Contributions

IWPACBB 2010 welcomes contributions reporting substantial, original and previously unpublished work in all areas of Bioinformatics, Chemoinformatics and Systems Biology. The papers can be presented from a formal, methodological, technical or applied point of view.Topics of InterestComputational areas of interest include, but are not limited to: - Knowledge Discovery and Data Mining techniques for the Analysis of high-throughput biological data (trancriptomics, proteomics, metabolomics, fluxomics).- Text Mining and Language Processing.- Machine Learning and Pattern Recognition.- Rough, Fuzzy and Hybrid Techniques.- Hidden Markov Models.- Bayesian Approaches.- Artificial Neural Networks.- Support Vector Machines.- Evolutionary Computing.- Case-Based Reasoning systems.- Non-linear dynamical analysis methods and Intelligent signal processing.- Feature selection.Biological areas of interest include, but are not limited to:- Sequence analysis.- Comparison and alignment methods.- Motif, gene and signal recognition.- Molecular evolution.- Phylogenetics and phylogenomics.- Determination or prediction of the structure of RNA and protein in two and three dimensions.- DNA twisting and folding.- Gene expression and gene regulatory networks.- Deduction of metabolic pathways.- Microarray design and analysis.- Proteomics.- Functional genomics.- Molecular docking and drug design.- Computational problems in genetics such as linkage and QTL analysis, linkage disequilibrium analysis in populations, and haplotype determination.- Molecular and cellular interactions.- Emergence of properties in complex biological systems.- Visualization of biological systems and networks.- Data and software integration.- In silico optimization of biological systems.- Metabolic engineering applications.- Cell simulation and modelling.- Metabolic, regulatory and signalling networks: properties, dynamics, inference and reverse engineering.- Metabolomics.