

Materials for this workshop

- Concepts: this presentation
- Hands-on session:
 - Dec2021handson.R
 - targets.txt
 - GSE60450_Lactation-GenewiseCounts.txt.gz

Please install the following library in Rstudio

Install.packages(magrittr)

Install.packages(edgeR)

Install.packages(org.Mm.eg.db)

Install.packages(tidyverse)

Install.packages(ggplot2)

Install.packages(statmod)

Intermediate RNA-seq data analysis

Gladstone Institutes

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Bioinformatics Core, GIDB

December, 7th 2021

Assumed background

- Familiarity with R and RStudio
- Familiarity with RNA-seq protocol
- Familiarity with basic concepts of statistics and hypothesis testing

Introductions

Michela Traglia

Statistician III

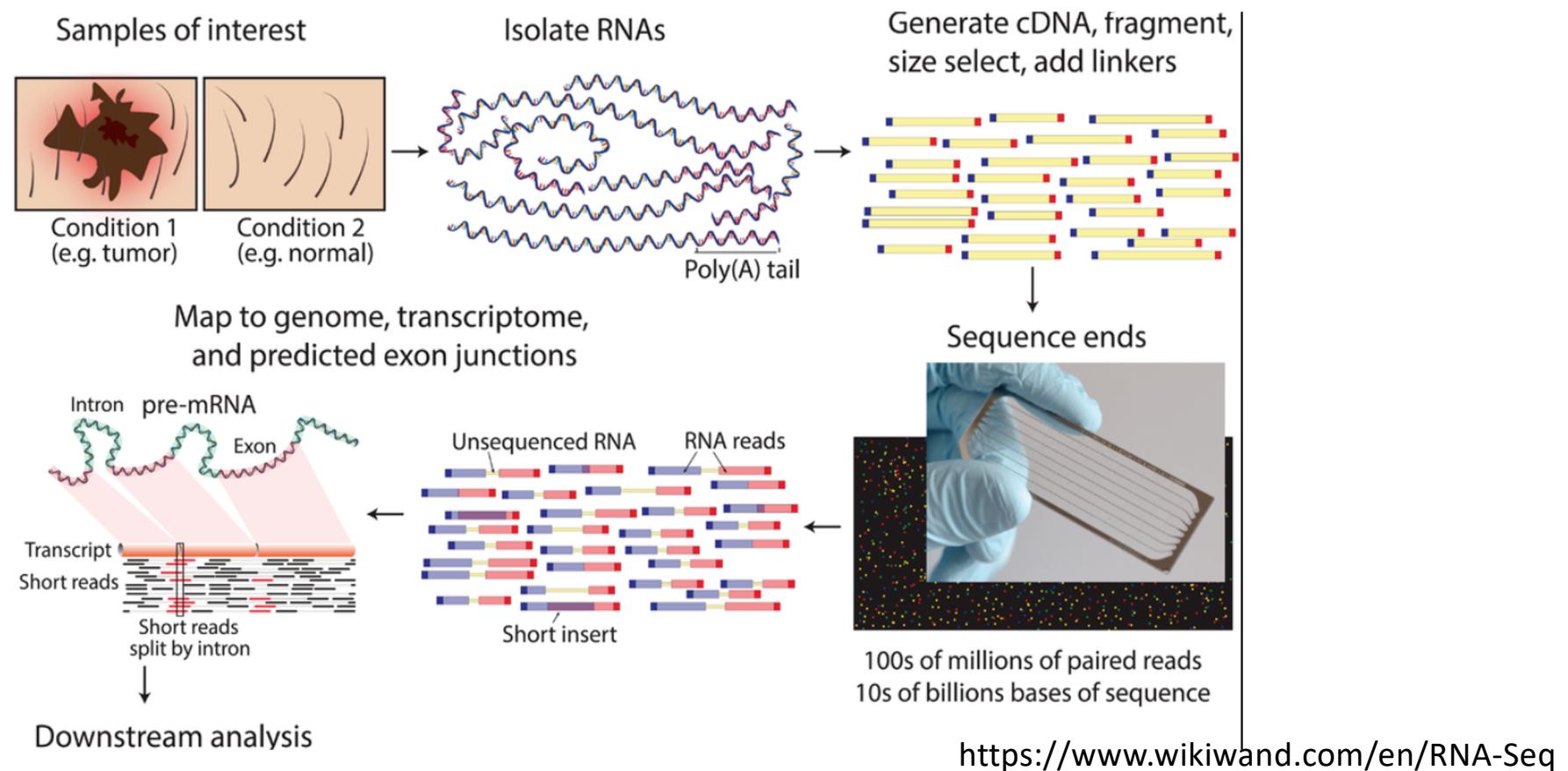
Min-Gyoung Shin

Bioinformatician II

Reuben Thomas

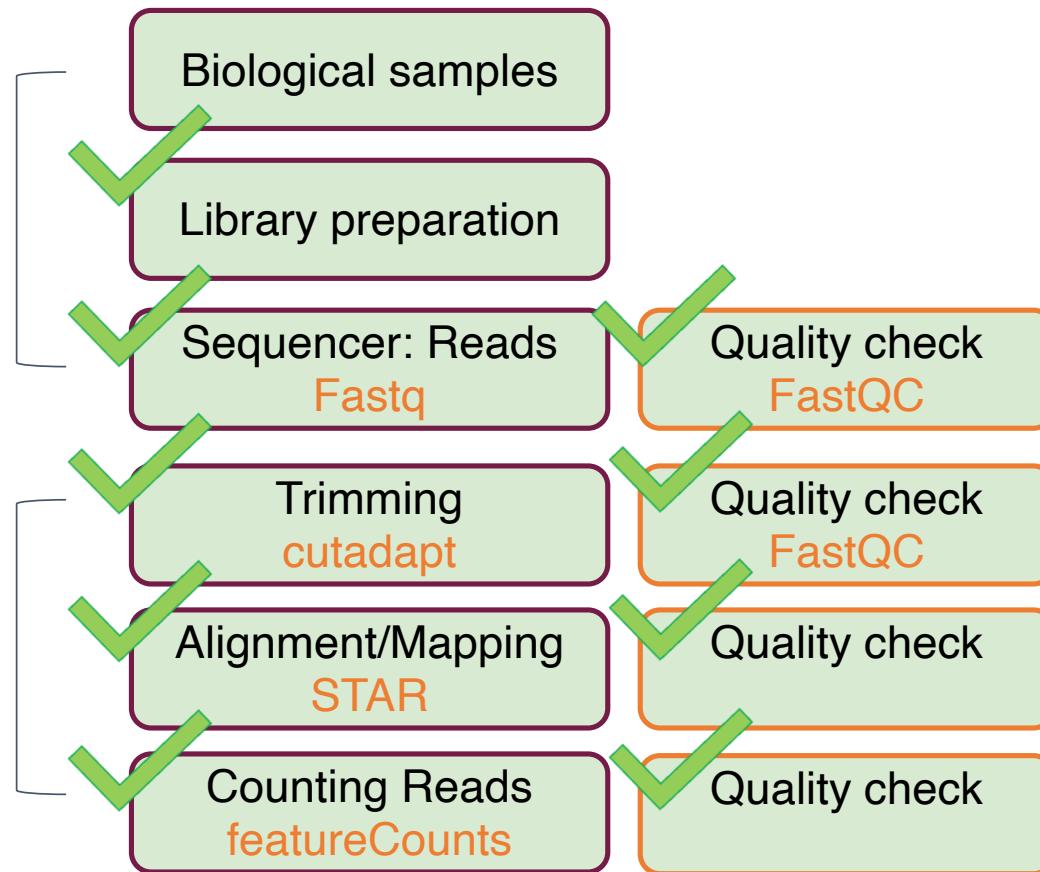
Associate Core Director

Typical RNA-seq protocol



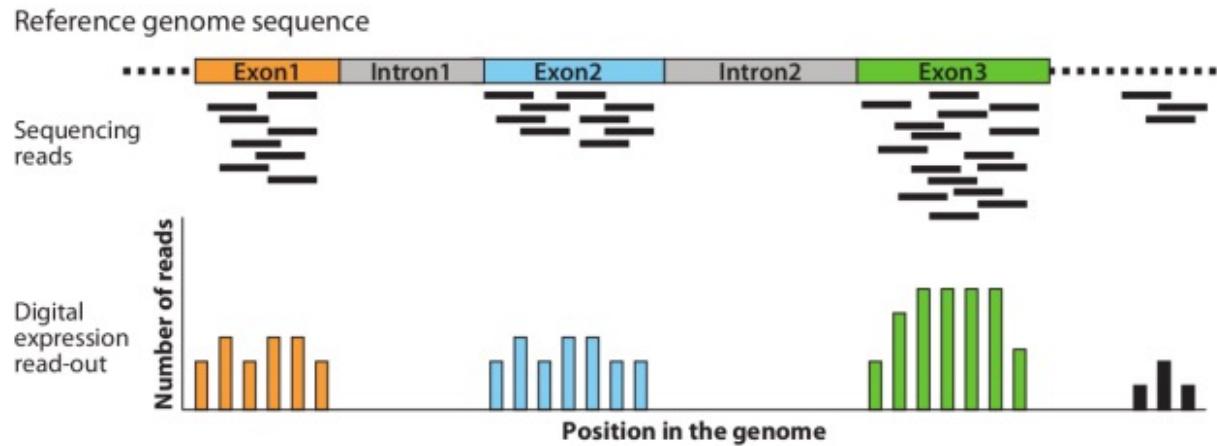
RNA-seq - analysis workflow

Session 1: Concepts + Demo



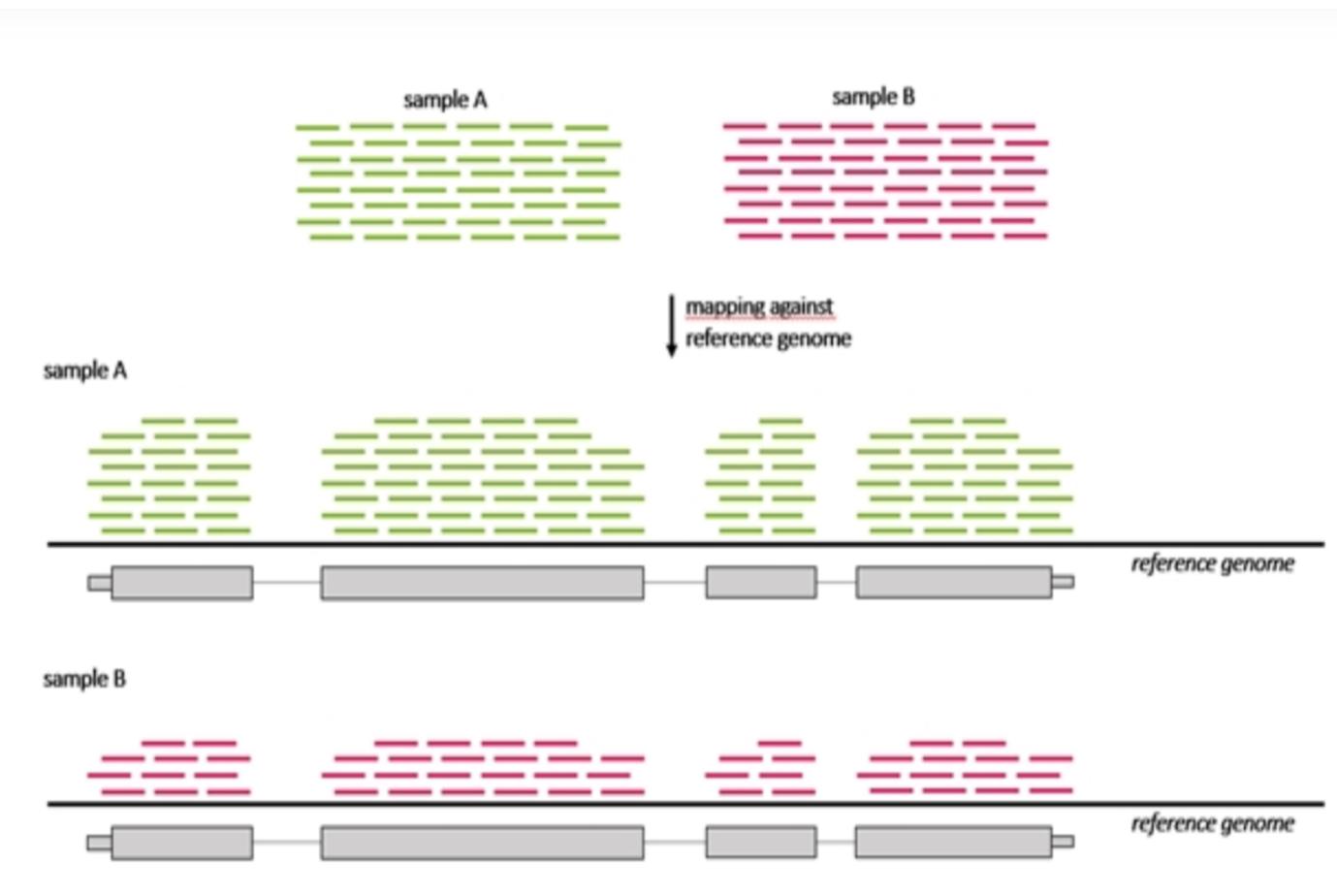
Session 2: Concepts + Demo

Goal of DEG analysis



Identify genes or molecular pathways that are differentially expressed (DE) between two or more biological conditions

Many steps to calculate the Differentially Expressed Genes (DEG) between sample A and B



DEG session - outline

- Steps for Differentially Expressed Gene analysis
- Real experiment
- Approach of DEG: edgeR
- Filtering genes
- Dealing with noisy data
- Normalization
- Exploratory visualization: MDS -PCA
- Fit the model for DEG and dispersion
- Which comparison and how to visualize the DEG

Reference for the workshop

F1000Research

F1000Research 2016, 5:1438 Last updated: 06 DEC 2018



Check for updates

SOFTWARE TOOL ARTICLE

REVISED From reads to genes to pathways: differential expression analysis of RNA-Seq experiments using Rsubread and the edgeR quasi-likelihood pipeline [version 2; referees: 5 approved]

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Dataset

Transcriptome analysis of luminal and basal cell subpopulations in the lactating versus pregnant mammary gland

- GEO accession: GSE60450
- Tissue of origin: Mammary glands of mouse
- Cell types: Basal stem-cell enriched cells (B) and committed luminal cells (L)
- Biological conditions: Virgin, Lactating (2 day) and Pregnant (18.5 day)
- # of groups: 2 cell types x 3 conditions = 6 groups
- # of replicates: 2 of each group

Files for the hands-on session

- [targets.txt](#)

Phenofile

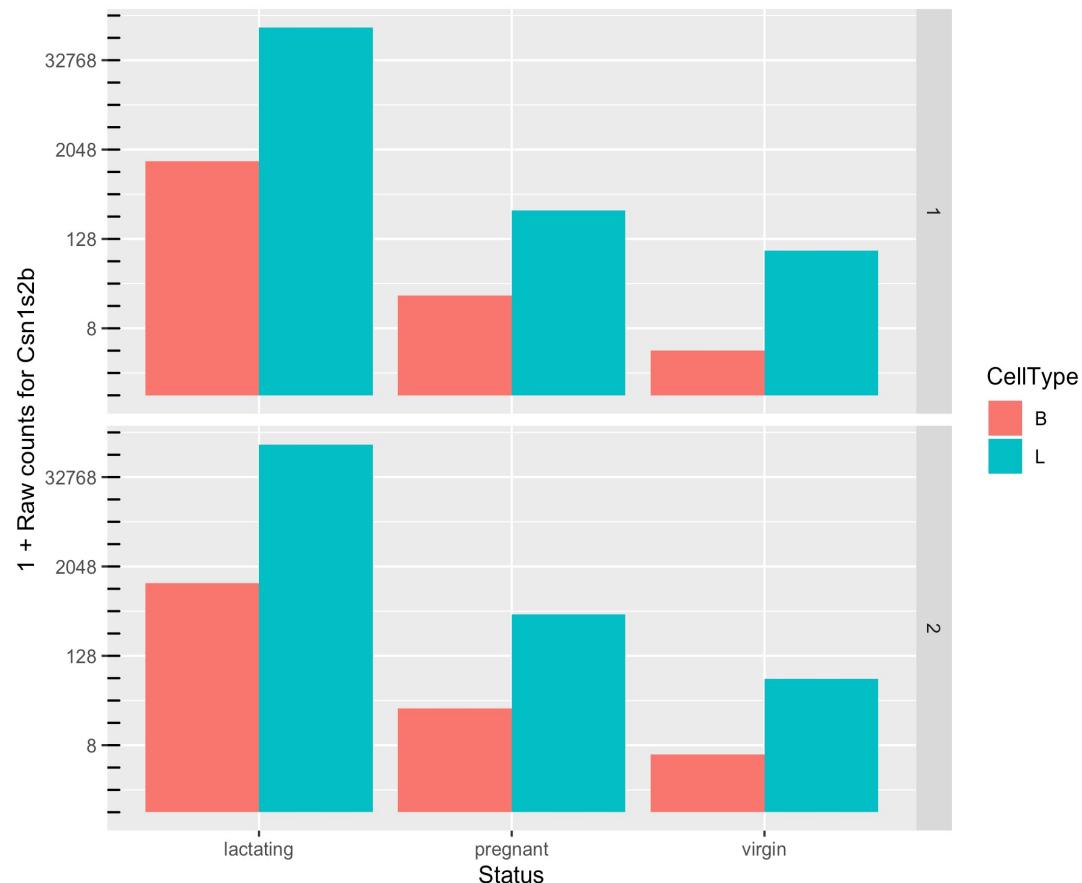
GEO	SRA	CellType	Status
MCL1.DG	GSM1480297	SRR1552450	B virgin
MCL1.DH	GSM1480298	SRR1552451	B virgin
MCL1.DI	GSM1480299	SRR1552452	B pregnant
MCL1.DJ	GSM1480300	SRR1552453	B pregnant
MCL1.DK	GSM1480301	SRR1552454	B lactating
MCL1.DL	GSM1480302	SRR1552455	B lactating
MCL1.LA	GSM1480291	SRR1552444	L virgin

- [GSE60450_Lactation-GenewiseCounts.txt.gz](#)

Counts for each sample for each gene(Entrez Gene Identifiers)

	Length	MCL1.DG	MCL1.DH	MCL1.DI	MCL1.DJ	MCL1.DK	MCL1.DL	MCL1.LA	MCL1.LB
497097	3634	438	300	65	237	354	287	0	0
100503874	3259	1	0	1	1	0	4	0	0
100038431	1634	0	0	0	0	0	0	0	0
19888	9747	1	1	0	0	0	0	10	3
20671	3130	106	182	82	105	43	82	16	25
27395	4203	309	234	337	300	290	270	560	464

Goal: To identify a set of genes that are differentially expressed

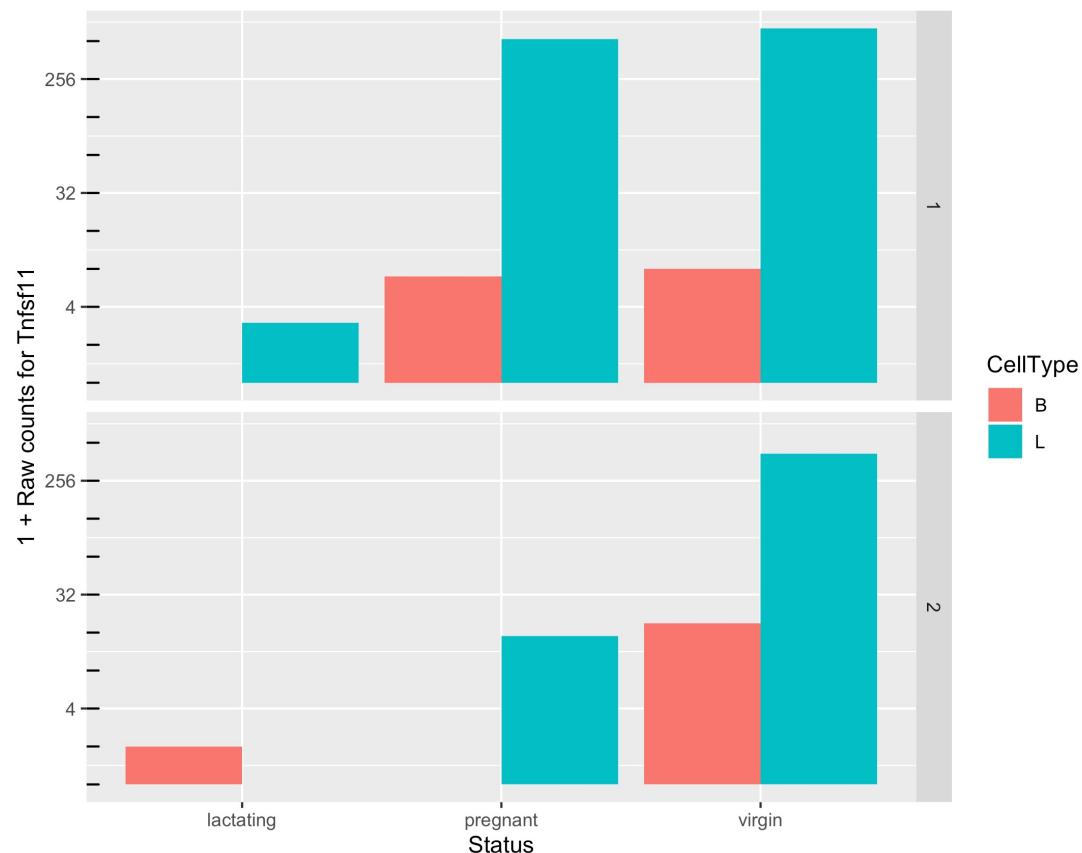


Which comparisons are we interested in?

Example:

1. B vs L,
2. B.lactating vs L.pregnant,
3. ...
4. All of them

Goal: To identify a set of genes that are differentially expressed



How do we ensure high power
for detection and high specificity
when faced with noise?

Can we make reliable
inferences for genes with very
low counts? What should we
consider “very low”?

Approach to identify DE genes: edgeR

- edgeR utilizes a theoretical model that captures some of the known processes leading to noise in counts data. (null model)
- Assume that the data is generated according to this model.
- Given any observed level of difference in mean expression levels of a gene, compute the probability that the observation will result from the null model. (p value)
- If the probability is very low (e.g., $p < 0.05$), infer that something may be happening that we did not account for in the null model. (e.g., biological processes in L cells for milk production)

Need to correct for multiple testing

- P value represents the chance that we may be wrong in calling something significantly differential. Example:
 - P = 0.01 means 1% chance that we may be wrong.
 - P = 0.50 means 50% chance that we may be wrong.
- More than 20k genes under consideration
- => if a certain difference in expression levels has only 1% chance of happening given the null model, it might be observed for 200 genes even if the null model were true for all the genes.
 - => 200+ false positives
- Hence, there is a need to adjust the p-values.
 - The more genes we test, the more we must adjust.
 - Reduce the number of tests by filtering out “uninteresting” genes.

“Uninteresting” genes

Filtering

- *Biological point of view*: minimal expression level of a gene -> translation into a protein -> biologically relevant
- *Statistical point of view*: low counts -> not enough statistical evidence.
Genes with consistently low counts are very unlikely be assessed as significantly DE

Why we need to normalize the counts

Identify and correct technical biases removing the least possible biological signal

- library prep, sequencing technology, ...

It is an essential step in the analysis of gene expression:

- to compare gene expressions from a same sample
- to compare genes from different samples (differential analysis)

Goals of normalization:

- 1) accurate estimation of gene expression levels
- 2) reliable differential expression analysis

Source of variability

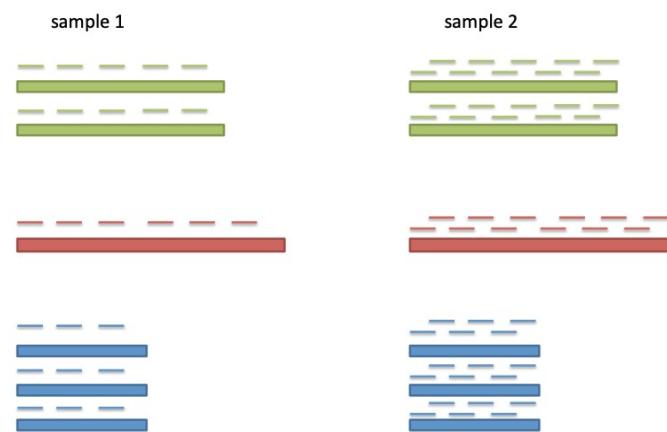
- Within-sample
 - Gene length
 - Nucleotide composition (GC content)
- Between-sample
 - Library size (number of mapped reads)
 - Batch effects

Gene-length and sequence depth

At the same expression level, a long gene will have more reads than a shorter one



Higher sequencing depth, higher counts



Factors other than differential gene expression that cause variation in counts

- Variation in sequencing depths => Need to normalize counts

Group	Total counts
B.virgin	23085177
B.virgin	21628857
B.pregnant	23919152
B.pregnant	22490570
B.lactating	21382233
B.lactating	19884434

Group	Total counts
L.virgin	20213223
L.virgin	21509988
L.pregnant	22073815
L.pregnant	21837341
L.lactating	24638939
L.lactating	24581591

Library size about 20M

Normalization for gene length

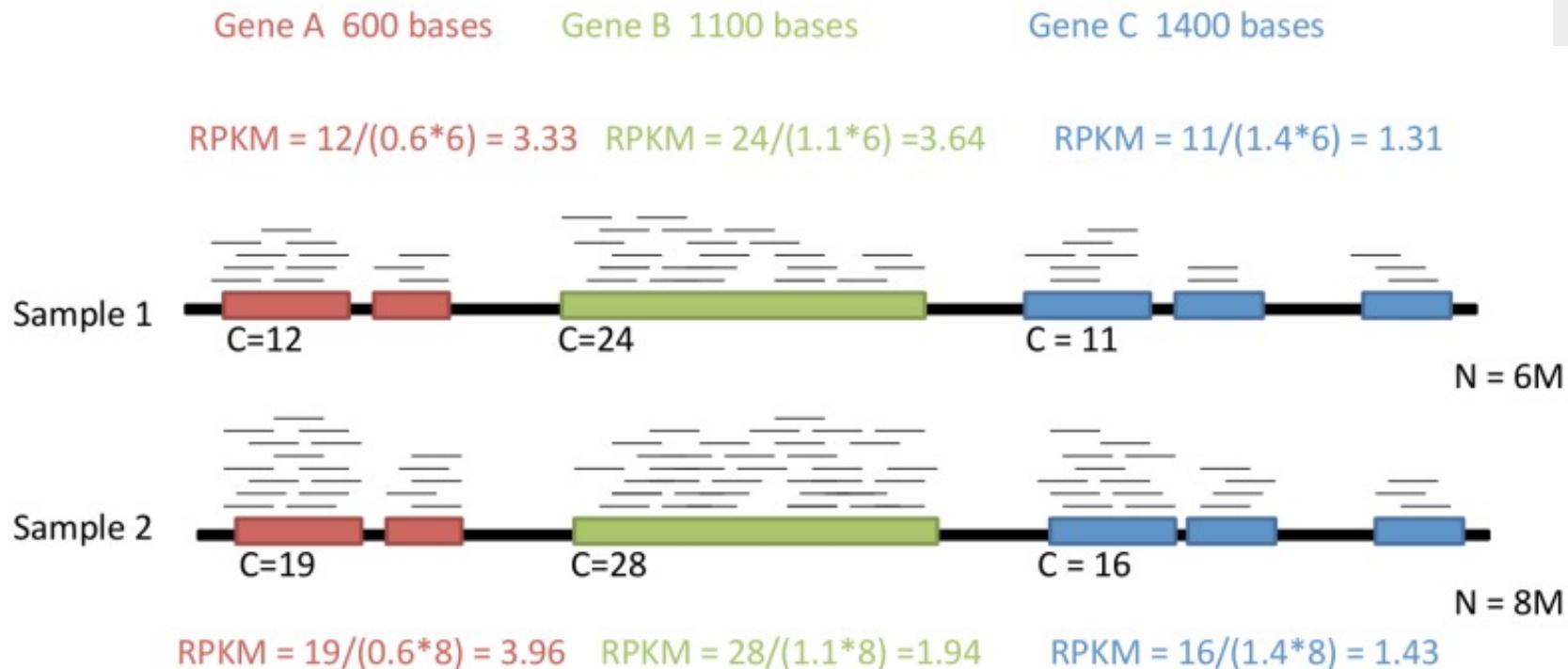
- Commonly used normalization method that includes gene length correction
 - TPM (Transcripts Per kilobase Million)
 - RPKM /FPKM (Reads/Fragments Per Kilobase per Million)

Not very relevant for samples comparisons

Proved to be inadequate and biased

RPKM: depth and length bias

$$RPKM_{ij} = \frac{10^9 \times k_{ij}}{N_j \times L_i},$$

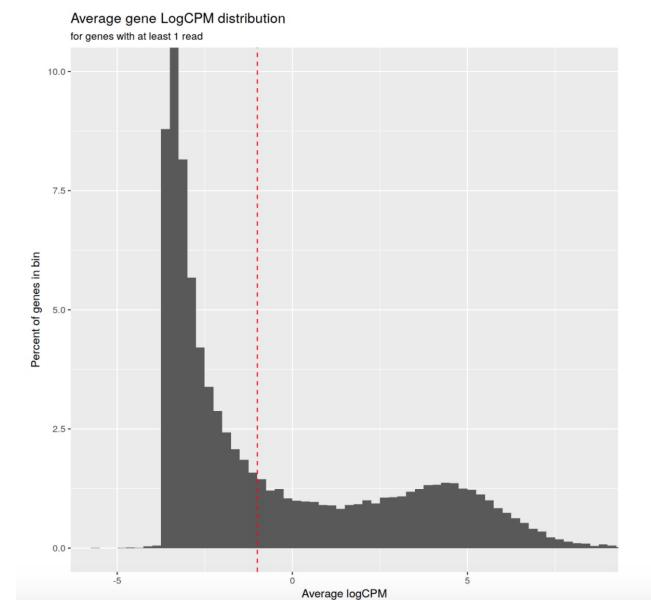


Library size - Count Per Million

A gene at least 10–15 counts in at least some libraries before it is considered to be expressed

Filter on count-per-million (CPM) values so as to avoid favoring genes that are expressed in larger libraries over those expressed in smaller libraries

Ex. a gene to be kept should have a cpm of 100 or greater for at least two samples



Between samples variation: observed counts depend on total reads sequenced and sample composition

Gene expression values should be compared among samples

- # reads for YFG = $\frac{\text{Amount of nucleic acid from YFG}}{\text{Total nucleic acid in sample}} \times \text{Total reads}$
- Need to normalize for difference in total reads between samples.
 - Might be enough if total nucleic acid is the same in both samples.
 - Example: technical replicates
- Need to account for difference in sample composition.
 - Assume that the large majority of genes are not differential.
 - Adjust counts such that for most genes, counts are not differential.

Scaling factors

Normalize for RNA composition by scaling factor

A few highly differentially expressed genes may have a strong influence on read counts -> minimizing effect of such genes

Assumption: A majority of transcripts is not differentially expressed

Between sample normalization

Normalize for RNA composition by a set of scaling factors that minimize the log-fold changes between the samples for most genes

- Reference sample: have the closest average expressions to mean of all samples
- Test samples: other samples

Scaling factor: weighted mean of log ratios between the test and reference, from a gene set removing most/lowest expressed genes (avg read counts) and genes with highest/lowest log ratios (differences in expression)

Normalization: Trimmed Mean of M-values

1. Choose a reference sample.
2. Compute the M and A values for all genes.
 $M = \log FC$ between ref and test; $A = \text{avg count gene}$
3. Filter genes that fall in the tails of M and A distributions.
4. Estimate variance of M values.
5. Estimate TMM --- the weighted average of trimmed M-values.
6. Size factor is 2^{TMM} .
7. Adjust such that these multiply to 1.

Other approaches to normalization

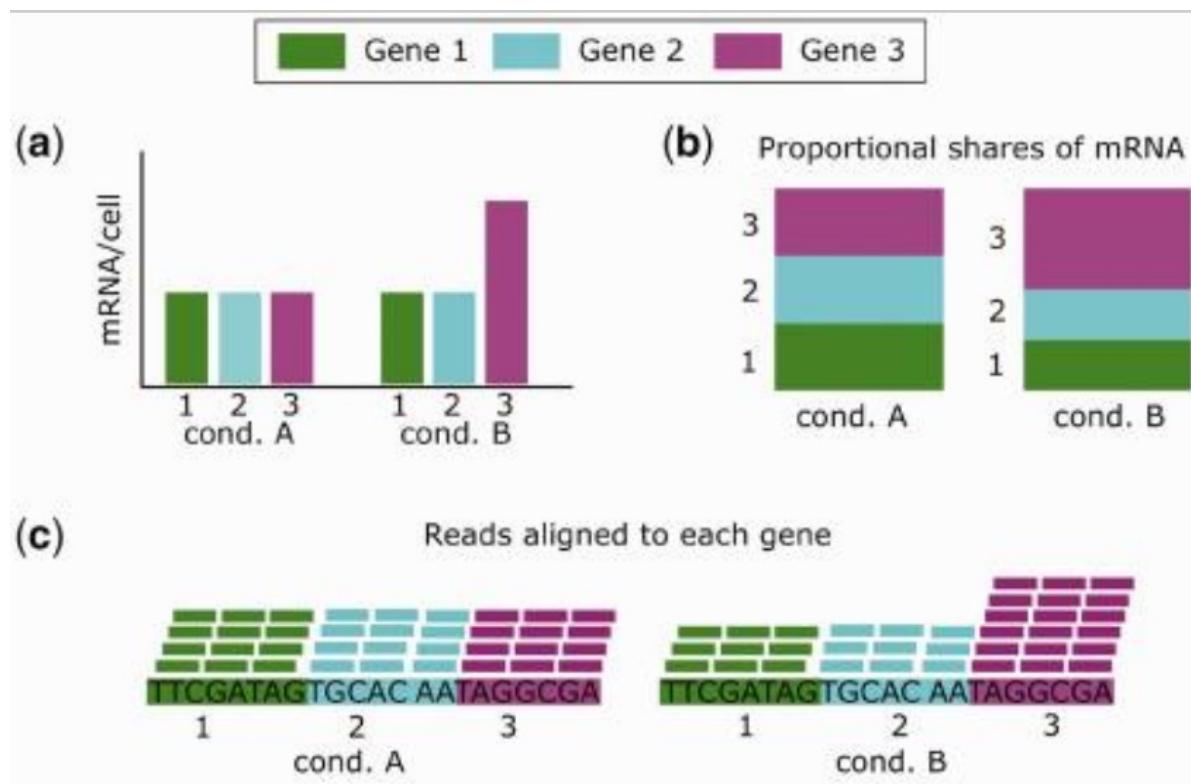
- RLE approach by Anders and Huber (2010)
 - Reference: geometric mean of all samples
 - Normalization factor: median ratio of each sample to the reference
 - Identical to TMM approach
 - R package DESeq
- Upper quartile normalization by Bullard et al (2010)
 - Normalization factor: 75% quantile of the counts for each sample
 - Not recommended in general
- Total number of reads : TC (Marioni et al. 2008)
- Control genes (housekeeping genes, spike-in) to estimate technical noise (RUVSeq - 2014)

Best practice to choose a normalization

An effective normalization should result in a stabilization of read counts across samples

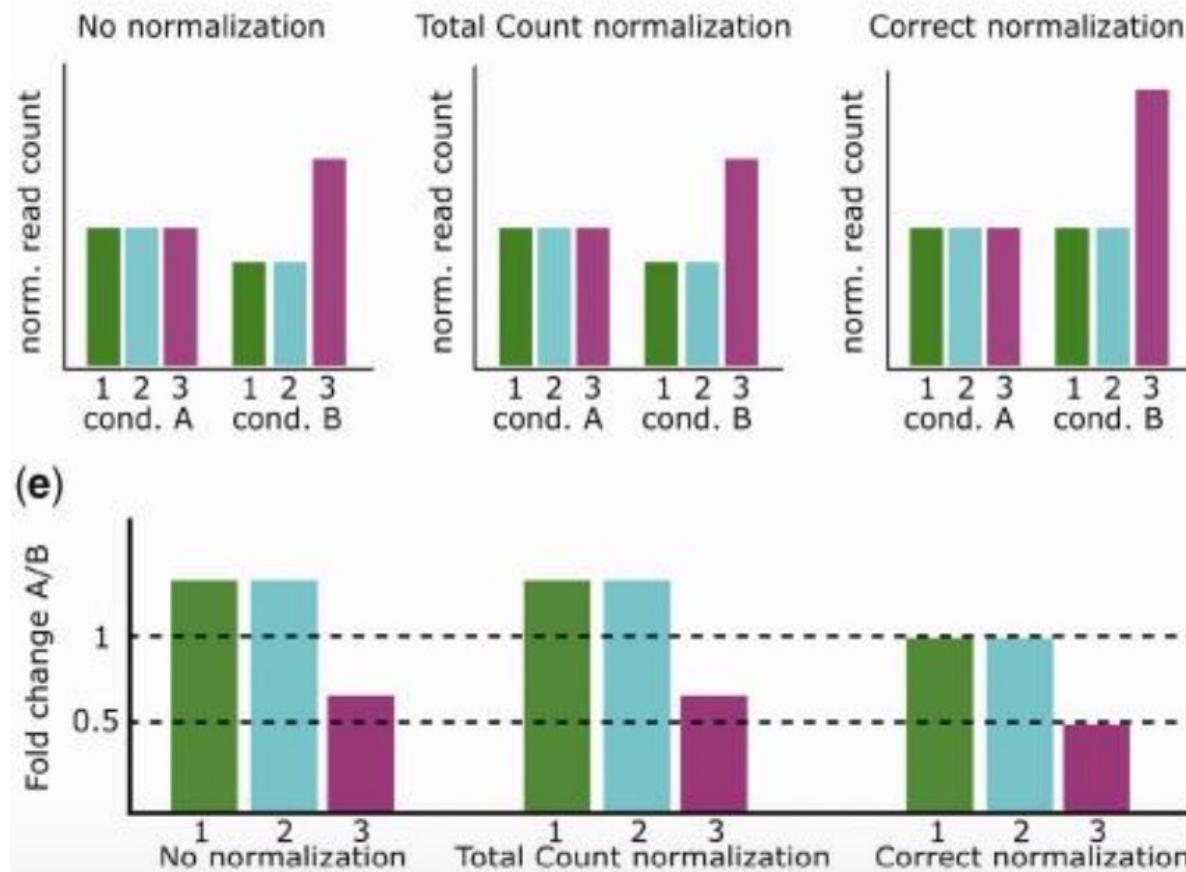
- TC, RPKM, UQ - Adjustment of distributions, implies a similarity between RNA repertoires expressed
- DESeq, TMM - More robust ratio of counts using several samples, suppose that the majority of the genes are not DE
- RUVSeq - Powerful when a large set of control genes can be identified

The goal is for differences in normalized read counts to represent differences in true expression



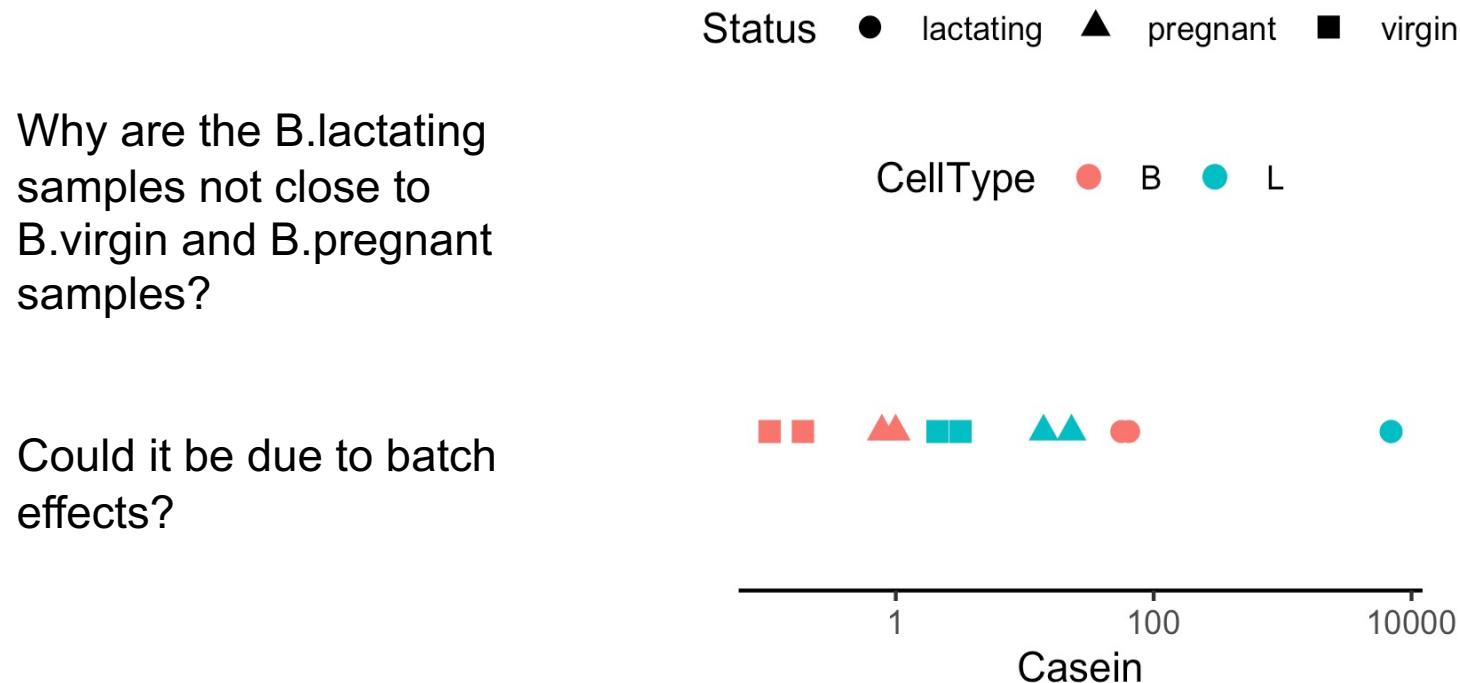
doi: [10.1093/bib/bbx008](https://doi.org/10.1093/bib/bbx008)

The goal is for differences in normalized read counts to represent differences in true expression



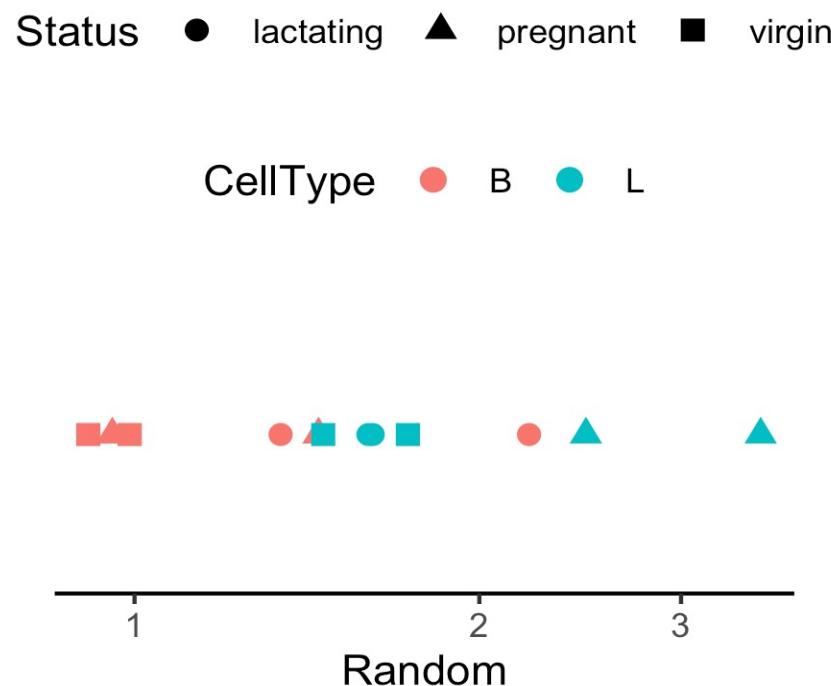
MDS and PCA plots

Expression level of Casein varies in a way that is strongly indicative of the effect of CellType and Status.



The distance between each pair of samples can be interpreted as the leading log-fold change between the samples for the genes that best distinguish that pair of samples.

In general, the way expression appears to vary across samples could be dominated by noise, batch effects, real signal, etc.

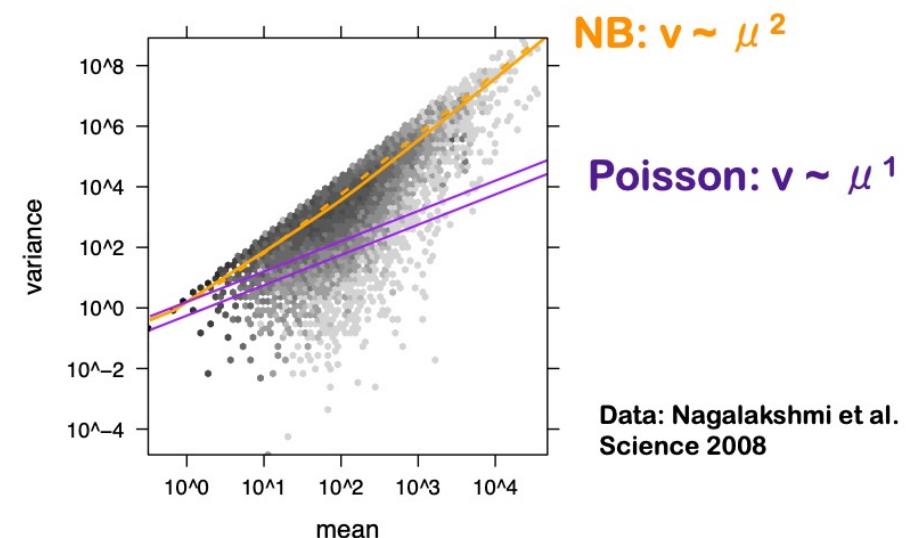


Fit the model: RNA-seq data and overdispersion between samples

The number of reads that are mapped into a gene was first modeled using a Poisson distribution

Assumption: assumes that mean and variance are the same

The variance grows faster than the mean in RNAseq data.



Overdispersion in RNA-seq data

- > counts from biological replicates tend to have variance exceeding the mean
- > underestimation of the biological variance increased type I error rate (probability to falsely declare a gene DE)

Three dispersion

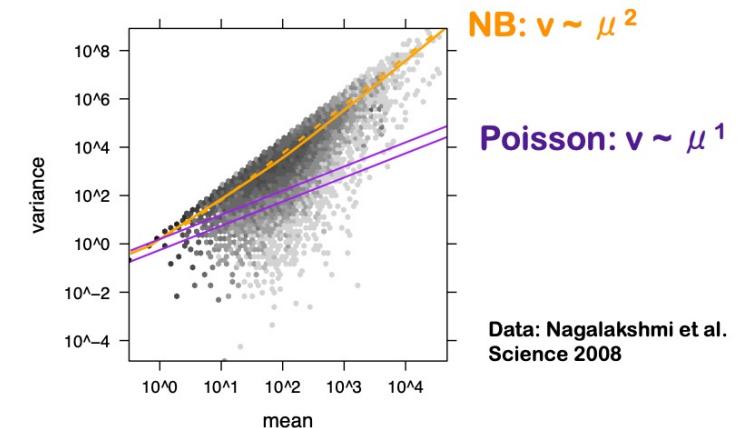
The negative binomial (NB) distribution alternative to model the read counts for each gene in each sample

The variance is always larger than the mean for the negative binomial ⇒ suitable for RNA-seq data

Many genes, few biological samples - difficult to estimate φ on a gene-by-gene basis

Using information across genes for stable estimates of φ .

3 ways to estimate φ : common, trended, tagwise (moderated)



Empirical Bayes moderated dispersion for each individual gene

Fitting the model: dispersion

Dispersion accounts for variability between biological replicates

- Common dispersion: a global dispersion estimate averaged across the genome
- Trended dispersion: dispersion of a gene is predicted from its abundance
- Tagwise dispersion: measure of the degree of inter-library variation for that tag – plotBCV

Empirical Bayes estimates need to be controlled for the possibility of outlier genes with exceptionally large or small individual dispersions (robust=TRUE)

Empirical Bayes estimates of dispersion parameters: Learning from the experience of others

- ◆ For an intuitive explanation by Bradley Efron, see link in description
- ◆ Original paper: Robbins, Herbert. *An Empirical Bayes Approach to Statistics*. (see description for complete reference)

glmQLFit and variance of gene counts

- NB dispersions - higher for genes with very low counts and decrease smoothly with abundance and to asymptotic to a constant value for genes with larger counts.
- Extended NB model to account for gene-specific variability from both biological and technical sources (quasi-likelihood)
 - 1) NB dispersion trend is used to describe the overall biological variability across all genes (fit GLM)
 - 2) For each gene-specific variability above and below the overall level (deviance) is picked up by the QL dispersion

edgeR statistical method

- Classic (pairwise comparisons between two or more groups), glm likelihood ratio test and glm quasi-likelihood F-tests
- QL for bulk RNA-seq:
 - + stricter error rate control (more rigorous dispersion and uncertainty)
 - + speed improvement compared to other quasi-methods
 - + appropriate for multiple treatment factors and with small # of biological replicates
 - + relative changes in expression levels between conditions (not absolute)

Limma package for large scale datasets

Get the DE genes – glmQLFTest and decideTestsDGE

- Identifies differential expression based on statistical significance regardless of how small the difference might be -> 5000 DE genes between the basal pregnant and lactating groups.
- Interested only in genes with large expression changes -> subset of genes more biologically meaningful.
- Modify the statistical test to evaluate variability as well as the magnitude of change of expression values -> expression changes greater than a specified threshold
- Not equivalent to a simple fold change cutoff.
- The total number of DE genes identified at an FDR of 5% can be shown with `decideTestsDGE()`

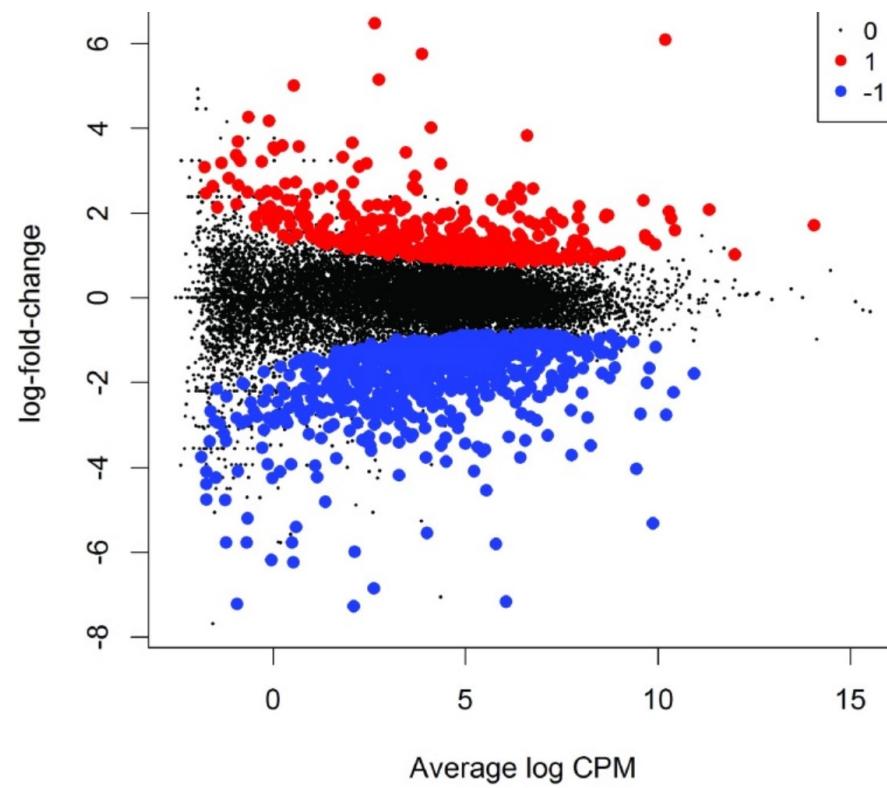
Get the DE genes - glmQLFTest

	genes	logFC	logCPM	F	PValue	FDR
PCDHA10	PCDHA10	-3.602	5.676	499.9	8.164e-11	1.354e-06
CHGA	CHGA	2.923	5.976	185.4	1.972e-08	0.0001635
ARRB1	ARRB1	-3.914	5.015	158.3	4.627e-08	0.0002019
TSSC2	TSSC2	3.175	3.301	156.8	4.869e-08	0.0002019

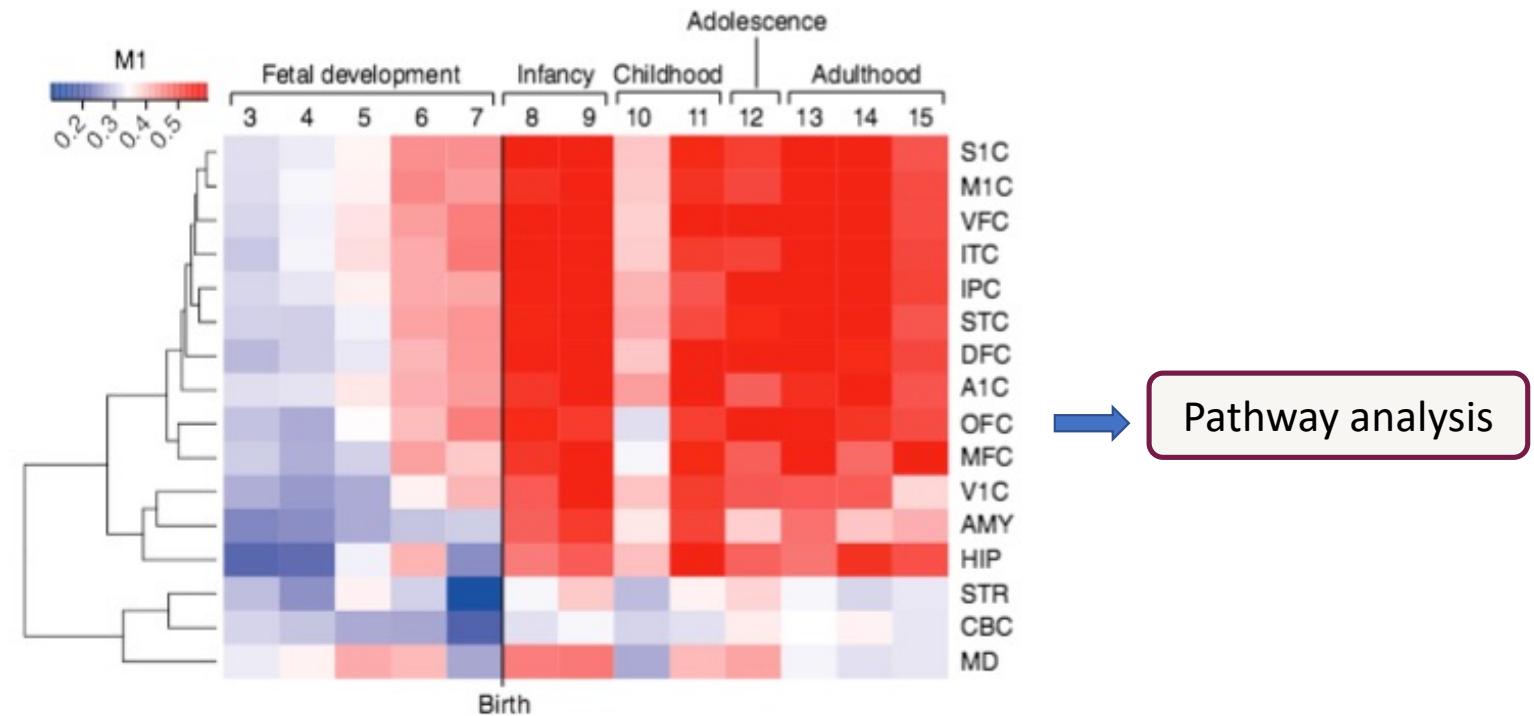
Complicated contrasts - makeContrasts()

- between lactating and pregnant mice is the same for basal cells as it is for luminal cells
- the interaction effect between mouse status and cell type

Over and under expressed genes



Visualization - heatmap



Color-coded heatmap of gradient of expression of genes, spanning fetal development to late adulthood and expressed in cortical regions

Your feedback is important to us!

At the end of the hands-on session:

Please take the survey ~3 min:

<https://www.surveymonkey.com/r/F75J6VZ>

Thank you!

Real data might need additional analyses choices that need experience.

Consult with the Gladstone Bioinformatics core for such scenarios and data.

Hands-on session

- Load and reformat the data
- Exploratory visualization : MA plot
- Create DGElist object and retrieve gene symbols
- Filter genes with inadequate information
- Normalize counts : *What's under the hood?*
- Exploratory visualization : MDS and PCA plots
- Define and fit a model
- Hypothesis testing (four example hypotheses)
- Save results as a table and explore in Excel



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