



# CAS Applied Bioinformatics: Next-Generation Sequencing Data Analysis

Advance your expertise in programming, analysis and interpretation

Develop practical skills in next-generation sequencing data analysis through a combination of lectures by experts, interactive exercises, and real-world case studies. You will gain a solid theoretical foundation and practical expertise in applied bioinformatics.

## Contents

This compact programme offers a comprehensive introduction to the analysis of sequencing data from Next-Generation Sequencing (NGS) and Oxford Nanopore Technologies (ONT). You will develop both a theoretical understanding and practical skills in applied bioinformatics, with a strong focus on reproducible workflows using widely used open-source tools.

The programme begins with fundamental programming skills needed in modern bioinformatics. You will work with Python, Git for version control, and Unix-based systems, gaining confidence in using command-line tools and Jupyter for interactive coding and scripting.

Building on this foundation, the second module focuses on the processing and analysis of raw sequencing data. Topics include key file formats such as FASTQ, BAM, and VCF, as well as essential steps like quality control, read alignment, variant calling, and metagenomics workflows using tools such as GATK.

The final module emphasizes the biological and clinical interpretation of sequencing results, applying statistical and visualization results. You will learn to perform gene expression analysis, pathway enrichment, and variant annotation using databases like Ensembl, ClinVar, and Kraken. Real-world case studies from research and clinical contexts ensure the direct applicability of all concepts.

## Target Group

This programme is for you if you work in life sciences, healthcare or research and want to build practical skills in bioinformatics. It is particularly relevant if you:

- Work with or plan to work with next-generation and nanopore sequencing data
- Are in life sciences or research, looking to analyse genomic or transcriptomic data

- Are a clinician who wants to interpret sequencing data in a clinical or translational context
- Work in biotech, pharma, or a related industry where sequencing analysis is becoming essential

You should have a basic understanding of molecular biology, some hands-on experience with a programming language such as Python, and strong motivation to strengthen your computational skills.

The admission criteria are outlined in the programme description on our website.

**Format**

The programme includes:

- 12 instruction days, held on Thursdays
- An individual project

On completing the programme, you will submit a written report and give a brief presentation summarizing the methodology, tools, and key findings of your project.

All lessons are online, with the option of attending the first and last day in person at FHNW Campus MuttENZ.

**Degree / ECTS**

Certificate of Advanced Studies FHNW Applied  
Bioinformatics: Next-Generation Sequencing Data Analysis  
/ 12 ECTS

**Location**

Online and FHNW Campus MuttENZ

**Programme Manager**

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**Further Information and Registration**

[www.fhnw.ch/applied-bioinformatics](http://www.fhnw.ch/applied-bioinformatics)

