

OUS/IBA Bioinformatics course - Level 2

Day: **Thursday, November 10th 2022**
Time: **12:45 - 15:30**
Venue: **University of Oslo, Domus Medica (DM4), L-257**



Application deadline: November 1st 2022

12:45 - 13:30 Part I: Theoretical introduction and short summary of level 1

After a brief repetition of required level 1 knowledge, we will give an introduction to:

- SNP calling and phylogenetic trees
- RNAseq and differential gene expression

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

13:30 - 13:45 Coffee break

13:45 - 15:30 Part II: Hands-on exercises

- Map to reference assembly and building of SNP trees in *Geneious* with PhyML (using Ebola virus isolates as an example)
- RNAseq and differential gene expression in *Geneious*

This course is a continuation of OUS/IBA bioinformatics course level 1 and requires some basic knowledge of whole genome assembly, including quality assessment of raw data, trimming and contig assembly. All applicants must have attended our beginner's course, however, we will give a short repetition of level 1 content at the beginning of the level 2 course.

Participants must bring their own laptops (limited to max 8 persons, on a first-come first-serve basis). A list of required preparations including instructions on how to install *Geneious* trial version will be provided a week before the course. If you have used a trial version of *Geneious* before, we will send you an educational license for this 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