OUS/IBA Bioinformatics course - Level 1

Day: **Monday, June 12th 2023**
Time: **09:30 - 12:00**
Venue: **University of Oslo, Domus Medica (DM4), L-257**

Application deadline: May 31st 2023

09:30 - 10:15   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.

10:15 - 10:30   Coffee break

10:30 - 12:00   Part II: Hands-on exercise

- 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 8 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/342140**

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 in September. Applicants who can't join the course in June will be offered a place on the waitlist.

Timo Lutter
Spesialingeniør/bioinformatiker, Seksjon for utvikling, MIK, OUS

OUS/IBA Bioinformatics course - Level 2

Day: **Monday, June 12th 2023**
Time: **12:45 - 15:30**
Venue: **University of Oslo, Domus Medica (DM4), L-257**

Application deadline: **May 31st 2023**

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/342140**

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 in September. Applicants who can't join the course in June will be offered a place on the waitlist.

Timo Lutter
Spesialingeniør/bioinformatiker, Seksjon for utvikling, MIK, OUS

OUS/IBA Bioinformatics course - Level 3

Day: **Tuesday, June 13th 2023**
Time: **09:30 - 16:00**
Venue: **University of Oslo, Domus Medica (DM4), L-257**

Application deadline: **May 31st 2023**

09:30 - 12:00   Part I: How to build a 16S rRNA pipeline in Geneious

We will start with a general introduction on workflows in *Geneious*, including example workflows, testing and debugging. Using raw data from 16S Sanger sequencing, we will explain the biological background and purpose of this pipeline, the advantage of local Blast search and every step of this pipeline from raw data to exported result files.

Participants will then build this pipeline on their own laptops (educational licenses for *Geneious* will be provided) with help of the instructors and a step-by-step handout

Analysis techniques covered will employ raw data from Sanger sequencing, but we will also provide additional exercises focusing on WGS and raw data from Illumina MiSeq.

12:00 - 12:45   Lunch break

12:45 - 16:00   Part II: Introduction to the command line tools

- Motivation: Why is it useful to learn command line?
- Basic commands, text manipulations and short exercises
- How to build a simple WGS pipeline using *Bash* (adapter and quality trimming with *BBDuk*, mapping to reference assembly with *Bowtie2*, de novo assembly with *SPAdes*)

This course is a continuation of the OUS/IBA bioinformatics course level 1+2 and requires some basic knowledge of whole genome assembly, including quality assessment of raw data, trimming and contig assembly. **To apply for this course, you must have attended in our level 1 course in the past, whereas level 2 is not a prerequisite.**

Participants must bring their own laptops (limited to max 8 persons, on a first-come first-serve basis). Educational licenses of Geneious will be provided for the hands-on part.

Please register at the following link: **https://nettskjema.no/a/342140**

Hospital employees of the Helse Sør-Øst region and IBA members will be prioritised for this bioinformatics course.

Timo Lutter, Jessin Janice & Stephan Frye
Bioinformaticians at Seksjon for utvikling, MIK, OUS