Program of Studies:	**Master Program Bioinformatics**
Name of the module:	**Special Lecture Bioinformatics: Modern Methods in Drug Discovery**
Abbreviation:	**BI-BM-1**
Subtitle:	-
Modules:	Lecture: 2 h (weekly) Tutorial: 1 h
Semester:	1st-3rd semester/ yearly during the winter term
Responsible lecturer:	PD Dr. Michael Hutter
Lecturer:	PD Dr. Michael Hutter
Language:	English (final exam also in German available)
Level of the unit/ Mandatory or not :	Graduate course / mandatory elective
Course type/weekly hours:	Lecture: 2 h (weekly) Tutorial: 1 h (weekly)
Total workload:	150 h = 48 h of classes and 102 h private study and assignments
Credits:	5

Entrance requirements:	- basic knowledge of Organic Chemistry and Genetics
	- knowledge spanning the scope of the lectures:
	  - Bioinformatik I + II
	  - Computational Chemistry
	  - Softwarewerkzeuge der Bioinformatik
	Students outside the master program bioinformatics need to have successfully passed *one* of the following courses to be admitted:
	- Bioinformatik II (bachelor program bioinformatics)
	- Computational Chemistry (bachelor program bioinformatics)
	- Softwarewerkzeuge der Bioinformatik
	- Structural Bioinformatics (master program bioinformatics)

Aims/Competences to be developed:	During the course the students will get familiar with current methods of bioinformatics, computer science, and chemoinformatics in the development of pharmaceutical drugs and their molecular targets also on the level of genes. Subsequently, the students should be able to set their mark within interdisciplinary research groups. The combination of knowledge from bioinformatics, machine learning, and other natural and life sciences is a demanding aspect of this course. Focus is the applicability of bioinformatical knowledge and machine learning techniques onto the field of pharmaceutically relevant tasks. The exercises play an important role in deepening the understanding:

	- about half of the exercises consist of application of computer programs onto selected biological systems and virtual screening issues. - the other half serves the consolidation and extension of special knowledge, such as working with substance data bases. In total, the emphasis is set on critical evaluation and interpretation of results in order to allow subsequent independent research and to strengthen scientific communication skills.
Content:	The focus of this course is the computer-based prediction of suitable pharmaceutical drugs and the search for new potential targets in the human genome. Following topics are covered: - molecular causes of typical diseases and mechanism of action of pharmaceutical drugs - virtual compound libraries and search strategies - *in silico* eADMET-models and filters, bioavailability - statistics and QSAR-methods - metabolism, toxicology and adverse side effects, also considering biomarkers - polymorphism und susceptible genes - identification of orthologous genes for deriving new targets and model organisms - current trends and strategies
Assessment/Exams:	Autonomous processing of 5 examination sheets that are handed out biweekly as homework. Two intermediate online tests. Admission to the final exam: at least 50% of points from the homework achieved or passing the two intermediate tests.
Grade:	Grade of the exam
Literature:	will be indicated during the lecture