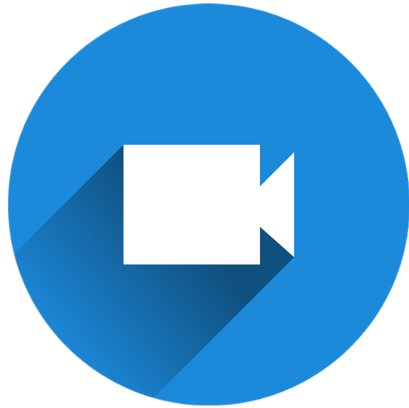# Long-read sequence analysis

Marco Kreuzer

Geert van Geest

Course etiquette

Video on
when
possible

Mute when
not speaking

Teachers

- **Valeria di Cola:** Training manager at SIB
- **Marco Kreuzer:** bioinformatician at IBU Bern
- **Geert van Geest:** Trainer at SIB/bioinformatician at IBU Bern
- **Guest lecture:** Alban Ramette

General learning outcomes

- Describe the **basics** behind **PacBio** SMRT sequencing and **Oxford Nanopore** Technology sequencing

- Use the command line to perform **quality control** and **read alignment** of long-read sequencing data

- **Develop** and execute a bioinformatics **pipeline** to perform an alignment-based analysis

- Answer **biological questions** based on the **analysis** resulting from the pipeline

Learning experiences

- Lectures
- Quiz questions
- Exercises
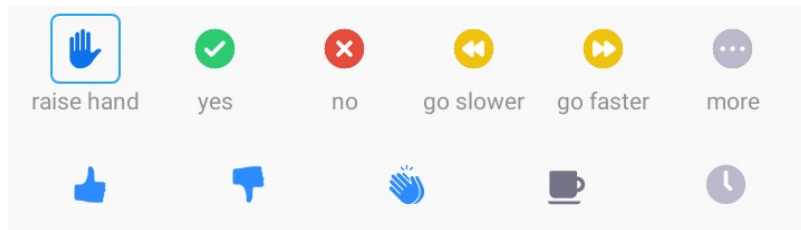- Group project

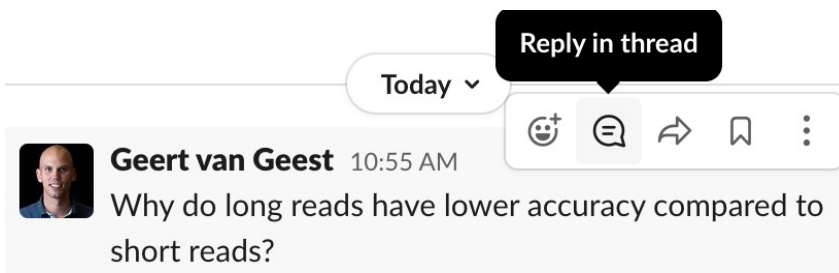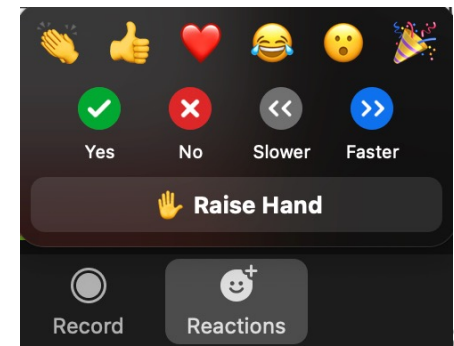# Question 1-3

Communication

- Course website:

https://sib-swiss.github.io/NGS-longreads-training/

- Slack

- Google docs

Asking questions

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

OR

Get to know each other

- Write in the google doc (5 minutes):
  - Three keywords about yourself
  - 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