E5444 Analysis of sequencing data

Lesson 2 – Projects description

Projects description

Group project

- During the semester <u>Group project (2-3</u> <u>persons</u>) – max 20 points – finished before the start of the exam period
- Aim: Analysis of NGS data from raw data to interpretation
- Data: Downloaded from databases or your own
- The projects will be defended last two weeks of the semester
- The project has to score **minimum 10 points**
- PROJECTS MUST BE SELECTED before 13.10.2023

Project

- Type of samples:
 - Bacteria/fungi/mouse/human/plant/metage nome
- Type of sequencing:
 - WGS, WMGS, RNAseq, variant calling, ITS/16S
- Possible aims and numbers of samples:
 - identification of strains (5-10) by WGS taxonomy/phylogeny
 - differentially expressed genes (min 10 per group) by RNAseq / functions/pathways
 - identification of mutations by targeted sequencing of mutations (min 10 per group)
 - identification of taxonomical composition /functional annotation (min 10 per group)

Data

- Own data or publicly available data
- Published article, with clear methodology and sample preparation
- Instrument:
 - Illumina (MiSeq, HiSeq, NextSeq, NovaSeq)
- Strategy:
 - RNA Seq, WGS, WES, WMGS, 16S/ITS
- Layout:
 - Single, Paired
- Organism:
 - Human, Mouse/Rat, Bacteria, Fungi, Plant
- Processing:
 - Raw read files