Workshop on Next-generation Sequencing Analysis

Detection of Copy Number Variation from Next Generation Sequencing Data with Total Variation Penalized Least Square Optimization
-Junbo Duan, Ji-Gang Zhang, John Lefante, Hong-Wen Deng and Yu-Ping Wang-

A Conceptual Data Model for a RNA-seq Pipeline
-Ruben Cruz Huacarpuma, Maristela Holanda, and Maria Emilia M. T. Walter-

Regularization of Sequence Data for Machine Learning
-Zhou Bai and Stefan C. Kremer-

SPATA: A Seeding and Patching Algorithm for de novo Transcriptome Assembly
-Zhiyu Zhao, Tin Nguyen, Nan Deng, Kristen Johnson, and Dongxiao Zhu-

A Novel Framework for Chimeric Transcript Detection Based on Accurate Gene Fusion Model
-Francesco Abate, Andrea Acquaviva, Giulia Paciello, Elisa Ficarra, Enrico Macii, Alberto Ferrarini, Massimo Delledonne, Simona Soverini, and Giovanni Martinelli-

A Fragment Based Alignment in Linear Space
-Jan Correa, Alba Melo, Ricardo Jacobi, and Azzedine Boukerche-

Evaluation of Normalization Methods for RNA-Seq Gene Expression Estimation
-Po-Yen Wu, John H. Phan, Fengfeng Zhou, and May Wang-

Workshop on Computational Advances in Molecular Epidemiology (CAME 2011)

Computational analysis of HIV-1 evolution and epidemiology
-Sergei L Kosakovsky Pond-

Network of Coordinated Substitutions in the Hepatitis B Virus Polymerase
-David S. Campo, Zoya Dimitrova, James Lara, Mike Purdy, Hong Thai, Sumathi Ramachandran,
Lilia Ganova-Raeva, Joseph Forbi, Chong-Gee Teo, and Yury Khudyakov

Variation in Physicochemical Properties of the Hypervariable Region 1 During Acute and Chronic Stages of Hepatitis C Virus Infection

Irina V Astrakhantseva, David S. Campo, Aufra Araujo, Chong-Gee Teo, Yury Khudyakov, and Saleem Kamili

Assessments of Intra- and Inter-Host Diversity of Hepatitis C Virus using Next Generation Sequencing and Mass Spectrometry

Zoya Dimitrova, David S. Campo, Sumathi Ramachandran, Gilberto Vaughan, Lilia Ganova-Raeva, Yulin Lin, Joseph Forbi, Guo-liang Xia, Pavel Skums, Brian Pearlman, Christiane Honisch, and Yury Khudyakov

CONDEX: COpy Number Detection in EXome Sequences

Arthi Ramachandran, Mariann Micsinai, and Itsik Pe’er

Viral Quasispecies Reconstruction from Amplicon 454 Pyrosequencing Reads

Nicholas Mancuso, Bassam Tork, Ion Mandoiu, Alex Zelikovsky, and Pavel Skums

Host-specific HCV evolution and response to the combined interferon and ribavirin therapy

James Lara, John E. Tavis, Maureen J. Donlin, William Lee, He-Jun Yuan, Brian Pearlman, Gilberto Vaughan, Joseph Forbi, Guo-liang Xia, and Yury Khudyakov

Modeling antigenic properties of the hepatitis C virus NS3 protein

James Lara and Yury Khudyakov

RNA-Seq based discovery and reconstruction of unannotated transcripts in partially annotated genomes

Serghei Mangul, Adrian Caciula, Ion Mandoiu, and Alex Zelikovsky

Visualization of tuberculosis patient and Mycobacterium tuberculosis complex genotype data via host-pathogen maps

Kristin Bennett, Cagri Ozcaglar, Janani Ranganathan, Srivatsan Raghavan, Jacob Katz, Dan Croft, Bulent Yener, and Amina Shabbeer

QColors: An Algorithm for Conservative Viral Quasispecies Reconstruction from Short and Non-Contiguous Next Generation Sequencing Reads

Austin Huang, Rami Kantor, Allison DeLong, Leeann Schrier, and Sorin Istrail

A Parametric Bayesian Method to Test the Association of Rare Variants

Yufeng Shen, Yee Him Cheung, Shuang Wang, and Itsik Pe’er

Modeling differential interferon resistance of HCV quasispecies

Serghei Mangul, Adrian Caciula, Ion Mandoiu, and Alex Zelikovsky

Visualization of tuberculosis patient and Mycobacterium tuberculosis complex genotype data via host-pathogen maps

Kristin Bennett, Cagri Ozcaglar, Janani Ranganathan, Srivatsan Raghavan, Jacob Katz, Dan Croft, Bulent Yener, and Amina Shabbeer

QColors: An Algorithm for Conservative Viral Quasispecies Reconstruction from Short and Non-Contiguous Next Generation Sequencing Reads

Austin Huang, Rami Kantor, Allison DeLong, Leeann Schrier, and Sorin Istrail

A Parametric Bayesian Method to Test the Association of Rare Variants

Yufeng Shen, Yee Him Cheung, Shuang Wang, and Itsik Pe’er

Modeling differential interferon resistance of HCV quasispecies

Serghei Mangul, Adrian Caciula, Ion Mandoiu, and Alex Zelikovsky

Visualization of tuberculosis patient and Mycobacterium tuberculosis complex genotype data via host-pathogen maps

Kristin Bennett, Cagri Ozcaglar, Janani Ranganathan, Srivatsan Raghavan, Jacob Katz, Dan Croft, Bulent Yener, and Amina Shabbeer

QColors: An Algorithm for Conservative Viral Quasispecies Reconstruction from Short and Non-Contiguous Next Generation Sequencing Reads

Austin Huang, Rami Kantor, Allison DeLong, Leeann Schrier, and Sorin Istrail

A Parametric Bayesian Method to Test the Association of Rare Variants

Yufeng Shen, Yee Him Cheung, Shuang Wang, and Itsik Pe’er

Modeling differential interferon resistance of HCV quasispecies
Pavel Skums, David S. Campo, Zoya Dimitrova, Gilberto Vaughan, Daryl T. Lau, and Yury Khudyakov

3rd Workshop on Data Mining for Biomarker Discovery (DMBD)

Multiobjective Optimization Shuffled Frog-leaping Biclustering ........................................... 151
Junwan Liu, Zhoujun Li, Xiaohua Hu, and Yiming Chen

Meta-Analysis of LC-MS Based Metabolomic Experiments ............................................. 157
Rency Varghese, Bin Zhou, and Habtom W. Rassom

Professional Tennis Player Ranking Strategy based Monte Carlo Feature Selection .............. 165
Ruifei Xie, Bin Han, Lihua Li, Juan Zhang, and Lei Zhu

saskPrimer - an Automated Pipeline for Design of Intron-Spanning PCR Primers in Non-Model Organisms ..................................................................................................................... 173
Wayne Clarke, Christine Sidebottom, Isobel Parkin, and Andrew Sharpe

Synthesizing Aligned Random Pattern Digraphs from Protein Sequence Patterns .......... 178
Annie En-Shiun Lee and Andrew K. C. Wong

Consistent Detection of Cancer biomarkers with Linear Models ................................... 186
Eulisa Rivera, Zahira Irizarry, Matilde Sánchez-Peña, Clara Isaza, Jaime Seguel, and Mauricio Cabrera-Rios

Brdicka Curve - a New Source of Biomarkers ................................................................. 193
Lenka Vyslouzilova, Vojtech Adam, Andrea Szaboova, Olga Stepankova, Rene Kizek, and Jiri Anyz

2nd Workshop on Integrative data analysis in systems biology (IDASB)

Ontology-based Functional Classification of Genes: Evaluation With Reference Sets and Overlap Analysis ...................................................................................................................................... 201
Sidahmed Benabderrahmane, Marie-Dominique Devignes, Malika Small-Taibonne, Amedeo Napoli, and Olivier Poch

A Web Interface for the Quantification of Microtubule Dynamics .................................... 209
Koon Kong, Adam Marcus, Paraskevi Giaanakakou, and May Wang

Finding a Longest Open Reading Frame of an Alternatively Spliced Gene ....................... 215
Neil Moore and Jerzy Jaromczyk

Multi-Source Kernel k-means for Clustering Heterogeneous Biomedical Data ................. 223
Systematic Discovery of Condition Specific Wnt Signaling Subnetworks .......................... 229
   Sudipto Saha and Rob Ewing

An Improved Data Integration Methodology for System Biology ........................................ 235
   Xiaodong Zhou and Ebenezer George

Associating Gene Functional Groups with Multiple Clinical Conditions using Jaccard Similarity... 241
   Noha A. Yousri and Dalal Elkaffash

Rapid Identification of Multi-PTMs Peptide Sequence Tags with a Graph Search Approach .......... 247
   Hui Li, Lauren Scott, Chunmei Liu, Legand Burge, and Mugizi Rwebangira

Rapid Generation of Peptide Sequence Tags with a Graph Search Algorithm .......................... 251
   Hui Li, Lauren Scott, and Chunmei Liu

Identifying Modular Function via Edge Annotation in Gene Correlation Networks using Gene Ontology Search .......................................................... 255
   Kathryn Dempsey, Ishwor Thapa, Dhundy Bastola, and Hesham Ali

Integrating Sequence Conservation Features and a Domain-Domain Interaction Network to Detect Disease-associated nsSNPs ............................................. 262
   Rui Jiang and Jiaxin Wu

Correlation of Genomics Features with the Date and Party Hub Distinction: a View from Three Dimensional Protein Structures ..................................................... 268
   Haiying Wang and Huiru Zheng

Development and Implementation of a Novel Computational Tool for an Efficient Construction of Drug-target Interactome ......................................................... 274
   Jingchun Sun, Paul Hart, and Zhongming Zhao

Workshop on Cancer Informatics

Classifying Six Glioma Subtypes from Combined Gene Expression and CNVs Data Based on Compressive Sensing Approach ......................................................... 282
   Yu-Ping Wang

Random Forest: A Reliable Tool For Patient Response Prediction ............................................. 289
   David Dittman, Taghi Khoshgoftaar, Randall Wald, and Amri Napolitano,

Optimal Delivery of Volumetric Modulated Arc Therapy (VMAT) for Moving Target .................... 297
Sairam Behera, Lech Papiez, and Ovidiu Daescu

An Adaptive Feature Reduction Algorithm for Cancer Classification Using Wavelet Decomposition of Serum Proteomic and DNA Microarray Data ......................................................... 305
Sabrina Rashid and Golam Morshed Maruf

Workshop on Computational Structural Bioinformatics

Ab initio Protein Structure Prediction Based on Memetic Algorithm and 3D FCC Lattice Model... 315
Jyh-Jong Tsay and Shih-Chieh Su

Rigid Region Pairwise Sequence Alignment ........................................................................ 319
Marko Zivanic, Ovidiu Daescu, and Anastasia Kurdia

Amino Acid Encoding Schemes for Machine Learning Methods ........................................ 327
Masood Zamani and Stefan C. Kremer

On the Energy of Bifurcated Hydrogen Bonds for Protein Structure Prediction .................. 334
Sajal Dash and Jack Snoeyink

Encoding Protein Structure with Functions on Graphs ...................................................... 338
Promita Bose, Xia Xia Yu, and Robert Harrison

Analysis of Relevant Physicochemical Properties in Obligate and Non-obligate Protein-protein Interactions ............................................................................................................ 345
Mina Maleki, Md. Mominul Aziz, and Luis Rueda

Recursive Protein Modeling: a Divide And Conquer Strategy for Protein Structure Prediction and Its Case Study in CASP9 ............................................................. 352
Jianlin Cheng, Jesse Eickholt, Zheng Wang, and Xin Deng

Protein Docking with Information on Evolutionary Conserved Interfaces .......................... 358
Irina Hashmi, Bahar Akbal-Delibas, Nurit Haspel, and Amarda Shehu

Protein Conformational Search with Geometric Projections ............................................. 366
Brian Olson, Farid Hendi, and Amarda Shehu

The Development of a Proteomic Analyzing Pipeline to Identify Proteins with Multiple Rms and Predict Their Domain Boundaries ................................................................. 374
Kyung Dae Ko, Chunmei Liu, Mugizi Robert Rwebangira, Legand Burge, and William Southerland

P.R.E.S.S. – An R-package for Exploring Residual-Level Protein Structural Statistics ............ 382
Yuanyuan Huang and Zhijun Wu

A Symmetry-driven BP Algorithm for the Discretizable Molecular Distance Geometry Problem

Antonio Mucherino, Carlile Lavor, and Leo Liberti

Hardware Simulation of Yeast Glycolytic Oscillations

Jorge Duarte, Pedro Moreno, and Jaime Velasco

Refinement of Docked Protein Complex Structures Using Evolutionary Traces

Bahar Akbal-Delibas, Irina Hashmi, Amarda Shehu, and Nurit Haspel

A Distance and Orientation Dependent Potential Energy Function with cluster energy

Lin Chen and Jing He

Normal mode analysis of protein structure dynamics based on residue contact energy

Weitao Sun

SCOP Family Fingerprints: An Information Theoretic Approach to Structural Classification of Protein Domains

Alberto Casagrande and Francesco Fabris

A Statistical Model of Overlapping Volume in Ligand Binding Cavities

Brian Chen and Soutir Bandypadhyay

Using Rigidity Analysis To Probe Mutation-Induced Structural Changes in Proteins

Filip Jagodzinski, Jeanne Hardy, and Ileana Streinu

Workshop on Bioinformatics for microRNA and Disease

Cluster Analysis of MiRNAs Microarray Data and Prediction of Lupeol’s Anti-cancer Path

Dachuan Liu, Cuihong Dai, and Dechang Xu

Identifying multiple stem-loops pre-miRNA using support vector machine

Xiaofeng Song, Minghao Wang, Yi-Ping Phoebe Chen, and Ping Han

Gene Sets Enrichment Analysis of miRNA Expression Profile

Tzu-Hung Hsiao, Hung-I Harry Chen, Patricia C. Sanchez-Diaz, Jaclyn Y. Hung, Yufei Huang, and Yidong Chen

4th Workshop on Biomolecular Network Analysis (IWBNA)

Topology-based scoring method for identification of responsive protein–protein interaction
subnetwork. .................................................................457
Shouguo Gao and Xujing Wang

Module Detection for Bacteria Based on Spectral Clustering of Protein-Protein Functional Association
Networks......................................................................465
Hongwei Wu, Yaming Lin, Fun Choi Chan, and Rocio Alba-Flores

Network Based Subcellular Localization Prediction for Multi-Label Proteins.........................473
Ananda Mondal, Jhih-rong Lin, and Jianjun Hu

VeNet: a Framework for the Analysis of Protein Interaction Networks through Vector Space
Embedding..................................................................481
Pietro Hiram Guzzi, Pierangelo Veltri, and Mario Cannataro

A New Functional Association-Based Protein Complex Prediction.................................488
Mingming Liu, Yanwei Huang, Liqing Zhang, and David Bevan

Using Semantic Similarity to Detect Features in Yeast Protein Complexes.........................495
Pietro Hiram Guzzi, Marianna Milano, Pierangelo Veltri, and Mario Cannataro

A Hierarchical Link Clustering based Approach for Identifying Protein Complexes by Incorporating
Core-Attachment Structure...........................................503
Yinhai Liu, Yang Yu, Chengjie Sun, Lei Lin, and Xiaolong Wang

Evaluation of Essential Genes in Correlation Networks using Measures of Centrality.............509
Kathryn Dempsey and Hesham Ali

Workshop on Biomedical and Health Informatics

Indoor Signage Detection Based on Saliency Map and Bipartite Graph Matching..................518
Shuihua Wang and Yingli Tian

Finding Objects for Blind People Based on SURF Features.................................................526
Ricardo Chincha and Yingli Tian,

Identifying Medicine Bottles by Incorporating RFID and Video Analysis..........................528
Faiz Hasanuzzaman, Yingli Tian, and Qingshan Liu

Learning from Positive and Unlabeled Documents for Automated Detection of Alternative Splicing
Sentences in MEDLINE Abstracts......................................530
Yang Chen, Manabu Torii, Chang-Tien Lu, and Hongfang Liu

Comparison of Classification Techniques-SVM and Naives Bayes to Predict the Arboviral