

Table of Contents

Keynote	1
Phylogenetic Analyses: Past, Present, and Future <i>Bernard M.E. Moret</i>	1
Genomics I	3
A Bayesian Framework for Marker Gene Taxonomic Classification Based on Sequence Alignment <i>Xiang Gao, Huaiying Lin, Kashi Revanna, Qunfeng Dong</i>	3
GraphPE: Refining Metagenome Binning by Use of Paired-end Graph of Contigs <i>Xianghui Liu, Rohan B. H. Williams</i>	9
Clustering Metagenome Sequences Using Canopies <i>Mohammad Arifur Rahman, Nathan LaPierre, Huzefa Rangwala, Daniel Barbara</i>	17
Improving Microbiome Classification with Dirichlet-Multinomial Models <i>Xiang Gao, Huaiying Lin, Qunfeng Dong</i>	25
Structure and Function	31
Evaluation of Protein Structural Models Using Random Forests <i>Renzhi Cao, Jie Hou, Taeho Jo, Jianlin Cheng</i>	31
Visual Experiments of Geometric Combinatorics for Neural Stem Cells and Their Derivatives <i>T. J. Peters, J. C. Conover, D. McManus, K. Pratt, K. D. Williams</i>	39
Classification of DNA Structure through Structure Network Analysis <i>Tanmay Kulshrestha, Ankita Gupta, Shibasish Chowdhury</i>	45
A Fast Algorithm for Finding Largest Common Substructures in Multiple RNAs <i>Jithendar Anandan, Eric Fry, Keith Monschke, Abdullah N. Arslan</i>	51
Systems Biology I	59
Approximate Frequent Subpath Mining Applied to Pangenomics <i>Alan Cleary, Brendan Mumeey, Thiruvarangan Ramaraj, Joann Mudge</i>	59
Determining Multifunctional Genes and Diseases in Human Using Gene Ontology <i>Hisham Al-Mubaid, Sasikanth Potu, M. Shenify</i>	65
A Local Search Algorithm for Clustering Large Biological Networks <i>Guy Coccimiglio, Salimur Choudhury</i>	73
Reconstructing Protein and Gene Phylogenies by Extending the Framework of Reconciliation <i>Esaie Kuitche, Manuel Lafond, Aïda Ouangraoua</i>	79
ChIP-GMM: A Gaussian Mixture Model for Inferring Binding Regions in ChIP-seq Profiles <i>Sharmi Banerjee, Xi Chen, Xiaowei Wu, Hehuang Xie, Jianhua Xuan, Wu-chun Feng</i>	87
Healthcare and Bioinformatics Applications	93
An In-Memory Database Platform for Systems Medicine <i>Milena Kraus, Matthieu-P. Schapranow</i>	93
A Pilot Study of Breast Cancer Patients: Can Machine Learning Predict Healthcare Professionals' Responses to Patient Emotions? <i>Luke Barracliffe, Ognjen Arandjelović, Gerry Humphrisy</i>	101

Fundamental Bounds for Sequence Reconstruction from Nanopore Sequencers <i>Abram Magner, Jarosław Duda, Wojciech Szpankowski, Ananth Grama</i>	107
Applications of Novel Graph Theoretic Methods to Clustering Autism Spectrum Disorders Phenotypes <i>John Matta, Thy Nguyen, Gunes Ercal, Tayo Obafemi-Ajayi</i>	113
Genomics II	121
ParSECH: Parallel Sequencing Error Correction with Hadoop for Large-Scale Genome <i>Arghya Kusum Das, Shayan Shams, Sayan Goswami, Richard Platania, Kisung Lee, Seung-Jong Park</i>	121
Finding Surrogate Controls in Pathway Enrichment Analysis using RNA-Seq Expression <i>Tham H. Hoang, Yue Zhao, Pujan Joshi, Seung-Huyn Hong, Dong-Guk Shin</i>	129
Towards Reliable Microarray Analysis and Design <i>Max Garzon, Sambriddhi Mainali</i>	135
Reconstruction of Ring Chromosomes Using Paired-End Sequencing Data <i>Matthew Hayes, Jeremy Pearson</i>	141
Systems Biology II	147
Parameter Identification of Nonlinear Biochemical Reaction Systems Using the Statistics-based Method <i>Xiaoying Zheng, Xiufen Zou, Zishu Pan</i>	147
Modularity in PPI Networks: Characteristics of Existing Networks and Models of Evolution <i>Min Ye, Xiuwei Zhang, Bernard M.E. Moret</i>	155
Network-based Differential Analysis of Hi-C Data <i>Lu Liu, Jianhua Ruan</i>	165
A Parallel Algorithm for Mining Maximal Cohesive Subgraphs <i>Aditya Goparaju, Saeed Salem</i>	173
Bioinformatics Applications I	179
Comparative study of Differential Evolutionary-Binary Particle Swarm Optimization (DE-BPSO) algorithm as a feature selection technique with different linear regression models for analysis of HIV-1 Integrase Inhibition features of Aryl β -Diketo Acids <i>Falguni Thakor, Ahmad Reza Hadaegh, Xiaoyu Zhang</i>	179
A Sequential Monte Carlo Sampler for Bayesian Phylogenetics <i>Liangliang Wang</i>	185
PF-Words: Biomedical Literature Based Protein Function Search <i>Wei Wei, Mike Wong, Anagha Kulkarni</i>	191
Detecting Haplotype Amplification in Cancer Sequencing Data <i>Weiwei Liu, Jingyang Gao, Zhongmeng Zhao, Rongrong Yang, Yu Geng, Tian Zheng, Xuanping Zhang, Xiao Xiao, Jiayin Wang</i>	197
Bioinformatics Applications II	203
Improving Peptide Identification by Considering Ordered Amino Acid Usage <i>Ahmed Alqurri, John Rose</i>	203
Non-parametric Quality Assessment of High-Content Screening Assays <i>Robert P. Trevino, Philippe C. Faucon, Thomas J. Lamkin, Steven A. Kawamoto, Ross Smith, Huan Liu</i>	209
Prediction of Biological Functions by Histone Modification Patterns Profiling <i>Yiou Xiao, Kishan G. Mehrotra, Chilukuri K. Mohan, Pratibha Choudhary, Ramesh Raina</i>	217
Genetic Information, Mutation Rates, and the Lore of the Error Threshold <i>Lee Altenberg</i>	223
Top-Down Correlation-Based Pattern Analysis and Feature Selection for Multi-Component FTIR Spectra <i>Ghada Badr, Najla Al-Ariefy</i>	231