



Introduction to Computational Biology

dr hab. inż. Krzysztof Giaro, prof. PG (GUT)

Computational Biology is a relatively new branch of computer science whose aim is to support biological research by computers. The lecture is devoted to presentation of selected algorithmic problems connected with the analysis of information obtained from biological sequences.

Topics:

- biological background
- the main areas of interest in Bioinformatics
- mathematical and algorithmic introduction
- biological sequence comparison
- algorithms for sequence alignment
- evolution of DNA
- sequence multialignment
- profile and consensus word
- progressive multialigning methods
- shotgun DNA sequencing
- sequencing by hybridization
- Eulerian circuits and paths
- hidden Markov models
- Baum-Welch algorithm
- Markov models for sequence profiles
- computer phylogenetics
- phylogenetic trees
- perfect phylogeny problem
- distance methods in phylogenetics
- parsimony method in phylogenetics
- maximum likelihood and Bayesian approach.



TERMINY WYKŁADÓW			
Data	Dzień tygodnia	Godzina	Sala
03.01.2011	Poniedziałek	15-18	sala 106 (Gmach Nowe ETI)
07.01.2011	Piątek	14-16	sala 232 (Gmach Nowe ETI)
10.01.2011	Poniedziałek	15-17	sala 106 (Gmach Nowe ETI)
14.01.2011	Piątek	14-16	sala 232 (Gmach Nowe ETI)
17.01.2011	Poniedziałek	15-17	sala 106 (Gmach Nowe ETI)
21.01.2011	Piątek	14-16	sala 232 (Gmach Nowe ETI)
24.01.2011	Poniedziałek	15-17	sala 106 (Gmach Nowe ETI)