9th International Conference on
Bioinformatics and Computational Biology (BICoB 2017)

PROGRAM

March 20–22, 2017

Waikiki Beach Marriott Resort and Spa
Honolulu, Hawaii, USA

Sponsored by

International Society for
Computers and Their Applications

64 White Oak Court
Winona, MN 55987
Phone: (507) 458-4517; e-mail: isca@isca-hq.org; website: www.isca-hq.org
9th International Conference on Bioinformatics and Computational Biology
(BICoB 2017)

SPONSOR

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# Schedule at a Glance

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<td>Conference opening (Milo 4-5)</td>
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<td>9:00am – 10:00am</td>
<td>Keynote (Milo 4-5)</td>
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<td>10:30am – 12:00pm</td>
<td>Session 1A</td>
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<td>Lunch break</td>
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<td>1:30pm – 3:00pm</td>
<td>Session 1B</td>
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<td>3:30pm – 5:30pm</td>
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<tr>
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<tr>
<td>10:30am – 12:00pm</td>
<td>Session 2A</td>
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<td>Conference Luncheon and Best Paper Award</td>
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<tr>
<td>2:00pm – 3:30pm</td>
<td>Session 2B</td>
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<td>4:00pm – 5:30pm</td>
<td>Session 2C</td>
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<tr>
<td>8:30am – 10:00am</td>
<td>Session 3A</td>
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<tr>
<td>10:15am – 12:00pm</td>
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Monday, March 20, 2017

8:00 a.m. – 3:30 p.m.  REGISTRATION – Coffee, tea, pastries – Lanai, Milo 4-5

8:45 a.m. – 9:00 a.m.  WELCOME – Milo 4-5
Hisham Al-Mubaid, University of Houston-Clear Lake, USA
Oliver Eulenstein, Iowa State University, USA
Qin Ding, East Carolina University, USA

9:00 a.m. – 10:00 a.m.  KEYNOTE SPEAKER
Prof. Günther Hasinger
University of Hawaii at Manoa, USA
The Power of Computing in Astrophysics
Location: Milo 4-5
Session Chair: Antoine Bossard (Kanagawa University, Japan)

10:00 a.m. – 10:30 a.m.  COFFEE BREAK

SESSION 1A

GENOMICS I
Monday March 20, 10:30 a.m. – 12:00 p.m., Milo 4
Session Chair: Thomas Peters (University of Connecticut, USA)

1.  A Bayesian Framework for Marker Gene Taxonomic Classification Based on Sequence Alignment
   Xiang Gao, Huaiying Lin, Kashi Revanna and Qunfeng Dong (Loyola University Chicago, USA)

2.  GraphPE: Refining Metagenome Binning by Use of Paired-end Graph of Contigs
   Xianghui Liu and Rohan B. H. Williams (Nanyang Technological University, Singapore)

3.  Clustering Metagenome Sequences Using Canopies
   Mohammad Arifur Rahman, Nathan LaPierre, Huzefa Rangwala and Daniel Barbara
   (George Mason University, USA)

4.  Improving Microbiome Classification with Dirichlet-Multinomial Models
   Xiang Gao, Huaiying Lin and Qunfeng Dong (Loyola University Chicago, USA)

12:00 p.m. – 1:30 p.m.  LUNCH BREAK ON OWN
**STRUCTURE AND FUNCTION**
Monday March 20, 1:30 p.m. – 3:00 p.m., Milo 4
Session Chair: Aïda Ouanegraoua (Université de Sherbrooke, Canada)

1. **Evaluation of Protein Structural Models Using Random Forests**
   Renzhi Cao (Pacific Lutheran University, USA), Jie Hou, Taeho Jo and Jianlin Cheng (University of Missouri, USA)

2. **Visual Experiments of Geometric Combinatorics for Neural Stem Cells and Their Derivatives**
   T. J. Peters, J. C. Conover, D. McManus, K. Pratt (University of Connecticut, USA) and K. D. Williams (Applied Medical Consulting, USA)

3. **Classification of DNA Structure through Structure Network Analysis**
   Tanmay Kulshrestha, Ankita Gupta and Shibasish Chowdhury (Birla Institute of Technology and Science, India)

4. **A Fast Algorithm for Finding Largest Common Substructures in Multiple RNAs**
   Jithendar Anandan, Eric Fry, Keith Monschke and Abdullah N. Arslan (Texas A&M University-Commerce, USA)

3:00 p.m. – 3:30 p.m. **COFFEE BREAK**

**SYSTEMS BIOLOGY I**
Monday March 20, 3:30 p.m. – 5:30 p.m., Milo 4
Session Chair: Jianlin Cheng (University of Missouri, USA)

1. **Approximate Frequent Subpath Mining Applied to Pangenomics**
   Alan Cleary, Brendan Mumey (Montana State University, USA), Thiruvarangan Ramaraj and Joann Mudge (National Center for Genome Resources, USA)

2. **Determining Multifunctional Genes and Diseases in Human Using Gene Ontology**
   Hisham Al-Mubaid, Sasikanth Potu (University of Houston - Clear Lake, USA) and M. Shenify (University of Baha, KSA)

3. **A Local Search Algorithm for Clustering Large Biological Networks**
   Guy Coccimiglio and Salimur Choudhury (Algoma University, Canada)

4. **Reconstructing Protein and Gene Phylogenies by Extending the Framework of Reconciliation**
   Esaie Kuitche (Universite de Sherbrooke, Canada), Manuel Lafond (University of Ottawa, Canada) and Aïda Ouanegraoua (Université de Sherbrooke, Canada)

5. **ChIP-GMM: A Gaussian Mixture Model for Inferring Binding Regions in ChIP-seq Profiles**
   Sharmi Banerjee, Xi Chen, Xiaowei Wu, Hehuang Xie, Jianhua Xuan and Wu-chun Feng (Virginia Tech, USA)
9:00 a.m. – 10:00 a.m.  KEYNOTE SPEAKER

Dr. Bernard Moret
EPFL (Swiss Federal Institute of Technology), Lausanne, Switzerland
Phylogenetic Analyses: Past, Present, and Future
Location: Milo 4-5
Session Chair: Oliver Eulenstein (Iowa State University, USA)

10:00 a.m. – 10:30 a.m.  COFFEE BREAK

SESSION 2A

HEALTHCARE AND BIOINFORMATICS APPLICATIONS
Tuesday March 21, 10:30 a.m. – 12:00 p.m., Milo 4
Session Chair: Matthew Hayes (Tennessee State University, USA)

1. An In-Memory Database Platform for Systems Medicine
   Milena Kraus and Matthieu-P. Schapranow (Hasso Plattner Institute, Germany)

   Luke Barracliffe, Ognjen Arandjelovic and Gerry Humphrisy (University of St Andrews, UK)

3. Fundamental Bounds for Sequence Reconstruction from Nanopore Sequencers
   Abram Magner (University of Illinois Urbana-Champaign, USA), Jaroslaw Duda, Wojciech Szpankowski and Ananth Grama (Purdue University, USA)

4. Applications of Novel Graph Theoretic Methods to Clustering Autism Spectrum Disorders Phenotypes
   John Matta (Southern Illinois University Edwardsville, USA), Thy Nguyen (Missouri State University, USA), Gunes Ercal (Southern Illinois University Edwardsville, USA) and Tayo Obafemi-Ajayi (Missouri State University, USA)

12:00 p.m. – 2:00 p.m.  CONFERENCE LUNCHEON AND BEST PAPER AWARD

LOCATION: Waikiki Ballroom
GENOMICS II
Tuesday March 21, 2:00 p.m. – 3:30 p.m., Milo 4
Session Chair: Tayo Obafemi-Ajayi (Missouri State University, USA)

1. ParSECH: Parallel Sequencing Error Correction with Hadoop for Large-Scale Genome
   Arghya Kusum Das, Shayan Shams, Sayan Goswami, Richard Platania, Kisung Lee
   and Seung-Jong Park (Louisiana State University, USA)

2. Finding Surrogate Controls in Pathway Enrichment Analysis using RNA-Seq Expression
   Tham H. Hoang, Yue Zhao, Pujan Joshi, Seung-Huyn Hong and Dong-Guk Shin
   (University of Connecticut, USA)

3. Towards Reliable Microarray Analysis and Design
   Max Garzon and Sambriddhi Mainali (The University of Memphis, USA)

4. Reconstruction of Ring Chromosomes Using Paired-End Sequencing Data
   Matthew Hayes and Jeremy Pearson (Tennessee State University, USA)

3:30 p.m. – 4:00 p.m.  COFFEE BREAK

SESSION 2C

SYSTEMS BIOLOGY II
Tuesday March 21, 4:00 p.m. – 5:30 p.m., Milo 4
Session Chair: Max Garzon (The University of Memphis, USA)

1. Parameter Identification of Nonlinear Biochemical Reaction Systems Using the Statistics-based Method
   Xiaoying Zheng, Xiufen Zou and Zishu Pan (Wuhan University, China)

2. Modularity in PPI Networks: Characteristics of Existing Networks and Models of Evolution
   Min Ye (EPFL Lausanne, Switzerland), Xiuwei Zhang (UC Berkeley, USA) and Bernard
   M.E. Moret (EPFL Lausanne, Switzerland)

3. Network-based Differential Analysis of Hi-C Data
   Lu Liu and Jianhua Ruan (The University of Texas at San Antonio, USA)

4. A Parallel Algorithm for Mining Maximal Cohesive Subgraphs
   Aditya Goparaju and Saeed Salem (North Dakota State University, USA)
8:00 a.m. – 11:00 a.m.  REGISTRATION – Coffee, tea, pastries – Lanai, Milo 4-5

SESSION 3A

BIOINFORMATIC APPLICATIONS I
Wednesday, March 22, 8:30 a.m. – 10:00 a.m., Milo 4
Session Chair: Lee Altenberg (University of Hawaii at Manoa, USA)

1. 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
   Falguni Thakor, Ahmad Reza Hadaegh and Xiaoyu Zhang (California State University San Marcos, USA)

2. A Sequential Monte Carlo Sampler for Bayesian Phylogenetics
   Liangliang Wang (Simon Fraser University, Canada)

3. PF-Words: Biomedical Literature Based Protein Function Search
   Wei Wei, Mike Wong and Anagha Kulkarni (San Francisco State University, USA)

4. Detecting Haplotype Amplification in Cancer Sequencing Data
   Weiwei Liu, Jingyang Gao (Beijing University of Chemical Technology, China), Zhongmeng Zhao, Rongrong Yang, Yu Geng, Tian Zheng, Xuanping Zhang, Xiao Xiao, Jiayin Wang (Xi’an Jiaotong University, China)

10:00 a.m. – 10:15 a.m.  COFFEE BREAK

SESSION 3B

BIOINFORMATIC APPLICATIONS II
Wednesday, March 22, 10:15 a.m. – 12:00 p.m., Milo 4
Session Chair: Liangliang Wang (Simon Fraser University, Canada)

1. Improving Peptide Identification by Considering Ordered Amino Acid Usage
   Ahmed Alqurr and John Rose (University of South Carolina, USA)

2. Non-parametric Quality Assessment of High-Content Screening Assays
   Robert P. Trevino, Philippe C. Faucon (Arizona State University, USA), Thomas J. Lamkin (Air Force Research Laboratory, USA), Steven A. Kawamoto (UES, USA), Ross Smith (Engility Corporation, USA) and Huan Liu (Arizona State University, USA)

3. Prediction of Biological Functions by Histone Modification Patterns Profiling
   You Xiao, Kishan G. Mehrotra, Chilukuri K. Mohan, Pratibha Choudhary and Ramesh Raina (Syracuse University, USA)

4. Genetic Information, Mutation Rates, and the Lore of the Error Threshold
   Lee Altenberg (University of Hawaii at Manoa, USA)

5. Top-Down Correlation-Based Pattern Analysis and Feature Selection for Multi-Component FTIR Spectra
   Ghada Badr (University of Ottawa, Canada) and Najla Al-Ariefy (King Saud University, Saudi Arabia)