

6th International Conference
on
**Bioinformatics and Computational
Biology (BICoB-2014)**

PROGRAM

March 24-26, 2014

Flamingo Hotel
Las Vegas, NV, USA

Sponsored by



International Society for
Computers and Their Applications

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Winona, MN 55987

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6th International Conference on Bioinformatics and Computational Biology (BICoB-2014)

SPONSOR

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Monday, March 24, 2014

8:00 a.m. - 4:00 p.m. **REGISTRATION – Coffee/tea/pastries – RR registration desk**

8:45 a.m. - 9:00 a.m. **WELCOME - Red Rock 7 Room**

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

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

Dr. Christopher Lee

University of California at Los Angeles, USA

Computational Experiment Planning and the Future of Big Data

Location: Red Rock 7 Room

10:00 a.m. – 10:30 a.m. COFFEE BREAK

SESSION 1A:

DATA MINING AND MACHINE LEARNING - 1

Monday, March 24 2014, 10:30 a.m. - 12:00 p.m., Lake Mead 1

Session Chair:

1. **Hierarchical Algorithm for Pattern Extraction from Biological Sequences**
Faouzi Mhamdi, Mehdi Kchouk
2. **Discovering Compounds That Activate Plant Immunity Using Machine Learning**
Takaya Yoshida, Nobutaka Kitahata, Hayato Ohwada, Kazuyuki Kuchitsu
3. **A K-means based approach for the design of Rotamer Libraries: Preliminary Results**
Sara Hernandez, Carlos Brizuela
4. **Semi-supervised Classification of Protein Sequences Using Burrows Wheeler Transformation-based Features**
Karthik Tangirala, Doina Caragea

SESSION 1B:

RNA AND DNA - 1

Monday, March 24 2014, 10:30 a.m. - 12:00 p.m., Lake Mead 2

Session Chair: -----

1. **Transcriptomic Analysis by RNA-Seq and Gene Enrichment Analysis**
Scott Nixon, Dianelys Gonzales Pena, Marcus Lawson, Robert McCusker,
Jason O'Connor, Robert Dantzer, Keith Kelley, Sandra Rodriguez-Zas

2. **A Novel 2-Dimensional Graphical Representation of DNA Sequences Using Weighted Vector Assignments**
Satoshi Mizuta, Kyohei Yamaguchi
3. **CircRNAFinder: a Tool for Identifying Circular RNAs Using RNA-Seq Data**
Xing Fu, Renyi Liu
4. **Advanced statistical analysis of RNA-seq differential gene expression profiles of animal gene-environment interactions**
Kelsey Caetano-Anolles, Scott Nixon, Sandra Rodriguez-Zas

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

SESSION 2A:

MEDICAL INFORMATICS AND APPLICATIONS

Monday, March 24 2014, 1:30 p.m. - 03:00 p.m., Lake Mead 1

Session Chair: -----

1. **C-Cell Detector: High-Throughput Data Processing Framework for the Detection and Identification of Biological Targets using Solid-State Micropores**
Abdul Hafeez, M.Mustafa Rafique, Ali R. Butt
2. **Semantics-Enabled Proactive and Targeted Dissemination of New Medical Knowledge**
Ismailcem Arpinar, Asmita Rahman, Priya Wadhwa, Lakshmish Ramaswamy, Ugur Kursuncu
3. **IN SEARCH OF OPTIMAL SPACE-FILLING CURVES FOR 3-D TO 1-D MAPPING: APPLICATION TO 3-D BRAIN MRI DATA**
Unal Sakoglu, Abdullah Arslan, Kushal Bohra, Heriberto Flores
4. **Potential Relationship Discovery Model Base on Context and Its Application in Lung Cancer Field**
Haishan Chen, Jing Lan, Xiaoxia Zhang, Xiaojiao Xu, Cui Wang, Qingqiang Wu

SESSION 2B:

GENES AND PROTEINS

Monday, March 24 2014, 1:30 p.m. - 03:00 p.m., Lake Mead 2

Session Chair: -----

1. **Analyzing Conservation Patterns and Its Influence on Identifying Protein Functional Sites**
Chun Fang, Tamotsu Noguchi, Hayato Yamana
2. **New Weighting Method of Protein Sequences for Protein Classification**
Faouzi Mhamdi, Salma Aouled, Elhaj Mohamed
3. **Predicting protein subcellular localization with reduced feature set**
Hisham Al-Mubaid, Izzat Alsmadi
4. **Understanding the impact of fractionation and dynamic exclusion on proteomics**
Cynthia Zavala, Scott Nixon, Bruce Southey, Cong Wu, Elena Romanova, Johnathan Sweedler, Sandra Rodriguez-Zas

3:00 p.m. – 3:30 p.m. Coffee Break

SESSION 3A:

BIOINFORMATICS APPLICATIONS - 1

Monday, March 24 2014, 3:30 p.m. - 05:30 p.m., Lake Mead 1

Session Chair: -----

- 1. Improved Shortest Path Edit Distance for Synonyms Identification**
Alex Rudyin, Min Song, James Geller
- 2. Evaluation of Significance Level Assignment of Database Search Programs using Monte Carlo Permutation Approach**
Malik Nadeem Akhtar, Bruce Robert Southey, Per E. Andren,
Jonathan V. Swendler, Sandra Luisa Rodriguez-Zas
- 3. Formal Analysis on Automated Model Abstractions on a System of Biochemical Reactions under Uncertainty**
Krishnendu Ghosh, John Schlipf
- 4. Impact of the Increased in the Biological Samples and Alternatives vs. Defaults Setting in the Transcripts Analysis.**
Dianelys Gonzalez-Pena, Nixon E Scott, Bruce R. Southey, Marcus A. Lawson, Robert H. McCusker, Robert Dantzer, Keith W. Kelley, Sandra L. Rodriguez-Zas
- 5. Accurate Discrimination of Outer Membrane Proteins Using Amino Acid Composition and Auto Covariance Derived From PSI-BLAST Profiles**
Lingyun Zou, Qingshan Ni

SESSION 3B:

DATA MINING AND MACHINE LEARNING - 2

Monday, March 24 2014, 3:30 p.m. - 05:00 p.m., Lake Mead 2

Session Chair: -----

- 1. Bursty Topic Detection Based on K-States Automaton Model: an Emerging Trend in Cancer Field**
Qingqiang Wu, Haibin Zhang, Qingqi Hong, Yan Zheng
- 2. Semi-supervised Self-training Approaches for Imbalanced Splice Site Datasets**
Ana Stanescu, Doina Caragea
- 3. A Probabilistic Roadmap-based Method to Model Conformational Switching of a Protein Among Many Functionally-relevant Structures**
Kevin Molloy, Amarda Shehu
- 4. Multi-Objective Optimization Techniques for Conformational Sampling in Template-Free Protein Structure Prediction**
Brian Olson, Amarda Shehu

Tuesday, March 25, 2014

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

**Dr. Maximilian M. Etschmaier
San Diego State University**

**Purposeful Systems: A Conceptual Framework for System Design, Analysis, and
Operation**

Location: Red Rock 7

10:00 a.m. – 10:30 a.m. COFFEE BREAK

SESSION 4A:

RNA AND DNA - 2

Tuesday, March 25 2014, 10:30 a.m. - 12:00 p.m., Lake Mead 1
Session Chair: -----

- 1. MITOCHONDRIAL DNA VARIATION ANALYSIS OF MENTAWAI POPULATION**
Todía Pediatama, Yoni Syukriani, Nurhalim Shahib
- 2. Decoding Methods for DNA Steganalysis**
Marc Beck, Ahmed Desoky, Eric Rouchka, Roman Yampolskiy
- 3. Evaluating Assembly Pipeline for Transcriptomes**
Natasha Pavlovikj, Sairam Behera, Kevin Begcy, Malachy Cambell,
Harkamal Walia, Jitender S Deogun
- 4. Analysis of Cancer Somatic Mutations Taking into Consideration Human Genetic Variations**
Bin He, Hanna Torkey, Azam Moosavi, Liqing Zhang

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

LOCATION: Red Rock 6

SESSION 5A:

**HIGH PERFORMANCE ALGORITHMS AND
HIGH-THROUGHPUT PROCESSING**

Tuesday, March 25 2014, 02:00 p.m. – 03:30 p.m., Lake Mead 1

Session Chair: -----

1. **Optimal Alignment of Three Sequences On A GPU**
Junjie Li, Sanjay Ranka, Sartaj Sahni
2. **Efficient Next-Generation DNA Sequencing Analysis in Hadoop**
Kareem Aggour, Dipen Sangurdekar, Vijay Kumar, Lee Newberg, Chinnappa Kodira
3. **Hybridization of Parallel Genetic Algorithm and Clustering Algorithm for Gene Expression Microarray Data Classification**
Olga Valenzuela, Ignacio Rojas
4. **Scalable Genome-Wide Discovery and Presentation of Motifs**
Marjan Trutschl, Phillip Kilgore, Urska Cvek, Rona Scott

3:30 p.m. – 4:00 p.m. Coffee Break

SESSION 6A:

BIOINFORMATICS APPLICATIONS – 2

Tuesday, March 25 2014, 04:00 p.m. – 05:30 p.m., Lake Mead 1

Session Chair: -----

1. **Explore transcription factor profiles in human pluripotent stem cells**
Jane Synnergren
2. **Vision-based Breast Self-Examination Hand Interaction Tracking using Sparse Optical Flow and Genetic Algorithm**
Melvin Cabatuan, Rey Masilang, Elmer Dadios, Laurence Gan Gim
3. **A Novel Approach to Approximate Parikh Matching for Comparing Composition in Biological Sequences**
Juan Mendivelso, Yoan Pinzon
4. **Creation of a database including a set of biological features related to protein sequences and their corresponding alignments.**
Olga Valenzuela, Ignacio Rojas

Wednesday, March 26, 2014

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

9:00 a.m. – 10:00 a.m. Tutorial

Dr. Satoshi Takahashi and Dr. Tokuro Matsuo

**University of Electro-Communications/Advanced Institute of Industrial
Technology**

Social Optimization with Computational Methods

Location: Lake Mead 1 & 2