Theoretical Bioinformatics

1. Basics of classical thermodynamics
2. Basics of enzyme kinetics
3. Statistical distributions: Gaussian, Poisson, Binomial and Extreme Value
4. Tests of statistical significance
5. Principal Component Analysis
6. Bayes' law and applications
7. Methods for performing and evaluating the regression of two sets of data
8. Methods for performing clustering of data
9. Dynamic programming in Bioinformatics
10. General features and algorithms for bio-sequence comparison
11. General features and algorithms for bio-structure comparison
12. Computation of scoring matrixes for sequence comparison
13. General features of machine learning based methods
14. Feed-Forward Neural Networks
15. Hidden Markov Models
16. Support Vector Machines
17. Kernel-based methods
18. Procedure for assessing the performance of machine learning methods.
19. Critical comparison of machine learning based methods
20. Mathematical tools for the structural and dynamical description of a complex biological system
21. Classification of large networks starting from their statistical parameters
22. Analysis of the stability of a 2 dimensional system described by non-linear differential equations
23. Normalization procedures for microarrays data
24. Simple data structures
25. Analysis of computational complexity of algorithms

Applied Bioinformatics

1. Critical evaluation of experimental data
2. Concepts of models for data analysis
3. Principle of protein structure stability and effects of variations
4. Principle of DNA and RNA structure stability and effects of variations
5. Chromatin remodelling and its biological meaning
6. The problem of sequence annotation
7. From protein sequence, to structure and function
8. Protein structure comparison: generating rules for sequence comparison and protein modelling
9. Local and global alignment methods and data base search
10. Principal biological data bases
11. A critical reading of UniProtKB files
12. Protein Domains: SCOP and CATH
13. Protein families and Pfam
14. Functional domains and evolution
15. Evolution did it: what can we learn from a pairwise structure comparison over the entire PDB
16. Methods for protein secondary structure prediction

17. Methods for protein tertiary structure prediction
18. GO terms and criteria for annotation by transfer
19. Protein-protein interaction networks
20. Protein transcription networks
21. Workflow of Next Generation Sequencing experiments and variation calling
22. DNA methylation and genome wide, high throughput technologies
23. Microarrays technologies for transcriptome analysis
24. Analysis of proteomics data
25. Making inference from diversity