

Introduction

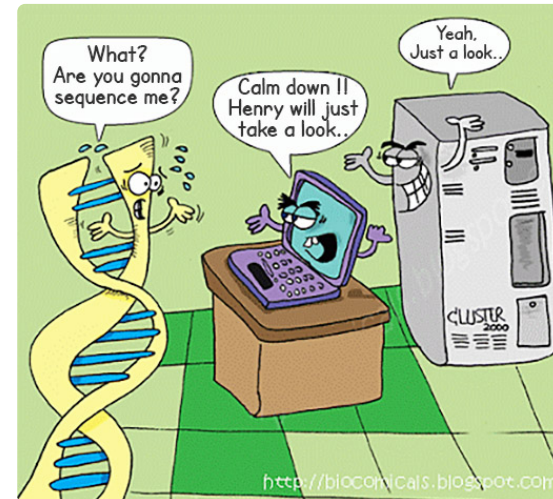
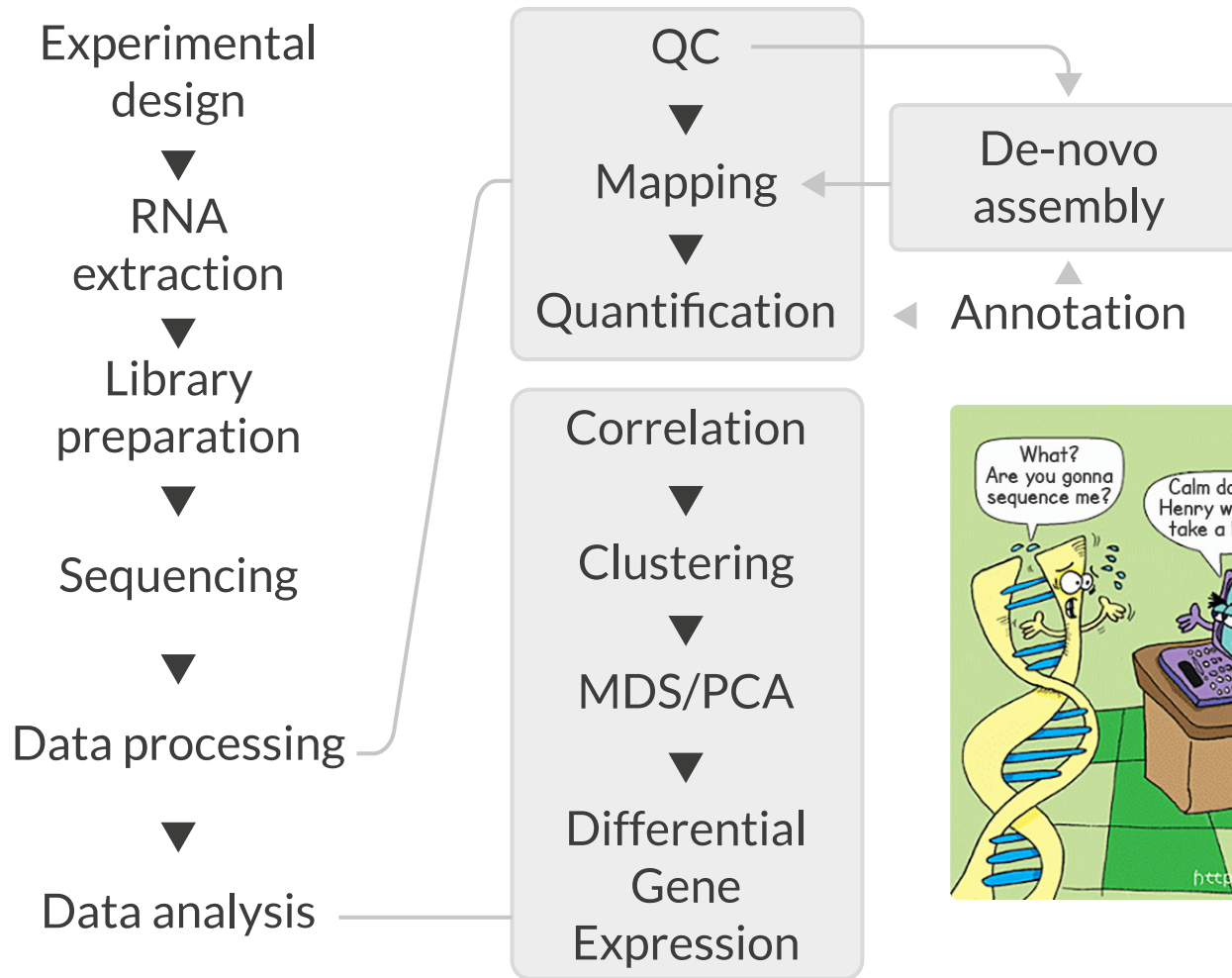
RNA-seq data analysis

Johan Reimegård | 3-June-2019

Welcome to RNAseq 2019

- General things before we start
 - WIFI
 - Toilets
 - Fika
 - Uppmax

Two days course



We are going to try to make this course interactive

- <https://youtu.be/Z9orbxoRofl>

And for that we need your help


- Presentations
 - Your name
 - Where you were born
 - Where you work
 - Favorite animal
 - Favorite plant
 - Favorite gene (if you have any)

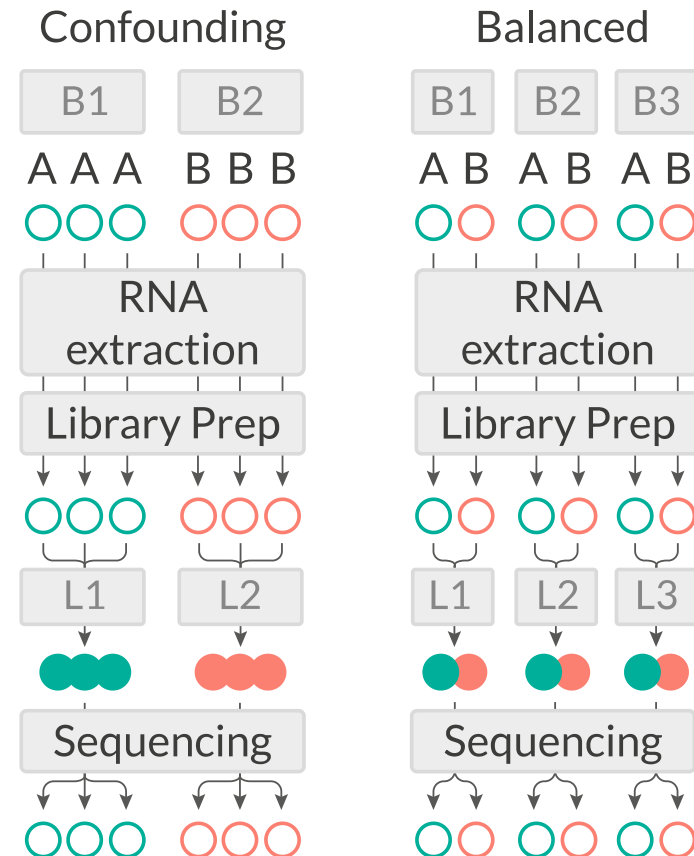
What are the things you need to consider when planning RNA-seq data analysis?




Experimental design

- Balanced design
- Technical replicates not necessary
(Marioni *et al.*, 2008)
- Biological replicates: 6 - 12 (Schurch *et al.*, 2016)
- ENCODE consortium
- Previous publications
- Power analysis


 [RnaSeqSampleSize](#) (Power analysis), [Scotty](#)
(Power analysis with cost)



 Busby, Michele A., *et al.* "Scotty: a web tool for designing RNA-Seq experiments to measure differential gene expression." *Bioinformatics* 29.5 (2013): 656-657

 Marioni, John C., *et al.* "RNA-seq: an assessment of technical reproducibility and comparison with gene expression arrays." *Genome research* (2008)

 Schurch, Nicholas J., *et al.* "How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use?." *Rna* (2016)

 Zhao, Shilin, *et al.* "RnaSeqSampleSize: real data based sample size estimation for RNA sequencing." *BMC bioinformatics* 19.1 (2018): 191

Which persons will have the most similar expression pattern





Thank you. Questions?

Johan Reimegård | 13-May-2019