
Editorial

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Biographical notes: Jie Liang is an Associate Professor in the Department of Bioengineering at the University of Illinois at Chicago and area leader in bioinformatics. He obtained his PhD degree from the University of Illinois at Urbana-Champaign in 1994. He was an NSF CISE postdoctoral research associate (1994–1996) at the National Center for Supercomputing and its Applications (NCSA) and the Beckman Institute. He then spent eight months as a visiting fellow at NSF Institute of Mathematics and Applications at Minneapolis. From 1997 to 1999, he was an Investigator at SmithKline Beecham Pharmaceuticals in King of Prussia, Pennsylvania. Dr. Liang's research interests in computational biology and bioinformatics include the areas of protein geometric shape computation, protein folding and protein binding, sampling techniques, evolutionary model of protein molecules, and large scale protein function prediction.

Dong Xu is a James C. Dowell Associate Professor and Director of the Digital Biology Laboratory in the Computer Science Department, University of Missouri, Columbia. He obtained his PhD from the University of Illinois, Urbana-Champaign in 1995. He worked as a Researcher at the National Cancer Institute and Oak Ridge National Laboratory. He has been involved in many areas of computational biology and bioinformatics, including protein structure prediction and analysis, high-throughput biological data analyses, computational proteomics, and *in silico* studies of plant and microbes.

This special issue is a collection of invited original papers presented at the 26th IEEE Engineering in Medicine and Biology Society (EMBS) held in San Francisco during September 1–5, 2004. The scope of these papers captures important areas of current research in bioinformatics and computational biology. The topics include development of algorithms for sequence analysis of both DNA and RNA sequences, for structure modelling of RNA and proteins, as well as methods and software for cellular function predictions and chromosome caryotyping.

At the sequence level, the paper by He et al. describes a combinatorial algorithm for tag SNP (single nucleotide polymorphism) selection through linear algebra formulations, with the goal of associating complex diseases to related SNPs. Zhang and Horvath discuss a method based on genetic algorithms to optimise fitness functions related to ridge regression to model the relationship between a quantitative trait and genetic markers in mice. Their method is designed for analysis of genomic data, where the number of features far exceeds the number of observations and where features can be highly correlated. Based on a fast and accurate approximate string-matching algorithm, the paper by Liu et al. focuses on a web-based software system for sequence acquisition and database construction, with application in ribosomal RNA gene (rRNA) sequence database.

At the structure level, the paper by Horesh and Unger discusses a clustering algorithm for detecting non-protein coding RNA molecules sharing common secondary structures. Garcia-Gomez et al. describe a method for modelling tRNA secondary structures based on the combination of stochastic context-free grammars and hidden Markov models. The work by Langlois et al. addresses an application of support vector machine for multi-class classification for recognising protein fold from sequence information.

At the cellular level, Joshi et al. discuss an integrated probabilistic method for cellular function prediction using micro-array gene expression profiles, in conjunction with predicted protein-protein interactions and annotations of known proteins in arabidopsis. Wu et al. consider the problem of caryotyping, or the automated classification of human chromosomes, and apply discrete optimisation algorithms to solve this problem.

A special issue in this journal can only include a small number of original papers. These papers demonstrate the breadth and depth of current research in bioinformatics and computational biology and represent a snapshot of a fast moving field.