

Preface.....	vii
--------------	-----

COMPUTATIONAL APPROACHES TO UNDERSTANDING THE EVOLUTION OF MOLECULAR FUNCTION

<i>Session Introduction.....</i>	1
Yana Bromberg, Matthew W. Hahn, Predrag Radivojac	
<i>Identification and Analysis of Bacterial Genomic Metabolic Signatures.....</i>	3
Nathan Bowerman, Nathan Tintle, Matthew DeJongh, Aaron A. Best	
<i>When should we NOT transfer functional annotation between sequence paralogs?</i>	15
Mengfei Cao, Lenore J. Cowen	
<i>ProSNet: integrating homology with molecular networks for protein function prediction.....</i>	27
Sheng Wang, Meng Qu, Jian Peng	
<i>On the power and limits of sequence similarity based clustering of proteins into families</i>	39
Christian Wiwie, Richard Röttger	

IMAGING GENOMICS

<i>Session Introduction.....</i>	51
Li Shen, Lee A.D. Cooper	
<i>Adaptive testing of SNP-brain functional connectivity association via a modular network analysis</i>	58
Chen Gao, Junghi Kim, Wei Pan	
<i>Exploring Brain Transcriptomic Patterns: A Topological Analysis Using Spatial Expression Networks..</i>	70
Zhana Kuncheva, Michelle L. Krishnan, Giovanni Montana	
<i>Integrative Analysis for Lung Adenocarcinoma Predicts Morphological Features Associated with Genetic Variations.....</i>	82
Chao Wang, Hai Su, Lin Yang, Kun Huang	
<i>Identification of Discriminative Imaging Proteomics Associations in Alzheimer's Disease via a Novel Sparse Correlation Model.....</i>	94
Jingwen Yan, Shannon L. Risacher, Kwangsik Nho, Andrew J. Saykin, Li Shen	
<i>Enforcing Co-expression in Multimodal Regression Framework</i>	105
Pascal Zille, Vince D. Calhoun, Yu-Ping Wang	

METHODS TO ENSURE THE REPRODUCIBILITY OF BIOMEDICAL RESEARCH

<i>Session Introduction.....</i>	117
Konrad J. Karczewski, Nicholas P. Tatonetti, Chirag J. Patel, Arjun K. Manrai, C. Titus Brown, John P.A. Ioannidis	
<i>Exploring the Reproducibility of Probabilistic Causal Molecular Network Models</i>	120

Ariella Cohain, Aparna A. Divaraniya, Kuixi Zhu, Joseph R. Scarpa, Andrew Kasarskis, Jun Zhu, Rui Chang, Joel T. Dudley, Eric E. Schadt

Reproducible Drug Repurposing: When Similarity Does Not Suffice 132
Emre Guney

Empowering Multi-Cohort Gene Expression Analysis to Increase Reproducibility 144
Winston A. Haynes, Francesco Vallania, Charles Liu, Erika Bongen, Aurelie Tomczak, Marta Andres-Terrè, Shane Lofgren, Andrew Tam, Cole A. Deisseroth, Matthew D. Li, Timothy E. Sweeney, and Purvesh Khatri

Rabix: An Open-Source Workflow Executor Supporting Recomputability and Interoperability of Workflow Descriptions 154
Gaurav Kaushik, Sinisa Ivkovic, Janko Simonovic, Nebojsa Tijanic, Brandi Davis-Dusenberry, Deniz Kural

Data Sharing and Reproducible Clinical Genetic Testing: Successes and Challenges 166
Shan Yang, Melissa Cline, Can Zhang, Benedict Paten and Stephen E. Lincoln

PATTERNS IN BIOMEDICAL DATA-HOW DO WE FIND THEM?

Session Introduction 177
Anna Okula Basile, Anurag Verma, Marta Byrska-Bishop, Sarah P. Pendergrass, Christian Darabos, H. Lester Kirchner

Learning Attributes of Disease Progression from Trajectories of Sparse Lab Values 184
Vibhu Agarwal, Nigam H. Shah

Computer Aided Image Segmentation and Classification for Viable and Non-Viable Tumor Identification in Osteosarcoma 195
Harish Babu Arunachalam, Rashika Mishra, Bogdan Armaselu, Ovidiu Daescu, Maria Martinez, Patrick Leavey, Dinesh Rakheja, Kevin Cederberg, Anita Sengupta, Molly Ni'sulleabhain

Missing Data Imputation in the Electronic Health Record Using Deeply Learned Autoencoders 207
Brett K. Beaulieu-Jones, Jason H. Moore, The Pooled Resource Open-Access ALS Clinical Trials Consortium

A Deep Learning Approach for Cancer Detection and Relevant Gene Identification 219
Padideh Danaee, Reza Ghaeini, David Hendrix

Development and Performance of Text-Mining Algorithms to Extract Socioeconomic Status from De-Identified Electronic Health Records 230
Brittany M. Hollister, Nicole A. Restrepo, Eric Farber-Eger, Dana C. Crawford, Melinda C. Aldrich, Amy Non

Genome-Wide Interaction with Selected Type 2 Diabetes Loci Reveals Novel Loci for Type 2 Diabetes in African Americans 242
Jacob M. Keaton, Jacklyn N. Hellwege, Maggie C. Y. Ng, Nicholette D. Palmer, James S. Pankow, Myriam Fornage, James G. Wilson, Adolfo Correa, Laura J. Rasmussen-Torvik, Jerome

I. Rotter, Yii-Der I. Chen, Kent D. Taylor, Stephen S. Rich, Lynne E. Wagenknecht, Barry I. Freedman, Donald W. Bowden

<i>Deep Motif Dashboard: Visualizing and Understanding Genomic Sequences Using Deep Neural Networks</i>	254
Jack Lanchantin, Ritambhara Singh, Beilun Wang, Yanjun Qi	
<i>Meta-Analysis of Continuous Phenotypes Identifies a Gene Signature that Correlates with COPD Disease Status</i>	266
Madeleine Scott, Francesco Vallania, and Purvesh Khatri	
<i>Predictive Modeling of Hospital Readmission Rates Using Electronic Medical Record-Wide Machine Learning: A Case-Study Using Mount Sinai Heart Failure Cohort</i>	276
Khader Shameer, Kipp W. Johnson, Alexandre Yahi, Riccardo Miotto, Li Li, Doran Ricks, Jebakumar Jebakaran, Patricia Kovatch, Partho P. Sengupta, Annette Gelijns, Alan Moskovitz, Bruce Darrow, David L. Reich, Andrew Kasarskis, Nicholas P. Tatonetti, Sean Pinney, Joel T. Dudley	
<i>Learning Parsimonious Ensembles for Unbalanced Computational Genomics Problems</i>	288
Ana Stanescu, Gaurav Pandey	
<i>Methods for Clustering Time Series Data Acquired from Mobile Health Apps</i>	300
Nicole Tignor, Pei Wang, Nicholas Genes, Linda Rogers, Steven G. Hershman, Erick R. Scott, Micol Zweig, Yu-Feng Yvonne Chan, Eric E. Schadt	
<i>A New Relevance Estimator for the Compilation and Visualization of Disease Patterns and Potential Drug Targets</i>	312
Modest von Korff, Tobias Fink, Thomas Sander	
<i>Network Map of Adverse Health Effects Among Victims of Intimate Partner Violence</i>	324
Kathleen Whiting, Larry Y. Liu, Mehmet Koyuturk, Gunnur Karakurt	
<i>Discovery of Functional and Disease Pathways by Community Detection in Protein-Protein Interaction Networks</i>	336
Stephen J. Wilson, Angela D. Wilkins, Chih-Hsu Lin, Rhonald C. Lua, Olivier Lichtarge	
PRECISION MEDICINE: DATA AND DISCOVERY FOR IMPROVED HEALTH AND THERAPY	
<i>Session Introduction</i>	348
Alexander A. Morgan, Dana C. Crawford, Josh C. Denny, Sean D. Mooney, Bruce J. Aronow, Steven E. Brenner	
<i>Opening the Door to the Large Scale Use of Clinical Lab Measures for Association Testing: Exploring Different Methods for Defining Phenotypes</i>	356
Christopher R. Bauer, Daniel Lavage, John Snyder, Joseph Leader, J. Matthew Mahoney, Sarah A. Pendergrass	
<i>A Powerful Method for Including Genotype Uncertainty in Tests of Hardy-Weinberg Equilibrium</i>	368

Andrew Beck, Alexander Luedtke, Keli Liu, Nathan Tintle

<i>Temporal Order of Disease Pairs Affects Subsequent Disease Trajectories: The Case of Diabetes and Sleep Apnea.....</i>	380
Mette Beck, David Westergaard, Leif Groop and Soren Brunak	
<i>MicroRNA-Augmented Pathways (mirAP) and Their Applications to Pathway Analysis and Disease Subtyping.....</i>	390
Diana Diaz, Michele Donato, Tin Nguyen, Sorin Draghici	
<i>Frequent Subgraph Mining of Personalized Signaling Pathway Networks Groups Patients with Frequently Dysregulated Disease Pathways and Predicts Prognosis.....</i>	402
Arda Durmaz, Tim A.D. Henderson, Douglas Brubaker, Gurkan Bebek	
<i>Human Kinases Display Mutational Hotspots at Cognate Positions Within Cancer.....</i>	414
Jonathan Gallion, Angela D. Wilkins, Olivier Lichtarge	
<i>MUSE: A Multi-locus Sampling-based Epistasis Algorithm for Quantitative Genetic Trait Prediction.....</i>	426
Dan He, Laxmi Parida	
<i>ceRNA Search Method Identified a MET-activated Subgroup Among EGFR DNA Amplified Lung Adenocarcinoma Patients.....</i>	438
Halla Kabat, Leo Tunkle, Inhan Lee	
<i>Improved Performance of Gene Set Analysis on Genome-Wide Transcriptomics Data when Using Gene Activity State Estimates.....</i>	449
Thomas Kamp, Micah Adams, Craig Disselkoen, Nathan Tintle	
<i>methylDMV: Simultaneous Detection of Differential DNA Methylation and Variability with Confounder Adjustment.....</i>	461
Pei Fen Kuan, Junyan Song, Shuyao He	
<i>Identify Cancer Driver Genes Through Shared Mendelian Disease Pathogenic Variants and Cancer Somatic Mutations</i>	473
Meng Ma, Changchang Wang, Benjamin Glicksberg, Eric Schadt, Shuyu D. Li, Rong Chen	
<i>Identifying Cancer Specific Metabolic Signatures Using Constraint-Based Models.....</i>	485
André Schultz, Sanket Mehta, Chenyue W. Hu, Fieke W Hoff, Terzah M. Horton, Steven M. Kornblau, Amina A. Qutub	
<i>Differential Pathway Dependency Discovery Associated with Drug Response across Cancer Cell Lines</i>	497
Gil Speyer, Divya Mahendra, Hai J. Tran, Jeff Kiefer, Stuart L. Schreiber, Paul A. Clemons, Harshil Dhruv, Michael Berens, Seungchan Kim	
<i>A Methylation-to-Expression Feature Model for Generating Accurate Prognostic Risk Scores and Identifying Disease Targets in Clear Cell Kidney Cancer</i>	509
Jeffrey A. Thompson, Carmen J. Marsit	
<i>De Novo Mutations in Autism Implicate the Synaptic Elimination Network</i>	521

Guhan Ram Venkataraman, Chloe O'Connell, Fumiko Egawa, Dorna Kashef-Haghghi, Dennis Paul Wall

<i>Identifying Genetic Associations with Variability in Metabolic Health and Blood Count Laboratory Values: Diving into the Quantitative Traits by Leveraging Longitudinal Data from an EHR</i>	533
Shefali S. Verma, Anastasia M. Lucas, Daniel R. Lavage, Joseph B. Leader, Raghu Metpally, Sarathbabu Krishnamurthy, Frederick Dewey, Ingrid Borecki, Alexander Lopez, John Overton, John Penn, Jeffrey Reid, Sarah A. Pendergrass, Gerda Breitwieser, Marylyn D. Ritchie	
<i>Strategies for Equitable Pharmacogenomic-Guided Warfarin Dosing Among European and African American Individuals in a Clinical Population</i>	545
Laura Wiley, Jacob VanHouten, David Samuels, Melinda Aldrich, Dan Roden, Josh Peterson, Joshua Denny	

SINGLE-CELL ANALYSIS AND MODELLING OF CELL POPULATION HETEROGENEITY

<i>Session Introduction</i>	557
Nikolay Samusik, Nima Aghaeepour, Sean Bendall	
<i>Production of a Preliminary Quality Control Pipeline for Single Nuclei RNA-Seq and Its Application in the Analysis of Cell Type Diversity of Post-Mortem Human Brain Neocortex</i>	564
Brian Aevermann, Jamison McCorrison, Pratap Venepally, Rebecca Hodge, Trygve Bakken, Jeremy Miller, Mark Novotny, Danny N. Tran, Francisco Diez-Fuertes, Lena Christiansen, Fan Zhang, Frank Steemers, Roger S. Lasken, Ed Lein, Nicholas Schork, Richard H. Scheuermann	
<i>Tracing Co-Regulatory Network Dynamics in Noisy, Single-Cell Transcriptome Trajectories</i>	576
Pablo Cordero, Joshua M. Stuart	
<i>An Updated Debarcode Tool for Mass Cytometry with Cell Type-Specific and Cell Sample-Specific Stringency Adjustment</i>	588
Kristin I. Fread, William D. Strickland, Garry P. Nolan, Eli R. Zunder	
<i>Mapping Neuronal Cell Types Using Integrative Multi-Species Modeling of Human and Mouse Single Cell RNA Sequencing</i>	599
Travis Johnson, Zachary Abrams, Yan Zhang, Kun Huang	

<i>A Spatiotemporal Model to Simulate Chemotherapy Regimens for Heterogeneous Bladder Cancer Metastases to the Lung</i>	611
Kimberly R. Kanigel Winner, James C. Costello	

<i>Scalable Visualization for High-dimensional Single-cell Data</i>	623
Juho Kim, Nate Russell, Jian Peng	

WORKSHOPS

<i>Harnessing Big Data for Precision Medicine: Infrastructures and Applications</i>	635
Kun-Hsing Yu, Steven N. Hart, Rachel Goldfeder, Qiangfeng Cliff Zhang, Stephen C. J. Parker, Michael Snyder	

<i>The Training of Next Generation Data Scientists in Biomedicine</i>	640
Lana Garmire, Stephen Gliske, Quynh C Nguyen, Jonathan H. Chen, Shamim Nemati, John D. Van Horn, Jason H. Moore, Carol Shreffler, Michelle Dunn	
<i>No-Boundary Thinking in Bioinformatics</i>	646
Jason H. Moore, Steven F. Jennings, Casey S. Greene, Lawrence E. Hunter, Andy D. Perkins, Clarlynda Williams-Devane, Donald C. Wunsch, Zhongming Zhao, Xiuzhen Huang	
<i>Open Data for Discovery Science</i>	649
Philip R.O. Payne, Kun Huang, Nigam H. Shah, Jessica Tenenbaum	