

OUS/IBA Bioinformatics course - Level 1

Day: **Thursday, November 10th 2022**
Time: **09:30 - 12:00**
Venue: **University of Oslo, Domus Medica (DM4), L-257**



Application deadline: November 1st 2022

09:30 - 10:15 Part I: Introduction to Whole Genome Sequencing

Theoretical introduction and applications in microbial whole genome sequence analysis:

- Basic whole genome sequence assembly and bioinformatics
- NGS read-to-reference alignment (contig assembly)

Analysis techniques covered will employ raw data from Illumina platforms (HiSeq/MiSeq).

After giving a short overview of Next Generation Sequencing, paired-end reads and the difficulties of whole genome assembly, we will address quality control of the raw data (FastQC), common file types and adapter/quality trimming. Differences between De novo assembly and mapping to an annotated reference genome will be explained, and we will present different software solutions and tools.

10:15 - 10:30 Coffee break

10:30 - 12:00 Part II: Hands-on exercise

- Quick explanation of associated file types
- Performing quality checks with FastQC (before and after trimming)
- Adapter and quality trimming
- Contig assembly and mapping to reference genome

Participants must bring their own laptops (limited to 8 persons, on a first-come first-serve basis). A list of required programs including instructions on how to install them will be provided before the course. You do not need any previous knowledge to attend this beginner's course.

Please register at the following link: <https://nettskjema.no/a/289651>

Hospital employees of the Helse Sør-Øst region, IBA members and applicants from outside of Oslo will be prioritised for this course. Depending on the number of registrations, we are considering to organize one repetition of this course on November 16th. Applicants who can't join the course on November 10th will be offered a place in the repetition course instead.

Timo Lutter
Spesialingeniør/bioinformatiker, Seksjon for utvikling, MIK, OUS