Program of Studies:	**Master Program Bioinformatics**
Name of the module:	**Data Structures and Algorithms**
Abbreviation:	**I-M-1**
Subtitle:	Core Lecture
Modules:	Lecture: 4 h (weekly) Tutorial: 2 h (weekly)
Semester:	1st -3rd semester/at least every two years
Responsible lecturer:	Prof. Dr. Kurt Mehlhorn
Lecturer:	Prof. Dr. Raimund Seidel, Prof. Dr. Kurt Mehlhorn
Language:	English
Level of the unit/ Mandatory or not:	Graduate course / mandatory elective
Total workload:	270 h = 90 h of classes and 180 h private study
Credits:	9
Entrance requirements:	For graduate students: C, C++, Java
Aims/Competences to be developed:	The students know standard algorithms for typical problems in the area's graphs, computational geometry, strings and optimization. Furthermore, they master a number of methods and data-structures to develop efficient algorithms and analyze their running times.
Content:	- graph algorithms (shortest path, minimum spanning trees, maximal flows, matchings, etc.) - computational geometry (convex hull, Delaunay triangulation, Voronoi diagram, intersection of line segments, etc.) - strings (pattern matching, suffix trees, etc.) - generic methods of optimization (tabu search, simulated annealing, genetic algorithms, linear programming, branch-and-bound, dynamic programming, approximation algorithms, etc.) - data-structures (Fibonacci heaps, radix heaps, hashing, randomized search trees, segment trees, etc.) - methods for analyzing algorithms (amortized analysis, average-case analysis, potential methods, etc.
Assessment/Exams:	- Regular attendance of classes and tutorials - Passing the midterm and the final exam - A re-exam takes place during the last two weeks before the start of lectures in the following semester.

Grade:	Will be determined from performance in exams, exercises and practical tasks. The exact modalities will be announced at the beginning of the module.
Literature:	Will be announced before the start of the course on the course page on the Internet.