

# **2010 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology**

**(CIBCB 2010)**

**Montreal, QC, Canada  
2 – 5 May 2010**



**IEEE Catalog Number: CFP10CIB-PRT  
ISBN: 978-1-4244-6766-2**

## Table of Contents

Supervised Learning of Maternal Cigarette-Smoking Signatures from Placental Gene Expression Data: A Case Study Chengpeng Bi, Carrie Vyhlidal and Steve Leeder	1
Exploring structural modeling of proteins for kernel-based enzyme discrimination Marco A. Alvarez and Changhui Yan	7
Towards a Temporal Modeling of the Genetic Network Controlling Systemic Acquired Resistance in <i>Arabidopsis thaliana</i> Alain B. Tchagang, Heather Shearer, Sieu Phan, Hugo Berube, Fazel Famili, Pierre Fobert and Youlian Pan	12
Modular Clustering of Protein-Protein Interaction Networks Nassim Sohaee and Christian V. Forst	20
DGA: Decomposition with Genetic Algorithm for Multiple Sequence Alignment Farhana Naznin, Ruhul Sarker and Daryl Essam	24
A Comparative Study of the Time-Series Data for Inference of Gene Regulatory Networks Using B-Spline Haixin Wang, James E. Glover and Lijun Qian	32
Integrating Multiple Scoring Functions to Improve Protein Loop Structure Conformation Space Sampling Yaohang Li, Ionel Rata, and Eric Jakobsson	37
Searching for a Single Mathematical Function to Address the Nonlinear Retention Time Shifts Problem in nanoLC-MS Data: Fuzzy-Evolutionary Computational Proteomics Approach Alan J. Barton	45
Classification of HIV-1 Protease Crystal Structures Using Random Forest, Linear Discriminant Analysis and Logistic Regression Gene M. Ko, A. Srinivas Reddy, Sunil Kumar, Barbara A. Bailey and Rajni Garg	53
Sequence Transformation to a Complex Signature Form for Consistent Phylogenetic Tree Using Extensible Markov Model Rao M. Kotamarti, Michael Hahsler, Douglas W. Raiford and Margaret H. Dunham	61
A fitness-independent evolvability measure for evolutionary developmental systems Yaochu Jin and Jens Trommler	69
Functional Data Classification for Temporal Gene Expression Data with Kernel-Induced Random Forests Guangzhe Fan, Jiguo Cao and Jiheng Wang	77
Identification of a Gene Expression Core Signature for Duchenne Muscular Dystrophy (DMD) via Integrative Analysis Reveals Novel	82

Potential Compounds for Treatment Norú Ichim-Moreno, Manuel Aranda and Christian R. Voolstra	
Support Vectors Based Correlation Coefficient for Gene and Sample Selection in Cancer Classification Piyushkumar A. Mundra and Jagath C. Rajapakse	88
Predicting Chemical Activities From Structures by Attributed Molecular Graph Classification Qian Xu, Derek Hao Hu, Hong Xue and Qiang Yang	95
Side Effect Machines for Quaternary Edit Metric Decoding Joseph Alexander Brown, Sheridan K. Houghten and Daniel Ashlock	103
Nearest Neighbor Training of Side Effect Machines for Sequence Classification Daniel Ashlock and Andrew McEachern	111
Identifying Essential Features for the Classification of Real and Pseudo MicroRNAs Precursors Using Fuzzy Decision Trees Na'el M. Abu-halaweh and Robert W. Harrison	119
A Regression Tree-based Gibbs Sampler to Learn the Regulation Programs in a Transcription Regulatory Module Network Jianlong Qi, Tom Michoel and Gregory Butler	126
Simulation of Oscillatory Dynamics of Blood Testosterone Levels Using the Crossover Method Amit Sabnis and Robert W. Harrison	134
Modeling Treatment and Drug Effects at The Molecular Level Using Hybrid System Theory Xiangfang (Lindsey) Li, Lijun Qian and Edward R. Dougherty	140
Speeding up Subcellular Localization by Extracting Informative Regions of Protein Sequences for Profile Alignment Wei Wang, Man-Wai Mak and Sun-Yuan Kung	147
Expanded Study of efn2 Thermodynamic Model Performance on RnaPredict, an Evolutionary Algorithm for RNA Folding Kay C. Wiese and Andrew G. Hendriks	155
Super-Resolution of Mammograms Jun Zheng, Olac Fuentes and Ming-Ying Leung	163
New Approaches to Clustering Microarray Time-Series Data Using Multiple Expression Profile Alignment Numanul Subhani, Luis Rueda, Alioune Ngom and Conrad Burden	170
Issues with the PipeAlign Phylogenomics Toolkit in Identifying Protein Subfamilies Christine Kehyayan and Gregory Butler	177
Missing Value Imputation Methods for Gene-Sample-Time Microarray Data Analysis Yifeng Li, Alioune Ngom and Luis Rueda	183

Mixing Patterns in a Global Influenza A Virus Network using Whole Genome Comparisons Adrienne E. Breland, Mehmet H. Gunes, Karen A. Schlauch and Frederick C. Harris Jr.	190
Computation Intelligence Method to Find Generic Non-coding RNA Search Models Jennifer A. Smith	198
An Exploration of Individual RNA Structural Elements in RNA Gene Finding Nicholas Erho and Kay Wiese	203
Neural Grammar Networks for Toxicology Christopher J.F. Cameron, Eddie Y.T. Ma and Stefan C. Kremer	212
Improved Prediction of Transcription Binding Sites from Chromatin Modification Data Kengo Sato, Tom Whittington, Timothy L. Bailey and Paul Horton	220
Using Decision Tree Learning to Study the Convergence of Phylogenetic Analyses Grant Brammer and Tiffani L. Williams	227
Detecting Retroviruses Using Reading Frame Information And Side Effect Machines Wendy Ashlock and Suprakash Datta	235
Machine Learning Approaches for Customized Docking Scores: Modeling of Inhibition of Mycobacterium tuberculosis Enoyl Acyl Carrier Protein Reductase Gary B. Fogel, Jonathan Tran, Stephen Johnson and David Hecht	243
Improved PCR Design for Mouse DNA by Training Finite State Machines Salik R. Yadav and Steven M. Corns	249
Paroxysmal Atrial Fibrillation Diagnosis Based on Feature Extraction and Classification B. Pourbabaee and C. Lucas	254
Classifying Cytochrome C Oxidase Subunit 1 by Translation Initiation Mechanism using Side Effect Machines Justin Schonfeld and Dan Ashlock	262
A Discrete Fourier Transform Method for Alignment of Visual Evoked Potentials İsmet Şahin and Nuri Yilmazer	269
Additive Noise Analysis on Microarray Data via SVM Classification Zejin Jason Ding and Yan-Qing Zhang	272
Applying neural networks to classify influenza virus antigenic types and hosts Pavan K. Attaluri, Zhengxin Chen and Guoqing Lu	279

Principal Components Analysis Filters Functionally Significant 285  
Peroxidase Motions  
Monique Laberge and István Kövesi