TTA Bioinformatics course – Level 2

Monday, September 10th 2018
Time: 11:00-17:00
Venue: University of Oslo, Domus Medica, PC-stua (R211)

Application deadline: **August 27th 2018**

Part I: Seminars 11:00 – 12:30:

Theoretical introduction to the course and short repetition of required level 1 content.

11:00 – 11:30	**Timo Lutter (TTA)** -	*SNP calling, phylogenetic tree building and whole genome alignment*
	Nermin Zecic (TTA) -	*RNAseq and differential gene expression*
11:30 – 12:00	**Henrik Hasman** **(Statens Serum Institut, DK)** -	*Identification of acquired antibiotic resistance genes with ResFinder*
12:00 – 12:30	**Jon Bolin (FHI)** -	*Mechanisms of foreign DNA acquisition and their detection in microbial genomes*
12:30 – 13:00	**Lunch**	

Part II: Hands-on exercises 13:00 – approx. 17:00:

- Map to reference assembly and building SNP trees in *Geneious* with RAxML (using Ebola virus isolates as an example)
- Basic alignments of bacterial genomes and draft genomes to detect large-scale evolutionary events (rearrangements/inversions) with *Mauve*
- RNAseq and differential gene expression in *Geneious*
- Introduction to *Center for Genomic Epidemiology* and *ResFinder* for identification of antimicrobial resistance genes

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 do recommend participants to attend in level 1 before signing up for this advanced course.

Participants of the hands-on session must bring their own laptops. A list of required preparations including instructions on how to install *Geneious* trial version will be provided end of August.

Please sign up for the course here: https://nettskjema.uio.no/answer/99244.html