# ISMB/ECCB 2009 Open Access Articles

**Bioinformatics Volume 25 #12, 2009**

## Stockholm, Sweden
## 27 June – 2 July 2009

**ISBN: 978-1-61567-446-6**

**Printed from e-media with permission by:**

Curran Associates, Inc.
57 Morehouse Lane
Red Hook, NY 12571

**Some format issues inherent in the e-media version may also appear in this print version.**

Copyright© (2009) by Oxford University Press
All rights reserved.

Printed by Curran Associates, Inc. (2009)

For permission requests, please contact Oxford University Press
at the address below.

Oxford University Press
2001 Evans Road
Cary, North Carolina 27513

Phone: (919) 677-0977
Fax: (919) 677-1714

jnlorders@oup-usa.org

**Additional copies of this publication are available from:**

Curran Associates, Inc.
57 Morehouse Lane
Red Hook, NY 12571 USA
Phone: 845-758-0400
Fax: 845-758-2634
Email: curran@proceedings.com
Web: www.proceedings.com

# TABLE OF CONTENTS

**Constrained Mixture Estimation for Analysis and Robust Classification of Clinical Time Series** ..... 1
*Ivan G. Costa, Alexander Schonhuth, Christoph Hafemeister, Alexander Schliep*

**Graph Theoretical Approach to Study eQTL: A Case Study of Plasmodium Falciparum** ..... 14
*Yang Huang, Stefan Wuchty, Michael T. Ferdig, Teresa M. Przytycka*

**A Classifier-based Approach to Identify Genetic Similarities Between Diseases** ..... 20
*Marc A. Schaub, Irene M. Kaplow, Marina Sirota, Chuong B. Do, Atul J. Butte, Serafim Batzoglou*

**Model-based Clustering of Array CGH Data** ..... 29
*Sohrab P. Shah, K-John Cheung Jr., Nathalie A. Johnson, Guillaume Alain, Randy D. Gascoyne, Douglas E. Horsman, Raymond T. Ng, Kevin P. Murphy*

**Viruses Selectively Mutate Their CD8+ T-cell Epitopes—A Large-scale Immunomic Analysis** ..... 38
*Tal Vider-Shalit, Ronit Sarid, Kobi Maman, Lea Tsaban, Ran Levi, Yoram Louzoun*

**Family Classification Without Domain Chaining** ..... 44
*Jacob M. Joseph, Dannie Durand*

**Identifying Novel Constrained Elements by Exploiting Biased Substitution Patterns** ..... 53
*Manuel Garber, Mitchell Guttman, Michele Clamp, Michael C. Zody, Nir Friedman, Xiaohui Xie*

**From Disease Ontology to Disease-ontology Lite: Statistical Methods to Adapt a General-purpose Ontology for the Test of Gene-ontology Associations** ..... 74
*Pan Du, Gang Feng, Jared Flatow, Jie Song, Michelle Holko, Warren A. Kibbe, Simon M. Lin*

**Alignment of the UMLS Semantic Network with Biotop: Methodology and Assessment** ..... 80
*Stefan Schulz, Elena Beisswanger, Laszlo Van Den Hoek, Olivier Bodenreider, Erik M. Van Mulligen*

**Ontology Quality Assurance Through Analysis of Term Transformations** ..... 88
*Karin Verspoor, Daniel Dvorkin, K. Bretonnel Cohen, Lawrence Hunter*

**Computing Galled Networks from Real Data** ..... 96
*Daniel H. Huson, Regula Rupp, Vincent Berry, Philippe Gambette, Chrisophe Paul*

**Genotype–Phenotype Associations: Substitution Models to Detect Evolutionary Associations Between Phenotypic Variables and Genotypic Evolutionary Rate** ..... 105
*Timothy D. O'Connor, Nicholas I. Mundy*

**Modeling Stochasticity and Robustness in Gene Regulatory Networks** ..... 112
*Abhisek Garg, Kartik Mohanram, Alessandro Di Cara, Giovanni De Micheli, Ioannis Xenarios*

**Grouped Graphical Granger Modeling for Gene Expression Regulatory Networks Discovery** ..... 121
*Aurelie C. Lozano, Naoki Abe, Yan Liu, Saharon Rosset*

**Clustered Alignments of Gene-expression Time Series Data** ..... 130
*Adam A. Smith, Aaron Vollrath, Christopher A. Bradfield, Mark Craven*

**KELLER: Estimating Time-varying Interactions Between Genes** ..... 139
*Le Song, Mladen Kolar, Eric P. Xing*

**Predicting Functionality of Protein–DNA Interactions by Integrating Diverse Evidence** ..... 148
*Duygu Ucar, Andreas Beyer, Srinivasan Parthasarathy, Christopher T. Workman*

**Probabilistic Retrieval and Visualization of Biologically Relevant Microarray Experiments** ..... 156
*Jose Caldas, Nils Gehlenborg, Ali Faisal, Alvis Brazma, Samuel Kaski*

**Proteome Coverage Prediction with Infinite Markov Models** ..... 165
*Manfred Claassen, Ruedi Aebersold, Joachim M. Buhmann*

**Fewer Permutations, More Accurate P-values** ..... 172
*Theo A. Knijnenburg, Lodewyk F. A. Wessels, Marcel J. T. Reinders, Ilya Shmulevich*

**A General Computational Method for Robustness Analysis with Applications to Synthetic Gene Networks** ..... 349
*Aurelien Rizk, Gregory Batt, Francois Fages, Sylvain Soliman*

**E-zyme: Predicting Potential EC Numbers from the Chemical Transformation Pattern of Substrate-product Pairs** ..... 359
*Yoshihiro Yamanishi, Masahiro Hattori, Masaaki Kotera, Susumu Goto, Minoru Kanehisa*

**Multi-locus Match Probability in a Finite Population: A Fundamental Difference Between the Moran and Wright–fisher Models** ..... 367
*Anand Bhaskar, Yun S. Song*

**Speeding Up HMM Algorithms for Genetic Linkage Analysis Via Chain Reductions of the State Space** ..... 376
*Dan Geiger, Christopher Meek, Ydo Wexler*

**A Multivariate Regression Approach to Association Analysis of a Quantitative Trait Network** ..... 386
*Seyoung Kim, Kyung-Ah Sohn, Eric P. Xing*

**Inference of Locus-specific Ancestry in Closely Related Populations** ..... 395
*Bogdan Pasaniuc, Sriram Sankararaman, Gad Kimmel, Eran Halperin*
**A Geometric Approach for Classification and Comparison of Structural Variants** ..... 404
*Suzanne Sindi, Elena Helman, Ali Bashir, Benjamin J. Raphael*
**Joint Estimation of Gene Conversion Rates and Mean Conversion Tract Lengths from Population SNP Data** ..... 413
*Junming Yin, Michael I. Jordan, Yun S. Song*
**Domain-oriented Edge-based Alignment of Protein Interaction Networks** ..... 422
*Xin Guo, Alexander J. Hartemink*
**Network-based Prediction of Metabolic Enzymes' Subcellular Localization** ..... 429
*Shira Mintz-Oron, Asaph Aharoni, Eytan Ruppin, Tomer Shlomi*
**IsoRankN: Spectral Methods for Global Alignment of Multiple Protein Networks** ..... 435
*Chung-Shou Liao, Kanghao Lu, Michael Baym, Rohit Singh, Bonnie Berger*
**Global Alignment of Protein–protein Interaction Networks by Graph Matching Methods** ..... 441
*Mikhail Zaslavskiy, Francis Bach, Jean-Philippe Vert*
**PICKY: A Novel SVD-based NMR Spectra Peak Picking Method** ..... 450
*Babak Alipanahi, Xin Gao, Emre Karakoc, Logan Donaldson, Ming Li*
**A Framework to Refine Particle Clusters Produced by EMAN** ..... 458
*Liya Fan, Fa Zhang, Gongming Wang, Zhiyong Liu*
**Pokefind: A Novel Topological Filter for Use with Protein Structure Prediction** ..... 463
*Firas Khatib, Carol A. Rohl, Kevin Karplus*
**REPETITA: Detection and Discrimination of the Periodicity of Protein Solenoid Repeats by Discrete Fourier Transform** ..... 471
*Luca Marsella, Francesco Sirocco, Antonio Trovato, Flavio Seno, Silvio C. E. Tosatto*
**Prediction of Sub-cavity Binding Preferences Using an Adaptive Physicochemical Structure Representation** ..... 478
*Izhar Wallach, Ryan H. Lilien*
**A Unified Statistical Model to Support Local Sequence Order Independent Similarity Searching for Ligand-binding Sites and Its Application to Genome-based Drug Discovery** ..... 487
*Lei Xie, Li Xie, Philip E. Bourne*
**Toward a Gold Standard for Promoter Prediction Evaluation** ..... 495
*Thomas Abeel, Yves Van De Peer, Yvan Saeys*
**DISCOVER: A Feature-based Discriminative Method for Motif Search in Complex Genomes** ..... 504
*Wenhie Fu, Pradipta Ray, Eric P. Xing*
**Predictions of RNA Secondary Structure by Combining Homologous Sequence Information** ..... 517
*Michiaki Hamada, Kengo Sato, Hisanori Kiryu, Toutai Mituyama, Kiyoshi Asai*
**Assessing Phylogenetic Motif Models for Predicting Transcription Factor Binding Sites** ..... 526
*John Hawkins, Charles Grant, William Stafford Noble, Timothy L. Bailey*
**Modeling Interactions Between Adjacent Nucleosomes Improves Genome-wide Predictions of Nucleosome Occupancy** ..... 535
*Shai Lubliner, Eran Segal*
**Efficient Exact Motif Discovery** ..... 550
*Tobias Marschall, Sven Rahmann*
**A Partition Function Algorithm for Interacting Nucleic Acid Strands** ..... 559
*Hamidreza Chitsaz, Raheleh Salari, S. Cenk Sahinalp, Rolf Backofen*
**Predicting and Understanding the Stability of G-Quadruplexes** ..... 587
*Oliver Stegle, Linda Payet, Jean-Louis Mergny, David J. C. MacKay, Julian Leon Huppert*
**Author Index**