IEEE GENISPS @ CSHL PROGRAM

WEDNESDAY, November 10—2:00 PM

SESSION 1  TUTORIALS

Chairperson:  M. Atwal, Cold Spring Harbor Laboratory, New York

Genome copy number measurements from hybridization and sequence read data
Michael Wigler, Boris Yamrom, Jud Kendell, Yoon-Ha Lee, Nick Navin, Kenny Ye.

Genetics and population genomics
Lucia Hindorff.
Presenter affiliation: NHGRI, National Institutes of Health, Bethesda, Maryland.

WEDNESDAY, November 10—5:00 PM

Wine and Cheese Party

WEDNESDAY, November 10—7:30 PM

SESSION 2  NETWORK BIOLOGY AND PATHWAY ANALYSIS

Chairperson:  Y. Huang, University of Texas, San Antonio

An iterated conditional mode solution for Bayesian factor modeling of transcriptional regulatory networks
Jia Meng, Jianqiu Zhang, Yidong Chen, Yufei Huang.
Presenter affiliation: University of Texas at San Antonio, San Antonio, Texas.
Pathway and network analysis probing epigenetic influences on chemosensitivity in ovarian cancer
Presenter affiliation: Philips Research, Briarcliff Manor, New York.

Optimal perturbation control of gene regulatory networks
Nidhal Bouaynaya, Roman Shiferenber, Dan Schonfeld.
Presenter affiliation: University of Arkansas at Little Rock, Little Rock, Arkansas.

A comparative study on sensitivities in Boolean Networks
Xiaoming Qian, Ewad Dougherty.
Presenter affiliation: University of South Florida, Tampa.

WEDNESDAY, November 10—9:00 PM

SESSION 3  ERROR ESTIMATION IN GENOMIC DATA

Chairperson: D. Schonfeld, University of Illinois, Chicago

Approximate expressions for the variances of non-randomized error estimators and CoD estimators for the discrete histogram rule
Ting Chen, Ulisses Braga-Neto.
Presenter affiliation: Texas A&M University, College Station, Texas.

Bayesian MMSE estimation of classification error and performance on real genomic data
Lori A. Dalton, Edward R. Dougherty.
Presenter affiliation: Texas A&M University, College Station, Texas.
THURSDAY, November 11—9:00 AM

Introduction by: Nevenka Dimitrova

KEYNOTE SPEAKER

Andrea Califano
Columbia University

“Elucidating master integrators of tumor-related phenotypes”

THURSDAY, November 11—10:15 AM

SESSION 4 GENE EXPRESSION STUDIES IN NEXT GEN SEQ

Chairperson: P. Beyerlein, University of Applied Sciences Wildau, Germany

Studying gene expression and regulation in cancer using Next Generation Sequencing
Gary Schroth.
Presenter affiliation: Illumina, Inc., Hayward, California.

Methylome-transcriptome relationship in the rat peripheral nervous system in health and chronic pain
Andreas Beutler.
Presenter affiliation: Mayo Clinic, Rochester, Minnesota.

Automatic learning from RNA-seq data—Unbiased transcriptome discovery using the Wildau In-silicO Sequence Analysis (WIOS) framework
Peter Beyerlein.
Presenter affiliation: University of Applied Sciences Wildau, Germany.
THURSDAY, November 11—1:00 PM

Introduction by: Haris Vikalo

KEYNOTE SPEAKER

Edward R. Dougherty
Texas A&M University

“Intervention in gene regulatory networks”

THURSDAY, November 11—2:15 PM

SESSION 5  DYNAMIC MODELING

Chairperson: J. Goutsias, Johns Hopkins University, Baltimore, Maryland

A screening method for dimensionality reduction in biochemical reaction system calibration
W. Garrett Jenkinson, John Goutsias.
Presenter affiliation: The Johns Hopkins University, Baltimore, Maryland.

Importance sampling method for efficient estimation of the probability of rare events in biochemical reaction systems
Zhouyi Xu, Xiaodong Cai
Presenter affiliation: University of Miami, Coral Gables, Florida.

THURSDAY, November 11—3:30 PM

SESSION 6  POSTER SESSION

CNC—DNA Copy Number Counter
Majid Alsagabi, Ahmed Tewfik.
Presenting author: University of Minnesota, Minneapolis.
Segregation-based subspace clustering for huge dimensional data
Majid Alsagabi and Ahmed Tewfik.
Presenting author: University of Minnesota, Minneapolis.

Cooperative miRNA target prediction algorithm
Claudia Coronnello, Panayiotis V. Benos.
Presenter affiliation: University of Pittsburgh, Pittsburgh, Pennsylvania.

Fast algorithms for recognizing retroviruses
Wendy Ashlock, Suprakash Datta
Presenter affiliation: York University, Toronto, Canada.

Sequence entropy and organization in H1N1 virus
Laurita Dos Santos, José Luiz Rybarczyk Filho, Günther J. L. Gerhardt.
Presenter affiliation: National Institute for Space Research, San José dos Campos, Brazil.

Using multiresolution transformations for predicting clinical outcomes from genome-wide data
Pablo Hennings-Yeomans, Gregory F. Cooper.
Presenter affiliation: University of Pittsburgh, Pittsburgh, Pennsylvania.

Exon-length distribution dynamics in genome evolution
Brian S. Hilbush, Jayson T. Durham.
Presenter affiliation: Real Time Genomics, Inc., San Francisco, California.

Applying a gene regulatory model to investigate the effect of copy number variations on gene expression values
Fang-Han Hsu, Erchin Serpedin, Yidong Chen, Edward R. Dougherty.
Presenter affiliation: Texas A&M University, College Station, Texas.

From biological pathways to regulatory networks
Ritwik K. Layek, Aniruddha Datta, Edward R. Dougherty.
Presenter affiliation: Texas A&M University, College Station, Texas.

Cancer therapy design based on pathway logic
Ritwik K. Layek, Aniruddha Datta, Edward R. Dougherty.
Presenter affiliation: Texas A&M University, College Station, Texas.
Inference of gene predictor set using Boolean satisfiability
Pey-Chang K. Lin, Sunil P. Khatri.
Presenter affiliation: Texas A&M University, College Station, Texas.

FastCaller, a new base caller for DNA re-sequencing
Fabian Menges, Bud Mishra.

SUTTA—Scoring-and-unfolding trimmed tree assembler
Giuseppe Narzisi.

Efficient designs for multiple gene knockdown experiments
Bobak Nazer, Robert D. Nowak.
Presenter affiliation: University of Wisconsin - Madison, Madison, Wisconsin.

Systematic synergy-based analysis of whole-genome association studies data exposes SNP-SNP interactions at the chip signals level
Hani Neuvirth, Ehud Aharoni, Noam Slonim.
Presenter affiliation: IBM Research Lab, Haifa, Israel.

Control of stochastic master equation models of genetic regulatory networks by approximating their average behavior
Ranadip Pal, Mehmet U. Caglar.
Presenter affiliation: Texas Tech University, Lubbock, Texas.

PicXAA-R—Probabilistic structural alignment of multiple RNA sequences using a greedy approach
Sayed M. Sahraeian, Byung-Jun Yoon.
Presenter affiliation: Texas A&M University, College Station, Texas.

A differential equation approach to model genetic similarities and differences between inner and outer cotyledons in Brassica napus during seed development
Alain Tchagang, Yi Huang, Hugo Bérubé, Fazel Famili, Jitao Zou, Youlian Pan.
Presenter affiliation: University of Minnesota.

Identification of genes involved in ovarian cancer platinum sensitivity through multi-modal Cox regression
Vinay Varadan, Sitharthan Kamalakaran, Nilanjana Banerjee, Angel Janevski, Nevenka Dimitrova.
Making a comparative assembler a pseudo de-novo assembler using minimum description length
Bilal Wajid, Erchin Serpedin.
Presenter affiliation: University of Engineering and Technology, Lahore, Pakistan; Texas A & M University, College Station, Texas.

An optimized version of GLM and PLM for QTL analysis
Liya Wang, Matthew W. Vaughn, Peter J. Bradbury, Lincoln D. Stein.

Dynamics, stability and consistency in representation of genomic sequences
Liming Wang, Dan Schonfeld.
Presenter affiliation: University of Illinois at Chicago, Chicago, Illinois.

Conditioning-based model for the regulatory activities of microRNAs in specific dietary contexts
Chen Zhao, Ivan Ivanov, Manasvi Shah, Laurie A. Davidson, Robert S. Chapkin, Edward R. Dougherty.
Presenter affiliation: Texas A&M University, College Station, Texas.

RMS bounds and sample size considerations for error estimation in linear discriminant analysis
Amin Zollanvari, Ulisses M. Braga-Neto, Edward R. Dougherty.
Presenter affiliation: Texas A&M University, College Station, Texas.

THURSDAY, November 11

BANQUET
Cocktails 6:00 PM  Dinner 6:45 PM

xi
FRIDAY, November 12—9:00 AM

Introduction by: Byung-Jun Yoon

KEYNOTE SPEAKER

W. Richard McCombie
Cold Spring Harbor Laboratory

“Finding a needle in a haystack”

FRIDAY, November 12—10:15 AM

SESSION 7 DATA CHALLENGES IN NEXT GENERATION SEQUENCING

Chairperson: N. Dimitrova, Philips Research, Briarcliff Manor, New York

De novo assembly of large genomes using cloud computing
Michael C. Schatz.

Practical NGS analysis on the cloud with Galaxy AMIs—Uncovering mitochondrial variation
Presenter affiliation: galaxyproject.org, University Park, Pennsylvania.

How and why do rates of different mutation types co-vary? Multivariate statistical analyses in the context of local genomic landscape
Guruprasad Ananda, Anton Nekrutenko, Francesca Chiaromonte, Kateryna Makova.
Presenter affiliation: Penn State University, University Park, Pennsylvania.
Detecting rare genetic variants in the Large-Scale 1000 Genomes Exome Resequencing Project
Presenter affiliation: Baylor College of Medicine, Houston, Texas.

Model-based sequential base calling for Illumina sequencing
Shreepriya Das, Haris Vikalo, Arjang Hassibi.
Presenter affiliation: The University of Texas at Austin, Austin, Texas.

FRIDAY, November 12—1:30 PM

SESSION 8 CLASSIFICATION AND STATISTICAL LEARNING

Chairperson: A. Tewfik, University of Minnesota, Minneapolis

Effects of partial reporting of classification results
Mohammadmahdi Rezaei Yousefi, Jianping Hua, Chao Sima, Edward R. Dougherty.
Presenter affiliation: Texas A&M University, College Station, Texas.

Subtype specific breast cancer event prediction
Herman Sontrop, Wim Verhaegh, Rene van den Ham, Marcel Reinders, Perry Moerland.

Inference of gene-regulatory networks using message-passing algorithms
Manohar Shamaiah, Sang Hyun Lee, Haris Vikalo.
Presenter affiliation: University of Texas at Austin, Austin, Texas.
SESSION 9  NETWORK-BASED METHODS IN COMPUTATIONAL BIOLOGY

Chairperson:  X. Qian, University of South Florida, Tampa

Finding steady states of large scale regulatory networks through partitioning
Ferhat Ay, Tamer Kahvec.
Presenter affiliation: University of Florida, Gainesville, Florida.

Graphlet alignment in protein interaction networks
Mu-Fen Hsieh, Sing-Hoi Sze.
Presenter affiliation: Texas A&M University, College Station, Texas.

Network propagation models for gene selection
Wei Zhang, Baryun Hwang, Baolin Wu, Rui Kuang.
Presenter affiliation: University of Minnesota, Minneapolis, Minnesota.

Approaches to and benefits of semi-quantitative modeling of biochemical network dynamics
Derek Ruths.
Presenter affiliation: McGill University, Montreal, Canada.

Hierarchical analysis of regulatory networks and cross-disciplinary comparison with the Linux call graph
Koon-Kiu Yan, Mark Gerstein.
Presenter affiliation: Yale University, New Haven, Connecticut.

Dynamic and static analysis of transcriptional regulatory networks in a hierarchical context
Nitin Bhardwaj, Mark Gerstein.
Presenter affiliation: Yale University, New Haven, Connecticut.