8th International Conference on Bioinformatics and Computational Biology (BICoB-2016)

PROGRAM

April 4 - 6, 2016

Las Vegas, Nevada, USA

Sponsored by



International Society for Computers and Their Applications

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8th International Conference on Bioinformatics and Computational Biology (BICoB-2016)

SPONSOR

International Society for Computers and Their Applications (ISCA)

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Monday, April 4th, 2016

8:00 a.m. - 4:00 p.m. REGISTRATION - Coffee/tea/pastries - RR Registration Desk

8:45 a.m. - 9:00 a.m. WELCOME - Room:

Hisham Al-Mubaid, University of Houston - Clear Lake, USA

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

Dr. Gordon K. Lee

San Diego State University, USA

Research Challenges in Intelligent Robotic Systems: From Evolutionary Methods to KASER's and KANSEI

Location: Red Rock 6

10:00 a.m. – 10:30 a.m. COFFEE BREAK – RR Registration Desk

SESSION 1A:

Biomedical Informatics

Monday, April 4, 2016, 10:30 a.m. - 12:00 p.m., Valley of the Fire Session Chair: Qin Ding

1. Prediction of Future Hospital Admissions – What is the Tradeoff between Specificity and Accuracy?

Leva Vasiljeva and Ognjen Arandjelovic

- 2. **Biomedical Text Classification with Improved Feature Weighting Method**Duong Nguyen, Mohamed Shenify and Hisham Al-Mubaid
- 3. Wearable Computing for Fully Automated Myocardial Infarction Classification
 Getie Zewdie and Momiao Xiong
- 4. Generating Hypothesis: Using Global and Local Features in Graph to Discover New Knowledge from Medical Literature

Vishrawas Gopalakrishnan, Kishlay Jha, Aidong Zhang and Wei Jin

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

STRUCTURE AND FUNCTION

Monday, April 4, 2016, 1:30p.m. - 03:10 p.m., Valley of the Fire Session Chair: Amir Vajdi

1. Clustering Protein Conformations Using a Dynamic Programming Based Similarity Measurement

Amir Vajdi and Nurit Haspel

- 2. Identification of Ubiquitylation Sites Through Nondominated Sorting Genetic Algorithm II
 Paulo Cardoso, Reginaldo Santos, Manoel Lima, Claudomiro Sales, Regiane Kawasaki and
 - Paulo Cardoso, Reginaldo Santos, Manoel Lima, Claudomiro Sales, Regiane Kawasaki and Vitcor Coelho
- 3. A Principled Comparative Analysis of Dimensionality Reduction Techniques on Protein Structure Decoy Data

Rohan Pandit and Amarda Shehu

4. Protein Structure Normal Mode Analysis on the Positive Semidefinite Matrix Manifold Xiao-Bo Li, Forbes Burkowski and Henry Wolkowicz)

3:00 p.m. - 3:30 p.m. Coffee Break



- 1. GiGA: Giraph-based Genome Assembler for Gigabase Scale Genomes
 - Praveen Kumar Kondikoppa, Arghya Kusum Das, Sayan Goswami, Richard Platania and Seung-Jong Park
- 2. A Pipeline for Identifying Integration Sites of Mobile Elements in the Genome using Next-Generation Sequencing

Raunag Malhotra, Daniel Elleder, Le Bao, David R Hunter, R. Acharya and Mary Poss

- 3. **Using Disk Based Index and Box Queries for Genome Sequencing Error Correction**Yarong Gu, Qiang Zhu, Xianying Liu, Youchao Dong, C. Titus Brown and Sakti Pramanik
- 4. A Scalable Solution for Finding Overlaps Between Sequences Using Map-Reduce
 Maan Haj Rachid and Qutaibah Malluhi

Tuesday, April 5th 2016

8:30 a.m. – 4:00 p.m. REGISTRATION – Coffee/tea/pastries – RR Registration Desk

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

BICOB – 2016 Keynote Talk

Dr. Vineet Bafna

University of California – San Diego

Learning to live the high life: decoding the genetic basis of adaptation

Location: Red Rock 6

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

BIOMEDICAL INFORMATICS II
SESSION 4A: Tuesday, April 5, 2016, 10:30 a.m. - 12:0

Tuesday, April 5, 2016, 10:30 a.m. - 12:00 p.m., Valley of the Fire

Session Chair: Raunaq Malhotra

1. MapBase: Declaratively Approaching Quality Biological ID Mapping using an On-demand Data Warehouse

Hasan Jamil

2. miRDiabetes: A microRNA-Diabetes Association Database Constructed by Classification on Literature

Hui Guo and Qin Ding

3. Parameter Estimation and Sensitivity Analysis of Biological systems with Memory Fathalla Rihan

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

LOCATION: Red Rock 7–8

SYSTEMS BIOLOGY Tuesday, April 5, 2016, 2:00 p.m. – 3:40 p.m., Valley of the Fire Session Chair: Mohamed Shenify

1. Synthesizing Large-Scale Species Trees using Guidance Trees

Jucheol Moon and Oliver Eulenstein

2. An alignment-free method for profiling microbial community

Diem-Trang Pham, Shanshan Gao and Vinhthuy Phan

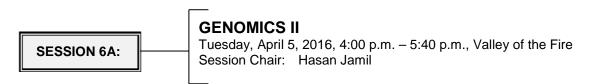
3. An Evaluation of Different Clustering Methods and Distance Measures Used for Grouping Metabolic Pathways

Sarah Kim, Matthew Pena, Mark Moll, George Giannakopoulos, George Bennett and Lydia Kavraki

4. Fast NeighborNet: Improving the Speed of the Neighbor-Net Phylogenetic Network Algorithm with Multithreading and a Relaxed Search Strategy

Jacob Porter

3:30pm - 4:00pm Coffee Break



1. Compromise or optimize? The breakpoint anti-median

Caroline Larlee, Alex Brandts and David Sankoff

- 2. Repeat complexity of genomes as a means to predict the performance of short-read aligners

 Quang Tran, Shanshan Gao, Nam S. Vo and Vinhthuy Phan
- 3. Sequential and Parallel LASSO: Novel Scalable Methods for eQTL Mapping
 Anhong He, Benika Hall, Jia Wen, Yingbin Liang and Xinghua Shi
- 4. Bit-Parallel Alignment with Substitution Scoring

Joshua Loving, Elizabeth Becker and Gary Benson