2009 International Joint Conferences on Bioinformatics, Systems Biology and Intelligent Computing

IJCBS 2009

SHANGHAI, CHINA
3 - 5 AUGUST 2009

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Proceedings

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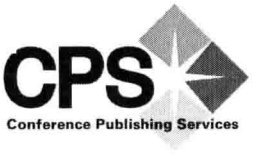

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2009 International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing

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Message from the General Chair

It is an exciting time for Bioinformatics, Genomics and Systems Biology, a time of continuous celebration of seemingly endless series of revolutionary inventions, and powerful next generation sequencing technologies. It is an exciting time to develop new powerful computational methods for deciphering the flood of genomic data and lay down foundations of Genome Biology.

It is an exciting time for Bioinformatics in China, where the growing number of researchers in the field has reached a critical mass, the level at which it is right to say that China became a major player in Bioinformatics along with Europe, Japan and the US.

I am delighted to see a number of high level papers submitted to the Shanghai International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing, the papers describing innovative approaches to long standing problems in genomic sequence analysis, prediction of structure and biological function as well as applications to molecular, personalized and alternative medicine.

Mark Borodovsky
General Chair

Message from the Program Chairs

Welcome to The 2009 International Joint Conferences on Bioinformatics, Systems Biology and Intelligent Computing (IJCBS'09) being held in Shanghai, China on August 3-5, 2009. Bioinformatics, Systems Biology and Intelligent Computing are synergistic disciplines that hold great promise for the advancement of research and development in designing intelligent systems to solve systems biology and translational bioinformatics problems. The IJCBS'09 is aimed at providing a common platform to bridge these very important interdisciplinary areas into an interactive forum, and bringing together top researchers, practitioners and students from around the world in order to promote scientific understanding and findings in computing intelligence and bioscience. It is sponsored by IEEE Computer Society, International Society of Intelligent Biological Medicine (ISIBM), USA National Science Foundation (NSF), National Natural Science Foundation of China (NSFC), Tongji University, and University of Southern Mississippi, USA.

The program committee consists of more than 100 committee members around the world who served as workshop chairs, session chairs, and peer reviewers. The IJCBS'09 received more than 240 submissions through the online submission systems or emails. The international nature of the IJCBS'09 is reflected in the geographical diversity of the submission pool. All submitted papers have been peer-reviewed by the program committee members or invited external reviewers. A total of 52 papers have been selected for full papers and oral presentation with an acceptance ratio of 22%, and registered authors are from 17 countries including Australia, Belgium, Canada, China, Denmark, Germany, India, Iran, Japan, Jordan, Portugal, Singapore, South Korea, Spain, Turkey, UK and USA. A number of other papers have been accepted as short papers or posters. The conference features eight distinguished keynote speakers, a panel, best paper awards and travel fellowships.

Many individuals have contributed to the success of this conference. Many thanks go to all the authors, invited speakers and conference organizers with special thanks to the general chair Dr. Mark Borodovsky, honorary general chairs Dr. Ruzena Bajcsy, Dr. Michael Waterman, Dr. Joydeep Ghosh and Dr. Changjun Jiang, and all steering committee members whose leadership ensures the success of this conference. Special thanks go to the organizing chair Dr. Weisheng Xu, and local organizing committee consisting of Drs. Jing Yao, Mingyu You, Youling Yu, and Yongqing Su for their assistance.

The help and support from the IEEE Computer Society is especially appreciated. Andrea Thibault-Sanchez from IEEE Conference Publishing Services (CPS) provided us much advice and answered our inquiries. The IEEE Computer Society editor, Juan Guerrero, did an outstanding job in preparing the proceedings.

We wish everybody an enjoyable and fruitful stay in Shanghai.

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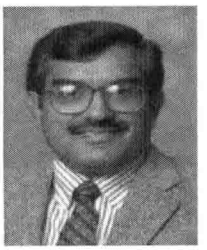
President of International Society of Intelligent Biological Medicine, Founder of GeneMark and Pioneer of Bioinformatics Research, Founder of Georgia Tech Bioinformatics Ph.D. Programs, Distinguished Regents' Professor and Director Center for the Bioinformatics and Computational Genomics, Georgia Institute of Technology, USA.



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Professor of Electrical and Computer Engineering

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Joydeep Ghosh

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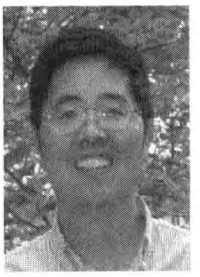

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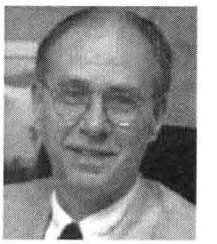
Yi Pan

Editor-in-chief of International Journal of Bioinformatics Research and Applications, series editor of Wiley Book Series on Bioinformatics, Associate Editor of 6 IEEE Transactions, winner of many awards, keynote speaker for over 10 conferences, and Chair of Department of Computer Science at Georgia State University, USA



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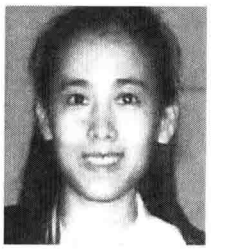
Member of United State National Academy of Science, Fellow of American Academy of Art and Sciences and Academician of French Académie des Sciences. Coeditor-in-Chief of Journal of Computational Biology, Editor-in-Chief of Lecture Notes in Bioinformatics, Lecture Notes in Computer Science (LNCS, Springer). Distinguished University Professor of University of Southern California, Los Angles, California, USA

Cathy H. Wu

Dr. Wu has conducted bioinformatics research since 1990 and developed several protein classification systems and databases. She has managed large software and database projects, led the bioinformatics effort of the Protein Information Resource (PIR) since 1999, and become the PIR Director in 2001. Her research interests include protein family classification and functional annotation, biological data integration, and literature mining.



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Aidong Zhang

Dr. Aidong Zhang is a professor in the Department of Computer Science and Engineering at the State University of New York at Buffalo and the director of the Buffalo Center for Biomedical Computing (BCBC). She is an author of more than 200 research publications and has served on many editorial boards of prestigious journals. Dr. Zhang is a recipient of the National Science Foundation CAREER Award and SUNY (State University of New York) Chancellor's Research Recognition Award. Dr. Zhang is an IEEE Fellow.

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Plenary

Keynote Abstracts

Locating a Few Useful Clusters in Large Biological Datasets: A Tale of Two Viewpoints

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I. Extended Abstract

A key application of clustering data obtained from sources such as microarrays, protein mass spectroscopy and phylogenetic profiles, is the detection of functionally related genes. Typically, only a small number of functionally related genes form meaningful groups, while the rest need to be ignored. Additional complications arise when there are several irrelevant experimental conditions, when the useful clusters occur at different resolutions/scales, and when genes participate in multiple biological processes, leading to multiple cluster memberships.

The pioneering work of Cheng and Church [1] focused a lot of attention to (bi)-clustering of microarray data. By identifying the most cohesive bi-clusters, i.e., subsets of genes and experiments over which there is coherent expression behavior rather than trying to cluster all the genes using all available features, the original biclustering approach was able to obtain more meaningful groups of genes. Since then a variety of improvements have been made using both biclustering oriented and subspace clustering oriented methods specialized for such data. However, these methods have provided limited progress, specially in the presence of a large number of irrelevant genes/conditions and due to the multi-membership problem.

We have recently developed two different approaches to simultaneously deal with all the complications of such microarray data analysis. These techniques are also relevant for certain other types of bioinformatics problems including spectroscopy data analysis. The first approach, Automated Hierarchical Density Shaving (Auto-HDS), is a framework that consists of a fast, hierarchical, density-based clustering algorithm and an unsupervised model selection strategy. Auto-HDS can automatically select clusters of different densities, present them in a compact hierarchy and rank individual clusters using an innovative stability criteria. This framework also provides a simple yet powerful 2-D visualization of the hierarchy of clusters that is useful for further interactive exploration. This approach is detailed in [2], which also present results on Gasch and Lee microarray datasets to show its effectiveness. Moreover, a public domain implementation called GeneDiver is available for practitioners to use via the internet, at http://www.ideal.ece.utexas.edu/ gunjan/genediver/.

An alternative approach to HDS is to specify a suitable data generation model, and then fit model parameters using the available data. For example, one can model observed data as a mixture of k multivariate Gassians, fit this mixture to data using the EM algorithm, and then get a k-cluster solution by assigning a given data point to the mixture component this is most likely to have produced it. How can one determine a suitable generative model for microarray data? A start can be made by noting that since clusters could exist in different subspaces of the feature space, a co-clustering algorithm that simultaneously clusters objects and features is often more suitable as compared to one that is restricted to traditional "one-sided" clustering. At the same time, it is important to discard irrelvant features and objects, and to allow arbitrary shaped and located co-clusters, including overlapping ones.

These objectives are achieved in two steps: In the first step, the Bregman Co-clustering algorithm [3] is adapted to automatically prune away non-informative data while simultaneously clustering both genes and conditions. This step results in finding co-clusters arranged in a grid structure, but only a predetermined number of rows and columns are assigned to the co-clusters. An agglomeration step then appropriately merges similar co-clusters to discover dense, arbitrarily positioned and even overlapping co-clusters.. The underlying probablity model related two a mixture model of exponential family distributions, where each mixture component is indexed by a pair of (row,col) cluster identity, and with a uniform background distribution to model the genes/conditions that are irrelevant.

The overall methodology has the following key features that distinguish it from existing co-clustering algorithms. (i) The ability to mine the most coherent co-clusters from large and noisy datasets; (ii) Detection of arbitrarily positioned and possibly overlapping co-clusters in a principled manner by iteratively minimizing a suitable cost function, (iii) Generalization to all Bregman divergences, including squared Euclidean distance, commonly used for clustering microarray data and I-divergence, commonly used for text data clustering; (iv) The ability to naturally deal with missing data values, without introducing random perturbations or bias in the data and (v) Efficient detection all the co-clusters simultaneously rather than sequentially, enabling scalability to large and high-dimensional datasets. For more details of the method and its empirically observed success, please refer to [4].

Given the two approaches that are philosophically and methodologically very different, the natural question is how does one determine the method that is most suitable? The

answer lies in the match of the dataset to certain modeling characteristics, showing that both approaches have complementary strengths, and that together, they form a formidable suite for catering to a wide range of bio-informatics related clustering requirements.

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