

NGS - quality control, alignment, visualisation

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Trainers/organisers

- **Valeria diCola:** Training manager at SIB
- **Geert van Geest:** trainer at SIB/bioinformatician at IBU Bern

Learning outcomes

- Understand the **basics** of the different NGS **technologies**
- Perform **quality control** for better downstream analysis
- **Align** reads to a **reference** genome
- **Visualize** the output

Learning experiences

- Lectures
- Polls + Quiz questions
- Exercises

Poll

Communication

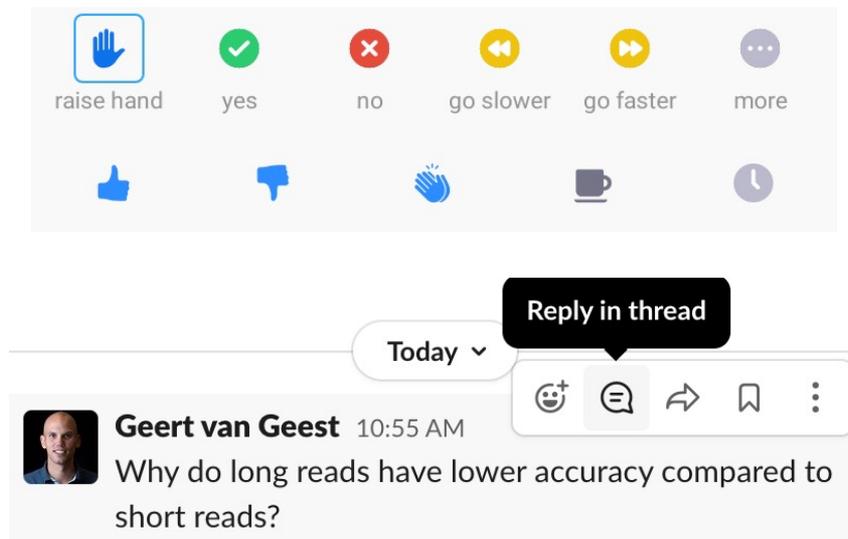
- Course website:

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

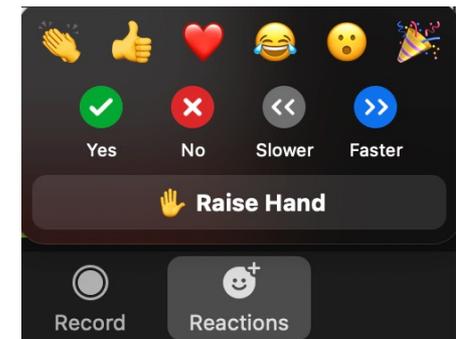
- Slack
- Google docs

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

- Introduction round
- Write three topics you want to learn about