

# International Conference on Intelligent Biology and Medicine (ICIBM 2014)

December 4-6, 2014, Sheraton Gunter Hotel, San Antonio, TX, USA

## Conference Agenda

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Dec 4, 2014

10:00 – 12:00pm: Registration

12:00-1:00pm: Session Chair: Yidong Chen  
Magnolia Room **Keynote: Single-Cell Analysis of Tumor Heterogeneity**  
Dr. Tim Huang, Professor and Chair,  
Department of Molecular Medicine, The University of Texas Health Science Center at San Antonio

1:00 – 1:15pm: Break

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Magnolia Room  
1:15-3:45pm **Tutorial 1: Proteomics and Metabolomics**  
Susan E Weintraub, Chair  
Steve Patrie  
Bill Alley and  
Michelle Zhang

3:45 – 4:00pm Break

4:00 – 5:30pm **Tutorial 2: Next-generation sequencing and data analysis**  
Yunlong Liu, Chair  
Kun Huang,

5:30-7:30 pm Reception and Poster session

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Baker Room  
1:15-3:45pm **Tutorial 3: Single-cell**  
Chun-Liang Chen, Chair  
Chenghang Zong  
Zhao Lai  
Yidong Chen

3:45-4:00pm Break

4:00-5:30pm **Tutorial 4: Metagenomics**  
Babu Guda, Chair  
Qunfeng Dong

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Dec 5, 2014

8:30-9:30am  
Magnolia Room

Session Chair: Zhongming Zhao

**Keynote: Identifying all of cancer's manifestations through integrated Pan-Cancer analysis**

Dr. Josh Stuart, Professor, Biomolecular Engineering Department Baskin Engineering Endowed Chair  
Associate Director, Center for Biomolecular Science and Engineering, University of California Santa Cruz

9:30 – 9:40 am Break

Magnolia Room

9:40 -12:00am: **Gene Regulation and Protein Interaction Networks, I**  
Session Chair: Dr. Feixiong Cheng

- 9:40 – 10:00am: A Translational Bioinformatic Approach In Identifying And Validating An Interaction Between Vitamin A And Cyp19a1, Santosh Philips, Guanglong Jiang, Lei Wang, Todd Skaar and Lang Li
- 10:00 – 10:20am: Global transcriptome analysis profiles metabolic pathways in traditional herb *Astragalus membranaceus* Bge. var. *mongolicus* (Bge.) Hsiao, Jing Chen, Xue-Ting Wu, Yi-Qin Xu, Yang Zhong, Yi-Xue Li, Jia-Kuan Chen, Xuan Li and Peng Nan
- 10:20 – 10:40am: BMRF-MI: integrative identification of protein interaction network by modeling the gene dependency, Xu Shi, Xiao Wang, Ayesha Shajahan, Leena Hilakivi-Clarke, Robert Clarke and Jianhua Xuan.
- 10:40 – 11:00am: Network-based stratification analysis of 13 major cancer types using mutations in panels of cancer genes, Xue Zhong, Hushan Yang, Shuyang Zhao, Yu Shyr and Bingshan Li.
- 11:00 – 11:20am: Network-based Gene Prediction for *Plasmodium falciparum* Malaria Towards Genetics-based Drug Discovery, Yang Chen and Rong Xu.
- 11:20 – 11:40am: Ishwor Thapa, Howard Fox and Dhundy Bastola. Co-expression network analysis of miRNA-142 over-expression in neuronal cells
- 11:40 – 12:00pm: Studying Tumorigenesis through Network Evolution and Somatic Mutational Perturbations in the Cancer Interactome, Feixiong Cheng and Zhongming Zhao (*highlight talk*)

Baker Room

9:45-12:00am: **Algorithms in NGS Data Analysis**  
Session Chair: Dr. Eric Chuang

- 9:40 – 10:00am: Hung-I Chen, Yuanhang Liu, Yi Zou, Zhao Lai, Devanand Sarkar, Yufei Huang and Yidong Chen. Differential expression analysis of RNA sequencing data by incorporating non-exonic mapped reads
- 10:00 – 10:20am: Adam Cornish and Chittibabu Guda. A comparison of variant calling pipelines using Genome in a Bottle as a reference
- 10:20 – 10:40am: Yang Xiang and Sarath Janga. Building integrated ontological knowledge structures with efficient approximation algorithms
- 10:40 – 11:00am: Qi Liu, Xue Zhong and Yu Shyr. Assessing Computational Steps for CLIP-Seq Data Analysis
- 11:00 – 11:20am: Yu-Ching Hsu, Yu-Chiao Chiu, Yidong Chen, Eric Y. Chuang and Tzu-Hung Hsiao. A gene set approach to analyze copy number alterations profiles of breast cancer
- 11:20 – 11:40am: Kashish Chetal and Sarath Chandra Janga. OperomeDB: a database of condition-specific transcription units in prokaryotic genomes
- 11:40 – 12:00pm: Amplification of Distant Estrogen Response Elements Deregulates Target Genes Associated with Tamoxifen Resistance in Breast Cancer, Pei-Yin Hsu (*highlight talk*)

Noon-1:30 pm: Lunch break

1:30-2:30 pm:  
Magnolia Room

Session Chair: Victor Jin

**Keynote: Genomic Medicine: Transforming Cancer Research and Care**

Dr. Lynda Chin, Professor and Chair,

Department of Genomic Medicine, Division of Cancer Medicine, The University of Texas MD Anderson Cancer Center

2:30 – 2:40 pm Break

Magnolia Room

2:40-6:00pm: **Gene Regulation and Protein Interaction Networks, II**

Session Chair: Drs. Yufang Jin, Yongsheng Bai

2:40 – 3:00pm MOST+: A de novo motif finding approach combining genomic sequence and heterogeneous genome-wide signatures, Yizhe Zhang, Yupeng He, Guangyong Zheng and Chaochun Wei.

3:00 – 3:20pm Kevin Zhu, Qi Liu, Yubo Zhou, Cui Tao, Hua Xu and Jingchun Sun. Oncogenes and tumor suppressor genes: comparative genomics and network perspectives

3:20 – 3:40pm Liang-Chin Huang, Ergin Soysal, W. Jim Zheng, Hua Xu and Jingchun Sun. A weighted and integrated drug-target interactome: drug repurposing for schizophrenia as a use case

3:40 – 4:00pm Finding pathway-modulating genes from a novel Ontology Fingerprint-derived gene network, Tingting Qin, Nabil Matmati, Lam Tsoi, Bidyut Mohanty, Nan Gao, Jijun Tang, Andrew Lawson, Yusuf Hannun and W. Jim Zheng (*highlight talk*)

**4:00 – 4:10pm Coffee Break**

4:10 – 4:30pm Nguyen T. Nguyen, Merry L. Lindsey and Yu-Fang Jin. Systems analysis of gene ontology and biological pathways post-myocardial infarction

4:30 – 4:50pm Yu-Chiao Chiu, Chin-Ting Wu, Tzu-Hung Hsiao, Yi-Pin Lai, Chuhsing K. Hsiao, Yidong Chen and Eric Y. Chuang. Co-modulation analysis of gene regulation in breast cancer reveals complex interplay between ESR1 and ERBB2 genes

4:50 – 5:10pm Comprehensive genome-wide transcription factor analysis reveals that a combination of high affinity and low affinity DNA binding is needed for human gene regulation, Junbai Wang, Agnieszka Malecka, Gunhild Trøen and Jan Delabie

5:10 – 5:30pm Lei Wang, Chiangwei Chang, Hong Liang, Heng-Yi Wu, Weixing Feng, Sara Quinney, Jin Li and Lang Li. How to Choose In Vitro Systems to Predict In Vivo Drug Clearance: A System Pharmacology Prospective

5:30 – 5:50: Emad Ramadan, Moataz Ahmed and Ahmed Naef. Bio-inspired Algorithm for Identifying Overlapping Clusters in Protein-Protein Interaction Networks

5:50 – 6:10pm Novel Bioinformatics Method for Identification of Genome-Wide Non-Canonical Spliced Regions Using RNA-Seq Data, Yongsheng Bai (*highlight talk*)

6:30-8:30pm Banquet

Baker Room

2:40-6:00pm **Metagenomics and Bioinformatics methods**

Session Chair: Drs. Chittibabu Guda, Patrick Zhao

2:40 – 3:00pm Akram Mohammed and Chittibabu Guda. Application of a hierarchical enzyme classification method reveals the role of gut microbiome in human metabolism

3:00 – 3:20pm Rong Xu, Quanqiu Wang and Li Li. A genome-wide systems analysis reveals strong link between colorectal cancer and trimethylamine N-oxide (TMAO), a gut microbial metabolite of dietary meat and fat

3:20 – 3:40pm Yukun Chen, Jingchun Sun, Liang-Chin Huang, Hua Xu and Zhongming Zhao. Classification Of Cancer Primary Sites Using Machine Learning And Somatic Mutations

3:40 – 4:00pm MeT-DB: A database of transcriptome methylation in mammalian cells, Lui Hui, Mario Flores, Jia Meng, Lin Zhang, Xinyu Zhao, Manjeet Rao, Yidong Chen and Yufei Huang (*highlight talk*)

**4:00 – 4:10pm Coffee Break**

4:10 – 4:30pm Yanhui Liang, Fusheng Wang, Darren Treanor, Derek Magee, George Teodoro, Yangyang Zhu and Jun Kong. A Framework for 3D Vessel Analysis with Whole Slide Images of Serial Liver Sections

4:30 – 4:50pm Pei-Fang Su, Yan Guo, Chung-I Li, Qi Liu, John Boice and Yu Shyr. Paired mitochondrial DNA data analysis using bivariate Poisson regression model

4:50 – 5:10pm Jun Li and Patrick Xuechun Zhao. Mining functional modules in heterogeneous biological networks using Multiplex PageRank method

5:10 – 5:30pm Shilin Zhao, Yan Guo, Quanhu Sheng, Mingsheng Guo, Brian Lehmann, Jennifer Pietenpol, David Samuels and Yu Shyr. RNAseq by Total RNA Library Identifies Additional lncRNA Compared to Poly(A) RNA library

5:30 – 5:50pm Weirong Cui, Yulan Qian, Xiaoke Zhou, Yuxin Lin, Junfeng Jiang, Jiajia Chen, Zhongming Zhao and Bairong Shen. Discovery and characterization of long intergenic non-coding RNAs (lincRNA) module biomarkers in prostate cancer: an integrative analysis of RNA-Seq data

5:50 – 6:10pm Detecting evolutionary strata on the human x chromosome in the absence of gametologous y-linked sequences, Ravi Shanker Pandey, Melissa Wilson Sayres and Rajeev Azad (*highlight talk*)

Dec 6, 2014  
8:30-9:30am  
Magnolia Room

Session Chair: Victor Jin

**Keynote: Make Big Data Useful: Horizontal and Vertical Data Integration to Study Genes, Networks and Diseases**

Dr. Jasmine Zhou, Professor,

Departments of Biological Sciences and Computer Science, University of Southern California

9:30 – 9:45am Break

Magnolia Room

9:45 – 1:15pm: **Epigenetics & Systems Biology**

Session Chair: Drs. Steve Qin and Jason Ernst

- 9:45 – 10:15am: Systematic epigenome imputation of over 4000 datasets, Jason Ernst
- 10:15 – 10:45am: Base-resolution methylation patterns accurately predict transcription factor bindings *in vivo*, Steve Qin
- 10:45 – 11:15am: Synthetic long read next generation sequencing, Jeremy Edwards
- 11:15 – 11:35am: Computational analysis reveals a correlation of exon-skipping events with splicing, transcription and epigenetic factors, Zhenqing Ye, Zhong Chen, Xun Lan, Stephen Hara, Benjamin Sunkel, Tim Huang, Laura Elnitski, Qianben Wang and Victor Jin (*highlight talk*)

11:35 – 11:50 am Coffee Break

- 11:50 – 12:20pm: Toward personalized cancer medicine: A cancer hallmark network framework, Edwin Wang
- 12:20 – 12:50pm: A comparative analysis of the cis-regulatory landscape between human and mouse, Feng Yue, Yin Shen, Samantha Kuan, Zhen Ye, Weisheng Wu, Ross Hardison, Mike Beer, Bing Ren & The mouse ENCODE consortium
- 12:50 – 1:10pm Prediction of promoters and enhancers using multiple DNA methylation-associated features, Woochang Hwang, Verity Oliver, Shannath Merbs, Heng Zhu and Jiang Qian.
- 1:10 – 1:30pm: Hong Cai, Timothy Lilburn, Changjin Hong, Jianying Gu, Rui Kuang and Yufeng Wang. Predicting and exploring network components involved in pathogenesis in the malaria parasite via novel subnetwork alignments

12:00pm

Meeting adjourn

Baker Room

9:45 – 1:15pm: **Biomarker Identification Methods**

Session Chair: Drs. Jianhua Ruan, Fuhai Li

- 9:45 – 10:05am Ghim Siong Ow and Vladimir Kuznetsov. Multiple signatures of a disease in potential biomarker space: Getting the signatures consensus and identification of novel biomarkers
- 10:05 – 10:25am Lin Wang, Fuhai Li, Jianting Sheng and Stephen T.C. Wong. A Computational Method for Clinically Relevant Cancer Stratification and Driver Mutation Module Discovery Using Personal Genomics Profiles
- 10:25 – 10:45am Jing Wang, Qi Liu and Yu Shyr. Dysregulated transcription across diverse cancer types reveals the importance of RNA-binding protein in carcinogenesis
- 10:45 – 11:05am: A Personalized Committee Classification Approach to Improving Prediction of Breast Cancer Metastasis, Md Jamiul Jahid, Tim Huang and Jianhua Ruan (*highlight talk*)

11:05 – 11:25am Coffee Break

- 11:25 – 11:50am Jian-Yu Shi, Zun Liu, Hui Yu and Yong-Jun Li. Drug Repositioning Via Drug-Target Pair Space Built by Within-Score and Between-Score Features
- 11:50 – 12:15pm William Budd, Greg Meyers, Jeri Dilts, Katherine O'Hanlon, John Woody, David Bostwick, John Drury and Thomas Reynolds. Next Generation Sequencing Reveals Disparate Population Frequencies Among Cytochrome P450 Genes: Clinical Pharmacogenomics of the CYP2 Family
- 12:15 – 12:40pm Fan Zhang, Mu Wang and Renee Drabier. Identification of novel alternative splicing biomarkers for breast cancer with LC/MS/MS and RNA-Seq
- 12:40 – 1:05pm Jasjit Banwait, Kaitlin Goettsch and Dhundy Bastola. Proteins localized to human mitochondria show structural element enrichment in their corresponding mRNA
- 1:05 – 1:25pm: Improve the prognostic estimation of cancer patients by incorporating the molecular data of tumor samples, Han Liang (*Highlight talk*)

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