Integrative Bioinformatics
BIOINF 4220 (4 ECTS credits)

Übersicht

Many biological research questions are centered around trying to understand how small changes in the organisms genome and environment can result in major changes in the cellular and organismal phenotype. Examples for such changes in phenotype can be different body height/weight, pathogenisis, or altered metabolic rates. To gain insights into the mechanism regulating how an organism functions, ideally the full underlying biological system needs to be understood and modeled. To do so, available measurements of the different layers in the central dogma (transcription, translation) and further cellular function (metabolism) have to be integrated.

This course thus deals with one of the central tasks of bioinformatics: integration and unification of biological data from different sources. Specifically, we well work with data sets for genome, transcriptome, proteome and phenome measurements and try to coax out mechanistic insights into the correlation between the genome and downstream processes (altered gene expression and altered metabolism).

Goals

- Data Integration using Python (and relevant packages)
- Genotype-Phenotype centered analyses (GWAS & PheWAS)
- Differential gene expression and pathway analysis
- eQTL (Expression Quantitative Trait Loci) Analysis based on pathway / network information

Requirements

- Master in Bioinformatics (or at least Bioinformatics 1 and 2)
- Proficient in a scripting language, preferably Python and/or willingness to pick the necessary skills prior (!) to the course

Evaluation

- To pass the practical course a report will have to be handed in. The grade is based on this report and passing requires an overall grade of 4.0 or better

Materials

Folien werden in der Vorlesung ausgegeben. Materialien und Folien werden zusätzlich auf der ILIAS Kursseite veröffentlicht.

Ecktermine

April
Preliminary meeting

21st August – 1st September
Practical Course

1st Oktober
Hand-in of report