Editorial

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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-2009, the 6th Bioinformatics and Biotechnology Symposium, held at University of Nebraska, Lincoln, Nebraska, USA, on October 9 and 10, 2009. The Symposium hosted more than 100 participants from 10 US states as well as five countries other than the USA. Over two days it featured four keynote speakers, 13 research talks, 44 posters,

and two talks about teaching computing and biology. Five full papers were selected for this special issue. We hope that you will find this special issue informative and that it motivates you to participate in future BIOT conferences. More information on the BIOT series (the current and past meetings) can be found at http://www.biotconf.org

The BIOT conference series have been a growing success. Founded at the University of Colorado at Colorado Springs, the conference has grown into a national event with an increasing number of international participants. The first two events, as well as BIOT-2007, have been held at the founding institution. The 3rd Symposium, BIOT-2006, took place at Brigham Young University in Provo, Utah, and BIOT-2008 was held at University of Texas at Arlington. In 2009, for the first time, BIOT was held in the Midwest, attracting researchers from 10 states across the US including Nebraska, Iowa, and Kansas. Participants also came from five countries other than the US. The conference now has a 9-member Steering Committee, representing 8 institutions in 6 states around the USA.

BIOT-2009 followed what has now become the tradition of the BIOT series. The BIOT-2009 provided an affordable scientific event whose goal was to showcase research and development activities in bioinformatics, computational biology, and biotechnology, and to promote future interdisciplinary activity and research in these areas. It brings together scientists in multiple disciplines: computer science, engineering, mathematics, statistics, bioinformatics, biotechnology, life sciences, and medical science. For BIOT-2009, we also received funding from National Science Foundation (DBI-0938224), with which we established a Student/Postdoc Travel Scholarship program. As a result, more than 45 students and postdocs who attended BIOT-2009 and presented their work were awarded the scholarships. All scholarship awardees participated in poster presentation and it fostered informal interactions between students, postdocs, and faculty. Keeping the conference as a single–track event also helped to keep the audience together and facilitated communication across disciplines.

All BIOT papers were peer reviewed by 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 three co-chairs. Based on this double review, five best papers have been invited for journal publication.

- Broom et al. describe in their paper, 'Bagged gene shaving for the robust clustering of high-throughput data', a clustering method based on the bootstrap aggregation (bagging) of gene shaving clusters, which overcomes the problem related to highly correlated variables within clusters.

- Dhawan et al. describe in 'Application of committee kNN classifiers for gene expression profile classification', a two-class classification system based on a committee of k-Nearest Neighbour (kNN) classifiers and its application to a set of microarray gene expression profiles from leukemia patients.

- Lai explores in 'Differential expression analysis of Digital Gene Expression data: RNA-tag filtering, comparison of t-type tests and their genome-wide co-expression based adjustments', if and how the 'soft filtering' strategy can be applied for analysing data generated by the deep sequencing techniques.

- Ma and Deogun present in 'Multiple genome alignment based on longest path in directed acyclic graphs', a simple and efficient algorithm for multiple genome sequence alignment. Their experiments show that the algorithm can correctly find the alignment, and runs faster than existing other methods.

- Stoutenburg et al. investigate in 'Scaling alignment of large ontologies', scalability issues in alignment of large-scale ontologies. They present an alignment algorithm that bounds processing by selecting optimal subtrees to align and show that this improves efficiency without significant reduction in precision.

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-2009. We hope that you will enjoy reading these manuscripts as much as the conference attendees enjoyed hearing their presentations.