



Swiss Institute of
Bioinformatics

INTRODUCTION TO SEQUENCING DATA ANALYSIS

Group work

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Adapted from previous year courses

Projects

Project 1: Variant analysis

Project 2: Long read RNA-seq

Project 3: Short-read RNA-seq

Data analysis steps

Go through all the steps performed in the course:

- » Quality control
- » Trimming
- » Alignment
- » Visualization

But also:

- » Perform counting for estimating gene expression

Data analysis steps (covered so far)

Go through all the steps performed in the course:

- » **Quality control**
- » **Trimming**
- » Alignment
- » Visualization

But also:

- » Perform counting for estimating gene expression

Projects

Project 1: Variant analysis

Project 2: Long read RNA-seq

Project 3: Short-read RNA-seq

Important

Do not only perform the calculations, also to **evaluate** the results

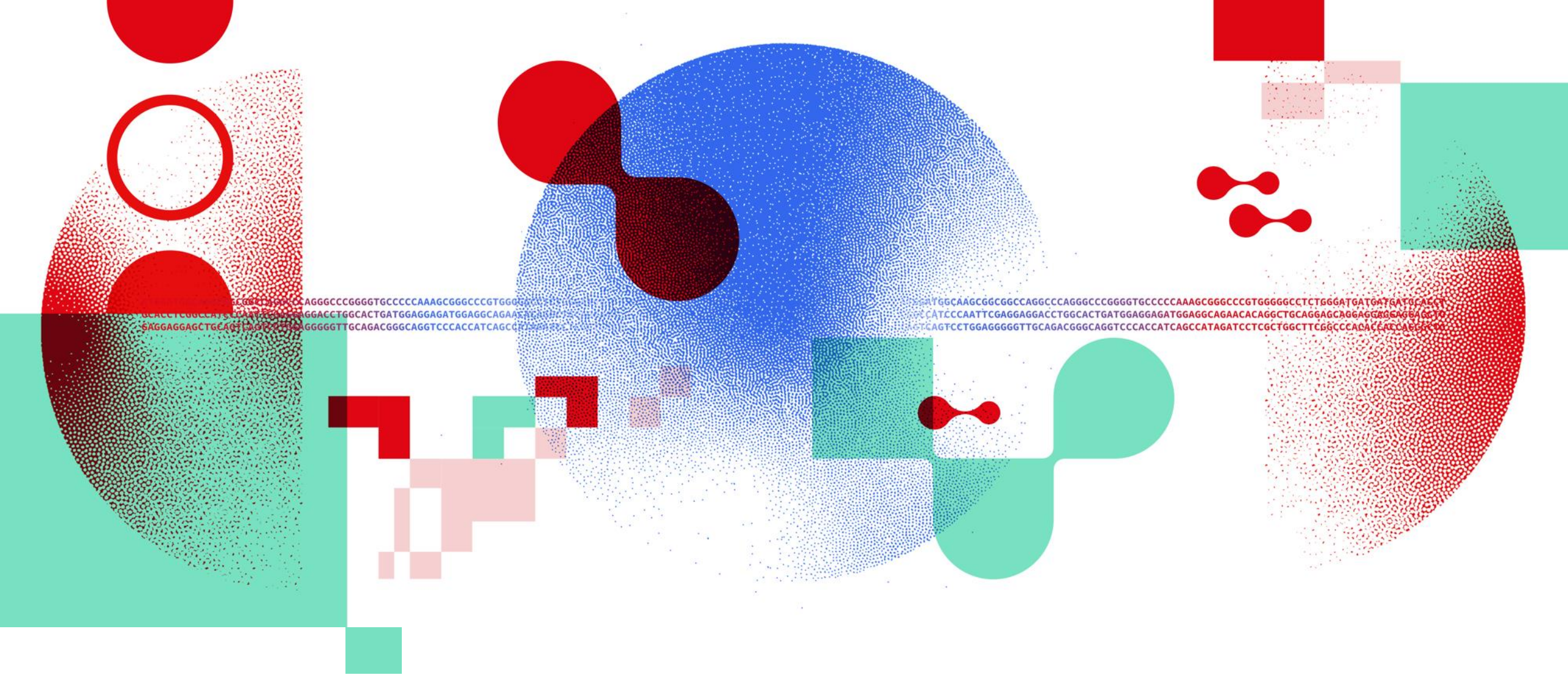
Be reproducible!!

In the afternoon of day 3, all groups will give a **5 minute presentation**

Bonus exercise

1. Run [clumpify.sh](https://www.biostars.org/p/225338/) after trimming, and then perform alignment:
<https://www.biostars.org/p/225338/>
 - How many reads [clumpify.sh](#) removed?
 - Check the alignment rate difference: before and after running [clumpify.sh](#)
2. Run Qualimap on aligned files:
http://qualimap.conesalab.org/doc_html/analysis.html
 - What extra information do you get?

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Thank you

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