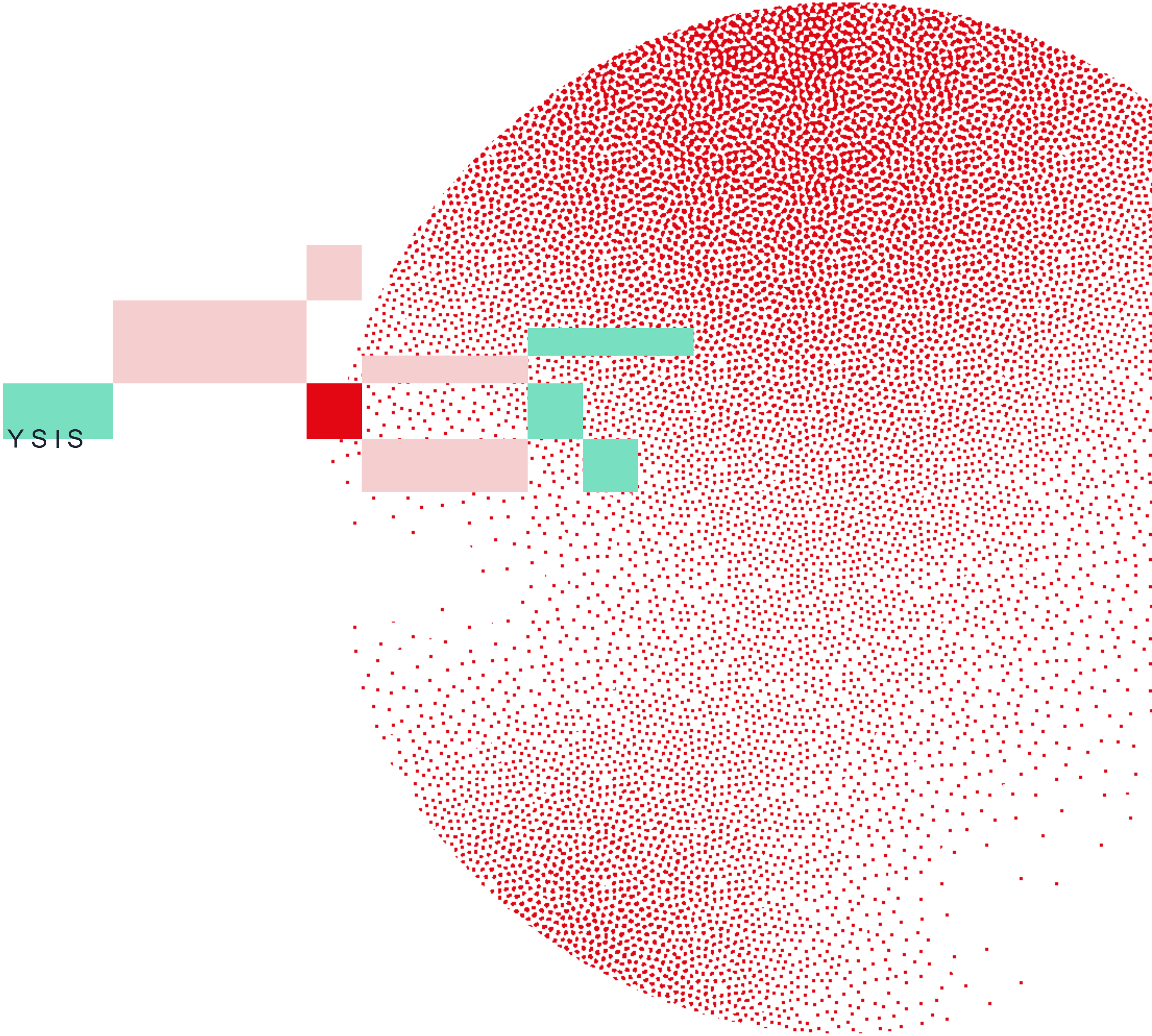
Swiss Institute of
Bioinformatics



INTRODUCTION TO SEQUENCING DATA ANALYSIS

Group work

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April 23-25, 2025
Adapted from previous year courses

elixir
SWITZERLAND

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

Important

Do not <u>only</u> **perform** the calculations, also to **evaluate** the results

Be **reproducible**!!

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

Working style

1. You can work individually and then compare results and present together.

2. You can work together as a group in you group specific folders: /group_work/

Bonus exercise

1. Run clumpify.sh after trimming, and the 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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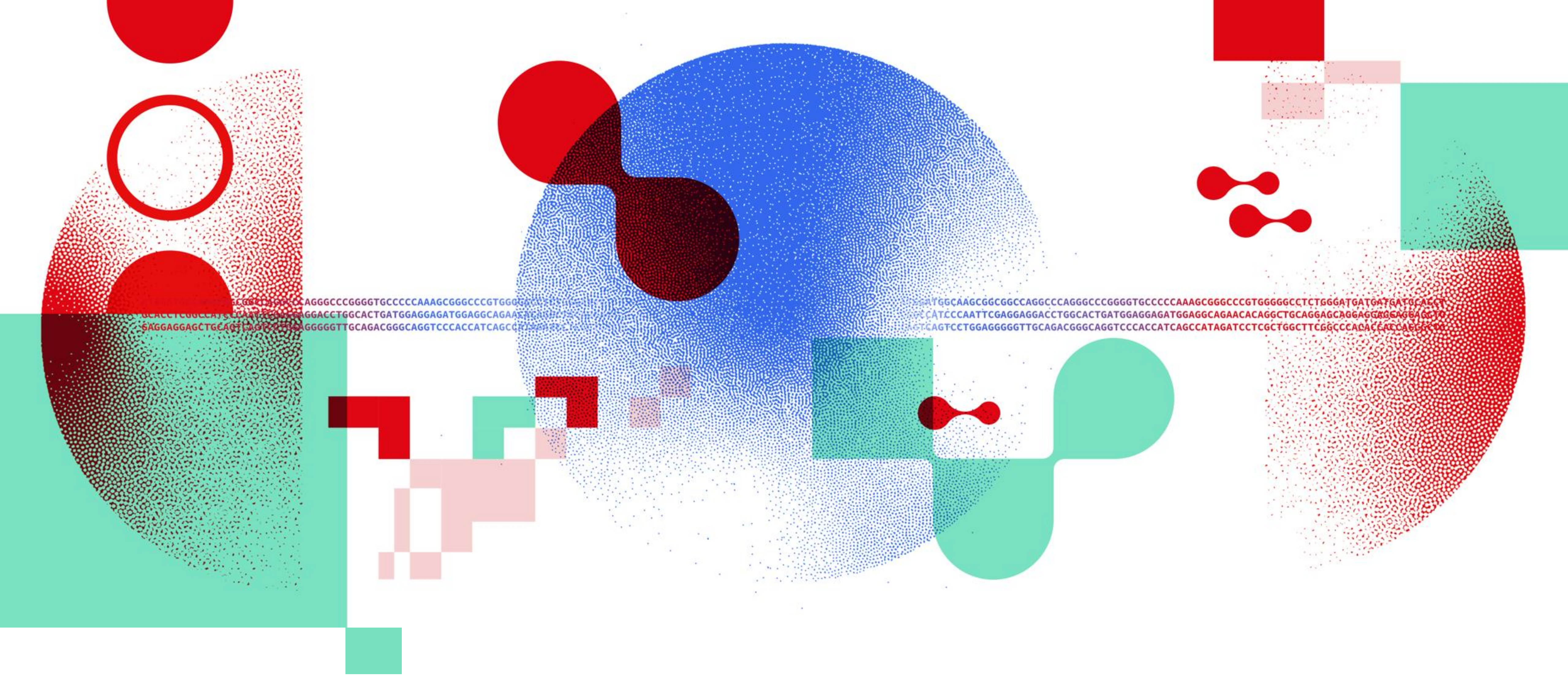

Thank you

DATA SCIENTISTS FOR LIFE

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