

Preface..... vii

ARTIFICIAL INTELLIGENCE FOR ENHANCING CLINICAL MEDICINE

<i>Session Introduction: Artificial Intelligence for Enhancing Clinical Medicine</i>	1
Roxana Daneshjou, Lukasz Kidzinski, Olga Afanasiev, Jonathan H. Chen	
<i>Predicting Longitudinal Outcomes of Alzheimer's Disease via a Tensor-Based Joint Classification and Regression Model</i>	7
Lodewijk Brand, Kai Nichols, Hua Wang, Heng Huang, Li Shen, for the ADNI	
<i>Robustly Extracting Medical Knowledge from EHRs: A Case Study of Learning a Health Knowledge Graph</i>	19
Irene Y. Chen, Monica Agrawal, Steven Horng, David Sontag	
<i>Increasing Clinical Trial Accrual via Automated Matching of Biomarker Criteria</i>	31
Jessica W. Chen, Christian A. Kunder, Nam Bui, James L. Zehnder, Helio A. Costa, Henning Stehr	
<i>Addressing the Credit Assignment Problem in Treatment Outcome Prediction Using Temporal Difference Learning</i>	43
Sahar Harati, Andrea Crowell, Helen Mayberg, Shamim Nemati	
<i>Multiclass Disease Classification from Microbial Whole-Community Metagenomes</i>	55
Saad Khan, Libusha Kelly	
<i>LitGen: Genetic Literature Recommendation Guided by Human Explanations</i>	67
Allen Nie, Arturo L. Pineda, Matt W. Wright, Hannah Wand, Bryan Wulf, Helio A. Costa, Ronak Y. Patel, Carlos D. Bustamante, James Zou	
<i>From Genome to Phenome: Predicting Multiple Cancer Phenotypes Based on Somatic Genomic Alterations via the Genomic Impact Transformer</i>	79
Yifeng Tao, Chunhui Cai, William W. Cohen, Xinghua Lu	
<i>Automated Phenotyping of Patients with Non-Alcoholic Fatty Liver Disease Reveals Clinically Relevant Disease Subtypes</i>	91
Maxence Vandromme, Tomi Jun, Ponni Perumalswami, Joel T. Dudley, Andrea Branch, Li Li	
<i>Monitoring ICU Mortality Risk with a Long Short-Term Memory Recurrent Neural Network</i>	103
Ke Yu, Mingda Zhang, Tianyi Cui, Milos Hauskrecht	
<i>Multilevel Self-Attention Model and Its Use on Medical Risk Prediction</i>	115
Xianlong Zeng, Yunyi Feng, Soheil Moosavinasab, Deborah Lin, Simon Lin, Chang Liu	
<i>Identifying Transitional High Cost Users from Unstructured Patient Profiles Written by Primary Care Physicians</i>	127
Haoran Zhang, Elisa Candido, Andrew S. Wilton, Raquel Duchon, Liisa Jaakkimainen, Walter Wodchis, Quaid Morris	

<i>Obtaining Dual-Energy Computed Tomography (CT) Information from a Single-Energy CT Image for Quantitative Imaging Analysis of Living Subjects by Using Deep Learning</i>	139
Wei Zhao, Tianling Lv, Rena Lee, Yang Chen, Lei Xing	

INTRINSICALLY DISORDERED PROTEINS (IDPS) AND THEIR FUNCTIONS

<i>Session Introduction: On the Importance of Computational Biology and Bioinformatics to the Origins and Rapid Progression of the Intrinsically Disordered Proteins Field</i>	149
Lukasz Kurgan, Predrag Radivojac, Joel L. Sussman, A. Keith Dunker	

<i>Many-to-One Binding by Intrinsically Disordered Protein Regions</i>	159
Wei-Lun Alterovitz, Eshel Faraggi, Christopher J. Oldfield, Jingwei Meng, Bin Xue, Fei Huang, Pedro Romero, Andrzej Kloczkowski, Vladimir N. Uversky, A. Keith Dunker	

<i>Disordered Function Conjunction: On the In-Silico Function Annotation of Intrinsically Disordered Regions</i>	171
Sina Ghadermarzi, Akila Katuwawala, Christopher J. Oldfield, Amita Barik, Lukasz Kurgan	

<i>De novo Ensemble Modeling Suggests that AP2-Binding to Disordered Regions Can Increase Steric Volume of Epsin but Not Eps15</i>	183
N. Suhas Jagannathan, Christopher W. V. Hogue, Lisa Tucker-Kellogg	

<i>Modulation of p53 Transactivation Domain Conformations by Ligand Binding and Cancer-Associated Mutations</i>	195
Xiaorong Liu, Jianhan Chen	

<i>Exploring Relationships Between the Density of Charged Tracts Within Disordered Regions and Phase Separation</i>	207
Ramiz Somjee, Diana M. Mitrea, Richard W. Kriwacki	

MUTATIONAL SIGNATURES

<i>Session Introduction: Mutational Signatures: Etiology, Properties, and Role in Cancer</i>	219
Max D.M. Leiserson, Teresa M. Przytycka, Roded Sharan	

<i>PhySigs: Phylogenetic Inference of Mutational Signature Dynamics</i>	226
Sarah Christensen, Mark D.M. Leiserson, Mohammed El-Kebir	

<i>TrackSigFreq: Subclonal Reconstructions Based on Mutation Signatures and Allele Frequencies</i>	238
Caitlin F Harrigan, Yulia Rubanova, Quaid Morris, Alina Selega	

<i>Impact of Mutational Signatures on microRNA and Their Response Elements</i>	250
Eirini Stamoulakatou, Pietro Pinoli, Stefano Ceri, Rosario Piro	

<i>DNA Repair Footprint Uncovers Contribution of DNA Repair Mechanism to Mutational Signatures</i>	262
Damian Wojtowicz, Mark D.M. Leiserson, Roded Sharan, Teresa M. Przytycka	

<i>Genome Gerrymandering: Optimal Division of the Genome into Regions with Cancer Type Specific Differences in Mutation Rates</i>	274
Adamo Young, Jacob Chmura, Yoonsik Park, Quaid Morris, Gurnit Atwal	

PATTERN RECOGNITION IN BIOMEDICAL DATA: CHALLENGES IN PUTTING BIG DATA TO WORK

<i>Session Introduction: Ongoing Challenges and Innovative Approaches for Recognizing Patterns Across Large-Scale Integrative Biomedical Datasets</i>	286
Shilpa Nadimpalli Kobren, Brett Beaulieu-Jones, Christian Darabos, Dokyoon Kim, Anurag Verma	

<i>Clinical Concept Embeddings Learned from Massive Sources of Multimodal Medical Data</i>	295
Andrew L. Beam, Benjamin Kompa, Allen Schmaltz, Inbar Fried, Griffin Weber, Nathan Palmer, Xu Shi, Tianxi Cai, Isaac S. Kohane	

<i>Assessment of Imputation Methods for Missing Gene Expression Data in Meta-Analysis of Distinct Cohorts of Tuberculosis Patients</i>	307
Carly A. Bobak, Lauren McDonnell, Matthew D. Nemesure, Justin Lin, Jane E. Hill	

<i>Towards Identifying Drug Side Effects from Social Media Using Active Learning and Crowd Sourcing</i>	319
Sophie Burkhardt, Julia Siekiera, Josua Glodde, Miguel A. Andrade-Navarro, Stefan Kramer	

<i>Microvascular Dynamics from 4D Microscopy Using Temporal Segmentation</i>	331
Shir Gur, Lior Wolf, Lior Golgher, Pablo Blinder	

<i>Using Transcriptional Signatures to Find Cancer Drivers with LURE</i>	343
David Haan, Ruikang Tao, Verena Friedl, Ioannis N Anastopoulos, Christopher K Wong, Alana S Weinstein, Joshua M Stuart	

<i>PAGE-Net: Interpretable and Integrative Deep Learning for Survival Analysis Using Histopathological Images and Genomic Data</i>	355
Jie Hao, Sai Chandra Kosaraju, Nelson Zange Tsaku, Dae Hyun Song, Mingon Kang	

<i>Machine Learning Algorithms for Simultaneous Supervised Detection of Peaks in Multiple Samples and Cell Types</i>	367
Toby Dylan Hocking, Guillaume Bourque	

<i>Learning a Latent Space of Highly Multidimensional Cancer Data</i>	379
Benjamin Kompa, Beau Coker	

<i>Scaling Structural Learning with NO-BEARS to Infer Causal Transcriptome Networks</i>	391
Hao-Chih Lee, Matteo Danieletto, Riccardo Miotto, Sarah T. Cherng, and Joel T. Dudley	

<i>PathFlowAI: A High-Throughput Workflow for Preprocessing, Deep Learning and Interpretation in Digital Pathology</i>	403
Joshua J. Levy, Lucas A. Salas, Brock C. Christensen, Aravindhnan Sriharan, Louis J. Vaickus	

<i>Improving Survival Prediction Using a Novel Feature Selection and Feature Reduction Framework Based on the Integration of Clinical and Molecular Data</i>	415
Lisa Neums, Richard Meier, Devin C. Koestler, Jeffrey A. Thompson	
<i>Bayesian Semi-Nonnegative Matrix Tri-Factorization to Identify Pathways Associated with Cancer Phenotypes</i>	427
Sunho Park, Nabhonil Kar, Jae-Ho Cheong, Tae Hyun Hwang	
<i>Graph-Based Information Diffusion Method for Prioritizing Functionally Related Genes in Protein-Protein Interaction Networks</i>	439
Minh Pham, Olivier Lichtarge	
<i>Tree-Weighting for Multi-Study Ensemble Learners</i>	451
Maya Ramchandran, Prasad Patil, Giovanni Parmigiani	
<i>A Literature-Based Knowledge Graph Embedding Method for Identifying Drug Repurposing Opportunities in Rare Diseases</i>	463
Daniel N. Sosa, Alexander Derry, Margaret Guo, Eric Wei, Connor Brinton, Russ B. Altman	
<i>PTR Explorer: An approach to identify and explore Post Transcriptional Regulatory mechanisms using proteogenomics</i>	475
Arunima Srivastava, Michael Sharpnack, Kun Huang, Parag Mallick, Raghu Machiraju	
<i>Two-stage ML Classifier for Identifying Host Protein Targets of the Dengue Protease</i>	487
Jacob T. Stanley, Alison R. Gilchrist, Alex C. Stabell, Mary A. Allen, Sara L. Sawyer, Robin D. Dowell	
<i>Network Representation of Large-Scale Heterogeneous RNA Sequences with Integration of Diverse Multi-omics, Interactions, and Annotations Data</i>	499
Nhat Tran, Jean Gao	
<i>Enhancing Model Interpretability and Accuracy for Disease Progression Prediction via Phenotype-Based Patient Similarity Learning</i>	511
Yue Wang, Tong Wu, Yunlong Wang, Gao Wang	
<i>Hadoop and PySpark for Reproducibility and Scalability of Genomic Sequencing Studies</i>	523
Nicholas R. Wheeler, Penelope Benckek, Brian W. Kunkle, Kara L. Hamilton-Nelson, Mike Warfe, Jeremy R. Fondran, Jonathan L. Haines, William S. Bush	
<i>CERENKOV3: Clustering and Molecular Network-Derived Features Improve Computational Prediction of Functional Noncoding SNPs</i>	535
Yao Yao, Stephen A. Ramsey	
PRECISION MEDICINE: ADDRESSING THE CHALLENGES OF SHARING, ANALYSIS, AND PRIVACY AT SCALE	
<i>Session Introduction: Precision Medicine: Addressing the Challenges of Sharing, Analysis, and Privacy at Scale</i>	547

Steven E. Brenner, Martha L. Bulyk, Dana C. Crawford, Alexander A. Morgan, Predrag Radivojac, Nicholas P. Tatonetti	
<i>Integrated Cancer Subtyping using Heterogeneous Genome-Scale Molecular Datasets</i>	551
Suzan Arslanturk, Sorin Draghici, Tin Nguyen	
<i>AnomiGAN: Generative Adversarial Networks for Anonymizing Private Medical Data</i>	563
Ho Bae, Dahuin Jung, Hyun-Soo Choi, Sungroh Yoon	
<i>Frequency of ClinVar Pathogenic Variants in Chronic Kidney Disease Patients Surveyed for Return of Research Results at a Cleveland Public Hospital</i>	575
Dana C. Crawford, John Lin, Jessica N. Cooke Bailey, Tyler Kinzy, John R. Sedor, John F. O'Toole, Williams S. Bush	
<i>Assessment of Coverage for Endogenous Metabolites and Exogenous Chemical Compounds Using an Untargeted Metabolomics Platform</i>	587
Sek Won Kong, Carles Hernandez-Ferrer	
<i>Coverage Profile Correction of Shallow-Depth Circulating Cell-Free DNA Sequencing via Multi-Distance Learning</i>	599
Nicholas B. Larson, Melissa C. Larson, Jie Na, Carlos P. Sosa, Chen Wang, Jean-Pierre Kocher, Ross Rowsey	
<i>PGxMine: Text Mining for Curation of PharmGKB</i>	611
Jake Lever, Julia M. Barbarino, Li Gong, Rachel Huddart, Katrin Sangkuhl, Ryan Whaley, Michelle Whirl-Carrillo, Mark Woon, Teri E. Klein and Russ B. Altman	
<i>Network-Based Matching of Patients and Targeted Therapies for Precision Oncology</i>	623
Qingzhi Liu, Min Jin Ha, Rupam Bhattacharyya, Lana Garmire, Veerabhadran Baladandayuthapani	
<i>The Power of Dynamic Social Networks to Predict Individuals' Mental Health</i>	635
Shikang Liu, David Hachen, Omar Lizardo, Christian Poellabauer, Aaron Striegel, Tijana Milenkovic	
<i>Implementing a Cloud Based Method for Protected Clinical Trial Data Sharing</i>	647
Gaurav Luthria, Qingbo Wang	
<i>Phenome-wide Association Studies on Cardiovascular Health and Fatty Acids Considering Phenotype Quality Control Practices for Epidemiological Data</i>	659
Kristin Passero, Xi He, Jiayan Zhou, Bertram Mueller-Myhsok, Marcus E. Kleber, Winfried Maerz, Molly A. Hall	
<i>Pathway and Network Embedding Methods for Prioritizing Psychiatric Drugs</i>	671
Yash Pershad, Margaret Guo, Russ B. Altman	
<i>aTEMPO: Pathway-Specific Temporal Anomalies for Precision Therapeutics</i>	683
Christopher Michael Pietras, Liam Power, Donna K. Slonim	

<i>Robust-ODAL: Learning from Heterogeneous Health Systems Without Sharing Patient-Level Data</i>	695
Jiayi Tong, Rui Duan, Ruowang Li, Martijn J. Scheuemie, Jason H. Moore, Yong Chen	
<i>Feature Selection and Dimension Reduction of Social Autism Data</i>	707
Peter Washington, Kelley Marie Paskov, Haik Kalantarian, Nathaniel Stockham, Catalin Voss, Aaron Kline, Ritik Patnaik, Brianna Chrisman, Maya Varma, Qandeel Tariq, Kaitlyn Dunlap, Jessey Schwartz, Nick Haber, Dennis P. Wall	
<i>Computationally Efficient, Exact, Covariate-Adjusted Genetic Principal Component Analysis by Leveraging Individual Marker Summary Statistics from Large Biobanks</i>	719
Jack Wolf, Martha Barnard, Xueting Xia, Nathan Ryder, Jason Westra, Nathan Tintle	

WORKSHOPS

<i>AI Ethics and Values in Biomedicine – Technical Challenges and Solutions</i>	731
Dragutin Petkovic, Lester Kobzik, Reza Ghanadan	
<i>Navigating Ethical Quandaries with the Privacy Dilemma of Biomedical Datasets</i>	736
Gamze Gursoy, Megan Doerr, John Wilbanks, Jennifer K. Wagner, Haixu Tang, Steven E. Brenner	
<i>Packaging Biocomputing Software to Maximize Distribution and Reuse</i>	739
William S. Bush, Nicholas Wheeler, Brett Beaulieu-Jones, Christian Darabos	
<i>Translational Bioinformatics: Biobanks in the Precision Medicine Era</i>	743
Marylyn Ritchie, Jason Moore, Ju Han Kim	