

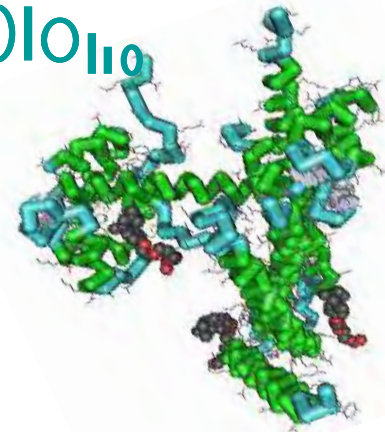
Course description: This course (1h lecture, 1h lab) gives students in all fields of life sciences an overview of the information publicly available in networking molecular databases. We will discuss how this information is generated and which tools can be applied to retrieve and analyze this information.

Goals and Objectives: This course explores the use of bioinformatics software and enables the students to apply it beyond the “default” settings by focusing on the underlying algorithms. Topics will span the entire field from identifying a single nucleotide sequence, functional integration and structural modeling to the analysis of entire ecosystems through metagenomics.



Sessions (1-3 lectures and labs per session):

- S1 Databases – Content and Access
- S2 Sequence Analysis
- S3 Comparative Sequence Analysis
- S4 Motifs and Patterns
- S5 Structure Predictions and Reliability
- S6 RNA structure, predictions and processing
- S7 Proteins – structure, function, and targeting
- S8 “Omics” databases and the HapMap project
- S9 Systems Biology Tools
- S10 Environmental Genomics



LAB: Students bring projects from their own research to the lab sections whenever possible. This enhances their interest in understanding and applying informatics and enriches their thesis work.