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Fa Zhang · Zhipeng Cai
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Bioinformatics Research and Applications

14th International Symposium, ISBRA 2018
Beijing, China, June 8–11, 2018
Proceedings

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Preface

On behalf of the Program Committee, we would like to welcome you to the proceedings of the 14th edition of the International Symposium on Bioinformatics Research and Applications (ISBRA 2018), held in Beijing, China, June 8–11, 2018. 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.

This year we received 138 submissions in response to the call for extended abstracts. The Program Committee decided to accept 24 of them for full publication in the proceedings and oral presentation at the symposium. We also accepted 30 for oral presentation; a list of these contributions can be found in this front matter. Furthermore, we received ten submissions in response to the call for short abstracts. The technical program also featured two keynote and two invited talks by four distinguished speakers: Prof. Ying Xu from the University of Georgia presented on mining omic data of large numbers of cancer tissue samples; Prof. Xuegong Zhang from Tsinghua University gave a primary view on single-cell bioinformatics; Prof. Xin Gao from King Abdullah University of Science and Technology introduced a graph-based biclustering method for mining phenotype data; Prof. Min Li from Central South University spoke on de novo genome assembly by using statistical characteristics of paired-end reads.

We would like to thank the Program Committee members and the additional reviewers for volunteering their time to review and discuss symposium papers. We would like to extend special thanks to the steering and general chairs of the symposium for their leadership, and to the finance, publicity, workshops, local organization, and publications chairs for their hard work in making ISBRA 2018 a successful event. Last but not least, we would like to thank all authors for presenting their work at the symposium.

April 2018

Fa Zhang
Min Li
Xiaohua Wan
Zhipeng Cai

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Abstracts of Invited Talks

A Primary View on Single-Cell Bioinformatics

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Abstract. Cells are not created equal. The Human Cell Atlas (HCA) project aims to build the atlas of all human cell types and cell states with their molecular signatures. Single-cell sequencing especially single-cell RNA-sequencing (scRNA-seq) is the key technology for obtaining the molecular signatures of a large amount of single cells at the whole transcriptome scale. It is a fundamental step toward the complete understanding of the human body, a super complex system composed of tens of trillions of cells that are all developed from a single cell. This opens the new broad field of single-cell biology. Single-cell biology converts each cell to a mathematical vector in the high-dimensional spaces of the expression of all genes and other molecular features. Therefore, single-cell bioinformatics, or the computational analyses of single-cell data, become the key component of all single-cell biology studies. This talk will give an overview of some key bioinformatics tasks in single-cell bioinformatics, and present examples of our on-going work on new methods for differential expression analysis and dimension reduction.

Searching for Roots of Cancer Development through Mining Large Scale Cancer Tissue Data and Modeling the Chemistry of Cellular Base-Acid Homeostasis

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Abstract. Over one million research articles have been published about cancer, but yet our understanding about cancer is undeniably little. We are yet to understand some of the most basic questions such as: (1) why some cancers such as pancreatic or liver cancers are so deadly while other cancers such as basal cell carcinoma are rarely life-threatening? or (2) why some cancers are highly drug resistant while other cancers are not? In this talk I will present some of our recent discoveries made through mining omic data of large numbers of cancer tissue samples. Our analyses strongly suggest that all cancer tissue cells have high levels of Fenton reactions, due to increased iron accumulation and H₂O₂ concentration at the disease sites, both being the result of persistent immune responses. A key consequence of the reaction is: it continuously produces OH⁻, to which the affected cells respond fiercely to maintain the pH homeostasis as changes in the intracellular pH would have profound impacts to the viability of the cells. We will demonstrate that cancer cells immobilize a wide range of metabolic activities through metabolic reprogramming, to keep the intracellular pH stable, including inhibition of the urea cycle, nucleotide synthesis, glycolytic ATP generation (Warburg effect) and even selection of mutations in specific amino acids. Some of the long-standing open questions can be answered naturally using our new model.

Gracob: A Graph-Based Constant-Column Biclustering Method for Mining Growth Phenotype Data

Xin Gao

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Abstract. Growth phenotype profiling of genome-wide gene-deletion strains over stress conditions can offer a clear picture that the essentiality of genes depends on environmental conditions. Systematically identifying groups of genes from such high-throughput data that share similar patterns of conditional essentiality and dispensability under various environmental conditions can elucidate how genetic interactions of the growth phenotype are regulated in response to the environment. In this talk, I will first demonstrate that detecting such “co-fit” gene groups can be cast as a less well-studied problem in biclustering, i.e., constant-column biclustering. Despite significant advances in biclustering techniques, very few were designed for mining in growth phenotype data. I will then propose Gracob, a novel, efficient graph-based method that casts and solves the constant-column biclustering problem as a maximal clique finding problem in a multipartite graph. We compared Gracob with a large collection of widely used biclustering methods that cover different types of algorithms designed to detect different types of biclusters. Gracob showed superior performance on finding co-fit genes over all the existing methods on both a variety of synthetic data sets with a wide range of settings, and three real growth phenotype data sets for *E. coli*, proteobacteria, and yeast.

De novo Genome Assembly by Using Statistical Characteristics of Paired-end Reads

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Abstract. DNA sequence is the carrier of genetic information, which guides the development of biological and functions of life. De novo genome assembly is aimed at acquiring a complete and accurate genome sequence, so it has become one of the fundamental issues in genome research for understanding the organization and process of life activities. However, de novo genome assembly still faces the challenges of repetitive regions in genome, sequencing errors, and uneven sequencing depth. In this talk, I will present our recent work as follows: (1) a sequence assembler based on the distributions of insert size and read, called EPGA. Through assessing the variation of the distribution of insert size, EPGA can solve problems introduced by some complex repetitive regions. And an improved assembler EPGA2 adopts error corrections and memory-efficient DSK to count k-mers; (2) a scaffolding method based on iterative strategy and linear programming to detect spurious edges, called BOSS. And scaffolding algorithm SCOP, which is the first method to classify the contigs and utilize the vertices and edges to optimize the scaffold graph; (3) a gap filling method called GapReduce, which aligns the paired-end reads to the scaffolds. For each gap, GapReduce determines two read sets, and then constructs De Bruijn graphs. GapReduce extracts paths from De Bruijn graphs to cover the gaps by using the characteristics of insert size and k-mer frequencies based on the partitioned read sets. Finally, the future development and challenges of de novo genome assembly will also be discussed.

List of Oral Presentations not Included in this Volume

Drug Repositioning based on Individual Bi-random Walks on a Heterogenous Network
Yuehui Wang, Maozu Guo, Yazhou Ren, Lianyin Jia and Guoxian Yu

Detecting Differential Consistency Network Modules
Jianwei Lu, Yao Lu, Yusheng Ding, Qingyang Xiao, Linqing Liu, Qingpo Cai, Yunchuan Kong, Yun Bai and Tianwei Yu

Joint SNMF Method for Finding Modules of Multiple Brain Networks
Lingkai Tang, Yulian Ding, Jie Zhang and Fang-Xiang Wu

Identifying Driver Genes Involving Gene Dyregulated Expression, Tissue-Specific Expression and Gene-Gene Network
Junrong Song, Feng Wang, Wei Peng and Jianxin Wang

Region-Based Interaction Detection in Genome-Wide Case-Control Studies
Sen Zhang, Wei Jiang, Ronald Cw Ma and Weichuan Yu

HiSSI: High-order SNP-SNP Interactions Detection based on Efficient Significant Pattern and Differential Evolution
Xia Cao, Jie Liu, Maozu Guo and Jun Wang

Detecting Horizontal Gene Transfer: A Probabilistic Approach
Gur Sevillya, Orit Adato and Sagi Snir

Predicting Comorbid Diseases with Geometric Embeddings of Human Interactome
Pakeeza Akram and Li Liao

A Novel Network Based Approach for Predicting Survivability of Breast Cancer Patients
Sheikh Jubair, Luis Rueda and Alioune Ngom

Directional Association Test Reveals High-Quality Putative Cancer Driver Biomarkers Including Noncoding RNAs
Hua Zhong and Mingzhou Song

Mining Information of Co-expression Network based on TGCA Data
Mi-Xiao Hou, Ying-Lian Gao, Jin-Xing Liu, Jun-Liang Shang, Rong Zhu and Sha-Sha Yuan

Identifying MicroRNA-Gene Networks Specific to Pathologic Stages in Colon Cancer
Benika Hall and Xinghua Shi

Cancer Driver Genes Discovery by Integrating Expression and Mutation Data
Ying Hui, Pi-Jing Wei, Junfeng Xia and Chun-Hou Zheng

DDIGIP: Predicting drug-drug interactions based on Gaussian Interaction profile kernels

Cheng Yan, Jianxin Wang, Yi Pan and Fang-Xiang Wu

A Novel Multi-Scale Local Sequence and Structural Representation for Identifying Protein-Protein Interfaces

Fei Guo and Jijun Tang

DEEPMEN: A New Method for Super-Enhancer Prediction based on Convolutional Neural Network

Hongda Bu, Jiaqi Hao, Yanglan Gan, Jihong Guan and Shuigeng Zhou

Data-driven Approach for Understanding the Mild Cognitive Impairment

Bingchen Yu, Meng Han, Liyuan Liu, Yan Huang, Yi Liang and Liqun Bai

InvBFM: Finding Genomic Inversions from High-throughput Sequence Data based on Feature Mining

Zhongjia Wu, Yufeng Wu and Jingyang Gao

Deep Feature Selection with Application to a Neisseria gonorrhoeae Antimicrobial Resistance Study

Jinhong Shi, Yan Yan, Matthew Links, Longhai Li, Michael Horsch and Anthony Kusalik

Jaccard/Tanimoto similarity test and statistical significance estimation methods to evaluate species co-occurrences

Neo Christopher Chung, B lazej Miasojedow, Micha l Startek and Anna Gambin

A Robustness Metric for Biological Data Clustering Algorithms

Yuping Lu, Charles A. Phillips and Michael A. Langston

CSA: A Web Service for the Complete Process of ChIP-Seq Analysis

Min Li, Li Tang, Fang-Xiang Wu, Yi Pan and Jianxin Wang

OffScan: A Universal and Fast CRISPR Off-Target Sites Detection Tool

Yingbo Cui, Minxia Cheng, Jiaming Xu, Xiangke Liao and Shaoliang Peng

GPRED-GC: A Gene PREDiction Model Accounting for 5'–3' GC Gradient

Prapaporn Techa-Angkoon, Kevin Childs and Yanni Sun

Detecting Diagnostic Biomarkers of Alzheimer's Disease by Integrating Gene Expression Data in Six Brain Regions

Lihua Wang and Zhi-Ping Liu

Revealing the Tipping Points in Infant Brain Development for Primates by High Throughput Data

Hui Tang, Ying Tang, Tao Zeng and Luonan Chen

A Framework using Topological Pathways for Deeper Analysis of Transcriptome Data

Yue Zhao, Stephanie Piekos, Tham H. Hoang and Dong-Guk Shin

Detecting Circular RNA from High-throughput Sequence Data with de Bruijn Graph

Xin Li and Yufeng Wu

Identification of Methylation States of DNA Regions for Illumina Methylation BeadChip

Ximei Luo, Yuming Zhao, Fang Wang, and Guohua Wang

Contents

Network Analysis and Modelling

Prediction of Drug Response with a Topology Based Dual-Layer Network Model.	3
<i>Suyun Huang and Xing-Ming Zhao</i>	
GRTR: Drug-Disease Association Prediction Based on Graph Regularized Transductive Regression on Heterogeneous Network	13
<i>Qiao Zhu, Jiawei Luo, Pingjian Ding, and Qiu Xiao</i>	
An Improved Particle Swarm Optimization with Dynamic Scale-Free Network for Detecting Multi-omics Features.	26
<i>Huiyu Li, Sheng-Jun Li, Junliang Shang, Jin-Xing Liu, and Chun-Hou Zheng</i>	
PBMarsNet: A Multivariate Adaptive Regression Splines Based Method to Reconstruct Gene Regulatory Networks	38
<i>Siyu Zhao, Ruiqing Zheng, Xiang Chen, Yaohang Li, Fang-Xiang Wu, and Min Li</i>	

Genomic Data Analysis

Bounds on Identification of Genome Evolution Pacemakers	51
<i>Sagi Snir</i>	
REXTAL: Regional Extension of Assemblies Using Linked-Reads	63
<i>Tunazzina Islam, Desh Ranjan, Eleanor Young, Ming Xiao, Mohammad Zubair, and Harold Riethman</i>	
A Scalable Reference-Free Metagenomic Binning Pipeline	79
<i>Terry Ma and Xin Xing</i>	

Cancer Data Analysis

The Review of the Major Entropy Methods and Applications in Biomedical Signal Research	87
<i>Guangdi Liu, Yuan Xia, Chuanwei Yang, and Le Zhang</i>	
Inferring Dysregulated Pathways of Driving Cancer Subtypes Through Multi-omics Integration.	101
<i>Kai Shi, Lin Gao, and Bingbo Wang</i>	

An Extension of Deep Pathway Analysis: A Pathway Route Analysis Framework Incorporating Multi-dimensional Cancer Genomics Data	113
<i>Yue Zhao</i>	

Hierarchical Similarity Network Fusion for Discovering Cancer Subtypes . . .	125
<i>Shuhui Liu and Xuequn Shang</i>	

Structure and Interaction

Sprites2: Detection of Deletions Based on an Accurate Alignment Strategy . . .	139
<i>Zhen Zhang, Jianxin Wang, Junwei Luo, Juan Shang, Min Li, Fang-Xiang Wu, and Yi Pan</i>	

KSIBW: Predicting Kinase-Substrate Interactions Based on Bi-random Walk	151
<i>Canshang Deng, Qingfeng Chen, Zhixian Liu, Ruiqing Zheng, Jin Liu, Jianxin Wang, and Wei Lan</i>	

XPredRBR: Accurate and Fast Prediction of RNA-Binding Residues in Proteins Using eXtreme Gradient Boosting	163
<i>Lei Deng, Zuojin Dong, and Hui Liu</i>	

A Biologically Meaningful Extension of the Efficient Method for Deleterious Mutations Prediction in RNAs: Insertions and Deletions in Addition to Substitution Mutations	174
<i>Alexander Churkin and Danny Barash</i>	

Screening of Sonic Hedgehog (Shh) Inhibitors in the Hedgehog Signaling Pathway from Traditional Chinese Medicine (TCM) Database Through Structure-Based Pharmacophore Design	179
<i>Ilmi Fadhillah Rizki, Mochammad Arfin Fardiansyah Nasution, Syafrida Siregar, Mega Maulina Ekawati, and Usman Sumo Friend Tambunan</i>	

Novel Inhibitors of T315I Mutant BCR-ABL1 Tyrosine Kinase for Chronic Myeloid Leukemia Disease Through Fragment-Based Drug Design	185
<i>Satya Anindita, Atika Marnolia, Hersal Hermana Putra, Muhammad Chandra Haikal, and Usman Sumo Friend Tambunan</i>	

HPC and CryoEM

On <i>k</i> -Mismatch Shortest Unique Substring Queries Using GPU	193
<i>Daniel W. Schultz and Bojian Xu</i>	

Memory-Efficient and Stabilizing Management System and Parallel Methods for RELION Using CUDA and MPI	205
<i>Jingrong Zhang, Zihao Wang, Yu Chen, Zhiyong Liu, and Fa Zhang</i>	

GPU Accelerated Ray Tracing for the Beta-Barrel Detection from Three-Dimensional Cryo-EM Maps	217
<i>Albert Ng, Adedayo Odesile, and Dong Si</i>	
A Fast Genome Sequence Aligner Based on Minimal Perfect Hash Algorithm Realized with FPGA Based Heterogeneous Computing Platform . . .	227
<i>Ke Huang, Shubo Yang, Zhaojian Luo, Ke Yang, Menghan Chen, Guopeng Wei, and Jian Huang</i>	
A Pattern Recognition Tool for Medium-Resolution Cryo-EM Density Maps and Low-Resolution Cryo-ET Density Maps	233
<i>Devin Haslam, Salim Sazzed, Willy Wriggers, Julio Kovcas, Junha Song, Manfred Auer, and Jing He</i>	
Machine and Deep Learning	
Combining Sequence and Epigenomic Data to Predict Transcription Factor Binding Sites Using Deep Learning	241
<i>Fang Jing, Shao-Wu Zhang, Zhen Cao, and Shihua Zhang</i>	
A Deep Learning Method for Prediction of Benign Epilepsy with Centrotemporal Spikes	253
<i>Ming Yan, Ling Liu, Sihan Chen, and Yi Pan</i>	
LSTM Recurrent Neural Networks for Influenza Trends Prediction	259
<i>Liyuan Liu, Meng Han, Yiyun Zhou, and Yan Wang</i>	
Predicting Gene-Disease Associations with Manifold Learning	265
<i>Ping Luo, Li-Ping Tian, Bolin Chen, Qianghua Xiao, and Fang-Xiang Wu</i>	
Data Analysis and Methodology	
On Approaching the One-Sided Exemplar Adjacency Number Problem	275
<i>Letu Qingge, Killian Smith, Sean Jungst, and Binhai Zhu</i>	
Prediction of Type III Secreted Effectors Based on Word Embeddings for Protein Sequences	287
<i>Xiaofeng Fu, Yiqun Xiao, and Yang Yang</i>	
Extending the Evolvability Model to the Prokaryotic World: Simulations and Results on Real Data	299
<i>Sagi Snir and Ben Yohay</i>	
Predicting Opioid Epidemic by Using Twitter Data	314
<i>Yubao Wu, Pavel Skums, Alex Zelikovsky, David Campo Rendon, and Xueting Liao</i>	

Analysis and Visualization Tools

Cluster Matching Distance for Rooted Phylogenetic Trees 321
Jucheol Moon and Oliver Eulenstein

RNA-Seq Data Analysis

Truncated Robust Principal Component Analysis and Noise Reduction
for Single Cell RNA-seq Data 335
*Krzysztof Gogolewski, Maciej Sykulski, Neo Christopher Chung,
and Anna Gambin*

Locality Sensitive Imputation for Single-Cell RNA-Seq Data 347
Marmar Moussa and Ion I. Măndoiu

Author Index 361