

**International Conference on Intelligent Biology and Medicine**  
**August 11-13, 2013**

**Sunday, August 11**

**Concurrent Workshop: Next Generation Sequencing [Chairs: Kun Huang and Dongxiao Zhu]  
(Centennial Ballroom C)**

11:00-11:05am

**Opening Remarks**

**Session I:**

11:05-11:35 am

**Degui Zhi:** “Genotype calling from NGS data: incorporating haplotype information in reads”

11:35am-12:05 pm

**Xin Jin:** “Profiling of different types of *de novo* and rare inherited mutations in autism spectrum disorders revealed by whole genome sequencing”

12:05-12:35 pm

**Haixu Tang:** “Spontaneous mutations in bacteria revealed by whole-genome re-sequencing”

12:35-1:30 pm

**Light Lunch\***

**Session II:**

1:30-2:00 pm

**Yuzhen Ye:** “Computational approaches for metagenomic mining”

2:00-2:30 pm

**Maureen Sator:** “PePr: a Peak-calling and Prioritization Pipeline for Identifying DNA-binding Sites in Replicated ChIP-seq Experiments”

2:30-3:00 pm

**Peilin Jia:** “Personalized mutation network analysis of putative cancer genes from next-generation sequencing data”

3:00-3:30 pm

**Break\***

**Session III:**

3:30-4:00 pm

**Yunlong Liu:** “Detection of allelic specific expression from RNA-seq data”

4:00-4:30 pm

**Kun Huang:** “Whole transcriptome analysis in pharmacogenomics applications”

4:30-5:00 pm

**Lee Cooper:** “Integrating Image Phenotypes with Genomics: Applications in Gliomas”

**Concurrent Tutorial I: Introduction to Proteome Informatics [Chair: David Tabb]  
(Vanderbilt Ballroom)**

9:00-10:10 am

**David Tabb:** “Identifying proteins through LC-MS/MS”

10:10-11:20 am	<b>Yao-yi Chen:</b> “Comparative and quantitative proteomics”
11:20-11:30 am	<b>Break</b>
11:30am -12:00 pm	<b>Matthew Chambers:</b> “Proteomic repositories and spectral libraries”
12:00-12:30 pm	<b>Xiaojing Wang:</b> “Proteogenomics through RNA-Seq/proteomic combination”

***Concurrent Tutorial II: Pathway and network analysis tutorial [Chair: Alexander Pico]  
(Vanderbilt Ballroom)***

1:30-2:20 pm	<b>Alexander Pico:</b> “Network visualization and analysis with Cytoscape”
2:20-2:30 pm	<b>Break</b>
2:30-3:20 pm	<b>Alexander Pico:</b> “Building pathway models for analysis with WikiPathways”
3:20-3:30 pm	<b>Break*</b>
3:30-4:20 pm	<b>Jing Wang:</b> “Integrating multidimensional omics data over biological networks with NetGestalt”
4:20-5:00 pm	<b>Alexander Pico/Jing:</b> Wang Q/A and hands on

**Sunday, August 11, Evening**

6:30-9:00 pm	<b>Welcome Reception - Centennial Ballroom A &amp; B</b>
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**Monday, August 12, Morning**

8:00-8:30 am	<b>Light Breakfast*</b>
8:30-8:40 am	<b>Opening Remarks – Kevin Johnson, Centennial Ballroom A &amp; B</b>
8:40-9:30 am	<b>Keynote – Lucila Ohno-Machado:</b> “Sharing clinical and genomic data for research: Is it simply a matter of trust?” – Centennial Ballroom A & B
9:30-9:40 am	<b>Break</b>

***Concurrent Session I: Next Generation Sequencing (NGS): Analysis and Tools [Chair: Yan Guo]  
Centennial Ballroom A***

9:40-10:00 am	<b>Yan Guo:</b> “Evaluation of read count based RNAseq analysis methods”
10:00-10:20 am	<b>Qi Liu:</b> “Gene and isoform expression signatures associated with tumor stage in kidney renal clear cell carcinoma”

10:20-10:40 am	<b>Jimmy Yi:</b> “QChIPat: a quantitative method to identify distinct binding patterns for two biological ChIP-seq samples”
10:40-10:50 am	<b>Break*</b>
10:50-11:10 am	<b>Bingshan Li:</b> “QPLOT: a quality assessment tool for next generation sequencing data”
11:10-11:30 am	<b>Xue Zhong:</b> “A comparison of microRNA sequencing reproducibility and noise reduction using mirVana and TRIzol isolation methods”
11:30-11:50 am	<b>Xinjun Zhang:</b> “Correcting imbalanced reads coverage in bacterial transcriptome sequencing with extreme deep coverage”

***Concurrent Session II: Network Analysis [Chair: Zhandong Liu]  
Centennial Ballroom C***

9:40-10:00 am	<b>Akshata Udyavar:</b> “Co-expression network analysis identifies Spleen Tyrosine Kinase (SYK) as an oncogenic driver in small-cell lung cancer”
10:00-10:20 am	<b>Xu Shi:</b> “mAPC-GibbsOS: An integrated approach for robust identification of gene regulatory networks”
10:20-10:40 am	<b>Zhandong Liu:</b> “Molecular pathway identification using biological network-regularized logistic models”
10:40-10:50 am	<b>Break*</b>
10:50-11:10 am	<b>Naresh Doni Jayavelu:</b> “Reconstructing dynamic activities of microRNAs in EGFR signaling”
11:10-11:30 am	<b>Patrick Xuechun Zhao:</b> “DeGNServer: deciphering genome-scale gene networks through high performance reverse engineering analysis”
11:30-11:50 am	<b>Xiaosheng Wang:</b> “Computational analysis of transcriptional circuitries in human embryonic stem cells reveals multiple and independent networks”
11:50am-1:30pm	<b>Luncheon – The Commodore Grille</b>

**Monday, August 12, Afternoon**

1:30-2:20 pm	<b>Keynote – Dan Roden:</b> “Genomic variation modulating drug response: discovery and implementation” – Centennial Ballroom A & B
2:20-2:30 pm	<b>Break</b>
2:30-3:45 pm	<b>Poster Session I, Vanderbilt Ballroom (submission ID: 2,27,59,60,61,66,68,72,73,74,77,80,81,83,84,90)</b>
3:45-4:00 pm	<b>Break*</b>

4:00-5:15pm

**Poster Session II, Vanderbilt Ballroom (submission ID:  
6,16,39,40,56,58,70,76,78,79,82,85,86,87,88,89,91)**

## **Monday, August 12, Evening**

6:30-7:20 pm

**Banquet** – Centennial Ballroom

**Keynote – Keith Dunker:** “An intrinsically disordered protein Swiss-knife-like toolkit for signaling diversification”

7:20-7:50 pm

**Award Ceremony,** Centennial Ballroom

## **Tuesday, August 13, Morning**

8:00-8:30 am

**Light Breakfast\***

8:30-9:20 am

**Keynote – Yixue Li:** “Genome sequences of wild and domestic bactrian camels” – Centennial Ballroom A & B

9:20-9:30 am

**Break**

### ***Concurrent Session III: Genomics [Chair: Lu Xie] Centennial Ballroom A***

9:30-9:50 am

**Satish Srinivasan:** “MetaID: A novel method for identification and quantification of metagenomic samples”

9:50-10:10 am

**Lu Xie:** “Identification of gene fusions from human lung cancer mass spectrometry data”

10:10-10:30 am

**Arindom Chakraborty:** “Simultaneous inferences based on empirical Bayes methods and false discovery rates in eQTL data analysis”

10:30-10:40 am

**Break\***

10:40-11:00 am

**Guohui Ding:** “The de novo sequence origin of two long non-coding genes from an inter-genic region”

11:00-11:20 am

**Lang Li:** “New aQTL SNPs for the CYP2D6 identified by a novel mediation analysis of genome-wide SNP arrays, gene expression arrays and CYP2D6 activity”

11:20-11:40 am

**Ramanandan Prabhakaran:** “Aeromonas phages encode tRNAs for their overused codons”

### ***Concurrent Session IV: Systems Biology [Chair: Charles A Phillips] Centennial Ballroom C***

9:30-9:50 am

**William Budd:** “A networks method for ranking microRNA dysregulation in cancer”

9:50-10:10 am

**Pei Hao:** “Expression sensitivity analysis of human disease related

	genes”
10:10-10:30 am	<b>Wei Xiong:</b> “The centrality of cancer proteins in human protein-protein interaction network: A revisit”
10:30-10:40 am	<b>Break*</b>
10:40-11:00 am	<b>Yu Xue:</b> “The human kinase-substrate phosphorylation network rewired by genetic polymorphisms is heavily associated with cancers”
11:00-11:20 am	<b>Charles A Phillips:</b> “Differential Shannon entropy and differential coefficient of variation: alternatives and augmentations to differential expression in the search for disease-related genes”
11:20-11:40 am	<b>Naresh Doni Jayavelu:</b> “Dynamics of regulatory networks in gastrin treated adenocarcinoma cells”
11:50-1:00 pm	<b>Box lunch – The Commodore Grille</b>

## Tuesday, August 13, Afternoon

### *Concurrent Session V: Computational Medicine [Chair: Vladimir Kuznetsov] Centennial Ballroom A*

1:00-1:20 pm	<b>Chao Wu:</b> “Computational drug repositioning through heterogeneous network clustering”
1:20-1:40 pm	<b>Fan Zhang:</b> “Novel alternative splicing isoform biomarkers identification from high-throughput plasma proteomics profiling of breast cancer”
1:40-2:00 pm	<b>Chifeng Ma:</b> “BRCA-Monet: a breast cancer specific drug treatment mode-of-action network for treatment effective prediction using large scale microarray database”
2:00-2:20 pm	<b>Junfeng Jiang:</b> “Post genome-wide association studies functional characterization of prostate cancer risk loci”
2:20-2:30 pm	<b>Break*</b>
2:30-2:50 pm	<b>Sukriti Goyal:</b> “Mechanistic insights into mode of action of novel natural cathepsin L inhibitors”
2:50-3:10 pm	<b>Vladimir Kuznetsov:</b> “Genome wide survival prognostic analysis stratifies of breast cancers on three subclasses discriminated by a novel grading signature”
3:10-3:30 pm	<b>Wei Chen:</b> “Supervised method for Periodontitis phenotypes prediction based on microbial composition using 16S rRNA sequences”
3:30-3:50 pm	<b>Fan Zhang:</b> “Multiple biomarker panels for early detection of breast cancer in peripheral blood”

***Concurrent Session VI: Intelligent Computing [Chair: Qingguo Wang]  
Centennial Ballroom C***

1:00-1:20 pm	<b>Yuan-Yuan Li:</b> “DCGL v2.0: from differential co-expression analysis to differential regulation analysis”
1:20-1:40 pm	<b>Vicky Wang:</b> “GeneTopics - interpretation of gene sets via literature-driven topic models”
1:40-2:00 pm	<b>Nihar Sheth:</b> “BOTUX: Bayesian--like Operational Taxonomic Unit eXaminer”
2:00-2:20 pm	<b>Qi Li:</b> “Localization of Drosophila embryos using active contours in channel spaces”
2:20-2:30 pm	<b>Break*</b>
2:30-2:50 pm	<b>Reka Kelemen:</b> “Classification of T cell movement tracks allows for prediction of cell function”
2:50-3:10 pm	<b>Jakob Lykke Andersen:</b> “Generic strategies for chemical space exploration”
3:10-3:30 pm	<b>Naresh Doni Jayavelu:</b> “Dynamic network of transcription in gastrin treated adenocarcinoma cells”
3:30-3:50 pm	<b>Jing Wang:</b> “PREAL: prediction of allergen protein by maximum relevance minimum redundancy (mRMR) feature selection”
3:50-4:00 pm	<b>Closing Remarks – Centennial Ballroom A &amp; B</b>

**\*Denotes refreshments served in the Parthenon Room**