

Scope and Topics

The main goal of the CIBB meetings is to provide a forum open to researchers from different disciplines to present and discuss problems concerning computational techniques in bioinformatics, systems biology and medical informatics with a particular focus on Neural Networks, Machine Learning, Fuzzy Logic, and Evolutionary Computation methods.

Technical areas addressed by CIBB 2010 include, but are not limited to:

- Sequence analysis, promoter analysis and identification of transcription factor binding sites
- Gene expression data analysis
- Methods for the integration of clinical and genetic data
- Algorithms for alternative splicing analysis
- Methods for the functional classification of genes
- Methods for the unsupervised analysis, validation and visualization of structures discovered in bio-molecular data
- Prediction of secondary and tertiary protein structures
- Mass spectrometry data analysis in proteomics
- Methods for comparative genomics
- Algorithms for molecular evolution and phylogenetic analysis
- Mathematical modelling and simulation of biological systems
- Heterogeneous data integration and data fusion for diagnostics
- Bio-molecular databases and data mining
- Algorithms for pharmacogenetics
- Bio-medical text mining and imaging
- Methods for diagnosis and prognosis
- Software tools for bioinformatics