

**39th Symposium on the Interface:
Computing Science and Statistics**

**Theme:
Systems Biology**

May 23–26, 2007

**DoubleTree Hotel
Philadelphia, Pennsylvania**

PROGRAM CHAIR

**Alan J. Izenman
Temple University**

PROGRAM CO-CHAIR

**Zoran Obradovic
Temple University**

The Interface Symposium is hosted by the **Center for Statistical & Information Science (Alan J. Izenman, Director)**, the **Department of Statistics**, and the **Center for Information Science & Technology (Zoran Obradovic, Director)**, Temple University.

Wednesday, 23rd May 2007

8:00 a.m. – 12:00 noon

ORCHESTRA ROOM

SHORT COURSE 1

**Computational Systems Biology of Cancer:
Measuring, Mining, & Modelling**

Bud Mishra

Courant Institute, New York University

1:30 p.m. – 5:30 p.m.

ORCHESTRA ROOM

SHORT COURSE 2

**Copy-Number Variation in the Genome:
Technologies, Statistics, & Applications**

John Marioni

**University of Cambridge, England
and**

Simon Tavare

**University of Cambridge, England
& University of Southern California**

6:00 p.m. – 8:00 p.m.

INTERFACE BOARD MEETING

8:00 p.m. – 10:00 p.m.

EVENING MIXER

Thursday, 24th May 2007

8:00 a.m. – 8:15 a.m.

ORMANDY WEST

WELCOME

Kenneth Soprano
Vice-President for Research & Graduate Studies
Temple University

8:15 a.m. – 9:45 a.m.

ORMANDY WEST

KEYNOTE ADDRESS

How the Genome and the Computer Have Changed
Biological Science

David Botstein
Princeton University

9:45 a.m. – 10:30 a.m.

BREAK

Technical sessions begin at 10:30 a.m.

10:30 a.m. – 12:10 p.m.

I-1 (ARIA-A)

Genetic Association Studies

Organizer: Charles Kooperberg, University of Washington

10:30 a.m. *Quantifying and Extracting Information in Whole-Genome Association Studies*, **Dan L. Nicolae**, University of Chicago

11:00 a.m. *An Adaptive Clustering Algorithm to Model Haplotype-Disease Association in Case-Control Association Studies*, **James Y. Dai**, University of Washington

11:30 a.m. *Patterns of Linkage Disequilibrium Reveal Errors and Deletions in Population Genetic Data*, **Paul Scheet**, University of Michigan

12:00 noon. *Floor Discussion*

I-2 (ARIA-B)

Statistical Methods in Proteomics

Organizer: Françoise Seillier-Moiseiwitsch, Georgetown University

10:30 a.m. *Statistical Preprocessing of Mass Spectrometry Data*, **Kevin Coombes**, MD Anderson Cancer Center, Houston

11:00 a.m. *Modeling and Spot Detection of Two-Dimensional Gels*, **Kimberley Sellers**, Georgetown University

11:30 a.m. *Analysis of 2D-Gels: A Global Approach*, **Valeriy Korostyshevskiy**, Georgetown University, & **Françoise Seillier-Moiseiwitsch**, Georgetown University

12:00 noon. *Floor Discussion*

I-3 (CONCERTO-A)

Problems and Prospects for Integrative Biology and the Grid

Organizers: J. Robert Beck, Fox Chase Cancer Center, Philadelphia

10:30 a.m. *Good Cells, Bad Cells, and the Grid*, **J. Robert Beck**, Fox Chase Cancer Center, Philadelphia

11:00 a.m. *Trustable Architectures for a Biomedical Research Grid*, **Frank J. Manion**, Fox Chase Cancer Center, Philadelphia

11:30 a.m. *Parallel Implementation of Nonnegative Matrix Factorization (NMF) Algorithms using High-Performance Computing (HPC) Cluster*, **Karthik Devarajan** and **Guoli Wang**, Fox Chase Cancer Center, Philadelphia

12:00 noon. *Floor Discussion*

I-4 (CONCERTO-B) **Modelling of Ethanol Abuse and HIV/AIDS**

Organizer: Yasmin H. Said, George Mason University

10:30 a.m. *Developing Integrative Models of the Interaction of Alcohol Use and HIV/AIDS Progression Using Behavioral and Biological "Bedside and Bench" Research*, **Kendall J. Bryant & Ron Braithwaite**, National Institute on Alcohol Abuse & Alcoholism/NIH

11:00 a.m. *Assessing Interventions Related to Negative Effects of Ethanol on HIV/AIDS Spread*, **Yasmin H. Said & Edward J. Wegman**, George Mason University

11:30 a.m. *Using Research Data to Parameterize Risky Sexual Behavioral and Alcohol Use*, **W.F. Wiczorek, K.S. Marczynski, T.H. Nochajski & S. Tetewsky**, Center for Health and Social Research, Buffalo State, Buffalo, NY

12:00 noon *Floor Discussion*

12:10 p.m. – 2:00 p.m.

LUNCH

2:00 p.m. – 3:40 p.m.

I-5 (ARIA-A)

Statistical Methods for Genetic Association Studies

Organizer: Gang Zheng, National Heart, Lung, and Blood Institute, Bethesda, MD

2:00 p.m. *Aspects of the Statistical Multiple Comparisons Problems in Genetic Association Studies of Sporadic Disease, Philip Rosenberg, National Cancer Institute, Bethesda, MD*

2:30 p.m. *Conditional Likelihood Methods for Haplotype-Based Association Analysis Using Matched Case-Control Data, Jinbo Chen, University of Pennsylvania*

3:00 p.m. *Two-Stage Analyses of Case-Control Genetic Associations, Gang Zheng, National Heart, Lung, and Blood Institute, Bethesda, MD*

3:30 p.m. *Floor Discussion*

I-6 (ARIA-B)

Proteomics Data Analysis

Organizer: Slobodan Vucetic, Temple University

2:00 p.m. *From Diverse Genomics Data to Protein-Protein Interaction Networks, Olga Troyanskaya, Princeton University*

2:30 p.m. *Enhancing the Analysis of MS Proteomic Profiles Using Prior Knowledge and Past Data Repositories, Milos Hauskrecht, University of Pittsburgh*

3:00 p.m. *Methods for Protein Identification and Quantification From Tandem Mass Spectrometry Data, Predrag Radivojac, Indiana University*

3:30 p.m. *Floor Discussion*

I-7 (CONCERTO-A)

Genomic Analysis Across Platforms

Organizer: Giovanni Parmigiani, Johns Hopkins University

2:00 p.m. *Multiple Laboratory Comparisons of Microarray Platforms, Rafael Irizarry, Johns Hopkins University*

2:30 p.m. *A Hierarchical Model and R Software for Finding Differential Gene Expression in Multiple High-Throughput Platforms*, **Robert Scharf**, Johns Hopkins University

3:00 p.m. *Finding significant large-average sample-variable blocks in high-dimensional data*, **Andrew Nobel**, University of North Carolina, Chapel Hill

3:30 p.m. *Floor Discussion*

I-8 (CONCERTO-B)

Systems Approaches for Alcohol Use Modelling

Organizer: Yasmin H. Said, George Mason University

2:00 p.m. *Systems Perspectives on Prevention of Alcohol-Related Problems: Research Opportunities and Resources*, **Gregory Bloss**, NIH/National Institute on Alcohol Abuse and Alcoholism

2:25 p.m. *Systems Ecology and Community Systems: Understanding Social Problems in Social Terms*, **Paul J. Gruenewald**, PIRE

2:45 p.m. *Applications of Small World Network Models in Alcohol Epidemiology*, **Robert A. Wilson**, University of Delaware

3:05 p.m. *Multilevel Examination of Neighborhood Influences on Drinking-and-Driving Behavior*, **W.F. Wiczorek; K.S. Marczynski; A. Delmerico; S.J. Tetewsky**, Buffalo State College, Buffalo, NY

3:30 p.m. *Floor Discussion*

C-1 (MAESTRO-A)

Analysis of Microarray Experiments

2:00 p.m. *An Iterative Nonparametric Quasi-Likelihood Method for Modeling Gene Expression Measurements*, **Qing Li, Nan Lin**, Washington University in St. Louis

2:20 p.m. *The High-level Similarity of Some Disparate Affymetrix GeneChip Expression Measures*, **Nandini Raghavan, Dhammika Amaratunga**, J&JPRD

2:40 p.m. *Graphical Modeling for Discrete Random Variables with Application to Tissue Microarray (TMA) Experiments*, **Corinne Dahinden, Peter Bühlmann**, ETH Zurich, Switzerland

3:00 p.m. *Consistent Probe Performance Yields Solutions Capable of Classification Across Independent Experiments*, **Kevin Thompson**, George Mason University

3:20 p.m. *Analysis of Comparative Genomic Hybridization Array Data Using Statistical Process Control*, **Xia Li, Adam Allred, Matthew Walter, Rhonda Ries, Timothy Ley**, and **William Shannon**, Washington University in St. Louis School of Medicine

3:40 p.m. – 4:00 p.m.

BREAK

4:00 p.m. – 5:40 p.m.

I-9 (ARIA-A)

Computational Analysis of Gene Regulation

Organizer: Vincent Carey, Harvard Medical School

4:00 p.m. *Learning Regulatory Programs That Accurately Predict Gene Expression*, **Christina Leslie**, Columbia University

4:30 p.m. *SVMs and Probabilistic Approaches for Classifying Promoters*, **Anirvan Sengupta**, Rutgers University

5:00 p.m. *Data-Driven Biophysical Modeling of Gene Expression Regulation*, **Harmen Bussemaker**, Columbia University

5:30 p.m. *Floor Discussion*

I-10 (ARIA-B)

Information Extraction from Biomedical and Clinical Text

Organizer: David Shera, Children's Hospital of Pennsylvania

4:00 p.m. *The Global Linguistic Challenge and Approaches*, **Kevin Cohen**, University of Colorado Health Science Center

4:30 p.m. *Mining the Bibliome: Supervised Extraction of Biomedical Entities from Text for Biological Application*, **Peter S. White**, Children's Hospital of Pennsylvania

5:00 p.m. *Striving to Make Text-Mining Useful for Disease-Gene Identification*, **Andrey Rzhetsky**, Columbia University

5:30 p.m. *Floor Discussion*

I-11 (CONCERTO-A)

Computational and Statistical Methods for Genome-Wide Studies of Biological Systems

Organizer: Sandrine Dudoit, University of California, Berkeley

Chair: Rebecka Jornsten, Rutgers University

4:00 p.m. *Systems Biology Insights From Host-Pathogen Interaction Studies*, **Imola K. Fodor**, Lawrence Livermore National Laboratory

4:30 p.m. *Simple Models for Integrating Gene Expression and Genetic Marker Data to Characterize Disease-Related Genes*, **Steve Horvath**, University of California, Los Angeles

5:00 p.m. *Enhancing Motif Finding Models Using Multiple Sources of Genome-Wide Data*, **Sunduz Keles**, University of Wisconsin

5:30 p.m. *Floor Discussion*

C-2 (CONCERTO-B)

Visualization of Biological Data

4:00 p.m. *Integrating Network Views and Inference with Explorase*, **Xiaoyong Sun**, **Michael Lawrence**, **Dianne Cook**, Iowa State University

4:20 p.m. *Network Models for time course microarray data*, **Inoue, L.Y.T., Telesca, D., Neira, M., Nelson, C., Gleave, M., Etzioni, R.**, University of Washington

4:40 p.m. *“Heated” 3D Scatterplots for the Simultaneous Display of cgh Array and Gene Expression Data*, **Juergen Symanzik**, Utah State University, and **William Shannon**, Washington University School of Medicine

5:00 p.m. *RJaCGH, a method for the analysis of CGH arrays with a Hidden Markov Model fitted via Reversible Jump MCMC*, **Oscar M. Rueda, Ramon Diaz-Uriarte**, Spanish National Cancer Center, Madrid, Spain

5:20 p.m. *Visualization and Analysis of High Resolution Cell Image Data*, **Roy Welsch**, Massachusetts Institute of Technology

7:00 p.m. – 10:30 p.m.

CONFERENCE BANQUET

A View of Systems Biology from 30,000 Feet

Richard Klavans
SciTech Strategies, Inc.

Friday, 25th May 2007

8:30 a.m. – 10:10 a.m.

I-12 (ARIA-A)
Data and Decision Fusion

Organizers: Frank Hsu, Fordham University, & Amy Braverman, JPL

8:30 a.m. *Uniform Random Guesses and Random Decision Forests*, **Tin K. Ho**, Bell Laboratories, Alcatel-Lucent

9:00 a.m. *A Censored-Data Approach to Modelling Partial Rankings on the Ranking Lattice*, **Guy Lebanon**, Purdue University

9:30 a.m. *Regulatory Module Discovery with Heterogeneous Data by Multipartite Coclustering*, **Li-San Wang**, University of Pennsylvania

10:00 a.m. *Floor Discussion*

I-13 (ARIA-B)
Computational Techniques for Structural Genomics

Organizer: Daisuke Kihara, Purdue University

8:30 a.m. *In Silico Prediction of Protein Interactions: Nothing That Nature Does Not Already Know*, **Carlos J. Camacho**, University of Pittsburgh

9:00 a.m. *From Sequences and Structures to Interactions of Proteins: Some Recent Developments*, **Yaoqi Zhou**, IUPUI, Indianapolis

9:30 a.m. *Surface-Shape-Based Protein Structure Classification and Search*, **Daisuke Kihara**, Purdue University

10:00 a.m. *Floor Discussion*

I-14 (CONCERTO-A)

Biological Networks

Organizer: Natasa Przulj, University of California, Irvine

8:30 a.m. *Predicting domain interactions from protein-protein interaction networks*

Teresa Przytycka, NIH/NLM/NCBI

8:50 a.m. *Learning Biology From Networks*, **Chris Wiggins**, Columbia University

9:15 a.m. *Geometric Local Structure in Biological Networks*, **Natasa Przulj**, University of California, Irvine

9:35 a.m. *Algorithmic and Analytical Methods for Functional Characterization of Molecular Interaction Networks*, **Mehmet Koyuturk**, Purdue University

10:00 a.m. *Floor Discussion*

I-15 (CONCERTO-B)

JCGS Highlights

Organizer: Luke Tierney, University of Iowa & David van Dyk, University of California, Irvine

Chair: David van Dyk, University of California, Irvine

8:30 a.m. *Simulating Two-Dimensional Gaussian Random Fields: Fast and Exact Algorithms*, **Hana Sevcikova**, University of Washington

9:00 a.m. *Flexible, Optimal Matching for Comparative Studies: A Network Flows Algorithm and an R Package*, **Ben B. Hansen**, University of Michigan, & **Stephanie Olsen Klopfer**, Merck Research Laboratories

9:30 a.m. *Mean-Mean Multiple Comparison Displays for Families of Linear Contrasts*, **Richard M. Heiberger**, Temple University

10:00 a.m. *Floor Discussion*

C-3 (MAESTRO-A)

Protein-Protein Interaction and Microarrays

8:30 a.m. *Integration Of Relational And Hierarchical Network Information: Prediction Of Protein Function*, **Xiaoyu Jiang**, **Eric Kolaczyk**, **Simon Kasifm**, Boston University

8:50 a.m. *Could Logistic Model Predict Yeast Protein-Protein Interaction from Subcellular Localization Pattern?*, **Junfeng Liu**, West Virginia University, **Hongyu Zhao**, Yale University, **Jun Tan**, & **E. James Harner**, West Virginia University

9:10 a.m. *A Computational Model and Simulation of Demyelination Phenomenon in Neuroimmunological Disorders*, **A. Zakharyan**, University of Colorado, **K. Kafadar**, University of Colorado, **D. Skundric**, Wayne State University School of Medicine, and **V. Zakarian**, University of Colorado

9:30 a.m. *Using 'Flex' Motifs in Predictive Modeling of Antisense Oligonucleotides to Radically Increase Success Rate*, **Tamara B. Sipes**, SciberQuest, Inc.

9:50 a.m. *Use of Dynamic Warping for the Alignment of DGGE Gels*, **David Baird**, AgResearch, Lincoln, New Zealand

10:10 a.m. – 10:30 a.m.

BREAK

10:30 a.m. – 12:10 p.m.

I-16 (ARIA-A)

Indexing and Search in Biological Data

Organizer: Mohammed J. Zaki, Rensselaer Polytechnic Institute

10:30 a.m. *Indexed Biosequence Similarity Search in the Age of Comparative Genomics*, **Jeremy Buhler**, Washington University in St. Louis

11:00 a.m. *Indexing for Success: Effective Index-Based Methods for Querying Biological Sequences*, **Jignesh Patel**, University of Michigan

11:30 a.m. *Querying and Mining in Graph Databases*, **Ambuj Singh**, University of California, Santa Barbara

12:00 noon. *Floor Discussion*

I-17 (ARIA-B)

Integrative Systems Biology in Cancer Research

Organizer: Ramana V. Davuluri, Ohio State University

10:30 a.m. *Stochastic Modelling and Estimation in Dynamic Cellular Networks*, **Mike West**, Duke University

11:00 a.m. *Integration of Annotations for Guiding Analysis of Signaling in Cancer Cells*, **Michael Ochs**, Fox Chase Cancer Center, Philadelphia

11:30 a.m. *Modern Data-Mining Tools in Predicting Cis-Regulatory Transcriptional Modules: A Case Study with a Random Forest Approach*, **Ramana Davuluri**, Ohio State University

12:00 noon. *Floor Discussion*

I-18 (CONCERTO-A)

Analysis of DNA Barcode Data

Organizer: Javier Cabrera, Rutgers University, & Woollcott K. Smith, Temple University

10:30 a.m. *DNA Barcoding: Linking Biodiversity, Biotechnology, and Bioinformatics*, **David Schindel**, Consortium for the Barcode of Life

11:00 a.m. *Weighted Chinese Restaurant Process for clustering barcodes*, **Javier Cabrera**, Rutgers University, **John Lau**, U Bristol, **Albert Y Lo**, Hong Kong UST

11:30 a.m. *Model-based species identification using DNA barcodes*, **Bogdan Pasaniuc**, **Sotirios Kentros**, **Ion Mandoiu**, University of Connecticut

12:00 p.m. *Floor Discussion*

I-19 (CONCERTO-B)

Best of SIAM Data Mining 2007

Organizer: Vipin Kumar

Chair: Arnold Goodman, University of California, Irvine

10:30 a.m. *Harmonium-Based Models for Semantic Video Representation and Classification*, **Jun Yang**, **Yan Liu**, **Eric Xing**, **Alexander Hauptmann**

10:50 a.m. *Less is More: Compact Matrix Decomposition for Large Sparse Graphs*,

Jimeng Sun, Yinglian Xie, Hui Zhang, Christos Faloutsos

11:10 a.m. *ROAM: Rule- and Motif-Based Anomaly Detection in Massive Moving Object Data Sets*, Xiaolei Li, Jiawei Han, Sangkyum Kim, Hector Gonzalez

11:30 a.m. *Multi-way Clustering on Relation Graphs*, Arindam Banerjee, Sugato Basu, Srujana Merugu

11:50 a.m. *Fast Newton-type Methods for the Least Squares Nonnegative Matrix Approximation Problem*, Dongmin Kim, Suvrit Sra, Inderjit Dhillon

C-4 (MAESTRO-A)

The Lasso and Variable Selection

10:30 a.m. *Drug Target Prediction Using Simultaneous Equation Models of Gene Regulatory Networks*, Yingchun Zhou, Elissa Burk, Tim Gardner, Eric Kolaczyk, Boston University

10:55 a.m. *GLARS: S-PLUS and R package for Generalized Least Angle Regression*, Tim Hesterberg, Insightful Corp.

11:20 a.m. *Estimating High-Dimensional Directed Acyclic Graphs with the PC-Algorithm*, Markus Kalisch, Peter Bühlmann, ETH, Zürich, Switzerland.

11:45 a.m. *The Group and Smoothed Lasso for High-Dimensional Data*, Lukas Meier, Peter Bühlmann, ETH Zürich, Switzerland

12:10 noon – 2:00 p.m.

LUNCH

2:00 p.m. – 3:40 p.m.

I-20 (ARIA-A)

Methods for Integrating Disparate Molecular Datasets for Prediction

Organizer: Peter S. White, Children's Hospital of Pennsylvania

2:00 p.m. *Integrative Genomics of Human Neuroblastoma: Promises and Pitfalls for Translation to the Clinic*, **John Maris**, Children's Hospital of Pennsylvania

2:30 p.m. *Data Integration for Disease Pathway Mapping*, **Michael Krauthammer**, Yale University

3:00 p.m. *Ontology Similarity Networks and Database Interoperability*, **Yves Lussier**, University of Chicago

3:30 p.m. *Floor Discussion*

I-21 (ARIA-B)

Roles of Protein Intrinsic Disorder in Interaction Networks

Organizer: Keith Dunker, Indiana University

Chair: Zoran Obradovic, Temple University

2:00 p.m. *The Interplay Between Alternative Splicing and Intrinsic Disorder and Its Implications on Multicellular Complexity*, **Pedro Romano**, Indiana University & Purdue University, Indianapolis

2:20 p.m. *Proteomics Studies of Intrinsically Unstructured Proteins (IUPs) in Mammalian Cells*, **Charles Galea**, St. Jude Children's Research Hospital, Memphis, TN

2:40 p.m. *Structure and Function of Rapidly-Evolving Proteins Involved in Yeast Protein-Interaction Networks*, **Celeste Brown**, University of Idaho

3:00 p.m. *Exploring Relationships Among Protein Disorders, Network Hubs, and Disease Targets in Protein Interactome Studies*, **Jake Chen**, Indiana University & Purdue University, Indianapolis

3:30 p.m. *Floor Discussion*

I-22 (CONCERTO-A)

IASC Session: Current Issues in Statistical Biocomputing

Organizer: Michael G. Schimek, Medical University of Graz, Austria, & Masaryk University, Brno, Czech Republic

2:00 p.m. *Pathway-Specific Predictors for Gene Expression Data*, **Alexander Ploner**, Karolinska Institute, Stockholm, Sweden

2:30 p.m. *A Median Absolute Deviation Method for Detecting Copy-Number Changes in Array-CGH Data*, **Eva Budinska**, Masaryk University, Czech Republic, **Eva Gelnarova**, Masaryk University, Czech Republic, & **Michael G. Schimek**, Medical University of Graz, Austria, & Masaryk University, Czech Republic

3:00 p.m. *Building Phenotypic Hierarchies From Nested Effects of Gene Perturbations*, **Florian Markowetz**, Princeton University, **Olga G. Troyanskaya**, Princeton University, & **Rainer Spang**, Max-Planck-Institute for Molecular Genetics, Berlin, Germany

3:30 p.m. *Floor Discussion*

C-5 (CONCERTO-B)

Mutations, Metatarsals, Metabolomics, Metabolics, and Maps

2:00 p.m. *Maximum Likelihood Estimation of Mutation Rates Under the Haldane Model*, **Qi Zheng**, Texas A&M University System School of Rural Public Health

2:20 p.m. *Using a Triangle to Diagnose and Evaluate a Skeletal Deformity*, **Philip H. Demp**, Temple University

2:40 p.m. *Detecting Peaks in Gas and Liquid Chromatography Mass Spectrometric Metabolomics Data*, **Michael Lawrence**, **Heike Hofmann**, **Suh-yeon Choi**, **Dianne Cook**, **Olga Nikolova**, **Eve Wurtele**, Iowa State University

3:00 p.m. *Indexing and Searching Databases of Metabolic Pathways*, **Robert Grossman**, University of Illinois at Chicago and Open Data Group, **Xiangjun Liu**, University of Illinois at Chicago, and **Greeshma Neglur**, University of Illinois at Chicago

3:20 p.m. *Strategies for Genome Scans in Complex Pedigrees Using Dense Marker Maps*, **Natascha Vukasinovic**, Monsanto Company, Animal Genomics and Breeding, St. Louis, MO

3:40 p.m. – 4:00 p.m.

BREAK

4:00 p.m. – 5:40 p.m.

I-23 (ARIA-A) **Immunological Proteomics**

Organizer: Keith Baggerly, MD Anderson Cancer Center

4:00 p.m. *The Biology of Immunological Assays: A Statistician's Perspective on Measuring Protein*, **Keith Baggerly**, MD Anderson Cancer Center

4:30 p.m. *Statistical Analysis of Reverse-Phase Protein Arrays*, **Shannon Neeley**, Rice University

5:00 p.m. *Issues in the Processing of Humoral Immune Response Array Data From Microarrays*, **Debashis Ghosh**, University of Michigan

5:30 p.m. *Floor Discussion*

I-24 (ARIA-B) **Inferring Genetic Networks from Genomics Data**

Organizer: Grace S. Shieh, Academia Sinica, Taiwan

4:00 p.m. *Computational Challenges for Modelling and Simulating Biological Pathways*, **Satoru Miyano**, University of Tokyo

4:30 p.m. *Inferring Genetic Regulatory Networks Using Genomics Data*, **Hongyu Zhao**, Yale University

5:00 p.m. *Is Less More?: On Statistical Investigation for Large Biological Networks*, **Henry Horng-Shing Lu**, National Chiao Tung University, Taiwan

5:30 p.m. *Floor Discussion*

I-25 (CONCERTO-A)

Best of CAMDA 2006

Organizer: Patrick McConnell, Duke University

4:00 p.m. *Bayesian Joint Disease-Marker-Expression Analysis Applied to Clinical Characteristics of Chronic Fatigue Syndrome*, **Madhuchhanda Bhattacharjee**, University of Lancaster, U.K.,

4:30 p.m. *Integration of Genetic and Genomic Approaches for the Analysis of Chronic Fatigue Syndrome Implicates Forkhead Box N1*, **Steve Horvath**, UCLA

5:00 p.m. *A Systems Genetic Analysis of Chronic Fatigue Syndrome: Combinatorial Data Integration From SNPs to Differential Diagnosis of Disease*, **Roumyana Kirova**, Oak Ridge National Laboratory, TN

5:30 p.m. *Floor Discussion*

C-6 (CONCERTO-B)

Gene Expression Data Analysis

4:00 p.m. *Genome-Wide Co-Expression Based Prediction of Differential Expressions*, **Yinglei Lai**, George Washington University

4:15 p.m. *A framework for learning classification models using whole genome DNA copy number data*, **Jie Cheng, Joel Greshock, Tal Zaks, Kwan Lee**, GlaxoSmithKline

4:30 p.m. *Gene Expression Data Analysis by Chemometric Methods*, **David X. Zhu, Richard J. Goeke, David L. Baker, James H. Hamburg, David E. Booth, Stephane E. Booth**, Kent State University

4:45 p.m. *Learning gene association networks from high dimensional data*, **Jie Cheng, Kwan Lee**, GlaxoSmithKline

5:00 p.m. *Tests for the Hypothesis of Exchangability*, **Reza Modarres**, George Washington University

5:15 p.m. *Learning of Regulatory Modules and Predictive Models of Global Transcriptional Dynamics: Application to the Extremophile Halobacterium NRC-1*,
Richard Bonneau, Nitin Baliga, Marc Faciotti, Vesteinn Thorsson, David Reiss,
Courant Institute, New York University

Saturday, 26th May 2007

8:30 a.m. – 10:10 a.m.

I-26 (ARIA-A)

Providing Biological “Confidence” from Computational Analyses

Organizer: Gregory E. Gonye, Thomas Jefferson University

8:30 a.m. *Pharmacovigilance Maps: Quantifying Associations Between Prescription Drugs and Adverse Reactions*, **Ronald Pearson**, Prosanos Corporation & Thomas Jefferson University

9:00 a.m. *Identification of Perturbation-Relevant Gene Regulatory Networks from Statistical Enrichment Analysis of Gene Co-Expression Clusters*, **Rajanikanth Vadigepalli**, Thomas Jefferson University

9:30 a.m. *Of microRNA Targets and microRNA Precursors*, **Isidore Rigoutos**, IBM Thomas J. Watson Research Center

10:00 a.m. *Floor Discussion*

I-27 (ARIA-B)

Statistical Learning and Management of Biological Data

Organizer: Parthasarathy Srinivasan, Ohio State University

8:30 a.m. *Using Molecular Data to Estimate the Evolution of Species – Not Just the Phylogeny of Genes*, **Dennis Pearl**, Ohio State University, & **Liang Liu**, Harvard University

8:50 a.m. *Machine-Learning Approaches for Drosophila Gene Expression Pattern Image Analysis*, **Jieping Ye**, Arizona State University, & **Sudhir Kumar**

9:10 a.m. *I-Sites 2007: Protein Local Structure Motifs Have Covariant Sequence Patterns*, **Chris Bystroff**

9:30 a.m. *Integration and Analysis of Complex, Heterogeneous and Interrelated Biological Data – Towards a New Generation of Biological Databases*, **Golan Yona**, Technion – Israel Institute of Technology & Cornell University

10:00 a.m. *Floor Discussion*

I-28 (CONCERTO-A)

Analysis of Microarray Gene Expression Data Using Excel, SAS, and S-Plus

Organizer: Richard M. Heiberger, Temple University

8:30 a.m. *An Office-Software- and Menu-Driven Interface to Advanced Statistics in Biological Sciences*, **Erich Neuwirth**, University of Vienna, Austria

9:00 a.m. *Distribution of microarray analysis graphics*, **Robert.C.Gagnon**, Glaxo-Smith-Klein

9:30 a.m. *Disseminating Statistical Methodology and Results via R and Excel: Two Examples*, **Balasubramanian Narasimhan**, Stanford University

10:00 a.m. *Floor Discussion*

C-7 (CONCERTO-B)

Clustering and Mixture Models

8:30 a.m. *Models for the Analysis of Antarctic Soil Samples*, **Lidia Rejto**, Alfred Renyi Mathematical Institute of the Hungarian Academy of Sciences, Budapest, Hungary, and University of Delaware, **Gabor Tusnady**, Alfred Renyi Mathematical Institute of the Hungarian Academy of Sciences, Budapest, Hungary, **Craig Cary**, University of Delaware, **Julie Smith**, University of Delaware

8:45 a.m. *Detection of Syntenic Regions in Bacterial Genomes Through Statistical Clustering*, **Siew-Ann Cheong**, Cornell University, **Paul Stodghill**, **Dave Schneider**, USDA Agricultural Research Service, **Chris Myers**, Cornell University

9:00 a.m. *Bayesian Modeling and Inference in Single Cell Dynamic Networks*, **Jarad Niemi**, Duke University

9:15 a.m. *Multi-level mixture models - flexible clustering of high-dimensional biological data*, **Rebecka Jornsten**, Rutgers University

9:30 a.m. *The k-means decomposition method for identifying biological functions of unknown transcripts in the yeast transcriptome*, **Sungchul Ji**, Rutgers University, **Wonsuk Yoo**, Wayne State University School of Medicine, and **Andrei Zinovyev**, The Curie Institute, Paris

9:45 a.m. *On Some Computational Issues in Marginal Latent Mixture Analysis*, **Yan Yang**, Arizona State University, **Douglas Simpson**, University of Illinois

10:10 a.m. – 10:30 a.m.

BREAK

10:30 a.m. – 12:10 p.m.

I-29 (ARIA-A)

Metrology and Inference of Complex Biological and Engineered Systems

Organizer: Z.Q. John Lu, National Institute of Standards & Technology (NIST)

10:30 a.m. *Standards in Microarray Gene Expression Experiments*, **Marc Salit**, NIST

11:00 a.m. *Bayesian Semiparametric Methods for Pathway Analysis*, **Inyoung Kim**, Yale University

11:30 a.m. *Sensitivity Analysis Methodology for a Complex System Computational Model*, **Jim Filliben**, NIST

12:00 noon. *Floor Discussion*

I-30 (ARIA-B)

Metagenome Informatics

Organizers: Hongwei Wu & Ying Xu, University of Georgia

10:30 a.m. *Assembling the Human Gut Biome*, **Mihai Pop**, University of Maryland

10:50 a.m. *Benchmarking the Fidelity of Metagenomic Sequences Using Simulated Datasets*, **Kostas Mavrommatis**, Joint Genome Institute

11:10 a.m. *On Incorporating Genomic Neighborhood Information for the Prediction of Orthologous Genes*, **Hongwei Wu**, University of Georgia

11:30 a.m. *Exploring Marine Metagenomics via the CAMERA (Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis) Project: An Initial Analysis of Protein Family Diversity Found in the Global Ocean Sampling Study*, **WeiZhong Li, Adam Godzik, John Wooley, & the CAMERA team**, University of California, San Diego

12:00 noon. *Floor Discussion*

I-31 (CONCERTO-A)

Tutorial on the Bridge Between Classical & Systems Biology: Systems Models of Nature, Uncertainty, and Real Collaboration

Organizer: Arnold Goodman, University of California, Irvine

10:30 a.m. *A Starter Kit for Systems Biology: First Useful and Usable System Model of Protein Cycle, Pursuit of Uncertainty, and Interdisciplinary Collaboration, [Arnold Goodman](#), University of California, Irvine*

12:00 noon. *Floor Discussion*

