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
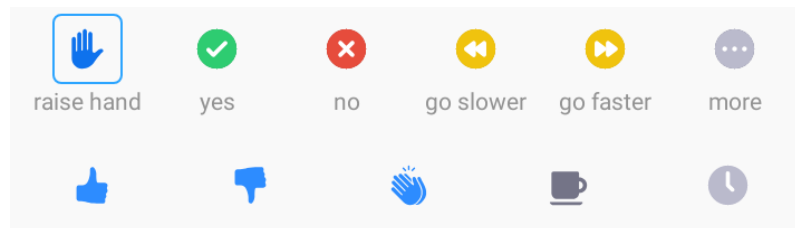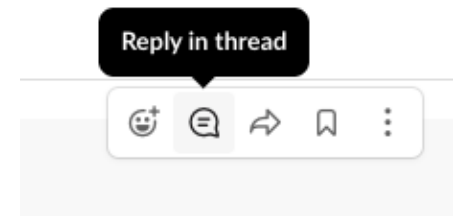- Exercises
- Miniproject

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:
  - #peer_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