

# ACM BCB 2014 Program

## REGISTRATION:

Saturday 7:30am-5pm/Sunday 8-11am/Monday 8-11am

Saturday September 20, 2014						
	Cardiff	Salon 1 & 2	Salon 3	Salon 4	Salon 5	Baycliff
8:30-10:30	ICIW		BigLS	CSBW	CNB-MAC	T1
10:30-11:00	Break					
11:00-1:00	ICIW		BigLS	CSBW	CNB-MAC	T5
1:00-2:00	Lunch					
2:00-4:00	ICIW	ParBio	BigLS	DL	CNB-MAC	T3
4:00-4:30	Break					
4:30-6:30	ICIW	IWBNA	BigLS	T2	CNB-MAC	T4

## TUTORIALS:

- T1:** Integrated Analysis of Next-Generation-Sequencing Data using Variant Tools  
Primary contact: Bo Peng [bpeng@mdanderson.org](mailto:bpeng@mdanderson.org)
- T2:** Informatics Approaches to Evidence-Based Medicine, with Emphasis on Systematic Reviews  
Primary contact: Aaron Cohen [cohenaa@ohsu.edu](mailto:cohenaa@ohsu.edu)
- T3:** Robot Motion Planning Methods for Modeling Structures and Motions of Biomolecules  
Primary contact: Amarda Shehu [amarda@gmu.edu](mailto:amarda@gmu.edu)
- T4:** Network Approaches in Aging Research with Focus on Biological Network Alignment  
Primary contact: Tijana Milenkovic [tmilenko@nd.edu](mailto:tmilenko@nd.edu)
- T5:** Computational Prediction of Protein-Protein Interfaces with Emphasis on Partner-Specific Protein-Protein Interaction  
Primary contact: Vasant G. Honavar [vhonavar@ist.psu.edu](mailto:vhonavar@ist.psu.edu)

## WORKSHOPS:

- BigLS:** Big Data in the Life Sciences  
Organizers: Ananth Kalyanaraman and Jaroslaw Zola
- CNB-MAC:** Computational Network Biology: Modeling, Analysis, and Control  
Organizers: Byung-Jun Yoon and Xiaoning Qian
- CSBW:** Computational Structural Bioinformatics  
Organizers: Jing Je, Amarda Shehu, Nurit Haspel, and Brian Chen
- ICIW:** Immunoinformatics and Computational Immunology  
Organizers: Vasant Honavar, Guanglan Zhang, and Lou T. Chitkushev
- IWBNA:** Biomolecular Network Analysis  
Organizers: Young-Rae Cho, Pietro H. Guzzi, and Pierangelo Veltri
- ParBio:** Parallel and Cloud-based Bioinformatics and Biomedicine  
Organizers: Mario Cannataro and John A. Springer
- DL:** Deep Learning in Bio- and Health Informatics  
Organizer: Pierre Baldi

**Sunday September 21, 2014**

8:45-9:00	<p align="center">Welcome Location: Salon 1-5 Session Chair: Pierre Baldi</p>	
9:00-10:00	<p align="center">Keynote 1 (CTB) Fine-Grained Phenotypes, Comorbidities and Disease Trajectories from Data Mining of Electronic Patient Records. Søren Brunak, Technical University of Denmark &amp; University of Copenhagen Session Chair: Pierre Baldi Location: Salon 1-5</p>	
10:00-10:30	<p align="center">Break</p>	
10:30-11:30	<p align="center">Industrial Session 1 Trends in Genomic Data and Big Data Analytics. Scott Kahn Vice President, Commercial Enterprise Informatics, Illumina, Inc. Session Chair: Anastasia Christianson Location: Salon 1-5</p>	
11:30-12:00	<p align="center">Published Highlights Session Chair: Umit Catalyurek Location: Salon 1-5</p> <p align="center">Automatic Training of Eukaryotic Gene Finding Algorithms. Mark Borodovsky</p> <p align="center">Predicting gene regulatory networks of soybean nodulation from RNA-Seq transcriptome data. Mingzhu Zhu, Jeremy Dahmen, Gary Stacey, and Jianlin Cheng.</p> <p align="center">Health Monitors for Chronic Disease by Gait Analysis with Mobile Phones. Joshua Juen, Qian Cheng, Valentin Prieto-Centurion, Jerry Krishnan, and Bruce Schatz.</p>	
12:00-1:00	<p align="center">Lunch Location: Rose Garden</p>	
1:00-3:30	<p align="center">Paper Session I</p>	
	<p align="center">Session S1 (CMS) Session Chair: Amarda Shehu Location A: Salon 4 &amp; 5</p>	<p align="center">Session S2 (BI) Session Chair: Leonard McMillan Location B: Salon 1-3</p>
1:00-1:30	<p>Graph-Theoretic Analysis of Epileptic Seizures on Scalp EEG Recordings. Nimit Dhulekar, Basak Oztan, Bülent Yener, Haluk O. Bingol, Gulcin Irim, Berrin Aktekin, and Canan Aykut Bingol.</p>	<p>IPED2: Inheritance Path based Pedigree Reconstruction Algorithm for Complicated Pedigrees. Dan He, Zhanyong Wang, Laxmi Parida, and Eleazar Eskin.</p>
1:30-2:00	<p>A Hadoop-Galaxy adapter for user-friendly and scalable data-intensive bioinformatics in Galaxy. Luca Pireddu, Simone Leo, Nicola Soranzo, and Gianluigi Zanetti.</p>	<p>Amb-EM: A SNP-based Prediction of HLA Alleles Using Ambiguous HLA Data. Vanja Paunic, Michael Steinbach, Abeer Madbouly, and Vipin Kumar.</p>
2:00-2:15	<p>Deep Autoencoder Neural Networks for Gene Ontology Annotation Predictions. Davide Chicco, Peter Sadowski, and Pierre Baldi.</p>	<p>Mining massive SNP data for identifying associated SNPs and uncovering gene relationships. Amy Webb, Aaron Albin, Zhan Ye, Majid Rastegar-Mojarad, Kun Huang, Jeffrey Parvin, Wolfgang Sadee, Lang Li, Simon Lin, and Yang Xiang.</p>

2:15-2:30	An Improved Algorithm for the Sorting by Reversals and Transpositions Problem. Ulisses Dias, Andre Rodrigues Oliveira, and Zanoni Dias.	PseudoLasso: Leveraging Read Alignment in Homologous Region to Correct Pseudogene Expression Estimates via RNASeq. Chelsea J.-T. Ju, Zhuangtian Zhao, and Wei Wang.
2:30-2:45	Data Mining to Aid Beam Angle Selection for Intensity-Modulated Radiation Therapy. Stuart Price, Bruce Golden, Edward Wasil, and Hao Zhang.	Focus: A New Multilayer Graph Model for Short Read Analysis and Extraction of Biologically Relevant Features. Julia Warnke and Hesham Ali.
2:45-3:00	omniClassifier: a Desktop Grid Computing System for Big Data Prediction Modeling John H. Phan, Sonal Kothari, and May D. Wang.	AccuRMSD: A Machine Learning Approach to Predicting Structure Similarity of Docked Protein Complexes. Bahar Akbal-Delibas, Marc Pomplun, and Nurit Haspel.
3:00-3:15	Spectral feature selection and its application in high dimensional gene expression studies. Zixing Wang, Peng Qiu, Wenlong Xu, and Yin Liu.	Large Highly Connected Clusters in Protein-Protein Interaction Networks . Suzanne Gallagher and Debra Goldberg.
3:15-3:30	Dynamic Coordinate Registration Method for Image-Guided Surgery. Xi Wen, Hong Wang, and Weiming Zhai.	Quantitative Trait Loci Mapping with Microarray Marker Intensities. Chen-Ping Fu, Fernando Pardo-Manuel de Villena, and Leonard McMillan.
3:30-4:00	Break	
4:00-6:00	SigBio community meeting Session Chair: Aidong Zhang Location: Salon 1-5	
6:00-8:00	Reception / Poster Session/ Demo/ Exhibit Location: Cardiff, Del Mar, Laguna, & Sunset Session Chairs: Yu-Ping Wang, Xiaohui Xie , and Dongxiao Zhu  DEMO 1: A Schema-Matching Tool for Alzheimer’s Disease Data Integration. Peeho Dewan, Naveen Ashish, and Arthur Toga, University of Southern California, Los Angeles, CA, USA  DEMO 2: The DOE Systems Biology Knowledgebase (KBase): Progress Towards a System for Collaborative and Reproducible Inference and Modeling of Biological Function. Robert Cottingham, Oak Ridge National Laboratory, Oak Ridge, TN, USA URL: <a href="http://kbase.us/">http://kbase.us/</a>	

**Monday September 22, 2014**

9:00-10:00	<p align="center">Keynote 2 (BI) Towards System Level Analysis of Tumor Heterogeneity. Teresa Przytycka, National Center for Biotechnology Information, National Institutes of Health Session Chair: Terry Gaasterland Location: Salon 1-5</p>	
10:00-10:30	<p align="center">Break</p>	
10:30-12:00	<p align="center">Paper Session II</p>	
	<p align="center">Session S3 (BI) Session Chair: Mark Borodovsky Location A: Salon 4 &amp; 5</p>	<p align="center">Session S4 (CTB) Session Chair: Jianlin Cheng Location B: Salon 1-3</p>
10:30-11:00	<p>FStitch: A fast and simple algorithm for detecting nascent RNA transcripts. Joseph Azofeifa, Mary Allen, Manuel Lladser, and Robin Dowell.</p>	<p>CNVnet: Combining Sparse Learning and Biological Networks to Capture Joint Effect of Copy Number Variants. Zhiyong Wang, Jinbo Xu, and Xinghua Shi.</p>
11:00-11:30	<p>InstantGenotype: A Non-parametric Model for Genotype Inference Using Microarray Probe Intensities. Chia-Yu Kao, Chen-Ping Fu, and Leonard McMillan.</p>	<p>Pathway Analysis with Signaling Hypergraphs. Anna Ritz and T. M. Murali.</p>
11:30-11:45	<p>Haplotype-Centered Mapping for Improved Alignments and Genetic Association Studies. Paul Bodily, Perry Ridge, Stanley Fujimoto, Quinn Snell, and Mark Clement.</p>	<p>Data-driven prediction of cancer cell fates with a non-linear model of signaling pathways. Fan Zhang, Chee Keong Kwoh, Min Wu, and Jie Zheng.</p>
11:45-12:00	<p>A Comparison of Combined P-value Methods for Gene Differential Expression Using RNA-Seq Data. Abdallah Eteleeb, Hunter Moseley, and Eric Rouchka.</p>	<p>Discovering Dysregulated Phenotype-Related Gene Patterns. Rami Alroobi and Saeed Salem.</p>
12:00-1:00	<p align="center">Lunch Location: Rose Garden</p>	<p align="center">Women in Bioinformatics Session Chair: May D. Wang Location B: Salon 1-3</p>
1:00-2:30	<p align="center">Paper Session III</p>	
	<p align="center">Session S5 (BI) Session Chair: Stefano Lonardi Location A: Salon 4 &amp; 5</p>	<p align="center">Session S6 (CTB) Session Chair: T.M. Murali Location B: Salon 1-3</p>
1:00-1:30	<p>Unconstrained Gene Tree Diameters for Deep Coalescence. Pawel Gorecki, Jaroslaw Paszek, and Oliver Eulenstein.</p>	<p>Improving identification of key players in aging via network de-noising. Boyoung Yoo, Huili Chen, Fazle Faisal, and Tijana Milenkovic.</p>
1:30-2:00	<p>Extracting phylogenetic signals from gene trees and its significance for species tree construction. Rasha Elhesha, Tamer Kahveci, Gordon Burleigh, and Ryan Cobb.</p>	<p>Integrated miRNA and mRNA Analysis of Time Series Microarray Data. Julian Dymacek and Nancy L. Guo.</p>
2:00-2:15	<p>Strand: Fast Sequence Comparison using MapReduce and Locality Sensitive Hashing. Jake Drew and Michael Hahsler.</p>	<p>Community Detection-based Features for Sequence Classification. Karthik Tangirala and Doina Caragea.</p>
2:15-2:30	<p>A Noise-Aware Method for Building Radiation Hybrid Maps. Raed Seetan, Anne Denton, Omar Al-Azzam, Ajay Kumar, M. Javed Iqbal, and Shahryar Kianian.</p>	<p>One Feature Doesn't Fit All: Characterizing Topological Features of Targets in Signaling Networks. Huey-Eng Chua, Sourav S Bhowmick, and Lisa Tucker-Kellogg.</p>
2:30-2:45	<p align="center">Break</p>	

2:45-4:15		Paper Session IV	
	Session S7 (BI) Session Chair: Filip Jagodzinski Location A: Salon 4 & 5	Session S8 (HI) Session Chair: Nurit Haspel Location B: Salon 1-3	
2:45-3:15	Fast Dendrogram-based OTU Clustering using Sequence Embedding. Thuy Diem Nguyen, Bertil Schmidt, and Chee Keong Kwoh.	A Novel Classification Method for Predicting Acute Hypotensive Episodes in Critical Care. Sakyajit Bhattacharya, Vaibhav Rajan, and Vijay Huddar.	
3:15-3:45	Learning Parameter Advisors for Multiple Sequence Alignment. Dan Deblasio and John Kececioglu.	icuARM-II: Improving the Reliability of Personalized Risk Prediction in Pediatric Intensive Care. Chih-Wen Cheng, Nikhil Chanani, Kevin Maher, and May D. Wang.	
3:45-4:00	COuplet Supertree by Equivalence Partitioning of taxa set and DAG formation. Sourya Bhattacharyya, and Jayanta Mukhopadhyay.	MotionTalk: Personalized home rehabilitation system for assisting patients with impaired mobility. Janani Venugopalan, Chih-Wen Cheng, and May Wang.	
4:00-4:15	Approximation Algorithms for Sorting by Signed Short Reversals. Gustavo Rodrigues Galvao and Zanoni Dias.	SideEffectPTM: An Unsupervised Topic Model to Mine Adverse Drug Reactions from Health Forums. Sheng Wang, Yanen Li, Duncan Ferguson, and Chengxiang Zhai.	
4:15-4:30	Break		
4:30-6:00		Paper Session V	
	Session S9 (BI) Session Chair: Brian Chen Location A: Salon 4 & 5	Session S10 (HI) Session Chair: Hongfang Liu Location B: Salon 1-3	
4:30-5:00	Scaled Sparse High Dimensional Tests for Localizing Sequence Variants. Shaolong Cao, Huaizhen Qin, Jian Li, Hong-Wen Deng, and Yu-Ping Wang.	SimConcept: A Hybrid Approach for Simplifying Composite Named Entities in Biomedicine. Chih-Hsuan Wei, Robert Leaman, and Zhiyong Lu.	
5:00-5:30	Prioritization of Genomic Locus Pairs for Testing Epistasis. Marzieh Ayati and Mehmet Koyuturk.	Joint Inference for End-to-End Coreference Resolution for Clinical Notes. Prateek Jindal, Dan Roth, and Carl A. Gunter.	
5:30-5:45	A Multiscale Hybrid Evolutionary Algorithm to Obtain Sample-based Representations of Multi-basin Protein Energy Landscapes. Rudy Clausen and Amarda Shehu.	Understanding User Intents in Online Health Forums. Thomas Zhang, Hyun Duk Cho, and Chengxiang Zhai.	
5:45-6:00	Constructing Burrows-Wheeler Transforms of Large String Collections via Merging. James Holt and Leonard Mcmillan.		
6:30-8:30	Banquet with best paper and best poster award Session Chairs: Wei Wang Location: Rose Garden		

**Tuesday September 23, 2014**

9:00-10:00	<p align="center">Keynote 3 (HI)  The Fractal-Like Architecture of the Learning Health System.  Leslie Lenert, Medical University of South Carolina  Session Chair: Bruce Schatz  Location: Salon 1-5</p>	
10:00-10:30	<p align="center">Break</p>	
10:30-12:00	<p align="center">Industrial Session 2  Session Chair: Bruce Schatz  Location: Salon 4-5</p> <p>Wearable Sensors: Moving from the Quantified Self to the Understood Self.  Steven Steinhubl  Director of Digital Health, Scripps Healthcare</p> <p>Rapid Learning Using Privacy-Preserving Distributed Data-Mining.  Balaji Krishnapuram  Director of Health Analytics, Siemens Healthcare</p>	<p align="center">Translational Bioinformatics Panel  Panel Chairs: Orly Alter and May D. Wang  Location: Salon 1-3</p> <p>Discovery of Principles of Nature from Matrix and Tensor Modeling of Large-Scale Molecular Biological Data.  Orly Alter, University of Utah</p> <p>Integrating Data from Discovery Research, Preclinical Studies and Clinical Trials.  Matthew J. Brauer, Genentech, Inc.</p> <p>Rank-Rank Hypergeometric Overlap (RRHO) Gene Expression Signature Comparison and the Benefits of Cross-Species Analysis.  Thomas G. Graeber, UCLA</p> <p>Comprehensive RNA-Seq Data Analysis Pipeline Investigation for Translational Genomics.  May D. Wang, Georgia Tech and Emory</p>
12:00-1:00	<p align="center">Lunch  Location: Seaview Terrace</p>	<p align="center">PhD Forum  Location: Cardiff, Del Mar, Laguna, &amp; Sunset Room held in the poster room—continues until 3 PM  Session Chair: Jean Gao</p>
1:00-2:30	<p align="center">Paper Session VI</p>	
	<p align="center">Session S11 (HI)  Session Chair: ChengXiang Zhai  Location A: Salon 4 &amp; 5</p>	<p align="center">Session S12 (CTB)  Session Chair: Xiaohui Xie  Location B: Salon 1-3</p>
1:00-1:30	<p>Towards a Natural Walking Monitor for Pulmonary Patients using Simple Smart Phones.  Joshua Juen, Qian Cheng, and Bruce Schatz.</p>	<p>Docking Features for Predicting Binding Loss due to Protein Mutation.  Norman Goodacre, Dr. Nathan Edwards, Dr. Mark Danielsen, Dr. Peter Uetz, and Dr. Cathy Wu.</p>
1:30-1:45	<p>Using Mobile Phones to simulate Pulse Oximeters: Gait Analysis predicts Oxygen Saturation  Qian Cheng, Joshua Juen, and Bruce Schatz.</p>	<p>Leveraging Hierarchy in Medical Codes for Predictive Modeling.  Anima Singh, Girish Nadkarni, John Guttag, and Erwin Bottinger.</p>
1:45-2:00	<p>Are We There Yet? Feasibility of Continuous Stress Assessment via Physiological Sensors in Field  Md. Mahbubur Rahman, Rummana Bari, Amin Ahsan Ali, Moushumi Sharmin, Andrew Raij, Karen Hovsepian, Syed Monowar Hossain, Emre Ertin, Ashley Kennedy, David H. Epstein, Michelle Jobes, Kenzie L. Preston, J. Gayle Beck, Satish Kedia, Kenneth D. Ward, Mustafa Al'Absi, and Santosh Kumar.</p>	

2:00-2:15	Conditional Random Fields for Morphological Analysis of Wireless ECG Signals. Annamalai Natarajan, Edward Gaiser, Gustavo Angarita, Robert Malison, Deepak Ganesan, and Benjamin Marlin.	A Flexible Volumetric Comparison of Protein Cavities can Reveal Patterns in Ligand Binding Specificity. Ziyi Guo, Trevor Kuhlengel, Steven Stinson, Seth Blumenthal, Soutir Bandyopadhyay, and Brian Chen.
2:15-2:30		Knowledge-based Search and Multi-objective Filters: Proposed Structural Models of GPCR Dimerization. Irina Hashmi, Daniel Veltri, Nadine Kabbani, and Amarda Shehu.
2:30-3:00	Break	
3:00-4:30	Paper Session VII	
	Session S13 (HI) Session Chair: Bruce Schatz Location A: Salon 4 & 5	Session S14 (CTB) Session Chair: Pierangelo Veltri Location B: Salon 1-3
3:00-3:30	Resolving Healthcare Forum Posts via Similar Thread Retrieval. Hyun Duk Cho, Parikshit Sondhi, Chengxiang Zhai, and Bruce Schatz.	Analysing the distribution of synaptic vesicles using a spatial point process model. Mahdieh Khanmohammadi, Rasmus Waagepetersen, Nicoletta Nava, Jens Nyengaard, and Jon Sparring.
3:30-4:00	Automating Risk of Bias Assessment for Clinical Trials. Iain Marshall, Joël Kuiper, and Byron Wallace.	Automated Ranking of Stem Cell Colonies By Translating Biological Rules to Computational Models. Adele Peskin, Steve Lund, Ya-Shian Li-Baboud, Michael Halter, Anne Plant, and Peter Bajcsy.
4:00-4:15	Modeling climate-dependent population dynamics of mosquito to guide public health policies. Aditya Vaidya, Angel Bravo-Salgado, and Armin Mikler.	Utilizing twilight zone sequence similarities to increase the accuracy of protein 3D structure comparison. Aleksandar Poleksic, and Paul Gray.
4:15-4:30	A Method for Reducing the Severity of Epidemics by Allocating Vaccines According to Centrality. Krzysztof Drewniak, Joseph Helsing, and Armin Mikler.	Challenges in Adapting Text Mining for Full text Articles to Assist Pathway Curation. Ravikumar Komandur Elayavilli, Kavishwar Wagholikar, and Hongfang Liu.