

# **2011 IEEE International Workshop on Genomic Signal Processing and Statistics**

**(GENSIPS 2011)**

**San Antonio, Texas, USA  
4-6 December 2011**



**IEEE Catalog Number: CFP11GEN-PRT  
ISBN: 978-1-4673-0491-7**

# Table of Contents

## Mon-Session: Next Generation Sequencing for Epigenetic Research

A Scalable, Flexible Workflow for MethylCap-Seq Data Analysis .....	1
<i>Benjamin Rodriguez, Hok-Hei Tam, David Frankhouser, Michael Trimarchi, Mark Murphy, Chris Kuo, Deval Parikh, Bryan Ball, Sebastian Schwind, John Curfman, William Blum, Guido Marcucci, Pearly Yan, Ralf Bundschuh</i>	
An Era/Modulator Regulatory Network in the Breast Cancer Cells .....	5
<i>Heng-Yi Wu, Yu Wang, P. Zheng, G. Jiang, Yunlong Liu, Kenneth P. Nephew, Tim H. M. Huang, Lang Li</i>	
Empirical Bayes Model Comparisons for Differential Methylation Analysis .....	9
<i>Mingxiang Teng, Yadong Wang, Curt Balch, Kenneth P. Nephew, Yunlong Liu, Lang Li, Seongho Kim</i>	
Chromatin signature analysis and prediction of genome-wide novel promoters using finite mixture model	13
<i>Cenny Taslim, Shili Lin, Kun Huang, Tim Huang</i>	

## Mon-Session: Gene Regulation Network I

Uncertainty-based Essentiality in Gene Regulatory Networks .....	17
<i>Xiaoning Qian, Byung-Jun Yoon, Edward R. Dougherty</i>	
The effect of certain Boolean functions in stability of networks with varying topology .....	21
<i>Vitor H. P. Louzada, Ronaldo F. Hashimoto, Fabricio M. Lopesy</i>	
A Cubature Kalman Filter Approach for Inferring Gene Regulatory Networks Using Time Series Data	25
<i>Amina Noor, Erchin Serpedin, Mohamed Nounou, Hazem Nounou</i>	
A novel critical time analysis approach for Genetic Regulatory Networks .....	29
<i>Sonal Bhattacharya, Ranadip Pal</i>	

## Mon-Session: Computational Methods for Therapeutic

Efficient Combinatorial Drug Optimization Through Stochastic Search .....	33
<i>Mansuck Kim, Byung-Jun Yoon</i>	
A novel approach for tumor sensitivity prediction and combination therapy design for targeted drugs ..	36
<i>Noah Berlow, Ranadip Pal</i>	
Modeling Cyclic and Acyclic Therapeutic Methods with Persistent Intervention Effect in Probabilistic Boolean Networks .....	38
<i>Mohammadmahdi R. Yousefi, Aniruddha Datta, Edward R. Dougherty</i>	
Predicting Drug Efficacy Based on the Integrated Breast Cancer Pathway Model .....	42
<i>Hui Huang, Xiaogang Wu, Sara Ibrahim, Marianne McKenzie, Jake Y. Chen</i>	

Identifying Genes Associated with Chemotherapy Response in Ovarian Carcinomas Based on DNA Copy Number and Expression Profiles .....	46
<i>Fang-Han Hsu, Erchin Serpedin, Tzu-Hung Hsiao, Alexander J.R. Bishop, Edward R. Dougherty, Yidong Chen</i>	
Assessing the Efficacy of Molecularly Targeted Agents by Using Kalman Filter .....	50
<i>Xiangfang (Lindsey) Li, Lijun Qian, Michael L. Bittner, Edward R. Dougherty</i>	
<b>Mon-Session: Gene Regulation Network II</b>	
Probabilistic consistency transformation for multiple alignment of biological networks .....	52
<i>Sayed Mohammad Ebrahim Sahraeian, Byung-Jun Yoon</i>	
Attractor Estimation and Model Refinement for Stochastic Regulatory Network Models .....	54
<i>Jason Knight, Edward Dougherty</i>	
Steady state probability approximation applied to stochastic model of biological network .....	56
<i>Md. Shahriar Karim, David M. Umulis, Gregory T. Buzzard.</i>	
Identification of biomarkers in breast cancer metastasis by integrating protein-protein interaction network and gene expression data .....	60
<i>Md Jamiul Jahid, Jianhua Ruan</i>	
Pathway Analysis in the Context of Bayesian Networks - Mathematical Modeling of Master and Canalizing Genes .....	64
<i>Chen Zhao, Ivan Ivanov, Michael L. Bittner, Edward R. Dougherty</i>	
Gene Network Inference via Sparse Structural Equation Modeling with Genetic Perturbations .....	66
<i>Xiaodong Cai, Juan Andres Bazerque, Georgios B. Giannakis</i>	
<b>Mon-Session: Data Integration</b>	
Improvement of GNs inference through biological data integration .....	70
<i>Fabio Fernandes da Rocha Vicente, Fabricio M. Lopes, Ronaldo F. Hashimoto</i>	
Multisource Biological Pathway Consolidation .....	74
<i>Mark S. Doderer, Zachry Anguiano, Uthra Suresh, Ravi Dashnamoorthy, Alexander J.R. Bishop, Yidong Chen</i>	
A Method For Finding Novel Associations Between Genome-Wide Copy Number And DNA Methylation Patterns .....	78
<i>Man-Hung Eric Tang, Vinay Varadan, Sid Kamalakaran, Michael Q. Zhang, Nevenka Dimitrova, James Hicks</i>	
Stochastic Modeling of Dynamic Effects of Copy Number Alterations upon Gene Expression Levels ...	83
<i>Fang-Han Hsu, Erchin Serpedin, Yidong Chen, Edward R. Dougherty</i>	
Efficient Cancer Therapy using Boolean Networks and Max-SAT-based ATPG .....	87
<i>Pey-Chang Kent Lin, Sunil P. Khatri</i>	
Designing Enhanced Classifiers Using Prior Process Knowledge: Regularized Maximum-Likelihood ....	91
<i>Mohammad Shahrokh Esfahani, Amin Zollanvari, Byung-Jun Yoon, Edward R. Dougherty</i>	

## **Mon-Session: Proteomics data processing**

Finding Effective Subnetwork Markers for Cancer by Passing Messages .....	95
<i>Byung-Jun Yoon</i>	
Application of Survival Analysis Methodology to the Quantitative Analysis of LC-MS Proteomics Data .....	97
<i>Carmen D. Tekwe, Alan R. Dabney, Raymond J. Carroll</i>	
Mapping of International Protein Index to Affymetrix Probe-Set Identifier for Correlating Genomics and Proteomics Expression Profiles in Multiple Myeloma .....	101
<i>Shweta S. Chavan , John D. Jr. Shaughnessy, Bart Barlogie, Ricky D. Edmondson</i>	
Multiple Reaction Monitoring: Modeling and Systematic Analysis .....	105
<i>Esmaeil Atashpaz-Gargari, Ulisses M. Braga-Neto, Edward R. Dougherty</i>	
Joint Corresponding Feature Identification and Alignment for Multiple LC/MS Replicates .....	108
<i>Jian Cui, Xuepo Ma, Jianqiu(Michelle) Zhang</i>	
Modeling and systematic analysis of LC-MS proteomics pipeline .....	112
<i>Youting Sun, Ulisses Braga-Neto, Edward R. Dougherty</i>	

## **Mon-Session: Next Generation Sequencing Data analysis and Application**

Enabling Atlas2 Personal Genome Analysis on the Cloud .....	117
<i>Uday S. Evani, Danny Challis, Jin Yu, Andrew R. Jackson, Sameer Paithankar, Matthew N. Bainbridge, Cristian Coar-fa, Aleksandar Milosavljevic, Fuli Yu</i>	
A Sequential Monte Carlo Base-calling Method for next-generation DNA Sequencing .....	121
<i>Xiaohu Shen, Haris Vikalo</i>	
Comparative Copy Number Variation from Whole Genome Sequencing .....	123
<i>Angel Janevski, Vinay Varadan, Sitharthan Kamalakaran, Nilanjana Banerjee, Nevenka Dimitrova</i>	
Beyond Seed Match: Improving miRNA Target Prediction using PAR-CLIP Data .....	127
<i>Mingzhu Lu, C. L. Philip Chen, Yufie Huang</i>	
Network-assisted Causal Gene Detection in Genome-wide Association Studies: An Improved Module Search Algorithm .....	131
<i>Peilin Jia, Zhongming Zhao</i>	

## **Tue-Session: Clustering and Classification Methods**

Classifier Error Estimator Performance in a Bayesian Context .....	135
<i>Lori Dalton, Edward R. Dougherty</i>	
Sample-Based Estimators for the Intrinsically Multivariate Prediction Score .....	139
<i>Ting Chen, Ulisses Braga-Neto</i>	
Clustering Gene Expression Data using Probabilistic Non-negative Matrix Factorization .....	143
<i>Belhassen Bayar, Nidhal Bouaynaya, Roman Shterenberg</i>	
Relationship between the accuracy of classifier error estimation and distribution complexity .....	147
<i>Esmaeil Atashpaz-Gargari, Chao Sima, Ulisses M. Braga-Neto, Edward R. Dougherty</i>	

Geometrical Modification Of Wavelet SVM Kernels And Its Application In Microarray Analysis .....	150
<i>Hong Cai , Yufeng Wang</i>	

S-score : a Novel Scoring Method of Gene Signatures for Molecular Classification .....	154
<i>Hung-I Harry Chen, Tzu-Hung Hsiao, Yidong Chen, Charles Keller</i>	

## Tue-Session: MicroRNA, Gene Networks, Next-Generation Sequencing Methods

Computational Prediction of microRNA Regulatory Pathways .....	158
<i>Dong Yue, Yidong Chen, Shou-Jiang Gao, Yufei Huang</i>	

Inference of a Genetic Regulatory Network model from limited time series data .....	162
<i>Saad Haider,Ranadip Pal</i>	

Modelling Oxidative Stress Response Pathways .....	166
<i>Sriram Sridharan, Ritwik Layek, Aniruddha Datta, Jijayanagaram Venkatraj</i>	

Clustering DNA methylation expressions using nonparametric beta mixture model .....	170
<i>Lin Zhang, Jia Meng, Hui Liu, Yufei Huang</i>	

A Novel Approach for Alignments Output Storage Problem Facing Clinical Scenarios .....	174
<i>Yiqi Lu ,Yaoliang Chen, Fuli Yu, Yanghua Xiao, Danfeng Xu</i>	

Personal Genome Privacy Protection with Feature-based Hierarchical Dual-stage Encryptions .....	178
<i>Xukai Zou, Peng Liu, Jake Y. Chen</i>	

## Tue-Session: ISIMB 2011

ECF sigma factor-associated regulatory networks in Streptomyces colicolor A3(2) .....	182
<i>Zhan Zhou, Qi Li, Julie Tudyk, Yong-Quan Li ,Yufeng Wang</i>	

Transcriptomic analysis using svd clustering and svm classification .....	186
<i>Hong Cai , Yufeng Wang</i>	

A Compton scattering suppression based Image reconstruction method for digital brest tomosynthesis .	190
<i>Shiyu Xu , Ying Chen</i>	

Effects of slice thickness filter in filtered backprojection reconstruction with parallel breast tomosynthesis imaging configuration .....	194
<i>Linlin Cong, Weihua Zhou ,Ying Chen</i>	

Targeting myocardial infarction-specific protein interactions using computational analyses .....	198
<i>Nguyen Nguyen, Xiaolin Zhang, Yunji Wang, Hai-Chao Han, Yufang Jin, Galen Schmidt, Richard A. Lange, Robert J. Chilton, Merry Lindsey</i>	

Mathematical modeling of macrophage activation in left ventricular remodeling post-myocardial infarction .....	202
<i>Yunji Wang, Yufang Jin, Yonggang Ma, Ganesh V Halade, Merry L. Lindsey</i>	

**Tue-Session: Poster**

Revision of the variational Bayesian method for uncovering Genes Regulatory Network .....	206
<i>Manuel Sanchez-Castillo, Isabel Maria Tienda-Luna, David Blanco-Navarro, Mar Del Carmen Carrion-Perez</i>	
A study of the effects of non-specific filtering on the gene expression data prior to statistical testing ...	210
<i>Jiaxiu He</i>	
Fast and Parallelized Greedy Forward Selection of Genetic Variants in Genome-Wide Association Studies	214
<i>Sebastian Okser, Tapio Pahikkala, Antti Airola, Tero Aittokallio, Tapio Salakoski</i>	
Peaking Phenomenon and Error Estimation for Support Vector Machines .....	218
<i>Sardar Afra, Ulisses Braga-Neto</i>	
Intervention in General Topology Gene Regulatory Networks .....	222
<i>Nidhal Bouaynaya, Mohammed Rasheed, Roman Shterenberg, Dan Schonfeld</i>	
Feature Set Enhancement via Hierarchical Clustering for Microarray Classification .....	226
<i>Mattia Bosio, Pau Bellot Pujalte, Philippe Salembier, Albert Oliveras-Verg</i>	
Minimum Description Length Based Selection of Reference Sequences for Comparative Assemblers ....	230
<i>Bilal Wajid, Erchin Serpedin</i>	

**Author Index**