READING VERSION OF MODULE DESCRIPTIONS
The module descriptions are not part of the Regulations; they are integrated into the First Amendment to the Module Catalog.

BIO-B-KM1: State of the Art in Biochemistry and Molecular Biology	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory module
Content and Objectives of Module	**Contents:** Current topics in biochemistry, biotechnology, molecular biology, genetics, cell biology and physiology with emphasis on eukaryotic and prokaryotic model organisms and the scientific fields of the participating professorships **Objectives:** – **Professional competence** Students acquire deep insights into the current state of research in selected topics in biochemistry, genetics, molecular biology, cell biology and physiology including suitable experimental approaches to solve scientific problems – **Methodological competence** Students learn to cope with specialist literature in English. – **Hands-on competence** Students develop the ability to phrase scientific questions during lectures, also in English.
Module examinations (number, form, scope):	Written exam, 120 min.
Independent study time (in hours):	90

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	3 x 2	-	-	-

Offered:	Winter semester
Prerequisite for taking the module:	None The following applies to the Master's Program in Bioinformatics (winter semester 2018/19): Requirement according to § 3 Disclipline -Specific Admission Regulations for the Master's Degree in Bioinformatics
Teaching unit(s):	Biology / Biochemistry

BIO-MBIB01: Introduction to databases and practical programming	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory / Elective module
Content and Objectives of Module	**Contents:** The students acquire basic programming skills in at least two programming languages as well as in dealing with Structured Query Language (SQL) databases. In addition, the students acquire learning skills in preparation for dealing with technical questions. Specifically: – The students learn the basics of procedural programming. Small software solutions are developed during the exercises, so they can also be used by non-programmers by providing a graphical user interface. – The database section deals with the basics of database theory, with emphasis on widely used database systems. **Objectives:** – **Professional competence** Students are familiar with the basic concepts of database theory, programming, and team collaboration. – **Methodological competence** Students are given the opportunity to use simple tasks from their field to demonstrate how computers can be used to arrive at a solution to a problem. – **Hands-on competence** Students can better define software requirements for solving specific problems and implement software solutions on a small scale.
Module examinations (number, form, scope):	Programming project, 90 min.
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture and Tutorial	1L + 3T	-	Exercises (50%)	-

Offered:	Winter semester
Prerequisite for taking the module:	None The following applies to the Master's Program in Bioinformatics (winter semester 2018/19): Requirement according to § 3 Disclipline -Specific Admission Regulations for the Master's Degree in Bioinformatics
Teaching unit(s):	Biology / Biochemistry

BIO-MBIB03: Programming expertise	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory / Elective module
Content and Objectives of Module	**Contents:** Imperative programming with C: code, compiler, linker; Simple types, variables, expressions; Input and output; Control structures, functions, parameters; Pointer (referential datatypes), arrays. Object-oriented programming with C ++ and Java: classes, objects, data elements, methods, constructors; Heredity and polymorphism; Abstract classes, interfaces, templates, generics; Definition and use of libraries; GUI programming; Threads (concurrent processes) Realization of typical algorithmic concepts: recursion, quick sorting, linked lists. **Objectives:** – **Professional competence** Acquiring programming expertise in a language relevant for network-driven bioinformatics problems. – **Methodological competence** Students learn approaches of object oriented programming. – **Hands-on competence** Students learn an object oriented programming language.
Module examinations (number, form, scope):	Written exam, 90 min with theoretical and practical part
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture and Tutorial	2L + 2T	-	Exercises (50%)	-

Offered:	Summer semester
Prerequisite for taking the module:	Recommended: MBIB01 The following applies to the Master's Program in Bioinformatics (winter semester 2018/19): Requirement according to § 3 Disclipline -Specific Admission Regulations for the Master's Degree in Bioinformatics
Teaching unit(s):	Biology / Biochemistry

BIO-MBIB04: Molecular, structural and evolutionary biology for informaticians	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory / Elective module
Content and Objectives of Module	**Contents:** The students will acquire basic knowledge of general principles of gene regulation (including transcription factors, promotors, enhancers, silencers, DNA binding), peculiarities of gene regulation in prokaryotes (including operon concept, lac operon, catabolite repression, glucose repression, cAMP , Regulating elements), specificities of gene regulation in eukaryotes (including special transcription factors and nuclear hormone receptors), splicing and processing of RNA, current techniques of molecular biotechnology and genome research (reporter genes, detection of DNA protein interactions, DNA sequencing, cloning Genes) as well as retroviruses. In addition, they will be exposed to historical development to the synthetic evolution theory as well as the fundamental evolutionary mechanisms. Micro- and macroevolutionary processes are explained and illustrated by examples. In this context, interactions between genotype and phenotype and molecular evolutionary processes are discussed. In addition, the students acquire knowledge about the principles of the polypeptide structure, the three-dimensional structure, stability and function of proteins, protein structure databases and techniques and programs of visualization and analysis of three-dimensional protein structures. **Objectives:** – **Professional competence** Acquiring knowledge from molecular, structural and evolutionary biology. – **Methodological competence** Students learn methods to quantify molecular processes. – **Hands-on competence** The students develop capabilities to use methods to quantify molecular processes.
Module examinations (number, form, scope):	Oral examination, 20 min.
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	4	-	-	-

Offered:	Summer semester
Prerequisite for taking the module:	None The following applies to the Master's Program in Bioinformatics (winter semester 2018/19): Requirement according to § 3 Disclipline -Specific Admission Regulations for the Master's Degree in Bioinformatics
Teaching unit(s):	Biology / Biochemistry

BIO-MBIP01: Algorithmic and Mathematical Bioinformatics	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory module
Content and Objectives of Module	**Contents:** The module covers basic techniques for the design and analysis of efficient algorithms, with emphasis on methods directly applicable to answer bioinformatics and systems biology questions. Topics include: search trees, greedy algorithms, dynamic programming, and divide-and-conquer strategy. The module also covers basic graph-theoretic algorithms and introduction to linear programming. The students will learn techniques of algorithm design and will analyze the correctness and complexity of algorithms. Used in this relation are basic techniques of proving mathematical claims. **Objectives:** **– Professional competence** The students will learn how to design and analyze algorithms applicable in the fields of bioinformatics and systems biology. Emphasis is placed on techniques for determining algorithm correctness and complexity. The students will learn to communicate an algorithm in a pseudocode form. **– Methodological competence** Acquisition of techniques for computational solution of optimization and counting problems in bioinformatics and systems biology. **– Hands-on competence** The students will acquire the skills to present an algorithm in a pseudocode form. Implementation of particular algorithms will be encouraged, in a programming language of their choice. Students will also prepare presentations that introduce a problem, present an algorithm which solves it, and determine the complexity (time and space).
Module examinations (number, form, scope):	Oral examination, 20 min.
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	2	-	Exercises (50%) and Quizzes (50%)	-
Tutorial	2	Presentation 10 min.	-	-

Offered:	Winter semester
Prerequisite for taking the module:	None
Teaching unit(s):	Biology / Biochemistry

BIO-MBIP02: Statistical Bioinformatics	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory module
Content and Objectives of Module	**Contents:** The module provides a general introduction to statistics with emphasis on practical usage of R. The topics covered include: concepts from probability theory and distributions in the analysis of large data, quality control of high-throughput bio-data, statistical testing, significance and multiple hypotheses testing, clustering, statistical models and inference, multidimensional analysis and visualization of large-scale data, regression and classification. Emphasis is also placed on brief introduction of the technologies used to generate high-throughput data as well as on reproducible research. **Objectives:** – **Professional competence** The students master the basics of descriptive and inferential statistics. They know basic methods for dimensionality reduction, multivariate regression and classification, and can apply them to address bioinformatics questions. They can perform statistical analyses in R. – **Methodological competence** The students can apply appropriate descriptive and inferential statistics as well as advanced methods for large-scale data analysis. – **Hands-on competence** The students are familiar with the statistical software R, and can use it to address bioinformatics questions using suitable methods.
Module examinations (number, form, scope):	Written exam, 90 min, with theoretical and practical parts
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	2	-	Exercises (50%) and Quizzes (50%)	-
Tutorial	2	Presentation 15 min.	-	-

Offered:	Winter semester
Prerequisite for taking the module:	None
Teaching unit(s):	Biology / Biochemistry

BIO-MBIP03: Bioinformatics of Biological Sequences (Evolutionary Genomics)	Number of credit points (CP): 6

Module type (mandatory or elective module):	Mandatory module
Content and Objectives of Module	**Content** The module introduces basic concepts from bioinformatics of biological sequences resulting from high-throughput experiments. The focus is on methods for the comparison of DNA and protein sequences. The module provides a thorough introduction in methods for the derivation of phylogenetic trees from sequences. Emphasis is placed on using freely available sequence databases as well as methods and applications of evolutionary genome research. **Objectives** – **Professional competence** The students master the fundamentals of the computer-based analysis of biological sequences in evolutionary context. – **Methodological competence** The students are able to analyze biological sequences with freely accessible software and to present and interpret the results. – **Hands-on competence** Students can independently process biological sequence data using free software and Linux system utilities.
Module examinations (number, form, scope):	Written exam, 90 min.
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture and Tutorial	2L + 2T	-	Exercises (80%)	-

Offered:	Winter semester
Prerequisite for taking the module:	None
Teaching unit(s):	Biology / Biochemistry

BIO-MBIP04: Analysis of Cellular Networks	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory module
Content and Objectives of Module	**Content** The module covers graph-theoretic approaches for analysis of large-scale biological data. Emphasis is placed on methods for reconstructing gene-regulatory, signaling, and metabolic networks with multivariate statistical techniques, as well as on techniques for integrating transcriptomics, proteomics, and metabolomics data with gene regulatory, protein-protein interaction, and metabolomics networks. Graph-theoretic approaches for clustering, comparison, and motif-discovery in biological networks are covered and used to answer questions from systems biology of plants to variety of cancers. **Objectives** – **Professional competence** Students master the basics of analyzing high-throughput data with network-driven techniques. – **Methodological competence** The students master the application of advanced clustering techniques, the generation of network models from high-throughput data, and the topological and statistical analysis of networks. – **Hands-on competence** Applicability of the learned methods to experimental data sets.
Module examinations (number, form, scope):	Written exam, 90 min, with theoretical and practical part
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	2	-	Quizzes (50%)	-
Tutorial	2	-	Exercises (50%)	-

Offered:	Summer semester
Prerequisite for taking the module:	Recommended: BIO-MBIB01, BIO-B-KM1
Teaching unit(s):	Biology / Biochemistry

BIO-MBIP06: Constraint-based Modeling of Cellular Networks	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory module
Content and Objectives of Module	**Content** The module provides an introduction to the computational approaches used in the constraint-based modeling framework. Introduction to linear, quadratic, and integer programming as well as bi-level programming is provided. Methods from constraint-based modeling framework cover flux balance analysis and its dynamic extensions as well as approaches for design of metabolic engineering strategies. All approaches are illustrated and applied with real-world metabolic networks. Concepts of flux and concentration couplings and their relations to elementary flux modes are highlighted. Approaches for prediction of phenotypes in mutants are also presented and critically examined with respect to uniqueness of solutions. **Objectives** – **Professional competence** A deeper understanding of metabolic networks and their manipulation to achieve a desired outcome (e.g. production of a compound of interest). Relations to modeling of other cellular networks in the constraint-based modeling framework are also established. – **Methodological competence** Usage of MATLAB and R to predict flux states of a cellular system and to use them for the comparison of experimental scenarios. – **Hands-on competence** Computational analysis of large-scale biological networks, demonstrating robustness of predictions, and integration of existing knowledge on sequences and ontologies with outcomes of the constraint-based modeling framework.
Module examinations (number, form, scope):	Written exam, 90 min with theoretical and practical part
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	2	-	Exercises (50%) and Quizzes (50%)	-
Tutorial	2	Presentation 10 min.	-	-

Offered:	Winter semester
Prerequisite for taking the module:	None
Teaching unit(s):	Biology / Biochemistry

BIO-MBIV01: Project work	Number of credit points (CP): 18
Module type (mandatory or elective module):	Mandatory module
Content and Objectives of Module	**Content** The project work consists of a supervised project in one of the following areas: integrative large-s analysis, modeling and simulation of cellular networks with integration of data, development of st toolboxes (computation and visualization) based on well-established methods. Successful completion of a written project report. The project report is to be a standalone research v scientific paper form. The report is to be composed of the following parts: abstract, introduction (inclu problem formulation), background, materials and methods, results, discussion, and conclusion. Th report is envisioned to contain no fewer than 30 pages. The results section is to describe preliminary res analysis of large data sets, development of computational methods, or the combination thereof. Stu encouraged to select a project from computational systems biology which combines at least two topics in the mandatory and elective lectures (e.g., sequence analysis, large-scale data, constraint-based mode theoretical systems biology). Emphasis is to be placed on conveying scientific results in a technicall form, comparing and contrasting the results to what has been published in literature, and identifying p further improvements. **Objectives** – **Professional competence** Students are introduced to the fundamentals of research work and to technical writing (e.g. problem form communication of results, discussion of findings). – **Methodological competence** Students acquire the skills to independently work on scientific questions, to compare and contrast met – **Hands-on competence** Students can peruse relevant primary literature (in English), acquire insights in one selected are computational expertise in one selected area of bioinformatics and systems biology research.
Module examinations (number, form, scope):	Project work as a scientific article (30-50 pages, including references)
Independent study time (in hours):	525

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exa (Number, form, scope)
		For completing the module	For admission to the module exam	
Tutorial	1	-	Presentation 20 min.	

Offered:	Any semester
Prerequisite for taking the module:	Recommended: Successful completion of all mandatory modules
Teaching unit(s):	Biology / Biochemistry

BIO-MBIW01: Data Integration in Cellular Networks	Number of credit points (CP): 6
Module type (mandatory or elective module):	Elective module
Content and Objectives of Module	**Content** The module provides thorough investigation of approaches intended for integration of large-scale high-throughput data in models of cellular networks. The module covers the approaches for context-specific network extraction, by using transcriptomics, proteomics, and metabolomics data, and for analyzing the specificity of the resulting predictions. In addition, methods that consider kinetic form of flux and allow for integration of metabolomics data, estimation of kinetic parameters, and consideration of thermodynamic constraints are covered in depth. In addition, emphasis is placed on classical and modern techniques for flux estimation from labeling data. Finally, approaches allowing for the integration of metabolic with signaling and gene regulatory networks are presented and validity of their predictions is assessed on real-world networks. **Objectives** – **Professional competence** Understanding the relevance and accuracy of flux estimation by integration of different data sources in large-scale cellular networks. – **Methodological competence** Methods for integration of data in models of biochemical reactions to estimate flux and kinetic parameters are mastered and used to address systems biology questions. – **Hands-on competence** Implementation of the methods covered during the lectures in MATLAB and R.
Module examinations (number, form, scope):	Written exam, 90 min with theoretical and practical part
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	2	Presentation 15 min.	-	-
Tutorial	2	-	Exercises (50%)	-

Offered:	Summer semester
Prerequisite for taking the module:	None
Teaching unit(s):	Biology / Biochemistry

BIO-MBIW02: Advanced methods for Analysis of Biochemical networks	Number of credit points (CP): 6
Module type (mandatory or elective module):	Elective module
Content and Objectives of Module	**Content** Topics from Chemical Reaction Network Theory (CRNT) are covered and illustrated on real-world networks. The topics focus on properties of steady-state concentrations in networks endowed with different types of kinetics (e.g., mass action, power law) and include: existence of positive steady state concentrations, multistationarity, stability from network structure alone, robustness and plasticity of concentrations upon changing environments. Relations of dynamic properties with presence of particular subnetworks are presented. The topics aim at discovery of structural properties which confer particular dynamic behavior which can be employed in synthetic biology studies. **Objectives** – **Professional competence** A deeper understanding of the mathematical and theoretical fundamentals of chemical reaction networks and the properties of their dynamics. – **Methodological competence** Learn mathematical methods which establish relationships between network structure, phenotypes, and biological functions. – **Hands-on competence** Strengthen the applications of MATLAB and stand-alone software applications to address problems in synthetic biology.
Module examinations (number, form, scope):	Oral examination 20 min.
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture and Tutorial	2L + 2T	-	Exercises (50%) and Quizzes (50%)	-

Offered:	Winter semester
Prerequisite for taking the module:	None
Teaching unit(s):	Biology / Biochemistry

BIO-MBIW03: Quantitative Genetics	Number of credit points (CP): 6
Module type (mandatory or elective module):	Elective module
Content and Objectives of Module	**Content** The module provides a critical view on computational approaches applied in classical and modern quantitative genetics. The students will obtain insights in the different populations used to determine the genetic basis of simple and complex traits. Emphasis is placed on mapping of quantitative trait loci, genome-wide association studies, and marker-assisted selection. The computational approaches deal with linear models and network-based extensions commonly applied for breeding and medical purposes. Exercises are carried out in R programming environment. **Objectives** – **Professional competence** Deeper understanding of the theoretical fundamentals of quantitative genetics and their application for breeding and medical purposes. – **Methodological competence** Statistical approaches and populations used for mapping of simplex and complex traits. – **Hands-on competence** Analysis and simulation of phenotype-genotype relationships with different population structures.
Module examinations (number, form, scope):	Written exam, 90 min with theoretical and practical part
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	2	Presentation 15 min.	-	-
Tutorial	2	-	Exercises (50%)	-

Offered:	Summer semester
Prerequisite for taking the module:	None
Teaching unit(s):	Biology / Biochemistry

<table>
<tr><td colspan="3">BIO-MBIW04: Image Processing and Phenotyping in Bioinformatics</td><td colspan="3">Number of credit points (CP): 6</td></tr>
<tr><td>Module type (mandatory or elective module):</td><td colspan="5">Elective module</td></tr>
<tr><td>Content and Objectives of Module</td><td colspan="5">Content
The module will provide students with a basic understanding of bioimage analysis and extended phenotyping. The students will be familiarized with basic image processing techniques and their applications in biological studies: experimental design, digitizing, segmentation, quantification and statistical analysis. Application-oriented work is central to this module. In addition, the module also covers other phenotyping methodologies used in systems biology and bioinformatics.

Objectives
– Professional competence
Basic and advanced techniques commonly applied in bioimage analysis and phenotyping are considered.
– Methodological competence
Students obtain knowledge about approaches for segmentation and extraction of biologically relevant features from images and high-throughput technologies.
– Hands-on competence
Variety of image-based phenotyping projects / questions is used to illustrate the computational approaches.</td></tr>
<tr><td>Module examinations (number, form, scope):</td><td colspan="5">Written exam, 90 min.</td></tr>
<tr><td>Independent study time (in hours):</td><td colspan="5">120</td></tr>
<tr><td colspan="6"></td></tr>
<tr><td rowspan="2">Courses
(type of teaching)</td><td rowspan="2">Contact time
(in semester hours)</td><td colspan="2">Supplementary exam work
(Number, form, scope)</td><td colspan="2">Module partial exam
(Number, form, scope)</td></tr>
<tr><td>For completing the module</td><td>For admission to the module exam</td><td></td></tr>
<tr><td>Lecture and Tutorial</td><td>2L + 2T</td><td>6-8 Hands-on projects</td><td>-</td><td>-</td></tr>
<tr><td colspan="6"></td></tr>
<tr><td colspan="3">Offered:</td><td colspan="3">Winter semester</td></tr>
<tr><td colspan="3">Prerequisite for taking the module:</td><td colspan="3">None</td></tr>
<tr><td colspan="3">Teaching unit(s):</td><td colspan="3">Biology / Biochemistry</td></tr>
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BIO-MBIW05: Structural Bioinformatics	Number of credit points (CP): 6
Module type (mandatory or elective module):	Elective module
Content and Objectives of Module	**Content** The module covers the biophysical principles underlying the structure of macromolecules. It provides a detailed overview of the principal methods for structure elucidation and modeling of three-dimensional structures of biological macromolecules and their interactions. The spectrum of methods ranges from molecular dynamics and energy minimization to homology modeling to statistical methods for structural prediction. Common programs for the analysis, modeling and comparison of three-dimensional structures are introduced and their applications are illustrated. **Objectives** – **Professional competence** The students have a basic understanding of the biophysical structural principles of macromolecules, especially proteins and RNA molecules. – **Methodological competence** The students know and master basic algorithms and software solutions for their analysis, comparison and prediction. – **Hands-on competence** Students are able to work independently in the area of structural modeling.
Module examinations (number, form, scope):	Written exam, 90 min.
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture	2	-	Quizzes (50%)	-
Tutorial	2	-	Exercises (50%)	-

Offered:	Summer semester
Prerequisite for taking the module:	None
Teaching unit(s):	Biology / Biochemistry

<table>
<tr><td colspan="3">BIO-MBIW06: Machine learning in bioinformatics</td><td colspan="3">Number of credit points (CP): 6</td></tr>
<tr><td>Module type (mandatory or elective module):</td><td colspan="5">Elective module</td></tr>
<tr><td>Content and Objectives of Module</td><td colspan="5">Content
The module covers basic and advanced methods for prediction and classification, with case studies from life sciences. Elements of deep learning and big data in the context of prediction and classification are considered. Cross-validation techniques as well as measures for goodness-of-fit are also introduced and their use in parameter selection is illustrated.

Objectives
– Professional competence
A deeper understanding of the mathematical and theoretical fundamentals of machine learning approaches.
– Methodological competence
Learn mathematical methods which can be used for predictive purposes in variety of machine learning applications.
– Hands-on competence
Strengthen the applications of R and other programming environments for machine learning in bioinformatics.</td></tr>
<tr><td>Module examinations (number, form, scope):</td><td colspan="5">Written exam, 90 min with theoretical and practical part</td></tr>
<tr><td>Independent study time (in hours):</td><td colspan="5">120</td></tr>
<tr><td colspan="6"></td></tr>
<tr><td rowspan="2">Courses
(type of teaching)</td><td rowspan="2">Contact time
(in semester hours)</td><td colspan="2">Supplementary exam work
(Number, form, scope)</td><td colspan="2">Module partial exam
(Number, form, scope)</td></tr>
<tr><td>For completing the module</td><td>For admission to the module exam</td><td colspan="2"></td></tr>
<tr><td>Lecture and Tutorial</td><td>2L + 2T</td><td></td><td>Exercises (50%) and Quizzes (50%)</td><td colspan="2"></td></tr>
<tr><td colspan="6"></td></tr>
<tr><td colspan="2">Offered:</td><td colspan="4">Summer semester</td></tr>
<tr><td colspan="2">Prerequisite for taking the module:</td><td colspan="4">None</td></tr>
<tr><td colspan="2">Teaching unit(s):</td><td colspan="4">Biology / Biochemistry</td></tr>
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<table>
<tr><td colspan="3">BIO-MBIW07: Integration of cellular layers and systems</td><td colspan="3">Number of credit points (CP): 6</td></tr>
<tr><td>Module type (mandatory or elective module):</td><td colspan="5">Elective module</td></tr>
<tr><td>Content and Objectives of Module</td><td colspan="5">Content
The module covers advanced methods for integration of diverse cellular networks from different cellular layers or organs / tissues resulting in a functional system. It also covers the integration of networks from different systems / organisms, allowing to draw eco-physiological conclusions. The module highlights how the deployed resource allocation strategy to ensure efficient usage of nutrient and energy in a biological system. Problems related to control of cellular states and crosstalk between systems are also treated.
Objectives
– Professional competence
A deeper understanding of the mathematical and theoretical fundamentals of integration of diverse networks across scales.
– Methodological competence
Learn methods which can be used for predictive purposes in ecophysiological applications.
– Hands-on competence
Strengthen the applications of R and MATLAB for modeling biological systems across scales.</td></tr>
<tr><td>Module examinations (number, form, scope):</td><td colspan="5">Oral exam, 20 min.</td></tr>
<tr><td>Independent study time (in hours):</td><td colspan="5">120</td></tr>
<tr><td colspan="6"></td></tr>
<tr><td rowspan="2">Courses
(type of teaching)</td><td rowspan="2">Contact time
(in semester hours)</td><td colspan="2">Supplementary exam work
(Number, form, scope)</td><td colspan="2">Module partial exam
(Number, form, scope)</td></tr>
<tr><td>For completing the module</td><td>For admission to the module exam</td><td></td></tr>
<tr><td>Lecture and Tutorial</td><td>2L + 2T</td><td>-</td><td>Exercises (50%) and Quizzes (50%)</td><td>-</td></tr>
<tr><td colspan="6"></td></tr>
<tr><td colspan="2">Offered:</td><td colspan="4">Summer semester</td></tr>
<tr><td colspan="2">Prerequisite for taking the module:</td><td colspan="4">None</td></tr>
<tr><td colspan="2">Teaching unit(s):</td><td colspan="4">Biology / Biochemistry</td></tr>
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<tr><td colspan="3">BIO-MBIW08: Analysis of big sequencing data</td><td colspan="3">Number of credit points (CP): 6</td></tr>
<tr><td>Module type (mandatory or elective module):</td><td colspan="5">Elective module</td></tr>
<tr><td>Content and Objectives of Module</td><td colspan="5">Content
The module will provide students practical and theoretical knowledge about the handling and analysis of high-throughput data. New techniques and use cases in this area will be presented and discussed.
The module takes place as two-week block course at the beginning of the exams ind internship period. Each day is starting with a lecture to introduce theoretical background. The other part of the day consists of guided hands-on exercises to improve the understanding. Working is done on a Linux server within a terminal. Extensive calculations can be run over night or several days on the server. Basic Linux understanding is required as well as some knowledge about the terminal Anyway, knowledge will be refreshed and strengthened.

Objectives
– Professional competence
The students can use high-throughput data for science and diagnostics
– Methodological competence
The students know basic properties and use cases of high-throughput sequencing technologies, the type of data as well the analysis and handling of big data.
– Hands-on competence
The students can work within the terminal on a server: handling of sequence data, quality control, genome and transcriptome assembly, mapping, identification of genome variants and predicting effects, gene expression analysis, identification of interactions, genetic maps and other common techniques.</td></tr>
<tr><td>Module examinations (number, form, scope):</td><td colspan="5">Written exam, 90 min with theoretical and practical part</td></tr>
<tr><td>Independent study time (in hours):</td><td colspan="5">90</td></tr>
<tr><td colspan="6"></td></tr>
<tr><td rowspan="2">Courses
(type of teaching)</td><td rowspan="2">Contact time
(in semester hours)</td><td colspan="2">Supplementary exam work
(Number, form, scope)</td><td colspan="2">Module partial exam
(Number, form, scope)</td></tr>
<tr><td>For completing the module</td><td>For admission to the module exam</td><td></td></tr>
<tr><td>Lecture and Tutorial</td><td>2L + 2T</td><td>3-5 Hands-on projects</td><td>-</td><td>-</td></tr>
<tr><td colspan="6"></td></tr>
<tr><td colspan="3">Offered:</td><td colspan="3">Winter semester</td></tr>
<tr><td colspan="3">Prerequisite for taking the module:</td><td colspan="3">None</td></tr>
<tr><td colspan="3">Teaching unit(s):</td><td colspan="3">Biology / Biochemistry</td></tr>
</table>

MAT-MBIP05: Introduction to Theoretical Systems Biology	Number of credit points (CP): 6
Module type (mandatory or elective module):	Mandatory module
Content and Objectives of Module	**Content** The course introduces the kinetic modeling based on the stochastic and deterministic formulation of biochemical reactions from selected biological systems. Mathematical models for the modeling of signaling pathways, gene regulatory and metabolic networks are presented and critically evaluated. Basic approaches for solving ordinary differential equations and analysis of stability of their fixed points are also presented. Computational implementation of the covered approaches is illustrated with hands-on exercises. **Objectives** – **Professional competence** The students can provide mathematical formulation of systems biology questions and can critically analyze models of biological systems. – **Methodological competence** The students master the basics of stochastic and deterministic modeling. They become aware of mathematical and computational methods for analysis of systems of differential equations. – **Hands-on competence** The students gain expertise in the computational analysis of systems of differential equations of small systems.
Module examinations (number, form, scope):	Written exam, 90 min or oral examination 30 min.
Independent study time (in hours):	120

Courses (type of teaching)	Contact time (in semester hours)	Supplementary exam work (Number, form, scope)		Module partial exam (Number, form, scope)
		For completing the module	For admission to the module exam	
Lecture and Tutorial	2L + 2T	-	Exercises (50%)	-

Offered:	Summer semester
Prerequisite for taking the module:	Recommended: BIO-MBIP01 or BIO-MBIP02
Teaching unit(s):	Mathematics