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## Editorial

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**Biographical notes:** Nikola Stojanovic received his PhD Degree in Computer Science and Engineering in 1997 from the Pennsylvania State University, University Park, PA. After five years of working on the Human Genome Project at the Whitehead Institute/MIT Center for Genome Research in Cambridge, MA, he joined the faculty of the University of Texas at Arlington in 2003, as an Assistant Professor. His research interests are in algorithms for genomic sequence analysis, phylogenetic studies and sequence alignments.

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This issue of the *International Journal of Bioinformatics Research and Applications (IJBRA)* features the extended versions of selected papers reported at BIOT 2008, the 5th Bioinformatics and Biotechnology Symposium, held in Arlington, Texas, USA, on October 17 and 18, 2008. The Symposium hosted around 100 participants from Italy, Japan, Mexico, and nine US states. Over two days it featured 17 research talks, two keynote speakers, 35 posters and a round-table discussion about the biotechnology and bioinformatics education. We hope that you will find the papers selected for this special journal issue informative, and that you will choose to yourself participate in a future BIOT conference. More information about the series, the current as well as past meetings, can be found at <http://www.biotconf.org>.

The BIOT series has been a growing success. Founded at the University of Colorado at Colorado Springs, in 2004, to address the need for scientific gatherings of this type in the Rocky Mountains area, the conference has grown into a national event with an increasing international participation. The first two meetings, as well as BIOT 2007, have been held at the founding institution, and the 3rd Symposium, BIOT 2006, took place at Brigham Young University in Provo, Utah. BIOT 2009 has been recently held at the University of Nebraska, Lincoln, and BIOT 2010 has been scheduled to take place at the University of Louisiana at Lafayette. The BIOT series has a permanent nine-member Steering Committee, representing eight academic institutions from seven states around the USA.

The symposium's objective is to showcase research and development activities in bioinformatics and computational biology, and biotechnology, and to stimulate future interdisciplinary activity and research in these areas. In accordance with what became its tradition, BIOT 2008 brought together scientists, engineers and other practitioners from biotechnology, bioinformatics and medical research community. It was conducted as a single-session event, further promoting its inter-disciplinary goal.

All BIOT papers have been rigorously peer-reviewed, by at least two, and in most cases three members of the Program Committee. The papers collected in this issue of

IJBRA have been selected based on the initial peer review scores, combined with the vote among the five Steering Committee members who attended the talks and independently evaluated the presentations.

Based on this double review, eight best papers have been invited for journal publication. In their manuscript 'Deterministic graph-theoretic algorithm for detecting modules in biological interaction networks' Chang et al. report on a new approach to the modularisation of nodes in graphs modelling biological systems using theory previously developed for social networks, and compare it with other existing schemes using Gene Ontology annotations. Paper on 'Assessing and improving the accuracy of detecting protein adaptation with the TreeSAAP analytical software' by McClellan and Ellison describes new developments in the performance evaluation of the author's software for detecting regions under selection in protein-coding genes using physicochemical amino acid properties. Danecek and Schein report on their work on the development and use of bioinformatics tools to compare the genomes of Flaviviruses stored in their comprehensive database, created to aid vaccine development, in 'Flavitrack analysis of the structure and function of West Nile non-structural proteins'. Manuscript 'An algorithm for the reconstruction of consensus sequences of ancient segmental duplications and transposon copies in eukaryotic genomes' by Singh et al. describes a novel method for the recognition of broken remnants of interspersed repeats in genomic sequences.

The next two papers, 'Strategies for enhanced annotation of a microarray probe set' by Powers et al. and 'Ranking through integration of protein-similarity for identification of cell-cyclic genes' by Dua et al. deal with issues in processing microarray data sets, biological interpretation in particular. In their manuscript on 'Scalable biomedical Named Entity Recognition: investigation of a database-supported SVM approach', Habib and Kalita address the issues in the classification of words in biomedical publications and report on the algorithm and software they have developed for this task. This collection concludes with the report on the use of alignment-free protein classifiers and Support Vector Machines for the identification of members of a protein family featuring high internal sequence divergence, in 'Mining Cytochrome b561 proteins from plant genomes', by Opiyo and Moriyama.

We are grateful to Dr. Yi Pan, the Editor-in-Chief of the IJBRA journal, for his continuous support of the BIOT series, and for his willingness to dedicate a special issue of IJBRA to BIOT 2008. We hope that you will enjoy reading these manuscripts as much as the conference attendees enjoyed hearing their presentations.