

International Conference on Intelligent Biology and Medicine

Program at-a-glance (June 10-12, 2018)

Sunday, June 10th

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| 12:00 | Registration opens | | |
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| CONCURRENT WORKSHOPS | | | |
| Room: Santa Monica | | Room: Grand Imperial North | |
| 1:00 - 2:30 | Dr. Yan Guo University of New Mexico Machine Learning | 1:00 - 2:30 | Dr. Feng Yue Pennsylvania State University 3D Genome Organization |
| 2:30 - 2:40 | <i>Break</i> | | |
| 2:40 - 4:10 | Chi Zhang; Xiao Dong Indiana University; Albert Einstein College of Medicine Single-cell Sequencing Analysis | 2:40 - 4:10 | Dr. Ting Wang Washington University WashU Epigenome Browser |
| 4:10 - 4:30 | <i>Coffee/Tea Break</i> | | |
| 4:30 - 5:20 | Keynote Lecture (Room: Grand Imperial North) Josh Denny, MD, MS Professor of Biomedical Informatics and Medicine Vanderbilt University Member, National Academy of Medicine Title: Huge cohorts, genomics, and clinical data to personalize medicine | | |
| 5:20 - 5:30 | <i>Break</i> | | |
| 5:30 - 7:30 | Poster Session (Room: Grand Imperial Foyer) | | |

Monday, June 11st

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| 7:30 - 8:30 | Registration Open and Buffet Breakfast | |
| 8:30 - 8:40 | Opening Remarks | |
| 8:40 - 9:30 | <p>Keynote Lecture (Room: Grand Imperial North)</p> <p>Paul Thomas, Ph.D. Associate Professor of Preventive Medicine Director of Division of Bioinformatics University of Southern California PI, Gene Ontology Consortium</p> <p>Title: Reconstructing the large-scale evolution of genomes and gene functions</p> | |
| 9:30 - 9:40 | <i>Break</i> | |
| 9:40 - 10:00 | <p>Eminent Scholar Talk (Room: Grand Imperial North)</p> <p>Xinghua Lu, MD, PhD Professor of Biomedical Informatics University of Pittsburgh</p> <p>Title: From Big Data to Bedside (BD2B): Precision Oncology in an Era of Artificial Intelligence</p> | |
| 10:00-10:05 | <i>Break for parallel session</i> | |
| CONCURRENT SESSIONS | | |
| Room: Grand Imperial North NGS & Tools Session Chair: Youping Deng | Room: Santa Monica Systems Biology Session Chair: Yin Liu | Room: Hollywood Bioinformatics Session Chair: Li Liu |

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| 10:05 -10:25 | <i>Development of somatic mutation signatures for risk stratification and prognosis in lung and colorectal adenocarcinomas</i> Mark Menor, Yong Zhu, Bin Jiang and Youping Deng | 10:05 -10:25 | <i>A Hidden Markov Model-based approach to reconstructing double minute chromosome amplicons</i> Ruslan Mardugalliamov, Kamal Al Nasr and Matthew Hayes | 10:05 -10:25 | <i>A Graph-based Algorithm for Estimating Clonal Haplotypes of Tumor Sample from Sequencing Data</i> Yixuan Wang, Rong Zhang, Xinyu Sun, Yu Geng, Jianye Liu, Zhongmeng Zhao, Xuanping Zhang, Yi Huang and Jiayin Wang |
| 10:25 - 10:45 | <i>Genomic copy number variations in large screening for pediatric sarcomas chemotherapy</i> Lijun Cheng, Pooja Chandra, Limei Wang, Karen Pollok, Pankita Pandya, Mary Murray, Jacquelyn Carter, Michael Ferguson, Mohammad Reza Saadatzadeh, Mashall Mark, Li Lang and Jamie Renbarger | 10:25 - 10:45 | <i>Classifying Mild Traumatic Brain Injuries with Functional Network Analysis</i> Francis San Lucas, John Redell, Dash Pramod and Yin Liu | 10:25 - 10:45 | <i>A new insight into underlying disease mechanism through semi-parametric latent differential network model</i> Yong He, Jiadong Ji, Lei Xie, Xinsheng Zhang and Fuzhong Xue |
| 10:45 - 11:05 | <i>Computational identification of deleterious synonymous variants in human genomes using a feature-based approach</i> Fang Shi, Yao Yao and Junfeng Xia | 10:45 - 11:05 | <i>scDNA: a fast and comprehensive tool for single-cell differential network analysis</i> Yu-Chiao Chiu, Tzu-Hung Hsiao, Li-Ju Wang, Yidong Chen and Yu-hsuan Shao | 10:45 - 11:05 | <i>Genetic-Epigenetic Interactions in Asthma Revealed by a Genome-Wide Gene-Centric Search</i> Vladimir Kogan, Joshua Millstein, Stephanie J London, Carole Ober, Steven R White, Edward T Naureckas, W James Gauderman, Daniel J Jackson, Albino Barraza-Villarreal, Isabelle Romieu, Benjamin A Raby and Carrie V Breton |
| 11:05 - 11:15 | Coffee/Tea Break | | | | |

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| 11:15 - 11:35 | <i>High scoring segment selection for pairwise whole genome sequence alignment with the maximum scoring subsequence and GPUs</i> Abdulrhman Aljouie, Ling Zhong and Usman Roshan | 11:15 - 11:35 | <i>Multiple transcription factors contribute to inter-chromosomal interaction in yeast</i> Yulin Dai, Chao Li, Guangsheng Pei, Dong Xiao, Guohui Ding, Zhongming Zhao, Yixue Li and Jia Peilin | 11:15 - 11:35 | <i>DLAD4U: deriving and prioritizing disease lists from PubMed literature</i> Junhui Shen, Suhas Vasaikar and Bing Zhang |
| 11:35 - 11:55 | <i>Detecting virus integration sites based on multiple related sequencing data by VirTect</i> Yuchao Xia, Yun Liu, Minghua Deng and Ruibin Xi | 11:35 - 11:55 | <i>Metabolomics of Mammalian Brain Reveals Regional Differences</i> William Choi, Mehmet Tosun, Cemal Karakas, Fatih Semerci, Zhandong Liu and Mirjana Maletic-Savatic | 11:35 - 11:55 | <i>A multitask bi-directional RNN model for named entity recognition on electronic medical records</i> Shanta Chowdhury, Xishuang Dong, Lijun Qian, Xiangfang Li, Yi Guan, Jinfeng Yang and Qiubin Yu |
| 11:55 - 12:15 | <i>Comprehensive assessment of genotype imputation performance</i> Shuo Shi, Na Yuan, Ming Yang, Zhenglin Du, Jinyue Wang, Sheng Xin, Jiayan Wu and Jingfa Xiao | 11:55 - 12:15 | <i>Boosting Gene Expression Clustering with System-Wide Biological Information: A Robust Autoencoder Approach</i> Hongzhu Cui, Chong Zhou, Xinyu Dai, Yuting Liang, Randy Paffenroth and Dmitry Korkin | 11:55 - 12:15 | <i>iMEGES: integrated Mental-disorder GENome score for prioritizing the susceptibility genes for mental disorders in personal genomes</i> Atlas Khan, Qian Liu and Kai Wang |
| 12:15 - 1:35 | Lunch Break - Buffet Lunches | | | | |
| 1:35 - 1:55 | Eminent Scholar Talk (Room: Grand Imperial North) Ting Wang, PhD Associate Professor of Genetics Washington University Title: Exploring the dark matter in genomics data | | | | |

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| 1:55 - 2:00 | Short Break | | | | |
| 2:00 - 2:50 | Keynote Lecture (Room: Grand Imperial North) Alex Hoffmann, Ph.D. Thomas M. Asher Professor of Microbiology Director of the Institute for Quantitative and Computational Biosciences University of California Los Angeles Title: Learning how to predict immune responses | | | | |
| 2:50 - 3:00 | Break for parallel sessions | | | | |
| CONCURRENT SESSIONS | | | | | |
| Room: Grand Imperial North NGS & Tools Session Chair: Lei Xie | | Room: Santa Monica Systems Biology Session Chairs: Matthew Hayes | | Room: Hollywood Medical Informatics Session Chairs: W. Jim Zheng | |
| 3:00 - 3:20 | <i>Reconstructing the High-resolution Chromosomal 3D structure by Hi-C Complex Network</i> Tong Liu and Zheng Wang | 3:00 - 3:20 | <i>Prediction of Protein Self-Interactions using Stacked Long Short-Term Memory from Protein Sequences Information</i> Yanbin Wang, Zhuhong You, Xiao Li, Tonghai Jiang, Li Cheng and Zhanheng Chen | 3:00 - 3:20 | <i>Building a high performance computing infrastructure for cancer research</i> W. Jim Zheng |
| 3:20 - 3:40 | <i>CeL-ID: Cell Line Identification using RNA-seq data</i> Tabrez A Mohammad, Yun S Tsai, Safwa Ameer, Hung-I H Chen, Yu-Chiao Chiu and Yidong Chen | 3:20 - 3:40 | <i>Circular RNA Expression Profiles during the Differentiation of Mouse Neural Stem Cells</i> Qichang Yang, Jing Wu, Jian Zhao, Tianyi Xu, Zhongming Zhao, | 3:20 - 3:40 | <i>Gene Fingerprint model for Literature based detection of the associations among complex diseases: A case study of COPD</i> Guocai Chen, Yuxi Jia, Lisha Zhu, |

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| | | | Xiaofeng Song and Ping Han | | Ping Li, Lin Zhang, Cui Tao and W. Jim Zheng |
| 3:40 - 4:00 | <p><i>Comparison of SureSelect and Nextera exome capture performance in single-cell sequencing</i></p> <p>Wendy Huss, Qiang Hu, Sean Glenn, Kalyan Gangavarapu, Jianmin Wang, Jesse Luce, Paul Quinn, Elizabeth Brese, Fenglin Zhan, Jeffrey Conroy, Gyorgy Paragh, Barbara Foster, Carl Morrison, Song Liu and Lei Wei</p> | 3:40 - 4:00 | <p><i>Identification of Gene Signatures from RNA-seq Data Using Pareto-optimal Cluster Algorithm</i></p> <p>Saurav Mallik and Zhongming Zhao</p> | 3:40 - 4:00 | <p><i>Early prediction of acute kidney injury following ICU admission</i></p> <p>Lindsay P. Zimmerman, Paul A. Reyfman, Angela D. R. Smith, Zexian Zeng, Abel Kho, L. Nelson SanchezPinto and Yuan Luo</p> |
| 4:00 - 4:10 | Coffee/Tea Break | | | | |
| 4:10 - 4:30 | <p><i>A PheWAS Study of a Large Observational Epidemiological Cohort of African Americans: the REGARDS Study</i></p> <p>Xueyan Zhao, Xin Geng, Vinodh Srinivasasainagendra, Suzanne Judd, Virginia Wadley, Orlando Gutierrez, Henry Wang, Ethan Lange, Leslie Lange, Daniel Woo, Fred Unverzagt, Monika Safford, Mary Cushman, Nita Limdi, Rakale Quarells, Donna Arnett, Marguerite Irvin and Degui Zhi</p> | 4:10 - 4:30 | <p><i>An experimental design framework for Markovian gene regulatory networks under stationary control policy</i></p> <p>Roosbeh Dehghannasiri, Mohammad Shahrokh Esfahani and Edward Dougherty</p> | 4:10 - 4:30 | <p><i>Epileptic foci localization based on mapping the synchronization of dynamic brain network</i></p> <p>Mei Tian, Wei Xiaoyan, Chen Ziyi, Tian Xianghua, Dong Nan, Li Dongmei and Zhou Yi</p> |
| 4:30 - 4:50 | <p><i>NanoMod: a computational tool to detect DNA modifications using</i></p> | 4:30 - 4:50 | <p><i>GSAE: an autoencoder with embedded gene-set nodes for</i></p> | 4:30 - 4:50 | <p><i>Dynamic Prediction of Hospital Admission with Medical Claim</i></p> |

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| | <p><i>Nanopore long-read sequencing data</i></p> <p>Qian Liu, Daniela C. Georgieva, Dietrich M. Egli and Kai Wang</p> | | <p><i>genomics functional characterization</i></p> <p>Hung-I Chen, Yu-Chiao Chiu, Tinghe Zhang, Songyao Zhang, Yufei Huang and Yidong Chen</p> | | <p><i>Data</i></p> <p>Tianzhong Yang, Yang Yang, Yugang Jia and Xiao Li</p> |
| 4:50 – 5:00 | <p><i>Joint Principal Trend Analysis for Longitudinal High-Dimensional Genomic Data</i></p> <p>Yuping Zhang and Zhengqing Ouyang (selected abstract talk)</p> | 4:50 – 5:00 | <p><i>Comparative gene co-expression network analysis of epithelial to mesenchymal transition reveals lung cancer progression stages</i></p> <p>Daifeng Wang, John Haley and Patricia Thompson (selected abstract talk)</p> | 4:50 – 5:10 | <p><i>Integrating Sentence Sequence Representation and Shortest Dependency Path into a Deep Learning Framework for Relation Extraction in Clinical Text</i></p> <p>Zhiheng Li, Zhihao Yang, Chen Shen, Jun Xu, Yaoyun Zhang and Hua Xu</p> |
| 5:00 – 5:10 | <p><i>Inferring Drug-Target Associations based on perturbational profiles in L1000 Data</i></p> <p>Pei-Han Liao, Tzu-Hung Hsiao, Liang-Chuan Lai, Mong-Hsun Tsai, Tzu-Pin Lu and Eric Y. Chuang (selected abstract talk)</p> | 5:00 – 5:10 | <p><i>Epigenomic Patterns Are Associated with Gene Haploinsufficiency and Predict Risk Genes of Developmental Disorders</i></p> <p>Siying Chen, Xinwei Han and Yufeng Shen (selected abstract talk)</p> | | |
| 5:10 – 5:20 | <p>Predict effective drug combination by deep believe network and Ontology Fingerprints</p> <p>Guocai Chen, Lam Tsoi, Hua Xu and W. Jim Zheng (selected abstract talk)</p> | 5:10 – 5:20 | <p><i>Genetic Association of Arterial Stiffness Index with Incident Coronary Artery Disease and Congestive Heart Failure</i></p> <p>Seyedeh Zekavat, Mary Haas, Krishna Aragam, Connor Emdin, Amit Khera, Derek Klarin, Hongyu Zhao and Pradeep Natarajan (selected abstract talk)</p> | 5:10 – 5:30 | |

Tuesday, June 12nd

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| 7:30 - 8:40 | Registration Open and Buffet Breakfast | |
| 8:40 - 9:30 | <p>Keynote Lecture (Room: Grand Imperial North)</p> <p>Jason Moore, Ph.D. Edward Rose, M.D. And Elizabeth Kirk Rose, M.D. Professor of Biostatistics, Epidemiology and Informatics Director, Institute for Biomedical Informatics University of Pennsylvania</p> <p>Title: Accessible artificial intelligence for data science</p> | |
| 9:30 - 9:40 | <i>Break</i> | |
| 9:40 - 10:00 | <p>Eminent Scholar Talk (Room: Grand Imperial North)</p> <p>Grace Xiao, Ph.D. Professor of Integrative Biology and Physiology UCLA</p> <p>Title: Deciphering the function of single-nucleotide variants in the RNA</p> | |
| 10:00 - 10:05 | <i>Break for parallel sessions</i> | |
| CONCURRENT SESSIONS | | |
| <p>Room: Grand Imperial North</p> <p>Cancer Genomics</p> <p>Session Chair: Bin Chen</p> | <p>Room: Santa Monica</p> <p>Systems Biology</p> <p>Session Chair: Fan Zhang</p> | <p>Room: Hollywood</p> <p>Computational drug discovery</p> <p>Session Chair: Zhifu Sun</p> |

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| 10:05 -10:25 | <i>Identification of exon skipping events associated with Alzheimer's disease in the human hippocampus</i> Seonggyun Han, Jason Miller, Seyoun Byun, Dokyoon Kim, Shannon Leigh Risacher, Andrew Saykin, Younghee Lee and Kwangsik Nho | 10:05 -10:25 | <i>Investigation of multi-trait associations using pathway-based analysis of GWAS summary statistics</i> Guangsheng Pei, Hua Sun, Yulin Dai, Peilin Jia and Zhongming Zhao | 10:05 -10:25 | <i>Drug-Drug Interaction Prediction based on Co-Medication Patterns and Graph Matching</i> Wen-Hao Chiang, Li Shen, Lang Li and Xia Ning |
| 10:25 -10:45 | <i>Brain-wide structural connectivity alterations under the control of Alzheimer risk genes</i> Jingwen Yan, Vinesh Raja V, Zhi Huang, Amico Enrico, Kwangsik Nho, Shaifen Fang, Olaf Sporns, Yu-Chien Wu, Andrew Saykin, Joaquin Goni and Li Shen | 10:25 -10:45 | <i>Lilikoi: an R package for personalized pathway-based classification modeling using metabolomics data</i> Sijia Huang, Fadhl Alakwaa and Lana Garmire | 10:25 -10:45 | <i>Predicting drug response of tumors from integrated genomic profiles by deep neural networks</i> Yu-Chiao Chiu, Hung-I Chen, Tinghe Zhang, Songyao Zhang, Li-Ju Wang, Yufei Huang and Yidong Chen |
| 10:45 -11:05 | <i>Context-sensitive Network Analysis Identifies Food Metabolites Associated with Alzheimer's Disease: An Exploratory Study</i> Yang Chen and Rong Xu | 10:45 -11:05 | <i>Gene2Vec: Distributed Representation of Genes Based on Co-Expression</i> Jingcheng Du, Peilin Jia, Yulin Dai, Cui Tao, Zhongming Zhao and Degui Zhi | 10:45 -11:05 | <i>Predicting Adverse Drug Reactions through Interpretable Deep Learning Framework</i> Sanjoy Dey, Heng Luo, Achille Fokoue-Nkoutche, Jianying Hu and Ping Zhang |
| 11:05 -11:15 | Coffee/Tea Break | | | | |
| 11:15 -11:35 | <i>Using natural language processing and machine learning to identify breast cancer local recurrence</i> | 11:15 -11:35 | <i>A robust fuzzy rule based integrative feature selection strategy for gene expression data in</i> | 11:15 -11:35 | <i>Predicting drug sensitivity of cancer cells with pathway activity inference</i> |

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| | Zexian Zeng, Sasa Espino, Ankita Roy, Xiaoyu Li, Seema Khan, Susan Clare, Xia Jiang, Richard Neapolitan and Yuan Luo | | TCGA Shicai Fan | | Xuwei Wang, Zhifu Sun, Michael Zimmerman, Andrej Bugrim and Jean-Pierre Kocher |
| 11:35 - 11:55 | <i>Identification of long non-coding RNA-related and –coexpressed mRNA biomarkers for hepatocellular carcinoma</i> Fan Zhang, Linda Ding, Li Cui, Robert Barber and Bin Deng | 11:35 - 11:55 | <i>Pessimistic optimization for modeling microbial communities with uncertainty</i> Meltem Apaydin, Liang Xu, Bo Zeng and Xiaoning Qian | 11:35 - 11:55 | <i>Application of Transfer Learning for Cancer Drug Sensitivity Prediction</i> Saugato Rahman Dhruba, Raziur Rahman, Kevin Matlock, Souparno Ghosh and Ranadip Pal |
| 11:55 - 12:15 | <i>Comparison of different functional prediction scores using a gene-based permutation model for identifying cancer driver genes</i> Alice Djotsa and Xiaoming Liu | 11:55 - 12:15 | <i>Evaluation of Top-Down Mass Spectral Identification with Homologous Protein Sequences</i> Ziwei Li, Yunlong Liu, Xiaowen Liu and Weixing Feng | 11:55 - 12:15 | <i>Large-scale mining disease comorbidity relationships from post-market drug adverse events surveillance data</i> Chunlei Zheng and Rong Xu |
| 12:15 - 1:30 | Lunch Break - Buffet lunch | | | | |
| 1:30 - 1:50 | Eminent Scholar Talk (Room: Grand Imperial North) Charles Wang, MD, PhD, MPH Professor & Director Center for Genomics Loma Linda University Title: Vegetarian diet-modulated epigenetic reprogramming/epigenetic clocks and longevity | | | | |
| 1:50 - 2:10 | <i>Award presentation</i> | | | | |
| 2:10 - 2:20 | <i>Coffee/Tea Break</i> | | | | |
| CONCURRENT SESSIONS | | | | | |

| Room: Grand Imperial North International PI Talk Session Chair: Yu Xue, Xiaofeng Song | | | | Room: Santa Monica Cancer Genomics Session Chair: Jun Wan | |
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| 2:20 - 2:40 | <i>Bioinformatics research on potential ability of circular RNA encoding protein</i> Xiaofeng Song | | | 2:20 - 2:40 | <i>Selecting precise reference normal tissue samples for cancer research using a deep learning approach</i> William Zeng, Benjamin Glicksberg, Yangyan Li, Bin Chen |
| 2:40 - 3:00 | <i>The impact of genetic admixture and natural selection on driving population differences in East Asia</i> Shuhua Xu | | | 2:40 - 3:00 | <i>Modeling of Hypoxia gene expression for three different cancer cell lines</i> Babak Soltanalizadeh, Erika Gonzalez Rodriguez, Vahed Maroufy and Hulin Wu |
| 3:00 - 3:20 | <i>Identification of functional PTM events in autophagy</i> Yu Xue | | | 3:00 - 3:20 | <i>Inferring gene-disease association by an integrative analysis of eQTL GWAS and Protein-Protein Interaction data</i> Jun Wang, Jiashun Zheng, Zengmiao Wang, Hao Li and Minghua Deng |
| 3:20 - 3:40 | <i>Tumor heterogeneity in hepatocellular carcinoma and intrahepatic cholangiocarcinoma</i> Ruibin Xi | | | 3:20 - 3:40 | <i>Network-based identification of critical regulators as putative drivers of human cleft lip</i> Aimin Li, Guimin Qin, Akiko Suzuki, Mona Gajera, Junichi Iwata, Peilin Jia, Zhongming Zhao |
| 3:40 | Adjourn | | | | |