RUHR UNIVERSITÄT BOCHUM

RUB

Module sheet

Title of module	II Bioinformatics
Module - coordinator	PD Dr. Mathias Lübben

Credit points	5	Semester(s) in which the module is taught	1
Contact hours	3	Workload	150 hours

Lecturer(s)	M. Lübben, A. Mosig,, Schlitter, R. Stoll
Type of teaching	Lecture (2 hours per week) Seminar (1 hour per week) During lectures and seminars discussions will be promoted; feedback regarding understanding and progress will be stimulated. Skills for efficient Computer application on complex questions in molecular genetics and protein biochemistry will be trained by including Computer practical classes
Relation to curriculum	Compulsory; For master students of Biology/Biotechnology and Biochemistry of RUB, this module is suitable as an elective lecture (needs more clarity-change as in previous modul).
Recommended prerequisites	No prerequisites from curriculum: Students taking this module will be expected to have a basic understanding of mathematics, genetics and molecular cell biology.
Aims	Students will acquire an overview of bioinformatics with respect to systemic and molecular biosciences and be enabled to apply them to case problems.
Learning outcome	Knowledge: Fundamentals of bioinformatics and databases have been learned. Skills: Students have acquired skills in: - applying computer programs as well as web-based services - work on programs in vector construction, analysis of gene structure etc. - homology search of sequences - theoretical concepts and strategies are concisely presented and further deepened by case studies. Competencies: As a primary goal, the student has learned how to solve case problems by practical computer exercises.
Contents of module	Introduction to bioinformatics, role of computers and of the internet for life sciences. Construction and use of DNA- and protein-related databases. Integration of databases. Bioinformatics search tools, search algorithms, profile and motif searches. Homology search of sequences (FASTA, BLAST) and special applications (PHI- and PSI-BLAST), statistical significance analysis of results. Construction of genomes, genes and proteins; splicing.

	Analysis of DNA and protein data by means of freely available and proprietary software tools; virtual cloning. Strategies of genome sequencing (microorganisms and higher organisms), "Next generation" sequencing methods; genome annotation. Comparison of DNA and protein sequences, binary and multiple sequence alignment, Needleman-Wunsch algorithm, dynamic programming, position-specific weight matrices and Hidden Markov models. Phylogenetic tree construction by distance matrix and by parsimony analysis, maximum likelihood methods, split- and quartet-based methods for phylogenetic network inference. Transcriptomics and proteomics: Analysis of the degree of utilization of genetic information by the cell (RNA and protein). Methods of structure determination for proteins (X-ray crystallography, NMR spectroscopy), structure validation (Pro-Check). Structural genomics, strategies of "structure factories". Use of RNA secondary structure prediction tools, introduction to RNA homology search and annotation. Motif discovery and motif search for transcription factor binding site modeling and recognition. Use of motif discovery and motif finding tools, and databases with transcription factor binding site profiles. Prediction of protein structures (secondary structure, neural networks, hydrophobicity analysis). Protein fold prediction, threading, homology modeling. Use of molecular graphics, application of viewers (RASMOL, PYMOL). Molecular mechanics, energy minimization and molecular dynamics.
Study and examination requirements; Forms of examination	Progress will be examined by means of assignments, which require the application of local computer programs as well as web-based services enabling the students to work on programs in vector construction, analysis of gene structure etc. 2-hour end-of-term written exam. The assessment will be based on 12 questions in free text. Students have to answer 9 questions to obtain full number of points
Literature	Arthur M. Lesk Introduction to Bioinformatics Verlag: Oxford University Press; Auflage: 0003 (20. März 2008) Sprache: Englisch ISBN-10: 0199208042 ISBN-13: 978-0199208043