

# Bioinformatics Algorithms: Introduction to Computational Molecular Biology (CMPT 441/711)

Fall 2014

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This is an introductory course on algorithmic aspects of bioinformatics with emphasis on biomolecular sequence analysis, next generation sequencing, probabilistic techniques, hidden markov models, phylogenetic analysis, RNA structure prediction and biomolecular networks. The course is intended for students in computer science, engineering, molecular biology and other biological sciences who would like to pursue basic understanding of mathematical and algorithmic tools in computational biology.

## Prerequisites

Elementary discrete mathematics, basic algorithms and data structures, and programming skills with a “real” programming language, e.g., C/C++ will be expected. Knowledge of elementary combinatorics and probability, fundamental algorithms for sorting, searching, hashing and dynamic programming, elementary graph algorithms would be very helpful.

## Textbook

*Bioinformatics Algorithms* by Neil Jones and Pavel Pevzner (MIT Press, 2004).

## Reference books (available from on-line bookstores)

*Algorithms on Strings, Trees and Sequences: Computer Science and Computational Biology* by Dan Gusfield (Cambridge University Press, 1997)

*Biological Sequence Analysis* by Durbin, Eddy, Krogh and Mitchison (Cambridge University Press, 1998)

## Exams and Assignments

There will be two midterm exams (each constituting to 25% of the final grade) and a final exam (constituting to 40% of the final grade). A further %10 of the final grade will be based on homework assignments.