

Getting started with containers

General introduction

Teachers

- **Gregoire Rossier:** Training manager at SIB
- **Roman Mylonas:** Bioinformatician at Protein Analysis Facility, Lausanne
- **Thomas Roder:** PhD candidate at IBU Bern
- **Geert van Geest:** trainer at SIB/bioinformatician at IBU Bern

Learning outcomes

- Understand the basic **concepts** and **terminology** associated with **virtualization** with **containers**
- Be able to **customize, store** and **share** a **containerized** environment with **Docker**
- Understand the essential **differences** between **Docker** and **Singularity**
- Be able to use **Singularity** to run **containers** on a **shared** computer **environment** (e.g. a HPC cluster)

Learning experiences

- Lectures
- Quiz questions
- Exercises

Quiz question 1A & 1B

Communication

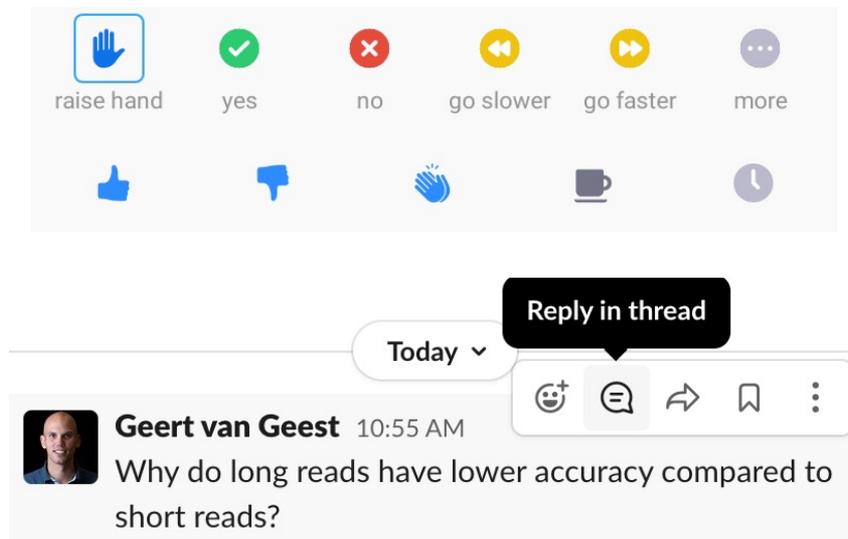
- Course website:

<https://sib-swiss.github.io/containers-introduction-training/>

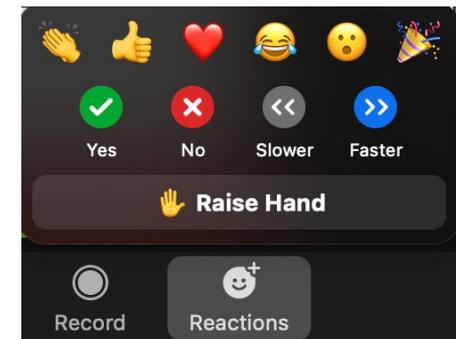
- Slack
- Google docs

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