

IEEE 6TH SYMPOSIUM ON BIOINFORMATICS & BIOENGINEERING

OCT. 16 – 18, 2006.

BIBE-06 Program

Day 1: Oct. 16, 2006

08:00 am – 09:00 am Registration & Breakfast

09:00 am – 10:00 am **Keynote Speaker**

10:00 am – 12:00 noon **Session 1 : Protein Structure, Function, and Classification**

<i>IUP : Intrinsic Unstructured Protein Prediction - A Software Tool</i>	Jack Yang, Mary Yang
<i>A Language Modeling Text Mining Approach to the Annotation of Protein Community</i>	Xiaodan Zhang, Daniel Wu, Xiaohua Zhou, Xiaohua Hu
<i>Novel Efficient Granular Computing Model for Protein Sequence Motifs and Structure Information Discovery</i>	Bernard Chen, Phang C. Tai, Robert Harrison, Yi Pan
<i>On Integrating Peptide Sequence Analysis and Relational Distance-Based Indexing</i>	Weijia Xu, Rui Mao, Shu Wang, Daniel Miranker
<i>Assessing protein function using a combination of supervised and unsupervised learning</i>	Jack Yang, Mary Yang, Okan K. Ersoy

12:00 noon – 01:30 pm Lunch Break

01:30 pm – 03:30 pm **Session 2: Pattern Discovery and Data Mining**

<i>Partition Frequency Distance based Filter Method for Finding Approximate Repetitions in DNA Sequences</i>	Di Wang, Guoren Wang, Baichen Chen, Qingquan Wu, Changyong Yu, Yi Zhao, Ge Yu
<i>Finding Patterns in Biological Sequences by Longest Common Subsequences and Shortest Common Supersequences</i>	Kang Ning, Hoong Kee Ng, Hon Wai Leong
<i>Mining the Database of Transcription Binding Sites</i>	Wei Peng, Tao Li, Giri Narasimhan
<i>Extending Pattern Branching to Handle Challenging Instances</i>	Jaime Davila, Sanguthevar Rajasekaran
<i>Discovering DNA Motifs with Nucleotide Dependency</i>	Francis Chin, Henry Leung

03:30 pm – 04:00 pm Coffee Break

04:00 pm – 06:00 pm **Session 3: Microarrays**

<i>Exploratory Tools for Follow-Up Studies to Microarray Experiments</i>	Kaushik Sinha, Ruoming Jin, Gagan Agrawal, Helen Piontkivska
<i>Mining Positive and Negative Co-regulation Patterns from Microarray Data</i>	Yuhai Zhao, Guoren Wang, Ying Yin, Ge Yu
<i>Building a Classifier for Integrated Microarray Datasets through Two-Stage Approach</i>	Youngmi Yoon, Jongchan Lee, Sanghyun Park
<i>IntClust: A Software Package for Clustering Replicated Microarray Data</i>	Wei Peng, Tao Li
<i>Quick Hierarchical Biclustering on Microarray Gene Expression Data</i>	Liping Ji, Kenneth Mock, Kian-Lee Tan

Day-2: Oct. 17, 2006

08:00 am – 09:00 am Registration & Breakfast

09:00 am – 10:00 am **Keynote Speaker**10:00 am – 12:00 noon **Session 4: Sequence Alignment and Database Search**

<i>An improved algorithm for the regular expression constrained multiple sequence alignment problem</i>	Abdullah Arslan, Dan He
<i>Large Grain Size Stochastic Optimization Alignment</i>	Perry Ridge, Hyrum Carroll, Dan Sneddon, Mark Clement, Quinn Snell
<i>Sequence Homology Search Based on Database Indexing Using the Profile Hidden Markov Model</i>	Sakti Pramanik, Qiang Xue, James Cole
<i>A Tool for Supporting Integration Across Multiple Flat-File Datasets</i>	Xuan Zhang, Gagan Agrawal
<i>Simplicity in RNA Secondary Structure Alignment: Towards biologically plausible alignments</i>	Rimon Mikhael, Guohui Lin, Eleni Stroulia

12:00 noon - 01:30 pm **Lunch Break**01:30 pm – 03:30 pm **Session 5: Phylogenies, Trees, and Visualization**

<i>Improving progressive alignment for phylogeny reconstruction using parsimonious guide-trees</i>	Usman Roshan, Dennis Livesay, Satish Chikkagoudar
<i>Learning the Tree of Phenotypes Using Genomic Data and VISDA</i>	Yuanjian Feng, Zuyi Wang, Yitan Zhu, Jianhua Xuan, David Miller, Robert Clarke, Eric Hoffman, Yue Wang
<i>Visualization of DNA/RNA Structure using Temporal CGRs</i>	Margaret Dunham, Donya Quick, Yuhang Wang, Monnie McGee, Jim Waddle
<i>Isolation and Visualization of Codon Usage Biases</i>	Douglas Raiford, Dan Krane, Travis Doom, Michael Raymer
<i>Evidence of Multiple Maximum Likelihood Points for a Phylogenetic Tree</i>	B-B Zhou, M. Tarawneh, D. Chu, P. Wang, C.Wang, A. Zomaya, R.Brent
<i>Finding Correlations in Functionally Equivalent Proteins by Integrating Automated and Visual Data Exploration</i>	Daniel A. Keim, Daniela Oelke, Royal Truman, Klaus Neuhaus

03:30 pm – 04:00 pm Coffee Break

04:00 pm – 06:00 pm **Session 6: DNA & RNA Sequence and Structure**

<i>A New Kernel Method for RNA Classification</i>	Xiaoming Wu, Jason T.L. Wang, Katherine G. Herbert
<i>RADAR: An Interactive Web-Based Toolkit for RNA Data Analysis and Research</i>	Mugdha Khaladkar, Vivian Bellofatto, Jason T. L. Wang, Bin Tian, Kaizhong Zhang
<i>Parsimony based approach to test the Evolving Master Gene hypothesis for human Alu repeats</i>	Sridhar Ramachandran, Travis Doom, Michael Raymer, Dan Krane
<i>An algorithm for string edit distance allowing substring reversals</i>	Abdullah Arslan
<i>A New Hybrid Approach for Unsupervised Gene Selection</i>	Young Bun Kim, Jean Gao

Day-3: Oct. 18, 2006

08:00 am – 09:00 am Registration & Breakfast

09:00 am – 10:00 am **Keynote Speaker**10:00 am – 12:00 noon **Session 7: Clustering, Similarity Metrics, and Near Neighbor Methods**

<i>Using Gene Clustering to Identify Discriminatory Genes with Higher Classification Accuracy</i>	Zhipeng Cai, Lizhe Xu, Yi Shi, Mohammad Salavatipour, Randy Goebel, Guohui Lin
<i>Semi-Supervised Clustering Models for Clinical Risk Assessment</i>	Yongyang Huo, Francisco Azuaje, Paul McCullagh, Roy Harper
<i>Prediction of Protein Function Using Common-Neighbors in Protein-Protein Interaction Networks</i>	Chuan Lin, Daxin Jiang, Aidong Zhang
<i>Determining Molecular Similarity for Drug Discovery using the Wavelet Riemannian Metric</i>	Elinor Velasquez, Emmanuel R. Yera, Rahul Singh
<i>Assigning Schema Labels Using Ontology and Hueristics</i>	Xuan Zhang, Ruoming Jin, Gagan Agrawal

12:00 noon – 01:30 pm **Lunch Break**01:30 pm – 03:30 pm **Session 8: Regulatory and Metabolic Networks and Bioengineering I**

<i>Optimal Multi-Objective Control Method for Discrete Genetic Regulatory Networks</i>	Osman Abul, Reda Alhadj, Faruk Polat
<i>Methods for Random Modularization of Biological Networks</i>	Zachary Saul, Vladimir Filkov
<i>Efficient Modularization of Weighted Protein Interaction Networks using k-Hop Graph Reduction</i>	Young-Rae Cho, Woochang Hwang, Aidong Zhang
<i>A Computational Inference Framework for analyzing Gene Regulation Pathway using Microarray Data</i>	D-G Shin, J. Bluis, Y-A Kim, W. Krueger, R.i Nori, N. Viniconis, H-W Wang, A. Wong, D. Rowe
<i>The Automation of SIBIOS Workflow Composition</i>	Xiang Xiao, Malika Mahoui, Zina Ben Miled, Bhavna Choudhury

03:30 pm – 04:00 pm Coffee Break

04:00 pm – 06:00 pm **Session 9: Bioengineering II**

<i>Using MEDLINE as Standard Corpus for Measuring Semantic Similarity in the Biomedical Domain</i>	Hisham Al-Mubaid, Hoa A. Nguyen
<i>Leveraging Chemical Background Knowledge for the Prediction of Growth Inhibition</i>	Lothar Richter, Stefan Hechtel, Stefan Kramer
<i>A Supervised Learning Approach to Predicting Coronary Heart Disease Complications in Type 2 Diabetes Mellitus Patients</i>	Marisol Giardina, Francisco Azuaje, Paul McCullagh, Roy Harper
<i>Prediction of labor for pregnant women using high-resolution mass spectrometry data</i>	J-H Oh, J. Gao, A. Nandi, P.Gurnani, P. B.Greenwood, K.P. Rosenblatt
<i>Noninvasive Study of the Human Heart using Independent Component Analysis</i>	Yi Zhu, T-L Chen, W. Zhang, T-P Jung, J-R Duann, S. Makeig, C-K Cheng
<i>The Role of Timing in Speech Perception and Speech Production Processes and its Effects on Language Impaired Individuals</i>	Anna Esposito & Nikolaos Bourbakis
<i>Analysis of Invariant Meta-features for Learning and Understanding Disable People's Emotional Behavior Related to Their Health Conditions</i>	N. Bourbakis ,A. Esposito & D. Kavvaki

End and closing remarks