

**2007 IEEE 7th International  
Symposium on  
BioInformatics and BioEngineering**

**Boston, Massachusetts  
14-17 October 2007**

**Volume 1 of 3**



**IEEE Catalog Number:**  
**ISBN:**

**07EX1893**  
**1-4244-1509-8**

# TABLE OF CONTENTS

## VOLUME I

### IEEE BIBE Plenary Keynote Lecture Notes (Part I)

<b>Intrinsically Disordered Proteins: Predictions and Applications.....</b>	<b>1</b>
<i>A. Keith Dunker, (Indiana University School of Medicine and School of Informatics, USA); Jack Y. Yang, (Harvard Medical School, Harvard University, USA); Christopher S. Oldfield, (Indiana University School of Informatics, USA); Zoran Obradovic, (Temple University, USA); Jingwei Meng, Pedro Romero (Indiana University School of Informatics, USA), Vladimir N. Uversky (Indiana University School of Medicine, USA)</i>	
<b>Stochasticity and Networks in Genomic Data.....</b>	<b>2</b>
<i>John Quackenbush (Harvard School of Public Health, Harvard University, USA)</i>	
<b>Decoding Novel Genomes: From Microbiomes to the Eukaryota.....</b>	<b>3</b>
<i>Mark Borodovsky (Georgia Institute of Technology, USA)</i>	
<b>Promoter Studies in the Human Genome: One Perspective on an Unfinished Story.....</b>	<b>4</b>
<i>Mary Qu Yang (National Human Genome Research Institute, National Institutes of Health (NIH), U.S. Department of Health and Human Services and Oak Ridge, DOE, USA); Laura L. Elnitski (National Human Genome Research Institute, National Institutes of Health (NIH), U.S. Department of Health and Human Services, USA)</i>	
<b>Protein Structure Prediction and Its Understanding Based on Machine Learning Methods.....</b>	<b>7</b>
<i>Yi Pan (Georgia State University, USA)</i>	
<b>Statistical Analysis of Nucleosome Occupancy and Histone Modification Data.....</b>	<b>8</b>
<i>Guocheng Yuan, Jun S. Liu (Harvard University, USA)</i>	
<b>An Investigation into the Feasibility of Detecting Microscopic Disease using Machine Learning.....</b>	<b>9</b>
<i>Mary Qu Yang (National Human Genome Research Institute, National Institutes of Health (NIH) and Oak Ridge, DOE, USA); Jack Y. Yang, (Harvard Medical School, Harvard University, USA)</i>	
<b>Nanobioinformatics: The Enabling Technology of Personalized Medicine .....</b>	<b>11</b>
<i>Linda K. Molnar (National Cancer Institute, National Institutes of Health (NIH), U.S. Department of Health and Human Services, USA)</i>	
<b>Intrinsically Disordered Proteins in Human Diseases.....</b>	<b>12</b>
<i>Vladimir N. Uversky (Indiana University School of Medicine, USA); Christopher S. Oldfield (Indiana University School of Informatics, USA); A. Keith Dunker (Indiana University, USA)</i>	
<b>Metallobiochemistry of Alzheimer’s Disease and Its Theranostic Agent Development.....</b>	<b>13</b>
<i>Xudong Huang (Harvard Medical School and Brigham and Women's Hospital, USA)</i>	

### Regular Research Papers (Part I).

#### Session 1: Protein Structure and Function

<b>Identification of Conserved Domain Combinations in <i>S.cerevisiae</i> Proteins.....</b>	<b>14</b>
<i>Suk Hoon Jung, Hee-Young Hur, Desok Kim, Dong-Soo Han (Information and Communications University, Korea)</i>	
<b>Multiclass Fuzzy Clustering Support Vector Machines for Protein Local Structure Prediction.....</b>	<b>21</b>
<i>Wei Zhong (University of South Carolina Upstate, USA); Jieyue He (Southeast University, China); Yi Pan (Georgia State University, USA)</i>	
<b>A New Alignment-Independent Algorithm for Clustering Protein Sequences .....</b>	<b>27</b>
<i>Abdellali Kelil, Shengrui Wang, Ryszard Brzezinski (Sherbrooke University, Canada)</i>	

<b>Metropolis-Hastings Algorithm and Continuous Regression for Finding Next-State Models of Protein Modification Using Information Scores .....</b>	<b>35</b>
David J. John, Jacquelyn S. Fetrow, James L. Norris ( <i>Wake Forest University, USA</i> )	
<b>Protein Function Prediction from Interaction Networks Using a Random Walk Ranking Algorithm .....</b>	<b>42</b>
Valerio Freschi ( <i>University of Urbino, Italy</i> )	
<b>Intrinsically Disordered Proteins: An Update .....</b>	<b>49</b>
A. Keith Dunker, ( <i>Indiana University School of Medicine and School of Informatics, USA</i> ); Jack Y. Yang, ( <i>Harvard Medical School, Harvard University, USA</i> ); Christopher S. Oldfield, ( <i>Indiana University School of Informatics, USA</i> ); Zoran Obradovic, ( <i>Temple University, USA</i> ); Jingwei Meng, Pedro Romero ( <i>Indiana University School of Informatics, USA</i> ); Vladimir N. Uversky ( <i>Indiana University School of Medicine, USA</i> );	
<b>Linking Protein Mass with Function via Organismal Massome Networks .....</b>	<b>59</b>
Gil Alterovitz ( <i>Harvard Medical School and Massachusetts Institute of Technology, USA</i> ); Eugenia Lyashenko ( <i>Columbia University, USA</i> ); Michael Xiang ( <i>Harvard Medical School, USA</i> ); Marco F. Ramoni ( <i>Harvard University and Massachusetts Institute of Technology, USA</i> )	
<b>Ensemble of Probabilistic Neural Networks for Protein Fold Recognition.....</b>	<b>66</b>
Yuehui Chen, Xueqin Zhang ( <i>University of Jinan, China</i> ); Mary Qu Yang ( <i>National Human Genome Research Institute, National Institutes of Health (NIH) and Oak Ridge, DOE., USA</i> ); Jack Y. Yang, ( <i>Harvard Medical School, Harvard University, USA</i> )	
 <b>Session 2: Microarray Data and Applications (Part A)</b>	
<b>HICCUP: Hierarchical Clustering Based Value Imputation Using Heterogeneous Gene Expression Microarray Datasets.....</b>	<b>71</b>
Qiankun Zhao ( <i>AOL Labs, China</i> ); Prasenjit Mitra, Dongwon Lee ( <i>Penn State University, USA</i> ); Jaewoo Kang ( <i>Korea University, Korea</i> )	
<b>On the Effectiveness of Constraints Sets in Clustering Genes.....</b>	<b>79</b>
Erliang Zeng, Chengyong Yang, Tao Li, Giri Narasimhan ( <i>Florida International University, USA</i> )	
<b>Integrate Qualitative Biological Knowledge to Build Gene Networks by Parallel Dynamic Bayesian Network Structure Learning.....</b>	<b>87</b>
Song Li ( <i>Iowa State University, USA</i> )	
<b>Finding Clusters of Positive and Negative Coregulated Genes in Gene Expression Data .....</b>	<b>93</b>
Kerstin Koch ( <i>Hasselt University, Belgium</i> ); Stefan Schönauer ( <i>University of Helsinki, Finland</i> ); Ivy Jansen, Jan van den Bussche, Tomasz Burzykowski ( <i>Hasselt University, Belgium</i> )	
<b>Pattern Cores and Connectedness in Cancer Gene Expression .....</b>	<b>100</b>
Noha A. Yousi, Mohamed S. Kamel ( <i>University of Waterloo, Canada</i> ); Mohamed A. Ismail ( <i>University of Alexandria, Egypt</i> )	
<b>PANP – A New Method of Gene Detection on Oligonucleotide Expression Arrays.....</b>	<b>108</b>
Peter Warren ( <i>Wyeth Research, USA</i> ); Deanne Taylor ( <i>Harvard School of Public Health, USA</i> ); Paolo G.V. Martini, Jennifer Jackson ( <i>EMD Serono, USA</i> ); Jadwiga Bienkowska ( <i>Biogen-Idec</i> )	
 <b>Session 3: Microarray Data and Applications (Part B)</b>	
<b>Cooperative Partitional-Divisive Clustering and Its Application in Gene Expression Analysis .....</b>	<b>116</b>
Rasha Kashef, Mohamed S. Kamel ( <i>University of Waterloo, Canada</i> )	
<b>On the Design of Oligos for Gene Synthesis.....</b>	<b>123</b>
Chris Thachuk ( <i>Simon Fraser University, Canada</i> ); Anne Condon ( <i>University of British Columbia, Canada</i> )	

<b>Evidence for Proximal to Distal Appendage Amputation Site Effects from Global Gene Expression Correlations Found in Newt Microarrays .....</b>	<b>131</b>
Kenneth A. Marx, John Sharko, Georges G. Grinstein ( <i>University of Massachusetts Lowell, USA</i> ); Shannon Odelberg ( <i>University of Utah School of Medicine, USA</i> ); Hans-Georg Simon ( <i>Northwestern University, USA</i> )	
<b>Denosing of Array-Based DNA Copy Number Data Using the Dual-tree Complex Wavelet Transform .....</b>	<b>137</b>
Nha Nguyen, Heng Huang, Soontorn Oraintara ( <i>University of Texas at Arlington, USA</i> ); Yuhang Wang ( <i>Southern Methodist University, USA</i> )	
<b>Quality Assessment of Affymetrix GeneChip Data Using the EM Algorithm and a Naïve Bayes Classifier .....</b>	<b>145</b>
Brian E. Howard, Imara Perera, Yang Ju Im, Heike Winter-Sederoff ( <i>North Carolina State University, USA</i> ); Beate Sick ( <i>Zurich University of Applied Science Winterthur, Switzerland</i> ); Steffen Heber ( <i>North Carolina State University, USA</i> )	
<b>Comparing Cancer and Normal Gene Regulatory Networks Based on Microarray Data and Transcription Factor Analysis.....</b>	<b>151</b>
Yu-Chun Lin, Hsiang-Yuan Yeh, Shih-Wu Cheng ( <i>National Tsing Hua University, Taiwan</i> ); Von-Wun Soo ( <i>National University of Kaohsiung, Taiwan</i> )	

#### **Session 4: Microarray Data and Applications (Part C)**

<b>Finding Cancer-Related Gene Combinations Using a Molecular Evolutionary Algorithm .....</b>	<b>158</b>
Chan-Hoon Park, Soo-Jin Kim, Sun Kim, Dong-Yeon Cho, Byoung-Tak Zhang ( <i>Seoul National University, Korea</i> )	
<b>A Two-Stage Gene Selection Algorithm by Combining ReliefF and mRMR .....</b>	<b>164</b>
Yi Zhang ( <i>Florida International University, USA</i> ); Chris Ding ( <i>University of Texas, USA</i> ); Tao Li ( <i>Florida International University, USA</i> )	
<b>Estimating Classification Error to Identify Biomarkers in Time Series Expression Data .....</b>	<b>172</b>
John H. Phan, May D. Wang ( <i>Georgia Institute of Technology, USA</i> )	
<b>Detection and Prediction of Alternative Splicing within Acceptor/Donor Sites in Pre-mRNA of Arabidopsis Thaliana.....</b>	<b>180</b>
Minseo Park, Deane L. Falcone, Kil-Young Yun, ( <i>University of Massachusetts, USA</i> ); Kil-Young Yun ( <i>Universtiy of Maine, USA</i> ); Karen M. Daniels ( <i>University of Massachusetts, USA</i> )	
<b>An Effective Interwoven Loop Design Application for Two-Channel Microarray Experiments .....</b>	<b>187</b>
Mehdi Pirooznia, Arun Rawat ( <i>The University of Southern Mississippi, USA</i> ); Ping Gong ( <i>SpecPro Inc., USA</i> ); Jack Y. Yang ( <i>Harvard Medical School, Harvard University, USA</i> ); Edward J. Perkins ( <i>US Army Engineer Research and Development Center, USA</i> ); Mary Qu Yang ( <i>National Human Genome Research Institute, National Institutes of Health (NIH), USA</i> ); Youping Deng ( <i>The University of Southern Mississippi, USA</i> )	
<b>SNPMiner: A Domain-Specific Deep Web Mining Tool.....</b>	<b>192</b>
Fan Wang, Gagan Agrawal ( <i>Ohio State University, USA</i> ); Ruoming Jin, Helen Piontkivska ( <i>Kent State University, USA</i> )	

#### **Session 5: Biomedical Engineering**

<b>Fast and Robust Detection of Epilepsy in Noisy EEG Signals Using Permutation Entropy.....</b>	<b>200</b>
Iman Veisi, Naser Pariz, Ali Karimpour ( <i>Ferdowsi University, Iran</i> )	
<b>A Robotic System for Real-Time Tumor Manipulation During Image Guided Breast Biopsy.....</b>	<b>204</b>
Vishnu Mallapragada, Nilanjan Sarkar, ( <i>Vanderbilt University, USA</i> ); Tarun K.Podder ( <i>Thomas Jefferson University Hospital, USA</i> )	
<b>Morphometric Analysis of Hippocampal Shape in Mild Cognitive Impairment: An Imaging Genetics Study.....</b>	<b>211</b>
Li Shen, Andrew J. Saykin ( <i>Indiana University School of Medicine, USA</i> ); Moo K. Chung ( <i>University of Wisconsin Madison, USA</i> ); Heng Huang ( <i>University of Texas at Arlington, USA</i> )	
<b>A Compartmentalized Approach to the Assembly of Physical Maps .....</b>	<b>218</b>
Serdar Bozdag, Timothy J. Close, Stefano Lonardi ( <i>University of California, Riverside, USA</i> )	

<b>Graph Theory Application in Cell Nucleus Segmentation, Tracking and Identification .....</b>	<b>226</b>
<i>Lelin Zhang, Hongkai Xiong, Kai Zhang (Shanghai Jiao Tong University, P.R. China); Xiaobo Zhou (Harvard Medical School, USA)</i>	
<b>An End-to-End Process for Cancer Identification from Images of Lung Tissue.....</b>	<b>233</b>
<i>Walker H. Land, Jr. (Binghamton University, USA); Dan McKee (Mansfield University, USA); Tatyana Zhukov, Dansheng Song, Wei Qian (University of South Florida, USA)</i>	
<b>Rat Mammary Fat Pad Segmentation and Growth Rate Evaluation in T1 Weighted MR Images.....</b>	<b>240</b>
<i>Bin Wang, Jianhua Xuan (Virginia Tech, USA); Matthew T. Freedman, Peter G. Shields (Georgetown University, USA); Yue Wang (Virginia Tech, USA)</i>	
<b>A Simulation-Based 3D Axon Axis Extraction in Confocal Fluorescence Microscopy Images.....</b>	<b>246</b>
<i>Kai Zhang, Hongkai Xiong (Shanghai Jiao Tong University, China); Xiaobo Zhou (The Methodist Hospital Research Institute and Cornell University, USA)</i>	
<b>Advancements in Automated Diagnostic Mammography .....</b>	<b>251</b>
<i>Walker H. Land, Jr., Alda Mizaku, Thomas Raway (Binghamton University, USA); John Heine, Claudia Berman, Nataliya Kovalchuk (H. Lee Moffitt Cancer Center and Research Institute and University of South Florida, USA)</i>	
<b>Calcium De-blooming in Coronary CT Images .....</b>	<b>257</b>
<i>Zhuangli Liang, W. Clem Karl (Boston University, USA); Synho Do, Udo Hoffmann, Thomas Brady, Homer Pien (Massachusetts General Hospital and Harvard Medical School, USA)</i>	
 <b>Session 6: Computational Methods in Bioinformatics</b>	
<b>Distance Preserving Dimension Reduction Using the QR Factorization or the Cholesky Factorization .....</b>	<b>263</b>
<i>Hyunsoo Kim, Haesun Park, Hongyuan Zha (Georgia Institute of Technology, USA)</i>	
<b>Discrete Methods for Association Search and Status Prediction in Genotype Case-Control Studies.....</b>	<b>270</b>
<i>Dumitru Brinza (University of California at San Diego, USA); Alexander Zelikovsky (Georgia State University, USA)</i>	
<b>A Multi-Objective Genetic Algorithm that Employs a Hybrid Approach for Isolating Codon Usage Bias Indicative of Translational Efficiency .....</b>	<b>278</b>
<i>Douglas Raiford, Dan E. Krane, Travis E. Doom, Michael L. Raymer (Wright State University, USA)</i>	
<b>Rapid Detection and Classification of Bacterial Contamination Using Grid Computing.....</b>	<b>286</b>
<i>Wamiq M. Ahmed, Bulent Bayraktar, Arun K. Bhunia, E. Dan Hirleman, J. Paul Robinson, Bartek Rajwa (Purdue University, USA)</i>	
<b>Sensitivity Analysis of Biomolecular Simulations Using Symbolic Models .....</b>	<b>294</b>
<i>Sadaf R. Alam, Nikhil Bhatia, Jeffrey S. Vetter (Oak Ridge National Laboratory, DOE, USA)</i>	
 <b>Session 7: Sequence Analysis</b>	
<b>Detecting and Assessing Conserved Stems for Accurate Structural Alignment of RNA Sequences.....</b>	<b>301</b>
<i>Xiaoyong Fang, Zhigang Luo (National University of Defense Technology, China); Bo Yuan, Zhenghua Wang (Ohio State University, USA)</i>	
<b>The RNA String Kernel for siRNA Efficacy Prediction .....</b>	<b>307</b>
<i>Shibin Qiu (Pathwork Diagnostics, Inc., USA); Terran Lane (University of New Mexico, USA)</i>	
<b>A Machine Learning Approach for Prediction of Lipid-Interacting Residues in Amino Acid Sequences.....</b>	<b>315</b>
<i>Stephanie Jiménez Irausquin (University of South Carolina, USA); Liangjiang Wang (Clemson University, USA)</i>	
<b>Assessing the Performance of Macromolecular Sequence Classifiers .....</b>	<b>320</b>
<i>Cornelia Caragea, Jivko Sinapov, Vasant Honavar, Drena Dobbs (Iowa State University, USA)</i>	
<b>Shortest Path Approaches for the Longest Common Subsequence of a Set of Strings .....</b>	<b>327</b>
<i>Marina Barsky, Ulrike Stege, Alex Thomo, Chris Upton (University of Victoria, Canada)</i>	

**Constrained RNA Structural Alignment: Algorithms and Application to Motif Detection in the Untranslated Regions of *Trypanosoma Brucei* mRNAs**.....334  
Mugdha Khaladkar (*New Jersey Institute of Technology, USA*); Vivian Bellofatto (*University of Medicine and Dentistry of New Jersey*); Jason T.L. Wang, Vandanaben Patel, Marvin K. Nakayama (*New Jersey Institute of Technology, USA*)

## Session 8: Systems Biology

**Optimizing Flow-based Modularization by Iterative Centroid Search in Protein Interaction Networks**.....342  
Young-Rae Cho, Woochang Hwang, Aidong Zhang (*State University of New York at Buffalo, USA*)

**Homomorphisms of Multisource Trees into Networks with Applications to Metabolic Pathways**.....350  
Qiong Cheng, Robert Harrison, Alexander Zelikovsky (*Georgia State University, USA*)

**Review of Systems Biology Simulation Tools for Translational Research** .....358  
Melissa Freedenberg, Chanchala Kaddi, Chang F. Quo, May D. Wang (*Georgia Institute of Technology, USA*)

**Combined Expression Data with Missing Values and Gene Interaction Network Analysis:  
A Markovian Integrated Approach**.....366  
Juliette Blanchet (*INRIA Rhône-Alpes, France*); Matthieu Vignes (*BioSS at Scottish Crop Research Institute, Scotland*)

**A Systematic Approach to Quantifying Evolutionary Functional Trends Across the Universal Tree of Life**.....374  
Gil Alterovitz, Taro Muso (*Harvard Medical School, USA*); Paresh Malalur (*Massachusetts Institute of Technology, USA*); Marco F. Ramoni (*Harvard Medical School, USA*)

## Session 9: Sequence and Structure

**Super Granular Shrink-SVM Feature Elimination (Super GS-SVM-FE) Model for Protein Sequence Motif Information Extraction**.....379  
Bernard Chen, Stephen Pellicer, Phang C. Tai, Robert Harrison, Yi Pan (*Georgia State University, USA*)

**False Discovery Rates in Identifying Functional DNA Motifs**.....387  
Osman Abul (*TOBB University of Economics and Technology, Turkey*); Geir Sandve, Finn Drablos (*Norwegian University of Science and Technology, Norway*)

**A Geometrical Model for the SNP Motif Identification Problem** .....395  
Gaofeng Huang, Peter Jeavons (*Oxford University, UK*)

**A Hierarchical Grow-and-Match Algorithm for Backbone Resonance Assignments Given 3D Structure**.....403  
Fei Xiong, Chris Bailey-Kellogg (*Dartmouth College, USA*)

**A Flexible Stem-Based Local Search Algorithm for Predicting RNA Secondary Structures Including Pseudoknots**.....411  
Xiang Chen, Si-Min He, Dong-Bo Bu, Run-Sheng Chen, Wen Gao (*Chinese Academy of Sciences, China*)

**Mining Conserved Structures of Enzymes from Functional Hierarchical Classification** .....418  
Yu-Feng Huang, Yu-Shin Lin, Tian-Wei Hsu, Chien-Kang Huang (*National Taiwan University, Taiwan*)

**Database Approaches and Data Representation in Structural Bioinformatics** .....425  
Kreshna Gopal, James C. Sacchettini, Thomas R. Ioerger (*Texas A&M University, USA*)

## Session 10: Bioinformatics Applications

**Identifying Genomic Regulators of Set-Wise Co-Expression**.....433  
Jung Hoon Woo (*Macrogen Inc., China*); Tian Zheng (*Columbia University, USA*); Ju Han Kim (*Seoul National University, China*)

**Tracing Lineage in Multi-Version Scientific Databases**.....440  
Mingwu Zhang, Daisuke Kihara, Sunil Prabhakar (*Purdue University, USA*)

<b>Resolving Scientific Service Interoperability with Schema Mapping.....</b>	<b>448</b>
Nadia Yacoubi Ayadi, Zoe Lacroix ( <i>Arizona State University, USA</i> )	
<b>A Machine Learning Approach to Pharmacological Profiling of the Quinone Scaffold in the NCI Database: A Compound Class Enriched in Those Effective Against Melanoma and Leukemia Cell Lines .....</b>	<b>456</b>
M.L. Ujwal ( <i>Eli Lilly &amp; Co. USA</i> ); Patrick Hoffman ( <i>Inforsense, USA</i> ); Kenneth A. Marx ( <i>University of Massachusetts Lowell, USA</i> )	
<b>Biomarker Selection for Predicting Alzheimer Disease using High-Resolution MALDI-TOF Data .....</b>	<b>464</b>
Jung Hun Oh, Young Bun Kim ( <i>The University of Texas, Arlington, USA</i> ); Prem Gurnani, Kevin P. Rosenblatt ( <i>University of Texas at Southwestern Medical Center, USA</i> ); Jean Gao ( <i>University of Texas at Arlington, USA</i> )	
<b>Multivariate Analysis of Imaging Mass Spectrometry Data .....</b>	<b>472</b>
Eric R. Muir, Ibrahima J. Ndiour, Nolwenn A. Le Goasduff, Richard A. Moffitt, Ying Liu, M.C. Sullards, A.H. Merrill, Jr., Yanfeng Chen, May D. Wang ( <i>Georgia Institute of Technology, USA</i> )	
<b>Phagocyte Transmigration Modeling Using System Dynamic Controls.....</b>	<b>480</b>
Jiaxing Xue, Jean Gao, Liping Tang ( <i>University of Texas at Arlington, USA</i> )	

## WORKSHOP PAPERS

### WORKSHOP on Bio-Nano-Info Integration for Personalized Medicine

<b>Toward a Nanobioinformatics Infrastructure for Nanotechnology-Based Prostate Cancer Therapeutic Response Tracking .....</b>	<b>486</b>
David Paik ( <i>Stanford University, USA</i> )	
<b>A Novel Approach for Signal Transduction Networks Simulation at a Mesoscopic Level.....</b>	<b>487</b>
Chenxi Shao, Hongli Deng ( <i>University of Science and Technology of China, China</i> )	
<b>Microtubule Dynamics Classification using a Statistical Model of the Movement of Outer Tips.....</b>	<b>495</b>
Christopher Alberti, Jean-Phillipe Villareal, Delano Billingsley, Koon Yin Kong ( <i>Georgia Institute of Technology, USA</i> ); Adam I. Marcus ( <i>Emory University, USA</i> ); Paraskevi Giannakakou ( <i>Cornell University, USA</i> ); May D. Wang ( <i>Georgia Institute of Technology, USA</i> )	
<b>Computer Aided Histopathological Classification of Cancer Subtypes .....</b>	<b>503</b>
Sohaib Waheed, Richard A. Moffitt, Qaiser Chaudry ( <i>Georgia Institute of Technology, USA</i> ); Andrew N. Young ( <i>Emory University, USA</i> ); May D. Wang ( <i>Georgia Institute of Technology, USA</i> )	
<b>Evolving Biological Behavior in Gene-Based Cellular Simulations .....</b>	<b>509</b>
John H. Phan, Richard A. Moffitt, Todd H. Stokes, May D. Wang ( <i>Georgia Institute of Technology, USA</i> )	
<b>Engineering Multifunctional Biologically-Amenable Nanomaterials for Interfacial Therapeutic Delivery and Substrate-Based Cellular Interrogation .....</b>	<b>517</b>
Mark Chen, Brian Huang, Eric Shin, Erik Robinson, Erik Pierstorff, Houjin Huang, Dean Ho ( <i>Northwestern University, USA</i> )	
<b>Non-Monotonic Radio-Sensitivity over Tumor Volumes on Adjuvant Radio Therapy - A New Insight on Cell Killing and Modeling .....</b>	<b>524</b>
Jack Y. Yang, ( <i>Harvard Medical School and Massachusetts General Hospital, USA</i> ); Mary Qu Yang ( <i>National Institutes of Health (NIH), USA</i> ); Andrzej Niemierko ( <i>Harvard Medical School and Massachusetts General Hospital, USA</i> ); Youping Deng ( <i>University of Southern Mississippi, USA</i> )	

### WORKSHOP on Joint Research in the Southern Illinois University, University of Illinois, and Oak Ridge National Laboratory, U.S. Department of Energy.

<b>Novel Materials for the Direct Removal of Water and Ions from the Body for Patients with Dialysis Needs .....</b>	<b>532</b>
Lisa Furby, Ravinder Gupta, Ajay Mahajan, Jarlen Don, Tsuchin Chu, Bakul Dave ( <i>Southern Illinois University at Carbondale, USA</i> ); Brad Schwartz ( <i>Southern Illinois University School of Medicine at Springfield, USA</i> )	

<b>A Robust Method for Generating Discriminative Gene Clusters .....</b>	<b>538</b>
Min Xu ( <i>University of Southern California, USA</i> ); Louxin Zhang ( <i>National University of Singapore, Singapore</i> ); Pei Li Zhou ( <i>Monash Univeristy, Australia</i> )	
<b>Biological Mechanism on a Chip: Modeling and Realization of Growth Hormone Secretion Mechanism.....</b>	<b>546</b>
John R. Shell, Yonglian Wang, Nazeih M. Botros ( <i>Southern Illinois University at Carbondale, USA</i> )	
<b>Retrieval Analysis of a Cementless Modular Total Hip Arthroplasty Prosthesis.....</b>	<b>553</b>
Manish Paliwal ( <i>The College of New Jersey, USA</i> ); D. Gordon Allan ( <i>Southern Illinois University School of Medicine at Springfield, USA</i> ); Peter Filip ( <i>Sothern Illinois University at Carbondale, USA</i> )	
<b>Trabecular Metal Patella Implanted into Soft-Tissue in a Post-Patellectomized Knee: A Case Report .....</b>	<b>559</b>
D. Gordon Allan ( <i>Sothern Illinois University School of Medicine at Springfield, USA</i> ); Manish Paliwal ( <i>The College of New Jersey, USA</i> ); Peter Filip ( <i>Southern Illinois University at Carbondale, USA</i> )	
<b>A Comparison Between Traditional Shift-and-Add (SAA) and Point-By-Point Back Projection (BP) - Relevance to Morphology of Microcalcifications for Isocentric Motion in Digital Breast Tomosynthesis (DBT) .....</b>	<b>563</b>
Ying Chen ( <i>Southern Illinois University Carbondale, USA</i> ); Joseph Y. Lo, James T. Dobbins, III ( <i>Duke University and Duke University Medical Center, USA</i> )	
<b>Methodology for Evaluating DNA Pattern Searching Algorithms on Multiprocessor .....</b>	<b>570</b>
Benfano Soewito, Ning Weng ( <i>Southern Illinois University at Carbondale, USA</i> )	
<b>An Efficient Compression Method for Multiplannar Reformulated Biomedical Images .....</b>	<b>578</b>
Qiang Cheng, Mehdi Zargham ( <i>Southern Illinois University at Carbondale, USA</i> )	
<b>A Computational Approach to Understand <i>Arabidopsis thaliana</i> and Soybean Resistance to <i>Fusarium solani</i> (Fsg).....</b>	<b>585</b>
Jiazheng Yuan, Mengxia Michelle Zhu, M. Javed Iqbal ( <i>Southern Illinois University at Carbondale, USA</i> ); Jack Y. Yang ( <i>Harvard Medical School, Harvard University, USA</i> ); David A. Lightfoot ( <i>Southern Illinois University at Carbondale, USA</i> )	
<b>Biostatistical Considerations of the Use of Genomic DNA Reference in Microarrays.....</b>	<b>593</b>
Yunfeng Yang ( <i>Oak Ridge National Laboratory, USA</i> ); Mengxia Michelle Zhu ( <i>Southern Illinois University at Carbondale, USA</i> ); Liyou Wu, Jizhong Zhou ( <i>University of Oklahoma, USA</i> )	
<b>Dynamic Load Balancing for Mining of Molecular Substructures using Genetic Algorithm .....</b>	<b>601</b>
Salahuddin Masum, Mohammed Yeasin ( <i>The University of Memphis, USA</i> )	
 <b>WORKSHOP on Progress Toward Petascale Applications in Bioinformatics And Computational Biology</b>	
<b>I/O Induced Scalability Limits of Bioinformatics Applications .....</b>	<b>609</b>
Robert Henschel, Matthias Mueller ( <i>Technische Universität Dresden, Germany</i> )	
<b>Large-Scale QM/MM Calculations of Electronic Excitations in Yellow Protein: Toward Petascale Level of Protein Calculations .....</b>	<b>614</b>
Marek Freindorf, Matthew D. Jones ( <i>State University at Buffalo, USA</i> ); Yihan Shao, Jing Kong ( <i>State University at Buffalo, and Q-Chem Inc. USA</i> ); Thomas R. Furlani ( <i>State University at Buffalo, USA</i> )	
<b>MotifNetwork: A Grid-Enabled Workflow for High-Throughput Domain Analysis of Biological Sequences: Implications for Annotation and Study of Phylogeny, Protein Interactions, and Intraspecies Variation.....</b>	<b>620</b>
Jeffrey Tilson ( <i>Renaissance Computing Institute, USA</i> ); Gloria Rendon ( <i>National Center for Supercomputing Applications, USA</i> ); Mao-Feng Ger, Eric Jakobsson ( <i>University of Illinois at Urbana-Champaign, USA</i> )	
<b>Toward Petascale Simulation of Cellular Microphysiology .....</b>	<b>628</b>
Scott B. Baden ( <i>University of California, San Diego, USA</i> ); Terrence J. Sejnowski, Thomas M. Bartol ( <i>The Salk Institute, USA</i> ); Joel Stiles ( <i>Pittsburgh Supercomputing Center and Carnegie Mellon University, USA</i> )	



## VOLUME II

### Special Sessions Papers

#### Session 11: Special Session on Computational Intelligence in Medical Informatics

- Silent Killing: An Object-Oriented View of Hypertension and Kidney Failures - Part I** .....635  
Jacqueline Signorini, Patrick Greussay (*University Paris 8, France*)
- Medical Image Retrieval Based on Bidimensional Empirical Mode Decomposition** .....641  
Wei Liu, Weidong Xu, Lihua Li (*Hangzhou Dianzi University, China*)
- A Modified Fuzzy Kohonen's Competitive Learning Algorithms Incorporating Local Information for MR Image Segmentation** .....647  
Jun Kong, Wenjing Lu, Jianzhong Wang, Na Che, Yinghua Lu (*Northeast Normal University, China*)
- An Efficient Modeling and Simulation System on the Kidney Matching, Distribution and Exchange Problems** .....654  
Siyuan Liu, Chao Liu (*Chinese Academy of Sciences, China*); Yu Liu (*Shandong University, China*); Chunzhe Zhao (*Chinese Academy of Sciences, China*)
- SiteSeeker – A Motif Discovery Tool** .....662  
Klaus Ecker, Lonnie Welch, Dazhang Gu (*Ohio University, USA*)

#### Session 12: Special Session on Evolutionary Systems Biology

- Modeling Protein Interaction Network and Mechanisms in Exocytosis** .....665  
Wen Zhou, Tian Xia, Jiansong Tong, Julie Dickerson, Bo Su, Xun Gu (*Iowa State University, USA*)
- Toward a Realistic Model for Gene Network Evolution** .....673  
Wenhai Chen (*Chinese Academy of Science, China*); Tian Xia (*Iowa State University, USA*); Tianzi Jiang (*Chinese Academy of Science, China*); Xun Gu (*Iowa State University, USA*)
- Application of Wavelet Transform to the MS-Based Proteomics Data Preprocessing** .....680  
Pan Du (*Northwestern University, USA*); Haihui Wang (*Beihang University, China*); Simon M. Lin, Warren A. Kibbe (*Northwestern University, USA*)
- Pathway Complements of Four *Yersinia*** .....687  
Jennifer L. Neary, Maribel Sanchez (*University of Texas at San Antonio, USA*); Timothy G. Lilburn (*American Type Culture Collection, USA*); Yufeng Wang (*University of Texas at San Antonio, USA*)
- An Improved Ant Colony Optimization Algorithm Based on Route Optimization and Its Applications in Travelling Salesman Problem** .....693  
Yi Zhang, Zhi-li Pei, Jin-hui Yang, Yan-chun Liang (*Jilin University, China*)
- Characterization of MYC Expression in Gefitinib Versus Acute Myeloid Leukemia Reveals Novel Therapeutic Targets** .....699  
James F. Courage, Saurabh Gupta, Yufeng Wang (*University of Texas at San Antonio, USA*)
- Hot and Cold: Spatial Fluctuation in HIV-1 Recombination Rates** .....707  
Misha L. Rajaram (*Iowa State University, USA*); Vladimir N. Mimin (*University of Washington, USA*); Marc A. Suchard (*University of California, Los Angeles, USA*); Karin S. Dorman (*Iowa State University, USA*)

### **Special Session 13: Special Session on Research in Bioinformatics, Neuroinformatics, and Systems Biology in East Asia**

<b>Computational Genome-Wide Discovery of Aberrant Splice Variations with Exon Expression Profiles.....</b>	<b>715</b>
Ryo Yoshida ( <i>Institute of Statistical Mathematics, Japan</i> ); Kazuyuki Numata, Seiya Imoto, Masao Nagasaki ( <i>University of Tokyo, Japan</i> ); Atsushi Doi ( <i>Gene Network International, Japan</i> ); Kazuko Ueno, Satoru Miyano ( <i>University of Tokyo, Japan</i> )	
<b>Mining Frequent Contiguous Sequence Patterns in Biological Sequences.....</b>	<b>723</b>
Tae Ho Kang, Jae Soo Yoo, Hak Yong Kim ( <i>Chungbuk National University, Korea</i> )	
<b>Efficient Methods for Biomedical Named Entity Recognition .....</b>	<b>729</b>
Shing-Kit Chan, Wai Lam ( <i>The Chinese University of Hong Kong, China</i> )	
<b>Stochastic Simulation Model for Patterned Neural Multi-Electrode Arrays.....</b>	<b>736</b>
Dong-Soo Kahng, Yoonkey Nam, Doheon Lee ( <i>Korea Advanced Institute of Science Technology, Korea</i> )	
<b>Classification of Enzyme Function from Protein Sequence based on Feature Representation.....</b>	<b>741</b>
Bum Ju Lee, Heon Gyu Lee, Jong Yun Lee, Keun Ho Ryu ( <i>Chungbuk National University, Korea</i> )	
<b>Inferring Behavioral-Level Circuits of <i>Caenorhabditis elegans</i> from the Topology of Its Wiring Diagram .....</b>	<b>748</b>
Yunkyoo Sohn ( <i>Korea Advanced Institute of Science Technology, Korea</i> ); Jaeseung Jeong ( <i>Korea Advanced Institute of Science Technology, Korea and Columbia University, USA</i> )	
<b>HAMMER Algorithm: Hashing with Arithmetic Modulo-4 for Motif Extraction of Regulatory Elements.....</b>	<b>753</b>
Huitao Sheng, Kishan Mehrotra, Chilukuri Mohan, Ramesh Raina ( <i>Syracuse University, USA</i> )	
<b>A Tale of Intronless Genes in Eukaryotic Genomes.....</b>	<b>759</b>
Meena Sakharkar, Kishore R. Sakharkar ( <i>Nanyang Technological University, Singapore</i> )	
<b>To Fuse or Not to Fuse.....</b>	<b>766</b>
Kishore R. Sakharkar, Meena Sakharkar ( <i>Nanyang Technological University, Singapore</i> )	

### **Session 14: Special Session on Sequence Alignment and Phylogenetic Analysis**

<b>Using Parsimony to Guide Maximum Likelihood Searches .....</b>	<b>774</b>
Kenneth Sundberg, Timothy O'Connor, Hyrum Carroll, Mark Clement, Quinn Snell ( <i>Brigham Young University, USA</i> )	
<b>QOMA2: Optimizing the Alignment of Many Sequences.....</b>	<b>780</b>
Xu Zhang, Tamer Kahveci ( <i>University of Florida, USA</i> )	
<b>A Reliable Metric for Quantifying Multiple Sequence Alignment.....</b>	<b>788</b>
Ken D. Nguyen, Yi Pan ( <i>Georgia State University, USA</i> )	
<b>Amino Acid Substitution Matrices Based on 4-Body Delaunay Contact Profiles.....</b>	<b>796</b>
Ahmet Sacan, I. Hakki Toroslu ( <i>Middle East Technical University, Turkey</i> )	
<b>A Heuristic for Phylogenetic Reconstruction Using Transposition .....</b>	<b>802</b>
Feng Yue ( <i>University of South Carolina, USA</i> ); Meng Zhang ( <i>Jilin University, China</i> ); Jijun Tang ( <i>University of South Carolina, USA</i> )	
<b>Phylogeny By Top Down Clustering Using a Given Multiple Alignment.....</b>	<b>809</b>
Abdullah N. Arslan, Peyman Bizargity ( <i>University of Vermont, USA</i> )	
<b>Reconstructing Mutational Pathways from Serial Evolutionary Trees.....</b>	<b>815</b>
Patricia Buendia ( <i>University of Miami, USA</i> )	

## Session 15: Special Session on Development of Algorithms for Solving Problems in Molecular Biology

- Towards Construction of Optimal Strip-Exchanging Moves** .....821  
Swapnoneel Roy, Ashok KumarThakur (*IBM India Pvt. Ltd., India*)
- Rough Overlapping Biclustering of Gene Expression Data**.....828  
Ruizhi Wang, Duoqian Miao, Gang Li, Hongyun Zhang (*Tongji University, P.R. China*)
- Using Domain-Based Structural Ensemble to Improve Structure Modeling**.....835  
Fa Zhang, Zhaoyun Ma, Zhiyong Liu (*Chinese Academy of Sciences, China*); Bo Yuan (*Shanghai Jiao Tong University, China*)
- Support Vector Regression with Feature Selection for the Multivariate Calibration of Spectrofluorimetric Determination of Aromatic Amino Acids** .....842  
Guo-Zheng Li, Hao-Hua Meng (*Nanjing University, China*); Mary Qu Yang (*National Human Genome Research Institute, National Institutes of Health (NIH), USA*); Jack Y. Yang (*Harvard Medical School, Harvard University, USA*)

## Session 16: Special Session on High-Throughput Data Analysis for Genomics and Proteomics

- Bottom-Up Multiple Row Addition Algorithms for the Biclustering-Problem**.....849  
Hyung-Won Koh (*ISAS - Institute for Analytical Sciences, Germany*); Lars Hildebrand (*University of Dortmund, Germany*)
- Fast Computation of Human Genetic Linkage**.....857  
Hongling Wang (*Columbus Children's Research Institute, USA*); Alberto Maria Segre (*University of Iowa, USA*); Yungui Huang (*Columbus Children's Research Institute, USA*); Jeffrey R. O'Connell (*University of Maryland, USA*); Veronica J. Vieland (*The Ohio State University, USA*)
- 3D Spectrum Analysis of DNA Sequence: Application to *Caenorhabditis elegans* Genome** .....864  
Afe Eloumi Oueslati, Zied Lachiri, Nouredine Ellouze (*ENIT, Tunis*)
- MotifNetwork: Genome-Wide Domain Analysis Using Grid-Enabled Workflows**.....872  
Jeffrey L. Tilson, Alan Blatecky (*Renaissance Computing Institute, USA*); Gloria Rendon (*National Center for Supercomputing Applications, USA*); Eric Jakobsson, Mao-Feng Ger (*University of Illinois at Urbana-Champaign, USA*)
- Profilins, Formins and Katanins as Flagellar Proteins of *Leishmania spp.*: A Genome-Based, Multi-StepBioinformatics-Driven Description** .....880  
Elton J.R. Vasconcelos, Ana C.L. Pacheco, João J.S. Gouveia, Fabiana F. Araújo, Michely C. Diniz, Michel T. Kamimura, Marcília P. Costa, Rodrigo Maggioni, Raimundo Araujo-Filho, Raimundo B. Costa, and Diana Magalhães de Oliveira (*Universidade Estadual do Ceará - UECE, Brazil*)

## Session 17: Special Session on Bio-Medical Soft Computing

- FPGA Acceleration of Phylogeny Reconstruction for Whole Genome Data** .....888  
Jason D. Bakos, Panormitis E. Elenis, Jijun Tang (*University of South Carolina, USA*)
- A Preliminary Study of Correlation between Depth and Path Length of GO Nodes with Gene Sequence Similarity**.....896  
Elham Khabiri (*University of Houston-Clear Lake, USA*)
- Mathematical Models and Optimization Discussions on EA System on AIDS/HIV Spread Estimating and Countermeasures Evaluating** .....900  
Siyuan Liu, Chao Liu, Chunzhe Zhao (*Chinese Academy of Sciences, China*); Yu Liu (*Shandong University, China*)

## Session 18: Special Session on Bio-Complexity

- Fractal Dimension of Mie Scattering Spectra for the Appraisal of Infected HeLa Cells in Cultures**.....908  
Radu Dobrescu (*Politehnica University of Bucharest, Romania*); Loretta Ichim (*Politehnica University of Bucharest, Romania and Romanian Academy, Romania*)
- Complexity-Theoretic Modeling of Biological Cyanide Poisoning as Security Attack in Self-Organizing Networks** .....914  
Jiejun Kong (*University of Florida, USA*); Xiaoyan Hong (*University of Alabama, USA*); Dapeng Wu (*University of Florida, USA*); Mario Gerla (*University of California, Los Angeles, USA*)
- Quantitative and Probabilistic Modeling in Pathway Logic**.....922  
Alessro Abate (*University of California, Berkeley, USA*); Yu Bai (*Stanford University, USA*); Nathalie Sznajder, *Ecole Normale Supérieure, France*; Carolyn Talcott, Ashish Tiwari (*SRI International, USA*)
- A 2D Vibration Array as an Assistive Device for Visually Impaired**.....930  
Dimitrios Dakopoulos, Sanjay K. Boddhu, Nikolaos Bourbakis (*Wright State University, USA*)

## Session 19: Special Session on Machine Learning Methods in Structural and Functional Genomics

- Characterizing and Predicting Catalytic Residues in Enzyme Active Sites Based on Local Properties: A Machine Learning Approach** .....938  
Leonardo Bobadilla, Ferno Niño, Edilberto Cepeda (*National University of Colombia, Colombia*); Manuel A. Patarroyo (*Fundacion Instituto de Inmunologia de Colombia, Colombia*)
- Predicting Protein-Protein Interaction Based on Fisher Scores Extracted from Domain Profiles** .....946  
Tapan Patel, Li Liao (*University of Delaware, USA*)
- A Novel Sequence-Structure Approach for Accurate Prediction of Resistance to HIV-1 Protease Inhibitors**.....952  
Majid Masso, Iosif I. Vaisman (*George Mason University, USA*)
- Prediction of Histone Modifications in DNA Sequences** .....959  
Tho Hoan Pham (*Hanoi National University of Education, Vietnam*); Tu Bao Ho, Dang Hung Tran, Kenji Satou (*Japan Advanced Institute of Science and Technology, Japan*)
- Feature Selection and Partial Least Squares Based Dimension Reduction for Tumor Classification**.....967  
Hua-Long Bu, Guo-Zheng Li (*Shanghai University, China*); Jack Y. Yang (*Harvard Medical School, USA*); Mary Qu Yang (*National Institutes Health (NIH), USA*)

## Session 20: Special Session on Pattern Recognition and Gene Discovery in Molecular Genetics

- $\alpha$ CORR: A Novel Algorithm for Clustering Gene Expression Data**.....974  
Hossam Sharara, Mohamed A. Ismail (*Alexandria University, Egypt*)
- An Intelligent System for Searching Genomic Sequences** .....982  
Vana Gummuluru (*University of Florida, USA*); Su-Shing Chen (*University of Florida, USA; and Shanghai Institute of Biological Sciences, China*)
- XML Encoding of Features Describing Rule-Based Modeling of Reaction Networks with Multi-Component Molecular Complexes** .....987  
Michael L. Blinov, Ion Moraru (*University of Connecticut Health Center, USA*)

## Session 21: Special Session on DNA Microarray Data Analysis

- BALBOA: Extending Bicluster Analysis to Classify ORFs using Expression Data** .....995  
Kenneth Bryan, Pádraig Cunningham (*University College Dublin, Ireland*)
- A Comprehensive Fuzzy-Based Framework for Cancer Microarray Data Gene Expression Analysis** .....1003  
Zhenyu Wang, Vasile Palade (*Oxford University, UK*)

<b>Ensemble of Kernel based Classifiers to Improve the Human Cancer Prediction using DNA Microarrays.....</b>	<b>1011</b>
Ángela Blanco, Manuel Martín-Merino ( <i>Universidad Pontificia de Salamanca, Spain</i> ); Javier De Las Rivas ( <i>Cancer Research Center (CIC-IBMCC, CSIC/USAL), Spain</i> )	
<b>Mining Order Preserving Patterns in Microarray Data by Finding Frequent Orders.....</b>	<b>1019</b>
Li Teng, Laiwan Chan ( <i>The Chinese University of Hong Kong</i> )	
<b>A New Smoothing Model for Analyzing Array CGH Data .....</b>	<b>1027</b>
Nha Nguyen, Heng Huang, Soontorn Oraintara, An Vo ( <i>University of Texas at Arlington, USA</i> )	
<b>Inference of Gene Regulatory Networks using Time Sliding Comparison and Transcriptional Lagging Time from Time Series Gene Expression Profiles .....</b>	<b>1035</b>
Sheehyun Kim, Dongsup Kim ( <i>Korea Advanced Institute of Science and Technology, Korea</i> )	

## Regular Research Papers (Part II)

### Session 22: Microarray Gene Expression Analysis

<b>Multivariate Feature Selection using Random Subspace Classifiers for Gene Expression Data .....</b>	<b>1041</b>
Vidya Kamath ( <i>University of South Florida and H. Lee Moffitt Cancer Center &amp; Research Institute, USA</i> ); Lawrence Hall ( <i>University of South Florida, USA</i> ); Timothy J. Yeatman, Steven A. Eschrich ( <i>H. Lee Moffitt Cancer Center &amp; Research Institute, USA</i> )	
<b>Gene Selection via Matrix Factorization .....</b>	<b>1046</b>
Fei Wang ( <i>Tsinghua University, China</i> ); Tao Li ( <i>Florida International University, USA</i> )	
<b>Mutual Information based Minimum Spanning Trees Model for Selecting Discriminative Genes.....</b>	<b>1051</b>
Fang Zhou, Jieyue He ( <i>Southeast University, China</i> ); Wei Zhong ( <i>University of South Carolina Upstate, USA</i> )	
<b>Gene-Markers Representation for Microarray Data Integration.....</b>	<b>1056</b>
Elena Baralis, Elisa Ficarra, Alessandro Fiori, Enrico Macii ( <i>Politecnico di Torino, Italy</i> )	
<b>Partial Mixture Model for Tight Clustering in Exploratory Gene Expression Analysis .....</b>	<b>1061</b>
Yinyin Yuan, Chang-Tsun Li ( <i>University of Warwick, UK</i> )	
<b>rSWTi: A Robust Stationary Wavelet Denoising Method for Array CGH Data .....</b>	<b>1066</b>
Yuhang Wang, Siling Wang ( <i>Southern Methodist University, USA</i> ); Andrew R. Zinn ( <i>UT Southwestern Medical Center at Dallas, USA</i> )	
<b>An Empirical CDF Approach to Estimate the Significance of Gene Ranking for Finding Differentially Expressed Genes .....</b>	<b>1071</b>
Jahangheer Shaik, E.O. George, Mohammed Yeasin ( <i>University of Memphis, USA</i> )	
<b>Gene Expression Profiling and Machine Learning to Understand and Predict Primary Graft Dysfunction .....</b>	<b>1076</b>
Monika Ray, Sekhar Dharmarajan ( <i>Washington University, USA</i> ); Johannes Freudenberg ( <i>Cincinnati Children's Hospital, USA</i> ); G. Alexander Patterson, Weixiong Zhang ( <i>Washington University, USA</i> )	
<b>Sensitivity and Consistency of Affymetrix GeneChip Normalization Methods.....</b>	<b>1081</b>
Jared Fox, Nik Brown ( <i>UCLA, USA</i> )	

### Session 23: Bioengineering (Part A) -- Deformable and 3D Modeling

<b>Statistical Shape Analysis of the Corpus Callosum in Subtypes of Autism.....</b>	<b>1087</b>
Qing He, Ye Duan, Judith Miles, Nicole Takahashi ( <i>University of Missouri-Columbia, USA</i> )	
<b>Simulation and Visualization of Menisci-Femur Contact using Patient-Specific Deformable Models.....</b>	<b>1092</b>
Ying Zhu ( <i>Georgia State University, USA</i> )	

**Improved Edge Map of Geometrical Active Contour Model based on Coupling to Anisotropic Diffusion Filtering** .....1097  
 Foued Derraz, Abdelmalik Taleb-Ahmed (*Valenciennes and Hainaut Cambresis University, France*);  
 Azzeddine Chikh, Fethi Bereksi-Reguig (*Abou Bekr Belkaid University, Algeria*)

**Analysis of Cardiac Wall Motion Estimation Methods**.....1102  
 Soroor Behbahani, Keivan Magholi (*Islamic Azad University, Iran*)

**Partial Transmission High-Speed Continuous Tracking Multi-Leaf Collimator for 4D Adaptive Radiation Therapy** .....1108  
 Tarun Podder, Ivan Buzurovic, Yida Hu, James M. Galvin, Yan Yu (*Thomas Jefferson University, USA*)

**Quantitative Analysis of Inter-Object Spatial Relationships in Biological Images** .....1113  
 Wamiq Ahmed, Magdalena Jonczyk, Ali Shamsaie, Arif Ghafoor, J. Paul Robinson (*Purdue University, USA*)

## **Session 24: Bioengineering (Part B) – Biomedical Image Processing I**

**Histogram Transformation for Inter-Modality Image Registration**.....1118  
 Joerg Meyer (*University of California at Irvine, USA*)

**The GPU on Biomedical Image Processing for Color and Phenotype Analysis**.....1124  
 Antonio Ruiz, Manuel Ujaldón, José Antonio Andrades, José Becerra (*University of Malaga, Spain*); Kun Huang,  
 Tony Pan, Joel Saltz (*Ohio State University, USA*)

**Tissue Identification in Ultrasound Images using Rayleigh Local Parameter Estimation** .....1129  
 Santiago Aja-Fernández, Marcos Martin-Fernández, Carlos Alberola-Lopez (*Universidad de Valladolid, Spain*)

**Exploring Cardioneural Signal from Noninvasive ECG Measurement** .....1134  
 Amirali Shayan Arani, Yi Zhu, Yi-Ning Cheng (*University of California San Diego, USA*); Shien-Fong Lin,  
 Peng-Sheng Chen (*Indiana University, USA*); Chung-Kuan Cheng (*University of California San Diego, USA*)

**MS Lesions Detection in MRI using Grouping Artificial Immune Networks**.....1139  
 Akmal Younis, Ahmed T. Soliman, Mansur R. Kabuka, Nigel M. John (*University of Miami, USA*)

**Non-Negative Tensor Factorization Based on Alternating Large-Scale Non-Negativity-Constrained Least Squares**.....1147  
 Hyunsoo Kim, Haesun Park (*Georgia Institute of Technology, USA*); Lars Eldén (*Linkoping University, Sweden*)

## **Session 25: Bioengineering (Part C) – Biomedical Image Processing II**

**A Computer Aided Tool for the Assessment of Human Sperm Morphology**.....1152  
 Henry Carrillo Lindado, Jorge Villarreal, Miguel Sotaquirá, Álvaro Goelkel, Ricardo Gutiérrez (*Universidad del Norte, Colombia*)

**Feature Estimation for Vocal Fold Edema Detection Using Short-Term Cepstral Analysis**.....1158  
 Benedito G. Aguiar Neto, Joseana M. Fechine, Silvana Cunha Costa (*Federal University of Campina Grande, Brazil*);  
 Menaka Muppa (*University of Washington, USA*)

**A New Hybrid Technique for Dermatological Image Registration**.....1163  
 Heng Huang (*University of Texas at Arlington, USA*); Paul Bergstresser (*University of Texas Southwestern Medical Center, USA*)

**PID Control based on BP Neural Network for the Regulation of Blood Glucose Level in Diabetes**.....1168  
 Chengwei Li (*Harbin Institute of Technology, China*); Ruiqiang Hu (*Yan Shan University, China*)

**Spatiotemporal Analysis of an Agent-Based Model of a Colony of Keratinocytes: A First Approach for the Development of Validation Methods** .....1173  
 Cesar Pichardo-Almarza, Rod Smallwood, S.A. Billings (*University of Sheffield, UK*)

## Session 26: Sequence Analysis and Sequence Alignment

- A Suffix Tree Construction Algorithm for DNA Sequences**.....1178  
Hongwei Huo (*Xidian University, China*); Vojislav Stojkovic (*Morgan State University, USA*)
- Identifying Fungal Regulatory Motif Patterns Using SCOPE, an Ensemble Learning Method Motif Finder**.....1183  
Viktor Martyanov, Larkin Elderon, Amy Gladfelter, Dhanalakshmi R. Nair, Robert H. Gross (*Dartmouth College, USA*)
- Computational Identification of Cis-regulatory Elements Associated with Pungency of Chili Peppers**.....1188  
Tieming Ji, Desh Ranjan, Jeanne Curry, Mary O'Connell (*New Mexico State University, USA*)
- Speeding Up Pairwise Sequence Alignments: A Scoring Scheme Reweighting Based Approach**.....1194  
Yong Gao, Michael Henderson (*University of British Columbia Okanagan, Canada*)
- Iterative Refinement of Repeat Sequence Specification Using Constrained Pattern Matching**.....1199  
Dan He, Abdullah N. Arslan, Yu He, Xindong Wu (*The University of Vermont, USA*)
- Differential Scoring for Systolic Sequence Alignment**.....1204  
Antonio de la Serna (*IEEE*)
- Determining Domain Similarity and Domain-Protein Similarity Using Functional Similarity Measurements of Gene Ontology Terms**.....1209  
Jennifer Leopold, Anne Maglia, Lisa Guntly (*University of Missouri - Rolla, USA*)
- Signal Representation and Processing of Nucleotide Sequences**.....1214  
Paul Cristea, Rodica Tuduce, Iulian Nastac (*University "Politehnica" of Bucharest, Romania*); Jan Cornelis, Rudi Deklerck (*Vrije Universiteit Brussel, Belgium*); Marius Andrei (*Google Inc., USA*)
- Cluster Analysis of Regulatory Sequences with a Log Likelihood Ratio Statistics-Based Similarity Measure**.....1220  
Huiru Zheng, Haiying Wang (*University of Ulster, UK*); Jinglu Hu (*Waseda University Japan*)

## Session 27: Bioengineering (Part D) – Biomedical Applications

- A PQRM-Based PACS System for Advanced Medical Services Under Grid Environment**.....1225  
Yong-Jie Ni, Chan-Hyun Youn, Byoung-Jin Kim, Young-Joo Han, Peng Liu (*Information and Communications University, Korea*)
- Middleware Based Inpatient Healthcare Information System**.....1230  
S.H. Hsieh, S.L. Hsieh, Y.C. Weng, T.H. Yang, Feipei Lai, P.H. Cheng, X.O. Ping, M.Y. Jan, J.C. Lin, C.H. Peng, K.H. Huang, L.F. Ko, C.H. Chen, K.P. Hsu (*National Taiwan University, Taiwan*)
- Generating Social Networks of Intimate Contacts for the Study of Public Health Intervention Strategies**.....1235  
Courtney R. Corley, Lindsey Brown, Armin R. Mikler (*University of North Texas, USA*); Diane J. Cook (*Washington State University, USA*); Karan Singh (*University of North Texas Health Science Center, USA*)
- YinYang Mental Squares – An Equilibrium-Based System For Bipolar Neurobiological Pattern Classification and Analysis**.....1240  
Wen-Ran Zhang, Karl Peace (*Georgia Southern University, USA*)
- Automatically Extracting Acronyms from Biomedical Text**.....1245  
Jared Fox, Nik Brown (*UCLA, USA*)
- Feature Extraction and Parameters Selection of Classification Model on Brain-Computer Interface**.....1249  
Mingyuan Zhao, Mingtian Zhou, Qingxin Zhu, Ping Yang (*University of Electronic Science Technology of China*)

## Session 28: Biological Networks

- Consistent Modeling, Integration and Simulation of Molecular Interaction Networks in Space-Time Dimension**.....1254  
Rui Chang (*Technical University of Munich, Germany*)

<b>Feature Reduction for Gene Regulatory Network Control .....</b>	<b>1260</b>
Mehmet Tan ( <i>University of Calgary, Canada</i> ); Faruk Polat ( <i>Middle East Technical University, Turkey</i> ); Reda Alhajj ( <i>University of Calgary, Canada</i> )	
<b>Graph Mining of Networks from Genome Biology .....</b>	<b>1265</b>
George Chin, Jr., Grant C. Nakamura, Daniel G. Chavarria, Heidi J. Sofia ( <i>Pacific Northwest National Laboratory, USA</i> )	
<b>Structural Prediction of Protein-Protein Interactions in <i>Saccharomyces Cerevisiae</i> .....</b>	<b>1270</b>
Martin S.R. Paradesi, Doina Caragea, William H. Hsu ( <i>Kansas State University, USA</i> )	
<b>Complete Backtranslation of Oligopeptides for Metabolic Pathways Exploration of Complex Environments Using Functional Microarrays .....</b>	<b>1275</b>
Mohieddine Missaoui, David R.C. Hill ( <i>Laboratoire d'informatique et de Modélisation et Optimization des Systèmes (LIMOS), France</i> ); Cécile Militon, Pierre Peyret ( <i>Laboratoire de Biologie des Protistes (LBP), France</i> )	
<b>A Structure Learning Algorithm for Inference of Gene Networks from Microarray Gene Expression Data Using Bayesian Networks.....</b>	<b>1280</b>
Kazuyuki Numata, Seiya Imoto, Satoru Miyano ( <i>University of Tokyo, Japan</i> )	
 <b>Session 29: Algorithms in Bioinformatics</b>	
<b>An Algorithm for Mining Fuzzy Association Rules Based on Immune Principles .....</b>	<b>1285</b>
Zhang Lei, Li Ren-hou ( <i>Xi'an Jiaotong University, China</i> ); Zhang Lei ( <i>Henan University of Science and Technology, China</i> )	
<b>Toward The Recognition Code Of Protein-DNA Recognition .....</b>	<b>1290</b>
Juan Shan, Yuxuan Wang, Changhui Yan ( <i>Utah State University, USA</i> )	
<b>Self-Optimizing Parallel Algorithms for Haplotype Reconstruction and Their Evaluation on the JPT and CHB Genotype Data.....</b>	<b>1294</b>
Dragoş Trincă, Sanguthevar Rajasekaran ( <i>University of Connecticut, USA</i> )	
<b>Reducing Folding Scenario Candidates in Pseudoknots Detection Using PLMM_DPSS Algorithm Integrated with Energy Filters.....</b>	<b>1299</b>
Xiaolu Huang, Hesham Ali ( <i>University of Nebraska at Omaha, USA</i> )	
<b>Exploring Topological Properties of NMR Graphs.....</b>	<b>1304</b>
Paulius Micikevicius ( <i>Armstrong Atlantic State University, USA</i> ); Narsingh Deo ( <i>University of Central Florida, USA</i> )	
<b>Probability Analysis on Associations of Adverse Drug Events with Drug-Drug Interactions.....</b>	<b>1308</b>
Yu-Ting Huang, Shih-Fang Lin, Chung-Cheng Chiu, Hsiang-Yuan Yeh, Von-Wun Soo ( <i>National Tsing Hua University, Taiwan</i> )	
 <b>Session 30: Bioinformatics Tools</b>	
<b>Combining Semantics, Context, and Statistical Evidence in Genomics Literature Search .....</b>	<b>1313</b>
Jay Urbain, Nazli Goharian ( <i>Illinois Institute of Technology, USA</i> ); Ophir Frieder ( <i>Georgetown University, USA</i> )	
<b>Graph and Topological Structure Mining on Scientific Articles.....</b>	<b>1318</b>
Fan Wang ( <i>The Ohio State University, USA</i> ); Ruoming Jin ( <i>Kent State University, USA</i> ); Gagan Agrawal ( <i>Ohio State University, USA</i> ); Helen Piontkivska ( <i>Kent State University, USA</i> )	
<b>Supervised HITS Algorithm for MEDLINE Citation Ranking .....</b>	<b>1323</b>
Ying Liu, Yongjing Lin ( <i>University of Texas at Dallas, USA</i> )	
<b>Storing Efficiently Bioinformatics Workflows.....</b>	<b>1328</b>
Michel Kinsy, Zoe Lacroix ( <i>Arizona State University, USA</i> )	



**Intelligent Interfaces for Mining Large-Scale RNAi-HCS Image Databases.....1333**  
Chen Lin, Wayne Mak, Pengyu Hong (*Brandeis University, USA*); Katharine Sepp (*Harvard Medical School, USA*);  
Norbert Perrimon (*Harvard Medical School and Howard Hughes Medical Institute, USA*)

**GPX: A Tool for the Exploration and Visualization of Genome Evolution .....1338**  
Neha Nahar, Lutz Hamel (*University of Rhode Island, USA*); Maria S. Poptsova, J. Peter Gogarten (*University of Connecticut, USA*)

**SBLAST: Structural Basic Local Alignment Searching Tools using Geometric Hashing .....1343**  
Tom Milledge (*Florida International University, USA*); Gaolin Zheng (*North Carolina Central University, USA*);  
Tim Mullins (*IBM Systems and Technology Group, USA*); Giri Narasimhan (*Florida International University, USA*)

## **Session 31: Protein Structural Prediction and Functional Analysis**

**G-Protein Coupled Receptor Subfamilies Prediction Based on Nearest Neighbor Approach .....1348**  
Mudassir Fayyaz, Adnan Mujahid (*Ghulam Ishaq Khan Institute of Engineering Science & Technology, Pakistan*);  
Asifullah Khan, Tae-Sun Choi (*Gwangju Institute of Science Technology, Korea*); Nadeem Iqbal (*Korea Advanced Institute of Science and Technology KAIST, Korea*)

**Protein Secondary Structure Prediction Using Genetic Neural Support Vector Machines .....1355**  
Anjum Reyaz-Ahmed, Yan-Qing Zhang (*Georgia State University, USA*)

**An HV-SVM Classifier to Infer TF-TF Interactions Using Protein Domains and GO Annotations .....1360**  
Xiao-Li Li (*Institute for Infocomm Research, Singapore*); Jun-Xiang Lee, Bharadwaj Veeravalli (*National University of Singapore, Singapore*); See-Kiong Ng (*Institute for Infocomm Research, Singapore*)

**Supervised Statistical and Machine Learning Approaches to Inferring Pairwise and Module-Based Protein Interaction Networks .....1365**  
Fiona Browne, Haiying Wang, Huiru Zheng, Francisco Azuaje (*University of Ulster at Jordanstown, UK*)

**Predicting Protein Subcellular Localizations Using Weighted Euclidian Distance.....1370**  
Jing Hu, Changhui Yan (*Utah State University, USA*)

**An Efficient Data Structure for Applying Multiple Seeds in Homology Search.....1374**  
Alireza Hadj Khodabakhshi (*Simon Fraser University, Canada*); Mehdi Mirzazadeh (*University of Waterloo, Canada*);  
Arvind Gupta (*Simon Fraser University, Canada*)

**A Mixture of Experts Method for Predicting Domain Boundaries in Proteins .....1379**  
Ian MacDonald (*College of Saint Rose, USA*); George Berg (*University at Albany, SUNY, USA*)

**SIGN: Reliable Protein Interaction Identification by Integrating the Similarity in GO and the Similarity in Protein Interaction Networks.....1384**  
Woochang Hwang, Taehyong Kim, Young-rae Cho, Aidong Zhang, Murali Ramanathan (*State University of New York at Buffalo, USA*)

## **Session 32: Bioinformatics Applications**

**Identification of Differential Flow Cytometry Expression .....1389**  
Elizabeth Rossin, Saumyadipta Pyne (*Broad Institute of MIT and Harvard, USA*); Florian Hahne (*German Cancer Research Center, Germany*); Philip L. De Jager (*Brigham & Women's Hospital, USA*)

**Performance Characterization of BLAST for the Grid .....1394**  
Enis Afgan, Purushotham Bangalore (*University of Alabama at Birmingham, USA*)

**Large-Scale Discovery of Regulatory Motifs Involved in Alternative Splicing .....1399**  
Sihui Zhao, Jihye Kim, Steffen Heber (*North Carolina State University, USA*)

**Semiparametric RMA Background-Correction for Oligonucleotide Arrays .....1404**  
Ionut Bebu, Françoise Seillier-Moiseiwitsch, Hongfang Liu (*Georgetown University, USA*)

<b>Alternative Splicing: Associating Frequency with Isoforms.....</b>	<b>1409</b>
<i>Anuradha Roy, Jennifer L. Leopold, Anne M. Maglia (University of Missouri - Rolla, USA)</i>	
<b>A Proposed Statistical Protocol for the Analysis of Metabolic Toxicological Data Derived from NMR Spectroscopy .....</b>	<b>1414</b>
<i>Benjamin Kelly, Paul Anderson, Nicholas Reo (Wright State University, USA); Nicholas DelRaso (Wright-Patterson AFB, USA); Travis Doom, Michael Raymer (Wright State University, USA)</i>	
<b>A Framework for Mass Spectral Quality Assessment without Prior Information .....</b>	<b>1419</b>
<i>Fang-Xiang Wu, Jiarui Ding (University of Saskatchewan, Canada); Guy G. Poirier (Laval University Medical Research Center (CHUL), Canada)</i>	
<b>Using Long Fragments to Reconstruct RNA Backbones .....</b>	<b>1424</b>
<i>Tapani Utriainen, Graham Kemp (Chalmers University of Technology, Sweden)</i>	
<b>A Modified Uniformization Method for the Chemical Master Equation .....</b>	<b>1429</b>
<i>Jingwei Zhang, Layne Watson (Virginia Polytechnic Institute and State University, USA)</i>	
<b>Decision Fusion of Circulating Markers for Breast Cancer Detection in Premenopausal Women .....</b>	<b>1434</b>
<i>Jonathan L. Jesneck, Sayan Mukherjee, Loren W. Nolte (Duke University, USA); Anna E. Lokshin (University of Pittsburgh, USA); Jeffrey R. Marks, Joseph Lo (Duke University, USA)</i>	

## **IEEE BIBE Plenary Keynote Lecture Notes (Part II)**

<b>Partial Least Squares Based Dimension Reduction with Gene Selection for Tumor .....</b>	<b>1439</b>
<i>Guo-Zheng Li; Xue-Qiang Zeng (Shanghai University, China); Jack Y. Yang (Harvard Medical School, Harvard University, USA); Mary Qu Yang (National Human Genome Research Institute, National Institutes of Health (NIH)), USA)</i>	
<b>Functional and Molecular Imaging: Key Components of Personalized Healthcare .....</b>	<b>1445</b>
<i>Steven E. Seltzer (Harvard Medical School and Brigham &amp; Women's Hospital, USA)</i>	
<b>Biomedical Literature Mining.....</b>	<b>1446</b>
<i>Xiaohua Hu (Drexel University, USA)</i>	
<b>An Overview of Bidirectional Promoters .....</b>	<b>1447</b>
<i>Mary Qu Yang (National Human Genome Research Institute, National Institutes of Health (NIH), U.S. Department of Health and Human Services and Oak Ridge, DOE, USA); Laura L. Elnitski (National Human Genome Research Institute, National Institutes of Health (NIH), U.S. Department of Health and Human Services, USA)</i>	
<b>Distributed wireless sensors on the Human Body .....</b>	<b>1448</b>
<i>Ruzena Bajcsy (University of California at Berkeley, USA)</i>	
<b>Transforming Medicine: Genomics, Bioinformatics, and Human Health .....</b>	<b>1449</b>
<i>Andreas D. Baxevas (National Human Genome Research Institute, National Institutes of Health (NIH), U.S. Department of Health and Human Services, USA)</i>	
<b>Integrative Biomedical Informatics .....</b>	<b>1450</b>
<i>Brain D. Athey (University of Michigan Medical School and National Center for Integrative Biomedical Informatics (NCIBI), USA)</i>	
<b>Bio-Nano-Info Integration for Personalized Medicine.....</b>	<b>1451</b>
<i>Eric Jakobsson (National Center for Biomimetic Nanoconductors and University of Illinois at Urbana-Champaign, USA); May D. Wang (Georgia Tech and Emory University); Linda Molnar (National Cancer Institute, National Institutes of Health, U.S. Department of Health and Human Services, USA)</i>	

## Tutorial Lecture Notes

<b>Using the Soybean Genome Database (SoyGD) To Display and Analyze a 1 Gbp Genome Sequence .....</b>	<b>1453</b>
David Lightfoot, Mengxia Michelle Zhu ( <i>Southern Illinois University, Carbondale, USA</i> )	
<b>Biometrics Intelligence Information Systems and Applications .....</b>	<b>1454</b>
Patrick S. P. Wang ( <i>Northeastern University, USA</i> )	
<b>Knowledge Modeling for High Content Screening of Multimedia Biological Data .....</b>	<b>1455</b>
Arif Ghafoor, J. Paul Robinson ( <i>Purdue University, West Lafayette, USA</i> )	
<b>Reconstructing Signal Transduction from Raw Genomic Data .....</b>	<b>1456</b>
Igor B. Zhulin ( <i>Oak Ridge National Laboratory, DOE, USA</i> )	
<b>Studying co-Regulation and Inter-regulation of Genes via eQTL Mapping .....</b>	<b>1457</b>
Tian Zheng ( <i>Columbia University, USA</i> )	
<b>Lecture on Progress Toward Petascale Applications in Bioinformatics and Computational Biology .....</b>	<b>1458</b>
Craig A. Stewart, Malinda Lingwall ( <i>Indiana University, USA</i> ); David Bade ( <i>Georgia Institute of Technology, USA</i> )	
<b>Performance Evaluation of a Scalable Molecular Dynamics Simulation Framework on a Massively-Parallel System .....</b>	<b>1459</b>
Sadaf R. Alam, Pratul K. Agarwal and Jeffery A. Kuehn ( <i>Oak Ridge National Laboratory, DOE, USA</i> )	

*Author Index for Volume I and II* ..... *Follows page 634*

*Author Index for Volume I and II* ..... *Follows page 1467*