THE 2009 INTERNATIONAL CONFERENCE ON BIOINFORMATICS & COMPUTATIONAL BIOLOGY

Edited by

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Preface:
It gives us great pleasure to introduce this collection of papers to be presented at the 2009 International Conference on Bioinformatics and Computational Biology (BIOCOMP'09), July 13 through 16, 2009, Las Vegas, USA. The Academic Co-Sponsors of this year’s conference include: United States Military Academy, Network Science Center, USA; Biomedical Cybernetics Laboratory, HST of Harvard University and MIT, USA; Argonne's Leadership Computing Facility of Argonne National Laboratory, USA; Functional Genomics Laboratory, University of Illinois at Urbana-Champaign, USA; Minnesota Supercomputing Institute, University of Minnesota, USA; Intelligent Data Exploration and Analysis Laboratory, University of Texas at Austin, Austin, Texas, USA; Harvard Statistics Department Genomics & Bioinformatics Laboratory, Harvard University, USA; Texas Advanced Computing Center, The University of Texas at Austin, Texas, USA; Center for the Bioinformatics and Computational Genomics, Georgia Institute of Technology, Atlanta, Georgia, USA; Bioinformatics & Computational Biology Program, George Mason University, Virginia, USA; Institute of Discrete Mathematics and Geometry, Vienna University of Technology, Austria; BioMedical Informatics & Bio-Imaging Laboratory, Georgia Institute of Technology and Emory University, Atlanta, Georgia, USA; Knowledge Management & Intelligent System Center (KMIS) of University of Siegen, Germany; National Institute for Health Research; Hawkeye Radiology Informatics, Department of Radiology, College of Medicine, University of Iowa, Iowa, USA; Institute for Informatics Problems of the Russian Academy of Sciences, Moscow, Russia; Medical Image HPC & Informatics Lab (MiHi Lab), University of Iowa, Iowa, USA; SECLAB
of University of Naples Federico II, University of Naples Parthenope, and the Second University of Naples, Italy; The University of North Dakota, Grand Forks, North Dakota, USA; Intelligent Cyberspace Engineering Lab., ICEL, Texas A&M University, USA; International Society of Intelligent Biological Medicine; and World Academy of Biomedical Sciences and Technologies. Corporate Co-Sponsors, Co-Sponsors At-Large and Organizers include: A number of university faculty members and their staff (names appear below and also on the cover of the proceedings); World Academy of Science (www.world-academy-of-science.org/); Computer Science Research, Education, and Applications Press; European Commission; Salford Systems, USA; Element CXI, California, USA; SuperMicro Computer, Inc., San Jose, California, USA; High Performance Computing for Nanotechnology (HPCNano); The International Council on Medical and Care Computing; The UK Department for Business, Enterprise & Regulatory Reform, UK; VMW Solutions Ltd.; Scientific Technologies Corporation; HoIP - Health without Boundaries; Hodges’ Health; Bentham Science Publishers; and GridToday. In addition to the above, several publishers of computer science and computer engineering books and journals, chapters and/or task forces of computer science associations/organizations from 9 countries, and developers of high-performance machines and systems provided significant help in organizing the conference. The program committee would like to thank all those who submitted papers for consideration. About 48% of the submissions were from outside the United States. Each submission was evaluated by at least two referees. The overall paper acceptance rate for regular papers was 27%; 10% of the remaining papers were accepted as short/poster papers. We are very grateful to the many colleagues who helped in organizing the conference. In particular, we would like to thank the members of the BIOCOMP’09 Program Committee who we hope will offer their help again in organizing the next year's conference (BIOCOMP’10). The BIOCOMP’09 Program Committee members were:

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• Prof. Alicia Troncoso, Head of CS Dept., Pablo de Olavide University, Seville, Spain
• Dr. Jack Yang, Editor-in-Chief, International Journal Functional Informatics and Personalized Medicine, Harvard University, USA
• Dr. Mary Qu Yang (Co Chair), National Human Genome Research Institute, National Institutes of Health, U.S. Department of Health and Human Services, USA
• Prof. Lotfi A. Zadeh, Member of National Academy of Engineering; Fellow of IEEE and ACM University of California, Berkeley, California, USA
• Prof. Yanqing Zhang, Georgia State University, Atlanta, Georgia, USA
• Dr. Leming Zhou, University of Pittsburgh, Pittsburgh, PA, USA
• Members of WORLDCOMP Task Force for Artificial Intelligence
• Members of WORLDCOMP Task Force for Computational Biology
• Members of WORLDCOMP Task Force for High-Performance Computing
• Members of WORLDCOMP Task Force for Pattern Recognition

We are indebted to the following distinguished speakers for accepting our invitation to present WORLDCOMP and individual conference tutorials: Prof. H. J. Siegel (Abell Endowed Chair Distinguished Professor of ECE and Professor of Computer Science, Colorado State University, Fort Collins, Colorado, USA); Dr. Sandeep Chatterjee (Chief Technology Officer / CTO, SourceTrace Systems); Prof. Ali Mohammad-Djafari (Directeur de recherche au CNRS, Centre National de la Recherche Scientifique, CNRS, France); Jay Xiong (International Software Automation, Inc., USA and ISA Shanghai, Ltd., P. R. China); Prof. Anura P. Jayasumana (Colorado State University, Fort Collins, Colorado, USA); Dr. Robert F. Erbacher (Utah State University, Utah, USA); Dr. Brian J. d'Auriol (Kyung Hee University, Republic of Korea); Dr. Michael L. Nelson (Graduate Program Director, Hodges University, Ft Myers, Florida, USA); Dr. Peter DePasquale (The College of New Jersey, USA); Dr. Mark Lewis (Trinity University, USA); Prof. Ray Kresman (Bowling Green State University, Bowling Green, Ohio, USA); Khanna Samratvivekanand Omprakash (University, V.V.Nagar, India); Dr. G. Subrahmanya VRK Rao (Cognizant Technology Solutions); Prof. Nitesh V. Chawla (University of Notre Dame, Indiana, USA); Dr. Peter Gecey (National Institute of Advanced Industrial Science and Technology, AIST, Japan); Prof. Asim Roy (Arizona State University, Arizona, USA); and Dr. Dan Steinberg (President and CEO of Salford Systems, Inc.)

We express our gratitude to keynote and invited speakers of WORLDCOMP and individual conference/tracks (a partial list at the time of this writing): Prof. Ian Foster (Father of Grid Computing, Distinguished Professor of CS & Director, Computation Institute, University of Chicago and Argonne National Laboratory, Illinois, USA); Dr. K. Eric Drexler (Father of Nanotechnology, Chief Technical Advisor, Nanorex); Prof. Viktor K. Prasanna (Charles Lee Powell Chair in Engineering; Professor of EE, CE, & CS; Executive Director of USC-Infosys Center for Advanced Software Technologies/ CAST, University of Southern California, USA);
Dr. Jose L. Munoz (Deputy Director, National Science Foundation / NSF Office of Cyberinfrastructure, OCI and NSF/ICI senior science advisor; former Director of ASCI); Dr. Sandeep Chatterjee (Co-founder, Chief Technology Officer and Vice President, SourceTrace Systems, Inc.); Dr. Rahul Razdan (CEO, Raztech LLC); Prof. P. M. A. Sloot (Director of the Institute for Informatics, University of Amsterdam, The Netherlands and Editor-in-Chief, Future Generation Computer Systems, Elsevier); Prof. Michael Bank (Holon Institute of Technology, Israel and inventor of Frequency Bank Signal, FBS); and the 2009 International Conference on Bioinformatics and Computational Biology Keynote Speakers Dr. Brian D. Athey (Professor of Biomedical Informatics, University of Michigan Medical School, USA; Head, NIH National Center for Integrative Biomedical Informatics; Director, Biomedical Informatics Program of Michigan Institute for Clinical & Health Research); and Dr. Yi Pan (Chair and Professor, Department of CS, Georgia State University, Atlanta, USA). We would also like to thank the followings: UCMSS (Universal Conference Management Systems & Support, California, USA) for managing all aspects of the conference; Dr. Tim Field of APC for managing the printing of the proceedings; and the staff of Monte Carlo Resort in Las Vegas for the professional service they provided. Last but not least, we would like to thank the Associate Editors, Drs. Youping Deng, Chien-Tsai Liu, Ashu M. G. Solo, and Yanqing Zhang. We present the proceedings of BIOCOMP’09.

Hamid R. Arabnia Mary Qu Yang
University of Georgia, USA National Institutes of Health, USA
General Co-Chairs & Coordinators, BIOCOMP’09

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SESSION 14: Keynote Lecture: The Emerging Field of Translational Bioinformatics - A National Perspective
Keynote Speaker: Dr. Brian D. Athey
Professor, Bioinformatics and Computational Biology and Professor of Departments of Psychiatry and Internal Medicine. Associate Director, U-M Center for Computational Medicine and Biology (CCMB). Director, Biomedical Informatics Program (BIP), Michigan Institute for Clinical and Health Research. Principal Investigator, NIH National Center for Integrative Biomedical Informatics. The University of Michigan Medical School, USA

Abstract

Translational Bioinformatics is an emerging interdisciplinary field of applied research and development that merges bioinformatics, clinical informatics, and clinical and translational research. Work done by my groups at the University of Michigan in our NIH National Center for Integrative Biomedical Informatics (NCIBI) and in our Biomedical Informatics Program of the U-M CTSA will illustrate the power and promise of this approach. Detailed examples illustrating the application of “Integrative Biomedical Informatics” to accelerate research and understanding of prostate cancer progression, metabolism and diabetes modeling, and of Bipolar Disorder will be given. Perspectives on how this problem-driven integrative approach enhances interactions with the NCBC, CTSA, BIRN, and caBIG national biomedical informatics communities will be described.

Biography

Dr. Brain D. Athey is Professor and Director of Biomedical Informatics, and a professor in the Departments of Psychiatry and Internal Medicine, and founding Associate Director of the Center for Computational Medicine and Biology, at the University of Michigan Medical School. Trained as a biophysicist, Athey is now recognized as one of the nation’s experts in
the new field of ‘Translational Bioinformatics’. In the Mid-1980s, Brian proposed the double helical crossed-linker model for the structure of chromatin, once quite controversial, it is now generally accepted. Brian established the first nationwide Internet2 Visible Human Project demonstration under contract with the National Library of Medicine, was Principal Investigator of the DARPA Virtual Soldier Project, and he currently heads the NIH National Center for Integrative Biomedical Informatics (NCIBI.org), one of seven NIH Roadmap Centers for Biomedical Computing. Brian is Director of the Biomedical Informatics Program in the Michigan Institute for Clinical and Health Research, and is national co-chair of the Clinical and Translational Sciences Award (CTSA) Informatics Key Function Committee (IKFC). He currently serves as a special advisor to the Director of the Division of Program Coordinator, Planning, and Strategic Initiatives (DPCPSI), in the office of the Director of the NIH. In 2000, Brian was named a Peace Fellow of the Federation of American Scientists (FAS.org) for his work in the 1990s to combat biological warfare and terrorism.

SESSION 15: Keynote Lecture: Protein Structure Prediction and Its Understanding Based on Machine Learning Methods

Keynote Speaker: Dr. Yi Pan
Chair and Professor, Department of Computer Science
Professor, Department of Computer Information Systems
Georgia State University, Atlanta, USA

Abstract

Understanding protein structures is vital to determining the function of a protein and its interaction with DNA, RNA and enzyme. The information about its conformation can provide essential information for drug design and protein engineering. While there are over a million known protein sequences, only a limited number of protein structures are experimentally determined. Hence, prediction of protein structures from protein sequences using computer programs is an important step to unveil proteins’ three dimensional conformation and functions. As a result, prediction of protein structures has profound theoretical and practical influence over biological study. The explanation of how a decision is made during prediction is also important for improving protein structure prediction and guiding the "wet experiments". In this talk, we will show how to use machine learning methods to improve the accuracy of protein structure prediction and to interpret prediction results. We will report our research on using neural networks, Support Vector Machines combined with Decision Tree and Association Rule for protein structure prediction, rule extraction and prediction interpretation. Evaluation and comparisons of various prediction and rule extraction systems will be presented and future research direction in this area will also be identified.

Biography

Yi Pan is the chair and a professor in the Department of Computer Science and a professor in the Department of Computer Information Systems at Georgia State University. Dr. Pan
received his B.Eng. and M.Eng. degrees in computer engineering from Tsinghua University, China, in 1982 and 1984, respectively, and his Ph.D. degree in computer science from the University of Pittsburgh, USA, in 1991. Dr. Pan's research interests include parallel and distributed computing, networking, and bioinformatics. Dr. Pan has published more than 100 journal papers with over 40 papers published in various IEEE/ACM journals. In addition, he has published over 150 papers in refereed conferences and co-edited 34 books (including proceedings). He has received many awards from agencies such as NSF, AFOSR, JSPS, IISF and Mellon Foundation.

Dr. Pan has served as an editor-in-chief or editorial board member for 15 journals including 5 IEEE Transactions. He has also served as a guest editor for many journals including IEEE/ACM Transactions on Computational Biology and Bioinformatics and IEEE Transactions on NanoBioscience. He has organized numerous international conferences and workshops. Dr. Pan has delivered over 10 keynote speeches at international conferences. Dr. Pan is an IEEE Distinguished Speaker (2000-2002), a Yamacraw Distinguished Speaker (2002), and a Shell Oil Colloquium Speaker (2002). He is listed in Men of Achievement, Who's Who in Midwest, Who's Who in America, Who's Who in American Education, Who's Who in Computational Science and Engineering, and Who's Who of Asian Americans.

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Volume I and II

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