

# International Conference on Intelligent Biology and Medicine

April 22-24, 2012

## Sunday, April 22, Afternoon

*Concurrent Workshop: Next Generation Sequencing [Chair: Kun Huang]  
(Vanderbilt Ballroom A)*

1:00-1:05 pm                      **Opening Remarks**

### *Session I: RNA-seq Data Analysis*

1:05-1:30 pm                      **“Alt Event Finder: A tool for extracting alternative splicing events from RNA-seq data.”** Ao Zhou, Marcus R. Breese, Yangyang Hao, Howard J. Edenberg, Lang Li, Todd C. Skaar, and Yunlong Liu. IUPUI

1:30-1:55 pm                      **“SASeq: A Selective and Adaptive Shrinkage Approach to Detect and Quantify Active Transcripts using RNA-Seq.”** Tin Nguyen, Nan Deng, and Dongxiao Zhu, Wayne State University

1:55-2:20 pm                      **“DFI: Gene Feature Discovery in RNA-seq Experiments from Multiple Sources.”** Hatice Gulcin Ozer, Jeffrey D. Parvin, Kun Huang. The Ohio State University

2:20-2:40 pm                      **Break**

### *Session II: NGS Data Sharing and Systems Biology*

2:40-3:20 pm                      **“Data Sharing: Between Promises and Practices.”** Chris Coldren, Vanderbilt University (*20 minutes presentation + 20 minutes public discussion*)

3:20-3:55 pm                      **“Bayesian Inference and Modularity Analysis of the Hierarchical Structure for Dynamic ER $\alpha$  Regulatory Networks.”** Binhua Tang, Hang-Kai Hsu, Pei-Yin Hsu, Russell Bonneville, Su-Shing Chen, Tim H-M Huang, and Victor X. Jin. The Ohio State University / University of Texas

3:55-4:20 pm                      **“Next-generation Sequencing-based Analysis of DNA Methylation Using MethylCap-seq: Sample Exclusion, Validation, and the Contribution of Replicate Lanes.”** Michael P Trimarchi, Mark Murphy, David Frankhouser, Benjamin Rodriguez, John Curfman, Guido Marcucci, Pearly Yan, and Ralf Bundschuh. The Ohio State University

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

1:05-1:50 pm                      **David Tabb:** “Identifying proteins through LC-MS/MS”

1:50-2:00 pm                      **Break**

2:00-2:45 pm                      **David Tabb:** “Comparing proteomes and recognizing protein modifications”

2:45-3:00 pm	<b>Break</b>
3:00-3:30 pm	<b>Xiaojing Wang:</b> “Building customized protein databases from RNA-seq data”
3:30-4:00 pm	<b>Qi Liu:</b> “Enhancing miRNA target identification through proteomics”
4:00-4:30 pm	<b>Bing Zhang:</b> “Relating protein modification to gene expression changes”
4:30-4:50 pm	<b>Questions and Answers</b>

## **Sunday, April 22, Evening**

6:00-9:00 pm	<b>Welcome Reception - Centennial Ballroom</b>
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## **Monday, April 23, Morning**

8:00-8:30 am	<b>Light Breakfast*</b>
8:30-8:40 am	<b>Opening Remarks – Centennial Ballroom A &amp; B</b>
8:40-9:30 am	<b>Keynote – Brian D. Athey:</b> “Introducing tranSMART: an open source and community-driven data sharing and analytics platform for translational research” – Centennial Ballroom A & B
9:30-9:40 am	<b>Break*</b>

### ***Concurrent Session I: Genomics [Chair: Qi Liu] Centennial Ballroom A***

9:40-10:00 am	<b>Kun Huang:</b> “Redistribution of H3K4me2 on Neural Tissue Specific Genes During Mouse Brain Development”
10:00-10:20 am	<b>Pei Hao:</b> “Optimizing hybrid assembly of next-generation sequence data from <i>Enterococcus faecium</i> : a microbe with highly divergent genome”
10:20-10:40 am	<b>Qi Liu:</b> “Steps to ensure accuracy in genotype and SNP calling from Illumina sequencing data”
10:40-10:50 am	<b>Break*</b>
10:50-11:10 am	<b>Jennifer M. Fettweis:</b> “Genomic sequence analysis and characterization of <i>Sneathia amnii</i> sp. nov.”
11:10-11:30 am	<b>Kun Huang:</b> “Gene Co-expression Analysis Predicts Chromosomal Aberration Loci Associated with Colon Cancer Metastasis”
11:30-11:50 am	<b>Paul Hale:</b> “Genome wide meta-analysis of genetic susceptible genes for Type 2 Diabetes”

***Concurrent Session II: Systems Biology 1 [Chair: Yufeng Wang]  
Centennial Ballroom C***

- 9:40-10:00 am                    **Yufeng Wang:** “Module-based Subnetwork Alignments Reveal Novel Transcriptional Regulators in Malaria Parasite Plasmodium falciparum”
- 10:00-10:20 am                   **Lu Xie:** “Differential combinatorial network analysis identifies key regulatory modules and miRNA regulators related to venous metastasis of hepatocellular carcinoma”
- 10:20-10:40 am                   **Zhiwei Cao:** “Potential metabolic mechanism of girls’ central precocious puberty: a network analysis on urine Metabonomics data”
- 10:40-10:50 am                   **Break\***
- 10:50-11:10 am                   **Jianhua Xing:** “A strategy to study pathway cross-talks of cells under repetitive exposure to stimuli”
- 11:10-11:30 am                   **Lijun Cheng:** “Gene Interaction Networks Based on Kernel Correlation Metrics”
- 11:30-11:50 am                   **Ru Shen:** “Mining functional subgraphs from cancer protein-protein interaction networks”
- 11:55am-1:25pm                   **Luncheon – The Commodore Grille**

**Monday, April 23, Afternoon**

- 1:30-2:20 pm                    **Keynote – Randolph A. Miller:** “A General Introduction to the Art and Practice of Clinical Decision Support” – Centennial Ballroom A & B
- 2:20-2:30 pm                    **Break\***

***Concurrent Session III: Algorithms and Methods [Chair: Frank Hsu]  
Centennial Ballroom A***

- 2:30-2:50 pm                    **Linxia Wan:** “Automatically Clustering Large-scale miRNA Sequences: Methods and Experiments”
- 2:50-3:10 pm                    **Carl Barton:** “Querying Highly Similar Sequences”
- 3:10-3:30 pm                    **D. Frank Hsu:** “Combining ChIP-seq Peak Detection Systems Using Combinatorial Fusion”
- 3:30-3:50 pm                    **Zhiwei Cao:** “Similarity between segments in protein conformational epitopes and MHC II peptides”
- 3:50-4:00 pm                    **Break\***
- 4:00-4:20 pm                    **Yufei Huang:** “A Bayesian Decision Fusion Approach for microRNA Target Prediction”
- 4:20-4:40 pm                    **Alexander Statnikov:** “New Methods for Separating Causes from Effects in Genomics Data”

4:40-5:00 pm **Murat Demirer:** “Sub-similarity Matching Based on Data mining with Dihedral Angles”

5:00-5:20 pm **Pei-Fang Su:** “Statistical aspects of omics data analysis using the random compound covariate”

***Concurrent Session IV: Intelligent Computing [Chair: Siddhartha Jonnalagadda]  
Centennial Ballroom C***

2:30-2:50 pm **Lijing Xu:** “Literature Aided Determination of Data Quality and Statistical Significance Threshold for Gene Expression Studies”

2:50-3:10 pm **Tingting Qin:** “Signaling network prediction by the Ontology Fingerprint enhanced Bayesian network”

3:10-3:30 pm **Cheng Zhu:** “A vertex similarity-based framework to discover and rank orphan disease-related genes”

3:30-3:50 pm **Yonghui Wu:** “Identifying the status of genetic lesions in cancer clinical trial documents using machine learning”

3:50-4:00 pm **Break\***

4:00-4:20 pm **Pei Hao:** “A cross-species analysis method to analyze animal models’ similarity to human’s disease state”

4:20-4:40 pm **Adeshola Adefioye:** “Multi-view Spectral Clustering and its Chemical Application”

4:40-5:00 pm **Siddhartha Jonnalagadda:** “A new iterative method to reduce workload in systematic review process”

5:00-5:20 pm **Michael Berry:** “PolyLens: Software for Map-based Visualization and Analysis of Genome-scale Polymorphism Data”

**Monday, April 23, Evening**

5:30pm-7:00pm **Poster Session and Refreshments  
Vanderbilt Ballroom**

**Tuesday, April 24, Morning**

8:30-9:20 am **Keynote – Wen-Hsiung Li:** “Protein Structure, Function and Classification” – Centennial Ballroom A & B

9:20-9:30 am **Break\***

***Concurrent Session V: Applications and Tools [Chair: Han Liang]  
Centennial Ballroom A***

9:30-9:50 am **Han Liang:** “BM-Map: an efficient software package for accurately allocating multireads of RNA-sequencing data”

9:50-10:10 am **Catherine Jayapandian:** “A Semantic Proteomics Dashboard (SemPoD) for Proteomics Data Management in Translational Research”

10:10-10:30 am	<b>Yupeng He:</b> “CTF: A CRF-based Transcription Factor Binding Site Finding System”
10:30-10:40 am	<b>Break*</b>
10:40-11:00 am	<b>Fei Ye:</b> “Analysis of High-Throughput RNAi Screening Data in Identifying Genes Mediating Sensitivity to Chemotherapeutic Drugs: Statistical Approaches and Perspectives”
11:00-11:20 am	<b>Sachin Shetty:</b> “Development of an Integrated Network Visualization and Graph Analysis Tool for Biological Networks”
11:20-11:40 am	<b>Jennifer M. Fettweis:</b> “Species-level classification of the vaginal microbiome”

***Concurrent Session VI: Systems Biology 2 [Chair: Jingchun Sun]  
Centennial Ballroom C***

9:30-9:50 am	<b>Adam Richards:</b> “Revealing functionally coherent subsets using a spectral clustering and an information integration approach”
9:50-10:10 am	<b>Kun Huang:</b> “Identify Condition Specific Gene Co-expression Networks”
10:10-10:30 am	<b>Meeta Pradhan:</b> “Cliques for identification of gene signatures for colorectal cancer across population”
10:30-10:40 am	<b>Break*</b>
10:40-11:00 am	<b>Jiang Qian:</b> “DNA Methylation Dependent Protein-DNA Interactions”
11:00-11:20 am	<b>Raphael Mourad:</b> “A dynamic time order network for time-series gene expression data analysis”
11:20-11:40 am	<b>ZhiHui (Jack) Luo:</b> “An iterative searching and ranking algorithm for prioritizing pharmacogenomics genes”
11:40-11:50 am	<b>Closing Remarks – Centennial Ballroom A &amp; B</b>
11:50-12:00 pm	<b>Box Lunch – The Commodore Grille</b>

**\*Denotes refreshments served in the Vanderbilt Ballroom**