Program of Studies:	**Master Program Bioinformatics**
Name of the module:	**Special Lecture Bioinformatics: Computational Methods for Epigenome Analysis**
Abbreviation:	**BI-BM-1**
Subtitle:	-
Modules:	Lecture and hands-on practical workshop
Semester:	Summer semester
Responsible lecturer:	JProf. Dr. Fabian Müller
Lecturers:	JProf. Dr. Fabian Müller, Prof. Dr. Jörn Walter
Language:	English
Level of the unit/ Mandatory or not :	Graduate course / mandatory elective
Total workload:	120 h = 12h lectures + 48h tutored hands-on workshop + 2h exam + 6h seminar + 64h private preparation
Credits:	4
Entrance requirements:	To enroll, students should have a basic knowledge in modern genomics and principles of epigenetics. They should have basic skills for script-based programming using the R language. The course will be limited to 24 (bioinformatics) students. Students who attended the lecture "Principles of Epigenetics" will be given priority. Non-bioinformatics students will be accepted on an individual basis if they can show that the requirements are met.
Aims/Competences to be developed:	This course offers a practical introduction to bioinformatics methods and tools used for NGS-based (NGS = next generation sequencing) epigenome analysis. The lecture will refresh the students' knowledge on epigenetic gene regulation, introduce a series of experimental methods to profile the epigenome and introduce into the theoretical background of bioinformatics methods and software tools used for data processing, quality control, exploratory analysis, differential analysis and integration of multiple data modalities. Four epigenomic data modalities will be discussed in detail: gene expression, DNA methylation, chromatin accessibility, histone modifications. The theoretical knowledge conveyed in the lecture will be solidified in a hands-on workshop in which the students will employ the introduced methods. Here, the students will work in groups of 2-3, each addressing one of the four epigenetic modalities mentioned above. Students will present their results in a final presentation at the end of the course.

Content:	- Introduction to epigenetic gene regulation - Experimental techniques and bioinformatic analysis for gene expression (RNA-seq) - Experimental techniques and bioinformatic analysis for DNA methylation (bisulfite-seq, microarrays, enrichment-based methods, etc.) - Experimental techniques and bioinformatic analysis for chromatin accessibility (ATAC-seq, DNase-seq, NOMe-seq, etc.) - Experimental techniques and bioinformatic analysis for histone modifications (ChIP-seq, CUT&RUN, etc.) - Integrative data analysis: Dimension reduction, clustering, differential analysis, segmentation, imputation - Emerging epigenome profiling technologies (including single-cell and multiome methods)
Assessment/Exams:	Students need to pass a written exam, based on the lecture content, prove that they successfully participated in the workshop by handing in a notebook-based protocol and give a 20-minute final presentation.
Grade:	The final grade will be given based on the exam and a check on the above criteria.
Literature:	Lecture slides, workshop handouts and problem sets are available on the course website and they will be disseminated in MS Teams.