

# Welcome to Clinical Cancer Genomics, vt 2025

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# Who are we?

## **Bioinformaticians @ MEB**

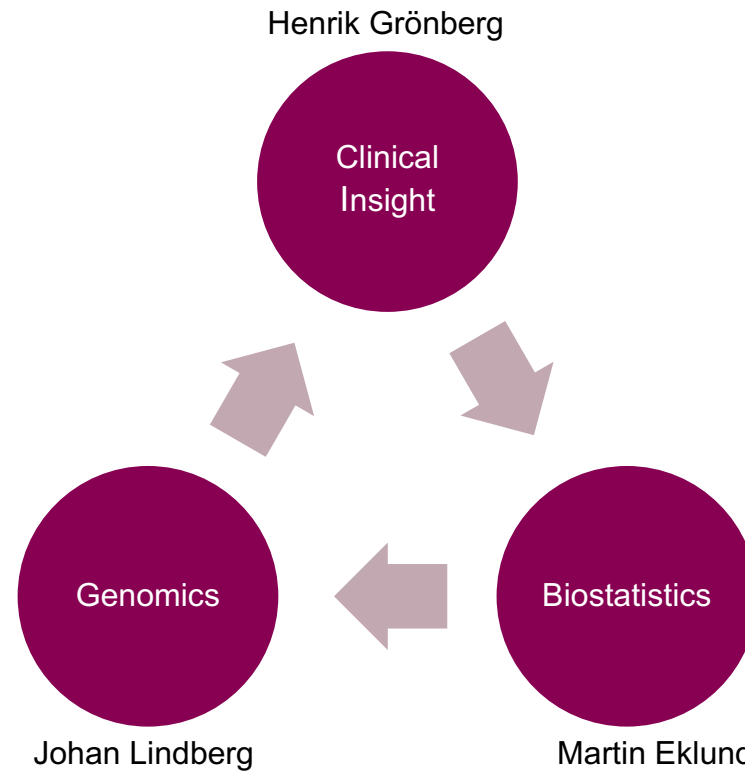
Venkatesh Chellappa  
Sarath Murugan  
Karthick Maniram  
Rebecka Bergstrom  
Markus Mayrhofer  
Nawal Hamidi  
Preeti Lakshman Kumar  
Anupriya Sadhasivam

## **Engineers**

Konstantin Carlberg  
Anastassija Kotsalaynen

## **Postdoc**

Sinja Taavitsainen

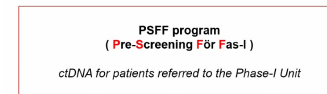
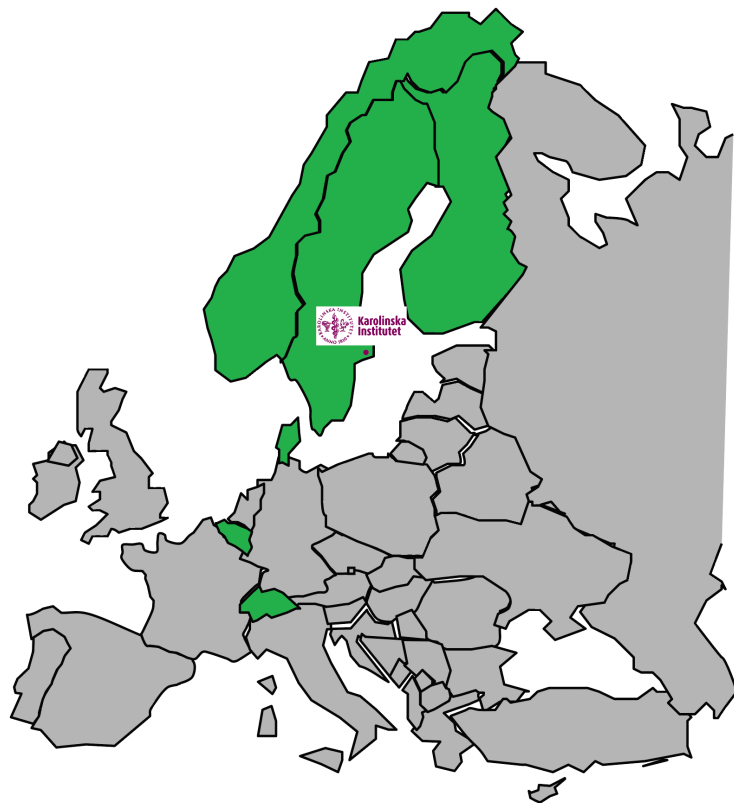


## **ProBio statisticians**

Alessio Crippa  
Andrea Discacciati

Others ...

# Cancer genomics team at KI

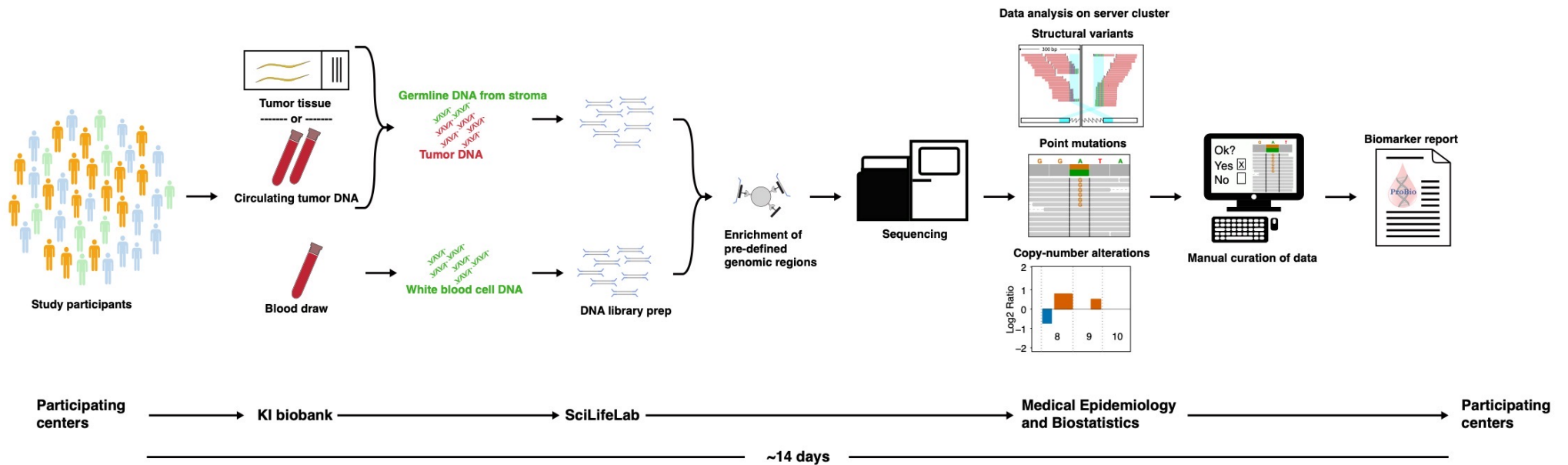


>50 sites in 6 European countries



Karolinska Institutet  
>6500 cases analysed

# Genomics infrastructure



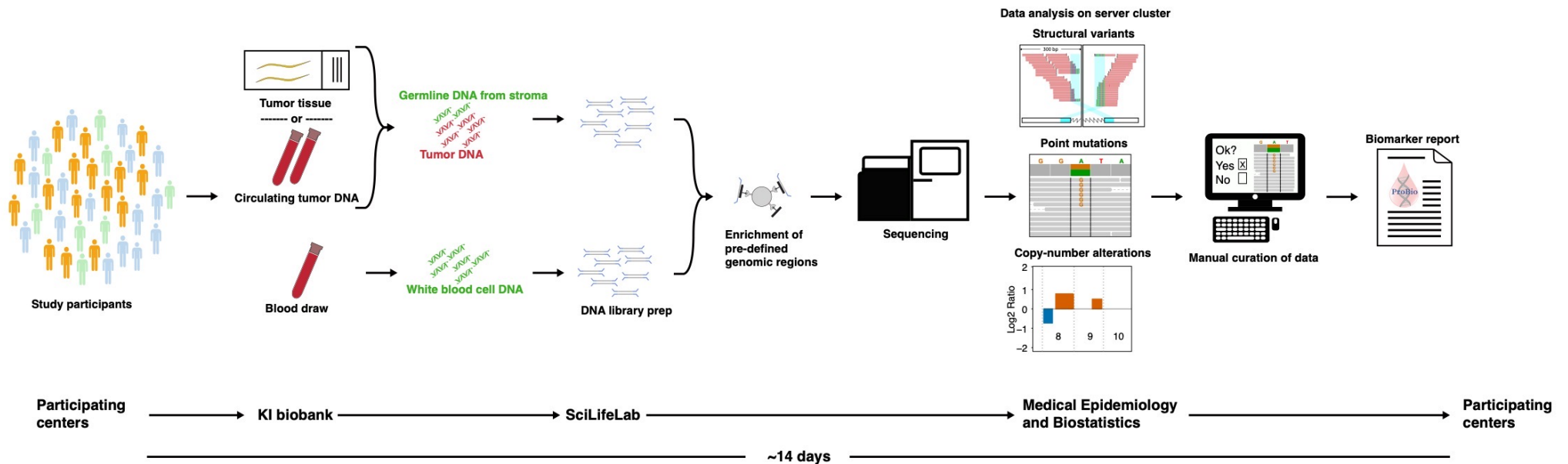


# The iPCM study - sponsored and run through the PCM program



## Aim

- To apply an existing research infrastructure to perform broad genomic profiling of all newly diagnosed advanced solid tumors (>2000) as a research project during one year in Stockholm
- To transfer all individual components of the research infrastructure to long-term PRAGMATIC solutions to facilitate routine implementation



Menti - Course overview

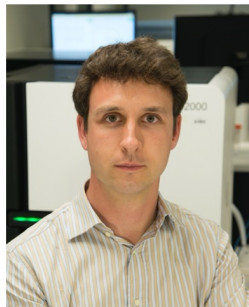
# Modified version of an existing course

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- <https://pmbio.org/course/>
- Course content under MIT license and Creative Commons.



Malachi Griffith, PhD  
Assistant Professor of Medicine  
Assistant Professor of Genetics  
Assistant Director, MGI

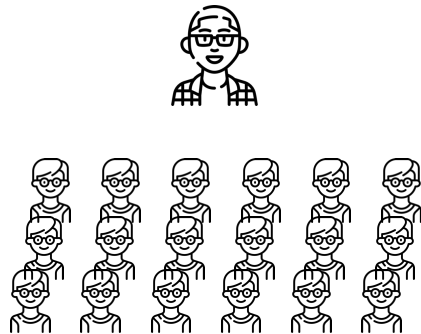


Obi Griffith, PhD  
Assistant Professor of Medicine  
Assistant Professor of Genetics  
Assistant Director, MGI

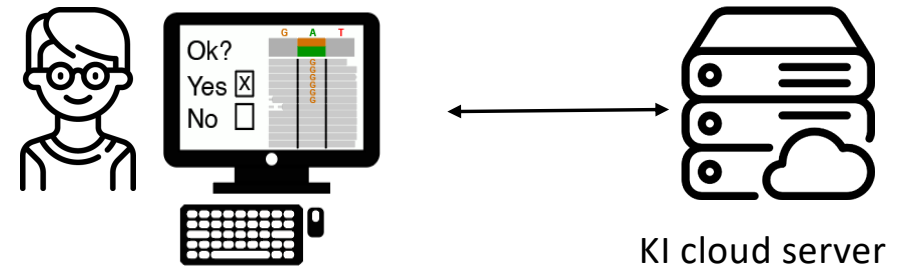
McDonnell Genome Institute, Washington University School of Medicine

# Set-up


## Lectures



## Practical sessions



<https://clinseq.github.io/>

**Clinical Cancer Genomics Course**

Search

**Clinical Cancer Genomics Course**

[Course Details](#)

Schedule

Lectures

**Pre-course setup**

Installation

Download Files

**Lab Session**

Day 1

Day 2

Day 3

WELCOME TO CLINICAL CANCER GENOMICS COURSE

This course aims to provide an introduction to cancer genomics and to support to obtain practical knowledge regarding how to apply state of the art methodology to interrogate the cancer genome in a routine clinical setting or a clinical trial setting. The course will include lectures covering the technology advancements that have enabled high-throughput analysis of cancer genomes and the knowledge that can be obtained by applying these technologies. This encompasses both laboratory sample processing and downstream bioinformatics. Lectures will be held in the mornings with computer-based exercises in the afternoon. The exercises will include processing and analysis of DNA- and RNA-sequencing data covering file formats, quality control aspects, identification of somatic variation, curation of identified somatic- and germline variants for clinical use, clonality estimation and annotation of variants.

The main objective of the course is to facilitate that students get an understanding of basic theory and obtain practical knowledge that will enable course participants to apply the covered methodologies in their own research- or clinical laboratory.

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Learning Outcomes

Contents of the course

Literature and other teaching material

Additional Information

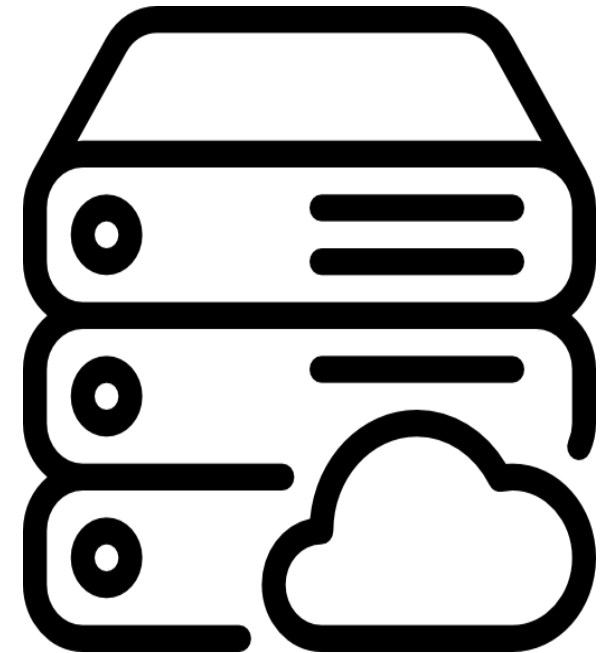
Course webpage, info, lectures and practical sessions.



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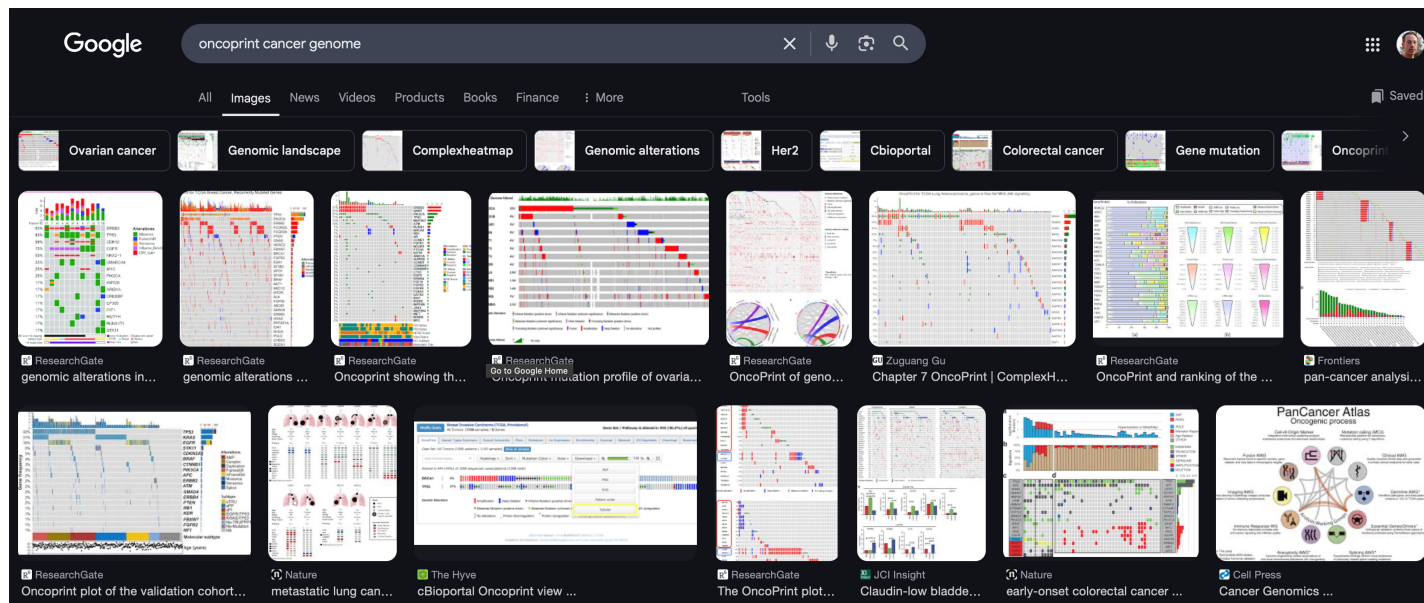
## KI Cloud Server – specs and etiquette

- A big VM - Intel Xeon Gold 5220R – 96 CPUs
- 512G RAM and 500GB SSD
- 4TB /nfs share (working area)
- Do not use **mv** or **rm** commands on any directory within **/nfs/course/inputs/** folder.
- Each of you will have your own working directory within **/nfs/course/students/**, please keep all your files within that directory



# Completion of the course

- Show for a course instructor each day that you have completed and understood the labwork.
  - During the exercises you get questions ...
- Examination task: During the two last days you will be given data from a set of 5-6 prostate cancer genomes. Each student will analyze the data and identify the main drivers/genomic phenotype of each cancer genome. Write a short summary per case and provide plots. We also want you to plot an oncoprint from the five cancer genomes.



Questions?