

Long-read sequence analysis

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Teachers

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- **Giancarlo Russo:** Expert Genome Informatics FGC Zurich
- **Geert van Geest:** Trainer at SIB/bioinformatician at IBU Bern

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 1A&B

Communication

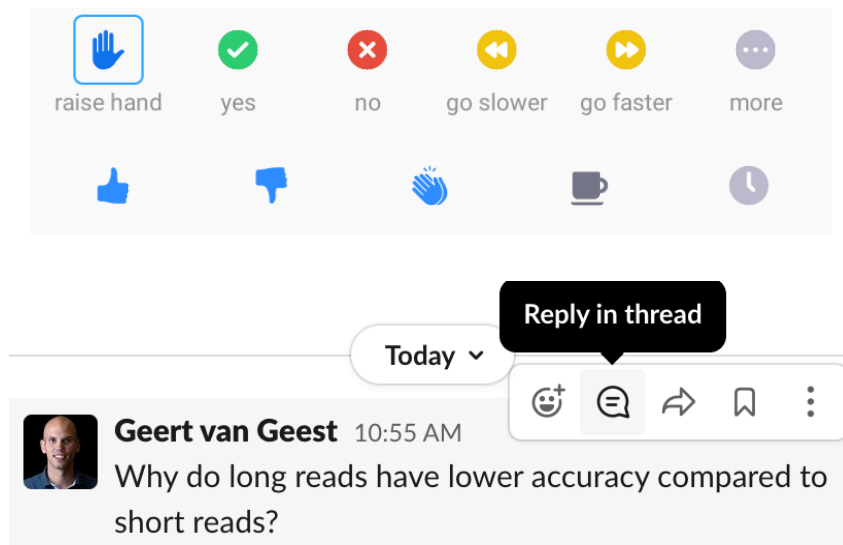
- Course website:

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

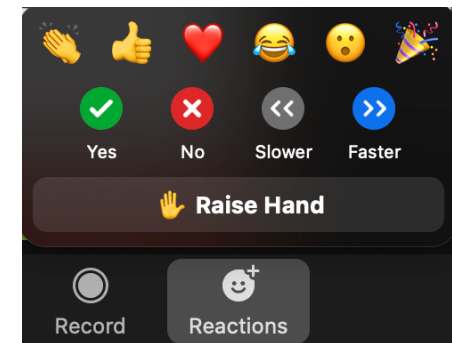
- Slack
- Google docs

Asking questions

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



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
 - 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