

Swiss Institute of Bioinformatics

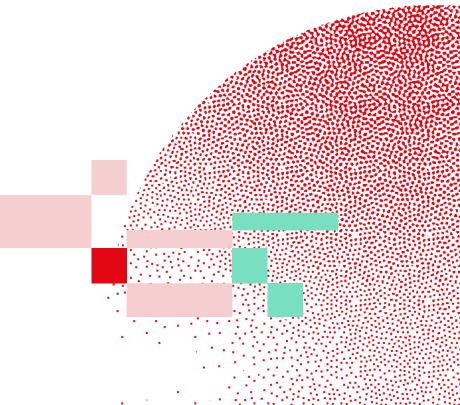
COURSE INTRODUCTION

# 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..





#### Code of conduct

- >> Learning can only be done in a safe environment
- >> We abide to the ELIXIR code of conduct during the course
- If you witness unacceptable behaviour that can't be dealt with with the people involved in this course, contact the <a href="COC oversight group">COC oversight group</a>
- >> More info: <a href="here">here</a>

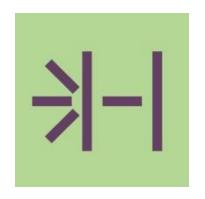






### Trainers/organizers

- >> 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

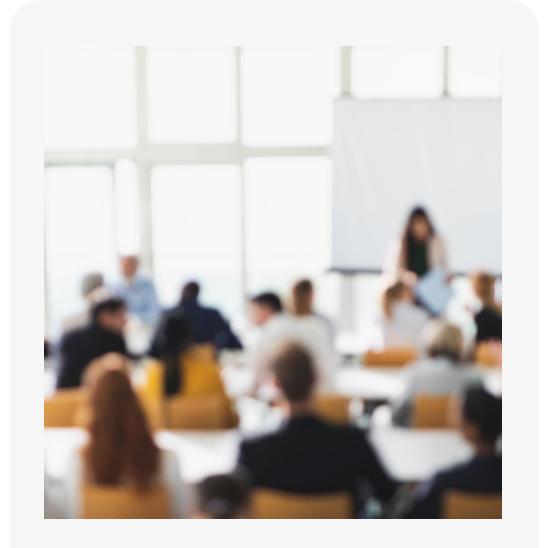
- >> Understand the difference between **germline** and **somatic** variants and the implication of computational analysis
- >>> Perform a somatic variant analysis on a paired sample (tumor normal) with GATK4
- >> Perform a somatic variant annotation with VEP and use the results to filter possible high-impact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





## Learning experiences

- Lectures
- >> Polls + quiz questions
- Exercises





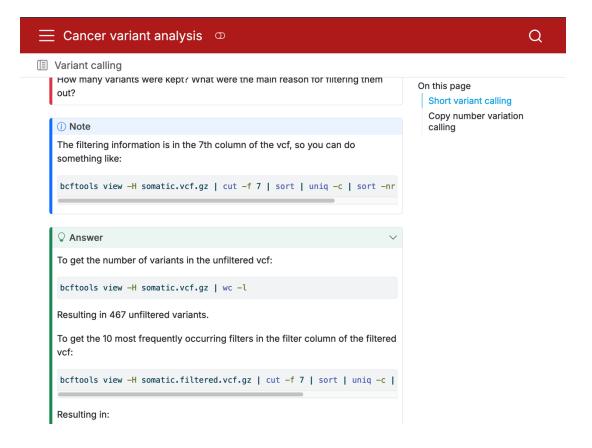




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#### Communication

- >> Course website: <a href="https://sib-swiss.github.io/cancer-variants-training/">https://sib-swiss.github.io/cancer-variants-training/</a>
- >> Shared document
- >> Slack

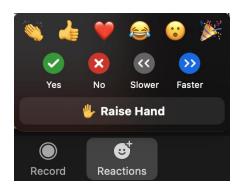


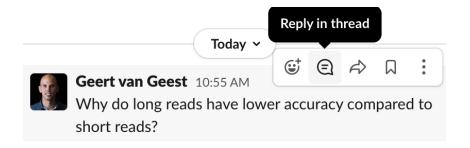




### Asking questions

- >> 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

