TTA Bioinformatics course – Level 2

Tuesday, October 29th 2019
Time: 13.00-16.00
Venue: University of Oslo, DM4 Domus Medica, L-257

Application deadline: **October 20th 2019**

13.00 - 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 tree building
• 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 - 16.00   Part II: Hands-on exercises

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

This course is a continuation of TTA bioinformatics course level 1 and requires some basic knowledge of whole genome assembly, including quality assessment of raw data, trimming and contig assembly. Although not a strict requirement, we recommend participants to attend level 1 before signing up for this advanced course.

Participants must bring their own laptops (limited to max 12 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 the course.

Please register at the following link: https://nettskjema.no/a/124938

We will be organizing a **bioinformatics level 3** *course on December 3rd 2019, where we will give an introduction to command line tools, whole genome alignment and how to build a WGS pipeline in Geneious.*

Timo Lutter & Nermin Zecic

TTA TURNING THE TIDE OF ANTIMICROBIAL RESISTANCE