows the derivative of the log-likelihood function with respect to the parameter τ :

$$\frac{dL}{d\tau} = \frac{1}{\tau} - \frac{1}{P} \frac{dP}{d\tau}$$

Below this, there are two expressions for the derivative of the log-likelihood function with respect to the parameter τ , both showing a similar form:

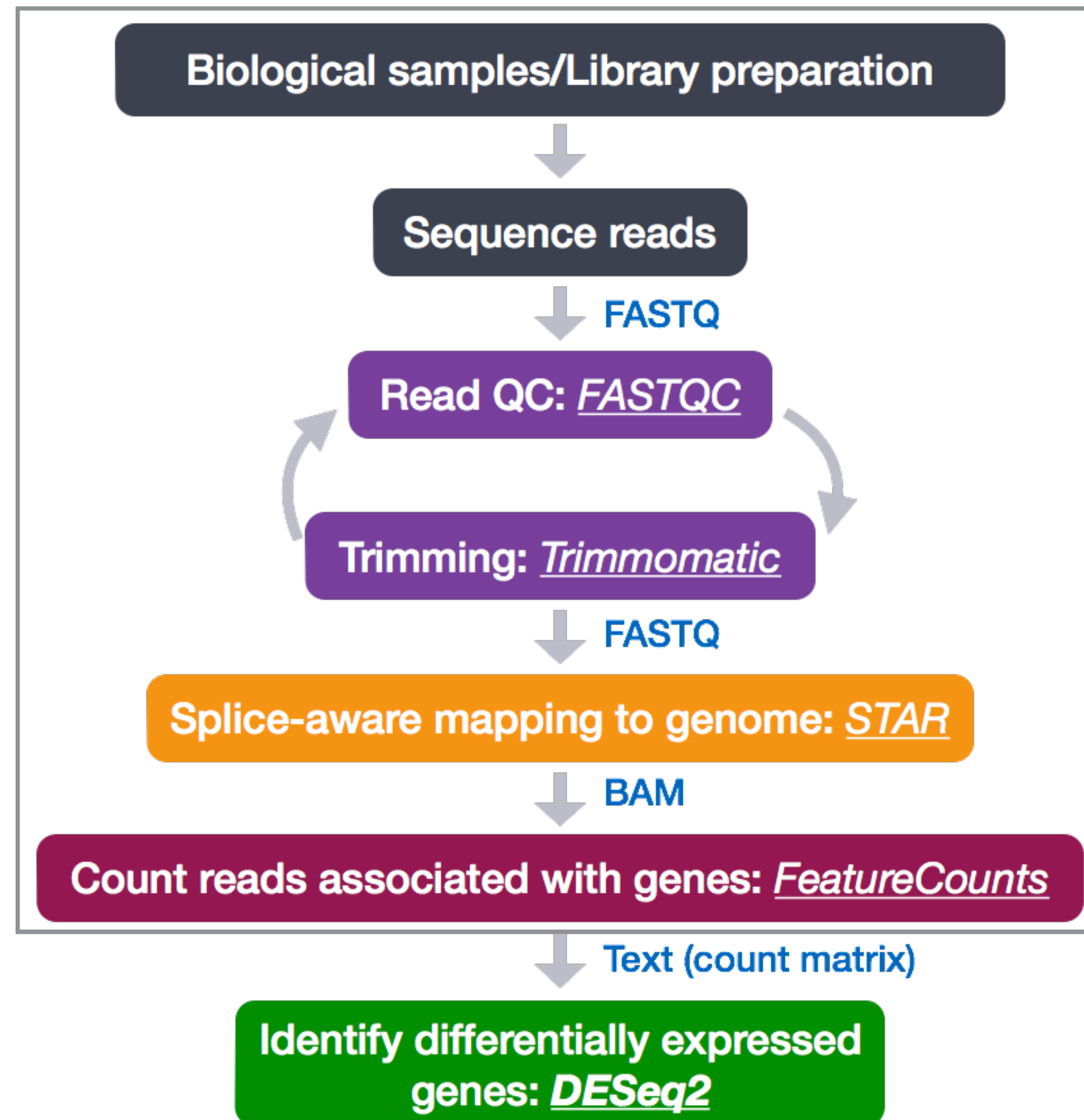
$$\frac{P_0 - P}{P} \sim \frac{1}{P}$$

Below these, there are two expressions for the log-likelihood function, both showing a similar form:

$$10^{-53}$$
$$10^{-26}$$

Below these, there are two expressions for the log-likelihood function, both showing a similar form:

$$10^8 \text{ } \{ \}$$
$$10^{10} (10^{11}) \}$$



From sequence data to count matrix


High-throughput sequencing data

	SRR1039508	SRR1039509	SRR1039512	SRR1039513	SRR1039516
ENSG000000000003	679	448	873	408	1138
ENSG000000000005	0	0	0	0	0
ENSG000000000419	467	515	621	365	587
ENSG000000000457	260	211	263	164	245
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High-throughput sequencing data

samples: want to see if differences across
condition are significant
(w.r.t. biological and technical variation)

features (e.g. genes)




	SRR1039508	SRR1039509	SRR1039512	SRR1039513	SRR1039516
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High-throughput sequencing data

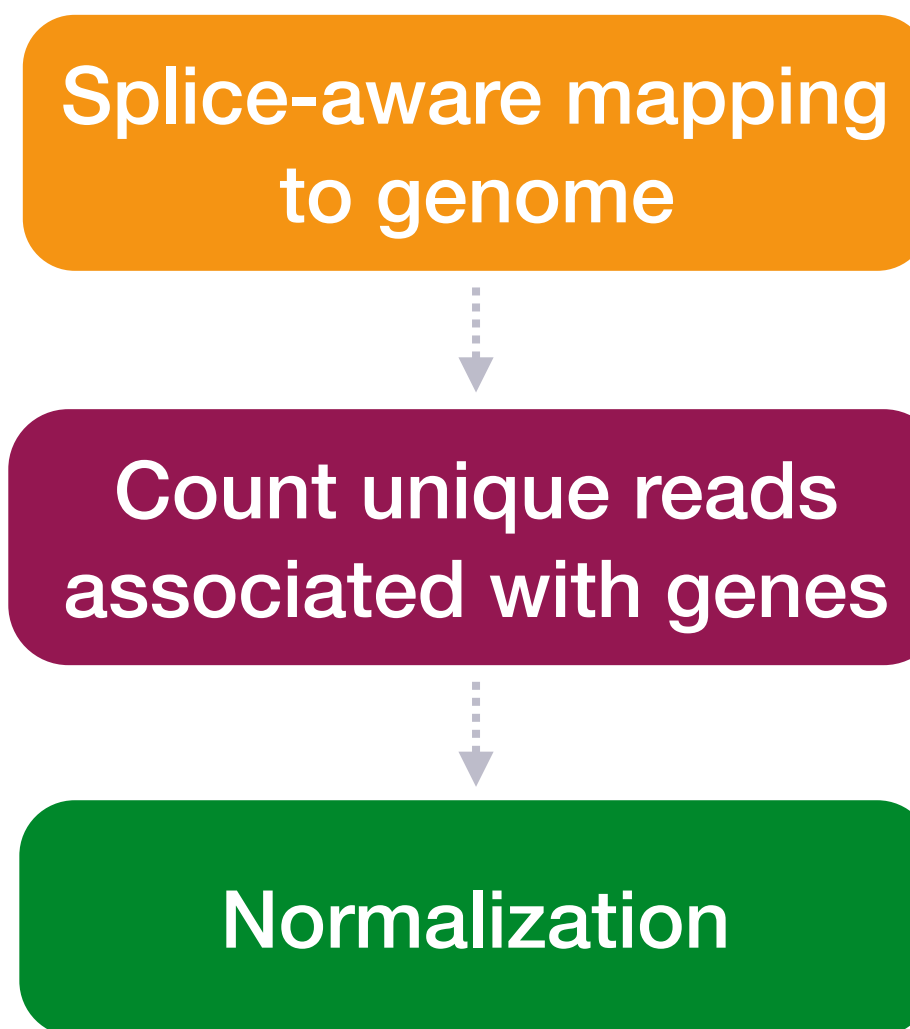
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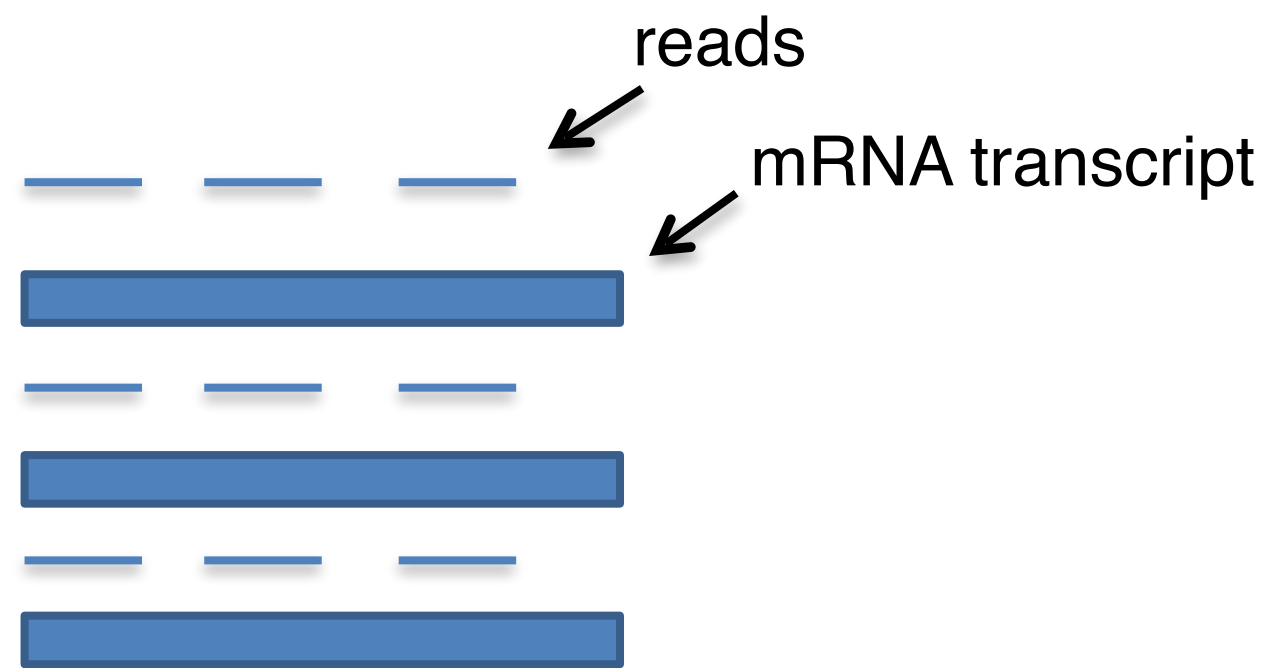
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- counts need an appropriate statistical model (normalization and variance modeling)

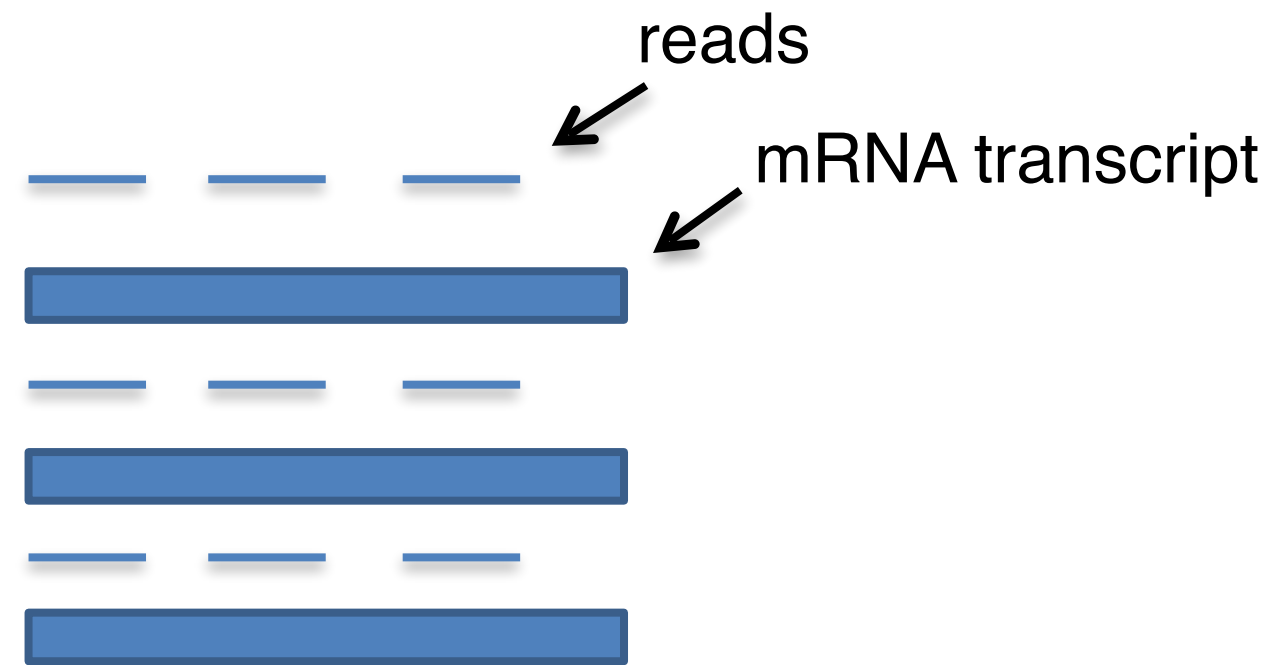


DE workflow :: normalization

mRNAs to reads



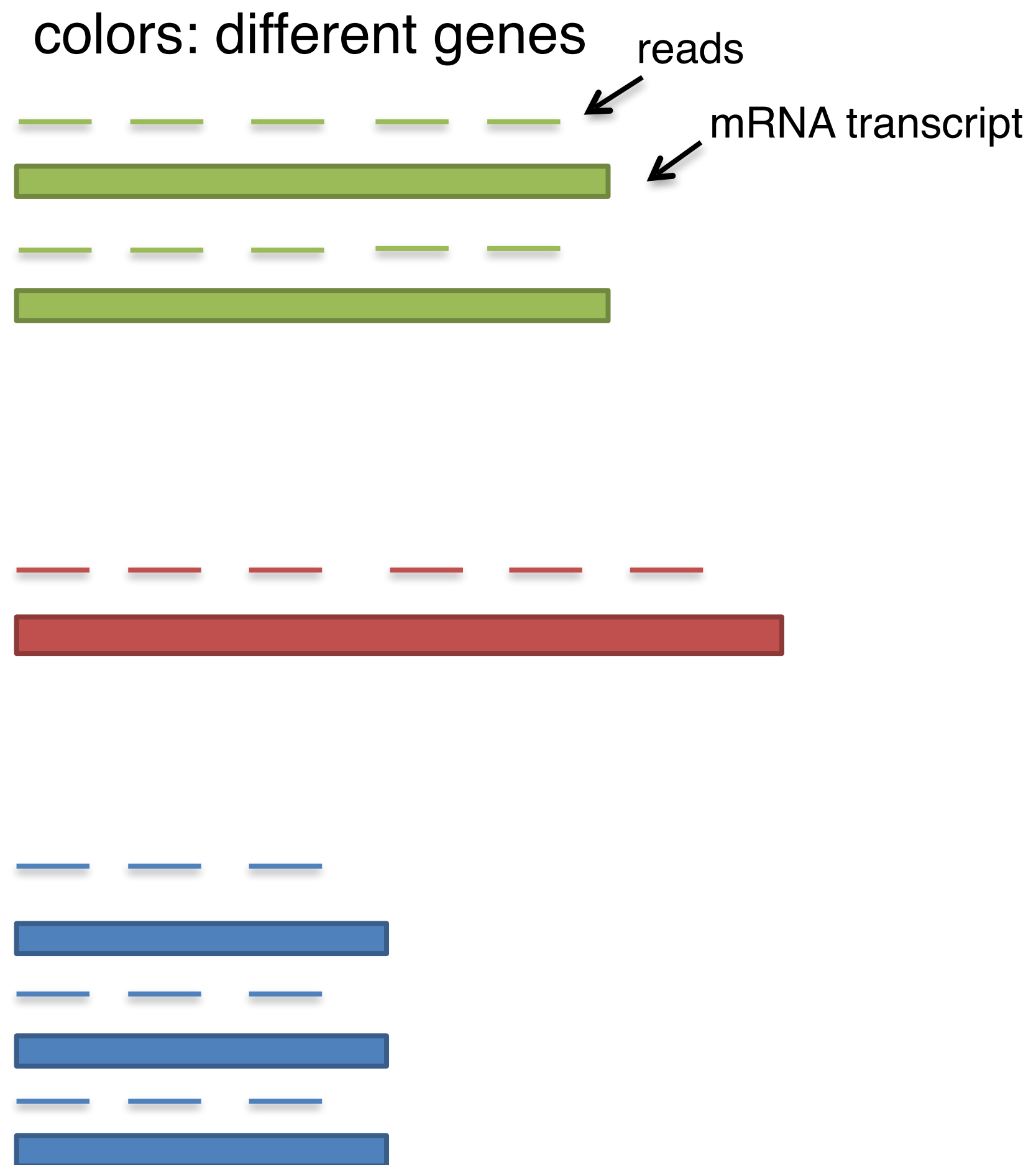
mRNAs to reads



count of mapped reads proportional to:

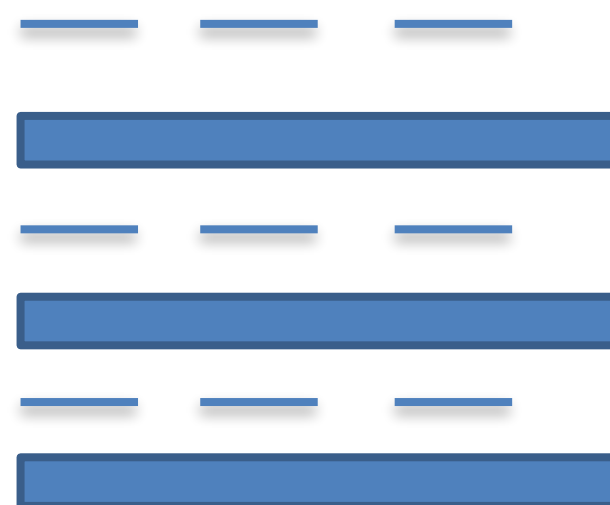
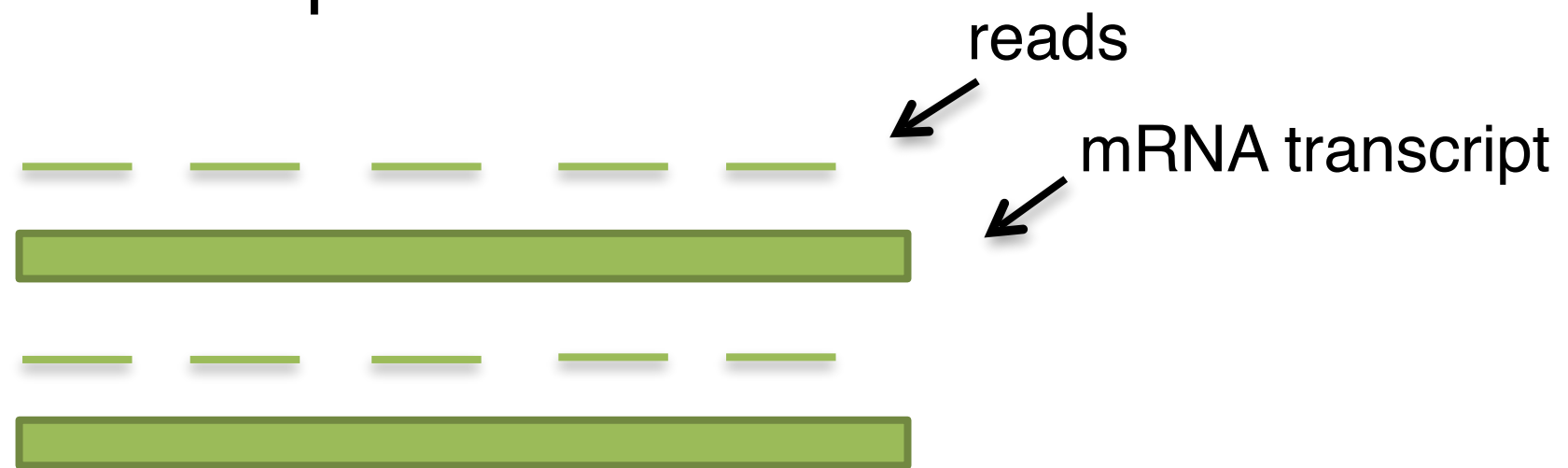
- expression of RNA
- length of gene
- sequencing depth
- library prep. factors (PCR)
- etc...

Length of gene



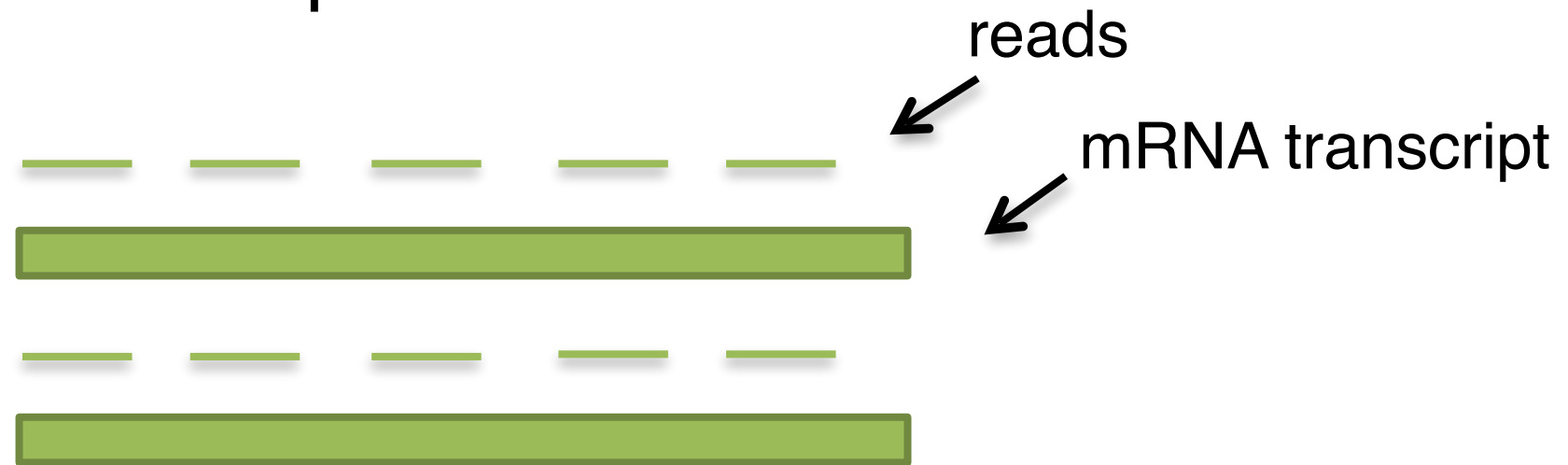
Sequencing depth

sample 1

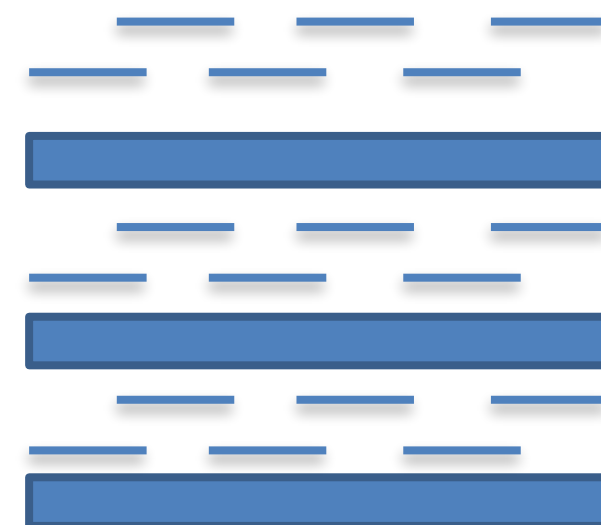
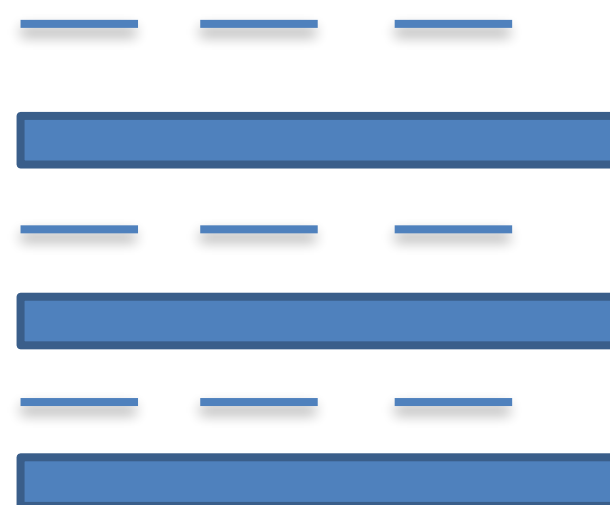


Sequencing depth

sample 1



sample 2



(Pre)-scaled measures of expression

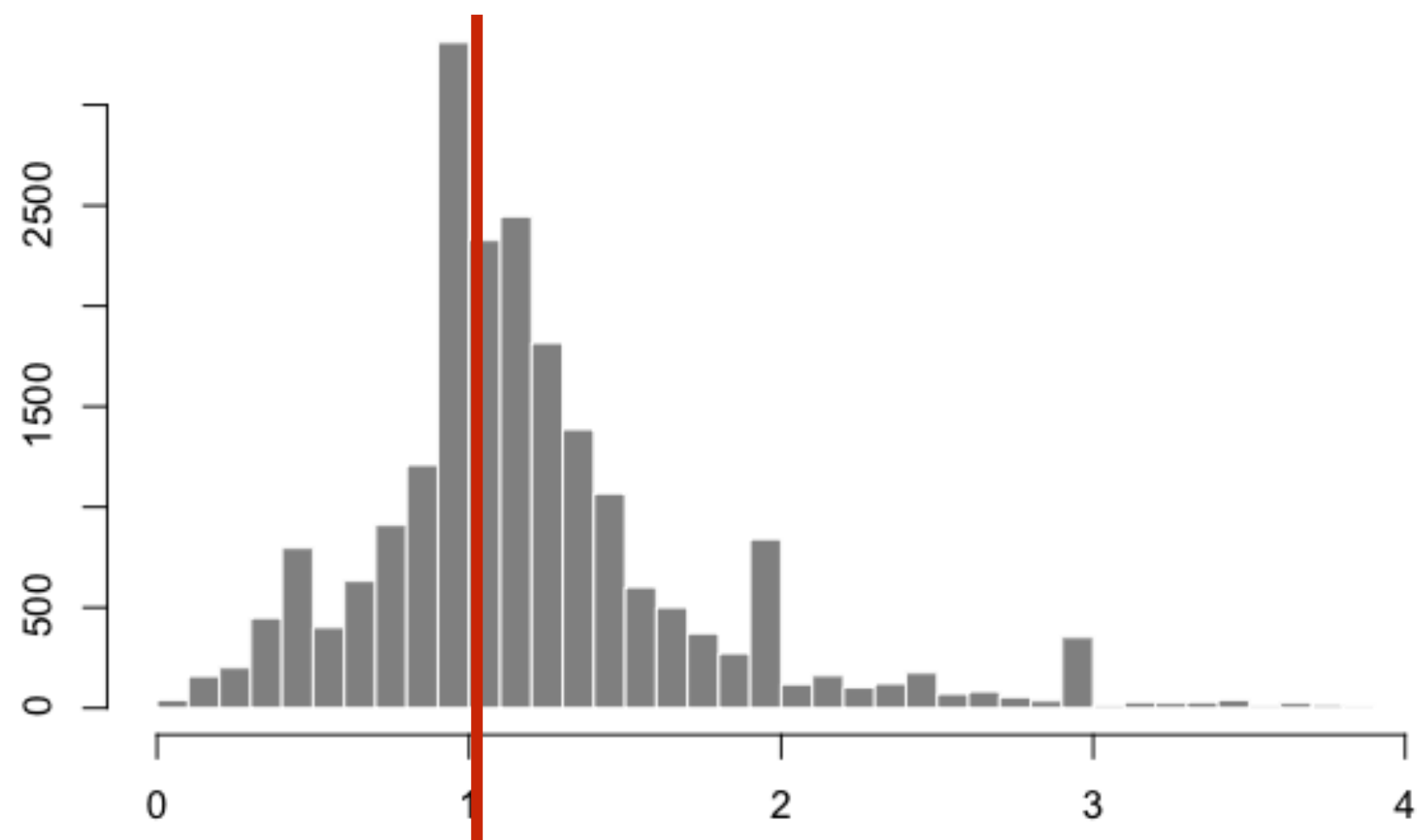
- ▶ CPM (counts per million) counts scaled by the total number of reads
- ▶ TPM (transcripts per million) the proportion of transcripts in your RNA (counts per base)
- ▶ (not recommended) RPKM (reads aligned per kilobase of exon per million reads mapped) – Mortazavi et al 2008
- ▶ (not recommended) FPKM (fragments per kilobase of exon per million fragments mapped). Same idea for paired end sequencing
- ▶ Tool-specific metrics for normalization

Raw counts should be used as input for
differential expression tools!

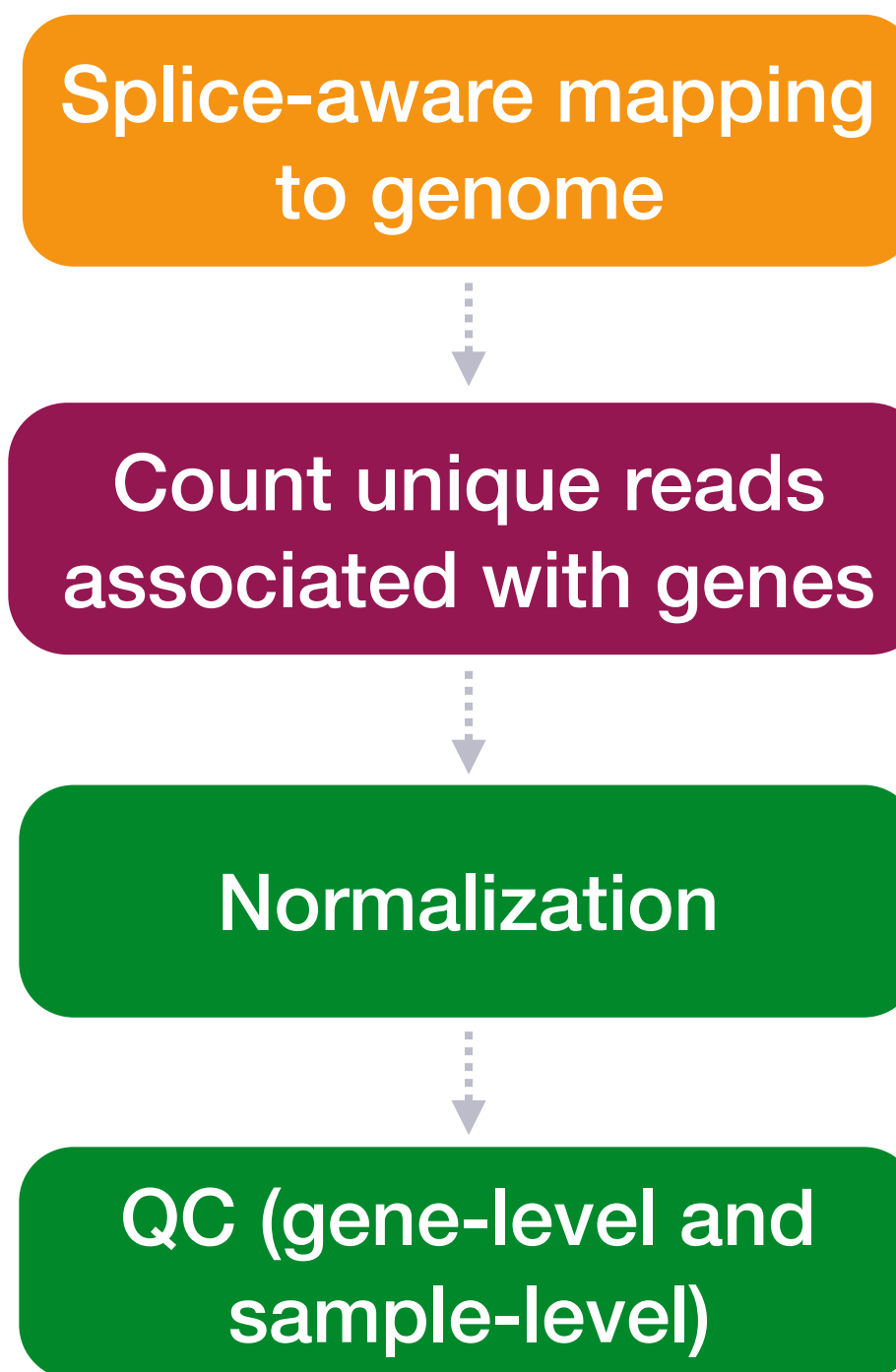
Median of ratios method

simple approach & works well
for each gene look at the count ratios:

sample 1 / pseudo-reference sample



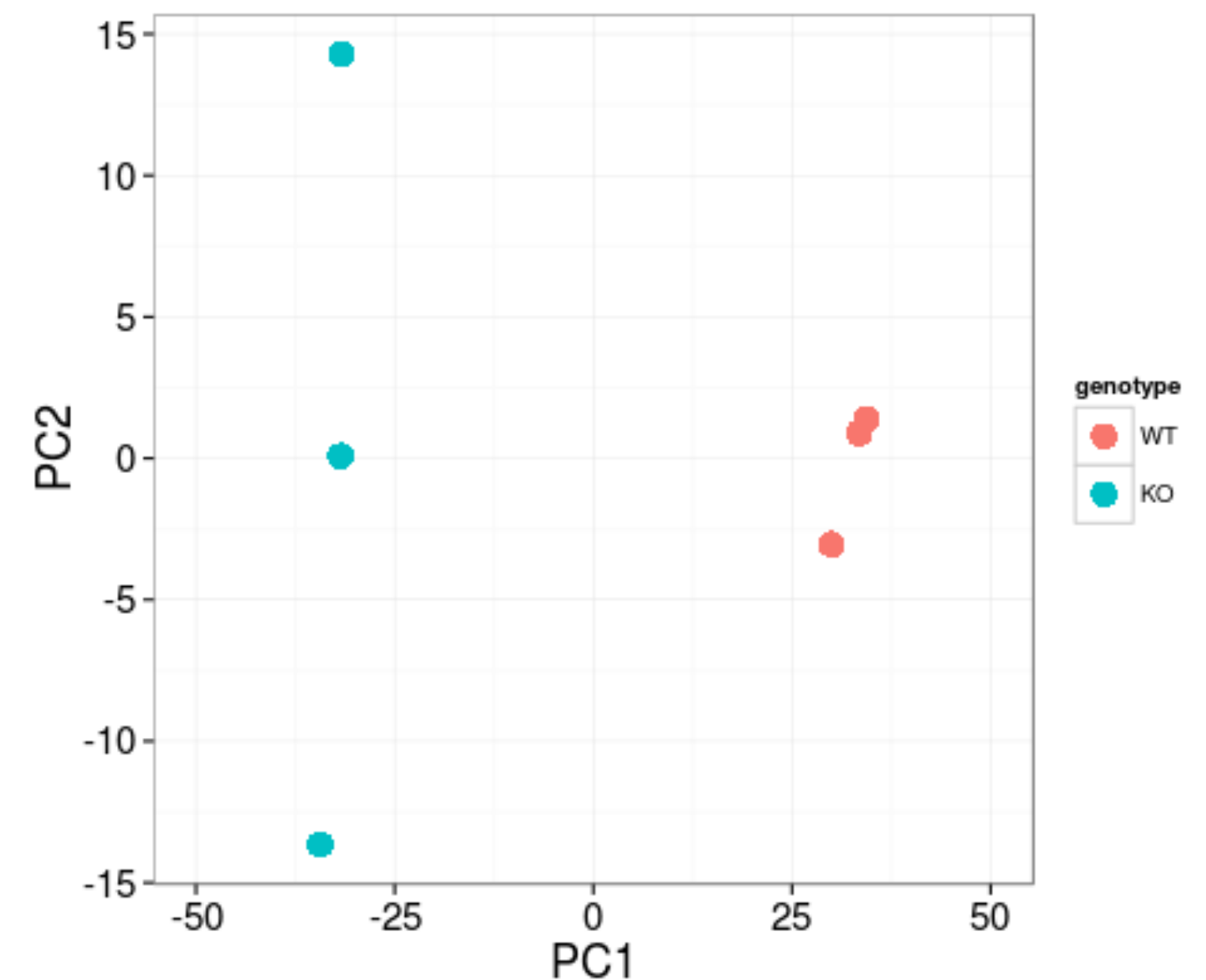
- in general: create a pseudo-reference-sample (row-wise geometric mean)
- calculate ratio of each sample to the reference
- take the median value as the normalization factor
- assumes that not *ALL* genes are DE (differentially expressed)
- **robust** to imbalance in up-/down- regulation and large numbers of DE genes



DE workflow :: quality control

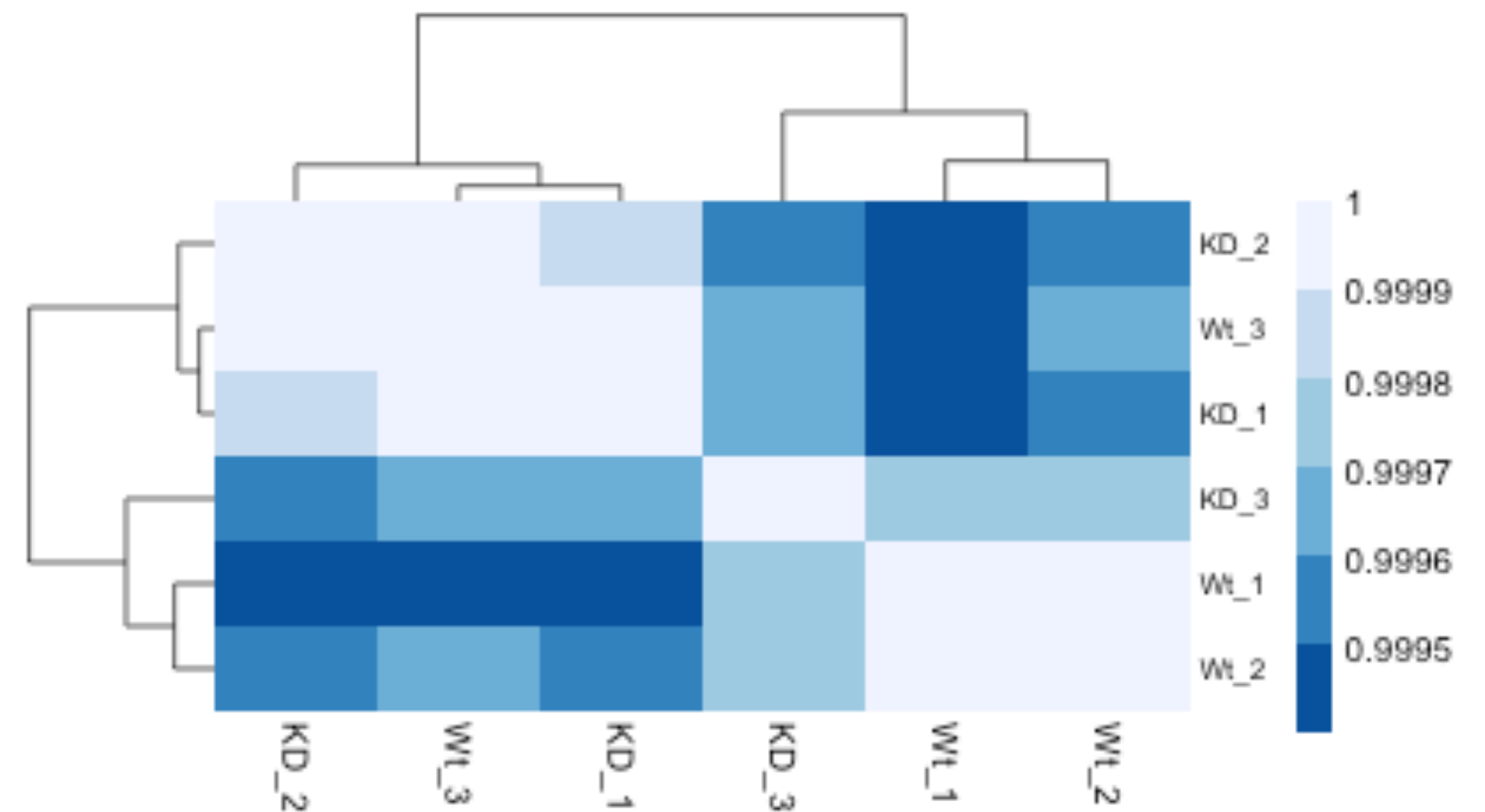
QC: Sample-level

- ▶ **Principal Component Analysis (PCA):** A technique used to emphasize variation and bring out strong patterns in a dataset (dimensionality reduction)
- ▶ Project a line through the data points in n dimensional space ($n = \text{genes}$)
- ▶ Measure how much variance there is from that line (the distance from each point to the line).
- ▶ PC1 explains highest variance, PC2 next highest etc.



QC: Sample-level

- ▶ Identify strong patterns in a dataset and potential outliers
- ▶ Correlation or distances for all pairwise combinations of samples.
- ▶ Generally high correlations with each other (values higher than 0.80)
- ▶ 'Blocks' indicate substructure in the data



QC: Gene-level filtering

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Genes with
zero counts

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Genes with extreme
count outlier



Genes with
zero counts



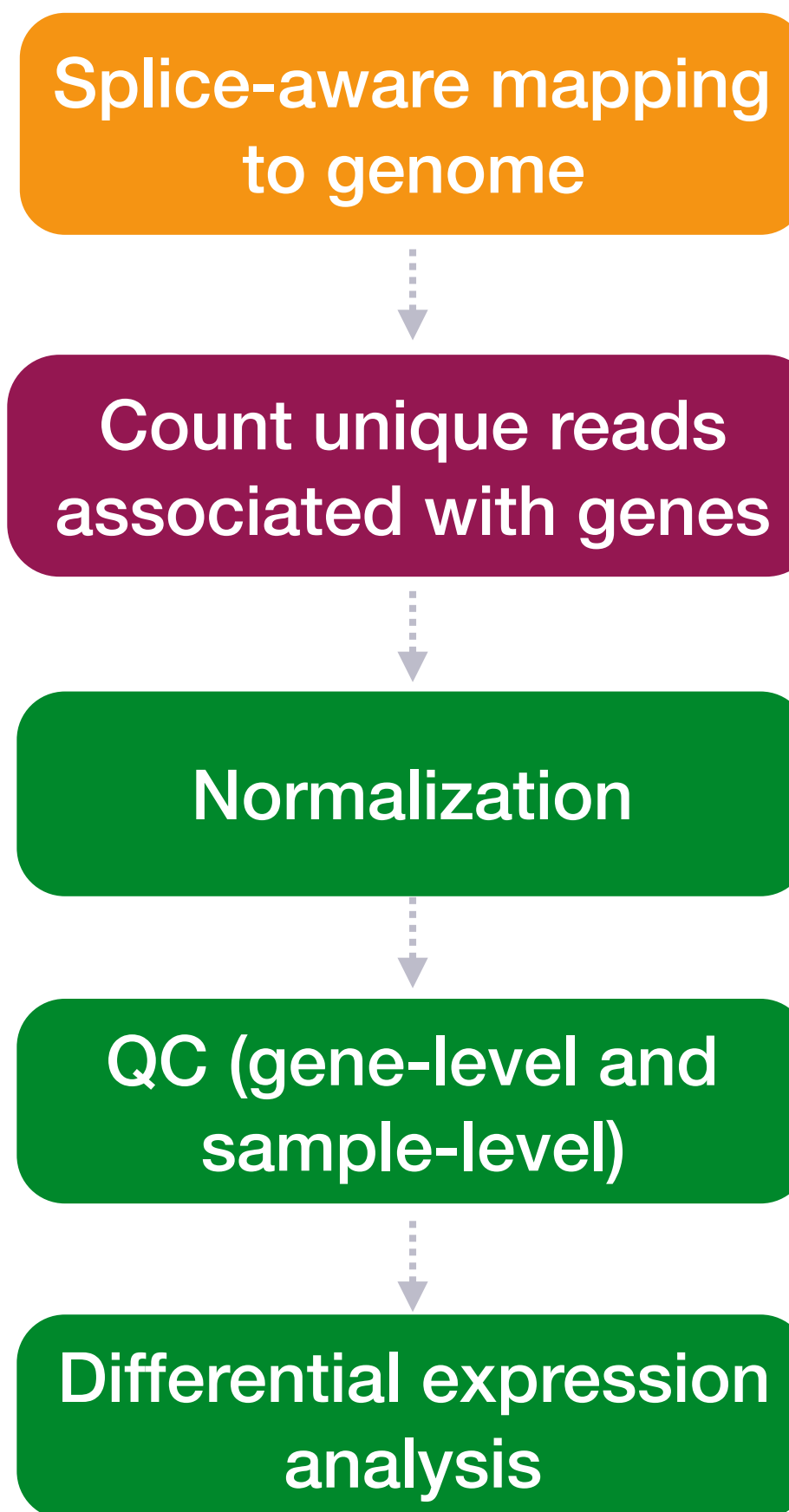
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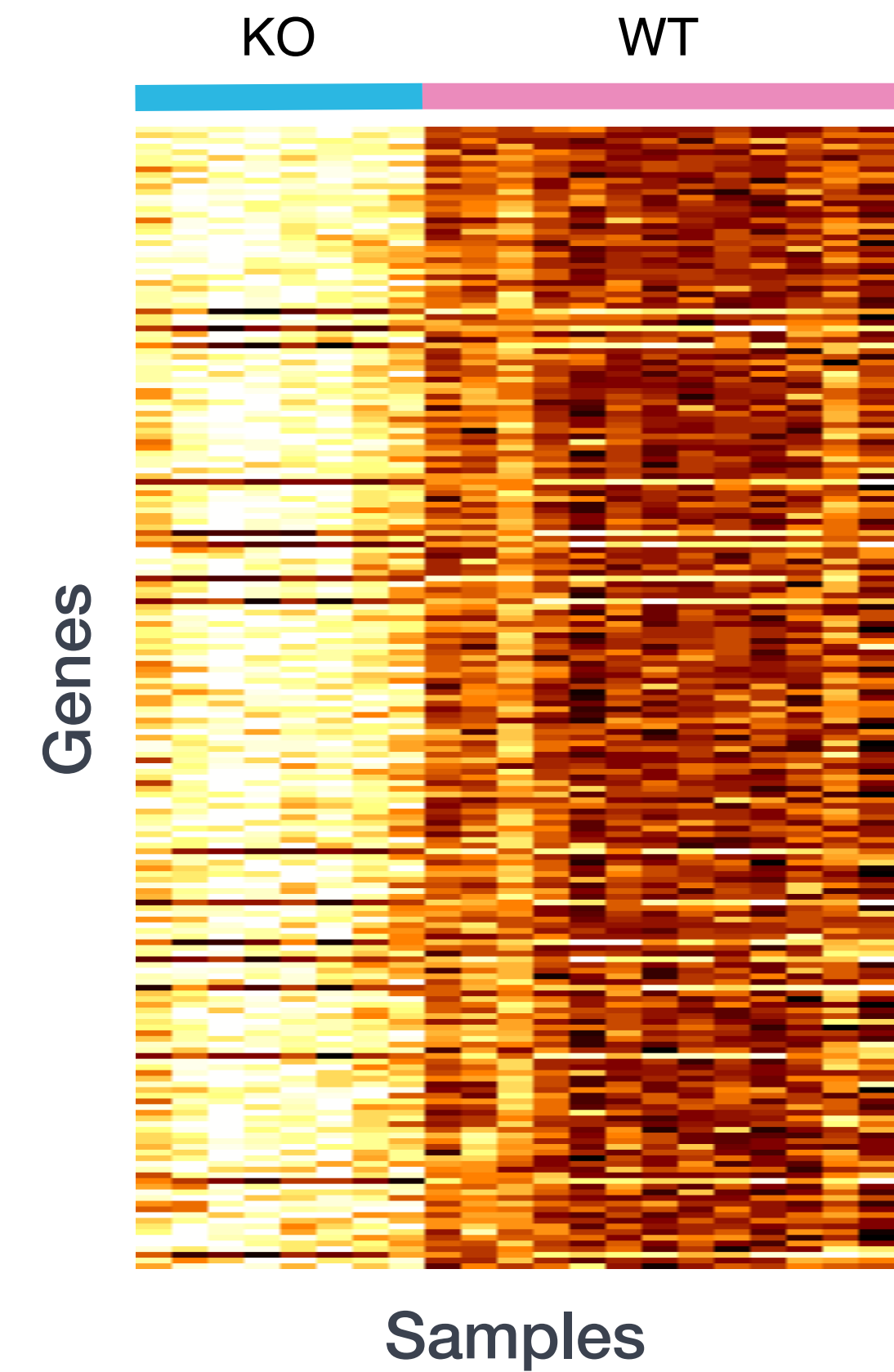
Genes with
zero counts

Genes with low mean
normalized counts
(‘Independent filtering’)



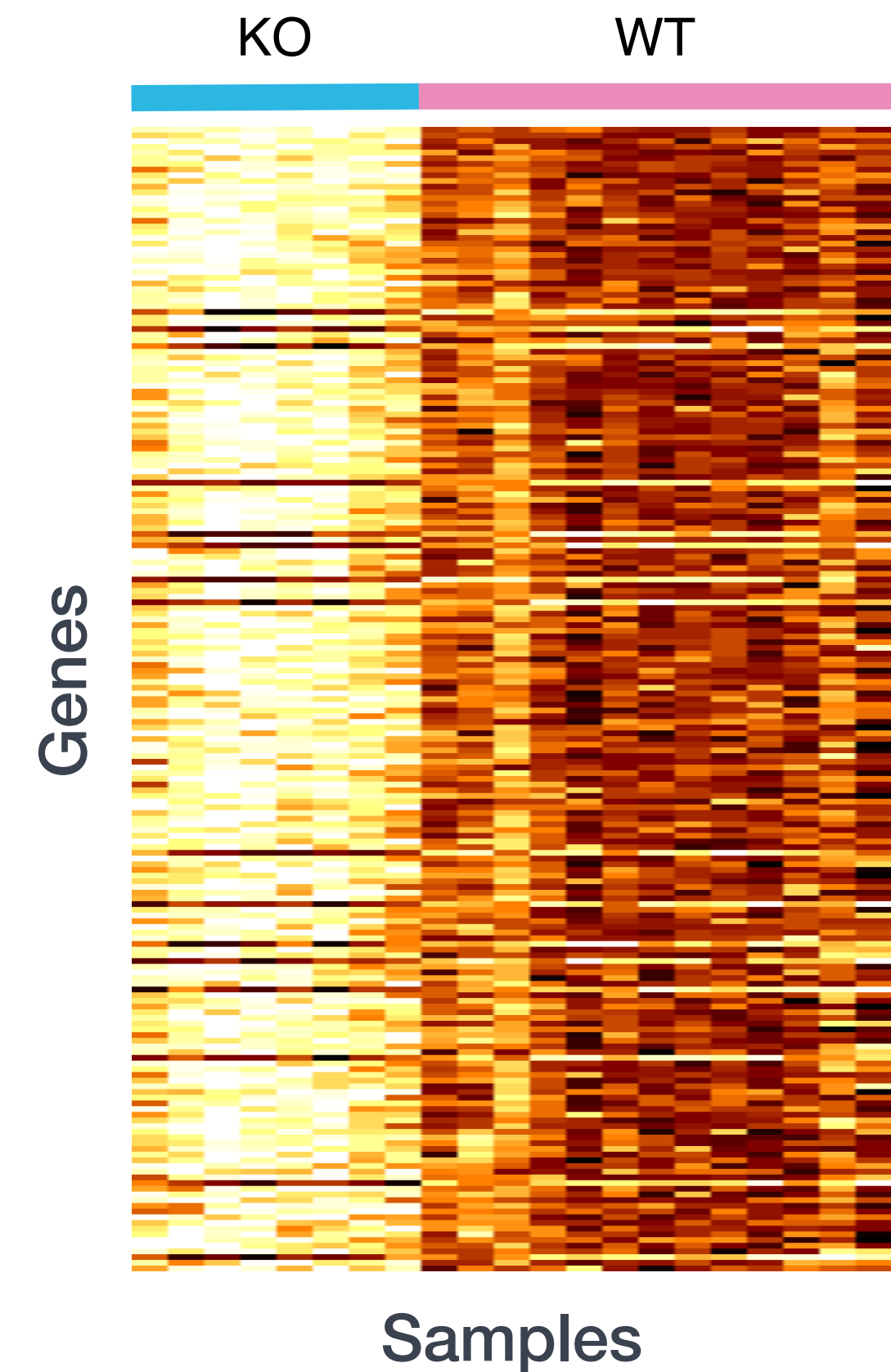
DE workflow :: differential expression

Identifying differences in gene expression



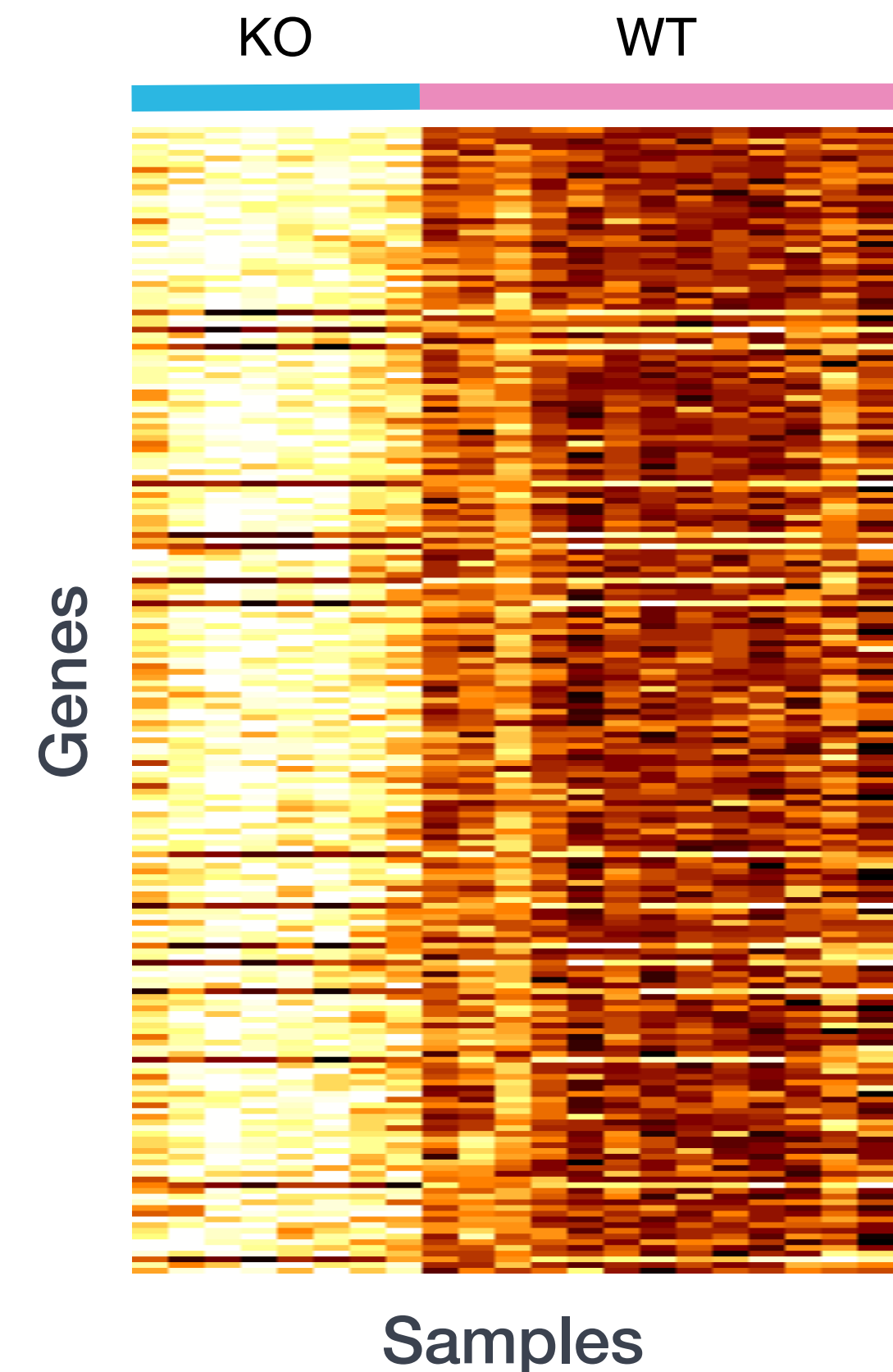
Identifying differences in gene expression

- ▶ Looking for genes that change in expression between two or more groups
 - ▶ case vs. control
 - ▶ correlation of expression with some variable or clinical outcome

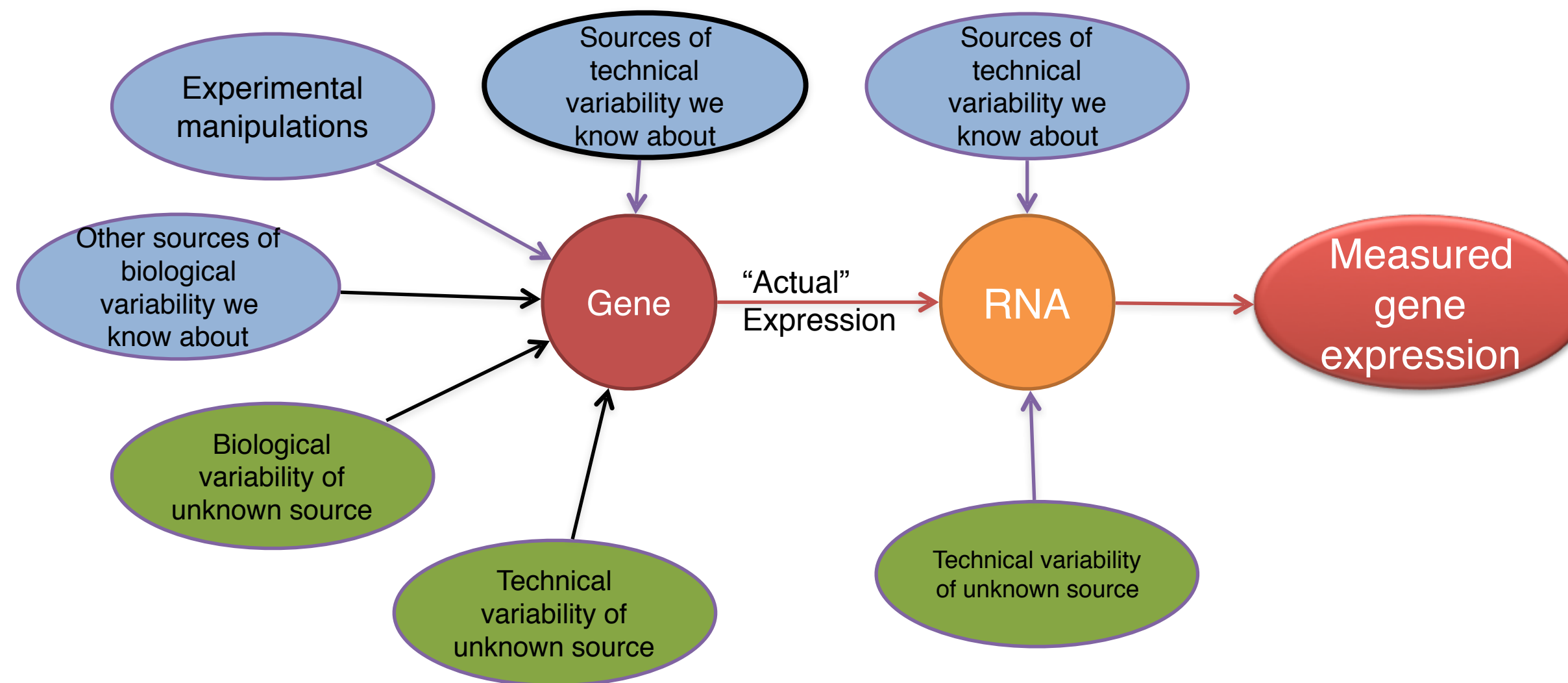


Identifying differences in gene expression

- ▶ Looking for genes that change in expression between two or more groups
 - ▶ case vs. control
 - ▶ correlation of expression with some variable or clinical outcome
- ▶ Rank the genes by how different they are between the two groups (based on fold change values). **Why does this not work?**



The measurement is the “sum” of many effects

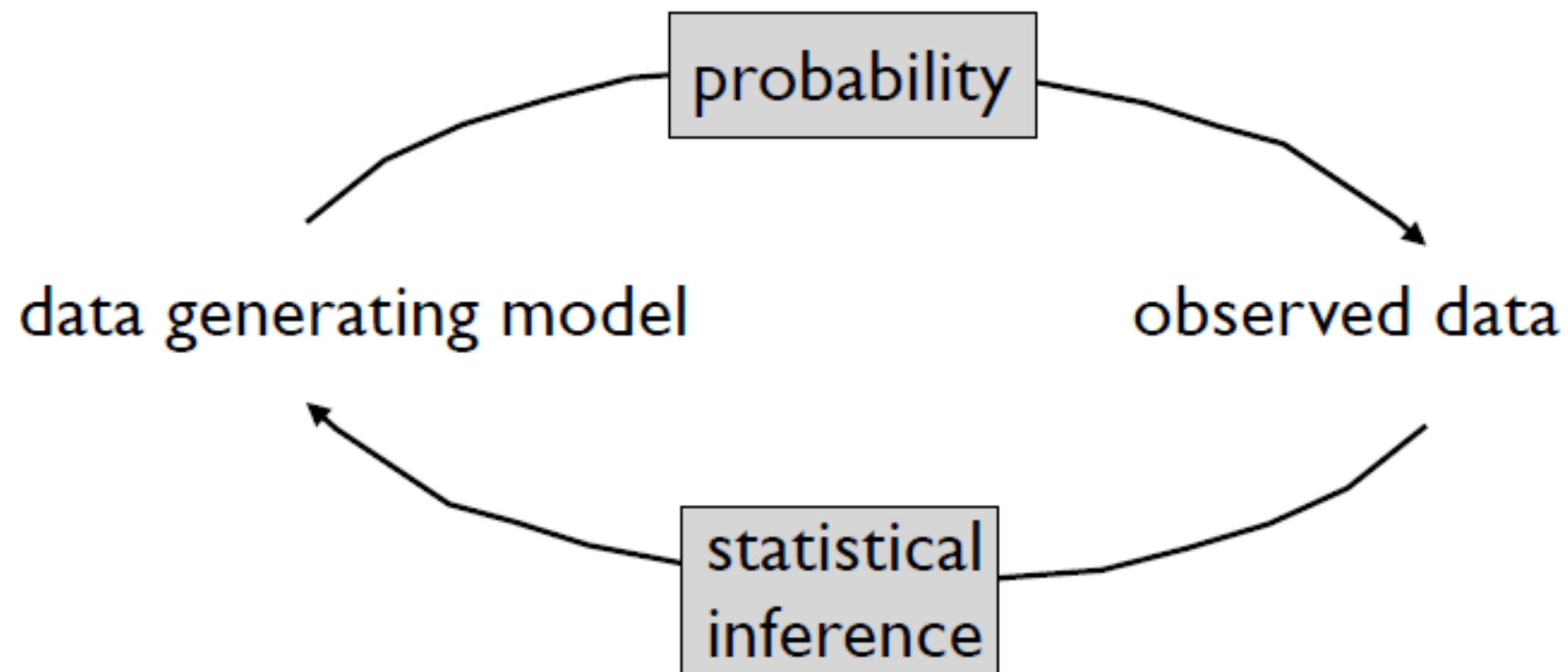


Modeling gene-level data

Courtesy of Paul Pavlidis, UBC

Making sense of data

Data is what we observe. We want to infer something about “where it came from”

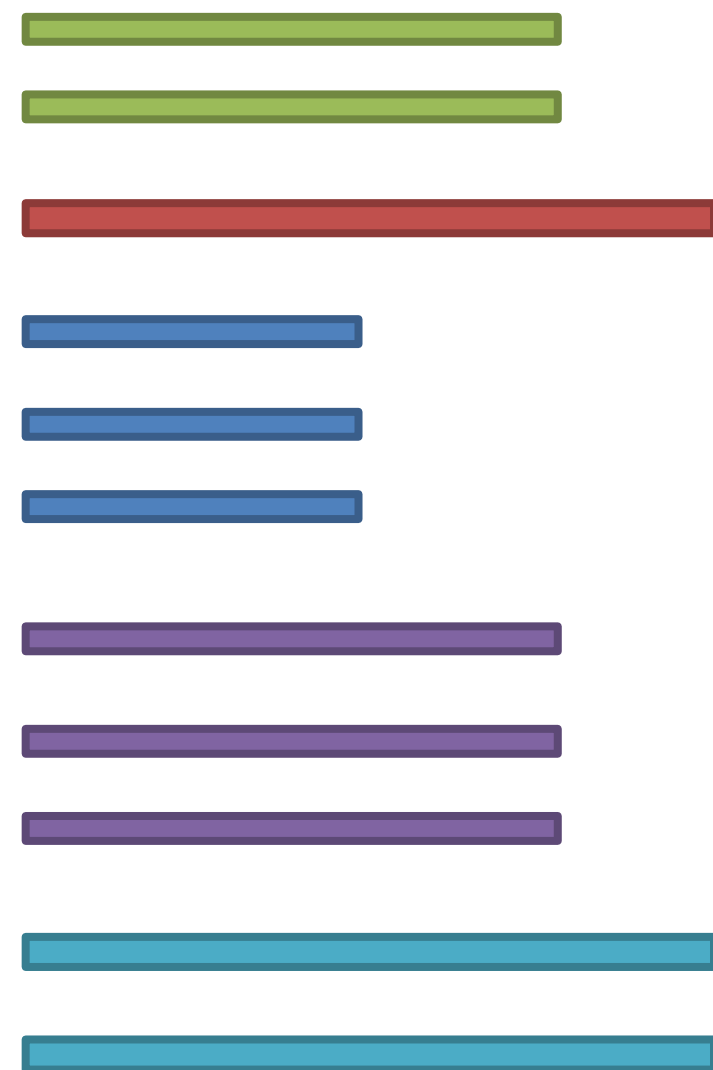


Characteristics of count data

- Discrete measurement for each gene
- Large dynamic range
- Not normally distributed
- Need regression models specific for count data; generalized linear models

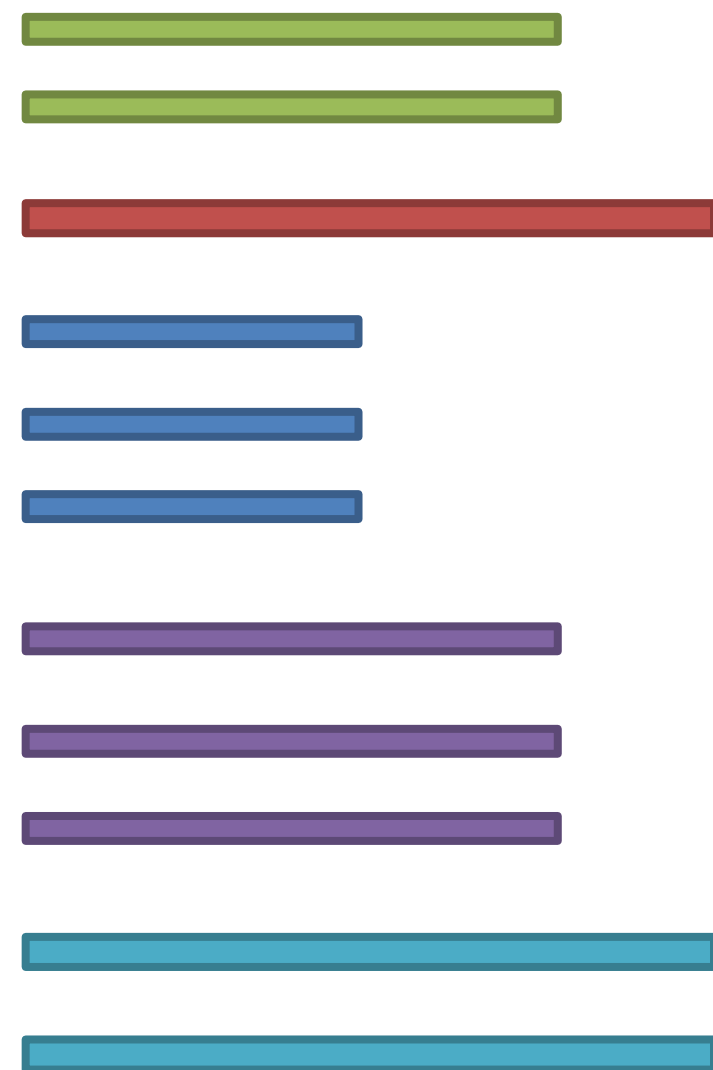
Distribution of Counts: Poisson versus Negative Binomial

If the proportions of mRNA stays exactly constant between biological replicates we can expect **Poisson distribution**.

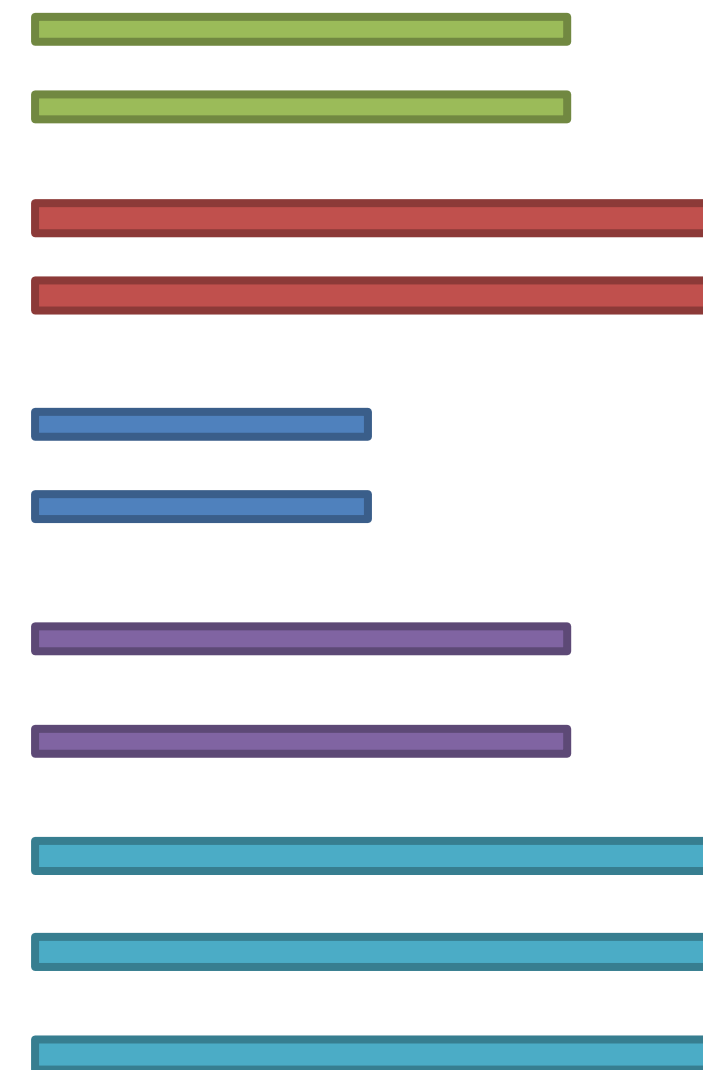


Distribution of Counts: Poisson versus Negative Binomial

If the proportions of mRNA stays exactly constant between biological replicates we can expect **Poisson distribution**.



But realistically, **biological variation** across sample units is expected and so a **Negative Binomial** distribution is more appropriate.



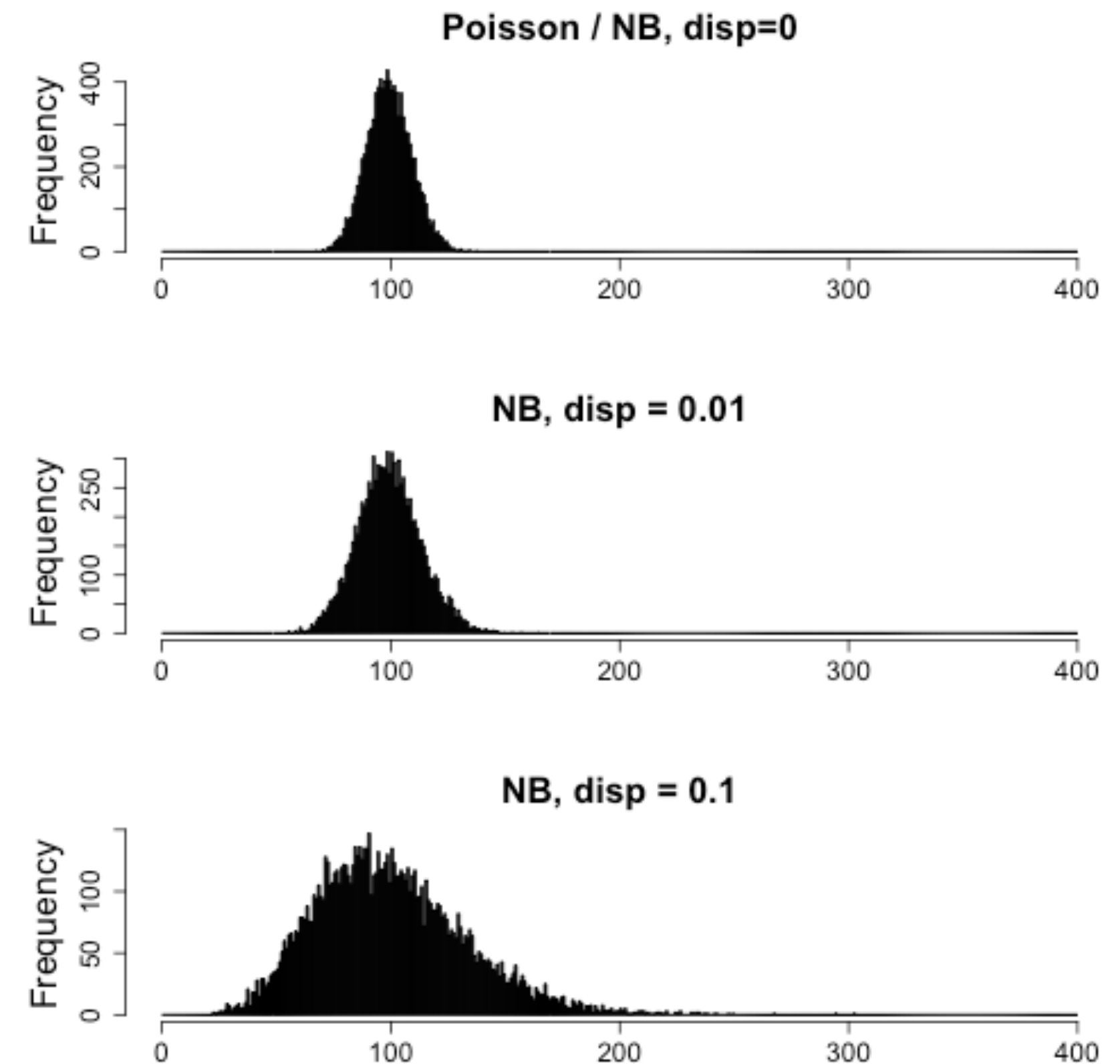
Biological vs. Technical Replicates

- ▶ **Biological replicates** represent multiple samples representing the same sample class
- ▶ **Technical replicates** represent the same sample but with technical steps replicated
- ▶ Usually **biological variance > technical variance**. They also allow us to make inferences about treatment groups

Biological replicates produce “over-dispersion” relative to Poisson

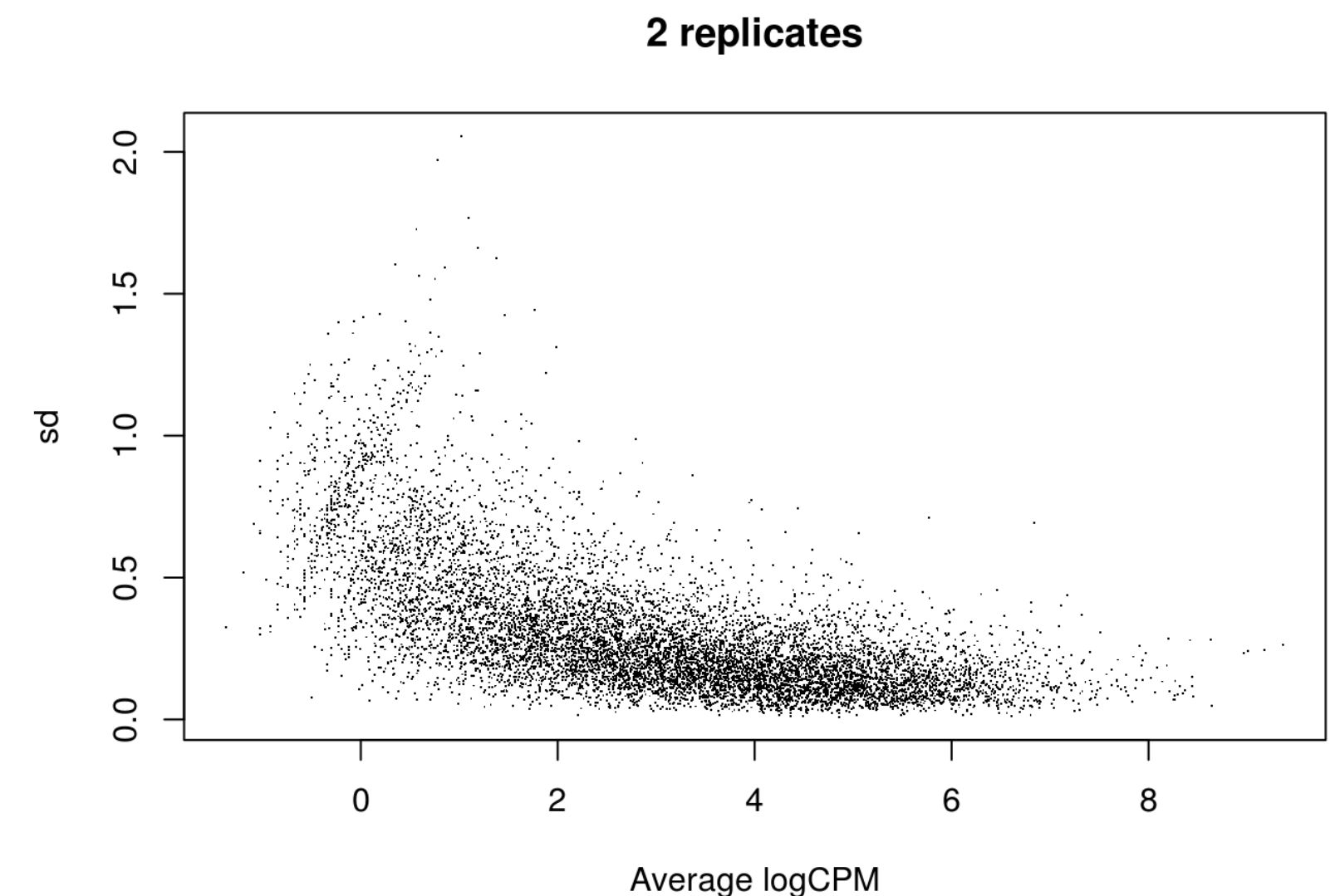
Poisson will underestimate the variability and the effect of the observed differences.

Instead we use the Negative Binomial.



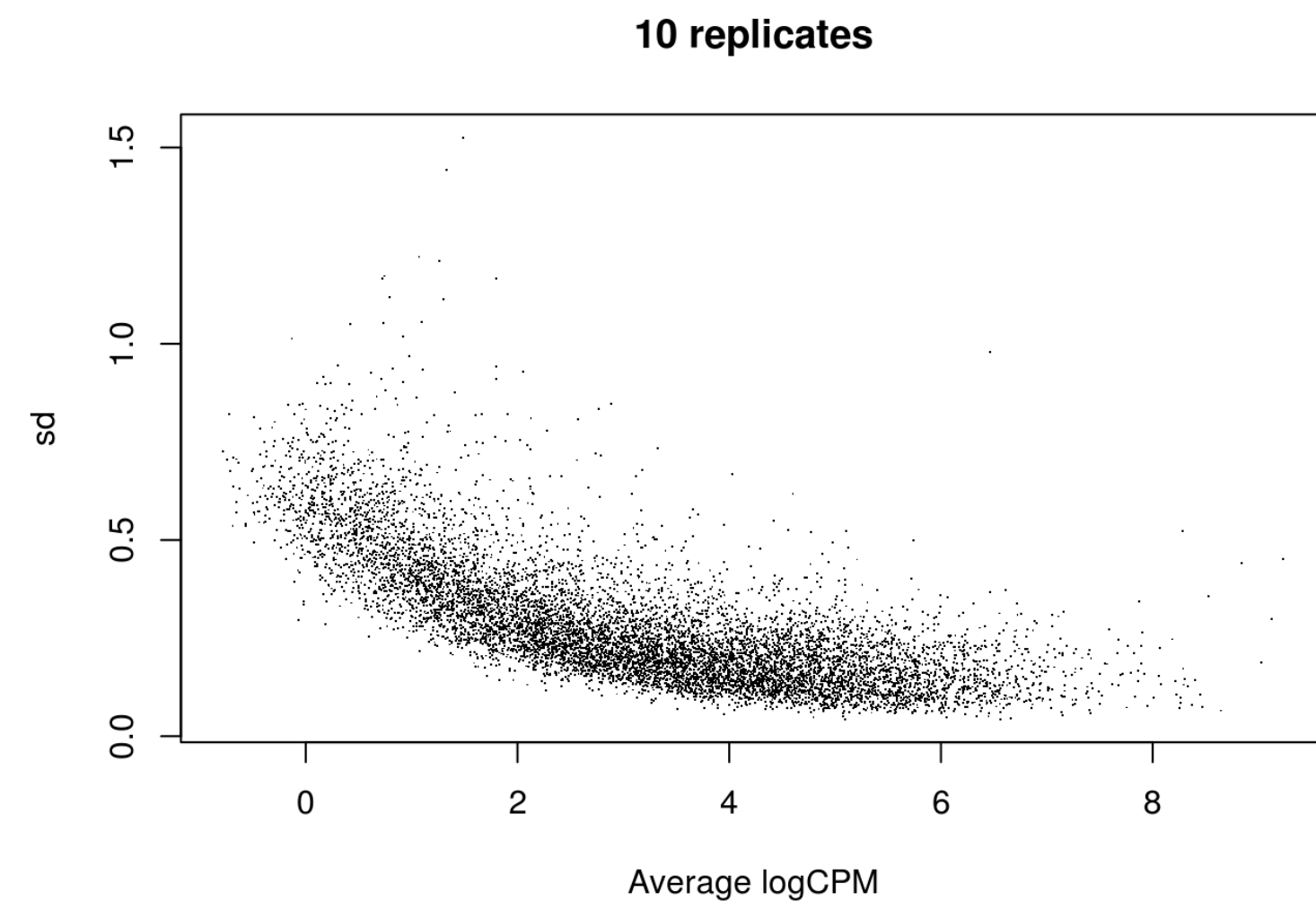
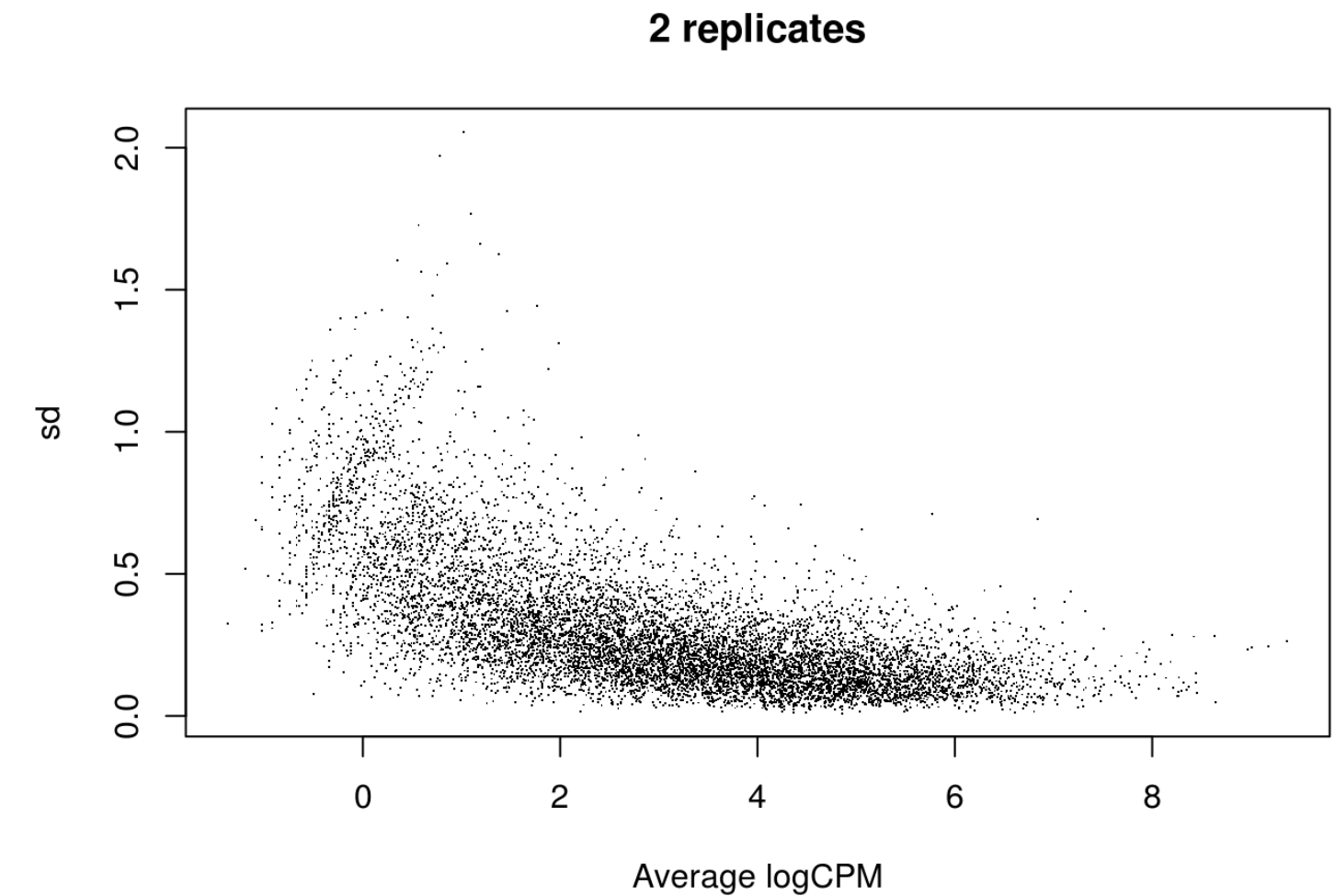
The need for more replicates

- ▶ Genes with larger average expression have on average larger observed variances across samples, This phenomena of 'having different scatter' is known as data heteroscedasticity.
- ▶ **Mean is not equal to variance**



Increase the number of replicates...

- ▶ Scatter tends to reduce
- ▶ Standard deviations of averages become smaller
- ▶ With smaller SD, you get more precise estimates of group means, and ultimately greater confidence in the ability to distinguish differences between sample classes



Counts are modeled using the Negative Binomial (NB) distribution

$$K_{ij} \sim \text{NB}(s_{ij}q_{ij}, \alpha_i)$$

We model read counts K_{ij} , as following the negative binomial distribution
with mean μ_i and **dispersion** α_i

Counts are modeled using the Negative Binomial (NB) distribution

raw count for gene i , sample j



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raw count for gene i , sample j

The mean is taken as a quantity of interest scaled by a normalization factor

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Counts are modeled using the Negative Binomial (NB) distribution

raw count for gene i , sample j

The mean is taken as a quantity of interest scaled by a normalization factor

one dispersion per gene

$$K_{ij} \sim \text{NB}\left(\overbrace{s_{ij} q_{ij}}^{\text{The mean is taken as a quantity of interest scaled by a normalization factor}}, \alpha_i\right)$$

We model read counts K_{ij} , as following the negative binomial distribution with mean μ_i and **dispersion** α_i

Within group variability is accounted for using the dispersion parameter

The **dispersion parameter** α_i , describes the variance of counts via:

$$\text{Var}(K_{ij}) = \mu_{ij} + \alpha_i \mu_{ij}^2$$



Poisson part:
sampling fragments

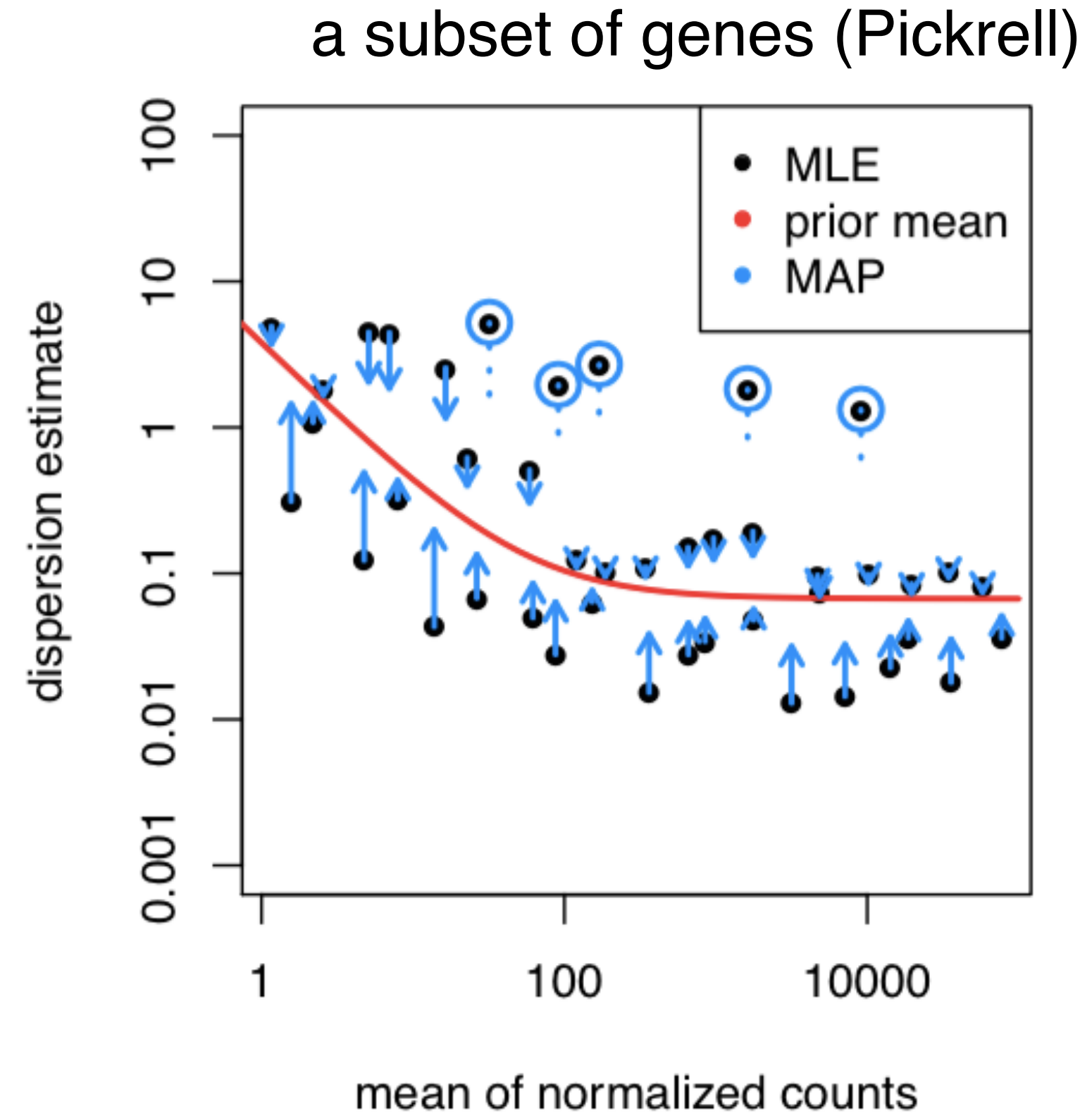
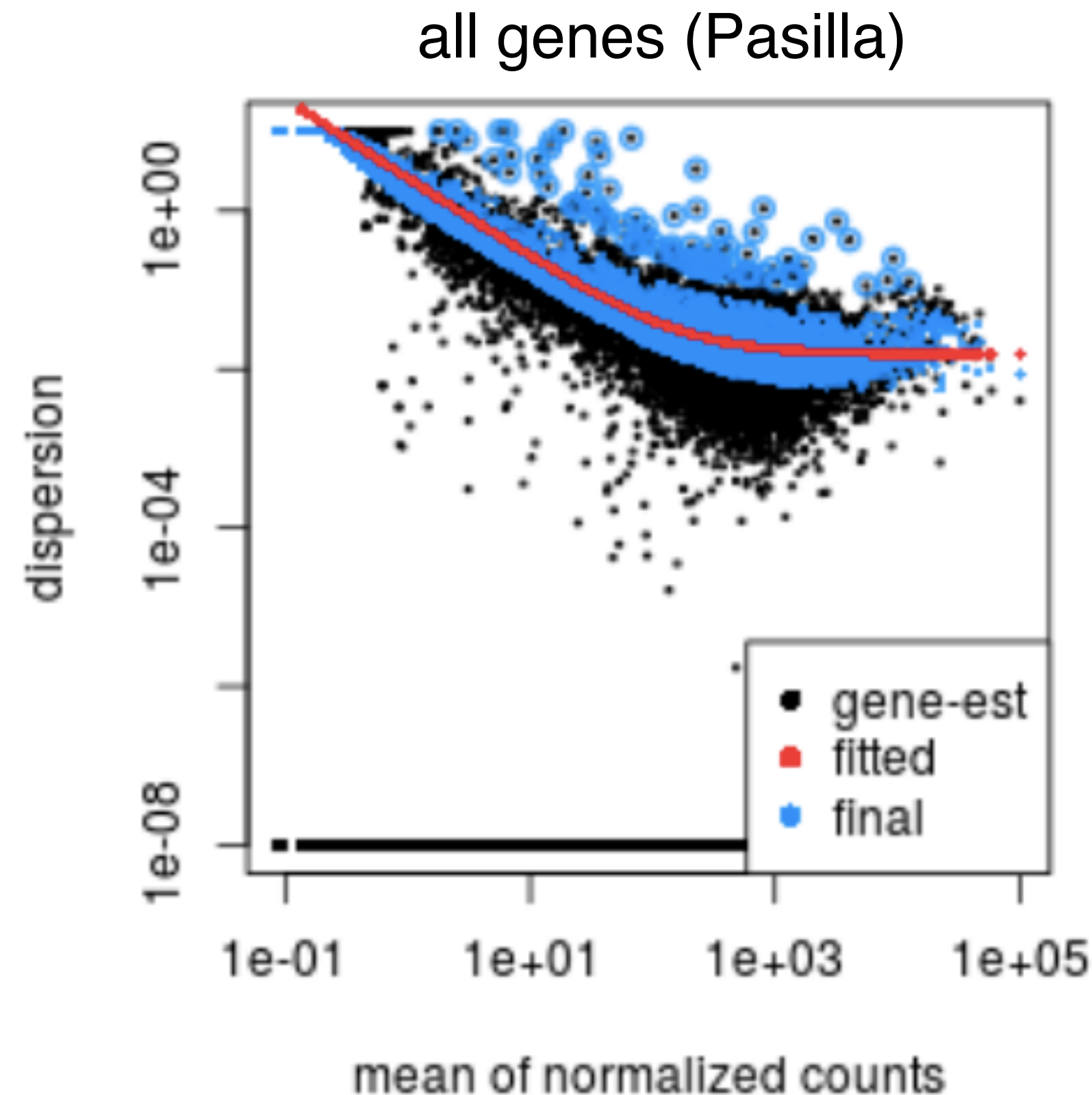


Extra variation
due to biological variance

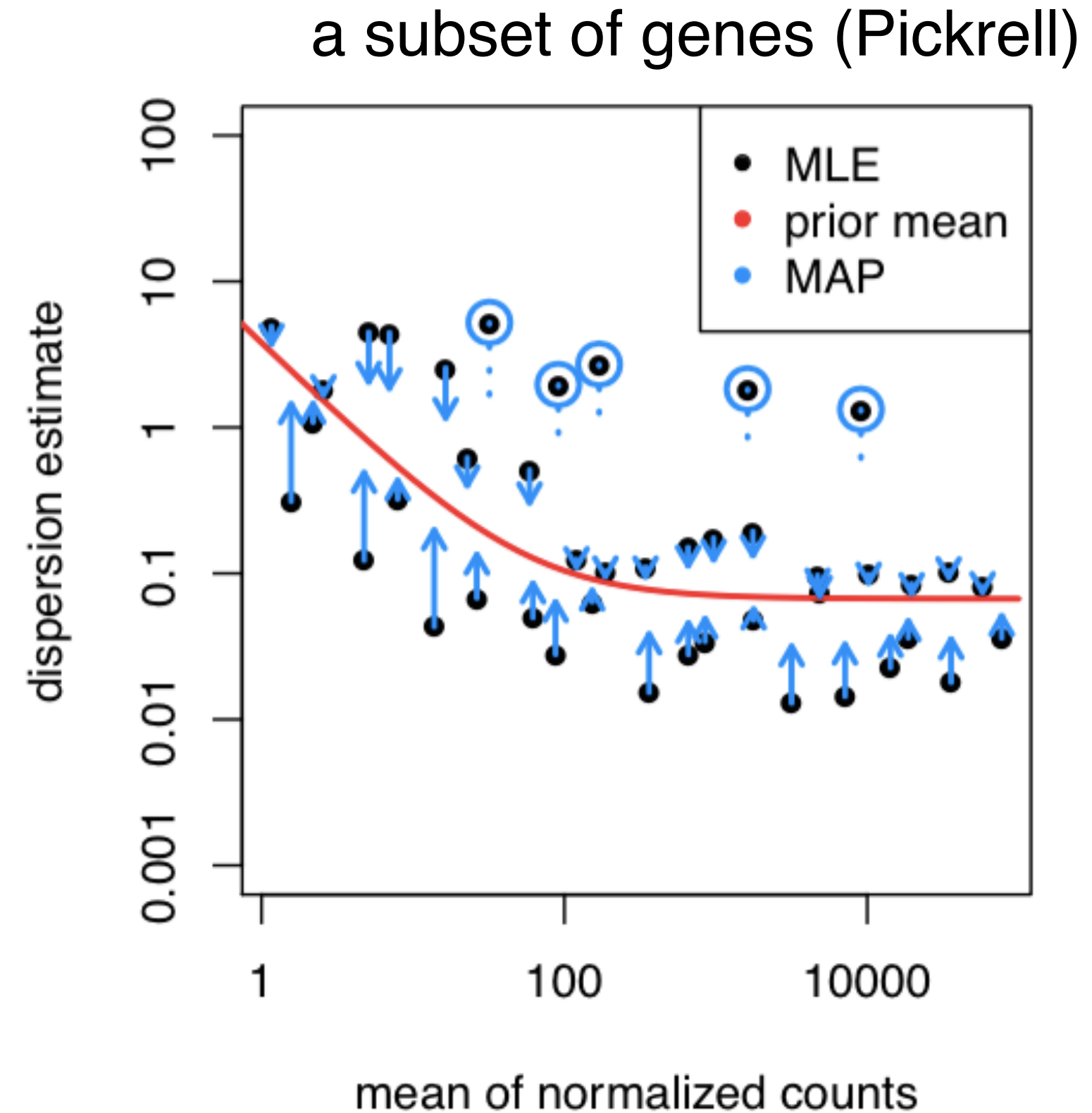
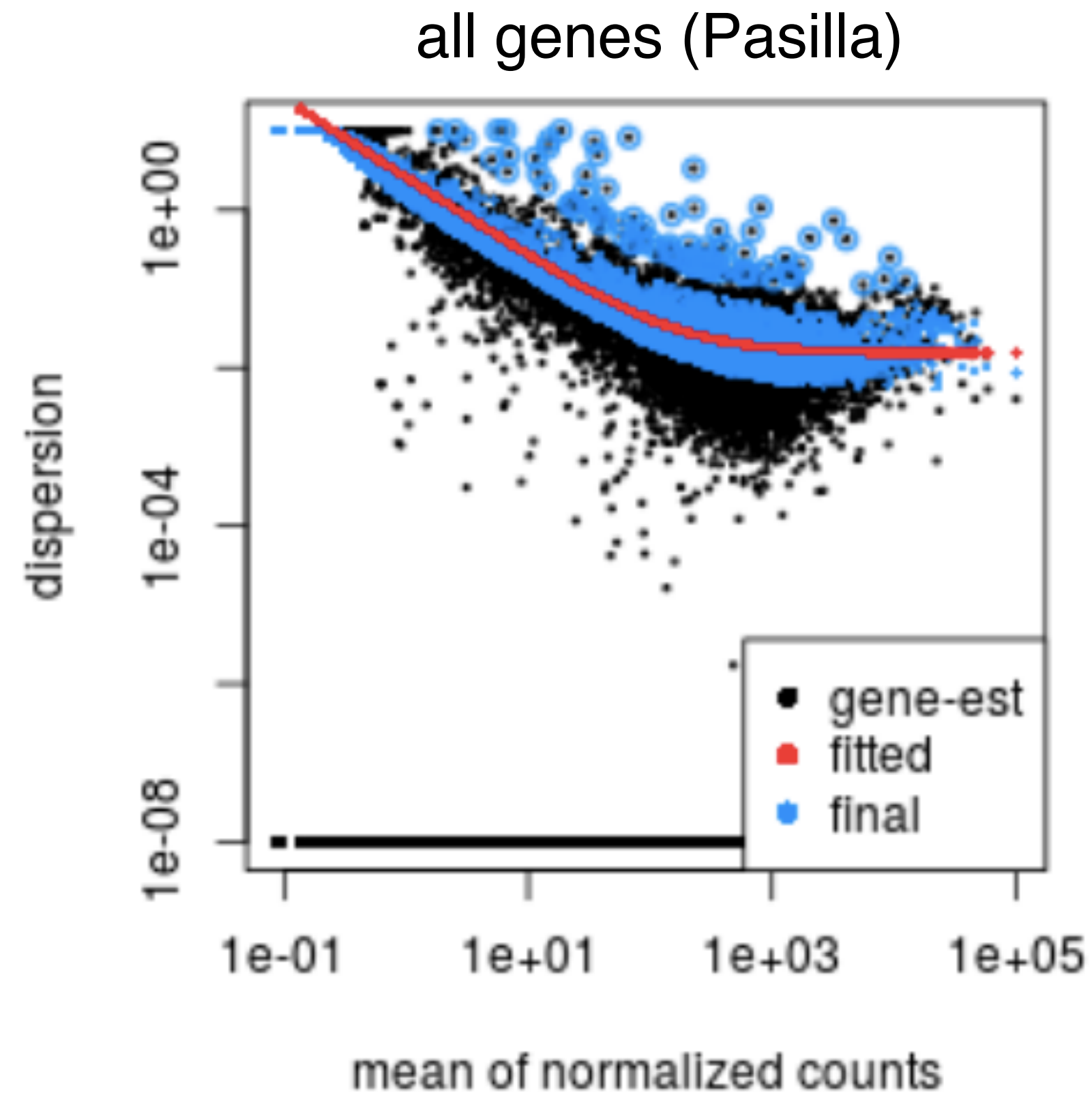
Shrinkage and dispersion

- Different genes naturally have different scales of biological variability
- Over all genes, there will be a distribution of reasonable estimates of dispersion
- With small sample size ($n=3-5$ replicates per group), we will make *very bad* estimates of gene-wise dispersion unless we **share information across genes**

Shrinkage of dispersion



1. Gene-wise estimate = just look at one gene (MLE)
2. Fitted dispersion trend = the middle for the prior
3. Final estimate = posterior, uses shared information (MAP)



The shrinkage procedure thereby helps avoid potential false positives, which can result from underestimates of dispersion

Differences across conditions

DESeq2

- Available through Bioconductor since 2013
- Publication: Genome Biology, Dec 2014.
main text written with non-statisticians in mind
- Builds on good ideas for dispersion estimation and use of GLM from the [DSS](#) and [edgeR](#) methods
- See bioconductor.org/install for installation
- Note that the latest Bioconductor packages are only available with **latest R version**. Bioconductor and R versions are *linked*

DESeq2 steps

count matrix (from featureCounts, htseq, tximport, etc.)



1. size factors (sequencing depth)
2. dispersion (biological variance)
3. *Wald* test or *likelihood ratio* test
4. build results table



Normalization



QC (gene-level and sample-level)



Differential expression analysis

Estimate size factors



Gene-wise dispersion estimation (ML)

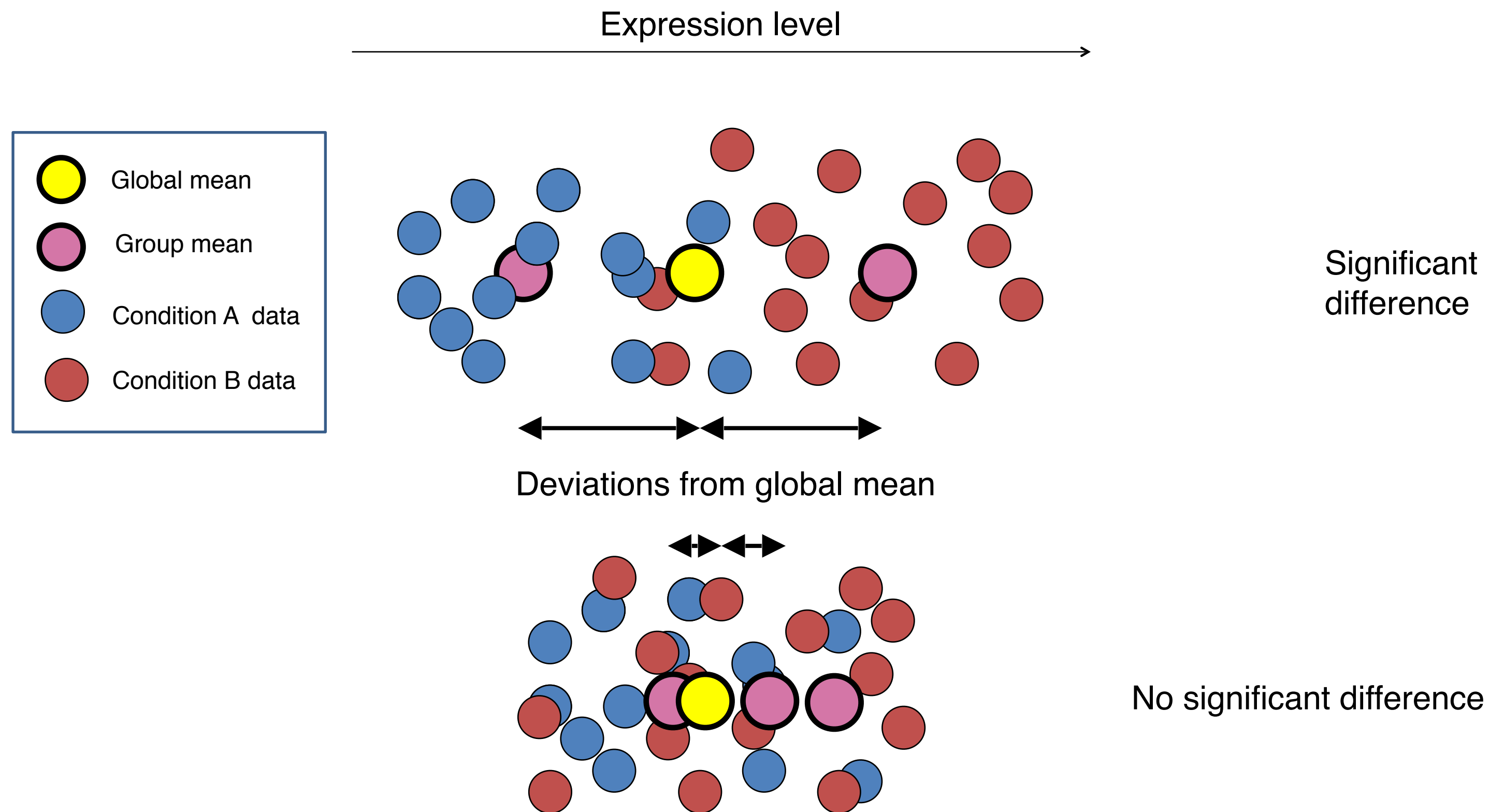


Shrink gene-wise dispersion estimates



GLM fit for each gene

Differences across two conditions



Differences across two conditions

- Describe experiment with formula, e.g.: ~ condition
- Per gene the design matrix looks like:

$$\begin{array}{lcl} \log_2 q1 & & 1 \quad 0 \\ \log_2 q2 & & 1 \quad 0 \\ \log_2 q3 & = & 1 \quad 1 \\ \log_2 q4 & & 1 \quad 1 \end{array}$$

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$$\begin{array}{l} \log_2 q1 \\ \log_2 q2 \\ \log_2 q3 \\ \log_2 q4 \end{array} = \begin{array}{|c|c|} \hline 1 & 0 \\ \hline 1 & 0 \\ \hline 1 & 1 \\ \hline 1 & 1 \\ \hline \end{array} \quad \boxed{\text{Intercept}}$$

All samples get an Intercept term

Differences across two conditions

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All samples get an Intercept term

The B condition samples also get a term that accounts for the difference between B and A

Differences across multiple conditions

- The design matrix now uses a column for each condition

$\log_2 q1$		1	1	0	0	
$\log_2 q2$		1	1	0	0	Intercept
$\log_2 q3$	=	1	0	1	0	conditionA
$\log_2 q4$		1	0	1	0	conditionB
$\log_2 q5$		1	0	0	1	conditionC
$\log_2 q6$		1	0	0	1	

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GLM: Generalized linear models

- ▶ Extension of linear models to non-normally distributed response data (in our case, negative binomial)
- ▶ Helps address the different mean-variance relationships
- ▶ GLM fit for a gene will return **coefficients indicating the overall expression** strength of the gene for each design matrix element

Contrasts

- A contrast is the comparison of coefficients we choose to evaluate

$\log_2 q1$		1	1	0	0	
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$\log_2 q3$	=	1	0	1	0	conditionA
$\log_2 q4$		1	0	1	0	conditionB
$\log_2 q5$		1	0	0	1	conditionC
$\log_2 q6$		1	0	0	1	

```
results(dds, contrast=c("condition", "B", "C"))
```

Hypothesis testing

Wald test

- ▶ use the shrunken estimate of the \log_2 fold-change divided by the SE
- ▶ this gives a Z-statistic which is compared to a standard normal distribution
- ▶ allows testing of individual coefficients, or contrasts of coefficients (i.e. two-level comparison)

Hypothesis testing

Wald test

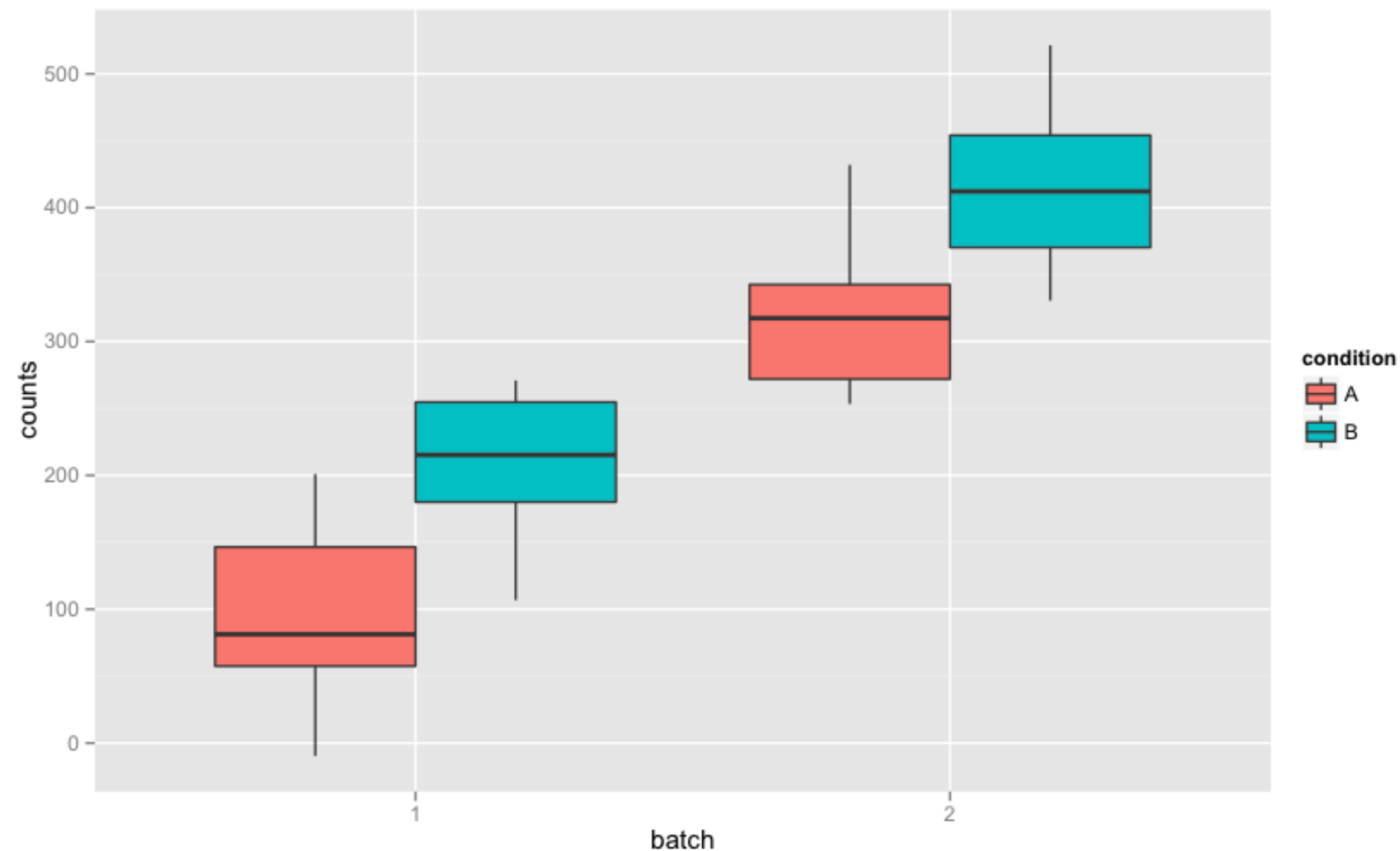
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Likelihood ratio test (LRT)

- ▶ examines two different models: full and reduced model (with some terms removed)
- ▶ determines if the increased likelihood of the data using the extra terms in the full model is more than expected if those extra terms are truly zero
- ▶ useful for identifying any gene that is changing in expression with respect to the biological factor of interest (useful for 3 or more levels)

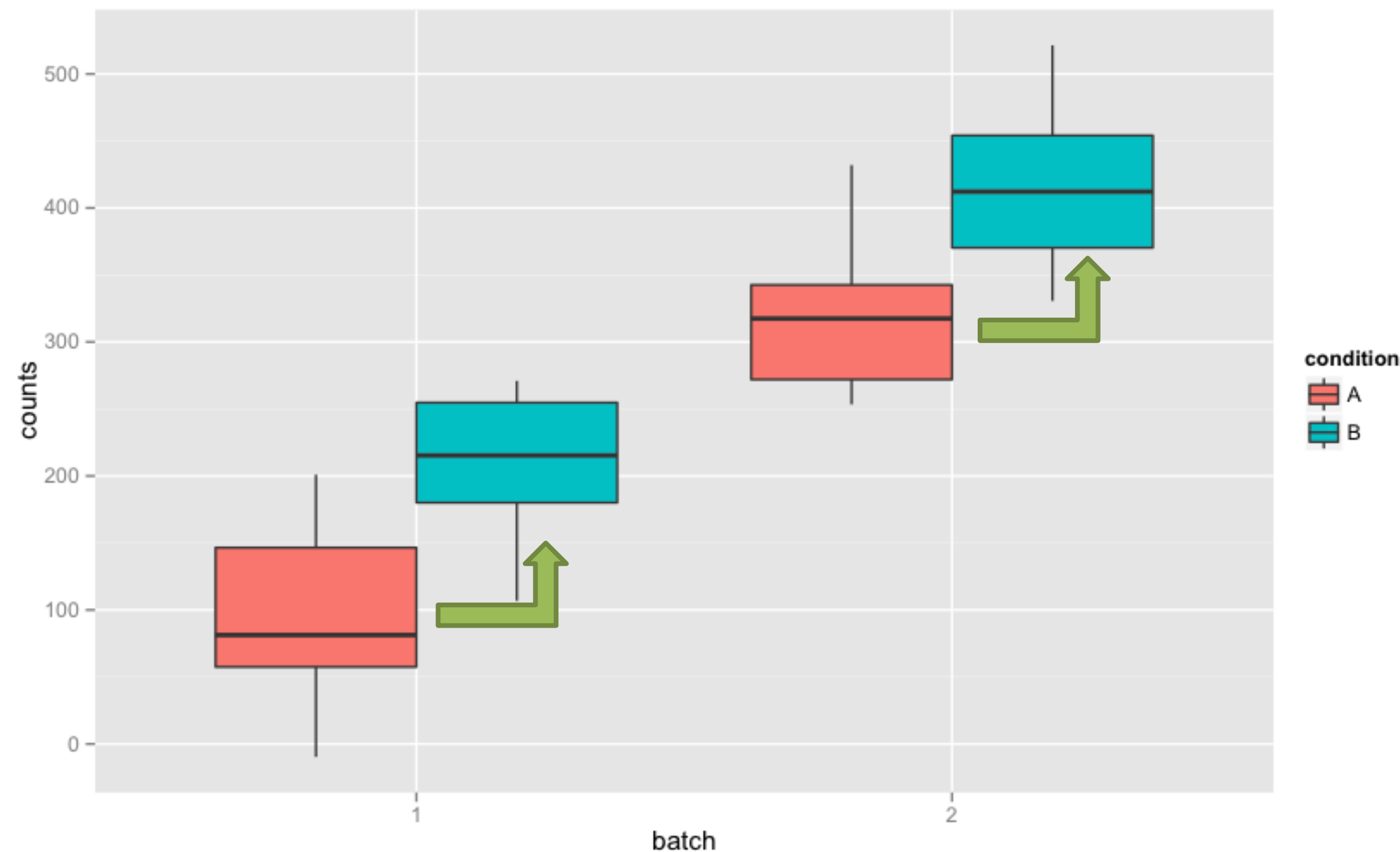
Controlling for different batches

- Using a design formula: $\sim \text{batch} + \text{condition}$, adds terms that control for batch differences
- If batches are unknown, possible to detect these with other methods: [svaseq](#), [RUVSeq](#)



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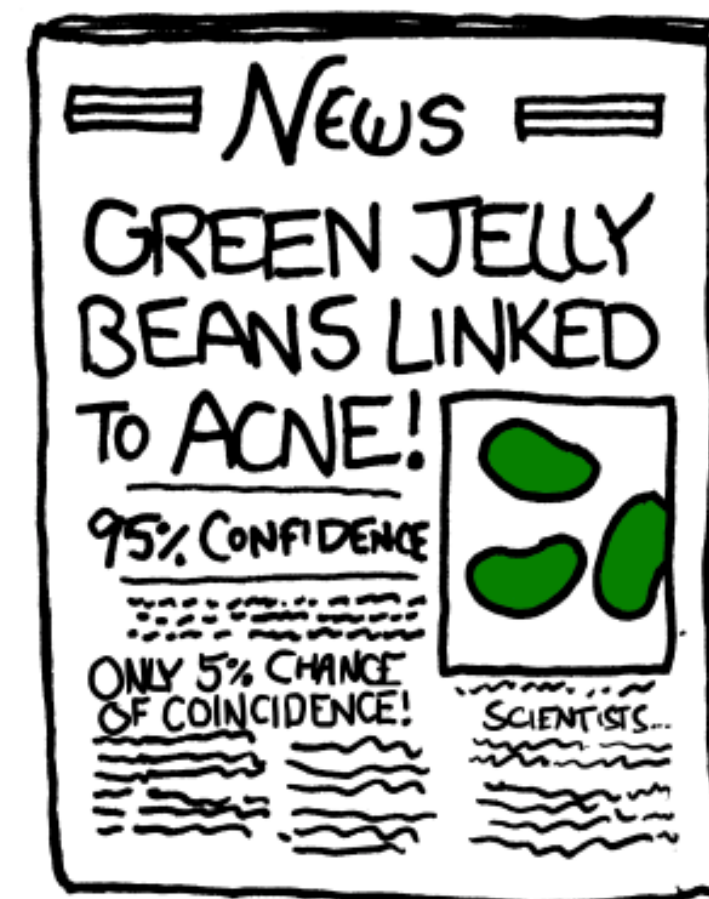
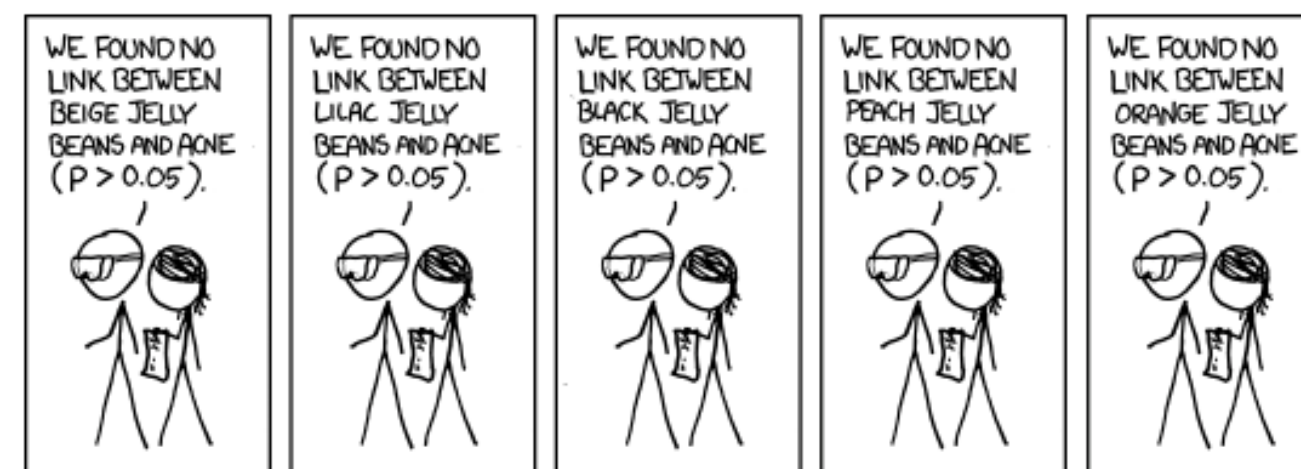
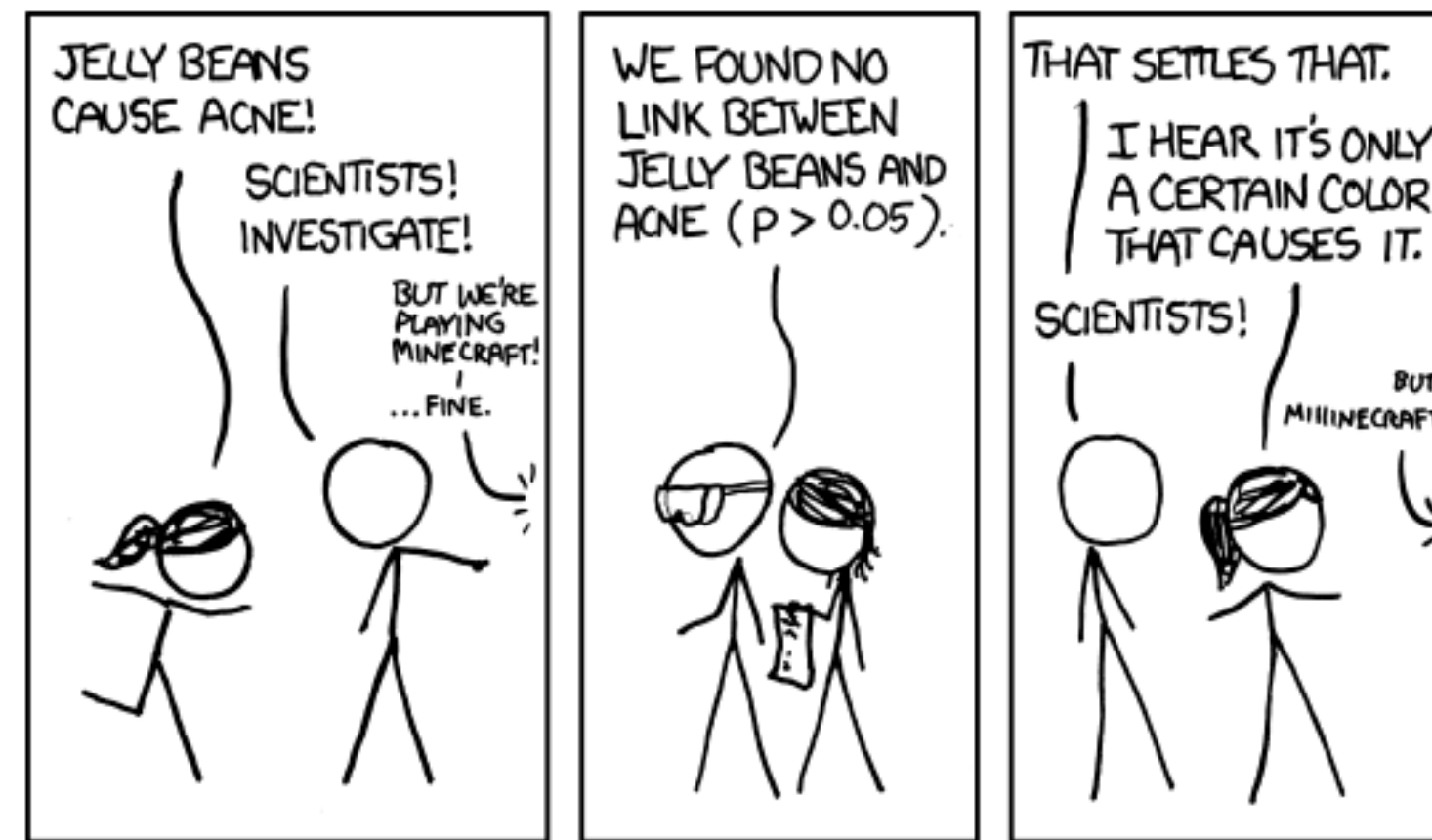
Complex designs

Want to test: treatment changes for enriched samples over baseline, controlling for individual effects

~individual + enrichment + treatment +
enrichment:treatment

indiv	.	enrich.	treat.
1	input	control	
1	IP	control	
1	input	treat	
1	IP	treat	
2	input	control	
2	IP	control	
2	input	treat	
2	IP	treat	
...			

Multiple test correction



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This is the multiple testing problem. The more tests we perform, the more we inflate the number of false positives observed.

Multiple test correction

Controlling the FWER

- ▶ Control α , the probability of making an error (false positive)
- ▶ **Bonferroni:** Reject any hypothesis with $p\text{-value} \leq \alpha/m$
 - ▶ Conservative; high probability of false negatives

Controlling the FDR

- ▶ FDR: false discovery rate: the expected percent of false predictions in the set of predictions
- ▶ **Benjamini-Hochberg:** Rank j / m multiplied by the FDR level
 - ▶ designed to control the FDR
- ▶ **Q-value:** The minimum FDR that can be attained when calling that feature significant

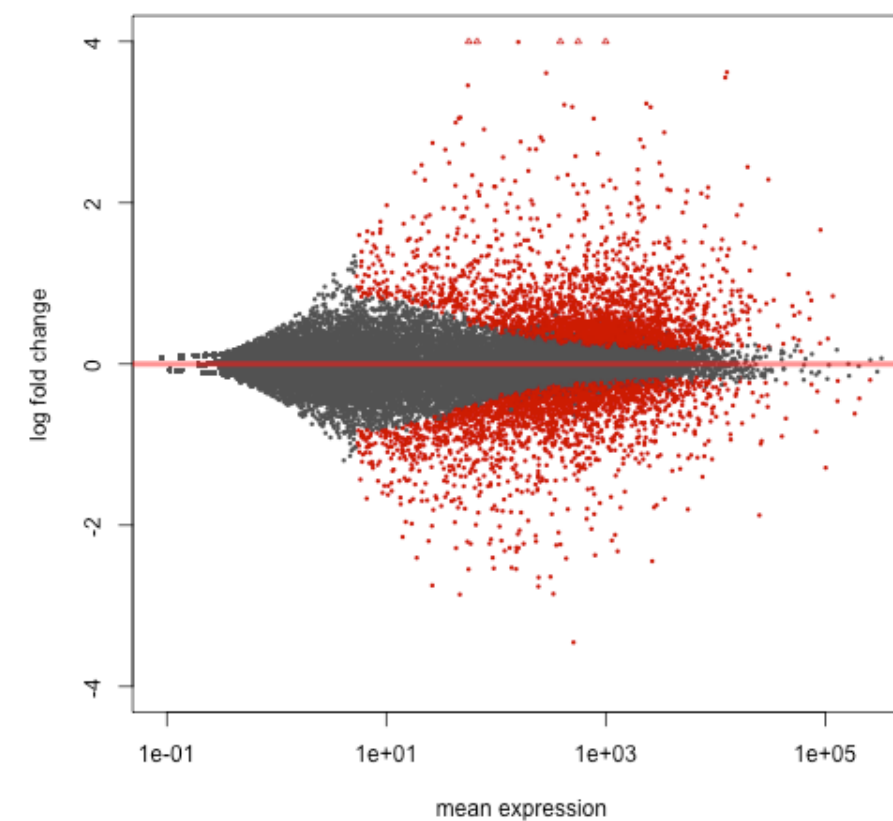
DE vs EDA

Two paths in DESeq2

Count matrix

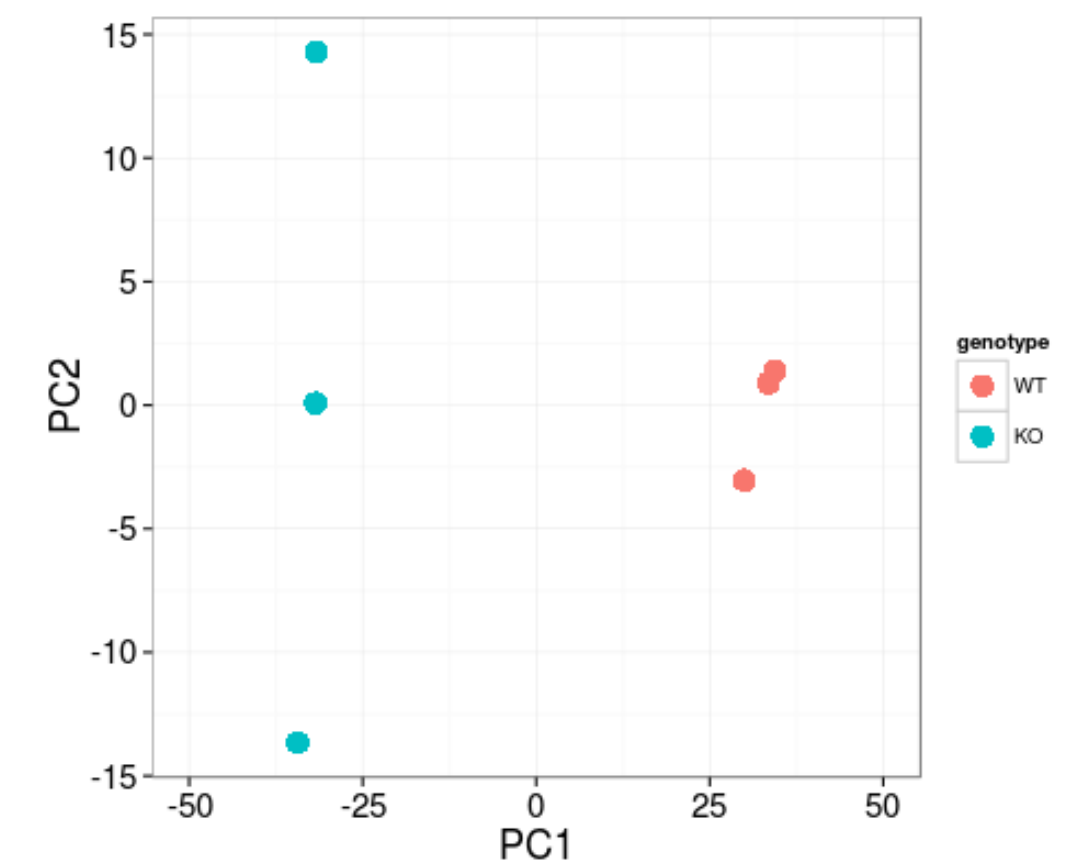
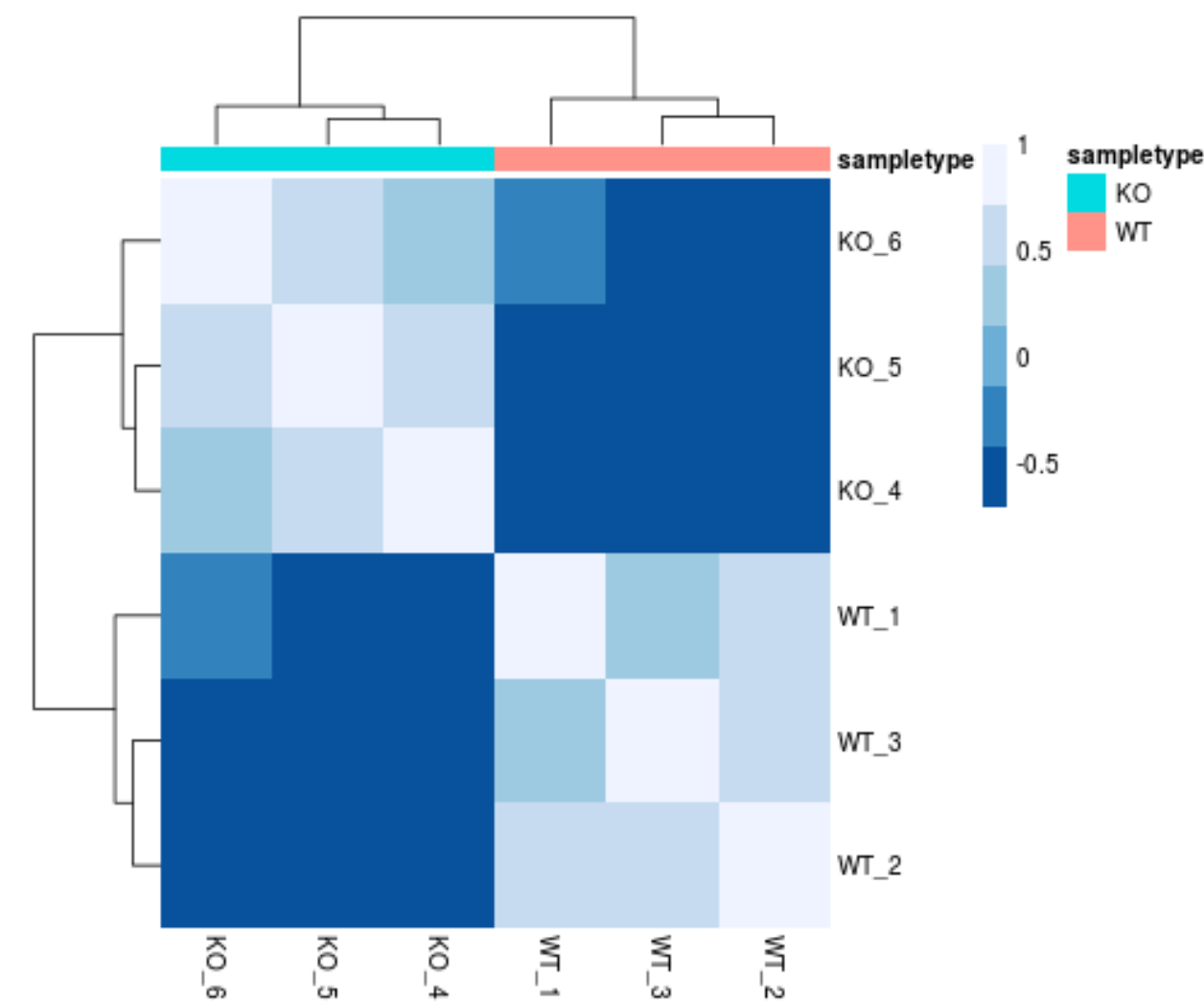
Differential expression

testing, p-values, FDR



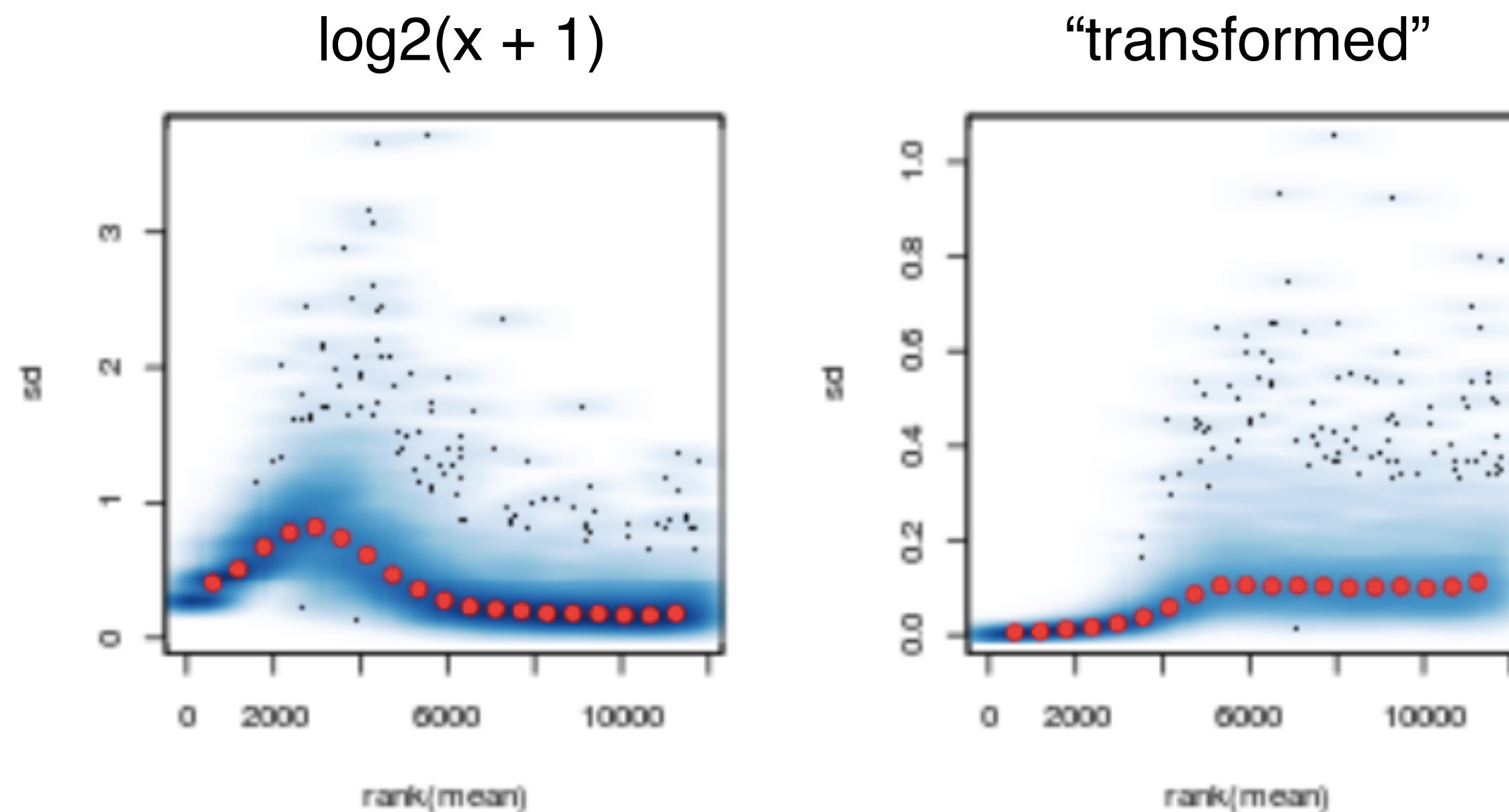
Transformations and
Exploratory Data Analysis (EDA)

clustering, heatmaps,
sample-sample distances



Transformations

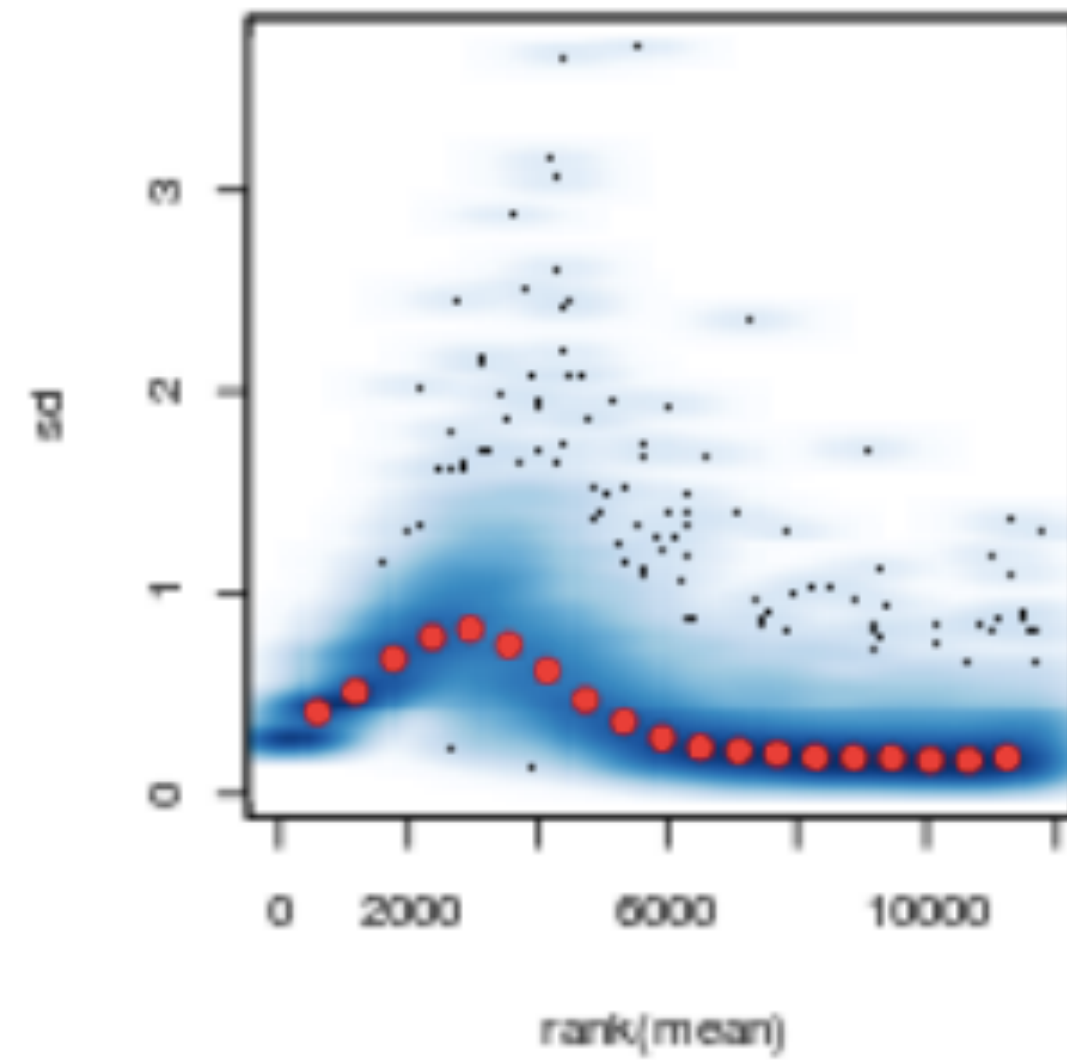
For comparison analyses when using unsupervised techniques, it can be useful to *transform* data. These techniques (VST and rlog) perform better when values have a similar dynamic range



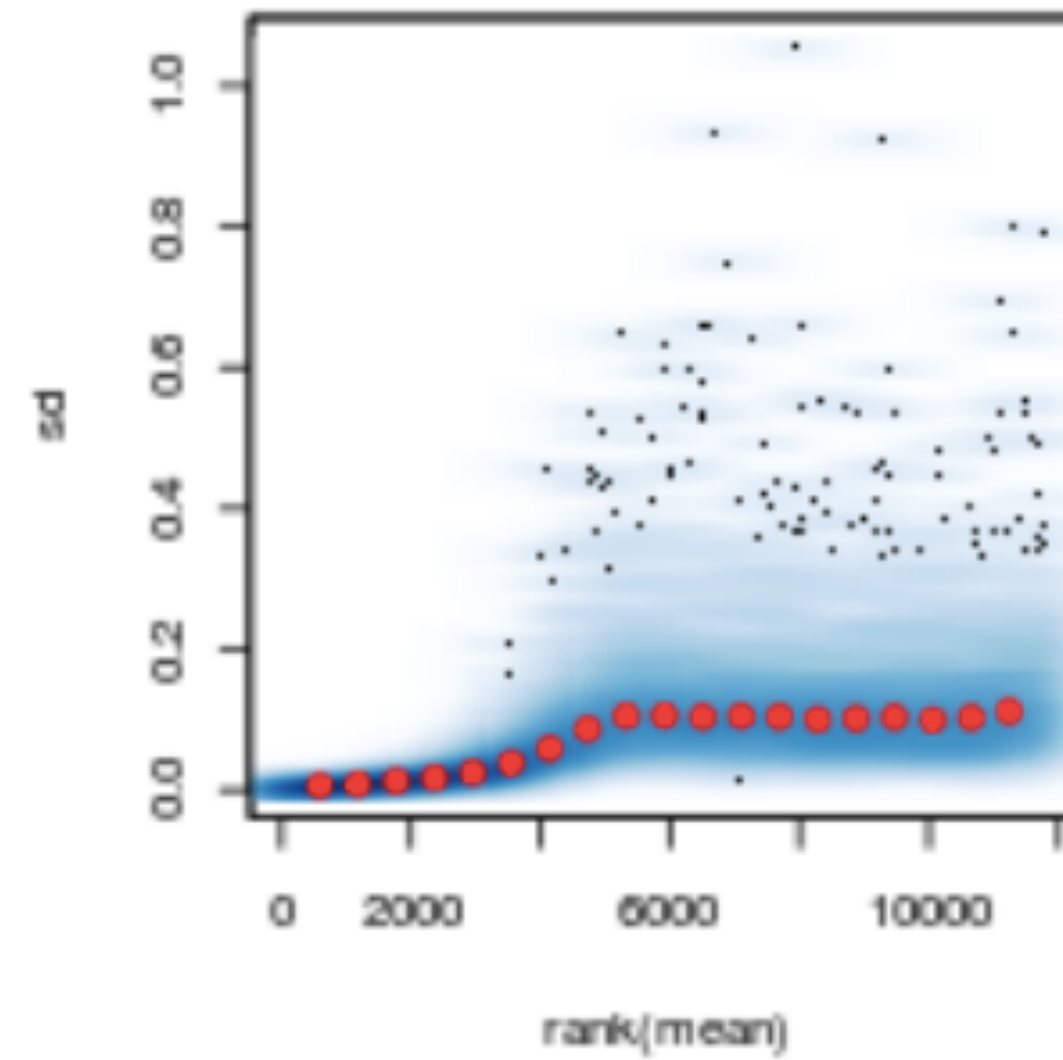
renders data *homoskedastic*
(variance of the gene is
stabilized across expression
levels)

rlog stabilizes variances along the mean

$\log_2(x + 1)$

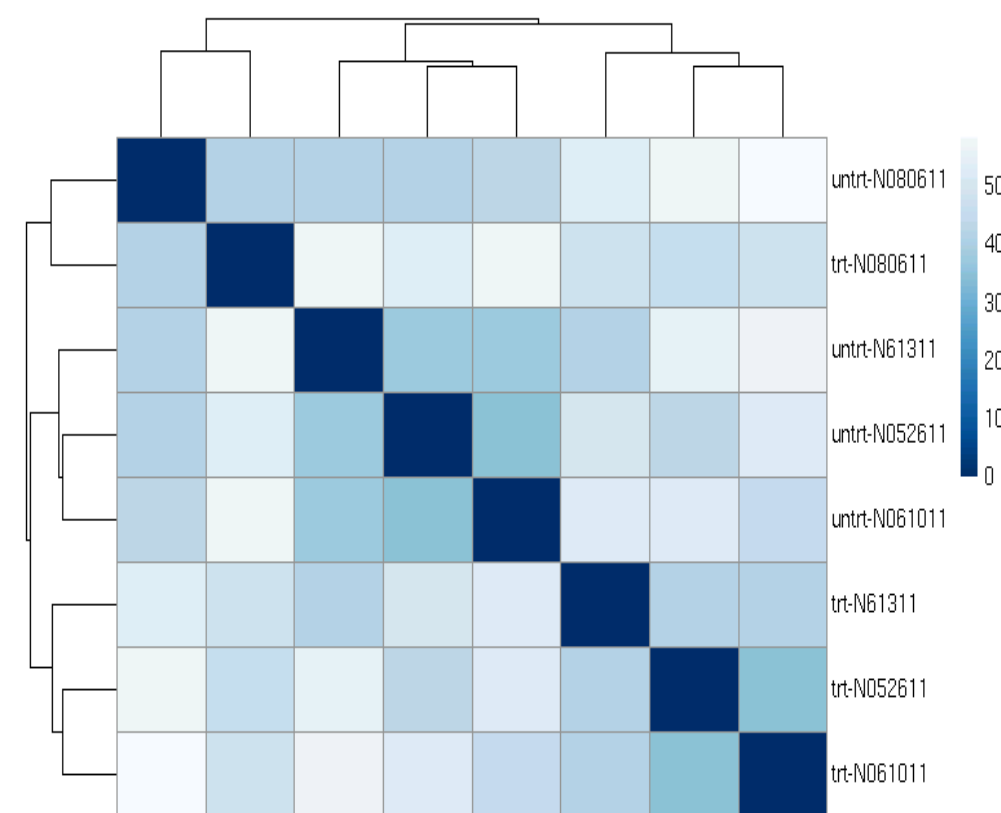
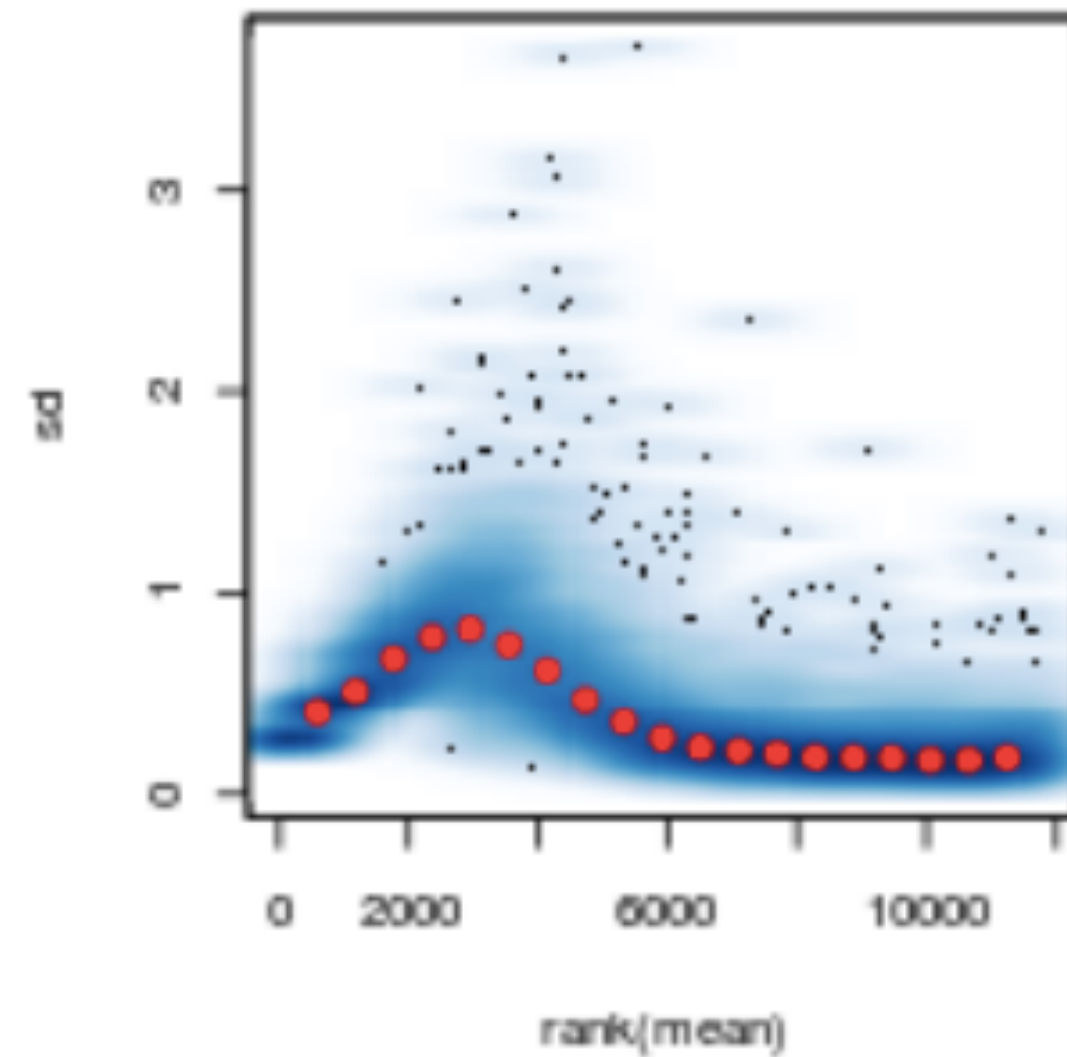


"rlog"

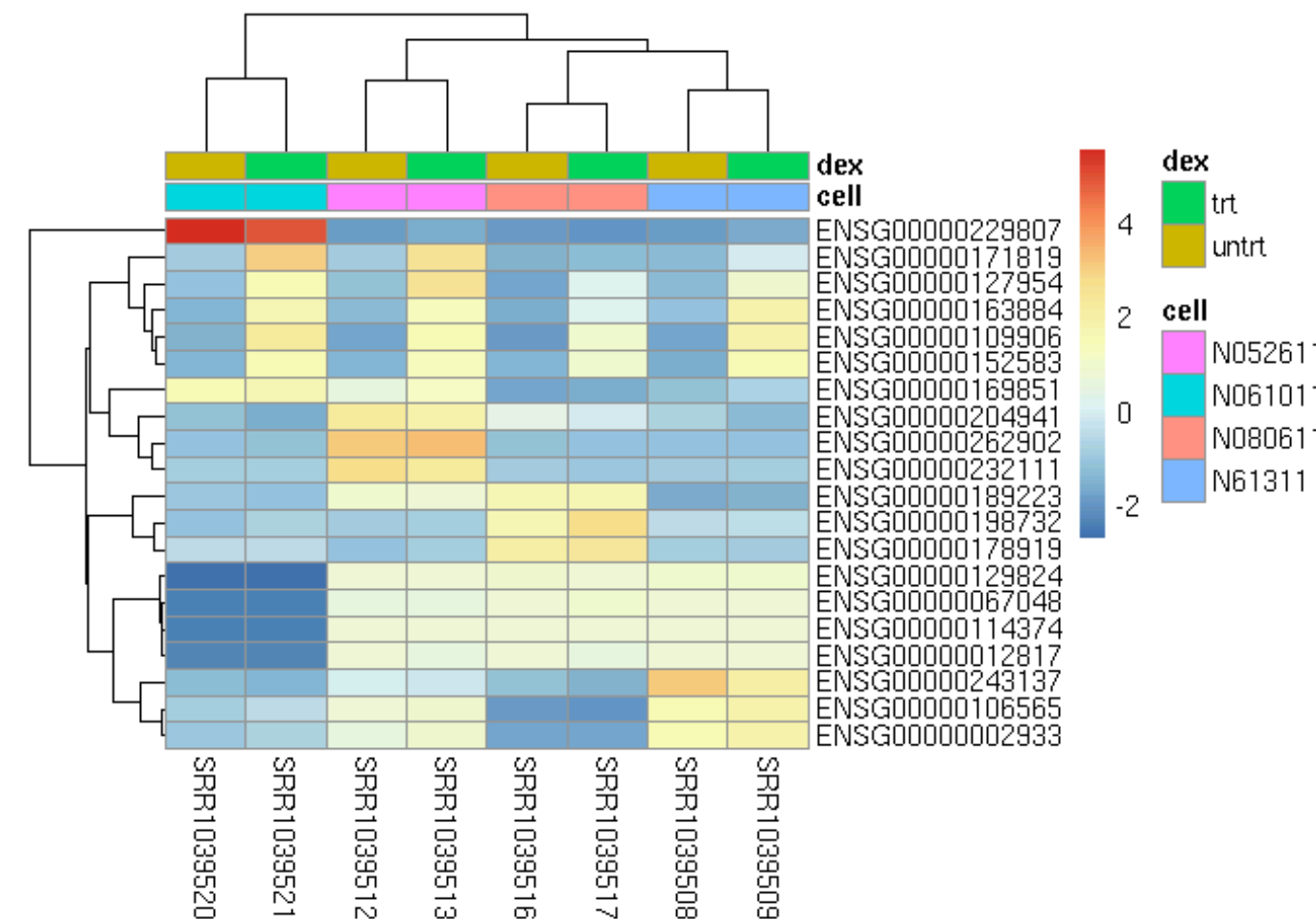
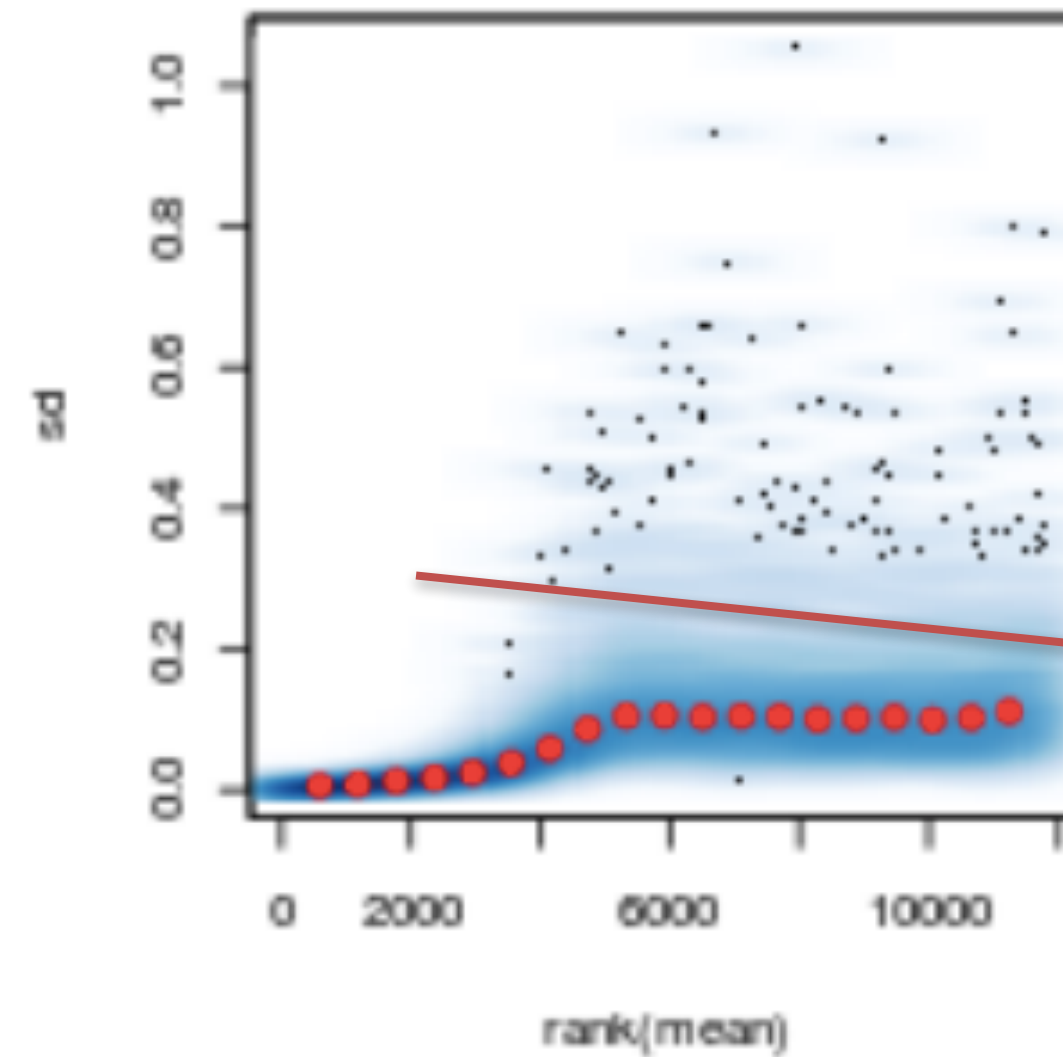


rlog stabilizes variances along the mean

$\log_2(x + 1)$



"rlog"



Moderating the high variance / low count genes Improves distances, clustering, visualizations

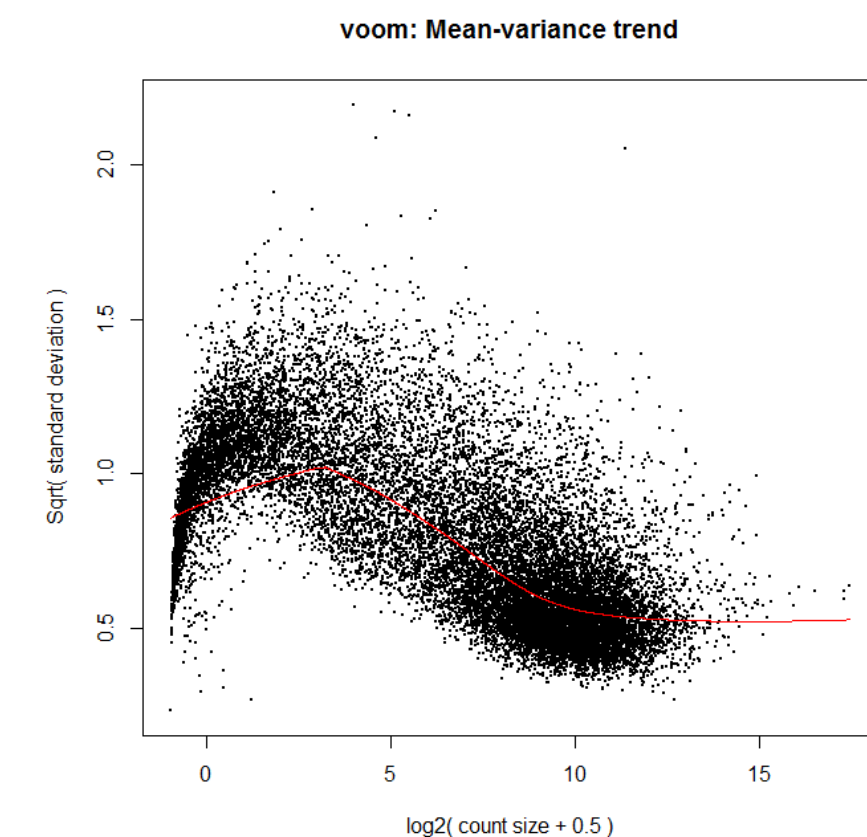
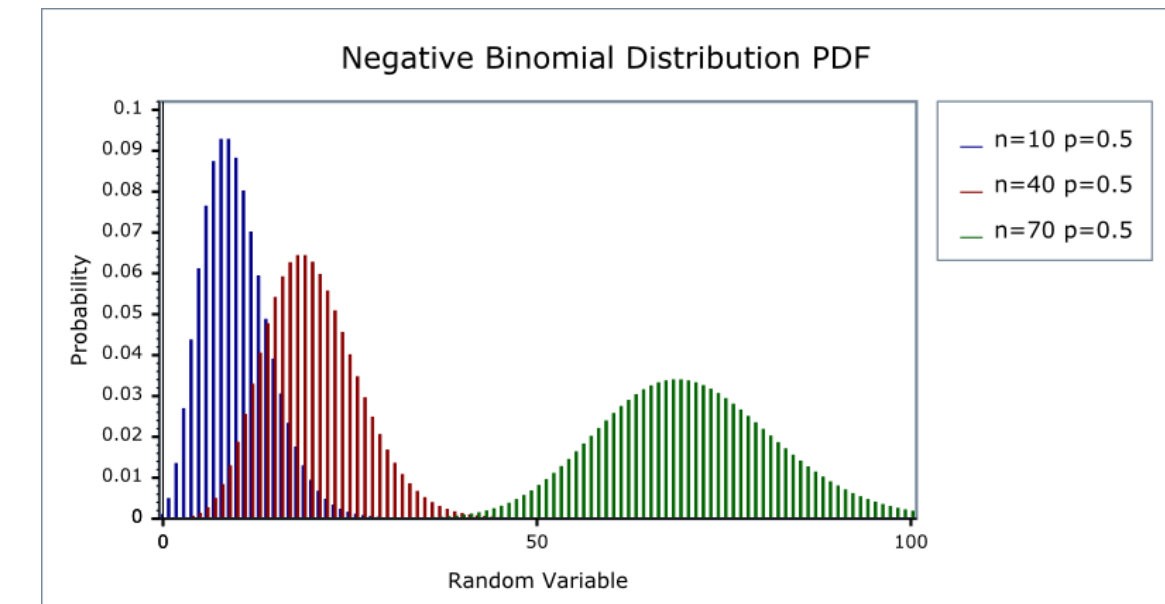
Variance stabilizing transform (VST)

- The variance stabilizing transformation is an earlier approach (from original DESeq) for transforming counts.
- Uses a function which is log-like but doesn't go to $-\text{Inf}$ at $x=0$.
- VST doesn't use size factors so is **better for data that has consistent sequence depth across samples**
- VST is closed form, so can be **better for large datasets ($n > 50$)** due to speed.

Comparison of methods

Count model vs linear model

- **DESeq2** and **edgeR** similar approach, similar results
 - very sensitive, may sometimes underestimate FDR
- **limma+voom** uses a linear model, weights determined by variance over mean
 - strong control of FDR, may be less sensitive for small sample size
 - recommended when number of biological replicates per group grows large (e.g. > 20)



Credits

RNA-seq statistical analysis and gene-level differential expression

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Dana-Farber Cancer Institute & Harvard TH Chan School of Public Health

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