

Swiss Institute of  
Bioinformatics

# Single cell transcriptomics

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# Trainers/organisers

- **Patricia Palagi:** Manager training group at SIB
- **Rachel Marccone:** Bioinformatician at SIB
- **Tania Wyss:** Bioinformatician at SIB and UNIL
- **Geert van Geest:** trainer at SIB/bioinformatician at IBU Bern

# Learning outcomes

- Distinguish **advantages** and **pitfalls** of scRNAseq
- **Design** your own scRNA-seq **experiment**
- Apply a **downstream analysis** using R

# Learning experiences

- Lectures
- Quiz questions
- Exercises

# Quiz question 1A & 1B

# Communication

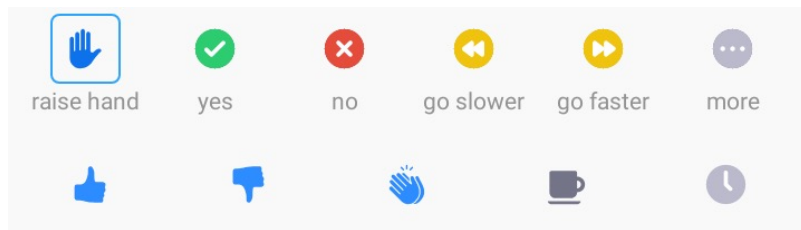
- Course website:

<https://sib-swiss.github.io/single-cell-training/>

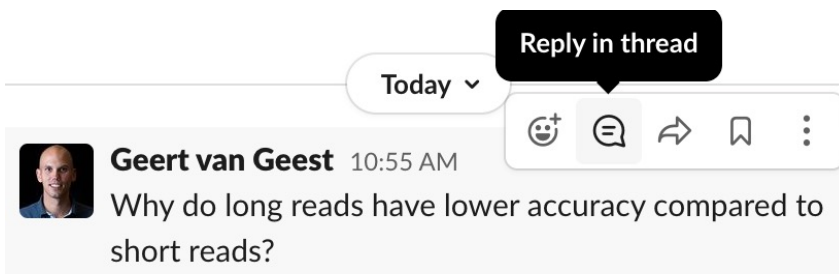
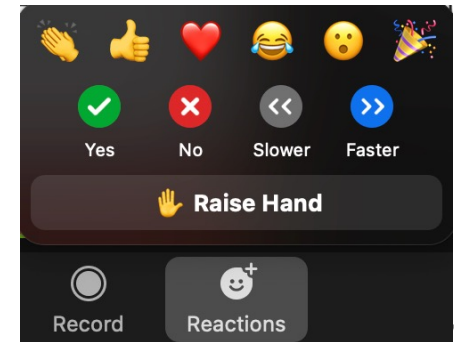
- Slack
- Google docs

# Asking questions

- During lectures: zoom functionality
- Personal interest questions: [#background](#)
- During exercises: [#q-and-a](#) on slack



OR



# Learning outcomes – per chapter



Long-read sequencing analysis



Introduction



Learning outcomes

**After having completed this chapter you will be able to:**

- Illustrate the difference between short-read and long-read sequencing
- Explain which type of invention led to development of long-read sequencing
- Describe the basic techniques behind Oxford Nanopore sequencing and PacBio sequencing
- Choose based on the characteristics of the discussed sequencing platforms which one is most suited for different situations



# Get to know each other

- Write in the google doc (5 minutes):
  - Three keywords about yourself (not necessarily about your profession)
  - Why you are joining this course, and what you want to learn
- You will discuss them in breakout rooms afterwards (15 minutes)
  - Introduce yourself based on what you've written in the doc