

Swiss Institute of Bioinformatics

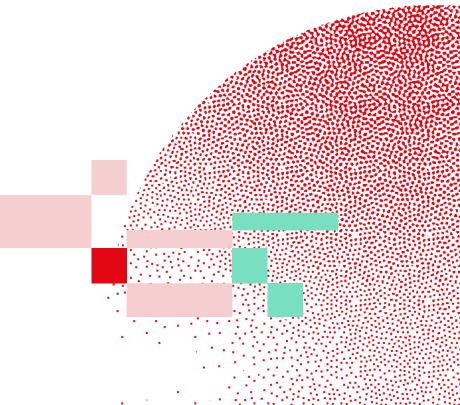
COURSE INTRODUCTION

Cancer variant analysis

Flavio Lombardo, Geert van Geest

13.12.2024







Course etiquette



Video on when possible



Mute when not speaking

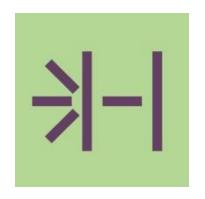
Use your **first** and **last** name as your Zoom ID Right-click on yourself > Rename..





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

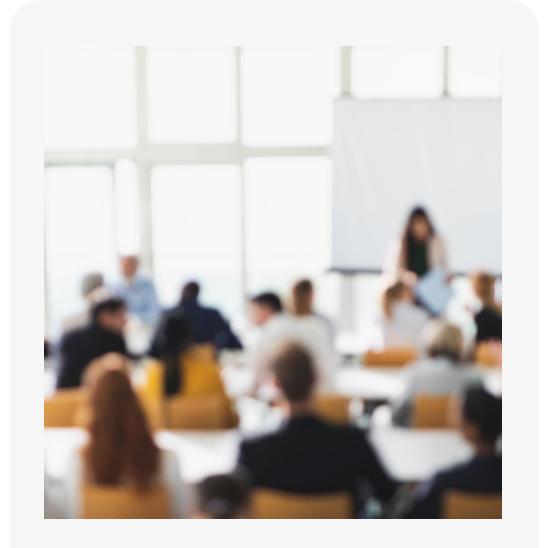
- >> Understand the difference between **germline** and **somatic** variants and the implication of computational analysis
- >>> Perform a somatic variant analysis on a paired sample (tumor normal) with GATK4
- >> Perform a somatic variant annotation with VEP and use the results to filter possible high-impact mutations in the cancer genome





Learning experiences

- Lectures
- >> Polls + quiz questions
- Exercises





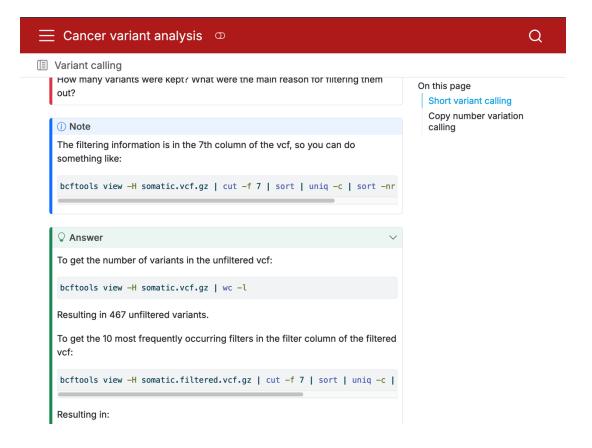




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Communication

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

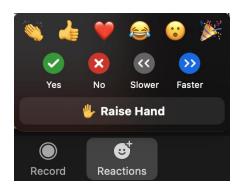


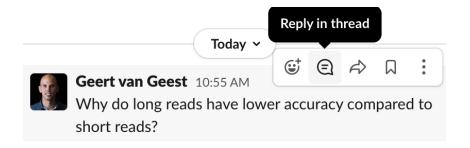




Asking questions

- >> During lectures: zoom functionality but the chat will be ignored
- >> During exercises: #q-and-a channel on Slack









Insert your text here

- >> First level
 - >> Second level



Introduction round

- >> Your name
- >> Where are you working
- >>> Why are you joining this course

