

TTA Bioinformatics course – Level 1

Tuesday, September 17th 2019

Time: 13.00-16.00

Venue: University of Oslo, DM4 Domus Medica, L-257

Application deadline: September 10th 2019

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 - 16.00 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 12 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/122628>

This course (or any previous level 1 course) is a requirement, if you want to participate in our advanced course on October 29th 2019, where we will give an introduction to command line tools and how to build a WGS pipeline in Geneious.

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