Analysis of high-dimensional biological data

Titel	Analysis of high-dimensional biological data	
Typ	Lecture with exercise	
Credits	6 ECTS	
Lehrform / SWS	3V + 1Ü	
Sprache	English	
Modulniveau	Master	
Arbeitsaufwand	Präsenzstunden	60 h
	Eigenstudium	120 h
	Gesamtaufwand	180 h
Intended Learning Outcomes	The students have a systematic overview of different methods to analyze high dimensional biological data. They have a critical understanding of their power and their specific limitations.	
Contents	The course covers important statistical methods and concepts for the analysis of high-dimensional biological high-throughput data. We will focus on bulk RNA-Seq, single-cell RNA-Seq, proteomic, metabolic, and, in particular, microbiome such as 16S rRNA and other amplicon data. Statistical topics include: ● Generative statistical models for count data ● Hypothesis testing for high-dimensional data ● Differential abundance and expression analysis ● High-Dimensional regression models for biological data ● Graphical models for network inference ● Deep learning models for high-throughput data	
Examination	Written exam or oral exam	
Media	Slide shows, blackboard presentation, videos	

Teaching and Learning Methods	The module consists of in-classroom lectures, recorded video lecture material, and an exercise. In the exercises, the methods presented in the lecture are applied to real data sets using the statistical software R. Students can work on the exercise sheets at home, and the exercise slot is used to discuss the solutions.
Turnus	Sommersemester
Modulverantwortlicher	Prof. Dr. Christian L. Müller
Dozenten	Prof. Dr. Christian L. Müller