Editorial

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Biographical notes: Jugal Kalita is a Professor in the Department of Computer Science at the University of Colorado at Colorado Springs. He received his PhD from the University of Pennsylvania in 1990. His areas of interest are bioinformatics, artificial intelligence, machine learning and natural language processing.

This issue of the *International Journal of Bioinformatics Research and Applications* (IJBRA) presents selected papers from BIOT-07, the Bioinformatics and Biotechnology Symposium, held in Colorado Springs, Colorado in October 2007. The symposium brought together about 75 researchers from around the USA and a few other countries.

The first BIOT two symposia were held in Colorado Springs, Colorado, in 2004 and 2005. In 2006, it was held in Provo, Utah. The 2007 symposium was held once again in Colorado Springs. The 2008 symposium was held in Arlington, Texas in October and a separate special issue of IJBRA is being planned based on a selection of papers from that symposium. The 2009 symposium is scheduled to be held in Lincoln, Nebraska, during the Fall.

Information about past and future BIOT symposia can be found on the Web at http://www.biotconf.org. The symposium has a standing Steering Committee comprising of academicians and researchers from around the USA. The symposium is fortunate to have a prestigious Program Committee from around the world. The symposium's Steering Committee invites researchers from around the world to send requests to serve on these two committees. The symposium also invites proposals from those interested in hosting the symposium in the future.

Dr. Yi Pan, Editor-in-Chief of IJBRA has been a patron of this symposium from its inception in 2004. We are grateful to Dr. Yi Pan for publishing a special issue of IJBRA with selected papers from BIOT-07.

We selected eight papers for publication in this special issue. The papers cover various topics in Bioinformatics and Computational Biology.

The first paper by Mitchell Koch, Bradley M. Broom and Devika Subramanian proposes a framework for learning robust models of cell signaling from high-throughput proteomic data. They use Bayesian networks and structure learning algorithms to achieve their objective. The authors use flow cytometry data to derive novel mechanisms for T-cell signaling network. The second paper by Xinye Cai, Praveen Koduru, Sanjoy Das and Stephen M. Welch presents a hybrid algorithm based on genetic algorithms and particle swarm optimisation for automated recovery of gene network structure.

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The algorithm takes as input gene expression time-series data and phenotypic data pertaining to plant flowering. The authors show that complex gene regulatory networks can be approximated with simple structures without significant deviation in performance.

In the third paper, Shuxing Zhang and Lei Du-Cuny discuss an easy-to-use and efficient software package for virtual screening in drug discovery. Their application, termed HiPCDock, implements a high-performance molecular docking prediction scheme that has performed very well in docking TK binders into enzymes and also in recovering real TK inhibitors from data. In the fourth paper, William L. Duax, Robert Huether, Vladimir Pletnev, Timothy C. Umland and Charles M. Weeks discuss the use of bioinformatics techniques to discover that the primordial members of the β -k-ACPR family of enzymes probably arose in the α -proteobacteria and are characterised by the presence of multiple open reading frames and an extreme codon and amino acid bias. In the fifth paper, S.O. Opiyo and E.N. Moriyama discuss the use of alignment-free methods based on Partial Least Squares (PLS) using physico-chemical to mine single and multiple-domain cyclophilins, a family of proteins that are celluar targets of immunosuppressant drugs. The PLS approach performed better than profile-HMMs and PSI-BLAST in identifying cyclophilins from Arabidopsis and rice genomes.

In the sixth paper, Rosy Das, Jugal Kalita and Dhruba K. Bhattacharyya propose a new dissimilarity measure for use in analysing gene-expression time-series data. They also present a graph-based clustering method for finding clusters in gene-expression time-series data using the new dissimilarity measure. They compare the results and find the new measure quite effective. In the seventh paper, Raja Loganantharaj says that genes that are members of the same cluster obtained after clustering gene array data are expected to have similar functions, but in reality it may not be the case because co-expression does not necessarily mean co-regulation. In order to improve the results of clustering, he integrates the expression data with data from diverse sources and uses a singular value decomposition approach as an effective data integrator.

In the eighth paper of this issue, Hyrum Carroll, Adam Teichert, Jonathan Krein, Kenneth Sundberg, Quinn Snell and Mark Clement discuss PSODA, a comprehensive phylogenetics package, including alignment, phylogenetic search under both parsimony and maximum likelihood, and visualisation and analysis tools. PSODA offers performance comparable to PAUP* in an open source package that aims to provide a foundation for researchers examining new phylogenetic algorithms.