Georg-August-Universität
Göttingen

Directory of Modules

zu der Prüfungs- und Studienordnung für den Master programme 'Computational Biology and Bioinformatics' (Amtliche Mitteilungen I Nr. 25/2022 S. 452)

This is a translation of the directory of modules as promulgated in Official Bulletin II No. 25, p. 452, dated June 09, 2022. Only those regulations published by the Georg-August-Universität Göttingen in its Official Bulletins are legally binding. Any claims to rights or titles resulting from the English translation of these regulations are expressly excluded.

Modules

Index by areas of study

I. Master programme "Computational Biology and Bioinformatics"

A total of 120 C have to be successfully completed according to the following regulation.

1. Core Studies (54 C)

A total of 54 C have to be successfully completed according to the following regulations.

Modules already completed in the Bachelor's programme cannot be considered again.

a. Bridging courses

Based on prior knowledge a total of at least **10C** out of the listed courses have to be succesfully completed. The mentor decides on this according to principles to be formulated by the examination board.

b. Compulsory course

The listed module of **8 C** has to be successfully completed.

c. Elective courses „Bioinformatics“

A total of at least **24 C** have to be successfully completed according to the following regulations.

d. Elective courses "Biology"

A total of at least **12 C** have to be successfully completed according to the following regulations. Modules completed according to No. 1C will not be considered again.

2. Area of Professionalization (36 C)

A total of 36 C have to be successfully completed according to the following regulations.

a. Compulsory course

The listed module of **12 C** has to be successfully completed.

b. Elective courses "Informatics"

A total of at least **12 C** have to be successfully completed. Based on prior knowledge and in agreement with the mentor modules listed under 1C and 1D (elective courses Biology or Bioinformatics) can be taken instead. Modules completed according to No. 1C will not be considered again.

c. Interdisciplinary key competencies

Modules amounting to a maximum of **12 C** from the university-wide module directory for key competencies or the examination regulations for study programmes offered by the Central Institution for Languages and Key Qualifications (ZESS) can be taken. The examination board decides on further selectable modules, which are to be announced in an appropriate manner.

3. Master thesis

30 C are awarded for successful completion of the master thesis.

Georg-August-Universität Göttingen Module B.Bio-NF.112: Biochemistry	6 C 4 WLH
Learning outcome, core skills: Students acquire basic knowledge of biochemical substances and an overview over elementary principles of biochemical reactions and learn the application of biochemical methods. They get insight into the basics of protein chemistry and genetics: DNA, RNA, enzymes, carbohydrates, lipids and cell membranes; basics of metabolism and signal transduction.	**Workload:** Attendance time: 56 h Self-study time: 124 h
Course: Grundlagen der Biochemie (Lecture)	4 WLH
Examination: Written examination (90 minutes) **Examination requirements:** Basic knowledge of biochemical reactions and its components as well as biochemical methods. Anabolism and catabolism of amino acids, carbohydrates, lipids and nucleic acids; synthesis and function of macromolecules; generation and accumulation of metabolic energy.	6 C

Admission requirements: none	**Recommended previous knowledge:** Basic knowledge in Biology
Language: German	**Person responsible for module:** Dr. rer. nat. Ellen Hornung
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 3 - 5
Maximum number of students: 20	
Additional notes and regulations: The combination of this module with module B.Bio.112 is not possible.	

Georg-August-Universität Göttingen **Module B.Bio-NF.116: General developmental and cell biology**	6 C 4 WLH

Learning outcome, core skills: The students learn about developmental aspects in cell biology; fundamental topics in developmental biology of animals and plants; classic and molecular-biological methods in developmental biology and model organisms.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Allgemeine Entwicklungs- und Zellbiologie (Lecture)	4 WLH
Examination: Written examination (90 minutes) **Examination requirements:** Students should be able to assess validity of statements, answer random control questions and describe and compare fundamental aspects from the fields: structure and compartments of cells, cytoskeleton, mitochondria, membrane structure and transport, contact and communication between cells, cell cycle, cell division, apoptosis, control of gene expression in eukaryotes, mechanisms in development, germ cells and fertilization, cleavage, principles in pattern formation, morphogenesis, gastrulation, neurulation, genesis of organs, cellular movement and shaping, methods from experimental embryology and developmental genetics, model organisms, formation of axis, genes for segmentation, homeotic selection genes, evolutionary developmental biology, neuronal development, stem cells and regeneration, homeostasis, origination of cancer, embryogenesis of plants, dormancy and germination, light dependent development, phytohormones, evolution and genetics during flower formation.	6 C

Admission requirements: none	**Recommended previous knowledge:** Basic knowledge in Biology
Language: German	**Person responsible for module:** Prof. Dr. Ernst A. Wimmer
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 3 - 5
Maximum number of students: 25	

Additional notes and regulations: The combination of this module with module B.Bio.116 is not possible.

Georg-August-Universität Göttingen **Module B.Bio-NF.125: Cell and molecular biology of plants**	6 C 4 WLH
Learning outcome, core skills: The students gain insight into the characteristics of plant cells, learn to know the relation between structure and function of organelles and the cell wall and get an overview of transport processes and intracellular signal transduction. They learn to know the model plant Arabidopsis thaliana and acquire knowledge in biosynthesis, signal transduction, effects of phytohormones and the molecular methods for adaption of plants to different abiotic and biotic stress factors. The students get an overview of current facts of phylogeny and biotechnology of algae.	**Workload:** Attendance time: 56 h Self-study time: 124 h
Course: Zell- und Molekularbiologie der Pflanze (Lecture)	4 WLH
Examination: Written examination (75 minutes) **Examination requirements:** Arabidopsis thaliana as model organism for research on cell- and molecular processes; methods for research on cell- and molecular processes; mechanisms of protein transport in different cell organelles and into the cell wall; mechanisms of signal transduction in plants; mechanisms of plant immunity.	6 C

Admission requirements: none	**Recommended previous knowledge:** Basic knowledge in Biology
Language: German	**Person responsible for module:** Prof. Dr. Christiane Gatz
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 3 - 5
Maximum number of students: 15	

Additional notes and regulations: The combination of this module with module B.Bio.125 is not possible.

Georg-August-Universität Göttingen **Module B.Bio-NF.130: Cognitive psychology**	3 C 2 WLH
Learning outcome, core skills: During the lectures, students get an introduction to Cognitive Psychology. They acquire solid knowledge about key concepts of this research area and relevant research methods. Students learn the fundamental principles of experimental work in this field, focusing on traditional theories and established paradigms as well as on psychophysiological methods.	**Workload:** Attendance time: 28 h Self-study time: 62 h

Course: Kognitionspsychologie (Lecture)	2 WLH
Examination: Written examination (45 minutes)	3 C
Examination requirements: The students should master the basics in Cognitive Psychology as taught in the lecture. They should be able to understand and describe connections between acquisition of cognitive skills, behavioral patterns, and psychophysiological correlates of (higher) cognitive functions, and to apply this knowledge to new situations.	

Admission requirements: BSc Biology: at least 40 C from the first study period	**Recommended previous knowledge:** none
Language: German	**Person responsible for module:** Prof. Dr. Annekathrin Schacht
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** from 3
Maximum number of students: 25	

Additional notes and regulations: The combination of this module with module B.Bio.130 is not possible.

Georg-August-Universität Göttingen **Module B.Bio.107: Statistics for biologists**	4 C 2 WLH
Learning outcome, core skills: After passing the module the students have a theoretical understanding of basic probabilistic terms and the elementary methods of the descriptive and conclusive statistics. They are able to conduct independently basic statistical tests and estimations.	**Workload:** Attendance time: 28 h Self-study time: 92 h
Course: Statistik (Lecture) It is recommended to attend the accompanying tutorials (2WLH).	2 WLH
Examination: Written examination (120 minutes) **Examination requirements:** The students should be able to apply the statistical approaches, methods and tests covered in the lecture to concrete situations. Here they should be able to find appropriate tests or approaches to solve the questions to a specific situation and solve the given problem numerically with this approach.	4 C

Admission requirements: none	**Recommended previous knowledge:** B.Mat.0811
Language: German	**Person responsible for module:** Prof. Dr. Michael Wibral
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: three times	**Recommended semester:** 2
Maximum number of students: 240	

Georg-August-Universität Göttingen **Module B.Bio.113: Applied bioinformatics**	10 C 7 WLH

Learning outcome, core skills: After passing the module the students will understand the structure of most databases in bioscientific research and be able to critically assess their content. They will learn to structure biological data and transfer the data to a database scheme. Furthermore the students learn the application of bioinformatical methods in particular on sequence data, biological networks and expression data.	**Workload:** Attendance time: 98 h Self-study time: 202 h

Course: Einführung in die angewandte Bioinformatik (Lecture)	4 WLH
Examination: Written examination (90 minutes) **Examination prerequisites:** regular participation in the practical training and successful completion of three exercises **Examination requirements:** The students should know suitable sources of biomedical information available in the internet. They should be able to design and explain simple database schemes. The students should be familiar with measurements for critical assessment of bioinformatical methods; different methods for sequence comparison; reconstruction of phylogenetic trees; application of concepts from information theory on the analysis of sequence data. The students should be able to describe basic characteristics and graph theoretical representations of biological networks and apply these concepts to data analysis.	10 C

Course: Internet-basierte Bioinformatik (Exercise)	3 WLH

Admission requirements: BSc Biology: at least 40 C from the first study period	**Recommended previous knowledge:** none
Language: German	**Person responsible for module:** Prof. Dr. Tim Beißbarth
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 3 - 5
Maximum number of students: 100	

Georg-August-Universität Göttingen

Module B.Inf.1101: Introduction to Computer Science and Programming

10 C
6 WLH

Learning outcome, core skills:

Studierende

- kennen grundlegende Begriffe, Prinzipien und Herangehensweisen der Informatik, kennen einige Programmierparadigmen und Grundzüge der Objektorientierung.
- erlangen elementare Grundkenntnisse der Aussagenlogik, verstehen die Bedeutung für Programmsteuerung und Informationsdarstellung und können sie in einfachen Situationen anwenden.
- verstehen wesentliche Funktionsprinzipien von Computern und der Informationsdarstellung und deren Konsequenzen für die Programmierung.
- erlernen die Grundlagen einer Programmiersprache und können einfache Algorithmen in dieser Sprache codieren.
- kennen einfache Datenstrukturen und ihre Eignung in typischen Anwendungssituationen, können diese programmtechnisch implementieren.
- analysieren die Korrektheit einfacher Algorithmen und bewerten einfache Algorithmen und Probleme nach ihrem Ressourcenbedarf.

Workload:

Attendance time:

84 h

Self-study time:

216 h

Course: Informatik I (Lecture, Exercise)	6 WLH

Examination: Klausur (90 Minuten) oder mündliche Prüfung (ca. 20 Min.)

10 C

Examination prerequisites:

Nachweis von 50% der in den Übungsaufgaben erreichbaren Punkte. Kontinuierliche Teilnahme an den Übungen.

Examination requirements:

In der Prüfung wird das Verständnis der vermittelten Grundbegriffe sowie die aktive Beherrschung der vermittelten Inhalte und Techniken nachgewiesen, z.B.

- Kenntnis von Grundbegriffen nachweisen durch Umschreibung in eigenen Worten.
- Standards der Informationsdarstellung in konkreter Situation umsetzen.
- Ausdrücke auswerten oder Bedingungen als logische Ausdrücke formulieren usw.
- Programmablauf auf gegebenen Daten geeignet darstellen.
- Programmcode auch in nicht offensichtlichen Situationen verstehen.
- Fehler im Programmcode erkennen/korrigieren/klassifizieren.
- Datenstrukturen für einfache Anwendungssituationen auswählen bzw. geeignet in einem Kontext verwenden.
- Algorithmen für einfache Probleme auswählen und beschreiben (ggf. nach Hinweisen) und/oder einen vorgegebenen Algorithmus (ggf. fragmentarisch) programmieren bzw. ergänzen.
- einfache Algorithmen/Programme nach Ressourcenbedarf analysieren.
- einfachsten Programmcode auf Korrektheit analysieren.
- einfache Anwendungssituation geeignet durch Modul- oder Klassenschnittstellen modellieren.

Admission requirements:	**Recommended previous knowledge:**

none	none
Language: German	**Person responsible for module:** Prof. Dr. Carsten Damm
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** from until
Maximum number of students: 300	

Georg-August-Universität Göttingen **Module B.Inf.1131: Data Science I: Algorithms and Processes**	6 C 4 WLH

Learning outcome, core skills:	**Workload:**
Die Studierenden • kennen die Phasen von Data Science Projekten und können diese definieren. • kennen die Rollen die typischerweise in Data Science Projekten involviert sind. • wissen was Regressionsprobleme sind und kennen verschiedene Modelle und Algorithmen zum Lösen von Regressionsproblemen. • wissen was Klassifikationsprobleme sind und kennen verschiedene Modelle und Algorithmen zur Klassifikationsproblemen. • wissen was Clustern ist und kennen verschiedene Modelle und Algorithmen zum Clustern von Daten. • wissen was Assoziationsregeln sind und kennen mindestens einen Algorithmus um Assoziationsregeln zu bestimmen. • kennen verschiedene Verfahren und Metriken zur Schätzung der Performanz von Modellen.	Attendance time: 56 h Self-study time: 124 h

Course: Data Science I: Algorithmen und Prozesse (Lecture, Exercise)	4 WLH
Examination: Written or oral examKlausur (90 Min.) oder mündliche Prüfung (ca. 20 Min.) **Examination requirements:** Definition des Prozesses von Data Science Projekten, Definition der Rollen in Data Science Projekten, Definition und Kenntnis von Klassifikationsalgorithmen, Definition und Kenntnis von Regressionsalgorithmen, Definition und Kenntnis von Assoziationsregeln, Definition und Kenntnis von Clustering, Kenntnis von Verfahren und Metriken zu Performanzschätzung von Modellen.	6 C

Admission requirements: none	**Recommended previous knowledge:** B.Inf.1101, B.Inf.1102
Language: German	**Person responsible for module:** Prof. Dr. Fabian Sinz
Course frequency: once a year	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 3
Maximum number of students: 50	

Georg-August-Universität Göttingen **Module B.Inf.1209: Software Engineering**	5 C 3 WLH

Learning outcome, core skills: Die Studierenden • kennen Geschichte, Definition, Aufgaben und Wissensgebiete der Softwaretechnik. • wissen was ein Softwareprojekt ist, welche Personen und Rollen in Softwareprojekten ausgefüllt werden müssen und wie Softwareprojekte in Unternehmensstrukturen eingebettet werden können. • kennen unterschiedliche Vorgehens- und Prozessmodelle der Softwaretechnik, • kennen deren Vor- und Nachteile und wissen wie die Qualität von Softwareentwicklungsprozessen bewertet werden können. • kennen verschiedene Methoden der Kosten- und Aufwandsschätzung für Softwareprojekte. • kennen die Prinzipien und verschiedene Verfahren für die Anforderungsanalyse für Softwareprojekte. • kennen die Prinzipien und mindestens eine Vorgehensweise für den Software Entwurf. • kennen die Prinzipien der Software Implementierung. • kennen die grundlegenden Methoden für die Software Qualitätssicherung.	**Workload:** Attendance time: 42 h Self-study time: 108 h

Course: Softwaretechnik (Lecture, Exercise) *Contents*: Software-Qualitätsmerkmale, Projekte, Vorgehensmodelle, Requirements-Engineering, Machbarkeitsstudie, Analyse, Entwurf, Implementierung, Qualitätssicherung	3 WLH
Examination: Klausur (90 Minuten) oder mündliche Prüfung (ca. 20 Min.) **Examination prerequisites:** B.Inf.1209.Ue: Erarbeiten und Vorstellen der Lösung mindestens einer Übungsaufgabe (Präsentation und schriftliche Ausarbeitung), sowie die aktive Teilnahme an den Übungen. **Examination requirements:** Definition und Aufgaben der Softwaretechnik, Definition Softwareprojekt, Personen und Rollen in Softwareprojekten, Einbettung von Softwareprojekten in Unternehmensstrukturen, Vorgehens- und Prozessmodelle und deren Bewertung, Aufwands- und Kostenabschätzung, Anforderungsanalyse, Design, Implementierung und Qualitätssicherung	5 C

Admission requirements: none	**Recommended previous knowledge:** B.Inf.1101, B.Inf.1801, B.Inf.1802
Language: German	**Person responsible for module:** Prof. Dr. Jens Grabowski
Course frequency: once a year	**Duration:** 1 semester[s]

Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 100	

Georg-August-Universität Göttingen

Module B.Inf.1231: Infrastructures of Data Science

6 C
4 WLH

Learning outcome, core skills:
Upon completion the course, students

- understand the basic functions of data science infrastructures and their significance.
- understand basic data types and their specifics.
- understand the most important technical infrastructures for storing and processing data locally and in the cloud as well as their advantages and disadvantages in relation to data science applications.
- can apply the concept of the data lake to basic data science problems.
- are able to apply the different steps of data pre-processing to selected data sets.
- can identify the characteristics of time series and graph data and are able to recall the functions of DBMSs designed for their processing.
- can present the basic tasks of data analysis platforms and can describe them using examples.
- can apply methods and tools for the presentation and visualisation of data.
- can model basic data science workflows and are able to transfer their knowledge to basic data science projects.

Workload:
Attendance time:
56 h
Self-study time:
124 h

Course: Infrastructures of Data Science (Lecture, Exercise)

4 WLH

Contents:

- Data types and their characteristics
- Common functions of data science infrastructures
- Storage, compute, and cloud infrastructures for data science
- Concept of a data lake
- Data pre-processing methods and selected tools
- Time series and graph data, the respective DBMS, and query languages
- Data analytics platforms
- Data presentation and visualization
- Data science workflows and selected infrastructure components

Examination: In-class, written exam (90 min) or oral exam (approx. 30 min.)
Examination prerequisites:
Students complete 50% of the homework exercises.
Examination requirements:
Through the examination students demonstrate that they are able to describe basic functions of (cloud-based) data science infrastructures as well as to specify and identify basic data types. Students can also prove their understanding of data lakes and can apply their knowledge of MapReduce and Hadoop in that particular context. They can analyse basic data pre-processing problems and sketch common solutions. Student can show that they understand time series and graph data as well as the corresponding DBMS and that they can present common tasks of data analysis platforms. Through the examination, students also demonstrate their ability to select appropriate methods for visualising data and show that they are able to create basic data science workflows.

6 C

Admission requirements: none	**Recommended previous knowledge:** Python and basic database knowledge (recommended, not mandatory)
Language: English	**Person responsible for module:** Hon.-Prof. Dr. Philipp Wieder
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** Bachelor: 3 - 6; Master: 1 - 2
Maximum number of students: 50	

Georg-August-Universität Göttingen **Module B.Inf.1236: Machine Learning**	6 C 4 WLH

Learning outcome, core skills: Students • learn concepts and techniques of machine learning and understand their advantages and disadvantages compared with alternative approaches • learn techniques of supervised learning for classification and regression • learn techniques of unsupervised learning for density estimation, dimensionality reduction and clustering • implement machine learning algorithms like linear regression, logistic regression, kernel methods, tree-based methods, neural networks, principal component analysis, k-means and Gaussian mixture models • solve practical data science problems using machine learning methods	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Machine Learning (Lecture) Bishop: Pattern recognition and machine learning. https://cs.ugoe.de/prml	2 WLH
Examination: Written examination (90 minutes) **Examination prerequisites:** B.Inf.1236.Ex: At least 50% of homework exercises solved. **Examination requirements:** Knowledge of the working principles, advantages and disadvantages of the machine learning methods covered in the lecture	6 C

Course: Machine Learning - Exercise (Exercise)	2 WLH

Admission requirements: none	**Recommended previous knowledge:** Knowledge of basic linear algebra and probability
Language: English	**Person responsible for module:** Prof. Dr. Alexander Ecker
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 4
Maximum number of students: 100	

Georg-August-Universität Göttingen **Module B.Inf.1237: Deep Learning**	6 C 4 WLH

Learning outcome, core skills: Students • learn concepts and techniques of deep learning and understand their advantages and disadvantages compared to alternative approaches • learn to solve practical data science problems using deep learning • implement deep learning techniques like multi-layer perceptrons, convolutional neural nerworks, recurrent neural networks, deep reinforcement learning • learn techniques for optimization and regularization of deep neural networks	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Deep Learning (Lecture) Goodfellow, Bengio, Courville: Deep Learning. https://www.deeplearningbook.org Bishop: Pattern Recognition and Machine Learning. https://cs.ugoe.de/prml	2 WLH
Examination: Written examination (90 minutes) **Examination prerequisites:** B.Inf.1237.Ex: At least 50% of homework exercises solved. **Examination requirements:** Knowledge of basic deep learning techniques, their advantages and disadvantages and approaches to optimization and regularization. Ability to implement these techniques.	6 C

Course: Deep Learning - Exercise (Exercise)	2 WLH

Admission requirements: none	**Recommended previous knowledge:** Basic knowledge of linear algebra and probability Completion of B.Inf.1236 Machine Learning or equivalent
Language: English	**Person responsible for module:** Prof. Dr. Alexander Ecker
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 5
Maximum number of students: 100	

Georg-August-Universität Göttingen **Module B.Inf.1240: Visualization**	5 C 3 WLH

Learning outcome, core skills: Knowledge of • the potentials and limitations of data visualization • the fundamentals of visual perception and cognition and their implications for data visualization. Students can apply these to the design of visualizations and detect manipulative design choices • a broad variety of techniques for visual representation of data, including abstract and high-dimensional data. Students can select appropriate methods on new problems • integration of visualization into the data analysis process, algorithmic generation and interactive methods	**Workload:** Attendance time: 42 h Self-study time: 108 h

Course: Visualization (Lecture, Exercise)	3 WLH
Examination: Practical project (2-3 weeks) with presentation and questions during oral exam in groups (approx. 20 minutes per examinee). **Examination prerequisites:** At least 50% of homework exercises solved. **Examination requirements:** Knowledge of potentials and limitations of data visualization, fundamentals of visual perception and their implications for good design choices, techniques for visual representation and how to use them.	5 C

Admission requirements: none	**Recommended previous knowledge:** Basic linear algebra and programming skills
Language: English	**Person responsible for module:** Prof. Dr. Bernhard Schmitzer
Course frequency: once a year	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 3 - 6
Maximum number of students: 50	

Georg-August-Universität Göttingen **Module B.Inf.1501: Algorithms in Bioinformatics I**	5 C 4 WLH

Learning outcome, core skills: Die Studierenden sollen die Spezifik der Modellbildung und der Algorithmik in der Bioinformatik kennen- und verstehen lernen. Ausgehend von konkreten biologischen Fragestellungen sollen Entwurf und Anwendung geeigneter Algorithmen verstanden werden.	**Workload:** Attendance time: 56 h Self-study time: 94 h

Course: Algorithmen der Bioinformatik I (Lecture, Exercise)	4 WLH
Examination: Oral examination (approx. 20 minutes) **Examination requirements:** Die Studierenden sollen die Spezifik der Modellbildung und der Algorithmik in der Bioinformatik kennen und verstehen. Ausgehend von konkreten biologischen Fragestellungen sollen die Studierenden die Fähigkeit haben, geeignete Algorithmen zu entwerfen und anzuwenden.	5 C

Admission requirements: B.Bio-NF.117: Genomanalyse	**Recommended previous knowledge:** Biologische und mathematische Grundkenntnisse
Language: German	**Person responsible for module:** Prof. Dr. Burkhard Morgenstern
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 3
Maximum number of students: 20	

Georg-August-Universität Göttingen **Module B.Inf.1504: Maschine Learning in Bioinformatics**	5 C 4 WLH
Learning outcome, core skills: Es sollen grundlegende Konzepte das maschinellen Lernens anschaulich vermittelt werden. Ziel ist das Verständnis der statistischen Voraussetzungen und der algorithmischen Umsetzung von maschinellen Lernverfahren. Dabei soll sowohl eine formale Beschreibung als auch die Implementation von einzelnen Methoden praktisch nachvollzogen werden können. Die Anwendungsmöglichkeiten der Methoden sollen vornehmlich im Kontext von mehrdimensionalen biomedizinschen Daten diskutiert und erprobt werden.	**Workload:** Attendance time: 56 h Self-study time: 94 h
Course: Maschinelles Lernen (Lecture, Exercise)	4 WLH
Examination: Oral examination (approx. 20 minutes)	5 C
Examination requirements: Die Studierenden können Konzepte des Maschinellen Lernens selbständig verstehen und anwenden.	

Admission requirements: none	**Recommended previous knowledge:** Biologische und mathematische Grundkenntnisse
Language: German	**Person responsible for module:** Dr. Peter Meinicke
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 3 - 5
Maximum number of students: 15	

Georg-August-Universität Göttingen **Module B.Inf.1801: Programming**	5 C 3 WLH

Learning outcome, core skills: Die Studierenden erlernen eine aktuelle Programmiersprache, sie • beherrschen den Einsatz von Editor, Compiler und weiteren Programmierwerkzeugen (z.B. Build-Management-Tools). • kennen grundlegende Techniken des Programmentwurfs und können diese anwenden. • kennen Standarddatentypen (z.B. für ganze Zahlen und Zeichen) und spezielle Datentypen (z.B. Felder und Strukturen). • kennen die Operatoren der Sprache und können damit gültige Ausdrücke bilden und verwenden. • kennen die Anweisungen zur Steuerung des Programmablaufs (z.B. Verzweigungen und Schleifen) und können diese anwenden. • kennen die Möglichkeiten zur Strukturierung von Programmen (z.B. Funktionen und Module) und können diese einsetzen. • kennen die Techniken zur Speicherverwaltung und können diese verwenden. • kennen die Möglichkeiten und Grenzen der Rechnerarithmetik (z.B. Ganzzahl- und Gleitkommarithmetik) und können diese beim Programmentwurf berücksichtigen. • kennen die Programmbibliotheken und können diese einsetzen.	**Workload:** Attendance time: 42 h Self-study time: 108 h

Course: Grundlagen der C-Programmierung (Block course)	3 WLH
Examination: Written examination (90 minutes), not graded **Examination requirements:** Standarddatentypen, Konstanten, Variablen, Operatoren, Ausdrücke, Anweisungen, Kontrollstrukturen zur Steuerung des Programmablaufs, Strings, Felder, Strukturen, Zeiger, Funktionen, Speicherverwaltung, Rechnerarithmetik, Ein-/Ausgabe, Module, Standardbibliothek, Präprozessor, Compiler, Linker	5 C

Admission requirements: none	**Recommended previous knowledge:** none
Language: German	**Person responsible for module:** Dr. Henrik Brosenne
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 120	

Georg-August-Universität Göttingen **Module B.Inf.1802: Training in Programming**	5 C 4 WLH
Learning outcome, core skills: Die Studierenden erlernen eine objektorientierte Programmiersprache, sie • kennen die gängigen Programmierwerkzeuge (Compiler, Build-Management-Tools) und können diese benutzen. • kennen die Grundsätze und Techniken des objektorientierten Programmentwurfs (z.B. Klassen, Objekte, Kapselung, Vererbung, Polymorphismus) und können diese anwenden. • kennen eine Auswahl der zur Verfügung stehenden Application Programming Interfaces (APIs) (z.B. Collections-, Grafik-, Thread-API) • können Dokumentationskommentare benutzen und kennen die Werkzeuge zur Generierung von API-Dokumentation. • kennen Techniken und Werkzeuge zur Versionskontrolle und können diese anwenden. • können Programme erstellen, die konkrete Anforderungen erfüllen, und deren Korrektheit durch geeignete Testläufe überprüfen. • kennen die Prinzipien und Methoden der projektbasierten Teamarbeit und können diese umsetzen.	**Workload:** Attendance time: 56 h Self-study time: 94 h
Course: Programmierpraktikum (Internship, Lecture)	
Examination: Projektarbeit (4-6 Wochen) und mündliche Prüfung (ca. 20 Minuten je zu prüfender Person) als Gruppenprüfung **Examination prerequisites:** B.Inf.1802.Ue: Lösung von 50% der Programmieraufgaben. **Examination requirements:** Klassen, Objekte, Schnittstellen, Vererbung, Packete, Exceptions, Collections, Typisierung, Grafik, Threads, Thread-Synchronisation, Prozess-Kommunikation, Dokumentation, Archive, Versionskontrolle	5 C

Admission requirements: B.Inf.1101	**Recommended previous knowledge:** B.Inf.1801
Language: German	**Person responsible for module:** Dr. Henrik Brosenne
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 80	

Georg-August-Universität Göttingen **Module B.Inf.1842: Programming for Data Scientists II**	5 C 3 WLH

Learning outcome, core skills:

Die Studierenden erlernen eine aktuelle Programmiersprache, sie

- beherrschen den Zugriff auf Daten aus verschiedenen Quellen, unter anderem aus lokalen Dateien und aus Datenbanken.
- kennen Programmbibliotheken zum machinellen Lernen und können diese anwenden um Modelle zu trainieren und auszuwerten.
- kennen Programmbibliotheken zu statistischen Tests und können diese anwenden.
- kennen Programmbibliotheken zur Visualisierung und können einfache Ergebnisgrafiken erstellen.

Workload:

Attendance time:
42 h
Self-study time:
108 h

Course: Programmierpraktikum für Data Scientists (Internship, Lecture)	3 WLH
Examination: Oral examination (approx. 20 minutes), not graded **Examination prerequisites:** Lösung von 50% der Programmieraufgaben und die erfolgreiche Teilnahme an einer großen Gruppenaufgabe **Examination requirements:** Kenntnis der Syntax und Semantik der Programmiersprache, Kenntnis von Bibliotheken und Befehlen zum maschinellen Lernen, statistischen Tests und zur Visualisierung.	5 C

Admission requirements: none	**Recommended previous knowledge:** B.Inf.1841
Language: German	**Person responsible for module:** N.N.
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 2
Maximum number of students: 50	

Georg-August-Universität Göttingen **Module M.Bio.101: General and applied microbiology**	12 C 14 WLH

Learning outcome, core skills: **Learning outcome:** Evolution and phylogenetic system; morphology and cell biology; communities and biocoenosis of bacteria and archaea; gene expression and molecular control (transcription, translation); posttranslational control, protein stability and proteomics; genetic networks; molecular switches and signal transduction; microbial developmental biology; mechanisms of pathogenicity of important pathogens; development of new antimicrobial agents; diversity of the metabolism in bacteria and archaea as basis for biotechnological applications; industrial microbiology. **Methods course:** Acquisition of biomolecular, genetic, and biochemical techniques for manipulation and analysis through experiments from current fields of research, e.g. structural analysis and classification of bacteria, transformation, isolation of DNA, sequencing of DNA, diagnostic and Real-time PCR, fluorescence microscopy, enzyme assays, cloning, protein purification. **Core skills:** Knowledge of microorganisms relevant for biotechnology and medicine, ability to identify these organisms and to analyse them with molecular methods. Independent acquisition of professional and critical dealing with knowledge from publications on current topics in microbiology.	**Workload:** Attendance time: 196 h Self-study time: 164 h

Course: General and applied microbiology (Lecture)	3 WLH
Examination: written examination covering lecture topics (90min, 90% of grade) and seminar presentation (15min, 10% of grade) **Examination prerequisites:** regular attendance in methods course and seminar, protocol	12 C

Course: General and applied microbiology (Seminar)	1 WLH

Course: Methods course: Signal transduction in bacteria (Practical course) or	

Course: Methods course: Isolation and characterisation of biotechnologically relevant microorganisms (Practical course)	10 WLH

Examination requirements: Detailed knowledge in cell biology, biochemistry and genetics of procaryotic microorgansims. Deepened knowledge of molecular biological, genetic and biochemical techniques to analyze procaryotes. Ability to critically present and reflect scientific publications.	

Admission requirements: can't be combined with key competence module M.Bio.141	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Jörg Stülke

Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 48	

Georg-August-Universität Göttingen **Module M.Bio.102: Molecular genetics and microbial cell biology**	12 C 14 WLH

Learning outcome, core skills: Advanced knowledge of molecular genetics and microbial cell biology through case studies of model systems of molecular mycology (yeasts and filamentous fungi). Acquisation of knowledge up to the "Review" level in one topic. **Methods course:** Research and project orientated acquisition of biomolecular, genetic, biochemical and cell biological techniques in the involved departments in small groups.	**Workload:** Attendance time: 196 h Self-study time: 164 h

Course: Molecular genetics and microbial cell biology (Lecture)	3 WLH
Course: Molecular genetics and microbial cell biology (Seminar)	1 WLH

Course: Methods course: Genetics/Cell biology (Practical course)	10 WLH

Examination: Written examination (90min, 80% of grade), oral presentation within seminar (15min, 10% of grade) and protocol (10 pages, 10% of grade) **Examination prerequisites:** regular attendance in seminar and methods course, protocol	

Examination requirements: • detailed knowledge in cell biology, biochemistry and genetics of eucaryotic microorgansims • deepened knowledge of molecular biological, genetic and biochemical techniques to analyze eucaryotes • detailed anaylsis and report of experiments • ability to reflect and present scientific paper	

Admission requirements: can't be combined with key competence module M.Bio.142	**Recommended previous knowledge:** • Watson, Molecular Biology of the Gene, Pearson, 6th Edition; • Alberts, Molecular Biology of the Cell, Garland, 5th Edition
Language: English	**Person responsible for module:** Prof. Dr. Gerhard Braus
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 24	

Georg-August-Universität Göttingen **Module M.Bio.105: Applied bioinformatics in molecular biosciences**	12 C 14 WLH

Learning outcome, core skills: Handling of programs, bioinformatic tools and databases with respect to data-driven Omics-based research, allowing to answer important questions of modern biology. Main topics are: • Application of bioinformatic approaches in molecular phylogeny, evolution, genome dynamics und (meta)Omics • Bioinformatic analysis of RNAs and proteins • Identification of motifs and genes • Generation and analysis of metabolic models and networks There's special focus on the analysis, visualisation and integration of big datasets generated by Omics approaches (e.g., genomics, transcriptomics, proteomics and metabolomics), which form the basis for a systemic understanding of organisms and communities.	**Workload:** Attendance time: 196 h Self-study time: 164 h

Course: Applied Bioinformatics in molecular biosciences (Internship)	10 WLH
Course: Applied Bioinformatics in molecular biosciences (Lecture)	3 WLH
Course: Applied Bioinformatics (Seminar)	1 WLH
Examination: presentation (30 min) approaches and results of the methods course (80% of grade) and seminar presentation (15 min, 20% of grade) **Examination prerequisites:** regular attendance in methods course and seminar, protocol or manuscript **Examination requirements:** Detailed knowledge in bioinformtic approaches with focus on (meta)omics-based analysis, detection of motifs and modeling of metabolic abilities. Ability to critically reflect and present scientific publications.	12 C

Admission requirements: Linux-course, B.Bio-NF117 or comparable modules	**Recommended previous knowledge:** Python and R
Language: English	**Person responsible for module:** Prof. Dr. Rolf Daniel
Course frequency: 1	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 12	

Georg-August-Universität Göttingen **Module M.Bio.106: Structural biochemistry**	12 C 14 WLH

Learning outcome, core skills: Methods in Structural Biochemistry, structure and function of biological macromolecules. Structure and folding of proteins, structure-function relationships, protein-protein and protein-nucleic acid complexes. Structure-based drug-design, molecular recognition. Handling of state of the art equipment, critical dealing with current biochemical topics, detailed analysis of experiments and their presentation. Independent acquisition of professional knowledge from publications by active participation in the seminar.	**Workload:** Attendance time: 196 h Self-study time: 164 h

Course: Structural biology (Lecture)	3 WLH
Examination: Written examination (90min, 80% of grade), oral presentation within seminar (15min, 10% of grade) and protocol (max 20 pages, 10% of grade) **Examination prerequisites:** regular participation in practical course and protocol	12 C

Course: Structural biology (Seminar)	1 WLH

Course: Structural biology (Practical course) *Contents*: Preparation of proteins and protein-RNA-complexes via affinity-, ion exchange- or gel filtration chromatography as well as ultracentrifugation. Characterization of recombinant proteins and macromolecular complexes (gel electrophoresis, spectroscopic methods). Biochemical analysis of protein-RNA-complexes, crystallization of proteins. Structural resolution of biological macromolecules using X-ray crystallography and cryo electron microscopy. Studies on dynamics and function of molecular machines.	10 WLH

Examination requirements: knowledge of the basics in structural biochemistry, especially: * biochemical and analytic methods used in the characterization of proteins and macromolecular complexes * characteristics of selected proteins and protein complexes * the basics of structural resolution and the structural characteristics of proteins and nucleic acids	

Admission requirements: can't be combined with key competence modules M.Bio.156 and M.Bio.166	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Ralf Ficner
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted:	**Recommended semester:**

twice	1
Maximum number of students: 20	

Georg-August-Universität Göttingen **Module M.Bio.107: Biochemistry and biophysics**	12 C 14 WLH

Learning outcome, core skills: Molecular biochemistry and biophysics of different classes of biomolecules, plant primary and secondary metabolism, lipid metabolism, lipids as signal molecules and secondary metabolites, biotechnological utilization and modification of storage substances, enzymes of lipid metabolism, modern biophysical methods for analysis of biomolecules Handling of state of the art equipment, critical dealing with current biochemical topics, detailed analysis of experiments and their presentation. Independent acquisition of professional knowledge from publications by active participation in the seminar.	**Workload:** Attendance time: 196 h Self-study time: 164 h

Course: Biochemistry and Biophysics (Lecture)	3 WLH
Examination: written examination covering lecture topics (90min, 80% of grade) and protocol (20 pages max, 20% of grade) **Examination prerequisites:** regular participation in methods course and protocol (max. 20 pages)	12 C

Course: Biochemistry and Biophysics (Tutorial)	1 WLH

Course: methods course: Biochemistry and Biophysics (Practical course) *Contents*: Biochemical analysis of carbohydrates, lipids, proteins and nucleic acids using photometric assays, electrophoresis, thin layer chromatography as well as fully automated analysis tools (HPLC/GC/GCMS). Spectroscopy of biomolecules (fluorescence, FT-IR, CD, UV/Vis), modern microscopy techniques (optical microscopy, scanning probe techniques), functional analysis of different membrane protein classes	10 WLH

Examination requirements: • basic knowledge of different classes of biomolecules and their metabolism • knowledge about spectroscopy of molecules • biotechnologic techniques using plants	

Admission requirements: can't be combined with M.Bio.157	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Ivo Feußner
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 48	

Georg-August-Universität Göttingen **Module M.Bio.141: General and applied microbiology**	3 C 3 WLH

Learning outcome, core skills: **Learning outcome:** Evolution and phylogenetic system; morphology and cell biology; communities and biocoenosis of bacteria and archaea; gene expression and molecular control (transcription, translation); posttranslational control, protein stability and proteomics; genetic networks; molecular switches and signal transduction; microbial developmental biology; mechanisms of pathogenicity of important pathogens; development of new antimicrobial agents; diversity of the metabolism in bacteria and archaea as basis for biotechnological applications; industrial microbiology. **Core skills:** Knowledge of microorganisms relevant for biotechnology and medicine, ability to identify these organisms and to analyse them with molecular methods.	**Workload:** Attendance time: 42 h Self-study time: 48 h

Course: lecture: General and applied microbiology (Lecture)	3 WLH
Examination: Written examination (90 minutes)	3 C

Examination requirements: detailed knowledge in cell biology, biochemistry and genetics of procaryotic microorgansims	

Admission requirements: can't be combined with core module M.Bio.101	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Jörg Stülke
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.142: Molecular genetics and microbial cell biology**	3 C 3 WLH

Learning outcome, core skills: Advanced knowledge of Molecular Genetics and microbial cell biology through case studies of model systems of molecular mycology (yeasts and filamentous fungi). Acquisation of knowledge up to the "Review" level in one topic.	**Workload:** Attendance time: 42 h Self-study time: 48 h

Course: Molecular genetics and microbial cell biology (Lecture)	3 WLH
Examination: Written examination (90 minutes)	3 C

Examination requirements: detailed knowledge in cell biology, biochemistry and genetics of eucaryotic microorgansims	

Admission requirements: Can´t be combined with core module M.Bio.102 or key competence module M.Bio.172.	**Recommended previous knowledge:** • Watson, Molecular Biology of the Gene, Pearson, 7th Edition • Alberts, Molecular Biology of the Cell, Garland, 5th Edition
Language: English	**Person responsible for module:** Prof. Dr. Gerhard Braus
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.144: Cellular and molecular biology of plant-microbe interactions**	3 C 3 WLH

Learning outcome, core skills: Introduction into theory and methods for the analysis of plant-microbe interactions on the cell biological and molecular level.	**Workload:** Attendance time: 42 h Self-study time: 48 h

Course: lecture: Plant-microbe-interactions (Lecture)	3 WLH
Examination: Written examination (54 minutes)	3 C

Examination requirements: knowledge of basic concepts in plant-microbe-interactions	

Admission requirements: Can´t be combined with core module M.Bio.104	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Christiane Gatz Prof. Dr. Volker Lipka
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.156: Structural biochemistry**	3 C 3 WLH

Learning outcome, core skills: Methods in Structural Biology,structure and function of biological macromolecules. Structure and folding of proteins, structure-function relationships, protein-protein and protein-nucleic acid complexes. Structure-based drug-design	**Workload:** Attendance time: 42 h Self-study time: 48 h

Course: lecture: Structural Biology (Lecture)	3 WLH
Examination: Written examination (90 minutes)	3 C

Examination requirements: The students show that they know the basics of structural biology. They are familiar with biochemical and analytical methods in protein and macromolecular complex- analysis. They have deepened knowledge about selected proteins and protein complexes. The students know the basics in structural resolution and structural characteristics of proteins.	

Admission requirements: can't be combined with M.Bio.105	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Ralf Ficner
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.157: Biochemistry and biophysics**	3 C 3 WLH

Learning outcome, core skills: Molecular biochemistry and biophysics of different classes of biomolecules, plant primary and secondary metabolism, lipid metabolism, lipids as signal molecules and secondary metabolites, biotechnological utilization and modification of storage substances, enzymes of lipid metabolism, modern biophysical methods for analysis of biomolecules Handling of state of the art equipment, critical dealing with current biochemical topics, detailed analysis of experiments and their presentation. Independent acquisition of professional knowledge from publications by active participation in the seminar.	**Workload:** Attendance time: 42 h Self-study time: 48 h

Course: lecture: Biochemistry and Biophysics (Lecture)	3 WLH
Examination: Written examination (90 minutes)	3 C

Examination requirements: • basic knowledge of different classes of biomolecules and their metabolism • knowledge about spectroscopy of molecules • biotechnologic techniques using plants	

Admission requirements: can't be combined with M.Bio.106	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Ivo Feußner
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 2
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.158: Enzyme catalysis and biological chemistry**	3 C 3 WLH

Learning outcome, core skills: Catalytic mechanisms of enzymes, mechanisms of macromolecular complexes, biocatalysis, kinetics und thermodynamics of biochemical reactions, chemical model systems of enzymes, synthesis of biooligomers, synthesis of ligands, ligation techniques, array technologies	**Workload:** Attendance time: 42 h Self-study time: 48 h

Course: lecture: Enzyme Catalysis and Chemical Biology (Lecture)	3 WLH
Examination: Written examination (90 minutes)	3 C

Examination requirements:

- knowledge about kinetics and thermodynamics of biochemical reactions
- knowledge about different organic synthesis mechanisms
- knowledge about catalytic mechanisms of enzyme

Admission requirements: can't be combined with M.Bio.107	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Kai Tittmann
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.172: Molecular genetics and microbial cell biology**	6 C 4 WLH

Learning outcome, core skills: Advanced knowledge of molecular genetics and microbial cell biology through case studies of model systems of molecular mycology (yeasts and filamentous fungi). Acquisation of knowledge up to the "Review" level in one topic.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Molecular genetics and microbial cell biology (Lecture)	3 WLH
Examination: Written examination (90min, 80% of grade), oral presentation within seminar (15min, 20% of grade) **Examination prerequisites:** regular attendance in seminar	6 C

Course: Molecular genetics and microbial cell biology (Seminar)	1 WLH

Examination requirements: • detailed knowledge in cell biology, biochemistry and genetics of eucaryotic microorgansims • deepened knowledge of molecular biological, genetic and biochemical techniques to analyze eucaryotes • ability to reflect and present scientific paper	

Admission requirements: can't be combined with M.Bio.102 or M.Bio.142	**Recommended previous knowledge:** • Watson, Molecular Biology of the Gene, Pearson, 7th Edition; • Alberts, Molecular Biology of the Cell, Garland, 5th Edition
Language: English	**Person responsible for module:** Prof. Dr. Gerhard Braus
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 6	

Georg-August-Universität Göttingen **Module M.Bio.176: Structural biochemistry**	6 C 4 WLH

Learning outcome, core skills: methods in Structural Biochemistry, structure and function of biological macromolecules, structure and folding of proteins, structure-function relationships, protein-protein and protein-nucleic acid complexes, Structure-based drug-design, molecular recognition. Critical dealing with current biochemical topics. Independent acquisition of professional knowledge from publications by active participation in the seminar.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Structural biochemistry (Lecture)	3 WLH
Examination: Written examination (90min, 80% of grade), oral presentation within seminar (15min, 20% of grade) **Examination prerequisites:** regular participation in seminar	6 C

Course: Structural biochemistry (Seminar)	1 WLH

Examination requirements: knowledge of the basics in structural biochemistry, especially: • biochemical and analytic methods used in the characterization of proteins and macromolecular complexes • characteristics of selected proteins and protein complexes • the basics of structural resolution and the structural characteristics of proteins and nucleic acids	

Admission requirements: can't be combined with M.Bio.106 and M.Bio.166	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Ralf Ficner Dr. Achim Dickmanns
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 5	

Georg-August-Universität Göttingen **Module M.Bio.310: Systems biology**	12 C 14 WLH

Learning outcome, core skills: Subject of this module are the formal description, modeling, analysis and simulation of complex interactions between the components (molecules, cells, organs) of living systems on different levels of abstraction. Biomolecular networks, like networks of metabolic signaling and transduction will be introduced and various graph based abstractions of interaction networks will be demonstrated (entity interaction graph, boolean networks, Petri networks). The students will get to know basics of the graph theory (analysis of paths, cluster coefficients, centrality, etc.) and they will learn how to apply the respective theory to biomolecular networks. The students will be introduced to different high-throughput techniques and their application to biomolecular networks. The simulation of molecular networks will be presented by selected examples.	**Workload:** Attendance time: 147 h Self-study time: 213 h

Course: Bioinformatics of systems biology (Lecture)	2 WLH
Examination: Oral examination (approx. 30 minutes)	6 C

Course: Bioinformatics of systems biology (Exercise)	2 WLH
Course: Bioinformatics of systems biology (Seminar)	1 WLH

Course: Methods course 'Modelling and analysis of biological systems' 3 weeks full time	9 WLH
Examination: Minutes / Lab report (max. 10 pages) **Examination prerequisites:** oral presentation (ca. 30 min), regular attendance	6 C

Examination requirements: Ability to model, analyze and simulate biomolecular networks	

Admission requirements: can't be combined with M.Bio.340	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Tim Beißbarth
Course frequency: each summer semester; verschieden; siehe Lehrveranstaltungen	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.323: Introduction to Bayesian Statsistics and Information Theory**	12 C 12 WLH

Learning outcome, core skills: The students learn the basic concepts and main applications of Bayesian Statistics, in particular Bayesian probabilities, parameter estimation and Bayesian credible intervals, importance and choice of prior distributions based on prior knowledge, Bayesian hypothesis testing, model tests and MCMC methods. All concepts will be presented in lectures and worked with in hands-on computer assignments. The module closes with a foray into information theory.	**Workload:** Attendance time: 195 h Self-study time: 165 h

Course: Introduction to Bayesian Inference and Information Theory (Lecture)	3 WLH
Course: Classical problems in Bayesian Interference (Seminar)	1 WLH

Course: Programmierkurs	8 WLH

Examination: Written examination (90 minutes) **Examination prerequisites:** regular attendance, oral presentation in seminar	12 C

Examination requirements: Knowledge of the foundations of Bayesian probabilities and statistics and the ability to solve simple classic problems in Bayesian Inference.	

Admission requirements: basic computer knowledge, basic experience in coding	**Recommended previous knowledge:** basics in probability calculation
Language: English	**Person responsible for module:** Prof. Dr. Michael Wibral
Course frequency: each winter semester	**Duration:**
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.340: Systems biology**	3 C 2 WLH

Learning outcome, core skills: Subject of this module are the formal description, modeling, analysis and simulation of complex interactions between the components (molecules, cells, organs) of living systems on different levels of abstraction. Biomolecular networks, like networks of metabolic signaling and transduction will be introduced and various graph based abstractions of interaction networks will be demonstrated (entity interaction graph, boolean networks, Petri networks). The students will get to know basics of the graph theory (analysis of paths, cluster coefficients, centrality, etc.) and they will learn how to apply the respective theory to biomolecular networks. The students will be introduced to different high-throughput techniques and their application to biomolecular networks. The simulation of molecular networks will be presented by selected examples.	**Workload:** Attendance time: 42 h Self-study time: 48 h

Course: Bioinformatics in systems biology (Lecture)	2 WLH
Examination: Oral examination (approx. 30 minutes)	3 C

Examination requirements: Ability to model, analyze and simulate biomolecular networks.	

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Tim Beißbarth
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 10	

Georg-August-Universität Göttingen **Module M.Bio.372: Matlab in neuroscience**	3 C 2 WLH

Learning outcome, core skills: Goal of the course is a general introduction into Matlab basics, with a focus on psychophysics and neuroscientific applications. The course teaches the knowledge and skills needed to understand existing Matlab code and to develop your own Matlab programs. The course consists of two parts, a more theoretically oriented lecture and a practical tutorial in which the weekly excercises will be discussed.	**Workload:** Attendance time: 28 h Self-study time: 62 h

Course: Matlab basics (Lecture)	1 WLH
Course: Matlab advanced (Tutorial)	1 WLH
Examination: Written examination (60 minutes) **Examination prerequisites:** Regular participation and performance of exercisess	3 C

Examination requirements: The students demonstrate that they can read and develop their own Matlab programs.	

Admission requirements: attendance of the lecture "Biologische Psychologie II/Kognitive Neurowissenschaften" or equivalent course.	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Alexander Gail
Course frequency: each summer semester; erste Semesterhälfte	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 20	

Additional notes and regulations: Die Veranstaltung ist geeignet für hoch motivierte Bachelor- und Master-Studierende der Psychologie, Biologie und Physik, die überdurchschnittliches Forschungsinteresse haben.

Georg-August-Universität Göttingen **Module M.Bio.375: Neurorehabilitation Technologies: Introduction and Applications**	2 C 2 WLH

Learning outcome, core skills: Students are able to describe the state of the art in Neurorehabilitation technologies and understand the basics of the related physiological processes. They are in a position to discuss and evaluate current trends as well as to recognize limitations of available assistive and (neuro)rehabilitation technology. The programming and lab exercises will allow students to address variety of practical Neurorehabilitation challenges.	**Workload:** Attendance time: 28 h Self-study time: 32 h

Course: Introduction to Neurorehabilitation Technologies (Seminar) *Contents*: • Basic motor physiology • Biophysiological signal acquisition and processing • Invasive and non-invasive man-machine interfaces • Upper limb related technologies • Lower limb related technologies • Feedback for sensory-motor integration and rehabilitation • Selected topics on advanced technologies and their applications	1 WLH
Examination: Presentation (approx. 20 min.) and written elaboration (max. 5 pages), not graded **Examination prerequisites:** Participation and successful completion of all laboratory exercises.	3 C

Course: Neurorehabilitation Technologies (Exercise) *Contents*: • Biophysiological signal acquisition and processing • Prosthesis control • Motion analysis	1 WLH

Examination requirements: Students show that they are able to present and critically reflect scientific publications. They are familiar with the basic principles of neurorehabilitation technologies.	

Admission requirements: none	**Recommended previous knowledge:** basic programming skills (B.Inf.1801/1802) basic knowledge in neurophysiology (B.Bio.123; M.Bio.304)
Language: English	**Person responsible for module:** Prof. Dr. Arndt Schilling; Dr. Marko Markovic
Course frequency: each winter semester1	**Duration:**

Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 16	

Additional notes and regulations:
Literature suggestions will be handed out at the beginning of each term. However, the students are expected to independently perform literature research on the selected topic.

Georg-August-Universität Göttingen **Module M.Biodiv.425: Evolution of embryophyta**	6 C 4 WLH

Learning outcome, core skills: The students get to know the current state of research in the field of the organismic evolution of embryophyta through study, presentation and discussion of latest case studies concerning speciation, history of evolution, chromosomal and genomic evolution, reproduction biology, evolution of traits and coevolution. They get an overview of novel theoretical and methodical research approaches to the comprehension of plant evolution. They acquire the ability to develop evolutionary hypotheses and are able to choose appropriate model systems and methods for their validation. The students acquire practical skills in presentation, interpretation and discussion of results (in scientific English). They are able to describe and understand evolutionary processes, hypotheses and methods and to give examples for case studies on terrestrial plants. They can discuss scientific results in English.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Speciation and evolution of land plants (Lecture) *Course frequency:* each winter semester	2 WLH
Course: Plant systematics and phycology (Seminar) *Course frequency:* each semester	2 WLH
Examination: Oral examinationabout the contents of the lecture (approx. 15 minutes) **Examination prerequisites:** participation in the seminar and oral presentation (45 minutes) **Examination requirements:** In the oral examination the students demonstrate their ability to understand and discuss evolutionary processes and hypotheses as well as their knowledge of case studies on terrestrial plants. In the seminar the students shall give talks in scientific English and present research results – preferably those of their master thesis.	6 C

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Elvira Hörandl
Course frequency: lecture: each winter semester, seminar: each semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 30	

Georg-August-Universität Göttingen **Module M.Biodiv.446: Molecular zoology and insect-biotechnology**	6 C 8 WLH

<table>
<tr><td>Learning outcome, core skills:
The module is aimed at students who want to gain in-depth knowledge of molecular genetic work in theory and practice. Relevant methods and experimental planning are taught theoretically and practically. Selected topics of molecular zoology are treated in depth in lectures and on the basis of current publications. Current developments of molecular methods in pest control and insect biotechnology will be covered.
Learning objectives:
• Application, experimental strategies and evaluation of different molecular biological methods.
• Gene function analysis in zoology: how to identify relevant genes and how to study their function in model and non-model organisms? (including genetic screens, reverse genetics (RNAi), genome editing (CRISPR/Cas9), transgenesis)
• Knowledge of databases of DNA, protein and gene function
• Identification of orthologous genes in different species
• Establishment of new molecular genetic model systems for zoological questions
• Advanced discussion of current research topics in molecular zoology
• Advanced discussion of recent approaches in insect biotechnology using molecular genetic methods (including pest control).
Students should be able to:
• design experimental strategies for the identification and analysis of gene function in non-model organisms
• design the establishment of new molecular genetic model systems
• be able to present and assess scientific questions on selected topics of molecular zoology.</td><td>Workload:
Attendance time:
112 h
Self-study time:
68 h</td></tr>
</table>

Course: Gene function analysis in diverse animals and applications in pest control (Lecture) *Contents*: molecular genetic methods; gene fuction analysis; selected topics from molecular zoology; most recent developments in insect biotechnology	2 WLH
Course: Topics of molecular zoology and insect biotechnology (Seminar)	2 WLH
Course: Molecular zoology and insect biotechnology (Exercise)	4 WLH
Examination: Oral Presentation (approx. 15 minutes)	6 C

Examination requirements: The students should be able to apply the contents and methods listed as “core skills” to new questions.	

Admission requirements: none	**Recommended previous knowledge:** none
Language:	**Person responsible for module:**

English	Prof. Dr. Gregor Bucher
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 8	

Additional notes and regulations: Das Modul kann nicht in Kombination mit B.Biodiv.370 belegt werden.

Georg-August-Universität Göttingen **Module M.Biodiv.479: Introduction to phylogenomics**	6 C 6 WLH
Learning outcome, core skills: The research field of phylogenomics comprises the utilization of genome and transcriptome data for the inference of phylogenetic trees. In this modul students will be introduced to the theoretical and practical knowledge of how to assemble genomes and transcriptomes and their annotation. Moreover, techniques to search for genes in such data will be presented (e.g., BLAST, hidden markov models). Additionally, the students will work with different alignment- and read mapping methods. Based on the assembled datasets different tree reconstruction methods will be conducted (Neighbor Joining, Maximum Parsimony, Maximum Likelihood, Bayesian Inference) and critically discussed. Within an accompanying seminar actual studies in the field of evolutionary genomics are presented and discussed. Students get an introduction into the Linux environment and the installation of all programs will be done independently. The command line will be mainly used for all analyses. Students will learn to perform genome-scale analyses for the reconstruction of phylogenetic trees. Within a seminar students will present recently published genomic studies in English language. In the last week, datasets will be analysed independently and results will be summarized as poster, which will be presented within a short talk.	**Workload:** Attendance time: 84 h Self-study time: 96 h
Course: Introduction to phylogenomics (Lecture)	1 WLH
Course: Introduction to phylogenomics (Seminar)	1 WLH
Course: Introduction to phylogenomics (Exercise)	4 WLH
Examination: Oral Presentation (approx. 15 minutes) **Examination prerequisites:** Short talk (ca. 12-15 minutes)	6 C
Examination requirements: Knowledge of how to reconstruct phylogenetic trees using genomic and transcriptomics data. Critical discussion of phylogenetic analyses and overview of actual controversies.	

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Christoph Bleidorn
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 1
Maximum number of students: 12	

Georg-August-Universität Göttingen **Module M.Biodiv.491: Next generation sequencing for evolutionary biology**	6 C 4 WLH

Learning outcome, core skills: The students acquire knowledge of the various systems and techniques for “next generation sequencing”. The focus of the module lies on the fast developing field of bioinformatics and data analysis. Lab methods are explained and discussed. The students learn the different possible applications for “next generation sequencing” data in evolutionary biology of animals and plants, for example biodiversity, evolution of traits, adaption, phylogeography, population genetics, hybridization, genotyping and QTL (quantitative trait locus) analyses. They get an overview of the theory and gain practical experiences in this new research area. They acquire the competence to choose suitable methods for evolutionary questions and to test hypotheses on non-model organisms. The students are able to list the differences and (dis)advantages of various “next generation sequencing” methods and to select suitable methods to analyze specific evolutionary questions by use of non-model organisms. They are able to compare and analyze the raw data of “next generation sequencing” and to annotate genes of a compared genome or transcriptome. The students shall present and discuss case studies from the field of “next generation sequencing” during the seminar in scientific English.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: M.Biodiv.491-2 Next generation sequencing: examples of botanical and zoological studies (Seminar)	0,5 WLH
Course: M.Biodiv.491-3 Analysis of next generation sequencing data (Exercise)	3 WLH
Course: M.Biodiv.491-1 Next generation sequencing: methods, data analysis and applications (Lecture)	0,5 WLH
Examination: Minutes / Lab report (max. 12 pages) **Examination prerequisites:** Oral presentation (max. 20 min.) **Examination requirements:** Knowledge of the various applications of „next generation sequencing“ in evolutionary biology of animals and plants. Overview of the theory and practical experiences in this new research area.	6 C

Admission requirements: none	**Recommended previous knowledge:** Speciation and evolution of land plants (Lecture: M.Biodiv.425). Basic knowledge about programs that deal with DNA conting assembly and multiple sequence alignment (e.g. Geneious) are advantageous
Language: English	**Person responsible for module:** Dr. Marc Appelhans
Course frequency:	**Duration:**

each summer semester	1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 12	

Georg-August-Universität Göttingen **Module M.Biodiv.600: Introduction to phylogenetics**	6 C 8 WLH

Learning outcome, core skills: The aim of phylogenetic systematics is to reconstruct evolutionary relationships of living things. A broad array of methods gives the opportunity to use molecular and morphological data to infer how life has diversified and changed over time. . In this modul students will be introduced to the theoretical and practical background of phylogenetics. The course includes an introduction to the description and delimitation of species, DNA barcoding, homology hypotheses, phylogenetic characters and character coding. Additionally, actual computational methods for the reconstruction of phylogenetic trees using molecular and morphological characters will be presented. Based on phylogenetic trees ancestral characters states and/or biogeographical patterns will be inferred. Based on the introduced methods the students will work independently on projects of exemplar datasets (e.g., diverse groups of insects or annelids, but maybe also from other animal groups). Within a seminar students will present recently published studies in the field of phylogenetic systematics in English language. In the last week, the student will present the results of the datasets they analysed in the form of a poster, which will be accompanied with a short talk.	**Workload:** Attendance time: 112 h Self-study time: 68 h

Course: Introduction to phylogenetics (Lecture)	1 WLH
Course: Introduction to phylogenetics (Seminar)	1 WLH
Course: Introduction to phylogenetics (Exercise)	6 WLH
Examination: Oral Presentation (approx. 15 minutes) **Examination prerequisites:** Talk (ca. 12-15 minutes)	6 C

Examination requirements: Basics of phylogenetic systematics, knowledge of how to reconstruct phylogenetic trees using computational methods. Interpretation of phylogenetic trees.	

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Christoph Bleidorn Dr. Maria Teresa Aguado Molina
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 1
Maximum number of students: 12	

Georg-August-Universität Göttingen **Module M.CoBi.501: Bioinformatics and its areas of application**	8 C 7 WLH

Learning outcome, core skills: The students will acquire knowledge on a diverse range of topics - both applied as well as purely bioinformatical. For this, there will be research-oriented lectures. On the applied side, these topics prominently feature - but are not limited to - the different types of "omics"-approaches available to answer biological questions (genomics, transcriptomics, phylogenomics, metabolomics, proteomics, CHIP-Seq, comparative genomics, phenomics etc). They will learn about feasibility and different approaches to data analysis. Furthermore, students will learn about the digitization of the biological sciences, featuring aspescts such as machine readable phenotypic annotation of morphology, phenotypic database, biological image analysis and more. Finally, the students will acquire knowledge on algorithmic and statistical aspects of bioinformatics, featuring the latest developments and challenges in the development of new bioinformatic tools for life sciences.	**Workload:** Attendance time: 98 h Self-study time: 142 h

Course: Bioinformatics and its areas of application (Lecture) *Contents*: This course provides an appetizer of the various applications and uses of bioinformatics - especially those represented by research on Göttingen Campus.	3 WLH
Course: IMPRS Genome Science (Lecture)	2 WLH
Course: Industry excursion (Excursion) *Contents*: excursion to companies that make use of bioinformatics/computational biology (and hire bioinformaticians and computational biologists)	2 WLH
Examination: Term Paper (max. 10 pages), not graded **Examination requirements:** Students show that they gained an overview of the diversity of areas of application for algorithmic and applied bioinformatics - including tools for computational biology to solve biological questions - as well as in depth knowledge on a topic of choice for the essay.	8 C

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Jan de Vries
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 1
Maximum number of students: 30	

Georg-August-Universität Göttingen **Module M.CoBi.502: Biology for (bio)informaticians**	10 C 6 WLH

Learning outcome, core skills: This course aims to teach the principles of biology required for aspiring bioinformaticians and computational biologists. The students will learn about the basics of the building blocks of life. An introduction to molecular biology will cover aspects of cell biology, developmental biology, principles of genetics and genome biology, microbiology, protein biology and enzymology, and biochemistry as well as metabolism. Furthermore, they will get a glimpse into biodiversity through an introduction organismal diversity across uni- and multicellular life. This will be contextualized by a basic (molecular) evolutionary biological framework. Finally, students will get a glimpse into how wet laboratory work is carried out.	**Workload:** Attendance time: 84 h Self-study time: 216 h

Course: Biology for (bio)informaticians (Lecture)	4 WLH
Course: Methods in biochemistry and microbiology (Internship)	2 WLH

Course: Biology for (bio)informaticians (Tutorial)	2 WLH
Examination: Written examination (90 minutes) **Examination prerequisites:** protocol	10 C

Examination requirements: knowledge of the basics in molecular biology (cell biology, microbiology, genetics, neurobiology, developmental biology, biochemistry) as well as biodiversity (microorganisms, plants, fungi, animals)	

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Kai Heimel
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 1
Maximum number of students: 20	

Georg-August-Universität Göttingen **Module M.CoBi.503: Advanced course in Computational Biology**	12 C
Learning outcome, core skills: The student learns how to independently perform a project in the area of bioinformatics and/or computational biology. Objective of this project can be the development, evaluation / benchmarking, and analysis of bioinformatic software tools, the automation of data processing, and the analysis of biological data with bioinformatic techniques; the scientific question addressed can revolve around bioinformatic problems, biological phenomena and related fields.	**Workload:** Attendance time: 280 h Self-study time: 80 h
Course: Lab course: 8 weeks, full-time (Internship) *Course frequency:* each semester	20 WLH
Examination: Oral examination (approx. 30 minutes) **Examination prerequisites:** scientific presentation and discussion of obtained results (in form of a protocol) **Examination requirements:** independent execution of a project in bioinformatics, proven ability to present own results	12 C

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Alle
Course frequency: not specified	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 30	

Georg-August-Universität Göttingen **Module M.CoBi.504: Comparative and Evolutionary Genomics**	12 C 14 WLH

Learning outcome, core skills: Students will acquire an understanding of the usage and usefulness of comparative approaches in analyzing large-scale biological data (foremost sequencing data). This will entail a hands-on experience with carrying out comparative analyses on genomic data. The students will learn how to analyze, evaluate, and present comparative data. Furthermore, students will read, present, and critically discus published comparative studies that cover current topics in comparative and evolutionary genomics. Main topics are: comparative genomics: more than evolutionary biology, introduction to evolutionary/tree thinking, the evolutionary forces that shape genomes, a common language for comparisons (ontologies, pathways and more), reconciliation of gene families and species trees, forward and reverse genetics in light of comparative genomics, major evolutionary transitions gleaned from genomics, phylogenomics, reticulate evolution.	**Workload:** Attendance time: 196 h Self-study time: 164 h

Course: Comparative and Evolutionary Genomics (Lecture) *Contents*: principles of evolutionary thinking,evolutionary concepts,analyses and useful software for comparative genomic analyses,phylogenomics,ancestral character state reconstruction, interpretation of data	4 WLH
Examination: protocol (10-20 pages; 70% of final grade); oral presentation in seminar(25 min + 20 min discussion; 30% of final grade) **Examination prerequisites:** regular attendance and active participation **Examination requirements:** Detailed knowledge on macro-evolutionary processes, evolutionary thinking, methods available to compare genomic data, background on methods to analyse comparative evolutionary questions with genomic data, interpretation of results	12 C

Course: Genomic insights into evolutionary processes (Seminar) *Contents*: reading and presenting a published article on comparative and evolutionary genomics, discussion among all participants on the presented work, feedback on presentation, discussions around evolutionary thinking	3 WLH
Course: Applying Comparative and Evolutionary Genomics (Internship)	7 WLH

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Jan de Vries
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**

Maximum number of students: 15	

Georg-August-Universität Göttingen **Module M.CoBi.505: Population Genomics**	6 C 8 WLH

Learning outcome, core skills: Students will acquire an understanding on the principles and concepts important for population genomic analyses and inferences. Dry data labs (practicals) will give them hands-on experience with various population genomic analyses and the software used to conduct them. Critical discussions of the dry labs will help them interpret results and increase their understanding of key evolutionary processes and methodological assumptions. After passing this course the students should be able to identify when population genomic approaches are useful and be able to set up an outline for a population genomic study.	**Workload:** Attendance time: 112 h Self-study time: 68 h

Course: Population genomics (Lecture) *Contents*: Basic genetics (mutations, alleles, polymorphisms, inheritance), Species concept & types of speciation, Phylogeny & tree-thinking, Evolutionary processes in populations (drift, bottleneck, radiation, migration, selection), Hardy-Weinberg-Equilibrium, High throughput sequencing for population genomics (e.g. genome resequencing, RAD-Seq), Population genetic and genomic analyses (e.g. GWAS, Fst, McDonald-Kreitman test), Coalescence theory and simulations, Application of population genomics	4 WLH

Course: Population genomics (Exercise) *Contents*: Answering basic questions/problems in genetics and population genetics, tree-thinking and phylogeny, handling of population genetic and genomic datasets, using different types of software to conduct population genetic and population genomic analyses, interpretation, presentation and discussion of the obtained results	4 WLH
Examination: written exam (80%), graded worksheets in practicals (20%) **Examination prerequisites:** regular attendance and fully completed worksheets **Examination requirements:** detailed knowledge on the background and principles of population genetics and genomics, phylogenetics and tree-thinking, methods and calculations to analyse population genetic/genomic problems, how to design a population genomic study, interpretation of population genetic/genomic data and results.	6 C

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Dr. Sophie de Vries
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**

Maximum number of students: not limited	

Georg-August-Universität Göttingen **Module M.Inf.1114: Algorithms on Sequences**	5 C 4 WLH

Learning outcome, core skills: We expect that the participants will gain an understanding of classical string-processing tools. They are supposed to understand and be able to use in various situations: classical text algorithms (e.g., pattern matching algorithms, edit distance), classical text indexing data structures (e.g., suffix arrays / trees), and classical combinatorial results that are useful in this context (e.g., periodicity lemmas).	**Workload:** Attendance time: 56 h Self-study time: 94 h

Course: Algorithms on Sequences (Lecture, Exercise) *Contents*: This course is an introduction into the theory of stringology, or algorithms on sequences of symbols (also called words or strings). Our main intention is to present a series of basic algorithmic and combinatorial results, which can be used to develop efficient word-processing tools. While the emphasis of the course is on the theoretical side of stringology, we also present a series of applications of the presented concepts in areas like data-compression or computational biology The main topics our course will cover are: basic combinatorics on words, pattern matching algorithms, data structures for text indexing (suffix arrays, suffix trees), text compression (Huffman encoding, Lempel-Ziv method), detection of regularities in words, algorithms for words with don't care symbols (partial words), word distance algorithms, longest common subsequence algorithms, approximate pattern matching. The presentation of each theoretical topic from the above will be accompanied by a brief discussion on its possible applications. Literature • T.H. Cormen, C.E. Leiserson, R.L. Rivest, C. Stein: Introduction to Algorithms (3rd Edition), MIT Press, 2009. • M. Crochemore, C. Hancart, T. Lecroq: Algorithms on Strings, Cambridge University Press, 2007. • M. Crochemore, W. Rytter: Jewels of Stringology, World Scientific, 2002. • D. Gusfield. Algorithms on strings, trees, and sequences: computer science and computational biology. Cambridge University Press, 1997.	4 WLH
Examination: Oral examination (approx. 20 minutes) **Examination requirements:** basic combinatorics on words, pattern matching algorithms, data structures for text indexing (suffix arrays, suffix trees), text compression (Huffman encoding, Lempel-Ziv method), detection of regularities in words, algorithms for words with don't care symbols (partial words), word distance algorithms, longest common subsequence algorithms, approximate pattern matching	5 C

Admission requirements: none	**Recommended previous knowledge:** none
Language:	**Person responsible for module:**

English	Prof. Dr. Florin Manea
Course frequency: irregular	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 50	

Georg-August-Universität Göttingen **Module M.Inf.1142: Semantic Web**	6 C 4 WLH
Learning outcome, core skills: Die Studierenden kennen die theoretischen Grundlagen sowie technischen Konzepte des Semantic Web. Sie können den Nutzen und die Grenzen der verwendeten Technologien einschätzen und in realen Szenarien abwägen. Sie sehen an einigen Beispielen, wo aktuelle wissenschaftliche Fragestellungen ansetzen.	**Workload:** Attendance time: 56 h Self-study time: 124 h
Course: Semantic Web (Lecture, Exercise)	4 WLH
Examination: Klausur (90 Min.) oder mündliche Prüfung (ca. 25 Min.) **Examination requirements:** Kenntnisse der theoretischen Grundlagen und technischen Konzepte des Semantic Web; Fähigkeit zum Abschätzen des Nutzens und der Grenzen der verwendeten Technologien; Fähigkeit zur Abwägung realer Szenarien; Fähigkeit zum Nachvollziehen wissenschaftlicher Fragestellungen und Vorgehensweisen.	6 C

Admission requirements: Datenbanken, Formale Systeme	**Recommended previous knowledge:** M.Inf.1243
Language: German, English	**Person responsible for module:** Prof. Dr. Wolfgang May
Course frequency: unregelmäßig	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 50	

Georg-August-Universität Göttingen

Module M.Inf.1232: Parallel Computing

6 C
4 WLH

Learning outcome, core skills:
Successfully completing the module, students are able to:

- define and describe the benefit of parallel computing
- specify the classification of parallel computers (Flyn classification)
- analytically evaluate the performance of parallel computing approaches (scaling/ performance models)
- know the parallel hardware and performance improvement approaches (cache coherence, pipeline, etc.)
- know the interconnects and networks and their role in parallel computing
- understand and develop sample parallel programs using different paradigms and development environments (e.g., shared memory and distributed models)
- expose to some applications of Parallel Computing through hands-on exercises

Workload:
Attendance time:
56 h
Self-study time:
124 h

Course: Parallel Computing (Lecture, Exercise)

4 WLH

Contents:
Successfully completing the lecture, students are able to:

- define and describe the benefit of parallel computing and identify the role of software and hardware in parallel computing
- specify the Flynn classification of parallel computers (SISD, SIMD, MIMD)
- analytically evaluate the performance of parallel computing approaches (Scaling/ Performance models)
- understand the different architecture of parallel hardware and performance improvement approaches (e.g., caching and cache coherence issues, pipeline, etc.)
- define Interconnects and networks for parallel computing
- architecture of parallel computing (MPP, Vector, Shared memory, GPU, Many-Core, Clusters, Grid, Cloud)
- design and develop parallel software using a systematic approach
- parallel computing algorithms and development environments (i.e. shared memory and distributed memory parallel programming)
- write parallel algorithms/programs using different paradigms and environments (e.g., POSIX Multi-threaded programming, OpenMP, MPI, OpenCL/CUDA, MapReduce, etc.)
- get exposed to some applications of Parallel Computing through exercises

References

- An Introduction to Parallel Programming, Peter S. Pacheco, Morgan Kaufmann (MK), 2011, ISBN: 978-0-12-374260-5.
- Designing and Building Parallel Programs, Ian Foster, Addison-Waesley, 1995, ISBN 0-201-57594-9 (Available online).

• Advanced Computer Architecture: Parallelism, Scalability, Programmability, Kai Hwang, Int. Edition, McGraw Hill, 1993, ISBN: 0-07-113342-9. • In addition to the mentioned text book, tutorial and survey papers will be distributed in some lectures as extra reading material.	
Examination: Klausur (90 Min.) oder mündliche Prüfung (ca. 20 Min.) **Examination requirements:** Parallel programming; Shared Memory Parallelism; Distributed Memory Parallelism, Single Instruction Multiple Data (SIMD); Multiple Instruction Multiple Data (MIMD); Hypercube; Parallel interconnects and networks; Pipelining; Cache Coherence; Parallel Architectures; Parallel Algorithms; OpenMP; MPI; Multi-Threading (pthreads); Heterogeneous Parallelism (GPGPU, OpenCL/CUDA)	6 C

Admission requirements: • Data structures and algorithms • Programming in C/C++	**Recommended previous knowledge:** • Computer architecture • Basic knowledge of computer networks and topologies
Language: English	**Person responsible for module:** Prof. Dr. Ramin Yahyapour
Course frequency: unregelmäßig	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 50	

Georg-August-Universität Göttingen **Module M.Inf.1501: Data Mining in Bioinformatics**	6 C 4 WLH

Learning outcome, core skills: Students will learn methods for analyzing multidimensional data, which play a crucial role in the study of biological systems. The aim is to understand the special properties of high-dimensional spaces and the statistical methods that can make structures in complex data accessible. Criteria for the selection and applicability of different methods should be understood in theoretical and practical aspects.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Data Mining in der Bioinformatik (Lecture)	2 WLH
Course: Rechnerübung zu Data Mining in der Bioinformatik (Block course)	2 WLH
Examination: Oral examination (approx. 20 minutes)	6 C

Examination requirements: After completing the module, the students should be able to independently understand and apply methods for analyzing complex data and to critically assess the limits of applicability.	

Admission requirements: none	**Recommended previous knowledge:** Algorithms in Bioinformatics, Machine Learning in Bioinformatics
Language: German, English	**Person responsible for module:** Dr. Peter Meinicke
Course frequency: unregelmäßig	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 15	

Georg-August-Universität Göttingen **Module M.Inf.1504: Algorithms in Bioinformatics II**	6 C 4 WLH

Learning outcome, core skills: Students learn algorithms for cluster analysis and analysis of RNA structures, gene prediction in eukaryotes, pattern recognition on sequences, and advanced methods of sequence alignment.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Algorithmen der Bioinformatik II (Lecture, Exercise)	4 WLH
Examination: Oral examination (approx. 20 minutes)	6 C

Examination requirements: After completion of the module, students should be able to apply known methods from computer science to bioinformatics problems and to critically assess the limits of their applicability.	

Admission requirements: none	**Recommended previous knowledge:** Basic knowledge of algorithms in bioinformatics, machine learning in bioinformatics, and molecular biology.
Language: German, English	**Person responsible for module:** Prof. Dr. Burkhard Morgenstern
Course frequency: unregelmäßig	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 15	

Georg-August-Universität Göttingen **Module M.Inf.2102: Advanced Statistical Learning for Data Science**	6 C 4 WLH
Learning outcome, core skills: Students will • learn concepts of advanced statistical methods and their scope of applications. These methods comprise the EM algorithm, Markov models, Hidden Markov Models, Markov chain Monte Carlo. • gain a solid understanding of ensemble learning algorithms. In particular, we will address additive tree approaches like boosting and Random Forest algorithms, as well as methods for ensemble optimization • learn strategies for model assessment and selection such as nested cross-validation, Monte Carlo validation, or permutation tests. Moreover, this will comprise measures of model quality and robustness. • acquire practical experience in the interpretation of machine learning models and learn required methods for feature selection, importance, stability, and robustness • learn techniques of statistical network inference, their implementation as well as their application to high-dimensional data.	**Workload:** Attendance time: 56 h Self-study time: 124 h
Course: Advanced Statistical Learning for Data Science (Lecture) Hastie, et al. Elements of Statistical Learning https://web.stanford.edu/~hastie/ElemStatLearn/ Bishop: Pattern Recognition and Machine Learning. https://cs.ugoe.de/prml	2 WLH
Examination: Written exam (90 min) or oral exam (approx. 20 min) **Examination prerequisites:** M.Inf.2102.Ex: At least 50% of homework exercises solved. **Examination requirements:** Knowledge of advanced statistical methods, ensemble learning, model assessment, and interpretation as well as statistical network inference. Evaluate their advantages and disadvantages and the ability to implement and interpret the results of these techniques.	6 C
Course: Statistical Learning in Data Science Exercise (Exercise)	2 WLH

Admission requirements: none	**Recommended previous knowledge:** Basic knowledge of linear algebra and probability Completion of B.Inf.1236 Machine Learning or equivalent
Language: English	**Person responsible for module:** Dr. Anne-Christin Hauschild; Dr. Michael Altenbuchinger
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 1 - 3

Maximum number of students: not limited	

Georg-August-Universität Göttingen **Module M.WIWI-QMW.0001: Generalized Regression**	6 C 4 WLH

Learning outcome, core skills: The students • gain an overview on extended regression modelling techniques that allow to analyse data with non-normal responses. • learn about approaches for modeling nonlinear effects in scatterplot smoothing. • get an introduction to additive models and mixed models for complex regression analyses. • learn how to implement these approaches using statistical software packages.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Generalized Regression (Lecture) *Contents*: Generalized linear models (binary and Poisson regression, exponential families, maximum likelihood estimation, iteratively weighted least squares regression, tests of hypotheses, confidence intervals, model selection and model checking, categorical regression models), nonparametric smoothing techniques (penalized spline smoothing, local smoothing approaches, general properties of scatterplot smoothers, choosing the smoothing parameter, bivariate and spatial smoothing, generalized additive models), mixed models, quantile regression Literatur: Fahrmeir, Kneib, Lang, Marx (2013): Regression - Models, Methods and Applications, Springer.	2 WLH
Course: Generalized Regression (Tutorial) *Contents*: Generalized linear models (binary and Poisson regression, exponential families, maximum likelihood estimation, iteratively weighted least squares regression, tests of hypotheses, confidence intervals, model selection and model checking, categorical regression models), nonparametric smoothing techniques (penalized spline smoothing, local smoothing approaches, general properties of scatterplot smoothers, choosing the smoothing parameter, bivariate and spatial smoothing, generalized additive models), mixed models, quantile regression	2 WLH
Examination: Written examination (90 minutes) or oral examination (approx. 20 minutes)	6 C

Examination requirements: In the exam, the students demonstrate their ability to choose, fit and interpret extended regression modeling techniques. They show a general understanding of the derived estimates and their interpretation in various contexts. The students are able to implement complex regression models using statistical software and to interpret the corresponding results. The exam covers contents of both the lecture and the exercise class.	

Admission requirements:	**Recommended previous knowledge:**

none	Module B.WIWI-QMW.0001: Linear Models
Language: English	**Person responsible for module:** Prof. Dr. Thomas Kneib
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 2
Maximum number of students: not limited	

Additional notes and regulations: The actual examination will be published at the beginning of the semester.

Georg-August-Universität Göttingen **Module M.WIWI-QMW.0002: Advanced Statistical Inference (Likelihood & Bayes)**	6 C 4 WLH

Learning outcome, core skills: Upon completion of the module, the students have acquired the following competencies: • foundations and general properties of likelihood-based inference in statistics, • bayesian approaches to statistical learning and their properties, • implementation of both approaches in statistical software using appropriate numerical procedures.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Advanced Statistical Inference (Likelihood & Baye) (Lecture) *Contents*: The likelihood function and likelihood principles, maximum likelihood estimates and their properties, likelihood-based tests and confidence intervals (derived from Wald, score, and likelihood ratio statistics), expectation maximization algorithm, Bootstrap procedures (estimates for the standard deviation, the bias and confidence intervals), Bayes theorem, Bayes estimates, Bayesian credible intervals, prior choices, computational approaches for Bayesian inference, model choice, predictions Literatur: Held, Sabanes Bové (2014): Applied Statistical Inference, Springer	2 WLH
Course: Advanced Statistical Inference (Likelihood & Bayes) (Exercise) *Contents*: The likelihood function and likelihood principles, maximum likelihood estimates and their properties, likelihood-based tests and confidence intervals (derived from Wald, score, and likelihood ratio statistics), expectation maximization algorithm, Bootstrap procedures (estimates for the standard deviation, the bias and confidence intervals), Bayes theorem, Bayes estimates, Bayesian credible intervals, prior choices, computational approaches for Bayesian inference, model choice, predictions	2 WLH
Examination: Written examination (90 minutes) or oral examination (approx. 20 minutes)	6 C

Examination requirements: The students demonstrate their general understanding of likelihood-based and Bayesian inference for different types of applications and research questions. They know about the advantages and disadvantages as well as general properties of both approaches, can critically assess the appropriateness for specific problems, and can implement them in statistical software. The exam covers contents of both the lecture and the exercise class.	

Admission requirements: none	**Recommended previous knowledge:** none
Language: English	**Person responsible for module:** Prof. Dr. Thomas Kneib

Course frequency: every year	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 1 - 2
Maximum number of students: not limited	

Additional notes and regulations: The actual examination will be published at the beginning of the semester.

Georg-August-Universität Göttingen **Module M.iPAB.0003: Statistical genetics, breeding informatics and experimental design**	6 C 4 WLH

Learning outcome, core skills: Novel biotechnological methods allow the production of very large data sets (gene sequences, genotypes, transcriptomes) at decreasing costs. Students learn about statistical and computational methods to use these records for breeding issues. Furthermore, the main experimental designs to plan, implement, and evaluate targeted and efficient experiments for data generation will be treated.	**Workload:** Attendance time: 56 h Self-study time: 124 h

Course: Statistical genetics, breeding informatics and experimental design (Lecture, Exercise)

4 WLH

Contents:

- Gene Expression Analysis
- Genome-wide association analysis
- QTL mapping
- Statistical hypothesis testing
- Regression methods
- Analysis of variance
- Multiple testing
- Experimental designs (block designs, randomized designs, Latin squares)
- Sample size estimation
- Introduction to programming
- Fundamentals of databases

Literature: Andrea Foulkes: Applied Statistical Genetics with R; Francis O'Donnel: Statistical Experiment Design and Interpretation; An Introduction with Agricultural Examples

Examination: Written examination (60 minutes) **Examination requirements:** Profound knowledge of statistic and informatics methods to use them for breeding issues.	6 C

Admission requirements: none	**Recommended previous knowledge:** Basics in statistics and genetics
Language: English	**Person responsible for module:** Prof. Dr. Armin Schmitt
Course frequency: each winter semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 20	

Georg-August-Universität Göttingen **Module M.iPAB.0014: Data Analysis with R**	3 C 2 WLH

Learning outcome, core skills: The students will be able to use methods provided by the statistical package R to perform the analysis of data sets that are typical in the life sciences. A core skill is the identification, usage and evaluation of online resources (e.g. packages and data sets).	**Workload:** Attendance time: 28 h Self-study time: 62 h

Course: Data Analysis with R (Block course, Lecture, Exercise) *Contents*: The fundamental concepts of the programming package R will be presented and deepened during practical exercises. Statistical methods will be recapitulated if necessary. Special emphasis is put on visualization methods. Literature: Wiki-book "R programming" https://en.wikibooks.org/wiki/R_Programming "R for Beginners" by Emanuel Paradis https://cran.r-project.org/doc/contrib/Paradis-rdebuts_en.pdf "R tips" by Paul E. Johnson http://pj.freefaculty.org/R/Rtips.pdf	2 WLH
Examination: Oral examination (approx. 20 minutes) **Examination requirements:** Ability to analyze typical data sets with the statistical package R and interpretation of the results.	3 C

Admission requirements: none	**Recommended previous knowledge:** Knowledge of basic statistics concepts
Language: English	**Person responsible for module:** Prof. Dr. Armin Schmitt
Course frequency: each semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** Master: 4
Maximum number of students: 24	

Georg-August-Universität Göttingen

Module M.iPAB.0017: Applied Bioinformatics with R

6 C
4 WLH

Learning outcome, core skills:
This module will cover the fundamental concepts of bioinformatics. Topics will include usage of relevant/modern biological databases and tools that are required to perform different analyses. Further, an introduction to multi-omics-data will be given, including genome, trancriptome and proteome analysis. This module aims to teach interested students fundamental analysis skills to evaluate biological data using bioinformatic techniques, and to become proficient in performing such analyses.

In more detail, following topics will be treated:

- Analysis of multi-omics data
- Standard databases in bioinformatics
- DNA sequence and genome analysis
- Variant calling techniques
- Sequence alignment
- Gene regulatory network analysis
- Clustering

The lecture will be based on the analysis of real data sets from agricultural research projects as far as possible.

Workload:
Attendance time:
56 h
Self-study time:
124 h

Course: Applied Bioinformatics with R (Lecture, Exercise)
Contents:
The course consists of lectures, exercises and a project work. After the lectures and the exercises the students will have to carry out a project work that must be finished within ten weeks after the end of the lectures. The students as well as the other research groups are welcome to suggest topics, possibly questions related to their master thesis can be treated. The project work should be a concise written report of about ten pages in which one or several of the techniques that were treated in the course are applied.

4 WLH

Examination: Oral examination (approx. 20 minutes, 75%) and term paper (max. 10 pages, 25%)
Examination requirements:

- Knowledge about the fundamental concepts of bioinformatics
- Knowledge about different databases in bioinformatics
- Analysis of biological data, interpretation and modeling og biological information and applying this to the solution of biological problems in any area involving molecular data.

6 C

Admission requirements: none	**Recommended previous knowledge:** Basic knowledge of R
Language: English	**Person responsible for module:** Prof. Dr. Armin Schmitt
Course frequency: each winter semester	**Duration:** 1 semester[s]

Number of repeat examinations permitted: twice	**Recommended semester:**
Maximum number of students: 30	

Georg-August-Universität Göttingen **Module SK.Bio-NF.7001: Neurobiology**	3 C 2 WLH

Learning outcome, core skills: The students should acquire comprehension in form and function of neurons and their anatomical and physiological features (genetics, subcellular organization, resting membrane potential, action potential generation, stimulus conduction, transmitter release, ion channels, receptors, second messenger cascades, axonal transport). The students acquire knowledge of the physiological basics of sensory systems (olfactory, gustatory, acoustic, mechanosensory and visual perception) as well as motor control. Based on this the students educe understanding for the relation between neuronal circuits and simple modes of behavior (central pattern generators, reflexes, and taxis movements). The students should conceptually learn how neuronal connections are modified by experience (cellular mechanisms of learning and memory) and should learn different types of modification of behavior based on experience and neuronal substrates. The students should acquire fundamental insight into the organization and function of brains and autonomous nervous systems of mammals and invertebrates. The neurobiological basis of behavioral control (orientation, communication, circadian rhythm and sleep as well as motivation and metabolism) is explained. The students will learn physiological and cellular mechanisms of aging and of neurodegenerative diseases.	**Workload:** Attendance time: 30 h Self-study time: 60 h

Course: Neurobiology (Lecture)	2 WLH
Examination: Written examination (90 minutes)	3 C

Examination requirements: The students should have the ability to assess coherence and facts of statements from the field of neurobiology; they should be able to answer questions on the structure and function of neurons and neuronal circuits. Furthermore they should be able to describe and compare neuronal basics of behavioral control, their experience-dependent modification and conceptual mechanisms of complex behavior; they should be able to describe and compare physiological mechanisms of sensory perception and different sensory modalities; they should be able to describe physiological and cellular mechanisms of aging and of neurodegenerative diseases.	

Admission requirements: none	**Recommended previous knowledge:** Basic knowledge in Biology
Language: English	**Person responsible for module:** Prof. Dr. Andre Fiala
Course frequency: each summer semester	**Duration:** 1 semester[s]
Number of repeat examinations permitted: twice	**Recommended semester:** 4 - 6
Maximum number of students: 30	

Additional notes and regulations:

The combination of this module with module SK.Bio.7001 is not possible.