

Guest Editorial for the 13th Asia Pacific Bioinformatics Conference

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THIS special section of the *IEEE/ACM Transactions on Computational Biology and Bioinformatics* is a selection of eight papers presented at the 13th Asia Pacific Bioinformatics Conference (APBC2015), which was held in HsinChu, Taiwan, 21-23 January 2015. The conference attracted 250 participants from around the world and included three invited keynote speakers, 53 oral and 49 poster presentations. The aim of this conference is to provide an international forum for researchers, professionals, and industrial practitioners to share their knowledge and ideas of how to surf the tidal wave of information in the area of bioinformatics and computational biology.

The eight selected papers cover diverse topics, including ontology, evolution, nucleosome positioning, single individual haplotyping, de novo sequencing of glycans, genome compression and biomedical experts mining, etc.

In "Using Semantic Association to Extend and Infer Literature-Oriented Relativity between Terms", L. Cheng, J. Li, Y. Hu, Y. Jiang, Y. Liu, Y. Chu, Z. Wang, and Y. Wang describes a new scoring method to compute the relationship between terms in an ontology. The proposed method identifies more statistically significant pairs of terms compared with the R-score and also achieves better TP and FP rates (ROC characteristics).

In "Cophylogenetic Reconciliation with ILP", N. Wieseke, T. Hartmann, M. Bernt, and M. Middendorf propose an ILP formulation of the problem of finding a cophylogenetic reconciliation that maximizes the number of cospeciations, then minimizes the number of host switches, then minimizes the number of host/parasite associations. The method proposed by the authors is the first ILP formulation of the problem to be applicable in practice due to a quadratic number of constraints, as opposed to previous results using a cubic number of them. The ideas proposed here could lead to further improvements in ILP formulations of the problem.

In "DPNuc: Identifying Nucleosome Positions Based on the Dirichlet Process Mixture Model", H. Chen, J. Guan, and S. Zhou provide a Markov chain Monte Carlo based approach to perform nucleosome positioning from ChIP-seq reads with no need of prior knowledge about nucleosomes. The authors compared the performance of different methods

using F scores and results comparing different methods are presented, showing the advantage of their method.

In "A Cooperative Co-Evolutionary Genetic Algorithm for Tree Scoring and Ancestral Genome Inference", N. Gao, Y. Zhang, B. Feng, and J. Tang presented a new phylogenetic algorithm for inferring ancestral genomes and for modeling the evolutionary processes, using the idea of cooperative co-evolution. In this method, each node of the phylogeny tree represents a population instead of an individual. The method provides better tree scoring and inferring ancestor results than current parsimony methods or maximum-likelihood methods.

In "LGH: A Fast and Accurate Algorithm for Single Individual Haplotyping (SIH) Based on a Two-Locus Linkage Graph", the authors presented a new method for solving the single individual haplotyping problem. They develop a fast and accurate heuristic algorithm to deal with the vertex labeling of the two-locus linkage graph which encode the information of aligned DNA fragments. In comparisons of three popular existing algorithms for SIH, the LGH algorithm shows faster and more accurate in both simulated and real data.

In "A Machine Learning Based Approach to de novo Sequencing of Glycans from Tandem Mass Spectrometry Spectrum", S. Kumozaki, K. Sato, and Y. Sakakibara propose a machine learning approach to de novo sequencing of glycans from MS/MS spectrum. The proposed algorithm employs Lagrangian relaxation, structured SVM, and core structure constraints to provide an efficient and effective framework. It shows sufficiently accurate results in two datasets of N-linked and O-linked glycans. In the future, the authors will further investigate a novel scoring model for considering intensities of MS/MS spectra to make better improvements.

In "CoGI: Towards Compressing Genomes as an Image", X. Xie, S. Zhou, and J. Guan proposed a novel approach, called "Compressing Genomes as an Image (CoGI)", that compresses genomes as a binary image. CoGI transforms genomic sequences to a 2D binary image, and then applies a rectangular partition coding algorithm to compress the image. Results show that the reference-based CoGI significantly outperforms some state-of-the-art methods in compression ratio and compression efficiency. It is believed that CoGI can serve as an effective and practical genome compressor.

In "BMExpert: Mining MEDLINE for Finding Experts in Biomedical Domains Based on Language Model", B. Wang, X. Chen, H. Mamitsuka, and S. Zhu develop a novel method called BMExpert for biomedical expert finding. BMExpert mines MEDLINE documents by considering three important

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factors: the relevance of documents to the topic, the importance of documents, and the associations between the documents and the experts. Results of evaluation experiments show that BMExpert outperforms three other biomedical expert finding services. It is believed that BMExpert will be useful for biomedical researchers who want to find experts in biomedical domain.

We would like to thank the authors of the selected papers for each of their individual excellent contributions. Special thanks go to the editorial staff of the *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, and all of the reviewers. We hope this fruitful collaboration continues for many future Asia Pacific Bioinformatics conferences.



Hsien-Da Huang received the bachelor's and PhD degrees from National Center University, Taiwan. He is a professor of the College of Biological Science and Technology, National Chiao Tung University, Taiwan and was appointed the vice dean in 2013. He is also the Chairman in the Department of Biological Science and Technology, and the Institute of Bioinformatics and Systems Biology at National Chiao Tung University. His laboratory investigates transcriptomics and metagenomics, which includes microRNAs and

small RNAs regulations, protein post-translational modifications, integrative analysis for microarray and next-generation sequencing data in conducting many biological applications and biomedical studies, clinical bioinformatics, and identifying novel biomarkers for diagnosis. One of the major contributions of his research is to establish a series of miRNA databases, computational tools, and integrated analysis platforms. For example, *miRTarBase*, which is the world-class miRNA-Target interaction (MTI) database, provides extensive experimental supports in all miRNA-related research, and it has been cited more than 200 times. His publications has been more than 100 papers in domestic and international journals (including *Science*, *Molecular Cell*, *Circulation*, *Journal of Clinical Investigation*, *The Journal of Clinical Investigation*, *PLoS Biology*, *Hepatology*, *Genome Biology*, *Cancer Research*, *Nucleic Acids Research*, *Biomaterials*, and *Oncogene*). In addition, more than 20 papers are published in *Nucleic Acids Research*. More information about him can be found at <http://isblab.life.nctu.edu.tw/pi.php>.



Yi-Ping Phoebe Chen received the BInfTech degree with first class honors and the PhD degree in computer science (bioinformatics) from the University of Queensland. She is a professor and chair and the director of research in the Department of Computer Science and Computer Engineering, La Trobe University, Melbourne, Australia. She is the chief investigator of the ARC Centre of Excellence in Bioinformatics. She is currently working on knowledge discovery technologies and is especially interested in their application to genomics and biomedical science. Her research focus is to find the best solutions for mining, integrating, and analyzing complex data structure and functions for scientific and biomedical applications. She has been working in the area of bioinformatics, health informatics, multimedia databases, query system, and systems biology, has coauthored more than 200 research papers, with many published in top journals and conferences. She is steering committee chair of the Asia-Pacific Bioinformatics Conference (founder) and the International Conference on Multimedia Modeling. She has been on the program committees of more than 100 international conferences, including top ranking conferences such as ICDE, ICPR, ISMB, CIKM, etc. More information about her can be found at <http://homepage.cs.latrobe.edu.au/ypchen/index.htm>.

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