

Introduction to Bioinformatics for NGS data

Course description:

In this course you will learn how to plan and conduct your own bioinformatic projects for NGS data in a reproducible and reliable way. This includes considerations of experimental designs and appropriate sequencing techniques for your preferred data. Moreover, we will cover important terms and basics of genomics, epigenomics and transcriptomics as well as common file types and tools for NGS data analysis. This will be complemented with practical exercises which do require a basic understanding of Bash. For this, we also offer an optional crash course for Bash one week prior to the course. Furthermore, you will learn to visualize genomic data in IGV with hands-on practice sessions and we will discuss where you can find published data and how you can choose appropriate tools for your NGS analysis. Eventually, you will also learn about good practices in bioinformatics including project and directory setup, tool installation and version control.

Topics:

- Fundamentals of NGS technologies
- Experimental design considerations
- Fundamentals of genomics
- Common file types and tools for NGS data
- Genome visualization
- Organization of bioinformatic projects
- Good practices in bioinformatics

Methods:

Presentations, Hands-on sessions and exercises, Q&A sessions

Format:

- Mode: online course on Teams
- Duration: 1 day (9 am – 5 pm)
- Language: English
- Participants: max. 20 persons

Requirements:

None, but very basic knowledge of Bash is beneficial.

Dates and Application:

You can view the current dates and register for this course on [CaMS](#).