Pacific Symposium on Biocomputing (PSB) 2016 Schedule

January 4-8, 2016, Big Island of Hawaii

Sunday, January 3, 2016

Registration

4:00-5:30pm	Registration	Ballroom Prefunction

Monday, January 4, 2016

Registration

7:30-9:30am	Registration	Ballroom Prefunction
12:00-2:00pm	Registration	Ballroom Prefunction
6:00-7:30pm	Registration	Kilohana Room

Workshops

9:00-12:00	Translational Bioinformatics 101 Speakers: Jessica Tenenbaum, Lewis Frey, Robert Freimuth, Subha Madhavan, Joshua Denny	Salon 2&3
9:00-12:00	Computational Approaches to Study Microbes and Microbiomes Speakers: Susan Holmes, Igor Zhulin Jouline, Tandy Warnow, Chad Myers, Yana Bromberg, Casey Greene, Fiona Brinkman, Wes Viles, Dan Knights, Serghei Mangul, James Foster, Nam-phuong Nguyen	Plaza

Break

12:00-1:30	Lunch on own

Workshop

1:30-4:30	Use of Genome Data in Newborns as a Starting Point for Life-Long Precision Medicine 1:30 Introduction and welcome 1:40 Robert Nussbaum, *Newborn screening and genome sequencing* 2:10 Stephen Kingsmore, *Integrating deep phenotyping and genome sequencing to enable precision medicine in neonatal intensive care units* 3:00 Jennifer Puck, *Using newborn dried blood spots to obtain deep sequence data for enhanced, early diagnosis* 3:30 Steven E. Brenner, *Analysis challenges of newborn genome sequences* 4:00 Sean Mooney, *Understanding the complex genetics of simple Mendelian traits*	Salon 2&3
1:30-4:30	Biomedical Applications of Topology and Abstract Algebras Speakers: Eric Neumann, Svetlana Lockwood	Plaza

Break

4:30-7:30	Dinner on own

Reception

		Kilohana
7:30-8:30pm	21st Anniversary Reception with Drinks and Desserts	

Tuesday, January 5, 2016

Registration		
7:30-9:00	Registration	Ballroom Prefunction
10:30-11:30	Registration	Ballroom Prefunction
1:00-2:00	Registration	Ballroom Prefunction
Breakfast		Ballroom Courtyard
7:30-8:30	PSB Breakfast	
Welcome		Salon 2&3
8:30-8:40	Welcome	
Session 1:	Innovative Approaches to Combining Genotype, Phenotype, Epigenetic, and Exposure Data for Precision Diagnostics	Salon 2&3
8:40-8:50	Introduction Melissa Haendel, Nicole Washington, Maricel Kann	
8:50-9:10	Invited Talk: Elissa Chesler *GeneWeaver: Finding relations among genes, phenotypes, and diseases from heterogeneous functional genomics data* Functional genomic studies of disease now encompass several decades of research resulting in a large volume of diverse associations of genes and their relations to the biological concepts reflected in experimental paradigms, diagnostic criteria and other disease related parameters. The GeneWeaver system is a platform for harmonizing and integrating the resulting gene lists, gene networks and descriptive meta-content to enable data-driven discovery of relations among experimental constructs and disease through user guided interrogation backed by powerful, efficient graph algorithms and dynamic visualization of results. Through this system, users can find convergent evidence from multiple species and experimental paradigms of a role for genes in disease related processes, align individual gene centric data sets to the database of known genomic data, identify model organism phenotypes and specific models that map onto various facets of human disease, and classify diseases and assays based on their intrinsic biological similarity rather than on extrinsic characteristics.	
9:10-9:25	*Discovering Patient Phenotypes Using Generalized Low Rank Models* Alejandro Schuler, Vincent Liu, Joe Wan, Alison Callahan, Madeleine Udell, David E. Stark, Nigam H. Shah	
9:25-9:40	*Diagnosis-Guided Method for Identifying Multi-Modality Neuroimaging Biomarkers Associated with Genetic Risk Factors in Alzheimer's Disease* Xiaoke Hao, Jingwen Yan, Xiaohui Yao, Shannon L. Risacher, Andrew J. Saykin, Daoqiang Zhang, Li Shen, for the ADNI	
9:40-9:55	*Metabolomics Differential Correlation Network Analysis of Osteoarthritis* Ting Hu, Weidong Zhang, Zhaozhi Fan, Guang Sun, Sergei Likhodi, Edward Randell, Guangju Zhai	
9:55-10:10	*Integrating Clinical Laboratory Measures and ICD-9 Code Diagnoses in Phenome-Wide Association Studies* Anurag Verma, Joseph B. Leader, Shefali S. Verma, Alex Frase, John	

Tuesday, January 5, 2016 (con't)

	Wallace, Scott Dudek, Daniel R. Lavage, Cristopher V. Van Hout, Frederick E. Dewey, John Penn, Alex Lopez, John D. Overton, David J. Carey, David H. Ledbetter, H. Lester Kirchner, Marylyn D. Ritchie, Sarah A. Pendergrass	
10:10-10:25	*Investigating the Importance of Anatomical Homology for Cross-Species Phenotype Comparisons Using Semantic Similarity* Prashanti Manda, Christopher J. Mungall, James P. Balhoff, Hilmar Lapp, Todd J. Vision	
Break		
10:25-10:50		
Keynote		Salon 2&3
10:50-12:00	*Creating a Gene X Phenome Catalog through Integration of Genome,Transcriptome, and EHR Data* Nancy Cox, with introduction by Russ Altman	
Lunch		Ballroom Courtyard
12:00-1:15	PSB Hosted Lunch	
Session 2:	Discovery of Molecularly Targeted Therapies	Salon 2&3
1:30-1:40	Introduction Philip R.O. Payne, Kun Huang, Nigam Shah	
1:40-2:00	Invited Talk: Scott Kahn *Balancing Short Term Dx with Longer Term Knowledge Creation* Paradoxically it seems as though the immediate needs to diagnose and treat a patient using genomic information can be at the expense of any longer term effort to aggregate such patient data for subsequent analysis and knowledge creation. This presentation will offer a different perspective that relies upon an open architecture in which patient reporting, cohort aggregation and analysis, and an extensible knowledgebase are all integrated with one another, and ultimately integrated within a healthcare organization's information infrastructure.	
2:00-2:15	*Collective Pairwise Classification for Multi-Way Analysis of Disease and Drug Data* Marinka Zitnik, Blaz Zupan	
2:15-2:30	*Computing Therapy for Precision Medicine: Collaborative Filtering Integrates and Predicts Multi-entity Interactions* Sam Regenbogen, Angela D. Wilkins, Olivier Lichtarge	
2:30-2:45	*An Integrated Network Approach to Identifying Biological Pathways and Environmental Exposure Interactions in Complex Diseases* Christian Darabos, Jingya Qiu, Jason H. Moore	
2:45-3:00	*Integrating Genetic and Structural Data on Human Protein Kinome in Network-Based Modeling of Kinase Sensitivities and Resistance to Targeted and Personalized Anticancer Drugs* Gennady M. Verkhivker	

Tuesday, January 5, 2016 (con't)

3:00-3:15	*A Framework for Attribute-Based Community Detection with Applications to Integrated Functional Genomics* Han Yu, Rachael Hageman Blair
Discussion Sessions	
3:15-4:15	Discovery of Molecularly Targeted Therapies
4:15-5:15	Innovative Approaches to Combining Genotype, Phenotype, Epigenetic, and Exposure Data for Precision Diagnostics
Break	
5:30	Dinner on own

Wednesday, January 6, 2016

Registration

7:30-8:30 Registration — Ballroom Prefunction

Breakfast — Ballroom Courtyard

7:30-8:30 PSB Breakfast

Announcements — Salon 2&3

8:30-8:40 Morning Announcements –

Session 3: Precision Medicine: Data and Discovery for Improved Health and Therapy — Salon 2&3

8:40-8:45 Introduction
Bruce Aronow, Steven Brenner, Sean Mooney, Alexander Morgan

8:45-9:20 Invited Talk: Jennifer Doudna
CRISPR Biology: A New Era in Genome Engineering
The advent of facile genome engineering using the bacterial RNA-guided CRISPR-Cas9 system in animals and plants is transforming biology. I will present a brief history of CRISPR biology from its initial discovery through the elucidation of the CRISPR-Cas9 enzyme mechanism, providing the foundation for remarkable developments using this technology to modify, regulate or visualize genomic loci in a wide variety of cells and organisms. These results highlight a new era in which genomic manipulation is no longer a bottleneck to experiments, paving the way to both fundamental discoveries in biology, with applications in all branches of biotechnology, and strategies for human therapeutics. Recent results regarding the molecular mechanism of Cas9 and its use for targeted cell-based therapies will be discussed.

9:20-9:35 *Multitask Feature Selection with Task Descriptors*
Victor Bellon, Veronique Stoven, Chloe-Agathe Azencott

9:35-9:50 *Knowledge Driven Binning and PheWAS Analysis in Marshfield Personalized Medicine Research Project Using BioBin*
Anna O. Basile, John R. Wallace, Peggy Peissig, Catherine A. McCarty, Murray Brilliant, Marylyn D. Ritchie

9:50-10:05 *Biofilter as a Functional Annotation Pipeline for Common and Rare Copy Number Burden*
Dokyoon Kim, Anastasia Lucas, Joseph Glessner, Shefali S. Verma, Yuki Bradford, Ruowang Li, Alex T. Frase, Hakon Hakonarson, Peggy Peissig, Murray Brilliant, Marylyn D. Ritchie

10:05-10:20 *Separating the Causes and Consequences in Disease Transcriptome*
Yong Fuga Li, Fuxiao Xin, and Russ B. Altman

10:20-10:35 *The Challenges in Using Electronic Health Records for Pharmacogenomics and Precision Medicine Research*
Sarah M. Laper, Nicole A. Restrepo, Dana C. Crawford

10:35-10:50 *Kidney Disease Genetics and the Importance of Diversity in Precision Medicine*
Jessica N. Cooke Bailey, Sarah Wilson, Kristin Brown-Gentry, Robert Goodloe, Dana C. Crawford

Wednesday, January 6, 2016 (con't)

Break

10:50-11:00

11:00-11:15	*Personalized Hypothesis Tests for Detecting Medication Response in Parkinson Disease Patients Using iPhone Sensor Data* Elias Chaibub Neto, Brian M. Bot, Thanneer Perumal, Larsson Omberg, Justin Guinney, Mike Kellen, Arno Klein, Stephen H. Friend, Andrew D. Trister
11:15-11:30	*PRISM: A Data-Driven Platform for Monitoring Mental Health* Maulik R. Kamdar, Michelle J. Wu
11:30-11:45	*Patient-Specific Data Fusion for Cancer Stratification and Personalised Treatment* Vladimir Gligorijevic, Noel Malod-Dognin, Natasa Przulj
11:45-12:00	*Bayesian Biclustering for Patient Stratification* Sahand Khakabimamaghani, Martin Ester
12:00-12:15	*Predicting Significance of Unknown Variants in Glial Tumors Through Sub-Class Enrichment* Alex M. Fichtenholtz, Nicholas D. Camarda, Eric K. Neumann
12:15-12:30	*One-Class Detection of Cell States in Tumor Subtypes* Artem Sokolov, Evan O. Paull, Joshua M. Stuart

Poster Session Lunch — Salon 1 and Ballroom Courtyard

12:30-2:30	Poster Session with Lunch (Posters on ODD numbered boards presented from 12:30-1:30) (Posters on EVEN numbered boards presented from 1:30-2:30)

Discussion Session — Salon 2&3

2:30-3:30	Precision Medicine: Data and Discovery for Improved Health and Therapy

ISCB Open Meeting — Salon 2&3

3:45-4:15	ISCB Open Meeting

Break

4:15 –	Dinner and evening on own

Thursday, January 7, 2016

Breakfast		Ballroom Courtyard
7:30-8:30	PSB Breakfast	
Announcements		Salon 2&3
8:30-8:40	Morning Announcements	
Session 4:	Social Media Mining for Public Health Monitoring and Surveillance	Salon 2&3
8:40-8:50	Introduction Graciela Gonzalez, Matthew Scotch, Karen Smith, John Brownstein, Abeed Sarker, Michael Paul, Azadeh Nikfarjam	
8:50-9:10	Invited Speaker: Abeed Sarker *Social media mining for pharmacovigilance-- challenges and progress* Social media is increasingly being used for public health monitoring tasks and the trend is likely to continue because of the rapid growth of data in this domain. This talk will focus on the DIEGO lab's efforts on social media mining for pharmacovigilance, and how the techniques and lessons learned can be used for performing related public health monitoring tasks from social media.	
9:10-9:25	*Towards Early Discovery of Salient Health Threats: A Social Media Emotion Classification Technique* Bahadorreza Ofoghi, Meghan Mann, Karin Verspoor	
9:25-9:40	*Monitoring Potential Drug Interactions and Reactions via Network Analysis of Instagram User Timelines* Rion Brattig Correia, Lang Li, Luis M. Rocha	
9:40-9:55	*Text Classification for Automatic Detection of E-Cigarette Use and Use for Smoking Cessation from Twitter: A Feasibility Pilot* Yin Aphinyanaphongs, Armine Lulejian, Duncan Penfold Brown, Richard Bonneau, Paul Krebs	
9:55-10:10	*Insights from Machine-Learned Diet Success Prediction* Ingmar Weber, Palakorn Achananuparp	
10:10-10:25	*Predicting Individual Well-Being Through the Language of Social Media* H. Andrew Schwartz, Maarten Sap, Margaret L. Kern, Johannes C. Eichstaedt, Adam Kapelner, Megha Agrawal, Eduardo Blanco, Lukasz Dziurzynski, Gregory Park, David Stillwell, Michal Kosinski, Martin E.P. Seligman, Lyle H. Ungar	
10:25-10:40	*Finding Potentially Unsafe Nutritional Supplements from User Reviews with Topic Modeling* Ryan Sullivan, Abeed Sarker, Karen O'Connor, Amanda Goodin, Mark Karlsrud, Graciela Gonzalez	
Discussion Sessions		Salon 2&3
10:40-11:40	Social Media Mining for Public Health Monitoring and Surveillance	
11:45-12:45	Regulatory RNA	
Break		
12:45-2:00	Lunch on Own	

Thursday, January 7, 2016 (con't)

NIH Open Meeting — Salon 2&3

2:00-3:30 NIH Meeting, moderated by Larry Hunter

Introduction to NLM Career Development Awards and Research Grants in Biomedical Informatics

Jane Ye, Program Officer, Division of Extramural Programs, NLM, NIH

Funding Computational Research at NIGMS, and the New MIRA Program

Rochelle Long, Acting Director, PPBC Division, NIGMS, NIH

A SWOT Analysis of Big Data @ the NIH

Philip E. Bourne, Associate Director for Data Science, National Institutes of Health

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Break

3:30-5:30

Dinner — Coconut Grove

5:30-7:30 Dinner Party

Keynote: — Salon 2&3

7:30-8:45 *Public Health Information in Social Networks*

Winter Mason, with introduction by Marylyn Ritchie

Please wear your PSB name tag and lanyard for admission to all events and hosted meals.

Friday, January 8, 2016

Breakfast		Ballroom Courtyard
7:30-8:30	Breakfast	
Closing		Salon 2&3
8:30-8:40	Closing Announcements	
Session 7:	Methods to Enhance the Reproducibility of Precision Medicine	Salon 2&3
8:40-8:50	Introduction Arjun Manrai, Chirag Patel, Nils Gehlenborg, Nicholas Tatonetti, John Ioannidis, Isaac Kohane	
8:50-9:05	*Dynamically Evolving Clinical Practices and Implications for Predicting Medical Decisions* Jonathan H. Chen, Mary K. Goldstein, Steven M. Asch, Russ B. Altman	
9:05-9:20	*Identification of Questionable Exclusion Criteria in Mental Disorder Clinical Trials Using a Medical Encyclopedia* Handong Ma, Chunhua Weng	
9:20-9:35	*Repurposing Germline Exomes of the Cancer Genome Atlas Demands a Cautious Approach and Sample-Specific Variant Filtering* Amanda Koire, Panagiotis Katsonis, Olivier Lichtarge	
9:35-9:50	*Reproducible Research Workflow in R for the Analysis of Personalized Human Microbiome Data* Benjamin Callahan, Diana Proctor, David Relman, Julia Fukuyama, Susan Holmes	
9:50-10:05	*Reproducible and Shareable Quantifications of Pathogenicity* Arjun K. Manrai, Brice L. Wang, Chirag J. Patel, Isaac S. Kohane	
Discussion Session		Salon 2&3
10:05-11:05	Methods to Enhance the Reproducibility of Precision Medicine	
Break		
11:05-12:30	Lunch on own	
Workshop		Salon 2&3
12:30-3:30	Social Media Mining Shared Task Workshop This workshop was designed to act as a platform for the application of state-of-the-art natural language processing systems on social media data. Using the DIEGO Lab Adverse Drug Reaction Twitter corpus, we prepared a shared task focusing on text classification and information extraction. Eleven teams participated in the shared task and several teams will be presenting their systems at the workshop. This workshop complements the Social Media Mining for Public Health Monitoring and Surveillance session.	

PSB over--see you next year!