Editorial

Mark J. Clement and Quinn O. Snell

Department of Computer Science,
Brigham Young University, USA
E-mail: clement@cs.byu.edu
E-mail: snell@cs.byu.edu

Biographical notes: Mark J. Clement is an Associate Professor in the Computer Science Department at Brigham Young University. His research has included new methods for phylogenetic analysis, sequence alignment and population genetics. He was responsible for the development of the TCS population genetics application as well as the DOGMA phylogenetic parallel processing system. In addition to his interests in bioinformatics, he has performed research in parallel processing and internet protocols and has published more than 65 papers in interdisciplinary venues.

Quinn O. Snell is an Associate Professor of Computer Science at Brigham Young University. His research areas are computational biology and parallel and distributed processing. He has been at Brigham Young University since 1997.

This issue of the *International Journal of Bioinformatics Research and Applications* (IJBRA) presents selected papers from BIOT-06, the Bioinformatics and Biotechnology Symposium, held in Provo, Utah, USA, in September of 2006. The Symposium brought together nearly 100 individuals from across the USA and as far away as Singapore and Pakistan.

Dr. Yi Pan, the Editor-in-Chief of IJBRA invited us to compile an issue of IJBRA with selected papers from BIOT-06. Information about past and future BIOT conferences can be found at http://biotconf.org. The nine papers selected for this issue cover a broad range of topics in bioinformatics and computational biology.

The first paper, 'Proteomic data mining using predicted peptide chromatographic retention times', by Tripet et al. presents a web-based tool for the prediction of peptide fragment retention times. They use their database of peptide fragments to enhance the identification of proteins. In their paper 'On predicting secondary structure transition', Loganantharaj and Philip discuss the use of machine-learning algorithms for the prediction of secondary structure transition, they present the degree of certainty for several machine-learning algorithms. Kimberly Baer and David McClellan report evidence that supports the co-evolution of cytochrom c_1 and the Rieske iron sulphur protein. Their paper 'Molecular co-evolution of the vertebrate cytochrome c_1 and rieske iron sulphur protein in the cytochrome bc_1 complex' shows examples of how each protein evolves in response to changes in the other protein to maintain overall function.

In 'Pharmacogenomics: analysing SNPs in the CYP2D6 gene using amino acid properties', Ebbert et al. present some of the issues surrounding the hope of pharmacogenomics. Amino acid chemical properties are used to identify four SNPs that may cause a person to be unable to metabolise certain drugs. They then move to the discussion of protein-protein interactions. In a collaborative effort between Sandia National Laboratories and the University of Southern California, Martin et al. present a computational method to predict protein-protein interactions with a high degree of accuracy. Their paper 'Inferring protein-protein interaction networks from protein complex data' demonstrates nearly 96% accuracy in predicting protein pair for a data set obtained from a cat melanoma cell line. Carroll et el. show the effects of gap open and gap extension penalties in multiple sequence alignment in their paper 'Phylogenies scores for exhaustive maximum likelihood and parsimony scores searches'. They show how these parameters greatly affect the distribution of phylogeny scores and the corresponding optimal phylogenies.

Chamala et al. present an interesting study of three SNPs in the mitochondrial subhaplogroups of the Pima Indians in their paper 'Evolutionary selective pressure on three mitochondrial SNPs is consistent with their influence on metabolic efficiency in Pima Indians'. Their results suggest a connection between two of the SNPs and metabolic efficiency. The next paper, 'A study of the repetitive structure and distribution of short motifs in human genomic sequences', by Singh et al. presents some of their findings from ongoing research into over-represented motifs in the human genome. They include an interesting discussion using over-representation for the determination of functional DNA elements. Finally, Yinglei Lai uses order statistical theory to propose the conservative adjustment of permutation *p*-values in the statistical analysis of microarrays in 'Conservative adjustment of permutation *p*-values when the number of permutations is limited'.

We enjoyed BIOT-06 and we hope that the papers in this issue of IJBRA provide a flavour of the research presented this year. We thank IJBRA and Dr. Yi Pan of Georgia State University for publishing the best papers from this conference in this venue. We encourage IJBRA readers to consider contributing to and attending the symposium in the future.