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Preface

The 12th edition of the International Symposium on Bioinformatics Research and Applications (ISBRA 2016) was held during June 5–8, 2016, in Minsk, Belarus. The symposium provides a forum for the exchange of ideas and results among researchers, developers, and practitioners working on all aspects of bioinformatics and computational biology and their applications.

There were 77 submissions received in response to the call for papers. The Program Committee decided to accept 42 of them for publication in the proceedings and for oral presentation at the symposium: 22 for Track 1 (an extended abstract) and 20 for Track 2 (an abridged abstract). The technical program also featured invited keynote talks by five distinguished speakers: Dr. Teresa M. Przytycka from the National Institutes of Health discussed the network perspective on genetic variations, from model organisms to diseases; Prof. Ion Mandoiu from the University of Connecticut spoke on challenges and opportunities in single-cell genomics; Prof. Alexander Schoenhuth from Centrum Wiskunde and Informatica spoke on dealing with uncertainties in big genome data; Prof. Ilya Vakser from the University of Kansas discussed genome-wide structural modeling of protein–protein interactions; and Prof. Max Alekseyev from George Washington University spoke on multi-genome scaffold co-assembly based on the analysis of gene orders and genomic repeats.

We would like to thank the Program Committee members and external reviewers for volunteering their time to review and discuss symposium papers. Furthermore, we would like to extend special thanks to the steering and general chairs of the symposium for their leadership, and to the finance, publicity, local organization, and publication chairs for their hard work in making ISBRA 2016 a successful event. Last but not least, we would like to thank all authors for presenting their work at the symposium.

June 2016

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Contents

Next Generation Sequencing Data Analysis

An Efficient Algorithm for Finding All Pairs $k$-Mismatch Maximal Common Substrings ......................................................... 3
  Sharma V. Thankachan, Sriram P. Chockalingam, and Srinivas Aluru

Poisson-Markov Mixture Model and Parallel Algorithm for Binning Massive and Heterogenous DNA Sequencing Reads ...................... 15
  Lu Wang, Dongxiao Zhu, Yan Li, and Ming Dong

FSG: Fast String Graph Construction for De Novo Assembly of Reads Data ................................................................. 27
  Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, Marco Previtali, and Raffaella Rizzi

OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads .......................................................... 40
  Takuya Moriyama, Yuichi Shiraishi, Kenichi Chiba, Rui Yamaguchi, Seiya Imoto, and Satoru Miyano

High-Performance Sensing of DNA Hybridization on Surface of Self-organized MWCNT-Arrays Decorated by Organometallic Complexes .......................................................... 52
  V.P. Egorova, H.V. Grushevskaya, N.G. Krylova, I.V. Lipnevich, T.I. Orekhovskaja, B.G. Shulitski, and V.I. Krot

Towards a More Accurate Error Model for BioNano Optical Maps .... 67
  Menglu Li, Angel C.Y. Mak, Ernest T. Lam, Pui-Yan Kwok, Ming Xiao, Kevin Y. Yip, Ting-Fung Chan, and Siu-Ming Yiu

HapIso: An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads .................. 80
  Serghei Mangul, Harry (Taegyun) Yang, Farhad Hormozdiari, Elizabeth Tseng, Alex Zelikovsky, and Eleazar Eskin

Protein-Protein Interactions and Networks

Genome-Wide Structural Modeling of Protein-Protein Interactions .... 95
  Ivan Anishchenko, Varsha Badal, Taras Dauzhkena, Madhurima Das, Alexander V. Tuzikov, Petras J. Kundrotas, and Ilya A. Vakser

Identifying Essential Proteins by Purifying Protein Interaction Networks ..... 106
  Min Li, Xiaopei Chen, Peng Ni, Jianxin Wang, and Yi Pan
Differential Functional Analysis and Change Motifs in Gene Networks to Explore the Role of Anti-sense Transcription .......................... 117
  Marc Legeay, Béatrice Duval, and Jean-Pierre Renou

Predicting MicroRNA-Disease Associations by Random Walking on Multiple Networks ............................................................ 127
  Wei Peng, Wei Lan, Zeng Yu, Jianxin Wang, and Yi Pan

Progression Reconstruction from Unsynchronized Biological Data using Cluster Spanning Trees .................................................. 136
  Ryan Eshleman and Rahul Singh

Protein and RNA Structure

Consistent Visualization of Multiple Rigid Domain Decompositions of Proteins ................................................................. 151
  Emily Flynn and Ileana Streinu

A Multiagent Ab Initio Protein Structure Prediction Tool for Novices and Experts ............................................................... 163
  Thiago Lipinski-Paes, Michele dos Santos da Silva Tanus,
  José Fernando Ruggiero Bachega, and Osmar Norberto de Souza

Filling a Protein Scaffold with a Reference ................................................. 175
  Letu Qingge, Xiaowen Liu, Farong Zhong, and Binhai Zhu

Phylogenetics

Mean Values of Gene Duplication and Loss Cost Functions ..................... 189
  Pawel Górecki, Jarosław Paszek, and Agnieszka Mykowiecka

The SCJ Small Parsimony Problem for Weighted Gene Adjacencies ............ 200
  Nina Luhmann, Amelyse Thévenin, Aïda Ouangraoua, Roland Wittler,
  and Cedric Chauve

Path-Difference Median Trees .............................................................. 211
  Alexey Markin and Oliver Eulenstein

NEMo: An Evolutionary Model with Modularity for PPI Networks ............. 224
  Min Ye, Gabriela C. Racz, Qijia Jiang, Xiwei Zhang,
  and Bernard M.E. Moret

Multi-genome Scaffold Co-assembly Based on the Analysis of Gene Orders
  and Genomic Repeats ..................................................................... 237
  Sergey Aganezov and Max A. Alekseyev
Sequence and Image Analysis

Selectoscope: A Modern Web-App for Positive Selection Analysis of Genomic Data .......................................................... 253
   Andrey V. Zaika, Iakov I. Davydov, and Mikhail S. Gelfand

Methods for Genome-Wide Analysis of MDR and XDR Tuberculosis from Belarus ......................................................... 258
   Roman Sergeev, Ivan Kavaliou, Andrei Gabrielian, Alex Rosenthal, and Alexander Tuzikov

Haplotype Inference for Pedigrees with Few Recombinations ................. 269
   B. Kirkpatrick

Improved Detection of 2D Gel Electrophoresis Spots by Using Gaussian Mixture Model ......................................................... 284
   Michal Marczyk

Abridged Track 2 Abstracts

Predicting Combinative Drug Pairs via Integrating Heterogeneous Features for Both Known and New Drugs ................................. 297
   Jia-Xin Li, Jian-Yu Shi, Ke Gao, Peng Lei, and Siu-Ming Yiu

SkipCPP-Pred: Promising Prediction Method for Cell-Penetrating Peptides Using Adaptive k-Skip-n-Gram Features on a High-Quality Dataset ....... 299
   Wei Leyi and Zou Quan

CPredictor 2.0: Effectively Detecting both Small and Large Complexes from Protein-Protein Interaction Networks .................................. 301
   Bin Xu, Jihong Guan, Yang Wang, and Shuigeng Zhou

Structural Insights into Antiapoptotic Activation of Bcl-2 and Bcl-xL Mediated by FKBP38 and tBid .................................................. 304
   Valery Veresov and Alexander Davidovskii

VAliBS: A Visual Aligner for Bisulfite Sequences ........................................ 307
   Min Li, Xiaodong Yan, Lingchen Zhao, Jianxin Wang, Fang-Xiang Wu, and Yi Pan

MegaGTA: A Sensitive and Accurate Metagenomic Gene-Targeted Assembler Using Iterative de Bruijn Graphs ......................... 309
   Dinghua Li, Yukun Huang, Henry Chi-Ming Leung, Ruibang Luo, Hing-Fung Ting, and Tak-Wah Lam
TRANScendence: Transposable Elements Database and De-novo Mining Tool Allows Inferring TEs Activity Chronology ........................................... 342
  Michal Startek, Jakub Nogłó, Dariusz Grzebelus, and Anna Gambin

Phylogeny Reconstruction from Whole-Genome Data Using Variable Length Binary Encoding ......................................................... 345
  Lingxi Zhou, Yu Lin, Bing Feng, Jieyi Zhao, and Jijun Tang

**Author Index** ................................................................. 347