TTA Bioinformatics course – Level 1

Wednesday, December 9th 2020
Time: 13.00-15.30
Venue: University of Oslo, DM4 Domus Medica, L-257

Application deadline: **November 30th 2020**

13.00 - 13.30 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.

13:30 - 13:45 Coffee break

13.45 - 15.30 Part II: Hands-on exercises

- 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 6 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/170608

*Due to Corona virus restrictions, the course will be limited to **6 participants**. If there are more applicants, we will organize a repetition of the course. In the event of cancellation due to updated infection control measures by the University of Oslo, we will postpone the course to 2021, and all accepted course participants will be given the chance to join.*

Timo Lutter & Marta Gómez Muñoz

TTA TURNING THE TIDE OF ANTIMICROBIAL RESISTANCE