

Introduction to Bioinformatics

Instructor: Jarek Meller, Dept. of Informatics, UMK & Biomedical Informatics, Cincinnati Children's Hospital Research Foundation, <http://folding.chmcc.org>

Philosophy of the course: students will learn about biological motivation, problem formulation and algorithmic solutions as well as practical protocols and bioinformatics tools being used to support genomic sciences.

Number of lectures: 20; each lecture 1.5 hours (30 hours in 10 two-lecture blocks).

Prerequisites: basic molecular biology, basic algorithmic concepts, homework assignments involving basic programming skills.

Suggested textbooks (that can also be used to acquire the skills mentioned above) include: Durbin, Eddy, Krogh and Mitchinson, "Biological Sequence Analysis" (ISBN 0 521 62971 3); Pevzner, "Computational Molecular Biology" (ISBN 0-262-16197-4); Gibson and Muse, "A Primer of Genomic Science" (ISBN 0-87893-234-8); Schwarz and Christianen, "Learning Perl".

Part I: Ground zero

Lecture 1&2: Browsing the genomes and other ABCs

Lecture 3&4: Sequence alignment tools and first applications

Lecture 5&6: Genome-wide expression profiling and genotyping

Part II: Problems and algorithms

Lecture 7&8: Motif finding and string matching

Lecture 9&10: Physical map and genome assembly

Lecture 11&12: Sequence alignment and Dynamic Programming

Lecture 13&14: Multiple alignment and profile Hidden Markov Models

Lecture 15&16: Phylogenetic trees and hierarchical clustering

Part III: Applications and integrated toolboxes

Lecture 17&18: Gene finding and annotation

Lecture 19&20: Protein structure prediction