

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:	1 st -3 rd Semester / at least once every two years
Responsible lecturer:	Prof. Dr. Kurt Mehlhorn
Lecturer:	Prof. Dr. Kurt Mehlhorn, Prof. Dr. R. Seidel
Language:	English
Level of the unit/ Mandatory or not	Graduate course / mandatory elective
Course type/weekly hours:	Lecture 4 h (weekly) Tutorial 2 h (weekly) Tutorials in groups of up to 20 students
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 areas 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:	<ul style="list-style-type: none"> - 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:	<ul style="list-style-type: none"> - Regular attendance of classes and tutorials - Passing the midterm and the final exam <p>A re-exam takes place during the last two weeks before the start of lectures in the following semester</p>
Literature:	Will be announced on the course website