SIGBio Record

Newsletter of the SIGBio
ACM Special Interest Group

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Editor in Chief's Notes:

2014 is the official year for the SIGBio community welcoming health informatics researchers into its ranks and incorporating health informatics topics into its flagship conference ACM BCB 2014.

The current issue presents the report on a IEEE International Conference on Healthcare Informatics (ICHI) 2013 Conference, by Christopher C. Yang. Also, the "Computer Scientist in Profile" section highlights Prof. Bruce Donald.
We thank contributors for this issue and hope that readers will find interesting topics related to their work in Bioinformatics andHealth Informatics area.

Pietro Hiram Guzzi, Young-Rae Cho, Pierangelo Veltri - SIGBio Record Editors

Notice to Contributing Authors to SIG Newsletters

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Note from Chair

Happy New Year to all members!

I hope to let everyone know that Health Informatics will be part of the main conference in ACM BCB 2014: The 5th ACM Conference on Bioinformatics, Computational Biology and Health Informatics. The call for workshops, call for tutorials and call for papers are included in this issue.

On a different note, SIGBio will hold its election this year in Fall for its officers and board of directors. The nomination committee members are:

Aidong Zhang , SUNY at Buffalo, Committee Chair

Pierre Baldi, University of California, Irvine

Mark Borodovsky, Georgia Institute of Technology

Pietro Hiram Guzzi, University Magna Graecia of Catanzaro

Vipin Kumar, University of Minnesota

Tekin Ozsoyoglu, Case Western Reserve University

Yi Pan, Georgia State University

Based on the SIGBio Bylaws, the election of Chair, Vice Chair, treasurer-secretary, and board of directors(six) will be conducted for the next term.

We would like to receive nominations for these positions (self nominations are welcome), and we would also like to receive input on any important issues that should be considered in the selection of the next officers.

Please submit your nominations and suggestions by May 31, 2014 to the chair of the

nomination committee, Aidong Zhang, azhang@buffalo.edu.

Aidong Zhang, SIGBio Chair

Aidong Zhang, University Distinguished Professor and Chair
Department of Computer Science and Engineering
State University of New York at Buffalo (UB)
338 Davis Hall
Buffalo, NY 14260

Computer Scientist in Profile:
Bruce R. Donald

Contributor: Amarda Shehu[1,2] [amarda@gmu.edu]
Dept. of [1]Computer Science, [2]Bioengineering
George Mason University, Fairfax, VA 22030
Tel: 703-993-4135   Fax: 703-993-1710

Of all the undergraduate majors that might steer someone towards an accomplished scientific career and prolific research in Artificial Intelligence, Robotics, and Computational Structural Biology, you would have a hard time circling 'Russian Language and Literature.' Yet, that is exactly how Bruce's journey started at Yale. Bruce fondly recalls his famous English and Literature professors, such as Harold Bloom and Victor Ehrlich, who left a deep impression on him and played no small part in Bruce eventually graduating *summa cum laude* in 1980. "The connection with Computer Science was there all along," says Bruce, "though I did not obtain any formal training in CS. I had been a hacker in high school, and I did take some LOGO and Fortran classes at MIT. I hung out with a group of programmers in school and had a job programming and selling one of the first personal computers, the MITS Altair 8800." He recalls that despite his interest in programming, at Yale he almost exclusively took only Humanities courses. The only other courses outside Humanities were a Physics, Calculus, and Artificial Intelligence course.

During the better half of his undergraduate studies and four years afterwards, Bruce was also a Research Analyst in the Laboratory for Computer Graphics and Spatial Analysis at the Harvard University Graduate School of Design, where he worked on Geographical Information Systems (GIS) and computer-aided architectural design. "In 1978 I just walked into the Harvard Graduate School of Design and convinced them I could program." They hired him. At first he was mostly attracted to the design, art, and visual connections. However, there was rigorous computer science that got him interested in theory. The lab was a hotbed of algorithms, GIS, graphics, and geometry. Eventually the administration urged Bruce to go back to graduate school. He was not quite sure what he wanted to do. So, he did the next logical thing.

Bruce simultaneously applied to Oxford in Russian literature and MIT in Computer Science. He was accepted to both. "MIT offered a stipend, whereas Oxford asked me to pay a lot, thousands of pounds." He goes on, "I do not know why MIT admitted me, but I was lucky to find a great advisor who trained me, Tomás Lozano-Pérez." In 1982, Bruce began working under the direction of Lozano-Perez at the MIT Artificial Intelligence Laboratory. He received the S.M. degree in Electrical Engineering and Computer Science, soon followed by a Ph.D. degree in Computer Science in 1987. His officemate at MIT, Mike Erdmann, urged Bruce to also study Mathematics. As a result, Bruce minored in Topology during his graduate studies, which he notes he still uses in his work today.

The next leg of the journey landed Bruce in Ithaca, N.Y., where he joined the Computer Science faculty at the Cornell University. At Cornell, Bruce also held a joint appointment in Applied Mathematics and co-founded the Cornell Robotics and Vision Laboratory. He got an early sign of the impact of his research when he received a National Science Foundation Presidential Young Investigator Award in 1989. He rose through the ranks of tenure by 1993.

Bruce spent more than a decade at Cornell before joining the Computer Science Department at Dartmouth in 1997. As if anticipating my question, he proceeds to tell me that the move happened organically. After obtaining tenure in 1993, he stayed in Ithaca an extra year to run the Masters Program, which he expanded from 6 to 80 students. Afterwards he took a sabbatical at Stanford as a visiting professor from 1994 to 1996. "I was very lucky to have a visiting position in Computer

Science and to work at Paul Allen's Company, Interval Research Corporation," he says. Bruce worked in Palo Alto, CA from 1995 to 1997. During this time, he became co-inventor of Embedded Constraint Graphics (ECG). Most importantly, he also met his wife, then a Neurobiology postdoctoral fellow at Stanford. They got married and looked for jobs. He hoped they could go back to Cornell or find positions in the West Coast. After spending one more year at Cornell trying to figure out how to solve the two-body problem, he got a surprise. Daniela Rus had just gone to Dartmouth as an Assistant Professor and helped Bruce and his wife find the right positions at Dartmouth. "That is how I ended up at Dartmouth," he says.

At Dartmouth, Bruce was named the Joan and Edward Foley Professor in 2003. During his time at Dartmouth, Bruce made significant contributions to robotics, including numerous scientific papers. "It was at Dartmouth that I started getting results in computational molecular biology," he recalls. The analogies with robotics gave Bruce a fresh perspective on computational problems involving molecular structures and some very exciting research directions. Indeed, in 2001, he was awarded a Guggenheim Fellowship for his advancement of algorithmic research on Structural molecular biology and proteomics. Since then, Bruce's research has advanced advanced protein design, molecular nanotechnology, and their biomedical applications. He has developed transformative algorithms for positive and negative protein design. He has extended the boundaries of what is possible with provable algorithms, in a series of end-to-end studies going from mathematics to novel algorithms to software to prospective experimental validation including binding, kinetics, stability, in vivo assays, and both NMR structures and crystal structures.

"I have been very lucky to have amazing collaborators with whom I have co-supervised students. That makes for the best science."

Bruce is now James B. Duke Professor of Computer Science at Duke University and Professor of Biochemistry in the Duke University Medical Center. He is a Fellow of the ACM and the IEEE for contributions in robotics, microelectromechanical systems, and computational molecular biology. In 2011, Bruce published a seminal book with MIT Press, "Algorithms in Structural Molecular Biology."

Bruce's efforts have significantly advanced computational structural biology. His algorithms have been experimentally demonstrated to have remarkable accuracy and predictive power. His algorithms have been applied prospectively to systems of significant biochemical and pharmacological interest. Seminal work includes reprogramming an antibiotic-producing enzyme (*PNAS 2009*), predicting MRSA resistance mutations to a new inhibitor (*PNAS 2010*), developing allosteric inhibitors of oncogenic protein-protein interactions (PPIs) in leukemia (*Chemistry & Biology 2007*), designing competitive inhibitors of PPIs to combat cystic fibrosis (*PLoS Comp. Biol. 2012*), designing molecular probes to selectively pull down broadly neutralizing antibodies against HIV-1 from donor sera (*Retrovirology 2012*), and designing a new antigenic MPER trimer for examining immunogenic responses to the HIV-1 viral coat protein gp41 (PDB id: 2m7w).

It is worth noting that Bruce is behind many structures deposited to the Protein Data Bank, which is a remarkable feat for a computer scientist. Bruce has developed breakthrough algorithms for structure determination from X-ray crystallography and NMR data, specifically for difficult systems including large proteins, symmetric proteins, and membrane proteins. For example, he has used his algorithms to solve challenging protein structures central in Cryptosporidosis (PDB id: 1QZF), cardiac calcium cycling (PDB id: 2HYN), and HIV (PDB id: 2M7W). Finally, he has developed biomedical microtechnology, including the world's smallest untethered controllable microrobots (*J.MEMS 2006, 2008*), massively-parallel distributed micromanipulation and microassembly, and carbon nanotube neural probes for intracellular recording in freely behaving animals (*PLoS 2013*).

With such a remarkably diverse and high-impact research contributions in molecular biology, it seems appropriate to pause and ask. "How does someone arrive at this point?" Bruce credits two sources to

his success. First, a diverse and accomplished research portfolio in Artificial Intelligence. "The second is my colleagues," he says. "My experimental collaborators have been instrumental to my ability to chart new paths in my scientific career and be successful. I have been lucky to co-supervise outstanding students with my collaborators."

Bruce is exceptionally proud of the accomplishments of his former Ph.D. and postdoctoral students. He tells me that many of them have gone to impressive positions and accomplishments as independent scientists with successful laboratories of their own. Perusing the detailed list he maintains on his lab's website, I realize I recognize many of them.
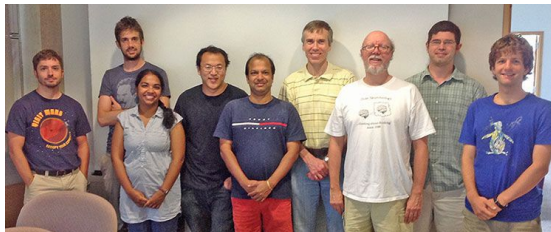
A recent photo of the Donald Lab.

"So, what is next?" I cannot resist to ask him. He shares with me his firm belief that his algorithms can revolutionize therapeutic treatment. "Our algorithms could enable the design of proteins and other molecules to act on today's undruggable proteins and tomorrow's drug-resistant diseases," he says. In the next few years, Bruce plans to develop novel protein design algorithms and software. He notes, "My goal is to use to them to (1) predict future resistance mutations to new drugs in pathogens responsible for deadly nosocomial and community-acquired infections; (2) design inhibitors of protein-protein interactions that address the underlying genetic defect in cystic fibrosis patients and alleviate their symptoms; and (3) discover, improve, and design broadly neutralizing antibodies against Human immunodeficiency virus (HIV)."

As we are approaching the end, it occurs to me that as a student of Literature, Bruce would have ideas of his own on how to bring the profile to a close and probably also have no trouble doing so in Russian. "How should I end?" I ask him. He seems prepared. "At a cartoon level, there are five major themes in Russian intellectual history: messianism, nationalism, anarchism, eschatologism, and socialism," he says. "If you perhaps morph 'nationalism' to 'disciplinary exceptionalism,' these are essentially the same figurative arteries in the heart of every successful biomedical laboratory and department."

IEEE International Conference on Healthcare Informatics 2013 Report

Christopher C. Yang
College of Computing and Informatics
Drexel University

The IEEE International Conference on Healthcare Informatics 2013 (ICHI 2013) served as the international forum concerned with the application of computer science principles, engineering principles, information technology, communication technology, and information science principles to address problems in healthcare, public health, everyday wellness as well as the related social and ethical issues. The First ICHI 2013 was organized in Philadelphia from September 8 to 11 in 2013.

ICHI 2013 brings together researchers, scientists, and practitioners to discuss their latest research and practices. ICHI is organized in three major tracks:

(1) **Systems Track** focuses on issues related building healthcare informatics systems such as architecture, framework, design, engineering, and application,
(2) **Analytics Track** focuses on data analytics,
(3) **Human Factors Track** focuses on understanding users or context, interface design, and user studies of healthcare informatics applications.

The three program committee co-chairs, Drs. Carlo Combi, Zhiyong Lu, and Yin-Leng Theng, together with over 160 program committee members developed the three-day conference program with 31 oral presentations and 24 poster presentations. There were also 3 keynote speeches, 14 extended abstracts, 1 tutorial, 1 panel, and a doctoral consortium.

There were 11 parallel oral presentation sessions covering topics on:
- Drug Management
- Health Text Analytics
- Health Risk Prediction
- Health Organization and Epidemiology
- Home-Assistance and Individual Care
- Interactivity and Modality
- Web-based Architectures and User Interactions
- Human Factors: Effects and Outcomes
- Human Factors: Applications

The contributing authors came from 21 countries and regions, including Belgium, Brazil, Canada, China, Denmark, France, Germany, India, Italy, Japan, Korea, Luxembourg, Netherlands, Portugal, Singapore, Slovenia, Spain, Sri-Lanka, Switzerland, United Kingdom, and United States. Over 150 participants attended the conference and exchanged their insights with the authors and the organizing committee. More details about the conference program can be found at http://cci.drexel.edu/ichi2013/.

The Award Selection Committee composed of five experts in healthcare informatics and the program committee co-chairs identified two best papers. The two Best Paper Awards were presented in the banquet on the second day of the conference. These two best papers were

- "A Publish/Subscribe Middleware for Body and Ambient Sensor Networks that Mediates between Sensors and Applications" by Christian Seeger, Kristof Van Laerhoven, Jens Sauer Alejandro Buchmann
- "Empirical Evaluation of Traditional vs. Hybrid Interaction Metaphors in a Multitask Healthcare Simulation" by Lauren Cairco Dukes, Jeffrey Bertrand, Manan Gupta, Rowan Armstrong, Tracy Fasolino, Sabarish Babu and Larry F. Hodges

Three keynote speeches were given in the morning and afternoon of the first day and in the morning of the second day of the conference Prof. Harold Thimbleby from Swansea University, UK, offered his insights on improving safety in medical devices and systems. Dr. Martin Kohn, IBM Chief Medical Scientist for Care Delivery Systems, talked about the Watson technologies in cognitive computing and healthcare. Professor Larry Smarr, Founding Director of the California Institute for Telecommunications and Information Technology (Calit2), talked about how to reveal the dynamics of our superorganism body digitally. There was a panel on Social Media and Patient-Centered Research. Ms. Rebecca Chiu, and Drs. Simon, Lin, Akhil Kumar, and Chris Yang discussed the impact of social media on patient community groups and its potential for timely knowledge discovery and patient-centered research, which complement the clinical-oriented research. Drs. Jimeng Sun and Chandan Reddy had given a tutorial on Big Data Analytics for Healthcare.

National Science Foundation (NSF) has provided generous partial support to organize the doctoral consortium. Over 25 doctoral students received financial traveling support to attend both of the doctoral consortium and the conference program. The doctoral consortium chairs, Drs. Giuseppe Pozzi and David Buckeridge, selected 13 doctoral students from Denmark, India, Portugal, United Kingdom, and United States to present their work in oral and poster formats in the three-hour program. Each doctoral student first received a one-on-one mentorship from senior healthcare informatics faculty. After presentations of the dissertation work by the selected doctoral students, there was also a panel discussing the latest development of healthcare informatics research and the career preparation of our doctoral students.

In addition, there were three affiliated workshops:

The International Workshop on Data Mining for Healthcare (DMH 2013) was a full-day workshop with 8 paper presentations covering topics on privacy and fraud, screening and diagnosis, data properties and management. Prof. Joydeep Ghosh from University of Texas at Austin and Dr. Robert Kaplan from National Institutes of Health had given the invited talks on predictive modeling of large healthcare data under privacy and challenges in the analysis of big data, respectively. In addition, Prof. Jaideep Srivastava had coordinated a panel on predictive modeling in healthcare to discuss the challenges, realities and opportunities.

The First Workshop on Mobile Cloud Computing in Healthcare (WMCCH 2013) was a half-day workshop covering the topics on the computational efficiency, false alarm rate reduction, and remote patient monitoring using mobile cloud computing technologies.

The Workshop on Hospital Readmission Prediction and Clinical Risk Management (HRPCRM 2013) was a half-day workshop covering the topics on readmission risk assessment, predictive modeling, prescriptive analytics, and temporal evaluation of risk factors. Dr. Scott Zasadil, the Chief Scientist of UPMC Health Plan, had given a keynote speech on "Readmissions; Models and More". The workshop was concluded by a panel discussion.

Healthcare Informatics with computing focus and interdisciplinary nature has drawn increasing attention in the recent years. We hope that the IEEE International Conference on Healthcare Informatics series will continue to serve as a platform for the researchers and practitioners in healthcare informatics to share their latest work annually. ICHI 2014 will be held in September in Verona, Italy. We hope that you will join us either as a presenter or a participant.

Call for Papers
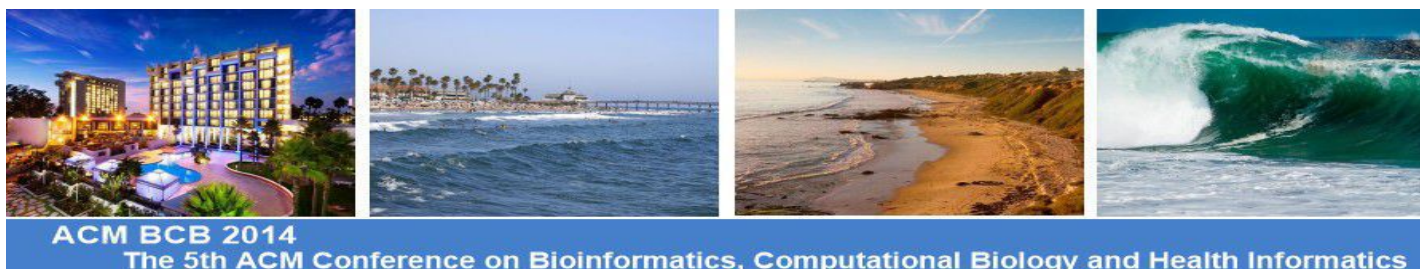
5th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics 2014

September 20-23, 2014, Newport Beach, CA, USA

http://www.cse.buffalo.edu/ACM-BCB2014/

The ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM BCB) is the flagship conference of the ACM SIGBio. This is the conference's fifth year, building upon the success of the first four meetings in Niagara Falls, Chicago, Orlando, and Washington DC. This year is the first to fully incorporate the new areas of Health Informatics.

ACM BCB 2014 will be held in Los Angeles CA during September 20-23, 2014. The conference offers a forum for premier interdisciplinary research linking computer science, mathematics, statistics, biology, bioinformatics, biomedical informatics, and health informatics. The past two decades have seen tremendous growth in the scale and complexity of biological and medical data. This conference serves to showcase leading-edge research on new technologies and techniques for gathering, processing, analyzing, and modeling these big data for a variety of scientific, clinical, and healthcare applications, from bench to bedside.

ACM BCB 2014 welcomes original submissions that have not been published or under review. Examples of relevant topics include the following, but are not limited to the areas of:

§ Sequencing and Analysis Methods
§ Gene Regulation and Transcription
§ Functional Genomics
§ Population, Evolution, and Comparative Genomics
§ Protein and RNA Structure and Function
§ Computational Systems Biology
§ Biomedical Image Analysis

§ Translational Bioinformatics
§ Medical Informatics and Medical Records
§ Knowledge Bases and Text Mining
§ Mobile Health and Sensor Applications
§ Population Health and Public Health Informatics
§ Cross-Cutting Computational Methods
§ Knowledge Representation and Machine Learning
§ Databases and Integration of Biomedical Data
§ Bioinformatics and Healthcare Infrastructure

Submitted manuscripts should not exceed 10 pages in ACM template on 8.5 x 11 inch paper (http://www.acm.org/sigs/publications/proceedings-templates). All submissions will be evaluated on their originality, technical soundness, significance, presentation, and interest to the conference attendees. All submitted papers will be reviewed by ACM-BCB's technical program committee. All accepted papers of registered authors will be included in the proceedings published by ACM Digital Library. Details for electronic submission can be found on the conference web portal at: http://www.cse.buffalo.edu/ACM-BCB2014/. The authors of selected papers will be invited to adapt their papers for a special issue of IEEE Transactions on Computational Biology and Bioinformatics (TCBB), a special issue of IEEE Journal of Biomedical and Health Informatics, a virtual issue of the DATABASE journal, and other prestigious journals.

Important Dates:
Paper submissions due : May 15, 2014
Notifications sent to authors: July 15, 2014
Camera-ready papers due : July 29, 2014

Steering Committee:

Aidong Zhang, State University of New York at Buffalo, Chair
Vasant Honavar, Penn State University, Conference Director

General Chairs:

Pierre Baldi, University of California, Irvine
Wei Wang, University of California, Los Angeles

Program Chairs:

Terry Gaasterland, University of California, San Diego
Ümit V. Çatalyürek, The Ohio State University

Bruce Schatz, University of Illinois at Urbana-Champaign

Workshop Chair:

Tamer Kahveci, University of Florida

Tutorial Chairs:

Vasant Honavar, Penn State University
Amarda Shehu, George Mason University

Poster Chairs:
Yu-Ping Wang, Tulane University
Dongxiao Zhu, Wayne State University

PHD Forum Chair:
Jean Gao, University of Texas at Arlington

Panel Chairs:
Orly Alter, University of Utah
May Wang, Georgia Institute of Technology

Exhibit/System Demo Chair:
Richard Lathrop, University of California, Irvine

Registration Chair:
Preetam Ghosh, Virginia Commonwealth University

Proceedings Chairs:
Jing Gao, State University of New York at Buffalo
Xinghua Mindy Shi, University of North Carolina

Industry Chairs:
Anastasia Christianson, AstraZeneca
Tanveer Syeda-Mahmood, IBM Almaden Research Center

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Jianlin Jack Cheng, University of Missouri, Columbia

Local Arrangement Chairs:
Xiaohui Xie, University of California, Irvine
Janet Ko, University of California, Irvine

ACM-BCB 2014 Call for Workshop and Tutorial Proposals

The 5th ACM BCB Conference on Bioinformatics, Computational Biology and Health Informatics to be held at the Marriott Hotel in Newport Beach, California, USA on September 20-23 2014 (http://www.cse.buffalo.edu/ACM-BCB2014) provides a premier forum for interdisciplinary and multidisciplinary research encompassing disciplines of computer science, mathematics, statistics, biology, bioinformatics, and health informatics.

1. Call for Workshop Proposals

The ACM-BCB-2014 organizing committee invites proposals for workshops to be held in conjunction with the conference. The purpose of a workshop is to provide participants with the opportunity to present and discuss novel research ideas on active and emerging topics in bioinformatics, computational biology and health informatics.

Workshops that focus on a challenge problem, such as (not limited to) flexible docking, computational drug design, or emerging topics, such as (not limited to) computational immunology and vaccinology, analysis of protein-RNA interactions, big data in bioinformatics, epigenomics, health related topics, and personal medicine are especially welcome. Please note that the conference does not have funding for invitation of workshop speakers. All workshop attendees are expected to register for the conference. Student participants in the workshops can apply for a limited number of student travel fellowships from the conference on a competitive basis.

The workshops organizers must be prepared to create a workshop web page to be linked to the main conference web page, announce the workshop and call for papers, gather submissions, conduct the review process and decide the final workshop program. The workshop proceedings will be part of ACM BCB 2014 proceedings. The logistics of the workshops will be coordinated with help from the ACM BCB-2014 organizers.

Workshop Proposals should be no more than 3 pages in length and must include the following:
• Workshop abstract, objectives, goals, relevance, and expected outcome
• One or more potential invited speakers
• Past workshops and other related recent workshops (if applicable)
• Preferred duration of the workshop (full day or half day)
• Contact information (address, email, and phone) for all organizers
• A designated contact person

Proposals should be submitted by email (with subject "ACM-BCB 2014 Workshop Proposal") to **Tamer Kahveci**(tamer@cise.ufl.edu) preferably in PDF format.

Key dates for the ACM-BCB Workshops:
Submission deadline:**March 1, 2014**
Notification of Acceptance:**March 15, 2014**

2. Call for Tutorial Proposals

ACM-BCB 2014 invites tutorials that address the interests of its varied audience of individuals interested in Bioinformatics and Computational Biology, and Health Informatics (BCB) including graduate students, researchers and educators from academia, and researchers and practitioners from industry and government.

We especially welcome proposals for tutorials that:
• Introduce a specific BCB topic, designed to make the topic (and the conference) more accessible to participants who are new to that topic.
• Provide a hands-on introduction to one or more databases, software tools, or other resources of broad interest to the conference participants.
• Provide a comprehensive review of the current state of the art in a specific BCB topic aimed at researchers and practitioners who are knowledgeable, but not necessarily experts in the topic.
• Present techniques from research fields e.g., machine learning, statistics, parallel computing, that are relevant to BCB research.
• Introduce new research problems, new application areas, or new or emerging technologies of relevance to BCB.

The tutorials will be held on September 20, 2014. We envision most tutorials to be 2 hours or 4 hours long although longer durations (in multiples of 2 hour slots) may be considered. Ideally, each tutorial must have more than one presenter and no more than three, preferably from different institutions, bringing different perspectives.

• Tutorial proposals should not exceed 5 pages, using an 11 point font for the text, and should include:
• Tutorial title
• Names and affiliations of presenters
• Tutorial abstract (200 words maximum, suitable for inclusion on the conference website)
• Tutorial description, including the objectives of the tutorial, its relevance to ACM-BCB 2014, description of the intended audience and background assumed of the audience, sufficient detail regarding the scope of material to be covered and the depth at which it will be covered.
• Desired tutorial length (if there is flexibility regarding length, please specify the topics to be included for each length).
• Information about other venues in which tutorials on the same topic have been or are planned to be presented, along with pointers to the relevant slides or other tutorial materials and a brief explanation of how the proposed tutorial differs from the other offerings.
• Brief professional biographies of presenters including their scientific and professional qualifications and experience (relevant research, teaching or tutorial presentation) and contact information.

Each proposal will be reviewed by the members of the ACM-BCB tutorial program committee, and ranked based on the significance of the proposed tutorial topic, overall quality of the proposal, the qualifications and experience of the presenters, and the tutorial's fit to the conference, and the number of tutorial slots and the space available.

Please email tutorial proposals to Tutorial Chairs:

Vasant Honavar, <u>vhonavar@ist.psu.edu</u>
Amarda Shehu, <u>amarda.shehu@gmail.com</u>

Key dates: To ensure full consideration, tutorial proposals must be received no later than **March 1, 2014**. Notifications of acceptance will be mailed by **March 15, 2014**.

The ACM-BCB-2014 organizing committee(<u>http://www.cse.buffalo.edu/ACM-BCB2014</u>)
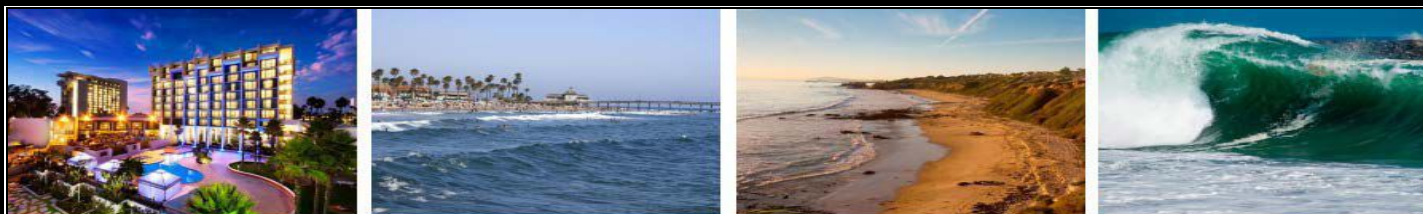
ACM BCB 2014
The 5th ACM Conference on Bioinformatics, Computational Biology and Health Informatics

Call for Papers, Workshops and Tutorials
ACM BCB: 5th ACM Conference on Bioinformatics, Computational Biology and Health Informatics 2014

September 20-23, 2014, Marriot Newport Beach, CA

http://www.cse.buffalo.edu/ACM-BCB2014

Key Dates

	Submission Deadline	Notification of Acceptance
Papers	May 15, 2014	July 15, 2014
Workshops	March 1, 2014	March 15, 2014
Tutorials	March 1, 2014	March 15, 2014

Organizing Committee

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- Janet Ko, University of California, Irvine

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The conference offers a forum for premier interdisciplinary research linking computer science, mathematics, statistics, biology, bioinformatics, biomedical informatics, and health informatics. The past two decades have seen tremendous growth in the scale and complexity of biological and medical data. This conference serves to showcase leading-edge research on new technologies and techniques for gathering, processing, analyzing, and modeling these big data for a variety of scientific, clinical, and healthcare applications, from bench to bedside.

We invite contributed papers, workshops and tutorials in the areas listed below. Please refer to the conference website for more details.

ACM BCB 2014 welcomes original submissions that have not been published and that are not under review by another conference or journal.

Topics

- **Sequencing and Analysis Methods**
- **Gene Regulation and Transcription**
- **Functional Genomics**
- **Population, Evolution, and Comparative Genomics**
- **Protein and RNA Structure and Function**
- **Computational Systems Biology**
- **Biomedical Image Analysis**
- **Translational Bioinformatics**
- **Medical Informatics and Medical Records**
- **Knowledge Bases and Text Mining**
- **Mobile Health and Sensor Applications**
- **Population Health and Public Health Informatics**
- **Cross-Cutting Computational Methods**
- **Knowledge Representation and Machine Learning**
- **Databases and Integration of Biomedical Data**
- **Bioinformatics and Healthcare Infrastructure**

Association for Computing Machinery
Advancing Computing as a Science & Profession

SIGBio
Bioinformatics, Computational Biology and Biomedical Informatics

SIGBIO Record - Call for contributions and Submission Guidelines

Submission categories

Submissions to the newsletter can be either on a special issue topic or on topics of general interest to the SIGBIO community.

These can be in any one of the following categories:
- Survey/tutorial articles (short) on important topics.
- Topical articles on problems and challenges
- Well-articulated position papers.
- Review articles of technical books, products and .
- Reviews/summaries from conferences, panels and special meetings within 1 to 4 pages [1500-2500 words]
- Book reviews and reports on relevant published technical books
- PhD dissertation abstracts not exceeding 10 pages
- Calls and announcements for conferences and journals not exceeding 1 page
- News items on the order of 1-3 paragraphs

Brief announcements Announcements not exceeding 5 lines in length can simply be sent as ASCII text to the
editors by e-mail. SIGBIO Record publishes announcements that are submitted as is without review.
Announcements cannot be advertisements and should be of general interest to the wider community. The Editor reserves the right to reject any requests for announcements at his discretion.
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