

# Long-read sequence analysis

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# Learning outcomes

- **Understand** 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
- Be able to do **differential isoform expression** analysis or a **repeat expansion** analysis based on long-read sequencing data

# Learning experiences

- Lectures
- Quiz questions
- Exercises
- Miniproject

# Question 1A&B

# Communication

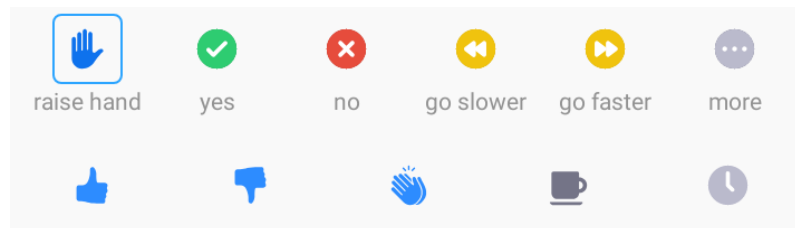
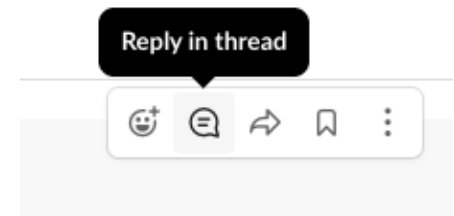
- Course website:

<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
  - if really stuck: **no** button in zoom
  - if finished: **yes** button in zoom



# 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