

# 2015 International Conference on Intelligent Biology and Medicine

Indianapolis, IN, USA

## Program at-a-glance (November 13-15, 2015)

Friday, Nov 13	1:00 - 2:00pm	Keynote #1 Jiajie Zhang, Rm 118	
	2:15 - 3:45pm	Tutorial #1 NGS data analysis Yan Guo, Rm 118	Tutorial #2 Bioimage informatics Kun Huang and Lee Cooper, Rm 206
	4:00 - 5:30pm		Tutorial #3 Top-down proteomics Xiaowen Liu, Rm 206
	5:30 - 7:30pm	Reception, 2 <sup>nd</sup> floor auditorium lobby	
Saturday, Nov 14	8:30 - 9:30am	Keynote #2 Chris Sander, Rm 118	
	9:50 - 12:20pm	Session #1 NGS data analysis Chair: Kun Huang, Rm 206	Session #2 Systems Biology Chair: Yufei Huang, Rm 208
	12:20 - 1:30pm	Lunch, Tower Dining	
	1:30 - 2:50pm	Session #3 NGS data analysis II Chair: Yongsheng Bai, Rm 206	Session #4 Integrative Genomics Chair: Ewy Mathe, Rm 208
	3:10 - 4:30pm	Session #5 Genomics and Genetics Chair: Yidong Chen, Rm 206	Session #6 Epigenomics, Proteomics, and Metabolomics Chair: Lei Liu, Rm 208
	4:50 - 6:20pm	Keynote #3 A. Keith Dunker, Rm 118	
	7:00 - 9:00pm	Banquet Rathskeller Restaurant (401 E Michigan St, Indianapolis, IN 46204)	
Sunday, Nov 15	8:30 - 9:30am	Keynote #4 Sylvia Plevritis	
	9:50 - 12:20pm	Session #7 Biomarker Discovery and Precision Medicine Chair: Yan Guo, Rm 206	Session #8 Pharmacogenetics and Systems Medicine Chair: Yidong Chen, Rm 208

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Conference Agenda (November 13-15, 2015)

## Friday, November 13, 2015

10:00 – 5:00pm	Registration (1 <sup>st</sup> floor lobby)	
1:00 – 2:00pm	Keynote lecture (Room 118)	12
	Dr. <b>Jiajie Zhang</b> , The University of Texas School of Biomedical Informatics	
	<i>Beyond Big Data: New Trends in Biomedical Informatics Research and Education</i>	
	Session chair: Dr. Zhongming Zhao	
2:00 – 2:15pm	Coffee Break	
2:15 – 5:30pm	Concurrent tutorial sessions	
2:15 – 5:30pm	Tutorial #1 (Room 118)	18
	<i>Next Generation Sequencing Data Analysis</i>	
	Dr. Yan Guo Vanderbilt University	
2:15 – 3:45pm	Tutorial #2 (Room 206)	18
	<i>Bioimage informatics with a focus on histology image analysis</i>	
	Dr. Lee Cooper, Emory University Dr. Kun Huang, The Ohio State University	
3:45 – 4:00pm	Break	
4:00 – 5:30pm	Tutorial #3 (Room 206)	19
	<i>Computational Challenges in Top-Down Proteomics</i>	
	Dr. Xiaowen Liu Indiana University Purdue University Indianapolis	
5:30 – 7:30pm	Poster and Reception 2 <sup>nd</sup> floor auditorium lobby	

## Morning, Saturday, November 14, 2015

8:00 – 4:30pm	Registration (1 <sup>st</sup> floor lobby)	
<b>8:30 – 9:30am</b>	<b>Keynote lecture (Room 118)</b>	<b>13</b>
	Dr. <b>Chris Sander</b> , Memorial Sloan-Kettering Cancer Center	
	<i>Systems Biology in Action: Prediction of Large Protein 3D Structures and Design of Cancer Combination Therapy</i>	
	Session chair: Dr. Lang Li	
9:30 – 9:50am	Coffee break (2 <sup>nd</sup> floor auditorium lobby)	
<b>9: 50 – 12:20pm</b>	<b>Concurrent session #1. NGS data analysis</b> <b>Session chair: Dr. Kun Huang</b> <b>Room 206</b>	
9:50 – 10:10am	<i>Whole genomic sequence analysis of Bacillus infantis: defining the genetic blueprint of strain NRRL B-14911, an emerging cardiopathogenic microbe,</i> <b>Chandirasegaran Massilamany</b> , Akram Mohammed, John Dustin Loy, Tanya Purvis, Bharathi Krishnan, Rakesh Halekote Basavalingappa, Christy M. Kelley, Chittibabu Guda, Raul G. Barletta, Etsuko N Moriyama, Timothy P. L. Smith and Jay Reddy.	20
10:10 – 10:30am	<i>Statistical Modeling for Sensitive Detection of Low-Frequency Single Nucleotide Variants,</i> <b>Yangyang Hao</b> , Pengyue Zhang, Xiaoling Xuei, Harikrishna Nakshatri, Howard Edenberg, Lang Li and Yunlong Liu.	20
10:30 – 10:50am	<i>Detection of high variability in gene expression from single-cell RNA-seq profiling,</i> <b>Hung-I Chen</b> , Yufang Jin, Yufei Huang and Yidong Chen.	21
10:50 – 11:10am	<i>XMRF: An R package to Fit Markov Networks to High-Throughput Genetics Data,</i> <b>Zhandong Liu</b> , Ying-Wooi Wan, Genevera I. Allen, Yulia Baker, Eunho Young and Pradeep Ravikumar	22
11:10 – 11:20am	Break	
11:20 – 11:40am	<i>Read-Split-Run: An improved bioinformatics pipeline for identification of genome-wide non-canonical spliced regions using RNA-Seq data,</i> <b>Yongsheng Bai</b> , Jeff Kinne, Brandon Donham, Justin Hassler and Randal Kaufman.	22
11:40 – 12:00am	<i>An Overview of Copy Number Variations in the Lung Adenocarcinomas,</i> Mathew Palakal and Meeta Pradhan, presented by <b>Swapna Vidhur Daulatabad</b>	23
12:00 – 12:20pm	<i>Mitochondria Single Nucleotide Variant Among Six Different Cell Types,</i> Pan Zhang, David Samuels, Yu Shyr and <b>Yan Guo</b>	24

## Morning, Saturday, November 14, 2015

<b>9: 50 – 12:20pm</b>	<b>Concurrent session #2. Systems Biology</b> <b>Session chair: Dr. Yufei Huang</b> <b>Room 208</b>	
9:50 – 10:10am	<i>Towards understanding brain-gut-microbiome connections in Alzheimer's disease, <b>Rong Xu</b> and Quanqiu Wang.</i>	24
10:10 – 10:30am	<i>Investigating cellular network heterogeneity and modularity in cancer: a network entropy and unbalanced motif approach, Feixiong Cheng, Chuang Liu, Bairong Shen and Zhongming Zhao, presented by <b>Junfei Zhao</b></i>	25
10:30 – 10:50am	<i>A genomics-based systems approach towards drug repositioning for rheumatoid arthritis, <b>Rong Xu</b> and Quanqiu Wang.</i>	26
10:50 – 11:10am	<b>Highlight Talk #1: Co-expression analysis in single cells</b> <b>Dr. Jiang Qian</b> (Johns Hopkins University)	17
11:10 – 11:20am	Break	
11:20 – 11:40am	<i>State Feedback Control Design for Boolean Networks, <b>Rongjie Liu</b> and Yufang Jin.</i>	26
11:40 – 12:00am	<i>A Matrix Rank Based Concordance Index for Evaluating and Detecting Conditional Specific Co-Expressed Gene Modules, <b>Zhi Han</b>, Jie Zhang, Guoyuan Sun, Gang Liu and Kun Huang.</i>	27
12:00 – 12:20pm	<i>Comprehensive Comparison of Molecular Portraits between Cell Lines and Tumor in Breast Cancer, <b>Lijun Cheng</b>, Guanglong Jiang, Shijun Zhang, Aida Yazdanparast, Meng Li, Yunlong Liu and Sai Inavolu.</i>	27
<b>12:20 – 1:30pm</b>	<b>Lunch (Tower Dining Cafeteria)</b>	

## Afternoon, Saturday, November 14, 2015

<b>1:30 – 2:50pm</b>	<b>Concurrent session #3. NGS data analysis II</b> <b>Session chair: Dr. Yongsheng Bai</b> <b>Room 206</b>	
1:30 – 1:50pm	<i>Benchmarking of de novo assembly algorithms for nanopore data reveals optimal performance of OLC approaches, <b>Yeesri Cherukuri</b> and Sarath Chandra Janga.</i>	28
1:50 – 2:10pm	<i>Lipopolysaccharide treatment induces genome-wide pre-mRNA splicing pattern changes in mouse bone marrow stromal stem cells, <b>Ao Zhou</b>, Meng Li, Bo He, Weixing Feng, Keith Dunker, Yunlong Liu and Yue Wang.</i>	29
2:10 – 2:30pm	<i>Whole blood transcriptional profiling comparison between different milk yield of Chinese Holstein cows using RNA-seq data, Xue Bai, Bin Liu, Xiaoyang Ji, Wenguang Zhang and <b>Yongsheng Bai</b>.</i>	29

## Afternoon, Saturday, November 14, 2015

2:30 – 2:50pm	<i>Improving De Novo Metatranscriptome Assembly via Machine Learning Algorithms</i> , Hussein Mohsen, <b>Haixu Tang</b> and Yuzhen Ye.	30
<b>1:30 – 2:50pm</b>	<b>Concurrent session #4. Integrative Genomics</b> <b>Session chair: Dr. Ewy Mathe</b> <b>Room 208</b>	
1:30 – 1:50pm	<i>An integrative genomics approach for identifying novel functional consequences of PBRM1 truncated mutations in clear cell renal cell carcinoma (ccRCC)</i> , <b>Yuanyuan Wang</b> , Xingyi Guo, Michael Bray and Zhongming Zhao.	31
1:50 – 2:10pm	<i>Structured Sparse CCA for Brain Imaging Genetics via Graph OSCAR</i> , <b>Lei Du</b> , Heng Huang, Jingwen Yan, Sungeun Kim, Shannon Risacher, Mark Inlow, Jason Moore, Andrew Saykin and Li Shen.	32
2:10 – 2:30pm	<i>Integrative Analysis of Somatic Mutations and Transcriptomic Data to Functionally Stratify Breast Cancer Patients</i> , Jie Zhang, Zachary Abrams, Jeffrey Parvin and <b>Kun Huang</b> .	32
2:30 – 2:50pm	<i>Inference of tumor proliferation networks from functional and genomic data</i> , Noah Berlow and <b>Ranadip Pal</b> .	33
2:50 – 3:10pm	Coffee break (2 <sup>nd</sup> Floor Auditorium Lobby)	
<b>3:10 – 4:30pm</b>	<b>Concurrent session #5. Genomics and Genetics</b> <b>Session chair: Dr. Yidong Chen</b> <b>Room 206</b>	
3:10 – 3:30pm	<i>Expression Quantitative Locus Mapping for Identification of Hotspots Using an Empirical Bayes Mixture Model</i> , <b>Guanglong Jiang</b> , Yingqiang Fu, Zhigao Li, Shirin Ardeshirrouhanifard, Pengyue Zhang, Lijun Cheng, Lang Li and Arindom Chakraborty.	33
3:30 – 3:50pm	<i>Computational Tools for Genome-wide R-loops Identification and Characterization</i> , <b>Rongjie Liu</b> and Yidong Chen.	34
3:50 – 4:10pm	<i>Concordance of copy number loss and down-regulation of tumor suppressor genes: a pan-cancer study</i> , Min Zhao and <b>Zhongming Zhao</b> .	34
4:10 – 4:30pm	<b>Highlight Talk #2: On understanding molecular mechanisms of disease and genome interpretation</b> <b>Dr. Predrag Radivojac</b> (Indiana University)	17

## Afternoon, Saturday, November 14, 2015

<b>3:10 – 4:30pm</b>	<b>Concurrent session #6. Epigenomics, Proteomics, and Metabolomics</b> <b>Session chair: Dr. Lei Liu</b> <b>Room 206</b>	
3:10 – 3:30pm	<i>An HMM-based Hierarchical Model for Detecting Methylation Sites in MeRIP-Seq Data</i> , <b>Xiaodong Cui</b> , Jia Meng, Manjeet Rao, Yidong Chen and Yufei Huang.	35
3:30 – 3:50pm	<i>Whole Genome Sequencing reveals Enhancer as major Methylation Target during Human pluripotent stem Cell early neural Induction</i> , Gang Liu, Yang Bai, <b>Lei Liu</b> , Jiaxi Zhou, Pei Su, Jie Wang, Biqing Li, Lisha Lu, Tao Xiong and Fei Wang.	36
3:50 – 4:10pm	<i>Genomic data mining reveals a rich repertoire of transport proteins in Streptomyces</i> , Zhan Zhou, Ning Sun, Shanshan Wu, Yong-Quan Li and <b>Yufeng Wang</b> .	36
4:10 – 4:30pm	<b>Highlight Talk #3: Metabolomics as a powerful tool in biomarkers studies: an example in lung cancer</b> <b>Dr. Ewy Mathe</b> (the Ohio State University)	17
4:30 – 4:50pm	Break	
<b>4:50 – 6:20pm</b>	<b>Keynote lecture (Room 118)</b>  Dr. <b>A. Keith Dunker</b> , Indiana University School of Medicine  <i>Intrinsically Disordered Protein and the Origins of Complex Multicellular Organisms</i>  Session chair: Dr. Yunlong Liu	<b>14</b>
<b>7:00 – 9:00pm</b>	<b>Banquet</b>  <i>Rathskeller Restaurant</i> Street address: 401 E Michigan St, Indianapolis, IN 46204	

## Morning, Sunday, November 15, 2015

8:00 – 12:00pm	Registration (1 <sup>st</sup> floor lobby)	
<b>8:30 – 9:30am</b>	<b>Keynote lecture (Room 118)</b>	<b>16</b>
	Dr. <b>Sylvia Plevritis</b> , Stanford University	
	<i>Optimizing Combination Cancer Therapy Based on Single Cell Analysis</i>	
	Session chair: Dr. Kun Huang	
9:30 – 9:50am	Coffee break (2 <sup>nd</sup> floor auditorium lobby)	
<b>9: 50 – 12:20pm</b>	<b>Concurrent session #7. Biomarker Discovery and Precision Medicine</b> <b>Session chair: Dr. Yan Guo</b> <b>Room 206</b>	
9:50 – 10:10am	<i>CrossLink: A Novel Method for Cross-Condition Classification of Cancer Subtypes</i> , Chifeng Ma, Konduru Sastry, Mario Flores, Salah Gehani, Issam Al-Bozom, Yusheng Feng, Erchin Serpedin, Lotfi Chouchane, Yidong Chen and <b>Yufei Huang</b> .	37
10:10 – 10:30am	<i>Digitalization of a non-irradiated acute myeloid leukemia model</i> , Rudong Li, Hui Cheng, Tao Cheng and <b>Lei Liu</b> .	37
10:30 – 10:50am	<i>A Method for Identifying Discriminative Isoform-Specific Peptides for Clinical Proteomics Application</i> , Fan Zhang and <b>Jake Chen</b> .	38
10:50 – 11:10am	Break	
11:10 – 11:30am	<i>Classification of breast cancer patients using somatic mutation profiles and machine learning approaches</i> , <b>Suleyman Vural</b> , Xiaosheng Wang and Chittibabu Guda.	39
11:30 – 11:50am	<i>Towards precision medicine-based therapies for glioblastoma: interrogating human disease genomics and mouse phenotypes</i> , <b>Yang Chen</b> , Zhen Gao, Bingcheng Wang and Rong Xu.	40
11:50 – 12:10am	<i>A novel integrated gene coexpression analysis approach reveals a prognostic three-transcription-factor signature for glioma molecular subtypes</i> , Sujuan Wu, Junyi Li, Mushui Cao, Jing Yang, Yi-Xue Li and Yuan-Yuan Li.	41
<b>9: 50 – 12:20pm</b>	<b>Concurrent session #8. Pharmacogenetics and Systems Medicine</b> <b>Session chair: Dr. Yidong Chen</b> <b>Room 208</b>	
9:50 – 10:10am	<i>A simple gene set-based method accurately predicts the synergy of drug pairs</i> , Yu-Ching Hsu, Yu-Chiao Chiu, Yidong Chen, <b>Tzu-Hung Hsiao</b> and Eric Chuang.	41

10:10 – 10:30am	<i>Leveraging Syntactic and Semantic Graph Kernels to Extract Pharmacokinetic Drug Drug Interactions from Biomedical Literature</i> , Yaoyun Zhang, <b>Heng-Yi Wu</b> , Jun Xu, Jingqi Wang, Ergin Soysal, Lang Li and Hua Xu.	42
10:30 – 10:50am	<i>Improving alignment accuracy on homopolymer regions for semiconductor-based sequencing technologies</i> , <b>Weixing Feng</b> , Dingkai Xue, Fengfei Song, Sen Zhao, Ziwei Li, Duojiao Chen, Yangyang Hao and Yunlong Liu.	43
10:50 – 11:10am	Break	
11:10 – 11:30am	<i>PageRank influence analysis of protein-protein association networks in the malaria parasite Plasmodium falciparum</i> , <b>Xinran Yu</b> , Timothy Lilburn, Hong Cai, Jianying Gu, Turgay Korkmaz and Yufeng Wang.	43
11:30 – 11:50am	<i>Identification of rifampin-regulated functional modules and related microRNAs in human hepatocytes based on the protein interaction network</i> , Jin Li, Ying Wang, <b>Lei Wang</b> , Xuefeng Dai, Wang Cong, Weixing Feng, Chengzhen Xu, Yulin Deng, Todd C Skaar, Hong Liang and Yunlong Liu.	44
11:50 – 12:10am	<i>Using a Computational Model of Cancer to Test the Effectiveness of Imatinib Resistant GIST Drug Regimes</i> , Malcolm Callis and <b>David Liebner</b> .	45