Welcome to ABC.10

12. December 2024
https://abc.au.dk
abcafe@au.dk
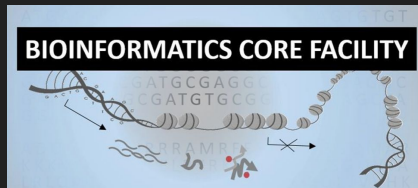
Agenda

- What's new

- Interesting things from you?

- Topic presentation

- Tutorial and/or open coding

What's new
Some updates

- We have a unified mail for the ABC:
  abcafe@au.dk
- Use our newsletter and suggestion forms at the homepage
  abc.au.dk

What's new
Some updates

- Next cafe dates
  - Jan 16
  - Jan 30
  - Feb 6
  - Feb 27
  - Mar 13

- You will always get an invitation if you are on the newsletter

Interesting things from you?

Topic presentation

Bulk RNA seq data alignment and quality control (QC)

Tutorial topic

~~Bulk RNA seq data alignment and quality control (QC)~~

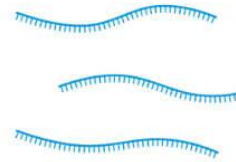Previous tutorials

RNA-seq
What is it?

It's a technology used to study RNA molecules in a biological sample
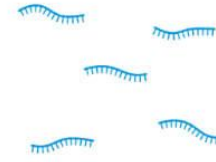
The purpose of RNA-seq:

- to quantify gene expression (what genes are active or not)
- to compare conditions or changes over time (healthy vs diseased, treated/stimulated vs untreated)
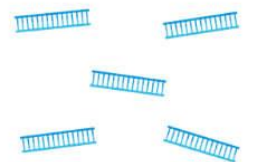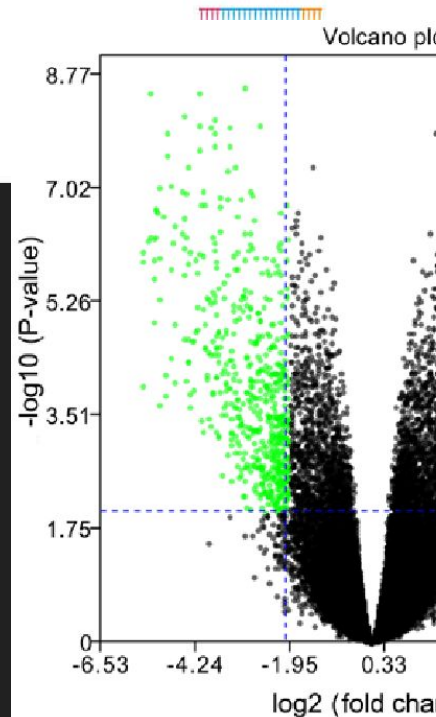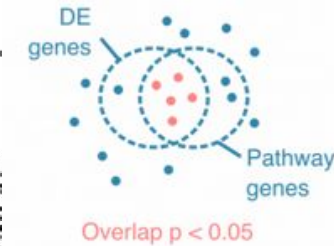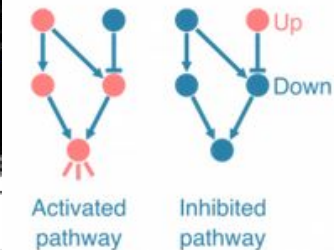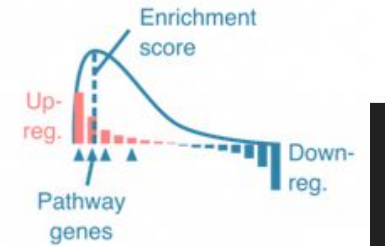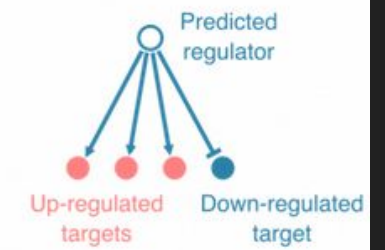
Raw RNA seq data
What are they?

- unprocessed results from sequencing RNA molecules from a sample (sometimes with a focus on a specific type of RNA, like mRNA)
- they're stored in FASTQ files, which contain
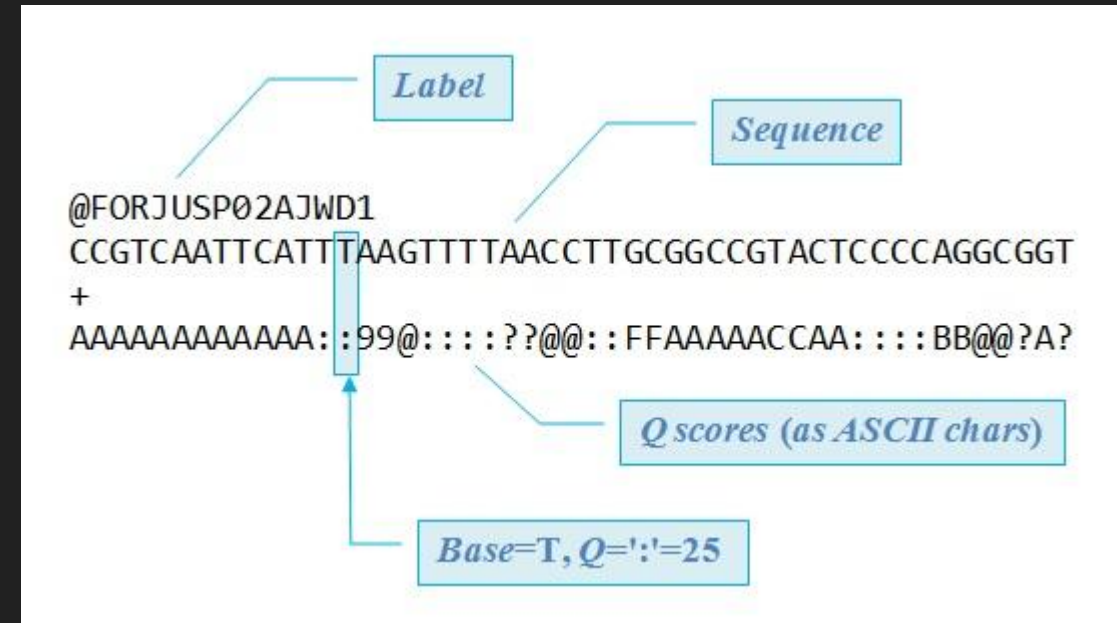   - line 1: the sequence identifier
    - line 2: the RNA sequence
    - line 3: a separator
    - line 4: the quality scores
    - extra: noise (adaptors, sequencing errors, or contamination)
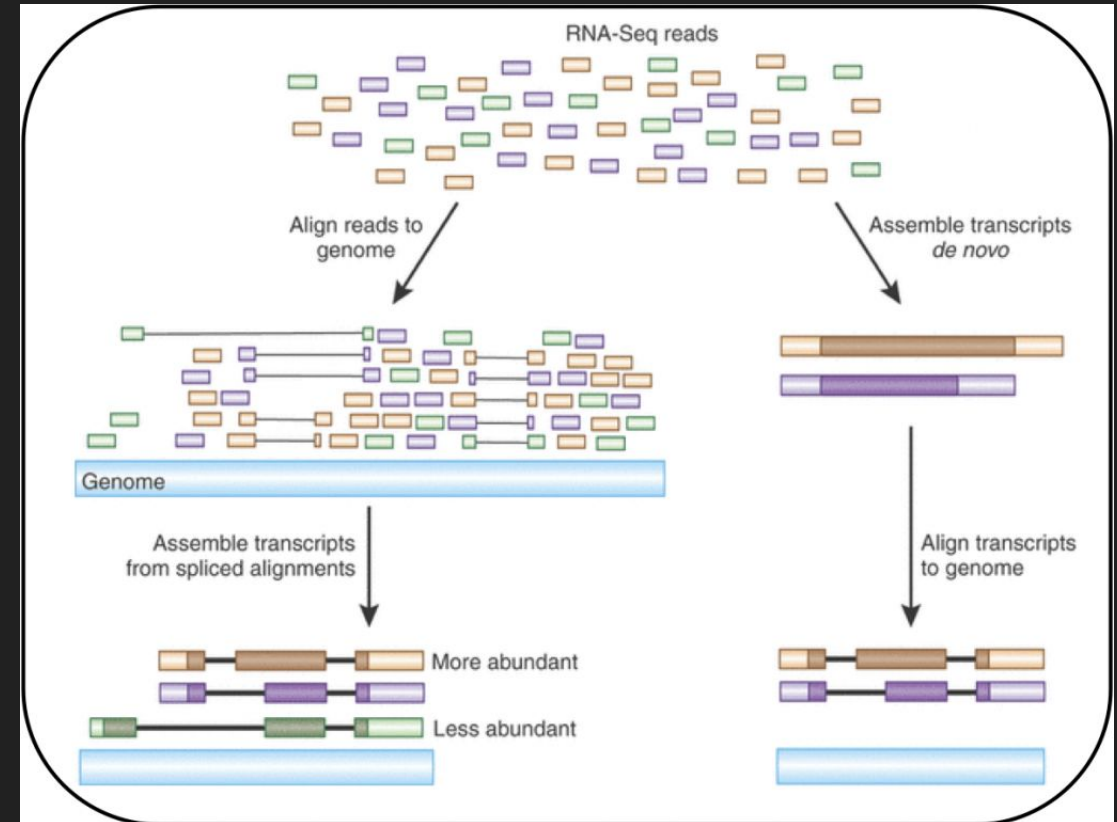
How to process RNA seq data

Alignment:
- preassembled reference genome
    - .fasta/.fa (reference genome) and .gft (annotation file)
- de novo assembly

Alignment tools:
- STAR, HISAT2, bowtie2

QC
- fastqc
- multiqc

Tutorial and open coding

At our home https://abc.au.dk/Documentation you can find

- Previous tutorials

- 1 conference workshop

Or you can code and ask for help or generic coding/bioinf/data science questions