

Second International Conference on  
Bioinformatics and Computational Biology  
(BICoB-2010)

**PROGRAM**

March 24-26, 2010

Sheraton Waikiki Hotel  
Honolulu, Hawaii USA

Sponsored by



International Society for  
Computers and Their Applications

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# Second International Conference on Bioinformatics and Computational Biology (BICoB-2010)

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**WEDNESDAY, MARCH 24, 2010**

7:30 a.m. – 5:00 p.m. CONFERENCE REGISTRATION – Ewa Room

Coffee/Tea/Pastries – Waianae Room

8:30 a.m. – 9:00 a.m. WELCOME and Opening Remarks (Kahuku Room)

Dr. Thomas Philip, CATA Program Chair  
Dr. Hisham Al-Mubaid, BICoB Program Chair

**9:00 a.m. – 10:00 a.m. - KEYNOTE ADDRESS**

**Prof. Christopher Lee**

University of California, Los Angeles

***“Mining the Structure of Biological Data through Selection Metrics”***

**Location: Kahuku Room**

10:00 a.m. – 10:30 a.m. COFFEE BREAK

**SESSION 1A:**

**MACHINE LEARNING IN BIOINFORMATICS**

Wednesday, March 24, 10:30 a.m. – 12:00 p.m., O’Ahu Room

Session Chair: Dr. Hisham Al-Mubaid, University of Houston-Clear Lake

1. **A GA based Approach for Image Shadow Removal using PCNN**  
Gh. Rezaei Rad and H. Jahani-rad (Iran University of Science and Technology, Iran)
2. **Multiple Kernel Learning for Fold Recognition**  
Huzefa Rangwala (George Mason University, USA)
3. **Iterative Split Adjustment for Building Multilabel Decision Trees**  
Aiyasha Ma and Ishwar Sethi (Oakland University, USA)

**SESSION 1B:**

**TEXT/LINGUISTIC APPLICATIONS**

Wednesday, March 24, 10:30 a.m. – 12:00 p.m., Waiialua Room

Session Chair: Dr. Jing Hu, Franklin & Marshall College

1. **Space-efficient Genome Comparisons with Compressed Full-text Indexes**  
Enno Ohlebusch and Simon Gog (University of Ulm, Germany)
2. **Specifications of Word Set in Linguistic Approach for Similarity Estimation**  
Satoshi Mizuta and Keishin Hanya (Hirosaki University, Japan)
3. **Phylogenomic Analysis Using Bayesian Congruence Measuring**  
Dazhuo Li, Eric C. Rouchka and Patrick Shafto (University of Louisville, USA)

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

**SESSION 2A:****BIOLOGICAL AND PPI NETWORKS**

Wednesday, March 24, 1:30 p.m. - 3:00 p.m., O’Ahu Room  
Session Chair: Dr. Mary M. Randolph-Gips, U. of Houston-Clear Lake

1. **GraMoFoNe: a Cytoscape Plugin for Querying Motifs without Topology in Protein-Protein Interactions networks**  
Guillaume Blin, Florian Sikora and Stéphane Vialette (Université Paris-Est, France)
2. **Biological Relevance Detection via Network Dynamic Analysis**  
Zheng Zhao, Huan Liu, Jiangxin Wang and Yung Chang (Arizona State University, USA)
3. **Metabolic Pathways Modeling using VHDL-AMS**  
Mary M. Randolph-Gips (University of Houston-Clear Lake, USA)

**SESSION 2B:****PROTEIN APPLICATIONS**

Wednesday, March 24, 1:30 p.m. - 3:00 p.m., Waialua Room  
Session Chair: Dr. Yaohang Li, North Carolina A&T State University

1. **Predicting Subcellular Localizations of Gram-negative Proteins with Improved Performance**  
Jing Hu (Franklin & Marshall College, USA)
2. **Bioinformatics Analysis of Physicochemical Properties of Protein Sorting Signals**  
Fan Zhang and Jianjun Hu (University of South Carolina, USA)
3. **Study of Computing Consolidation Techniques in Computational Protein Loop Structure Modeling**  
Yaohang Li and Douglas Wardell (North Carolina A&T State University, USA)

3:00 p.m. – 3:30 p.m.

**COFFEE BREAK**

**SESSION 3A:****BIOINFORMATICS and DISEASE RELATED TASKS**

Wednesday, March 24, 3:30 p.m. – 5:30 p.m., O’Ahu Room  
Session Chair: Dr. Hisham Al-Mubaid, U. of Houston-Clear Lake

1. **Delay Differential Models in Dynamic Diseases**  
Fathalla A. Rihan (United Arab Emirates University, UAE)
2. **Identification of Similarities among MS/MS Spectra from Human Brain**  
Alan J. Barton, Arsalan S. Haqqani and Julio J. Valdés (National Research Council Canada, Canada)
3. **On Building a Quantitative Food-Disease-Gene Network**  
Hui Yang, Abhishek Sharma, Rajesh Swaminathan and Vilas Ketkar (San Francisco State University, USA)
4. **Disease Classification using Gene Similarity and GO Annotations**  
Hisham Al-Mubaid (University of Houston-Clear Lake, USA)

**SESSION 3B:**

**DNA APPLICATIONS**

Wednesday, March 24, 3:30 p.m. – 5:00 p.m., Waialua Room  
Session Chair: Dr. Desh Ranjan, Old Dominion University

- 1. Algebraic Theory of DNA Recombination**  
Sergei R. Sverchkov (Novosibirsk State University, Russia)
- 2. DNADigest: In silico Tool for Customized Digestion of Nucleic Acid Sequences**  
Sina Vivekanandan, Avinash Panigrahi, Sunil Kumar and Randeep Singh (Philips Research Asia-Bangalore, India)
- 3. Computational and Biological Approach to Understand the 3' UTR-Mediated Posttranscriptional Regulation of Alfalfa Cytosolic Glutamine Synthetase Genes**  
Bindu Simon, Champa Sengupta-Gopalan, Pavan K. Yelavarthi (New Mexico State University, USA) and Desh Ranjan (Old Dominion University, USA)

**THURSDAY, March 25, 2010**

**8:00 a.m. – 5:15 p.m. - CONFERENCE REGISTRATION – Ewa Room  
Coffee/Tea/Pastries – Waianae Room**

**9:00 a.m. – 10:00 a.m. - KEYNOTE ADDRESS**

**Prof. Axel Timmermann  
University of Hawaii**

***“Understanding Global Warming: the Role of Supercomputers”***

**Location: Kahuku Room**

**10:00 a.m. – 10:30 a.m. COFFEE BREAK**

**SESSION 4A:**

**ALGORITHMIC TECHNIQUES with BIOINFORMATICS APPLICATIONS**

Thursday, March 25, 10:30 a.m. – 12:00 p.m., O’Ahu Room

Session Chair: Dr. Oliver Eulenstein, Iowa State University

- 1. A New Relational KMR Based Algorithm for Microsatellite Identification**  
Nahla El Zant El Kadhi (Ahlia University, Bahrain)
- 2. SMS-Forbid: An Efficient Algorithm for Simple Motif Problem**  
Tarek El Falah (University of Tunis, Tunisia and University of Rouen, France), Thierry Lacroq (University of Rouen, France) and Mourad Elloumi (University of Tunis, Tunisia)
- 3. Triplet-Supertrees constructed from Minimum Triplet Presentations**  
Max Homilius (Max-Planck-Institute for Mol. Genetics, Germany), J. Gordon Burleigh (University of Florida, USA) and Oliver Eulenstein (Iowa State University, USA)

**SESSION 4B:**

**GENE and PROTEIN APPLICATIONS**

Thursday, March 25, 10:30 a.m. – 12:00 p.m., Waiialua Room

Session Chair: Dr. Hui Yang, San Francisco State University

- 1. Scaling the Gene Duplication Problem Towards the Tree of Life**  
André Wehe (Iowa State University, USA) and J. Gordon Burleigh (University of Florida, Gainesville, USA)
- 2. Nonlinear Retention Time Shifts in nanoLC-MS Data: A Fuzzy-Evolutionary Computational Proteomics Approach**  
Alan J. Barton and Arsalan S. Haqqani (National Research Council Canada, Canada)
- 3. Folding-aware and Structure-conscious 3D Substructures in Folding Data: Identification and Applications**  
Hui Yang, Saurabh Gupte, Runtang Wang and Rahul Parte (San Francisco State University, USA)

**12:30 p.m. – 2:30 p.m. CONFERENCE LUNCHEON**

**Location: Ni’Ihau Room**

**CONFERENCE AWARDS**

**and**

**ISCA ANNUAL GENERAL ASSEMBLY**

**SESSION 5A:****RNA SEQUENCES and CLUSTERING**

Thursday, March 25, 2:30 p.m. – 4:00 p.m., O’Ahu Room  
Session Chair: Dr. Michela Taufer, University of Delaware

- 1. Clustering Micro-RNA Array Data Using an Information Fusion-Based Approach with Multiple Types of Input Data**  
Jane Synnergren, Alper Özdoğan and Björn Olsson (University of Skövde, Sweden) and Peter Sartipy (Cellartis AB, Sweden)
- 2. miRSAT & miRCDB: An Integrated MicroRNA Sequence Analysis Tool and a Cancer-Associated MicroRNA Database**  
Boya Xie, Robert Hochberg, Qin Ding and Di Wu (East Carolina University, USA)
- 3. A Dynamic Programming Algorithm for Finding the Optimal Segmentation of an RNA Sequence in Secondary Structure Predictions**  
Abel Licon, Michela Taufer (University of Delaware, USA) and Ming-Ying Leung, Kyle L. Johnson (The University of Texas at El Paso, USA)

**SESSION 5B:****DATA MINING and MACHINE LEARNING IN BIOINFORMATICS**

Thursday, March 25, 2:30 p.m. – 4:30 p.m., Waiialua Room  
Session Chair: Dr. Pengyu Hong, Brandeis University

- 1. Integrative Biomarker Discovery for Breast Cancer Metastasis from Gene Expression and Protein Interaction Data Using Error-tolerant Pattern Mining**  
Rohit Gupta, Smita Agrawal, Navneet Rao, Ze Tian, Rui Kuang, and Vipin Kumar (University of Minnesota, USA)
- 2. A Method to Identify Protein Names with Iterative Extension of Training Data Set**  
Kazunori Miyamishi, Tomonobu Ozaki and Takenao Ohkawa (Kobe University, Japan)
- 3. An Improved Model for Gene Cluster Inference**  
Xiao Yang and Srinivas Aluru (Iowa State University, USA)
- 4. Novel Morphological Phenotypes Discovery in High-Content Screens Using Underused Features**  
Chen Lin and Pengyu Hong (Brandeis University, USA), Chris Bakal (The Institute of Cancer Research London, UK), and Norbert Perrimon (Harvard Medical School, USA)

**FRIDAY, MARCH 26, 2010**

**8:00 a.m. – 10:30 a.m. CONFERENCE REGISTRATION – Coffee/Tea/Pastries  
(Waianae Room)**

**SESSION 6A:**

**TREES and GRIDS with BIOINFORMATICS APPLICATIONS**

Friday, March 26, 9:00 a.m. – 10:30 a.m., O’Ahu Room

Session Chair: Dr. Hisham Al-Mubaid, University of Houston-Clear Lake

- 1. Corrected Statistical Distance and Probability Constrained Optimization in Reconstruction of Phylogenetic Trees**  
D. A. Thomas, J. F. Weng and I. Mareels (The University of Melbourne, Australia)
- 2. A Grid-Enabled Problem Solving Environment for QTL Analysis in R**  
Mahen Jayawardena, Carl Nettelblad, Salman Zubair Toor (Uppsala University, Sweden), Per-Olov Östberg, Erik Elmroth (Umeå University, Sweden), and Sverker Holmgren (Uppsala University, Sweden)
- 3. A More Efficient Closest String Problem**  
Ruixuan Zhao (Sun Yat-Sen University, China) and Ning Zhang (University of Waterloo, Canada)