2012 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology

Program

Catamaran Resort Hotel & Spa, San Diego, May 9-12, 2012

Day 1 Wednesday, May 9, 2012

First Floor, *Bahia Belle*

08:00 AM – 04:00 PM	**Registration**
09:00 AM – 09:30 AM	**Breakfast**
09:30 AM – 11:30 AM	**Tutorial TSA: Molecular Biology for Computational Scientists: A Tutorial Introduction** *Instructor: Wendy Ashlock*
11:30 AM – 1:00 PM	**Lunch Break**
01:00 PM – 03:00 PM	**Tutorial TSB: A Survey of Representations for Bioinformatics and Computational Biology** *Instructor: Daniel Ashlock*
03:00 PM – 03:15 PM	**Afternoon Tea and Coffee**
03:15 PM – 05:15 PM	**Tutorial TSC: Lab Techniques and Biological Data for Computational Scientists** *Instructor: Thomas Kiehl*
05:30 PM – 07:00 PM	**Reception**

Day 2 Thursday, May 10, 2012

First Floor (oral), and Second Floor (posters), *William D. Evans*

08:00 AM – 04:00 PM	**Registration**
07:30 AM – 08:00 AM	**Breakfast**
08:00 AM – 08:15 AM	**Opening Remarks**
08:15 AM – 09:15 AM	**Keynote by Prof. Philip E. Bourne, Chair: Yaochu Jin**
09:15 AM – 09:30 AM	**Morning Tea and Coffee**

Session GSA: Modeling, Simulation, and Optimization of Biological Systems
Thursday, May 10, 9:30AM-11:30AM, Chair: Gary Fogel

09:30AM   Biological Pathway Completion Using Network Motifs and Random Walks on Graphs [#1056]
Maya El Dayeh and Michael Hahsler
Southern Methodist University, United States

09:50AM   Towards Predictive Structure-based Models of Evolved Drug Resistance [#1034]
David Hecht and Gary B. Fogel
Southwestern College, United States; Natural Selection, Inc., United States

10:10AM   Blind Identification of Post-translational Modifications via Dynamic Time Warping Model [#1047]
Hui Li and Chunmei Liu
Department of Systems and Computer Science Howard University, United States

10:30AM   A Model of Competitive Exclusion in Plants [#1052]
Daniel Ashlock and Erin Wild
University of Guelph, Canada

10:50AM   Evolution in silico of genes with multiple regulatory modules on the example of the Drosophila segmentation gene hunchback [#1059]
Alexander Spirov and David Holloway
SUNY Stony Brook, United States; British Columbia Institute of Technology, Canada

11:10AM   Searching a Multicellular Model to Tame Tumor-Induced Angiogenesis [#1074]
Gregory J. Podgorski and Nicholas S. Flann
Biology Department, Utah State University, United States; Computer Science Department, Utah State University, United States

11: 30 AM – 1:00 PM   **Lunch Break**

Session GSB: Analysis and Visualization of Large Data Sets
Thursday, May 10, 1:00PM-3:00PM, Chair: Jonathan Clark

1:00PM   Assessing Reliability of Protein-Protein Interactions by Gene Ontology Integration [#1009]
George Montanez and Young-Rae Cho
Carnegie Mellon University, United States; Baylor University, United States

1:20PM   Cluster Visualization and Nonlinear Projection Techniques for Biological Sequences [#1019]
Christos Ferles and William-Scott Beaufort
National Technical University of Athens, Greece; Hellenic Center for Marine Research, Greece

1:40PM   Novel Visualisation Methods for Protein Data [#1050]
Shahzad Mumtaz, Ian T. Nabney and Darren Flower
Aston University Birmingham, United Kingdom

2:00PM   An Efficient Machine Learning Approach to Low-Complexity Filtering in Biological Sequences [#1057]
Christopher Barber and Christopher Oehmen
Pacific Northwest National Laboratory, United States

2:20PM   Detecting Aberrant Signal Transduction Pathways From High-throughput Data Using GIST Algorithm [#1062]
Jinghua Gu, Jianhua Xuan, Chen Wang, Li Chen, Tian-Li Wang and Ie-Ming Shih
Virginia Tech, United States; Johns Hopkins Medical Institutions, United States

2:40PM   GPU-Accelerated Machine Learning Techniques Enable QSAR Modeling of Large HTS Data [#1069]
Edward Lowe, Mariusz Butkiewicz, Nils Woetzel and Jens Meiler
Vanderbilt University, United States

03:00 PM – 03:20 PM   **Afternoon Tea and Coffee**

Session GSC: Biomedical Data Modeling and Mining
Thursday, May 10, 3:20PM-4:40PM, Chair: Daniel Ashlock

3:20PM Exploring Genetic Variability in Drug Therapy by Selecting a Minimum Subset of the Most Informative Single Nucleotide Polymorphisms through Approximation of a Markov Blanket in a Kernel-induced Space [#1039]

Qiang Lou, Henry P. Parkman, Michael R. Jacobs, Evgeny Krynetskiy and Zoran Obradovic

Center for Data Analytics and Biomedical Informatics, Temple University, United States; Gastroenterology Section, School of Medicine, Temple University, United States; School of Pharmacy, Temple University, United States; Jayne Haines Center for Pharmacogenomics and Drug Safety; School of Pharmacy, Temple University, United States

3:40PM A Method for Design of Data-tailored Partitioning Algorithms for Optimizing the Number of Clusters in Microarray Analysis [#1060]

Milan Vukicevic, Boris Delibasic, Obradovic Zoran, Jovanovic Milos and Suknovic Milija

University of Belgrade, Serbia and Montenegro; Temple University, United States

4:00PM GOcSim: GO Context-Driven Similarity [#1075]

Kamal Taha and Ramez Elmasri

Khalifa University of Science, Technology and Research, United Arab Emirates; University of Texas at Arlington, United States

4:20PM Evolving a Social Fabric to Fit and Epidemic Profile [#1078]

Daniel Ashlock and Elizabeth Shiller

University of Guelph, Canada

Plenary Poster Session PS: Plenary Poster Session
Thursday, May 10, 5:00PM-6:30PM, Chair: Steven Corns

P101 Optimal Cut Finding for the Hierarchical Clustering Using Background Information [#1005]

Askar Obulkasim, Gerrit Meijer and Mark van de Wiel

Department of Epidemiology and Biostatistics, VU University Medical Center, Netherlands; Department of Pathology, VU University Medical Center, Netherlands

P102 Using Structural Domains to Predict Obligate and Non-obligate Protein-protein Interactions [#1007]

Mina Maleki, Michael Hall and Luis Rueda

University of Windsor, Canada

P103 Protein Secondary Structure Prediction Using BLAST and Exhaustive RT-RICO, the Search for Optimal Segment Length and Threshold [#1013]

Leong Lee, Jennifer Leopold and Ronald Frank

Austin Peay State University, United States; Missouri University of Science and Technology, United States

P104 Protein Model Assessment Using Extended Fuzzy Decision Tree with Spatial Neighborhood Features [#1017]

Anjum Chida, Robert Harrison and Yan-Qing Zhang

Georgia State University, United States

P105 Developing a novel integrated model of p38 MAPK and glucocorticoid signalling pathways [#1021]

Alex Holehouse, Xian Yang, Ian Adcock and Yike Guo

Imperial College London, United Kingdom

P106 Robust Integrated Framework for Effective Feature Selection and Sample Classification and Its Application to Gene Expression Data Analysis [#1032]

Shang Gao

University of Calgary, Canada

P107 Multi-Centre Retrospective Study Design in Survival Analysis [#1036]

Corneliu Arsene and Paulo Lisboa

Automation Research Institute, Bucharest, Romania, Romania; Liverpool John Moores University, Liverpool, United Kingdom, United Kingdom

P108 SMISB : System to Manage Minimum Information from omics' studies for Systems Biology [#1040]

Kyung Dae Ko, Amen Mashariki, Chunmei Lui and Legand Burge

Dept. of System and Computer Science, Howard University, United States; Applied Physics Laboratory, Johns Hopkins University, United States

P109 Collabarating Viusulization on Large Dataset for Protein-Protein Interaction Network [#1045]

Hui Li and Chunmei Liu

Department of Systems and Computer Science of Howard University, United States

P110 Hybrid Metaheuristic for Multi-objective Biclustering in Microarray Data [#1055]

Khedidja Seridi, Laetitia Jourdan and El-Ghazali Talbi

INRIA Lille-Nord Europe/LIFL/CNRS, France

P111 A Comparative Analysis of Evolutionary Algorithms and Mahalanobis-Taguchi System for Breast Cancer Classification [#1064]

Benjamin Daniels, Steven Corns and Elizabeth Cudney

Missouri University of Science and Technology, United States

P112 Assessing Network Characteristics of Cancer-Associated Genes in Metabolic and Signaling Networks [#1066]

Deanna Petrochilos and Neil Abernethy

PhD Candidate, United States; Assistant Professor, United States

P113 bcl::ChemInfo - Qualitative Analysis of Machine Learning Models for Activation of HSD involved in Alzheimer's Disease [#1071]

Mariusz Butkiewicz, Edward Lowe and Jens Meiler

Vanderbilt University, United States

P114 Automated Plant Identification using Artificial Neural Networks [#1073]

Jonathan Clark, David Corney and Lilian Tang

University of Surrey, United Kingdom

P115 Quasi-cyclic Codes Exhibiting the Gene Regulatory Network of the Cell Cycle [#1084]

Vida Ravanmehr and Bane Vasic

Department of Electrical and Computer Engineering, University of Arizona, United States

Day 3 Friday, May 11, 2012

First Floor, *William D. Evans*

08:00 AM – 04:00 PM   **Registration**

08:00 AM – 08:30 AM   **Breakfast**

Special Session SSA: Machine Learning and Computational Intelligence in Biomedicine
Friday, May 11, 8:30AM-9:50AM, Room: Room Shell, Chair: Alfonso Maurizio Urso, Chengpeng Bi

8:30AM Large-Scale Computation of Pediatric Growth Percentiles with Fuzzy Logic Justification of Parameter Selection [#1014]

Chengpeng Bi and Steve Leeder

Children's Mercy Hospitals, United States

8:50AM An Ontology Design Methodology for Knowledge-Based Systems with Application to Bioinformatics

[#1025]

Antonino Fiannaca, Massimo La Rosa, Riccardo Rizzo, Alfonso Urso and Salvatore Gaglio

ICAR-CNR, National Research Council of Italy, Italy; DICGIM, University of Palermo, Italy

9:10AM   Learning to Predict Health Status of Geriatric Patients from Observational Data [#1035]

Yi Yang, Alex Hauptmann, Ming-Yu Chen, Yang Cai, Ashok Bharucha and Howard Wactlar

Carnegie Mellon University, United States

9:30AM   Sequence Learning: Analysis and Solutions for Sparse Data in High Dimensional Spaces [#1067]

Zhou Bai and Stefan Kremer

School of Computer Science, University of Guelph, Canada

09:50 AM   **Morning Tea and Coffee**

Special Session SSB: Computational Intelligence for Microarray Data Analysis
Friday, May 11, 10:10AM-11:30AM, Chair: Alioune Ngom, Yifeng Li

10:10AM   Latent growth curve modeling of incomplete time-course data in microarray gene expression studies [#1030]

Qihua Tan, Mads Thomassen and Torben Kruse

Odense University Hospital, Denmark

10:30AM   Hybrid Feature Selection Method for Biomedical Datasets [#1038]

Saul Solorio-Fernandez, Jose Fco. Martinez-Trinidad, Jesus Ariel Carrasco-Ochoa and Yan-Qing Zhang

Computer Science Department National Institute for Astrophysics, Optics and Electronics, Mexico; Department of Computer Science Georgia State University, United States

10:50AM   An Integrative Bioinformatic Approach for Identifying Subtypes and Subtype-specific Drivers in Cancer [#1044]

Peikai Chen, Y. S. Hung, Yubo Fan and Stephen T.-C. Wong

The University of Hong Kong, Hong Kong; Baylor College of Medicine, United States; The Methodist Hospital Research Institute, United States

11:10AM   A New Kernel Non-Negative Matrix Factorization and Its Application in Microarray Data Analysis [#1079]

Yifeng Li and Alioune Ngom

University of Windsor, Canada

11: 30 AM – 1:00 PM   **Lunch Break**

Special Session SSC: Gene Regulatory Networks I
Friday, May 11, 1:00PM-2:20PM, Chair: Sanjoy Das

1:00PM   Functional characterization of miRNAs in prostate cancer using functional protein networks [#1003]

Mohammed Alshalalfa, Ala Qabaja, Tarek Bismar and Reda Alhajj

University of Calgary, Canada

1:20PM   Combining Genetic Oscillators and Switches using Evolutionary Algorithms [#1012]

Spencer Thomas and Yaochu Jin

University of Surrey, United Kingdom

1:40PM   On the Performance of Particle Swarm Optimization for Parameterizing Kinetic Models of Cellular Networks [#1046]

Natalie Berestovsky, Riya Fukui and Luay Nakhleh

Department of Computer Science, Rice University, United States

2:00PM   Utilizing Stochastic Model Checking to Analyze Genetic Circuits [#1080]
        Curtis Madsen, Chris Myers, Nicholas Roehner, Chris Winstead and Zhen Zhang
        University of Utah, United States; Utah State University, United States

02:20 PM – 02:40 PM   **Afternoon Tea and Coffee**

Session GSD: Protein Structure, Function, and Interaction
Friday, May 11, 2:40PM-4:40PM, Chair: Kay Wiese

2:40PM   Prediction of crystal packing and biological protein-protein interactions [#1008]
        Sridip Banerjee, Luis Rueda and Mina Maleki
        University of Windsor, Canada
3:00PM   Comparison of RSH with Shape Signatures and MACT Technique for Shape Analysis of HIV-1 Protein [#1015]
        Srinivas Reddy Alla, Himali Desai, Sunil Kumar and Rajni Garg
        Lajolla Bioengineering Institute, Lajolla, California San Diego, CA 92121, United States; Electrical and Computer Engineering Department, San Diego State University, San Diego, CA 92182, United States; Computational Science Research Center, San Diego State University, San Diego, CA 92182, United States
3:20PM   idock: A Multithreaded Virtual Screening Tool for Flexible Ligand Docking [#1023]
        Hongjian Li, Kwong-Sak Leung and Man-Hon Wong
        Chinese University of Hong Kong, Hong Kong
3:40PM   Exhaustive RT-RICO Algorithm for Mining Association Rules in Protein Secondary Structure [#1061]
        Leong Lee, Jennifer Leopold and Ronald Frank
        Austin Peay State University, United States; Missouri University of Science and Technology, United States
4:00PM   Non-Coding RNA Gene Finding with Combined Partial Covariance Models [#1068]
        Wenbo Jiang and Kay Wiese
        Simon Fraser University, Canada
4:20PM   Molecular Distance Geometry Optimization using Geometric Build-up and Evolutionary Techniques on GPU [#1070]
        Levente Fabry-Asztalos, Istvan Lorentz and Razvan Andonie
        Central Washington University, United States; Transilvania University, Romania

07:00 PM – 9:00 PM **Conference Banquet** in *Board Room*

Day 4 Saturday, May 12, 2012

Aviary Ballroom

08:00 AM – 8:30 AM   **Breakfast**

Special Session SSD: Gene Regulatory Networks II
Saturday, May 12, 8:30AM-9:50AM, Room: Shell, Chair: Sanjoy Das

8:30AM   Matrix Factorization for Transcriptional Regulatory Network Inference [#1081]
        Michael Ochs and Elana Fertig
        Johns Hopkins University, United States
8:50AM   Reconstruction and update robustness of the mammalian cell cycle network [#1082]

Gonzalo Ruz and Eric Goles

Universidad Adolfo Ibanez, Chile

9:10AM A NonGaussian Factor Analysis Approach to Transcription Network Component Analysis [#1083]

Shikui Tu, Runsheng Chen and Lei Xu

The Chinese University of Hong Kong, Hong Kong; Institute of Biophysics, Chinese Academy of Sciences, China

9:30AM Information Theoretic Methods for Modeling of Gene Regulatory Networks [#1085]

Amina Noor, Erchin Serpedin, Mohamed Nounou, Hazem Nounou, Nady Mohamed and Lotfi Chouchane

Texas AM University, United States; Texas AM University at Qatar, Qatar; Weill Cornell Medical College, Qatar

09:50 AM **Morning Tea and Coffee**

Session GSE: Motif Analysis and Detection
Saturday, May 12, 10:10AM-11:30AM, Chair: Sheridan Houghten

10:10AM Multiple Worlds Model for Motif Discovery [#1028]

Joseph Alexander Brown

University of Guelph, Canada

10:30AM Learning relationships between over-represented motifs in a set of DNA sequences [#1037]

Oksana Korol and Marcel Turcotte

University of Ottawa, School of Electrical Engineering and Computer Science, Canada

10:50AM Quantitative Analysis of Redundancy in Evolution of Developmental Systems [#1018]

Lisa Schramm, Yaochu Jin and Bernhard Sendhoff
TU Darmstadt, Germany; University of Surrey, UK; Honda Research Institute Europe, Germany

11:10AM A MultiObjective Genetic Algorithm with Side Effect Machines for Motif Discovery [#1063]

Farhad Alizadeh Noori and Sheridan Houghten

Brock University, Canada

11: 30 AM – 1:00 PM   **Lunch Break**

Session GSF: Bio-Image Analysis
Saturday, May 12, 1:00PM-2:00PM, Chair: Yaochu Jin

1:00PM Data Mining Techniques for AFM- Based Tumor Classification [#1031]

Stephan Hutterer, Gerald Zauner, Marlene Huml, Rene Silye and Kurt Schilcher

University of Applied Sciences Upper Austria, Austria; University of Applied Sciences Upper Austria, Austria; Neuropathic Hospital Wagner-Jauregg Department of Pathology, Austria

1:20PM Hybrid Feature Extractor for Harlequin Ladybird Identification Using Color Images [#1053]

Mohd Ayob

University of York, United Kingdom

1:40PM Graph Based MRI Brain Scan Classification and Correlation Discovery [#1072]

Seth Long and Lawrence Holder

Washington State University, United States

Competition CS: Competition Session
Saturday, May 12, 2:00PM-3:30PM, Chair: Daniel Ashlock

03:30 PM   **Closing Remarks**