11th International Conference on

Bioinformatics and Computational Biology (BICOB 2019)

PROGRAM

March 18-20, 2019

Waikiki Beach Marriott Resort and Spa Honolulu, Hawaii, USA

Sponsored by



International Society for Computers and Their Applications

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11th International Conference on **Bioinformatics and Computational Biology** (BICOB 2019)

SPONSOR

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Schedule at a Glance

		Milo 4-5
	8:45am – 9:00am	Conference opening (Milo 4-5)
	9:00am – 10:00am	Keynote (Milo 4-5)
	10:30am – 12:00pm	Session 1A
Monday, March 18	12:00-1:30pm Lunch break (on your own)	
	1:30pm – 3:00pm	Session 1B
	3:30pm – 5:00pm	Session 1C

		Milo 4-5	
	9:00am – 10:00am	Keynote (Milo 4-5)	
	10:30am – 12:00pm	Session 2A	
Tuesday, March 19	12:00-2:00pm Conference Luncheon and Best Paper Award (Waikiki Ballroom)		
	2:00pm – 3:30pm	Session 2B	

Monday, March 18, 2019

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. Tamer Kahveci University of Florida, USA

Computational Analysis of Interactomes: Challenges, Solutions, and Opportunities

Location: Milo 4-5

Session Chair: Hisham Al-Mubaid (University of Houston-Clear Lake, USA)

10:00 a.m. - 10:30 a.m. COFFEE BREAK

DNA SEQUENCE ASSEMBLY ALIGNMENT, AND ANALYSIS

Monday March 18, 10:30 a.m. – 12:00 p.m., Milo 4-5

Session Chair: Elena Harris (California State University, Chico, USA)

1. HPC-BLAST: Distributed BLAST for Modern HPC Clusters

Shane Sawyer, Mitchel Horton, Chad Burdyshaw, Glenn Brook (University of Tennessee, USA) and Bhanu Rekapalli (BioTeam Inc., USA)

2. gcn.MOPS: Accelerating cn.MOPS with GPU

Mohammad Alkhamis and Amirali Baniasadi (University of Victoria, Canada)

3. Identifying DNA Sequence Motifs of Pdx-1 and NeuroD1 Transcription Factors

Hassan Aldarwish, David Keller and Elena Harris (California State University, Chico, USA)

4. DALIGNER Performance Evaluation on Intel Xeon Phi Architecture

Evaldo Costa, Gabriel Silva and Marcello Teixeira (Universidade Federal do Rio de Janeiro, Brazil)

12:00 p.m. – 1:30 p.m. LUNCH BREAK ON OWN

GENOME ANALYSIS AND NGS Monday March 18, 1:30 p.m. – 3:00 p.m., Milo 4-5 Session Chair: Oliver Eulenstein (Iowa State University, USA)

1. An Enrichment Method For Mapping Ambiguous Reads To Reference Genome For NGS Analysis

Yuan Liu, Yongchao Ma, Evan Salsman, Frank Manthey, Elias Elias, Xuehui Li and Changhui Yan (North Dakota State University, USA)

2. Comparison of Type I Interferon Expression in Adult and Neonatal Mice during Respiratory Viral Infection

Zifeng Liang (Miss Hall's School, USA)

- 3. Understand Effective Coverage by Mapped Reads using Genome Repeat Complexity Shanshan Gao, Quang Tran and Vinhthuy Phan (University of Memphis, USA)
- 4. The Polygraph: A Data Structure for Genome Alignment and Variation Detection
 Masaki Fujimoto, Cole Lyman and Mark Clement (Brigham Young University, USA)

3:00 p.m. - 3:30 p.m. COFFEE BREAK

MACHINE LEARNING IN BIOINFORMATICS

Monday March 18, 3:30 p.m. – 5:00 p.m., Milo 4-5

Session Chair: Freimut Bodendorf (University of Eriangen-Nuremberg, Germany)

1. Improving Classification with CNNs using Wavelet Pooling with Nesterov-Accelerated Adam

Allison Rossetto and Wenjin Zhou (University of Massachusetts Lowell, USA)

2. Predicting high-cost patients by Machine Learning: A case study in an Australian private hospital group

Isabella Eigner (University of Eriangen-Nuremberg, Germany), Freimut Bodendorf (University of Eriangen-Nuremberg, Germany) and Nilmini Wickramasinghe (Epworth HealthCare & Deakin University, Australia)

3. A New Look at Codon Usage and Protein Expression

Gabriel Wright, Anabel Rodriguez, Patricia Clark (University of Notre Dame, USA) and Scott Emrich (University of Tennessee, USA)

4. Prediction of MoRFs Based on n-gram Convolutional Neural Network

Chun Fang (Shandong University of Technology, China), Yoshitaka Moriwaki (The University of Tokyo, Japan), Caihong Li (Shandong University of Technology, China) and Kentaro Shimizu (The University of Tokyo, Japan)

Tuesday, March 19, 2019

8:00 a.m. – 3:30 p.m.

REGISTRATION – Coffee, tea, pastries – Lanai, Milo 4-5

9:00 a.m. - 10:00 a.m. KEYNOTE SPEAKER

Dr. Kelvin Richards
Director, International Pacific Research Center
University of Hawaii

MODELING EARTH'S OCEAN AND ATMOSPHERE: THE CHALLENGE OF CAPTURING RELEVANT SCALES

Location: Milo 4-5

Session Chair: Gordon Lee (San Diego State University, USA)

10:00 a.m. - 10:30 a.m. COFFEE BREAK

CANCER RESEARCH
Tuesday March 19, 10:30 a.m. – 12:00 p.m., Milo 4-5
Session Chair: Fred Harris (University of Nevada, Reno, USA)

- 1. Robust Fuzzy Cluster Ensemble on Cancer Gene Expression Data
 - Yan Yan, Tin Nguyen, Bobby Bryant and Fred Harris (University of Nevada, Reno, USA)
- 2. A SVM Model for Candidate Y-chromosome Gene Discovery in Prostate Cancer

Wageesha Rasanjana (University of Moratuwa, Sri Lanka), Sanduni Prasadi (University of Peradeniya, Sri Lanka), Indika Perera (University of Moratuwa, Sri Lanka) and Dulani Meedeniya (University of Moratuwa, Sri Lanka)

3. Colorectal Cancer Outcome Prediction from H&E Whole Slide Images using Machine Learning and Automatically Inferred Phenotype Profiles

Xingzhi Yue, Neofytos Dimitriou and Ognjen Arandjelovic (University of St Andrews, United Kingdom)

4. Petri nets and ODE as complementary tools in analysis of signaling pathways

Daria Kogut (Silesian University of Technology, Poland), Kaja Gutowska (Poznan University of Technology, Poland), Aleksandra Poterała-Hejmo (Silesian University of Technology, Poland), Jarosław Śmieja (Silesian University of Technology, Poland), Dorota Formanowicz (Poznan University of Medical Sciences, Poland) and Piotr Formanowicz (Poznan University of Technology and Polish Academy of Sciences, Poland)

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

LOCATION: Waikiki Ballroom

BIOINFORMATICS ALGORITHMS AND ANALYSIS
Tuesday March 19, 2:00 p.m. – 3:30 p.m., Milo 4-5
Session Chair: Tara Scully (The George Washington University, USA)

1. Equipping Decoy Generation Algorithms for Template-free Protein Structure Prediction with Maps of the Protein Conformation Space

Ahmed Bin Zaman and Amarda Shehu (George Mason University, USA)

2. Statistical Analysis of GLCM Texture Features and Microstructures in SEM Images of Crassostrea virginica Exposed to Atrazine

Abia Khan, Kavery Nivana Theethira Poonacha and Tara Scully (The George Washington University, USA)

3. Connecting Molecular Energy Landscape Analysis with Markov Model-based Analysis of Equilibrium Structural Dynamics

Kazi Lutful Kabir, Nasrin Akhter and Amarda Shehu (George Mason University, USA)

4. Prediction Of Novel Pirna Rat Clusters Based On Mouse Pirna Clusters Using Downstream and Upstream Analysis

Tamer Aldwairi (Ursinus College & Mississippi State University), Andy Perkins (Mississippi State University, USA) and Federico Hoffmann (Mississippi State University, USA)

3:30 p.m. – 4:00 p.m. COFFEE BREAK