



ISBRA 2017

**13th International Symposium on Bioinformatics
Research and Applications (ISBRA)**

**May 29 - June 2, 2017
Honolulu, Hawaii, USA**

<http://alan.cs.gsu.edu/isbra17/>

**The ISBRA 2017 will take place in Milo 4/5 at Waikiki
Beach Marriott Resort & Spa.**

Message from the General Chair



I am delighted to welcome you to the 13th International Symposium on Bioinformatics Research and Applications (ISBRA 2017) being held at Waikiki Beach Marriott Resort & Spa, Honolulu, Hawaii. We are honored to serve the international community by bringing together scholars, scientists and students from academia, laboratories, and industry to this premier meeting.

We would like to express our gratitude to the Program Chairs Zhipeng Cai, Ovidiu Daescu, and Min Li for putting together a terrific technical program. We thank the program committee and reviewers for their hard work, and also thank all authors who submitted papers and abstracts for their contributions. We believe that you will enjoy all contributed and keynote talks this week!

We are grateful to the Steering Committee Chair Yi Pan for help in coordinating ISBRA 2017. We thank the Finance Chair Anu Bourgeois for her outstanding job in managing the bank account and registration system. We also thank the Publicity Chairs Chunyu Ai Shaoliang, Peng, Xiang Wan, Gangman Yi, for their assistance in publicizing the symposium. We thank the Publication Chair Pavel Skums for his efforts in assembling Springer Proceedings and the Award Chair Raj Sunderraman for selecting award recipients.

Last but not least, we would like to thank our sponsors: the National Science Foundation, Georgia State University and CCF Task Force on Bioinformatics. Thanks to their generous support we have been able to award travel fellowships to several graduate students and post-doctoral scholars from different countries of the world.

We hope you will have a wonderful time at the symposium and enjoy Hawaii - the beautiful beaches, volcanos and waterfalls.

Alexander Zelikovsky, Georgia State University

ISBRA 2017 General Chair

Message from the Program Chairs



On behalf of the Program Committee, we would like to welcome you to the 13th edition of the International Symposium on Bioinformatics Research and Applications (ISBRA 2017), held in Honolulu, Hawaii, May 29 to June 2, 2017. 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 118 submissions in response to the call for extended abstracts. The Program Committee decided to accept 27 of them for full publication in the proceedings and oral presentation at the symposium. We also accepted 24 of them for oral presentation and short abstract publication in the proceedings. Furthermore, we also received 18 submissions in response to the call for short abstracts.

The technical program invited keynote talks by Prof. Michael Q. Zhang from The University of Texas at Dallas and Tsinghua University. Prof. Zhang reviewed the history of computational genome regulation and then introduced some new biochemical (BL-Hi-C), biophysical (super-resolution imaging), and Bioinformatics (MICC, 3CPET, FIND) technology developments that may be used for studying 3D genomes and disease markers in the near future.

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 2017 a successful event. Last but not least we would like to thank all authors for presenting their work at the symposium.

Zhipeng Cai, Georgia State University, USA
Ovidiu Daescu, University of Texas at Dallas, USA
Min Li, Central South University, China

ISBRA 2017 TPC Co-Chairs

Keynote Speakers



Michael Q. Zhang

Computational Biology of Genome Regulation from 1D to 3D

The University of Texas at Dallas & Tsinghua University

Cell fate determination and transformation is intimately related to chromatin interaction and 3D genome structure. Many 1D cancer or other developmental regulatory disease markers, such as GWAS SNPs/CNVs, heritable or somatic mutations, gene fusions, viral insertion hotspots, epimutations, etc., are often linked to dis-regulation of cis-regulatory elements to their target genes through altered 3D DNA loops. I will review the history of computational genome regulation and then introduce some new biochemical (BL-Hi-C), biophysical (Super-resolution imaging) and Bioinformatics (MICC, 3CPET, FIND) technology developments that may be used for studying 3D genomes and disease markers in the near future.

Bio: Dr. Zhang got his B.S. in Mech. Eng. from USTC and joined the first CUSPEA (initiated by T.D. Lee) group studying physics in USA in 1981. After getting Statistical Physics PhD from Rutgers University in 1987, he became a postdoc at the Courant Institute of Mathematics at NYU until he became a Genome Research fellow at CSHL in 1991. Dr. Zhang started his Computational Genomics Lab there in 1996 and became full professor in 2002. He became 1000-Talent guest professor of Tsinghua University in 2009 and moved to The University of Texas at Dallas as the Cecil H. and Ida Green Distinguished endowed chair Professor in 2010. Dr. Zhang is currently the director of Center for Systems Biology at UT Dallas and the co-director of Center for Synthetic and Systems Biology at Tsinghua U.

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Sponsors



National Science Foundation



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CCF Task Force on Bioinformatics

ISBRA 2017 Agenda

May 29, Monday

18:00pm to 19:30pm

Reception

Venue: Waikiki Terrace

20:00pm to 21:00pm

ISBRA 2018 Organization Committee Meeting

Venue: Milo 4/5

May 30, Tuesday

7:00 am to 8:00 am

Registration

8:00 am to 8:10 am

Opening Remarks

8:10 am to 10:10 am

Session 1: Cancer Analysis & Prediction

Session Chair: Yaohang Li, Old Dominion University

Copy Number Aberration Based Cancer Type Prediction with Convolutional Neural Networks

Yuchen Yuan, Yi Shi, Xianbin Su, Xin Zou, Qin Luo, Weidong Cai, Zeguang Han and David Dagan Feng.

Prediction of Time to Tumor Recurrence in Ovarian Cancer: Comparison of Three Sparse Regression Methods

Mahsa Lotfi, Burook Misganaw and Mathukumalli Vidyasagar.

Predicting Human Microbe-Disease Associations via Binary Matrix Completion

Jian-Yu Shi, Hua Huang, Yan-Ning Zhang and Siu-Ming Yiu.

Characterization of Kinase Gene Expression and Splicing Profile in Prostate Cancer with RNA-Seq Data

Huijuan Feng, Tingting Li and Xuegong Zhang.

Histopathological Diagnosis for viable and non-viable tumor prediction for Osteosarcoma using Convolutional Neural Network

Rashika Mishra, Ovidiu Daescu, Patrick Leavey, Dinesh Rakheja and Anita Sengupta.

Relating Diseases Based on Disease Module Theory

Peng Ni, Min Li, Ping Zhong, Guihua Duan and Fangxiang Wu.

10:10 am to 10:40 am

Coffee Break

10:40 am to 12:00 pm

Session 2: Network Analysis

Session Chair: Xinghua Shi, University of North Carolina at Charlotte

Reconstructing One-Articulated Networks with Distance Matrices

Kuang-Yu Chang, Yun Cui, Siu Ming Yiu and Wing-Kai Hon.

Identifying Conserved Protein Complexes across Multiple Species via Network Alignment

Bo Song, Jianliang Gao, Xiaohua Hu, Yu Sheng and Jianxin Wang.

Constructing an Integrative MicroRNA eQTL Network on Ovarian Cancer: A Label Propagation Approach Utilizing Multiple Networks

Benika Hall, Andrew Quitadamo and Xinghua Shi.

Computational methods for the prediction of drug-target interactions from drug fingerprints and protein sequences by stacked auto-coder deep neural network

Lei Wang, Zhu-Hong You, Xing Chen, Shi-Xiong Xia, Feng Liu, Xin Yan and Yong Zhou.

12:00 pm to 13:30 pm

Luncheon

Venue: Milo 4/5 Lanai

13:30 pm to 15:30 pm

Session 3: Transcriptomics

Session Chair: Ion Mandoiu, University of Connecticut

Analysis of paired miRNA-mRNA microarray expression data using a stepwise multiple linear regression model

Yiqian Zhou, Rehman Qureshi and Ahmet Sacan.

Clustering Single Cell RNA-seq Data using TF-IDF based Methods

Marmar Moussa and Ion Mandoiu.

CircMarker: A Fast and Accurate Algorithm for Circular RNA Detection

Xin Li, Chong Chu, Jingwen Pei, Ion Mandoiu and Yufeng Wu.

Multiple model species selection for transcriptomic and functional analysis

Tun-Wen Pai.

IsoTree: De Novo Transcriptome Assembly from RNA-seq Reads

Jin Zhao, Haodi Feng, Daming Zhu, Chi Zhang and Ying Xu.

RNA Transcriptome Mapping with GraphMap

Krešimir Križanović, Ivan Sović, Ivan Krpeljik and Mile Šikić.

15:30 pm to 16:00 pm

Coffee Break

16:00 pm to 18:00 pm

Session 4: Proteomics

Session Chair: Xiaowen Liu, Indiana University-Purdue University Indianapolis

A graph-based approach for proteoform identification and quantification using homogeneous multiplexed top-down tandem mass spectra

Kaiyuan Zhu and Xiaowen Liu.

A New Estimation of Protein-level False Discovery Rate

Guanying Wu, Xiang Wan and Baohua Xu.

A generalized approach to predicting protein-protein interactions between virus and host

Xiang Zhou, Byungkyu Park, Daesik Choi and Kyungsook Han.

Unfolding the Protein Surface for Pattern Matching

Heng Yang, Chunyu Zhao and Ahmet Sacan.

Estimation of Intensities of Reactions Triggered by Electron Transfer in Top-Down Mass Spectrometry

Michał Aleksander Ciach, Mateusz Krzysztof Łacki, Błażej Miasojedow, Frederik Lermyte, Dirk Valkenburg, Frank Sobott and Anna Gambin.

Construction of Protein Backbone Fragments Libraries on Large Protein Sets using a Randomized Spectral Clustering Algorithm

Wessam Elhefnawy and Yaohang Li.

18:30 pm to 20:00 pm

Banquet & Keynote

Venue: Milo 3

Computational Biology of Genome Regulation from 1D to 3D

Michael Q. Zhang (The University of Texas at Dallas & Tsinghua University)

May 31, Wednesday

8:00 am to 10:00 am

Session 5: Analysis and Visualization Tools

Session Chair: Joshua Loving, Boston University

DeepSort: Deep Convolutional networks for Sorting Haploid Maize Seeds

Balaji Veeramani, John Raymond and Pritam Chanda.

Mapping paratope and epitope residues of antibody pembrolizumab via molecular dynamics simulation

Wenping Liu and Guangjian Liu.

A New 2-Approximation Algorithm for rSPR

Lusheng Wang, Zhi-Zhong Chen and Youta Harada.

PhenoSimWeb: a web tool for measuring and visualizing phenotype similarities using HPO

Jiajie Peng, Hansheng Xue, Bolin Chen, Qinghua Jiang, Xuequn Shang and Yadong Wang.

An SIMD Algorithm for Wraparound Tandem Alignment

Joshua Loving, John Scaduto and Gary Benson.

PhAT-QTL: A Phase-Aware Test for QTL detection

Meena Subramaniam, Noah Zaitlen and Jimmie Ye.

10:00 am to 10:30 am

Coffee Break

10:30 am to 12:10 pm

Session 6: Genomic Data Analysis

Session Chair: Gabriel Valiente, Technical University of Catalonia

Unbiased Taxonomic Annotation of Metagenomic Samples

Bruno Fosso, Graziano Pesole, Francesc Rosselló and Gabriel Valiente.

An improved approach for reconstructing consensus repeats from short sequence reads

Chong Chu, Jingwen Pei and Yufeng Wu.

Efficiently Mining Multi-mers in a Variety of Biological Sequences

Jingsong Zhang, Jianmei Guo, Xiaoqing Yu, Xiangtian Yu, Weifeng Guo, Tao Zeng and Luonan Chen.

GRSR: a Tool for Deriving Genome Rearrangement Scenarios from Multiple Unichromosomal Genome Sequences

Dan Wang and Lusheng Wang

Genetic Algorithm Based Beta-Barrel Detection for Medium Resolution Cryo-EM Density Maps

Albert Ng and Dong Si.

12:10 pm to 13:30 am

Luncheon

Venue: Milo 4/5 Lanai

13:30 pm to 15:30 pm

Session 7: Phylogenetics

Session Chair: Siu-Ming Yiu, The University of Hong Kong

Coestimation of Gene Trees and Reconciliations under a Duplication-Loss-Coalescence Model

Bo Zhang and Yi-Chieh Wu.

A median solver and phylogenetic inference based on DCJ sorting

Ruofan Xia, Jun Zhou, Lingxi Zhou, Jijun Tang and Bing Feng.

Reconstruction of Real and Simulated Phylogenies Based on Quartet Plurality Inference

Eliran Avni and Sagi Snir.

Phylogenetic Tree Reconciliation: Mean Values for Fixed Gene Trees

Pawel Gorecki, Alexey Markin, Agnieszka Mykowiecka, Jaroslaw Paszek and Oliver Eulenstein.

On the Impact of Uncertain Gene Tree Rooting on Duplication-Transfer-Loss Reconciliation

Soumya Kundu and Mukul S. Bansal.

Addressing the Threats of Inference Attacks on Traits from Individual Genomic Data

Zaobo He, Yingshu Li, Ji Li and Jiguo Yu.

15:30 pm to 16:00 pm

Coffee Break

16:00 pm to 17:30 pm

Session 8: Network & Machine Learning (6 short)

Session Chair: Yufeng Wu, University of Connecticut

Extracting Depression Symptoms from Social Networks and Web Blogs via Text Mining

Long Ma, Zhibo Wang and Yanqing Zhang.

[A Probabilistic Approach to Multiple-Instance Learning](#)

Silu Zhang, Yixin Chen and Dawn Wilkins.

[Net2Image: A network representation method for identifying cancer-related genes based on TensorFlow](#)

Bolin Chen, Yuqiong Jin and Xuequn Shang.

[Differential Privacy Preserving Genomic Data Releasing via Factor Graph](#)

Zaobo He, Yingshu Li and Jinbao Wang

[Computational prediction of influenza neuraminidase inhibitors using machine learning algorithms and recursive feature elimination method](#)

Li Zhang, Haixin Ai, Qi Zhao, Junfeng Zhu, Wen Chen, Xuewei Wu, Liangchao Huang, Zimo Yin, Jian Zhao and Hongsheng Liu.

[In silico simulation of signal cascades in biomedical networks based on the production rule system](#)

Sangwoo Kim and Hojung Nam

June 1, Thursday

8:00 am to 10:00 am

Session 9: Machine Learning & High Performance Computing

Session Chair: Fa Zhang, Chinese Academy Of Sciences

[Biomedical Event Extraction via Attention-Based Bidirectional Gated Recurrent Unit Networks Utilizing Distributed Representation](#)

Lishuang Li, Jia Wan and Jieqiong Zheng.

[Computer Assisted Segmentation Tool: A Machine Learning Based Image Segmenting Tool for TrakEM2](#)

Augustus Tropea, Janey Valerio and S. Seth Long.

[Efficient Computation of Motif Discovery on Intel Many Integrated Core \(MIC\) Architecture](#)

Kaiwen Huang, Xiangke Liao, Yutong Lu and Shaoliang Peng.

[Accelerating Electron Tomography Reconstruction Algorithm ICON using the Intel Xeon Phi Coprocessor on Tianhe-2 Supercomputer](#)

Zihao Wang, Yu Chen, Jingrong Zhang, Lun Li, Xiaohua Wan, Zhiyong Liu, Fei Sun and Fa Zhang.

Predicting Diabetic Retinopathy and Identifying Interpretable Biomedical Features Using Machine Learning Algorithms

Hsin-Yi Tsao, Pei-Ying Chang and Emily Chia-Yu Su.

Big data analysis for bioinvasion

Chenyu Wang, Shengling Wang and Liran Ma.

10:00 am to 10:30 am

Coffee Break

10:30 am to 12:00 pm

Session 10: Data Analysis (6 short)

Session Chair: Wooyoung Kim, University of Washington Bothell

A new probability way to understand protein-protein interface formation mechanism at amino acid level

Yongxiao Yang and Xinqi Gong.

Detecting Potential Adverse Drug Reactions using Association Rules and Embedding Models

Kai Guo, Hongfei Lin, Bo Xu, Zhihao Yang, Jian Wang, Kan Xu and Yuanyuan Sun.

NemoLib: A Java library for efficient network motif detection

Andrew Andersen and Wooyoung Kim

A Genetic Algorithm for Finding Discriminative Functional Motifs in Long Non-Coding RNAs

Brian Gudenas and Liangjiang Wang

Heterogeneous Cancer Cell Line Data Fusion for Identifying Novel Response Determinants in Precision Medicine

Jeremiah Emidih

Modeling the Spread of HIV and HCV Infections Based on Identification and Characterization of High-Risk Communities Using Social Media

Deeptanshu Jha, Pavel Skums, Alex Zelikovsky, Yury Khudyakov, Rahul Singh

12:00 pm to 13:30 pm

Luncheon

Venue: Milo 4/5 Lanai

13:30 pm to 15:30 pm

Session 11: Modeling

Session Chair: Jun Meng, Dalian University of Technology

**Modeling the Molecular Distance Geometry Problem
Using Dihedral Angles**

Michael Souza, Carlile Lavor and Rafael Alves.

**What's hot and what's not? - Exploring trends in
bioinformatics literature using topic modeling and
keyword analysis**

Alexander Hahn, Somya Mohanty and Prashanti Manda.

**Structure Modeling and Molecular Docking Studies of
Schizophrenia Candidate Genes, Synapsins 2 (SYN2) and
Trace Amino Acid Receptor (TAAR6)**

**Naureen Khattak, Sheikh Sehgal, Yongsheng Bai and
Youping Deng.**

**Drug response prediction model using a component based
structural equation modeling method**

Sungtae Kim and Taesung Park.

**Accurate Prediction of Haplotype Inference Errors by
Feature Extraction**

Rogério Rosa and Katia Guimaraes.

**Detecting Change Points in fMRI Data via Bayesian
Inference and Genetic Algorithm Model**

**Xiuchun Xiao, Bing Liu, Jing Zhang, Xueli Xiao and Yi
Pan.**

15:30 am to 16:00 pm

Coffee Break

16:00 pm to 18:00 pm

Session 12: Data Analysis (7 short)

Session Chair: Bin Xue, University of South Florida

**Using the precision medicine analytical method to
investigate the impact of the aerobic exercise on the
hypertension for the middle-aged women**

**Wei Zhou, Guangdi Liu, Jiong Luo, Tingran Zhang and
Le Zhang.**

**Genome-wide analysis of response regulator genes in
*Solanum lycopersicum***

Jun Cui, Ning Jiang, Jun Meng and Yushi Luan.

**Evaluating the Impact of Encoding Schemes on Deep
Auto-encoders for DNA Annotation**

Ning Yu, Zeng Yu, Feng Gu and Yi Pan.

In Silico Evolution of HCV Quasispecies

Alexander Artyomenko, Pelin B. Icer, Pavel Skums and Alex Zelikovsky

Metabolic analysis of metatranscriptomic data from planktonic communities

Igor Mandric, Sergey Knyazev, Cory Padilla, Frank Stewart, Ion Mandoiu and Alex Zelikovsky

A Fully Automatic Geometric Parameters Determining Method For Electron Tomography

Yu Chen, Zihao Wang, Lun Li, Xiaohua Wan, Fei Sun and Fa Zhang.

Multi-threshold Sequential-voting in Decision-tree Based Meta-prediction

Bin Xue

June 2, Friday

8:00am – 9:00am

ISBRA 2018 Planning Committee Meeting and Breakfast

12:00 pm to 13:30 pm

ISBRA 2018 Organizing Committee Meeting and Lunch

Venue: Milo 4/5
