

Analysis of next-generation sequencing data

PhD course, 5 ECTS, June 28-July 2, each day 9 am to 5 pm

Location: Bioinformatics Research Center, Aarhus University, Building 1110

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Sign up by email to teachers or through AU Summer University

Aims:

Learning the basics of next generation sequencing analysis in practice

Topics:

Sequencing methods, short and long reads

SNP calling

De novo assembly

Reference-based mapping

Single-cell transcriptomics

Metagenomics

Exercises:

Introduction to Galaxy, GATK, Samtools, IGV

Introduction to Jupyter notebooks and Python

Grooming of reads

Building bioinformatics workflows

Mapping of Illumina and PacBio reads to reference

De novo assembly of PacBio reads

SNP/indel calling, filtering and annotation

Gene models

Analysis of scRNA-seq data

Bring your own data! – or use our examples from white clover and humans

No prior experience with next-generation sequencing data analysis needed

