

2009 IEEE International Conference on Bioinformatics and Biomedicine Workshop

(BIBMW 2009)

**Washington, DC, USA
1 – 4 November 2009**



**IEEE Catalog Number: CFP0926D-PRT
ISBN: 978-1-4244-5120-3**

TABLE OF CONTENTS

WORKSHOP 1: APPLICATIONS OF MACHINE LEARNING IN BIOINFORMATICS

Clustering Microarray Time-series Data using Expectation Maximization and Multiple Profile Alignment	1
<i>Numanul Subhani, Luis Rueda, Alioune Ngom, Conrad J. Burdeny</i>	
A Comparison of Data Mining Approaches in the Categorization of Oral Anticoagulation Patients	7
<i>Francesco Archetti, Ilaria Giordani, Enza Messina, Giulia Ogliari, Daniela Mari</i>	
Evaluation of Weight Matrix Models in the Splice Junction Recognition Problem	13
<i>Leonardo G. Tavares, Heitor S. Lopes, Carlos R. Erig Lima</i>	
Relational Clustering and Bayesian Networks for Linking Gene Expression Profiles and Drug Activity Patterns	19
<i>E. Fersini, I. Giordani, E. Messina, F. Archetti</i>	
A Ground Truth Based Comparative Study on Detecting Epistatic SNPs	25
<i>Li Chen, Guoqiang Yu, David J. Miller, Lei Song, Carl Langefeld, David Herrington, Yongmei Liu, Yue Wang</i>	
A New Distance Distribution Paradigm to Detect the Variability of the Influenza-A Virus in High Dimensional Spaces	31
<i>Mosaab Daoud, Stefan C. Kremer</i>	
CGM: A Biomedical Text Categorization Approach Using Concept Graph Mining	37
<i>Said Bleik, Min Song, Aaron Smalter, Jun Huan, Gerald Lushington</i>	
On a General Method for Matrix Factorisation Applied to Supervised Classification	43
<i>Vladimir Nikulin, Geoffrey J. McLachlan</i>	
Domain Content Based Protein Function Prediction Using Incomplete GO Annotation Information	49
<i>Lirong Tan, Zhiwen Yu, Hau-San Wong</i>	
Selection of Negative Examples in Learning Gene Regulatory Networks	55
<i>Michele Ceccarelli, Luigi Cerulo</i>	
A Novel Graph-based Selection Wrapper for Learning Enhancement in a Semi-supervised Manner	61
<i>Zhenggang Chang, Jieyue He, Wei Zhongy, Yi Panz</i>	
A Graph Algorithm for Extracting Features from Transcription Factor Binding Sites	67
<i>Chunmei Liu, Yinglei Song, Junfeng Qu, Anietie U. Andy</i>	
Learning Parameters for Non-coding RNA Sequence-Structure Alignment	72
<i>Yinglei Song, Chunmei Liu, Junfeng Qu</i>	

WORKSHOP 2: COMPUTATIONAL STRUCTURAL BIOINFORMATICS

Polynomial-Time Disulfide Bond Determination Using Mass Spectrometry Data	77
<i>William Murad, Rahul Singh, Ten-Yang Yen</i>	
Density-Based Classification of Protein Structures Using Iterative TM-score	85
<i>David Hoksza, Jakub Galgonek</i>	
A Global Optimization Algorithm for Protein Surface Alignment	91
<i>P. Bertolazzi, G. Liuzzi, C. Guerra</i>	
Upper Bounds for Foldings in the FCC-HP Protein Model	99
<i>Abu Dayem Ullah, Kathleen Steinhöfel</i>	
Node Degree Distribution in Amino Acid Interaction Networks	105
<i>Omar Gaci, Stefan Balev</i>	
Matching Observed Alpha Helix Lengths to Predicted Secondary Structure	111
<i>Brian Cloteaux, Nadezhda Serova</i>	
Tracing Conformational Changes in Proteins	118
<i>Nurit Haspel, Mark Moll, Matthew L. Baker, Wah Chiu, Lydia E. Kavraki</i>	
Prediction of Protein Long-Range Contacts Using GaMC Approach with Sequence Profile Centers	126
<i>Peng Chen, Jinyan Li</i>	
Generalized Spring Tensor Models for Protein Fluctuation Dynamics and Conformation Changes	134
<i>Tu-Liang Lin, Guang Song</i>	
Computational Testing of Protein-Protein Interactions	142
<i>Ataur R. Katebi, Andrzej Kloczkowski, Robert L. Jernigan</i>	

An Artificial Backbone of Hydrogens for Finding the Conformation of Protein Molecules	150
<i>C. Lavor, A. Mucherino, L. Liberti, N. Maculan</i>	
Discrimination of Thermophilic and Mesophilic Proteins.....	154
<i>Todd J. Taylor</i>	
Sequence-based B-cell Epitope Prediction by Using Associations in Antibody-Antigen Structural Complexes	163
<i>Liang Zhao, Jinyan Li</i>	
An Efficient Geometric Build-up Algorithm for Protein Structure Determination with Sparse Exact Distance Data	171
<i>Robert T. Davis, Claus Ernst, Di Wu</i>	
Effect of Sidechain Anisotropy on Residue Contact Determination.....	179
<i>Weitao Sun, Jing He</i>	
How Does the Periodicity Associated with Nucleosomal DNA Reflect on Its Intrinsic Curvature?	187
<i>T. Murlidharan Nair</i>	

WORKSHOP 3: DATA MINING FOR BIOMARKER DISCOVERY

Data Mining for Biomarker Discovery: The Time is Ripe	192
<i>Vincent S. Tseng, Hui-Huang Hsu, Jake Y. Chen</i>	
A Cooperative Feature Gene Extraction Algorithm that Combines Classification and Clustering	194
<i>Chi Kin Chow, Hailong Zhu, Jessica Lacy, Mark W. Lingen, Winston Patrick Kuo, Keith Chan</i>	
Lasso based Gene Selection for Linear Classifiers.....	200
<i>Songfeng Zheng, Weixiang Liu</i>	
Discover Significant Associations of Orthologous Simple Sequence Repeat Patterns with Gene Ontology Terms	206
<i>Chien-Ming Chen, Chia-Sheng Chuang, Zhen-Li Huang, Tun-Wen Pai</i>	
Meta-Analysis of Cancer Microarray Data Reveals Signaling Pathway Hotspots.....	211
<i>Pankaj Chopra, Jaewoo Kang, Seung-Mo Hong</i>	
Seed-weighted Random Walks Ranking Method and Its application to Leukemia Cancer Biomarker Prioritizations	217
<i>Tianxiao Huan, Xiaogang Wu, Zengliang Bai, Jake Y. Chen</i>	
A Two-Phase Clustering Approach for Peak Alignment in Mining Mass Spectrometry Data	223
<i>Lien-Chin Chen, Yu-Cheng Liu, Chi-Wei Liu, Vincent S. Tseng</i>	

WORKSHOP 4: DATA MINING IN FUNCTIONAL GENOMICS

Mapping Short Reads to a Genome Without Using Hash Look-Up Table Algorithm and Burrows Wheeler Transformation.....	228
<i>Chun Yuan Lin, Ming-Yuan Huang, Chia-Han Chu, Petrus Tang, Chuan Yi Tang</i>	
Cluster Validation: An Integrative Method for Cluster Analysis.....	234
<i>Mahesh Visvanathan, Adagarla B. Srinivas, Gerald Lushington, Peter Smith</i>	
A Topology-Sharing Based Method for Protein Function Prediction via Analysis of Protein Functional Association Networks	239
<i>Pingzhao Hu, Hui Jiang, Andrew Emili</i>	
Identification of Structured Motifs	245
<i>Huitao Sheng, Kishan Mehrotra, Chilukuri Mohan, Ramesh Raina</i>	
Mining Association Rules among Gene Functions in Clusters of Similar Gene Expression Maps	250
<i>Li An, Zoran Obradovic, Desmond Smith, Olivier Bodenreider, Vasileios Megalooikonomou</i>	

WORKSHOP 5: GRAPH TECHNIQUES FOR BIOMEDICAL NETWORKS

EpICS: A System for Genome-wide Epistasis and Genetic Variation Analysis using Protein-Protein Interactions	256
<i>Kazi Zakia Sultana, Anupam Bhattacharjee, Hasan Jamil</i>	
PathMapper-An Integrative Approach for Oncogene Pathway Identification	262
<i>Asha Vijayan, Bessey Elen Skariah, Bipin G. Nair, Gerald H. Lushington, Shabarinath Subramaniam, Mahesh Visvanathan</i>	
Gene Prioritization Using a Probabilistic Knowledge Model.....	267
<i>Shuguang Wang, Milos Hauskrecht, Shyam Visweswaran</i>	

Towards Automatic Extraction of Social Networks of Organizations in Pub-Med Abstracts	274
<i>Siddhartha Jonnalagadda, Philip Topham, Graciela Gonzalez</i>	
MetNetGE: Visualizing Biological Networks in Hierarchical Views and 3D Tiered Layouts	282
<i>Ming Jia, Sivakumar Swaminathan, Eve Syrkin Wurtele, Julie Dickerson</i>	

WORKSHOP 6: NLP APPROACHES FOR UNMET INFORMATION NEEDS IN HEALTH CARE

NLP-NG - A New NLP System for Biomedical Text Analysis	290
<i>Robert P. Futrelle, Jeff Satterley, Tim McCormack</i>	
Speech Recognition in a Dialog System for Patient Health Monitoring.....	296
<i>Lucian Galescu, James Allen, George Ferguson, Jill Quinn, Mary Swift</i>	
Investigating and Annotating the Role of Citation in Biomedical Full-Text Articles	302
<i>Hong Yu, Shashank Agarwal, Nadya Frid</i>	
Automated Classification of Radiology Reports for Acute Lung Injury: Comparison of Keyword and Machine Learning Based Natural Language Processing Approaches.....	308
<i>Imre Solti, Colin R. Cooke, Fei Xia, Mark M. Wurfel</i>	
Extracting Templates from Radiology Reports using Sequence Alignment	314
<i>Shengyang Wu, Curtis P. Langlotz, Paras Lakhani, Lyle H. Ungar</i>	
Information Flow in Intensive Care Narratives.....	319
<i>Hanna Suominen, Helja Lundgren-Laine, Sanna Salanterä, Helena Karsten, Tapio Salakoski</i>	
Evaluating the Weighted-keyword Model to Improve Clinical Question Answering.....	325
<i>Yong-Gang Cao, John Ely, Hong Yu</i>	

POSTERS

Modeling the Temporal Interplay of Molecular Signaling and Gene Expression by using Dynamic Nested Effects Models.....	330
<i>Benedict Anchang, Rainer Spang, Peter J. Oefner, Mohammad Sadeh, Juby Jacob, Marcel O. Vlad, Achim Tresch</i>	
Constructing Gene-Expression Based Survival Prediction Model for Non-Small Cell Lung Cancer (NSCLC) in All Stages and Early Stages	331
<i>Ying-Wooi Wan, Nancy Lan Guo</i>	
The Mutation at H254 of Organophosphorus Hydrolase Increases the Substrate Specificity of Profenofos.....	332
<i>Shih-Chong Tsai, Kuen-Jou Wei, Chia-Chi Lin, Chu-His Fan</i>	
Information- and Graph-Theoretic Analysis of Bacterial Two Component System.....	333
<i>Kwangmin Choi, Sun Kim</i>	
Knowledge Management for Systems Biology and Translational Medicine. Experiences from the EU BioBridge project.....	334
<i>Dieter Maier, Philipp Krubasik, Sascha Losko, Miguel Hernandez, Jordi Villa I Freixa</i>	
Mining Gene-Related Information from Biomedical Literature	335
<i>Catalina O Tudor, K Vijay-Shanker, Carl J Schmidt</i>	
Computational Analysis Using CisFind of The 3'UTR of Cytosolic Glutamine Synthetase Genes Involved in Posttranscriptional Regulation	336
<i>Bindu Vasudevan-Simon, Champa Sengupta-Gopalan, Pavan K Yelavarthi, Desh Ranjan</i>	
iMOWSE, a Scoring Scheme Bridging in silico and in vitro Digestion in Peptide Mass Fingerprints	337
<i>Stephen Kwok-Wing Tsui, Ka-Kit Leung</i>	
The Classification of a Protein from Its Primary Sequence Using Functional and Structural-Specific PSSMs in Quantitative Measurement.....	338
<i>Kyung Dae Ko, Yoo Jin Hong, Damian B. Van Rossum, Randen L. Patterson</i>	
Development of dbOGAP: A Bioinformatics Resource of O-GlcNAcylated Proteins and Site Prediction	339
<i>Zhang-Zhi Hu, Manabu Torii, Jinlian Wang, Hongfang Liu, Gerald W. Hart</i>	
Predicting Functional Sites in Biological Sequences Using Canonical Correlation Analysis	340
<i>Alvaro J. Gonz'alez, Li Liao, Cathy H. Wu</i>	
Prediction of Biological Pathways with Integrated Information	341
<i>Li Jin, Keith S. Decker, Alexander J. Stachnik, Carl J. Schmidt</i>	
Gene-set Cohesion Analysis Tool (GCAT): A Literature Based Web Tool for Calculating Functional Cohesiveness of Gene Groups.....	342
<i>Lijing Xu, Ramin Homayouni, Nicholas A Furlotte, Kevin E. Heinrich, E. Olusegun George, Michael W. Berry</i>	

Mining Impact of Protein Modifications on Protein-Protein Interactions from Literature	343
<i>Amy Siu, Cecilia Arighi, Jules Nchoutmboue, Catalina O. Tudor, K. Vijay-Shanker, Cathy H. Wu</i>	
Discovery of Cancer-Related New Drug Target Proteins from Re-Constructed Human Disease Network Based on Protein-Protein Interaction Network	344
<i>Yoon Kyeong Lee, Hak Yong Kim</i>	
Microbial Dynamics of Human Obesity	345
<i>James Robert White, Mihai Pop</i>	
SAMON: Sleep Apnea MONitoring	346
<i>Alfredo Burgos, Alfredo Goñi, Arantza Illarramendi, Jesús Bermúdez</i>	
Inhibition Study of the SOD-Cu/Zn of Taenia Solium by Computational Methods	347
<i>Ponciano García-Gutiérrez, Abraham Landa, Arturo Rojo-Domínguez</i>	
Learning a Highly Resolved Tree of Phenotypes Using Genomic Data Clustering	348
<i>Yuanjian Feng, David J. Miller, Robert Clarke, Eric P. Hoffman, Yue Wang</i>	
Physical Markov Model for Protein Structure Prediction	349
<i>Yeona Kang, Charles M. Fortmann</i>	
Integration of Mutual Information and Text Mining Methods for Extracting Gene-Gene Interactions from Gene Expression Data	350
<i>David H. Millis, Jeffrey L. Solka, Lakshmi K. Matukumalli</i>	
Correlation between Computed Equilibrium Secondary Structure Free Energy and siRNA Efficiency	351
<i>Puranjoy Bhattacharjee, Naren Ramakrishnan, Lenwood S. Heath, Alexey V. Onufriev</i>	
Toward Real Time Image to Mesh Conversion for Non Rigid Registration	352
<i>Panagiotis Foteinos, Andrey Chernikov, Nikos Chrisochoides</i>	
Author Index	