

2009 IEEE International Conference on Bioinformatics and Biomedicine

(BIBM 2009)

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



IEEE Catalog Number: CFP09BIB-PRT
ISBN: 978-1-4244-5254-5

2009 IEEE International Conference on Bioinformatics and Biomedicine

BIBM 2009

Table of Contents

Preface

Conference Committees

Program Committee

Additional Referees

Session 1: Genomics and Molecular Structure, Function, and Evolution

Sequence-Based Prediction of Protein Folding Rates Using Contacts, Secondary Structures and Support Vector Machines	3
<i>Guan Ning Lin, Zheng Wang, Dong Xu, and Jianlin Cheng</i>	
Bioinformatics Pipeline for Identification of Binding Motifs of Flexible Protein Tethers	9
<i>Jeffrey L. Ram and Yi Lu</i>	
Extremal Optimization for the Protein Structure Alignment	15
<i>Hengyun Lu, Genke Yang, and Lam Fat Yeung</i>	
Biological Feature Incorporated Alignment for Cross Species Analysis on Carbohydrate Binding Modules	20
<i>Wei-Yao Chou, Shu-Chuan Lin, Rong-Yuan Huang, Ting-Ying Jiang, Chien-Jung Chen, Chia-Mao Wu, Chuan-Yi Tang, Margaret Dah-Tsyr Chang, Wei-I Chou, and Hao-Teng Chang</i>	
Accurate Prediction of Stability Changes in Bacteriophage T4 Lysozyme upon Single Amino Acid Replacements	26
<i>Majid Masso, Tariq Alsheddi, and Iosif I. Vaisman</i>	
High Throughput Short Read Alignment via Bi-directional BWT	31
<i>T. W. Lam, Ruiqiang Li, Alan Tam, Simon Wong, Edward Wu, and S. M. Yiu</i>	
Neural Grammar Networks in QSAR Chemistry	37
<i>Eddie Y. T. Ma and Stefan C. Kremer</i>	

Predicting Yeast Synthetic Lethal Genetic Interactions Using Protein Domains	43
<i>Bo Li and Feng Luo</i>	
Detection of Gene Orthology Based on Protein-Protein Interaction Networks	48
<i>Fadi Towfic, M. Heather West Greenlee, and Vasant Honavar</i>	
Assessment of Gene Annotation Accuracy by Inferring Transcripts from RNA-Seq	54
<i>Jeffrey Martin, Wenhan Zhu, Nicholas Bergman, and Mark Borodovsky</i>	
An Algorithm for the Discovery of Phenotype Related Metabolic Pathways	60
<i>Matthew C. Schmidt and Nagiza F. Samatova</i>	
Protein Long Disordered Region Prediction Based on Profile-Level Disorder Propensities and Position-Specific Scoring Matrixes	66
<i>Bin Liu, Lei Lin, Xiaolong Wang, Xuan Wang, and Yi Shen</i>	
ChemAlign: Biologically Relevant Multiple Sequence Alignment Using Physicochemical Properties	70
<i>Hyrum Carroll, Mark Clement, Quinn Snell, and David McClellan</i>	
3D Rotation Invariant Features for the Characterization of Molecular Density Maps	74
<i>Min Xu, Shihua Zhang, and Frank Alber</i>	
Fast Motif Selection for Biological Sequences	79
<i>Pavel Kuksa and Vladimir Pavlovic</i>	
Inexact Local Alignment Search over Suffix Arrays	83
<i>Mohammadreza Ghodsi and Mihai Pop</i>	
Derivation of Transcriptional Regulatory Relationships by Partial Least Squares Regression	88
<i>Mehmet Tan, Faruk Polat, and Reda Alhajj</i>	
Statistical Methods for Detecting Latent Periodicity in Biological Sequences: Solving a Problem of Small-Size Samples	92
<i>M. Chaley, N. Nazipova, E. Teplukhina, G. Tyulbasheva, and V. Kutyrkin</i>	
Session 2: Computational Systems Biology	
Modeling Protein Interaction Networks with Answer Set Programming	99
<i>Timur Fayruzov, Martine De Cock, Chris Cornelis, and Dirk Vermeir</i>	
Restructuring Protein Interaction Networks to Reveal Structural Hubs and Functional Organizations	105
<i>Young-Rae Cho and Aidong Zhang</i>	
High Functional Coherence in k-Partite Protein Cliques of Protein Interaction Networks	111
<i>Qian Liu, Yi-Ping Phoebe Chen, and Jinyan Li</i>	
Exploratory Analysis of Protein Translation Regulatory Networks Using Hierarchical Random Graphs	118
<i>Daniel Duanqing Wu, Xiaohua Hu, and Tingting He</i>	

Qualitative Motif Detection in Gene Regulatory Networks	124
<i>Zina M. Ibrahim, Ahmed Y. Tawfik, and Alioune Ngom</i>	
Towards Reliable Isoform Quantification Using RNA-Seq Data	130
<i>Brian E Howard and Steffen Heber</i>	
Identifying Gene Signatures from Cancer Progression Data Using Ordinal Analysis	136
<i>Yoon Soo Pyon and Jing Li</i>	
Side Effect Prediction Using Cooperative Pathways	142
<i>Mutsumi Fukuzaki, Mio Seki, Hisashi Kashima, and Jun Sese</i>	
DASSO-MB: Detection of Epistatic Interactions in Genome-Wide Association Studies Using Markov Blankets	148
<i>Bing Han, Meeyoung Park, and Xue-wen Chen</i>	
Disease Classification Based on the Activities of Interacting Molecular Modules with Condition-Responsive Correlation	154
<i>Sejoon Lee, Eunjung Lee, Kwang H. Lee, and Doheon Lee</i>	
A Multi-task Feature Selection Filter for Microarray Classification	160
<i>Liang Lan and Slobodan Vucetic</i>	
A 2-Stage Approach for Inferring Gene Regulatory Networks Using Dynamic Bayesian Networks	166
<i>Akther Shermin and Mehmet A. Orgun</i>	
Microarray Biclustering with Crowding Based MOACO	170
<i>Junwan Liu, Zhoujun Li, Xiaohua Hu, and Yiming Chen</i>	
Using Gene Pair Combinations to Improve the Accuracy of the PAM Classifier	174
<i>Pankaj Chopra, Jaewoo Kang, and Jinseung Lee</i>	
The Analysis of Arabidopsis thaliana Circadian Network Based on Non-stationary DBNs Approach with Flexible Time Lag Choosing Mechanism	178
<i>Yi Jia and Jun Huan</i>	

Session 3: Medical Informatics and Translational Bioinformatics

Biofilm Image Segmentation Using Optimal Multi-level Thresholding	185
<i>Darío Rojas, Luis Rueda, Alioune Ngom, Homero Urrutia, and Gerardo Carcamo</i>	
Model-Based ECG Denoising Using Empirical Mode Decomposition	191
<i>Yan Lu, Jingyu Yan, and Yeung Yam</i>	
Extraction of Respiratory Rate from Impedance Signal Measured on Arm: A Portable Respiratory Rate Measurement Device	197
<i>Sardar Ansari, Kayvan Najarian, Kevin Ward, and Mohamad Hakam Tiba</i>	

Integrated Analysis of Pharmacokinetic, Clinical, and SNP Microarray Data Using Projection onto the Most Interesting Statistical Evidence with Adaptive Permutation Testing	203
<i>Stan Pounds, Xueyuan Cao, Cheng Cheng, Jun Yang, Dario Campana, William E. Evans, Ching-Hon Pui, and Mary V. Relling</i>	
Building a Standards-Based and Collaborative E-Prescribing Tool—MyRxPad	210
<i>Stuart J. Nelson, Kelly Zeng, and John Kilbourne</i>	
RIC: Ranking with Interaction Chains and Its Application in Computational Clinical Proteomics Studies	216
<i>Jieun Jeong and Jake Y. Chen</i>	
Towards Identification of Human Disease Phenotype-Genotype Association via a Network-Module Based Method	222
<i>Jeffrey Q. Jiang, Andreas W. M. Dress, and Ming Chen</i>	
Multiagent Approach for Identifying Cancer Biomarkers	228
<i>Ala Qabaja, Mohammed Alshalalfa, Reda Alhajj, and Jon Rokne</i>	
Feature Extraction for Pulse Waveform in Traditional Chinese Medicine by Hemodynamic Analysis	234
<i>Yan Haixia, Wang Yiqin, Liu Zhaorong, Guo Rui, Li Fufeng, Run Fengying, and Hong Yujian</i>	
Differential Predictive Modeling for Racial Disparities in Breast Cancer	239
<i>Indranil Palit, Chandan K. Reddy, and Kendra L. Schwartz</i>	
Identifying MiRNA and Imaging Features Associated with Metastasis of Lung Cancer to the Brain	246
<i>Sara Nasser, Aarati R. Ranade, Shravan Sridhart , Lisa Haney, Ronald L. Korn, Michael B. Gotway, Glen J. Weiss, and Seungchan Kim</i>	
Evolution of the Probability of an MPM (Multiple Primary Malignancy) after a First Colon Tumor	252
<i>Alberto Cavallo, Cocetta Dodaro, and Andrea Renda</i>	
An Efficient Noise Cancellation Technique to Remove Noise from the ECG Signal Using Normalized Signed Regressor LMS Algorithm	257
<i>Mohammad Zia Ur Rahman, Rafi Ahamed Shaik, and D. V. Rama Koti Reddy</i>	
Using Forearm Electromyograms to Classify Hand Gestures	261
<i>Gene Shuman</i>	
A Device for Detecting and Counting Bites of Food Taken by a Person during Eating	265
<i>Yujie Dong, Adam Hoover, and Eric Muth</i>	
Nonlinear Dynamical and Entropic Complexity Measures as Indicators of Nonstationarities in Short-Term ECG Signals	269
<i>Rafal Ladysz</i>	

Clinical Attribute Network for Chronic Lymphocytic Leukemia	279
<i>Abhisek Kundu, Hatice Gulcin Ozer, Tara Borlawsky, Kristin C. Circle, Kun Huang, and Philip Payne</i>	
Hospital Admission Prediction Using Pre-hospital Variables	283
<i>Jiexun Li, Lisan Guo, and Neal Handly</i>	
Hybrid SVM for Multiclass Arrhythmia Classification	287
<i>Aniruddha J. Joshi, Sharat Chandran, V. K. Jayaraman, and B. D. Kulkarni</i>	
Traumatic Pelvic Injury Outcome Prediction by Extracting Features from Relevant Medical Records and X-Ray Images	291
<i>Wenan Chen, Rebecca Smith, Simina Vasilache, Kayvan Najarian, Kevin Ward, Charles Cockrell, and Jonathan Ha</i>	
Session 4: Cross-Cutting Computational Methods and Bioinformatics Infrastructure	
A Fast, Semi-automatic Brain Structure Segmentation Algorithm for Magnetic Resonance Imaging	297
<i>Kevin Karsch, Qing He, and Ye Duan</i>	
Pancreas Modeling from IVGTT Data Using a Deterministic Optimal Search Method	303
<i>Dayu Lv and Bill Goodwine</i>	
GemAffinity: A Scoring Function for Predicting Binding Affinity and Virtual Screening	309
<i>Kai-Cheng Hsu, Yen-Fu Chen, and Jinn-Moon Yang</i>	
A Novel Deterministic-Stochastic Crossover Method for Simulating Biochemical Networks	315
<i>Amit Sabnis and Robert W. Harrison</i>	
GAM: Genomic Assemblies Merger: A Graph Based Method to Integrate Different Assemblies	321
<i>Alberto Casagrande, Cristian Del Fabbro, Simone Scalabrin, and Alberto Policriti</i>	
Activated Germinal-Center B Cells Undergo Directed Migration	327
<i>Mark J. O'Connor, Anja E. Hauser, Ann M. Haberman, and Steven H. Kleinstein</i>	
Accurate Estimation of Genomic Deletions and Normal Cell Contamination by Bayesian Analysis of Mixtures	332
<i>Guoqiang Yu, Bai Zhang, Jianfeng Xu, Ie-Ming Shih, and Yue Wang</i>	
Determination of Major Lineages of <i>Mycobacterium tuberculosis</i> Complex Using Mycobacterial Interspersed Repetitive Units	338
<i>Minoo Aminian, Amina Shabbeer, and Kristin P. Bennett</i>	
Towards a Better Ranking for Biomedical Information Retrieval Using Context	344
<i>Xiaoshi Yin, Xiangji Huang, and Zhoujun Li</i>	

Ensemble Learning Based on Active Example Selection for Solving Imbalanced Data Problem in Biomedical Data	350
<i>Min Su Lee, Sangyoong Oh, and Byoung-Tak Zhang</i>	
Application of Kernel Functions for Accurate Similarity Search in Large Chemical Databases	356
<i>Xiaohong Wang, Jun Huan, Aaron Smalter, and Gerald H. Lushington</i>	
A Hybrid Method to Discover and Rank Cross-Disciplinary Associations	362
<i>Yue W. Webster, Ranga C. Gudivada, Ernst R. Dow, Jacob Koehler, and Mathew Palakal</i>	
Biomedical Relationship Extraction from Literature Based on Bio-semantic Token Subsequences	366
<i>Jayasimha R. Katukuri, Ying Xie, and Vijay V. Raghavan</i>	
A Protein-Protein Interaction Prediction Method Embracing Intra-protein Domain Cohesion Information	371
<i>Woo-Hyuk Jang, Suk Hoon Jung, Bo-ra Hyun, and Dong-Soo Han</i>	
BioCLink: A Probabilistic Approach for Improving Genomics Search with Citation Links	375
<i>Xiaoshi Yin, Xiangji Huang, and Zhoujun Li</i>	
DNAjig: A New Approach for Building DNA Nanostructures	379
<i>Md. Muksitul Haque, Ananth Kalyanaraman, Amit Dhingra, Nehal Abu-Lail, and Kaori Graybeal</i>	
Enhancing Pathway Based Analysis Using Different Weighting Schemes	384
<i>Sook S. Ha, Inyoung Kim, and Jianhua Xuan</i>	
Analyzing DNA Copy Number Changes Using Fused Margin Regression	388
<i>Yuanjian Feng, Guoqiang Yu, Tian-Li Wang, Ie-Ming Shih, and Yue Wang</i>	
Enabling Data Analysis on High-Throughput Data in Large Data Depository Using Web-Based Analysis Platform - A Case Study on Integrating QUEST with GenePattern in Epigenetics Research	392
<i>Terry Camerlengo, Hatice Gulcin Ozer, Pearly Yan, Jeffrey Parvin, Tim Huang, Kun Huang, Mingxiang Teng, Lang Li, Yunlong Liu, Francisco Perez, and Tahsin Kurc</i>	
Applying Feature Coupling Generalization for Protein-Protein Interaction Extraction	396
<i>Yanpeng Li, Hongfei Lin, and Zhihao Yang</i>	
Real-Time Non-rigid Registration of Medical Images on a Cooperative Parallel Architecture	401
<i>Yixun Liu, Andriy Fedorov, Ron Kikinis, and Nikos Chrisochoides</i>	
A Generalized Multivariate Approach for Correlation-Based Pattern Discovery from Replicated Molecular Profiling Data	405
<i>Dongxiao Zhu, Guorong Xu, and Lipi R. Acharya</i>	
A Genetic Association Study between Breast Cancer and Osteoporosis Using Transitive Text Mining	411
<i>Bi-Hua Cheng, Harsha Gopal Vaka, and Snehasis Mukhopadhyay</i>	

Bacterial Foraging Optimization Algorithm Integrating Tabu Search for Motif Discovery	415
<i>Linlin Shao and Yuehui Chen</i>	
Discovering Temporal Associations among Significant Changes in Gene Expression	419
<i>Hashmat Rohian, Aijun An, Jiashu Zhao, and Xiangji Huang</i>	
Bayesian Classifier for Anchored Protein Sorting Discovery	424
<i>Fan Zhang and Jianjun Hu</i>	

Author Index