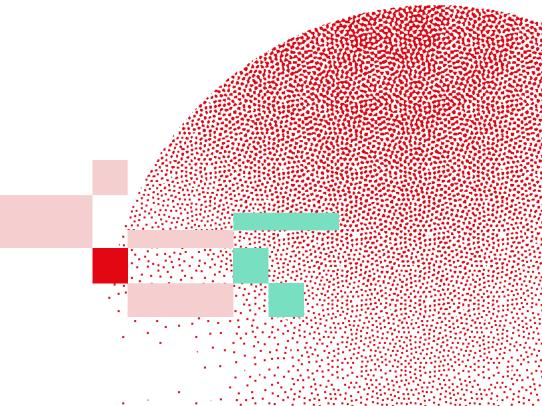COURSE INTRODUCTION

Cancer variant analysis

Flavio Lombardo, Geert van Geest

13.12.2024

Course etiquette

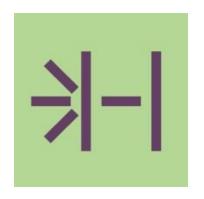**Video on when possible**

Mute when not speaking

Use your **first** and **last** name as your Zoom ID
Right-click on yourself > Rename..

SIB

Trainers/organizers

>> **Diana Marek:** training coordinator at SIB

>> **Flavio Lombardo:** Computational Biologist at the University Hospital Basel

>> **Geert van Geest:** Trainer at SIB + Bioinformatician at Interfaculty Bioinformatics Unit Bern University
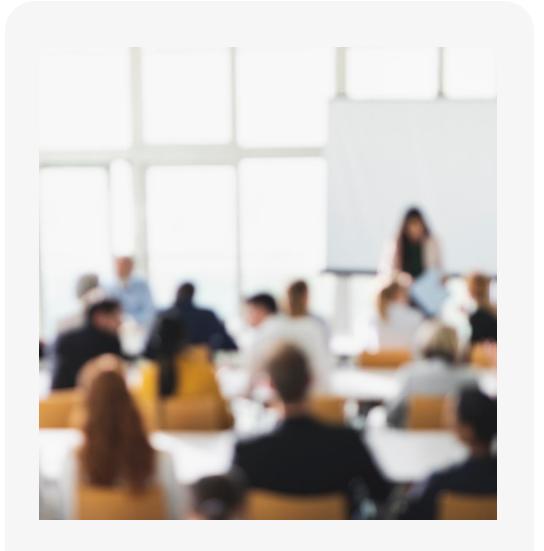
Learning outcomes

▸ Understand the difference between **germline** and **somatic** variants and the implication of computational analysis

▸ **Perform** a somatic **variant analysis** on a **paired** sample (tumor – normal) with GATK4

▸ Perform a somatic **variant annotation** with VEP and use the results to filter possible **high-impact mutations** in the cancer genome

Learning experiences

>> Lectures
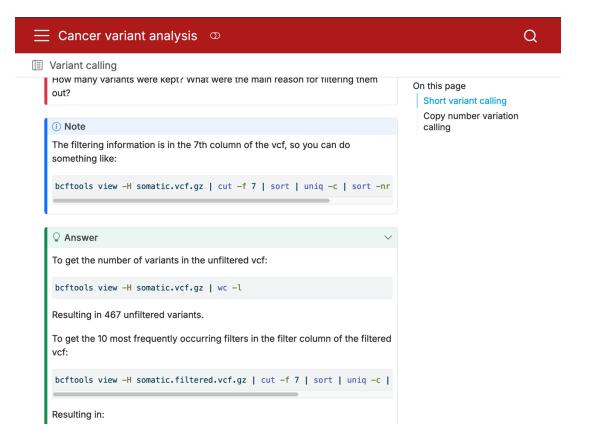
>> Polls + quiz questions

>> Exercises

Question

Communication

∷ Course website: https://sib-swiss.github.io/cancer-variants-training/
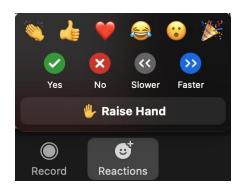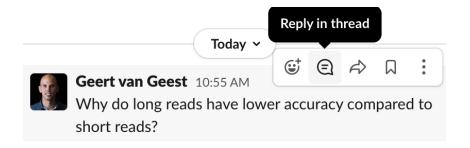
∷ Shared document

∷ Slack

Asking questions

» During lectures: zoom functionality – **but the chat will be ignored**

» During exercises: #q-and-a channel on Slack

Introduction round

>> Your name

>> Where are you working

>> Why are you joining this course