Bioinformatics in Genomics and Proteomics (KRS504)

Objective

This course will be structured in a bottom-up method. It will lead from the basic building blocks of information, namely nucleotides in the genome, to their functional translation as proteins. Each important stage, such as transcription, translation, transformation, protein folding, and so forth, will be examined from three points of view, namely from the perspective of genomics, proteomics and bioinformatics. Most topics will only be introduced on a high level omitting most detail, which will be introduced in the follow-up course KRS505, which will assume that topics learned in this course are already known.

Course Structure

The course consists of both, lecture and practical exercises which will parallel the topics introduced in the lecture. Practical exercises are purely *in silico*, meaning that no wet lab experiments will be performed in this course.

At the beginning a small literature research project will be given to each participant who shall present the findings as a short 15 min presentation. The last day of this course will not have a practical exercise; instead participants will present their projects and the final exam will also take place that day.

Grading

30%   Research Project with Presentation
30%   General participation, in class work, and homework
40%   Final Exam
tba   Optionally, a project can be implemented

Books

Genes IX: Lewin, B, ISBN: 978-0763752224
Bioinformatics: Oregon, CA, Jones DT, and Thornton JM, ISBN: 1-85996-054-5
Molecular Biology and Genomics: Mulhardt, C, ISBN: 978-0120885466

Course Schedule

1. Introduction to Genomics
   a. Nucleotides and Sequence
   b. Patterns and Motives
   c. Transcription
   d. Translation
2. Computational Analysis of the Genome
   a. Pattern and Motive Discovery
   b. Similarity Analysis
   c. Evolutional Distance and Heritage Trees
   d. Gene Prediction
3. Introduction to Proteomics
   a. Functional Genomics
   b. Protein Folding and Modifications
   c. Motives and Patterns
   d. Proteome(s)
4. Methods in Proteomics
   a. Protein Extraction
   b. Gel Based Protein Separation
   c. More Separation Methods
   d. Denaturation Renaturation Digestion
5. Protein Identification
   a. Edman Degradation
   b. Mass spectrometry (MS)
   c. Computational Analysis of MS
   d. Protein identification