IEEE 7th BIBE Tentative Program (Subject to Change)
Harvard Medical School New Research Building
Everyday 7:00am~7:50am: On-site Registrations and Registrations pick-up

7:00am~7:50am: On-site Registrations and Registrations pick-up
Oct 14th, 2007 Sunday Morning: (Lunch Box will be delivered during the program)
Harvard Medical School New Research Building
Harvard Medical School Conference Center Amphitheater (500 attendees).
Plenary Keynote Lecturers
8:00am~8:10am: Opening Remarks by Dr. Larry Hall, President of IEEE/SMC
Welcome to the conference center at Harvard Medical by Dr. Jack Y. Yang

8:10am-9:00am Keynote Plenary Session on Integrative Biomedical Informatics. Chair: Keith Dunker

Plenary Keynote Lecturer: Dr. Brian D. Athey (University of Michigan and National Center for Integrative Biomedical Informatics)

9:00 am– 9:50am Keynote Plenary Session on Stochasticity and Networks in Genomic Data.
Chair: Jack Y. Yang
Plenary Keynote Lecturer: Dr. John Quackenbush (Harvard University)

9:50am~ 10:40am Plenary Keynote Session on Transmembrane Proteins (Tentative) Chair: Lawrence O. Hall
Plenary Keynote Lecturer: **Dr. Mary Qu Yang** (NIH and Oak Ridge, DOE)

10:40am~ 11:30am Keynote Plenary Session on Image Guided Therapy.

Chair: Xudong Huang
Plenary Keynote Lecturer: Dr. Ferenc A. Jolesz (Harvard Medical School)

11:30am-12:15am : Keynote Plenary Session on Protein Structure Prediction and Its Understanding Based on Machine Learning Methods. Chair: Georges Grinstein
Plenary Keynote Lecturer: Dr. Yi Pan (Georgia State University)

12:15am~1:00pm: Plenary Keynote Session on Statistical Analysis of nucleosome occupancy and histone modification data
Chair: Youping Deng
Plenary Keynote Speaker: Jun S. Liu (Harvard University and Massachusetts Institute of Technology)

Oct 14th, 2007 Sunday afternoon
Harvard Medical School New Research Building 3rd Floor (parallel sessions 1pm - 6pm)
Harvard Medical School Conference Center Rotunda
Cutting-Edge Research Tutorial Lectures

1:10-1:45pm Cutting-Edge Research Tutorial Session on Intrinsically Disordered Proteins in Human Diseases Biometrics Intelligent Information Systems and Applications. Chair: Yunlong Liu

Lecturer: **Dr. Vladimir N. Uversky** (Indiana University School of Medicine)

1:45pm~2:20pm Cutting-Edge Research Tutorial Session on Biometrics Intelligent Information Systems and Applications Chair: Vasile Palade (Tentative)

Lecturer: **Dr. Patrick S. Wang** (Northeastern University)

2:20pm~2:55pm Cutting Edge Research Tutorial Session on Knowledge Modeling for High Content Screening of Multimedia Biological Data Chair: Aidong Zhang (Tentative)

Lecturer: **Dr. Arif Ghafoor** (Purdue University)

2:55pm~3:30pm Cutting-Edge Research Tutorial Session on Reconstructing signal transduction from raw genomic data

Chair: Nazeih Botros(Tentative)

Lecturer: **Dr. Igor B. Zhulin** (Oak Ridge National Lab and University of Tennessee).

3:30pm~4:05pm Cutting Edge Research Tutorial Session Manipulation and Control of Friction at the Atomic Scale

Chair: Igor Zhulin

Lecture: **Dr. Yehuda Y. Braiman** (Oak Ridge National Laboratory)

4:05pm~4:40pm Cutting-Edge Research Tutorial Session on Using The Soybean Genome Database (SoyGD) To Display and Analyze a 1 Gbp genome sequences. Chair: Lonnie Welch (Tentative)

Lecturer: **Dr. David Lightfoot** (Southern Illinois University),

4:40pm~5:15pm Big Red supercomputer and HPSS archival storage system via the TeraGrid

Chair: TBA

Lecturer: **Dr. Craig Stewart**

5:15pm~5:50pm Cutting Edge Research Tutorial Session Studying co-regulation and inter-regulation of genes via eQTL mapping Chair: Stephen Wong (Tentative)

Lecturer: **Dr. Tian Zheng** (Columbia University),

Oct 14th, 2007 Sunday
Harvard Medical School New Research Building
HIM Room Workshop (Nano Medicine)
Workshop Title: “Bio-Nano-Info Integration for Personalized Medicine”
Organizers and Co-Chairs:

Professor May D. Wang, Ph.D., Georgia Institute of Technology and Emory University
http://www.bio-miblab.org
Dr. Linda Molnar, National Cancer Institute
http://nano.cancer.gov
Professor Eric Jakobsson, Ph.D. University of Illinois at Urbana-Champaign
http://www.mcb.uiuc.edu/faculty/profile/960
Workshop Schedule:
2007, Oct. 14 (Sunday), 8:30am-5:30pm, both oral session and poster session
8:00am-8:30am, Setting Up Poster, Speakers Getting Ready for Presentation

8:30am-9:00am	Linda Molnar, Ph.D. National Cancer Institute Nanobioinformatics: The Enabling Technology of Personalized Medicine
9:00am-9:30am	Shankar Subramaniam, Ph.D. University of California, San Diego Scientific Data Management
9:35am-10:05am	Chi-Ming Ho, Ph.D. University of California, Los Angeles Efficient Search for the Optimal Control of Biological Systems
10:05am-10:30am	Coffee Break
10:30am-11:00am	Eric Jakobsson, Ph.D. University of Illinois, Urbana-Champaign Towards a Functional Domain Ontology
11:05am-11:35am	Tom Deisboeck, MD, Massachusetts General Hospital Multi-scale Brain Tumor Modeling
11:35am-12:00pm	Poster-Preview
12:00pm-1:00pm	Lunch and poster viewing
1:00pm-1:25pm	Andrew Young, MD/Ph.D. Emory University /Grady Health System, Personalized Biomarker Identification and Quantification for Cancer Diagnosis
1:30pm-1:55pm	Dean Ho, Ph.D. Northwestern University Engineering Multifunctional Biologically-amenable Nanomaterials for Interfacial Therapeutic Delivery and Substrate-Based Cellular Interrogation
2:00pm-2:25pm	David Sept, Ph.D. Washington University Informatics Resource for Nanotechnology Research in Cancer Diagnostics and Therapeutics
2:30pm-2:55pm	Coffee Break
2:55pm-3:20pm	David S. Paik, Ph.D. Stanford University Toward a Nanobioinformatics Infrastructure for Nanotechnology-based Prostate Cancer Therapeutic Response
3:25pm-3:50pm	May D. Wang, Ph.D. Georgia Institute of Technology and Emory University caNanoSuite: An Integrated Bionanotechnology Information Management System for Cancer Nanoparticle Therapeutic Development
3:55pm-4:05pm	Linda Molnar, Ph.D. National Cancer Institute Closing Remarks
4:05pmpm-5:30pm	Poster Viewing

Oct 14th, 2007 Sunday
Workshop Midwest and Oak Ridge National Lab. (parallel session)
Chair: Igor Zhulin, Oak Ridge National Laboratory, DOE.

4:10pm~4:30pm 213: Lisa Furby, Ravinder Gupta, Ajay Mahajan, Jarlen Don, Tsuchin Chu, Bakul Dave and Brad Schwartz. Novel Materials for the Direct Removal of Water and Ions from the Body for Patients with Dialysis Needs
4:30pm~4:50pm 259: Min Xu and Louxin Zhang. A Robust Method for Generating Discriminative Gene Clusters
4:50pm~5:10pm 283: John Shell, Yonglian Wang and Nazeih Botros. Biological Mechanism on a Chip: Modeling and Realization of Growth Hormone Secretion Mechanism
5:10pm~5:30pm 393: George Chin, Grant Nakamura and Heidi Sofia. Graph Mining of Networks from Genome Biology
Regular session paper Part II: 6 Bioengineering D(2) – Biomedical Applications
5:30pm~5:50pm free slot
5:50pm~6:10pm 110: Courtney D. Corley, Lindsey Brown, Armin R. Mikler and Karan Singh. *Generating social networks of intimate contacts for the study of public health intervention strategies*

Oct 14th, 2007 Sunday afternoon
Harvard Medical School New Research Building
Harvard Medical School Conference Center Bray Room
Special session (Parallel Session)
Session 1 (180 min) 1pm-4:00pm
Special Session: Research in bioinformatics, neuroinformatics, and systems biology in East Asia (180 min)
Chairs: Dr. Doheon Lee, Korea Advanced Institute of Science and Technology
Dr. Sun Kim, Indiana University
Dr. Hyunsoo Kim, Georgia Institute of Technology

1:10pm~1:30pm 61 Ryo Yoshida, Kazuyuki Numata and Seiya Imoto. Computational Genome-Wide Discovery of Aberrant Splice Variations with Exon Expression Profiles
1:30pm~1:50pm 311 Tae Ho Kang, Jae Soo Yoo and Hak Yong Kim. Mining Frequent Contiguous Sequence Patterns in Biological Sequences
1:50pm~2:10pm 299 Shing-Kit Chan and Wai Lam. Efficient Methods for Biomedical Named Entity Recognition
2:10pm~2:30pm 329 Dong-Soo KAHNG, Yoonkey Nam and Doheon Lee. A Specific Purpose Neural Simulator with a Stochastic Spike Generation Model for Multi-electrode Arrays
2:30pm~2:50pm 314 Bum Ju Lee, Heon Gyu Lee and Keun Ho Ryu. Classification of Enzyme Function from Protein Sequence based on Feature Representation
2:50pm~3:10pm 309 Yunkyu Sohn and Jaeseung Jeong. Inferring Behavioral-level Circuits of Caenorhabditis elegans from the Topology of its Wiring Diagram
3:10pm~3:30pm 354 Huitao Sheng, Kishan Mehrotra, Chilukuri Mohan and Ramesh Raina. HAMMER Algorithm: Hashing with Arithmetic Modulo-4 for Motif Extraction of Regulatory Elements
3:30pm~3:50pm 122: Joerg Meyer. Histogram Transformation for Inter-Modality Image Registration

Session 2 (60 min)
Special Session: Bio-Medical Soft Computing (60 min)
Chairs: Dr. Andrew H. Sung, Dr. Srinivas Mukkamala, and Dr. Qingzhong Liu New Mexico Tech
3:50pm~4:10pm 347: Jason Bakos, Panormitis Elenis, and Jijun Tang, FPGA Acceleration of Phylogeny Reconstruction for Whole Genome Data
4:10pm~4:30pm 380: Elham Khabiri and Hisham Al-Mubaid. A Preliminary Study of Correlation between Depth and Path Length of GO Nodes with Gene Sequence Similarity

4:30pm~4:50pm 307: Siyuan Liu, Chao Liu, Chunzhe Zhao and Yu Liu. Mathematical Models and Optimization Discussions on EA System on AIDS/HIV Spread Estimating and Countermeasures Evaluating

Regular session paper Part II: 6 Bioengineering D(3) – Biomedical Applications

Chair: Dr. Patrick S. Wang, Northeastern University

4:50pm~5:10pm 398: Jingwei Zhang and Layne T. Watson. A Modified Uniformization Method for the Chemical Master Equation

5:10pm~5:30pm150: Yu-Ping Wang. Classification of Multi-color Fluorescence In Situ Hybridization (M-FISH) Images with Multi-Spectral Wavelet Representations

5:30pm~5:50pm: 339: Benedito Aguiar , Silvana Costa, Joseana Fechine and Menaka Muppa. *Feature Estimation for Vocal Fold Edema Detection Using Short-term Cepstral Analysis* (Regular Paper)

5:50pm~6:15pm: Hamid Arabnia. "Future Generation of High-Performance Computing"

7:00am~7:50am: On-site Registrations and Registrations pick-up

Oct 15th, 2007, Monday Morning (Lunch box will be delivered during the program)

Harvard Medical New Research Building

Harvard Medical School Conference Center Amphitheater (500 audiences).

Plenary Keynote Lecturers

8:00am~8:10am Greetings and Introduction to personalized medicine at Harvard Medical School and BWH.

Plenary Opening Remark Speaker: Dr. Gary Gottlieb President of BWH and Professor of Harvard Medical School

(Hosted by **Dr. Andy Baxevanis,** Deputy Scientific Director, National Human Genome Research Institute

8:10-9:00am Keynote Plenary Session on personalized medicine, bioinformatics and bioengineering, Chair: TBA

Plenary Keynote Lecturer: Dr. Steven Seltzer (Harvard University, Harvard Medical School).

9:00am~9:50am Keynote Plenary Session on Transforming Medicine: Genomics, Bioinformatics, and Human Health, Chair: Hamid Arabnia

Plenary Keynote Speaker: Dr. Andy Baxevanis (National Human Genome Research Institute, National Institutes of Health, U. S. Department of Health and Human Services)

9:50am~10:40am Opening Keynote Plenary Session on Intrinsically Disordered Proteins Predictions and Applications, Chair: Yanqing Zhang

Opening Plenary Keynote Speaker: Dr. A. Keith Dunker (Indiana University and Purdue University)

10:40am~11:25am Keynote Plenary Session on Promoter studies in the human genome: one perspective on an unfinished story, Chair: TBA

Plenary Keynote Speaker: Dr. Laura L. Elnitski (National Human Genome Research Institute, National Institutes of Health, U. S. Department of Health and Human Services)

11:25am~12:15am Keynote Plenary Session on Distributed wireless sensors on the Human Body

Distributed wireless sensors on the Human Body, Chair: Jack Y. Yang (Tentative)

Plenary Keynote Speaker: Dr. Ruzena Bajcsy (University of California, Berkeley and Member of United State National Academy of Engineering and Member of the Institute of Medicine of National Academies)

12:15pm~1:00pm: Plenary Keynote Session on Data Mining and Bioinformatics, Chair: Eric Jakobsson (Tentative)
Plenary Keynote Speaker: Tony Xiaohua Hu (Drexel University)

Oct 15th, 2007, Monday afternoon
Harvard Medical School New Research Building
Harvard Medical Conference Center 3rd Rotunda, 1:00pm-2:00pm

1:10pm-1:45pm Cutting-Edge Research Tutorial Session on Decoding Novel Genomes: From Microbiomes to the Eukaryota, Chair: Linda Monlar (Tentative)
Lecturer: Dr. Mark Borodovsky (George Institute of Technology)
1:45pm-2:35pm **Supercomputing and Applications in Medical Imaging**
Keynote Speaker: **Dr. Hamid R. Arabnia** (The University of Georgia, Georgia, USA; Editor-in-Chief, The Journal of Supercomputing (Springer); Chair, WORLDCOMP)

Oct 15th, 2007, Monday afternoon
Rotunda (2 to 7) **Workshop Mid-west and Oak Ridge National Lab. DOE** (parallel session)
Chair: Laura L. Elnitski, National Human Genome Research Institute, NIH, US DHHS.
2:10pm~2:30pm 305: Manish Paliwal, D. Gordon Allan and Peter Filip. Retrieval Analysis of a Cementless Modular Total Hip Arthroplasty Prosthesis
2:30pm~2:50pm 306: D. Gordon Allan, Manish Paliwal and Peter Filip. Trabecular Metal Patella Implanted into Soft-Tissue in a Post-Patellectomized Knee: A Case Report
2:50pm~3:10pm 323: Ying Chen, Joseph Lo and James Dobbins. A comparison between traditional shift-and-add (SAA) and point-by-point back projection (BP) -- relevance to morphology of microcalcifications for isocentric motion in Digital Breast tomosynthesis (DBT)
3:10pm~3:30pm 371: Benfano Soewito and Ning Weng. Methodology for Evaluating DNA Pattern Searching Algorithms on Multiprocessor

Break: 3:30pm - 3:35pm
Chair: Yunfeng Yang Oak Ridge National Laboratory
3:35pm~3:55pm 390: Qiang Cheng and Mehdi Zargham. An Efficient Compression Method for Multiplanar Reformulated Biomedical Images
3:55pm~4:15pm 395: Jiazheng Yuan, Michelle Mengxia Zhu, Javed Iqbal, Jack Y. Yang and David Lightfoot. A Computational Approach to Understand Arabidopsis thaliana and Soybean Resistance to Fusarium solani (Fsg) s
4:15pm~4:35pm 403: Yunfeng Yang, Michelle Mengxia Zhu, Liyou Wu and Jizhong Zhou. Biostatistical Considerations of the Use of Genomic DNA Reference in Microarrays
4:35pm~4:55pm 387: Salahuddin Mohammad Masum and Mohammed Yeasin. Dynamic Load Balancing for Mining of Molecular Substructures using Genetic Algorithm

Oct 15th, 2007, Monday afternoon
Workshop on progress toward petascale applications in bioinformatics and computational biology
Chair: Dr. Craig Stewart, Indiana University
4:55pm~5:15pm 173: Robert Henschel and Matthias S. Mueller. I/O Induced Scalability Limits of Bioinformatics Applications (Workshop on progress toward petascale applications in bioinformatics and computational biology)

5:15pm~5:35pm 204: Marek Freindorf, Matthew Jones, Jing Kong and Tom Furlani. Large-Scale QM/MM Calculations of Electronic Excitations in Yellow Protein: Toward Petascale Level of Protein Calculations (Workshop on progress toward petascale applications in bioinformatics and computational biology)

5:35pm~5:55pm 203: Jeffrey Tilson, Gloria Rendon, Mao-Feng Ger, Alan Blatecky and Eric Jakobsson. MotifNetwork: Genome-Wide Domain Analysis using Grid-enabled Workflows (Workshop on progress toward petascale applications in bioinformatics and computational biology)

5:55pm~6:15pm 70: Scott Baden, Terrence Sejnowski, Thomas Bartol and Joel Stiles. Toward Petascale Simulation of Cellular Microphysiology (Workshop on progress toward petascale applications in bioinformatics and computational biology

6:15pm~6:35pm: 237: Chengwei Li and Ruiqiang Hu. *PID Control based on BP Neural Network for the Regulation of Blood Glucose Level in Diabetics* (Regular Paper)

6:35pm~6:55pm: 145: Cesar Pichardo-Almarza, Rod Smallwood and S. A. Billings. *Spatiotemporal Analysis of an Agent-Based Model of a Colony of Keratinocytes: A First Approach for the Development of Validation Methods*

Oct 15th, 2007, Monday afternoon

Harvard Medical School New Research Building

Harvard Medical School Conference Center 216 room (1 to 6pm) (parallel session)

Regular session paper Part I: 1 Protein Structures (140 min) 1pm-3:40pm

Chairs: Drs. Vladimir N. Uversky and Marco F. Ramoni, Indiana University

1:10pm~1:30pm 79: Suk Hoon Jung, Hee-Young Hur, Desok Kim and Dong-Soo Han. *Identification of Conserved Domain Combinations in S.cerevisiae Proteins*

1:30pm~1:50pm 80: Wei Zhong, Jieyue He and Yi Pan. *Multiclass Fuzzy Clustering Support Vector Machines for Protein Local Structure Prediction*

1:50pm~2:10pm 184: Abdellali Kelil, Shengrui Wang and Ryszard Brzezinski. *A New Alignment-Independent Algorithm for Clustering Protein Sequences*

2:10pm~2:30pm 88: David John, Jacquelyn Fetrow and James Norris. *Metropolis-Hastings Algorithm and Continuous Regression for finding Next-State Models of Protein Modification using Information Scores*

2:30pm~2:50pm 71: Valerio Freschi. *Protein function prediction from interaction networks using a random walk ranking algorithm*

2:50pm~3:10pm 422: A. Keith Dunker, Christopher J. Oldfield, Jingwei Meng, Pedro Romero, Jack Y. Yang, Zoran Obradovic, and Vladimir N. Uversky: Intrinsically Disordered Protein: An Update

3:10pm~3:30pm 429: Gil Alterovitz, Eugenia Lyashenko, Michael Xiang, and Marco F. Ramoni. Linking Protein Mass with Function via Organismal Massome Networks

Break: 3:30pm - 3:35pm

Regular session paper Part I: 2 Microarray Data and Applications A (120 min) 3:35pm-5:35pm

Chairs: Dr. David Lightfoot, Southern Illinois University

3:35pm~3:55pm 158: Qiankun Zhao, Prasenjit Mitra, Dongwon Lee and Jaewoo Kang. *HICCUP: Hierarchical Clustering Based Value Imputation using Heterogeneous Gene Expression Microarray Datasets*

3:55pm~4:15pm 74: Erliang Zeng, Chengyong Yang, Tao Li and Giri Narasimhan. *On the Effectiveness of Constraints Sets in Clustering Genes*

4:15pm~4:35pm 214: Song Li. *Integrate Qualitative Biological Knowledge to build Gene Networks by Parallel Dynamic Bayesian Network Structure Learning*

4:35pm~4:55pm 94: Kerstin Koch, Stefan Schoenauer, Ivy Jansen, Jan Van den Bussche and Tomasz Burzykowski. *Finding Clusters of Positive and Negative Coregulated Genes in Gene Expression Data*

4:55pm~5:15pm 372: Noha A. Yousri, Mohamed Kamel and Mohamed Ismail. *Pattern Cores And Connectedness in Cancer Gene Expression*

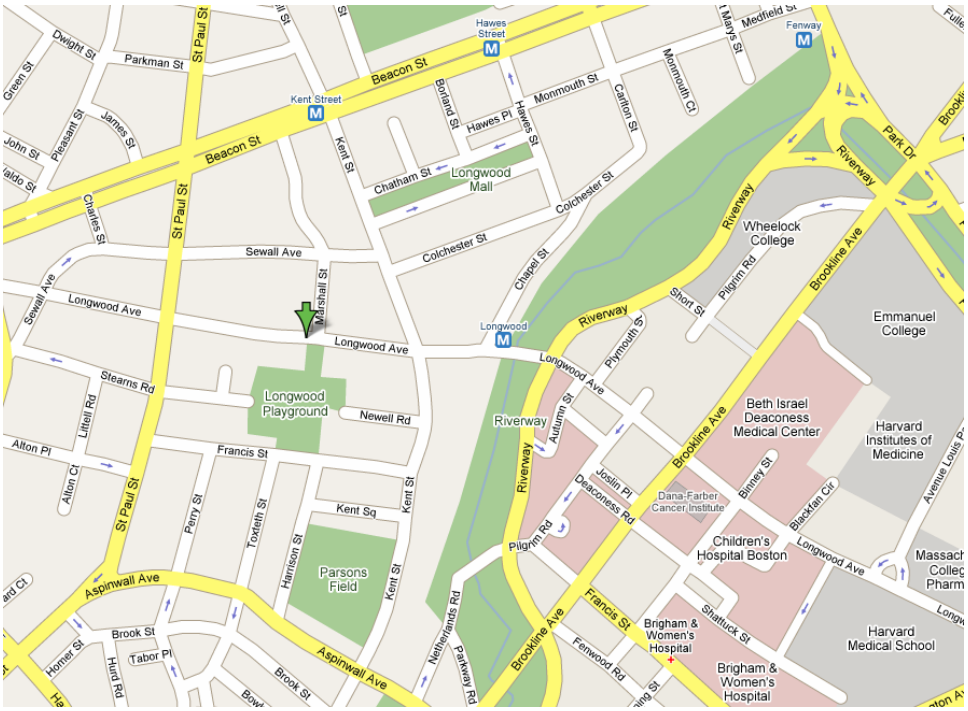
5:15pm~5:35pm 424: Peter Warren, Deanne Taylor, Jadwiga Bienkowska, Paolo Martini, Jennifer Jackson: PANP – a New Method of Gene Detection on Oligonucleotide Expression Arrays

5:35pm~5:55pm: 109: Cornelia Caragea, Jivko Sinapov, Drena Dobbs and Vasant Honavar. Assessing the Performance of Biological Sequence-Based Predictors (Regular Paper)

Oct 15th, 2007 Monday Night

6:30pm~10:00pm: Banquet at Longwood Inn hotel, 617-566-8615

123 Longwood Ave, Brookline, MA



7:00am~7:50am: On-site Registrations and Registrations pick-up

Oct 16th, 2007, Tuesday Morning three tracks:

Harvard Medical School New Research Building

Harvard Medical School Conference Center HIM (parallel session)

Regular session paper Part I: 3 Microarray Data and Applications B (120 min) 8am - 10am

Chair: Dr. Klaus Ecker, Ohio University

8:00am~8:20am 365: Rasha Kashef and Mohamed Kamel. *Cooperative Partitional-Divisive Clustering and Its Application in Gene Expression Analysis*

8:20am~8:40am 188: Chris Thachuk and Anne Condon. *On the Design of Oligos for Gene Synthesis*

8:40am~9:00am 330: Kenneth Marx, John Sharko and Georges Grinstein. *Evidence for Proximal to Distal Limb Amputation Site Effects from Global Gene Expression Correlations Found in Newt Microarrays*

9:00am~9:20am 200: Nha Nguyen, Heng Huang, Soontorn Oraintara and Yuhang Wang. *Denoising of Array-Based DNA Copy Number Data Using The Dual-tree Complex Wavelet Transform*

9:20am~9:40am 192: Brian Howard, Steffen Heber, Imara Perera, Yang Ju Im, Heike Winter-Sederoff and Beate Sick. *Quality Assessment of Affymetrix GeneChip Data using the EM Algorithm and a Naive Bayes Classifier*

9:40am~10:00am 60: Yu-Chun Lin, Hsiang-Yuan Yeh, Shih-Wu Cheng and Von-Wun Soo. *Comparing Cancer and Normal Gene Regulatory Networks Based on Microarray Data and Transcription Factor Analysis*

Break 10am~10:05am

Regular session paper Part I: 4 Microarray Data and Applications C (120 min) 10:15am-12:15pm

Chair: Dr. Chris Ding, University of Texas at Arlington

10:05am~10:25am 374: Chan Hoon Park, Soo-Jin Kim, Sun Kim, Dong-Yeon Cho and Byoung-Tak Zhang. Finding Cancer-related Gene Combinations Using a Molecular Evolutionary Algorithm

10:25am~10:45am 350: Yi Zhang, Chris Ding and Tao Li. *A Two-Stage Gene Selection Algorithm by Combining ReliefF and mRMR*

10:45am~11:05am 149: John H. Phan and May D. Wang. Estimating Classification Error to Identify Biomarkers in Time Series Expression Data

11:05am~11:25am 67: Minseo Park, Deane L. Falcone, Kil-Young Yun and Karen M. Daniels. *Detection and Prediction of Alternative Splicing within Acceptor/Donor Sites in pre-mRNA of Arabidopsis thaliana*

11:25am~11:45am 120: Jung Hun Oh, Young Bun Kim, Jean Gao, Animesh Nandi, Prem Gurnani and Kevin P. Rosenblatt. *Biomarker Selection in Alzheimer Disease using High-Resolution MALDI-TOF Data*

11:45am~12:05am 89: Fan Wang, Gagan Agrawal, Ruoming Jin and Helen Piontkivska. *SNPMiner: A Domain-Specific Deep Web Mining Tool*

Oct 16th, 2007, Tuesday Morning

Harvard Medical School New Research Building

Harvard Medical School Conference Center Bray Room (parallel session)**:**

Regular session paper Part II: 3 Bioengineering B – Biomedical Image Processing II (120 min) 8am-10am

Chair: Qiang Cheng, Southern Illinois University

8:00am~8:20am 100: Vidya Kamath, Timothy Yeatman and Steven Eschrich. Multivariate Feature Selection using Random Subspace Classifiers for Gene Expression Data (Microarray session)

8:20am~8:40am 356: Antonio Ruiz, Manuel Ujaldon, José Antonio Andrades, José Becerra, Kun Huang, Tony Pan and Joel Saltz. *The GPU on biomedical image processing for color and phenotype analysis*

8:40am~9:00am 318: Santiago Aja-Fernandez, Marcos Martin-Fernandez and Carlos Alberola-Lopez. *Tissue Identification in Ultrasound Images using Rayleigh Local Parameter Estimation*

9:00am~9:20am 117: Amirali Shayan Arani, Yi Zhu and Chung-Kuan Cheng. *Exploring Cardioneural Signal from Noninvasive ECG Measurement*

9:20am~9:40am 376: Akmal Younis, Ahmed Soliman and Nigel John. MS Lesions Detection in MRI Using Grouping Artificial Immune Networks

9:40am~10:00am 129: Hyunsoo Kim, Haesun Park and Lars Eld\'{e}n. Non-negative Tensor Factorization Based on Alternating Large-scale Non-negativity-constrained Least Squares

Break 10am~10:05am

Regular session paper Part II: 4 Bioengineering C -- Deformable and 3D Modeling (100 min) 10:15am-11:55am

Chair: Ken Marx, University of Massachusetts Lowell

10:05am~10:25am 262: Qing He, Ye duan, Judith Miles and Nicole Takahashi. *Statistical Shape Analysis of the Corpus Callosum in Subtypes of Autism*

10:25am~10:45am 408: M. Kinsy and Z. Lacroix. Storing Efficiently Bioinformatics Workflows

10:45am~11:05am 76: DERRAZ Foued, TALEB-AHMED Abdelmalik and CHIKH Azzeddine. *Improved edge map of geometrical active contour model based on coupling to anisotropic diffusion filtering*

11:05am~11:25am 171: Tarun Podder, Ivan Buzurovic, Yida Hu, James Galvin and Yan Yu. Partial transmission high-speed continuous tracking multi-leaf collimator for 4D adaptive radiation therapy
11:25am~11:45am 183: wamiq ahmed, Magdalena Jonczyk, Ali Shamsaie, Arif Ghafoor and Joseph Robinson. *Quantitative Analysis of Inter-object Spatial Relationships in Biological Images*
11:45am~12:05pm: 328: Xiao-Li Li, Jun-Xiang Lee, Bharadwaj Veeravalli, and See-Kiong Ng An HV-SVM Classifier to Infer TF-TF Interactions using Protein Domains and GO Annotations

Oct 16th, 2007, Tuesday Morning
Harvard Medical School New Research Building
Harvard Medical School Conference Center Room 214: Special Session (parallel session)
8am-9:40am
Special Session: High-throughput data analysis for genomics and proteomics) (100 min)
Chair: Dr. Jean Gao, University of Texas at Arlington
8:00am~8:20am 62: Hyung-Won Koh and Lars Hildebrand. Bottom-Up Multiple Row Addition Algorithms for the Biclustering-Problem
8:20am~8:40am 103: Hongling Wang, Alberto Segre, Yungui Huang, Jeffrey O'Connell and Veronica J. Vieland. Fast Computation of Human Genetic Linkage
8:40am~9:00am 47: Jeffrey Tilson, Gloria Rendon, Mao-Feng Ger and Eric Jakobsson. *MotifNetwork: A Grid-enabled Workflow for High-throughput Domain Analysis of Biological Sequences*
9:00am~9:20am 181: Elton Vasconcelos, Ana Pacheco, João Gouveia, Fabiana Araujo, Michely Diniz, Daniel Viana, Marcilia Costa, Rodrigo Maggioni, Raimundo Araujo-Filho, Raimundo Costa and Diana Oliveira. *Profilins, Formins and Katanins as Flagellar Proteins of Leishmania spp.: a Genome-based, Multi-Step Bioinformatics-driven Description*
9:20am~9:40am 402: afef elloumi oueslati. 3D spectrum analysis of DNA sequence: application to C. elegans genome (NP)
9:40am~10:00am: 327. Fang Zhou, Jieyue He and Wei Zhong. Mutual Information based Minimum Spanning Trees Model for Selecting Discriminative Genes (microarray session)

Break: 10:00am-10:05am
Special Session: Development of Algorithms for Solving Problems in Molecular Biology (80min)
Chairs: Dr. Saurabh Sinha, University of Illinois Urbana-Champaign
10:05am~10:25am 249: Swapnoneel Roy and Ashok Kumar Thakur. Towards Construction of Optimal Strip-Exchanging Moves
10:25am~10:45am 209: Sadaf R. Alam, Pratul K. Agarwal and Jeffery A. Kuehn, Performance Evaluation of a Scalable Molecular Dynamics Simulation Framework on a Massively-Parallel System
10:45am~11:05am 189: Fa Zhang, Lin Xu, Zhiyong Liu and Bo Yuan. Using Domain-Based Structural Ensemble to Improve Structure Modeling
11:05am~11:25am 405: Jean Gao, Phagocyte Transmigration Modeling Using System Dynamic Controls
11:25am~11:45am: 97:Elena Baralis, Elisa Ficarra, Alessandro Fiori and Enrico Macii. *Gene-Markers Representation for Microarray Data Integration* (microarray session)
11:45am~12:05pm: 340: Yinyin Yuan and Chang-Tsun Li. *Partial Mixture Model for Tight Clustering in Exploratory Gene Expression Analysis* (microarray session)

Oct 16th, 2007, Tuesday Afternoon four tracks:
Harvard Medical School New Research Building
Harvard Medical School Conference Center HIM: (parallel session)

Regular session paper Part I: 5 Bioinformatics Computational Method (140 min) 1pm-3:20pm

Chair: Alex Zelikovsky, Georgia State University

1:00pm~1:20pm 35: Dumitru Brinza and Alex Zelikovsky. *Discrete Methods for Association Search and Status Prediction in Genotype Case-Control Studies*

1:20pm~1:40pm 341: wamiq ahmed, Bulent Bayraktar, Arun Bhunia, E Hirleman, J Robinson and Bartek Rajwa. *Rapid detection and classification of bacterial contamination using grid computing*

1:40pm~2:00pm 174: Sadaf R Alam, Nikhil Bhatia and Jeffrey S Vetter. *Sensitivity Analysis of Biomolecular Simulations using Symbolic Models*

2:00pm~2:20pm 139: Lisa Guntly, Jennifer Leopold and Anne Maglia. Determining Domain Similarity and Domain-Protein Similarity Using Functional Similarity Measurements of Gene Ontology Terms

2:20pm~2:40pm ??

2:40pm~3:00pm 194: Sihui Zhao, Jihye Kim and Steffen Heber. Large-scale Discovery of Regulatory Motifs Involved in Alternative Splicing

3:00pm~3:20pm 101: Douglas Raiford, Dan Krane, Travis Doom and Michael Raymer. A Multi-Objective Genetic Algorithm that Employs a Hybrid Approach for Isolating Codon Usage Bias Indicative of Translational Efficiency

Break: 3:20pm - 3:25pm

Regular session paper Part I: 6 Biomedical Engineering (160 min) 3:25pm-6:15pm

Chair: Li Shen, Indiana University School of Medicine

3:25pm~3:45pm 77: Vishnu Mallapragada, Nilanjan Sarkar and Tarun K. Podder. *A Robotic System for Real-time Tumor Manipulation During Image Guided Breast Biopsy*

3:45pm~4:05pm 81: Li Shen, Andrew J. Saykin, Moo K. Chung and Heng Huang. *Morphometric Analysis of Hippocampal Shape in Mild Cognitive Impairment: An Imaging Genetics Study*

4:05pm~4:25pm 132: Serdar Bozdag, Stefano Lonardi and Timothy Close. *A Compartmentalized Approach to the Assembly of Physical Maps*

4:25pm~4:45pm 221: LELIN ZHANG, Hongkai Xiong, Kai Zhang and Xiaobo Zhou. *Graph Theory Application in Cell Nucleus Segmentation, Tracking and Identification*

4:45pm~5:05pm 33: Walker Land. *An End-to-End Process for Cancer Identification from Images of Lung Tissue.*

5:05pm~5:25pm 115: Bin Wang, Jianhua Xuan, Matthew T. Freedman, Peter G. Shields and Yue Wang. Rat Mammary Fat Pad Segmentation and Growth Rate Evaluation in T1 Weighted MRI Images

5:25pm~5:45pm 208: Kai Zhang, Hongkai Xiong, Xiaobo Zhou and Stephen Wong. *A Simulation-Based 3D Axon Axis Extraction in Confocal Fluorescence Microscopy Images* (Regular Paper)

5:45pm~6:05pm Zhuangli Liang, Synho Do, Clem Karl, Udo Hoffmann, Thomas Brady and Homer Pien. Calcium De-blooming in Coronary CT Images

6:05pm~6:25pm 413: Mehdi Pirooznia, Arun Rawat, Jack Yang, Mary Qu Yang, Edward J. Perkins, Youping Deng. An effective Interwoven Loop Design Application for Two-Channel Microarray Experiments

Oct 16th, 2007, Tuesday Afternoon

Harvard Medical School New Research Building

Harvard Medical School Conference Center Bray Room: (parallel session) (1pm to 4pm)

Regular session paper Part II: 5 Sequence (140 min) 1pm-3:20pm

Chair: Jouline, Igor B, Oak Ridge National Laboratory

1:00pm~1:20pm 378: Hongwei Huo and Vojislav Stojkovic. *A Suffix Tree Construction Algorithm for DNA Sequences*

1:20pm~1:40pm 244: Viktor Martyanov, Larkin Elderon, Amy Gladfelter, Dhanalakshmi Nair and Robert H. Gross. Identifying Fungal Regulatory Motif Patterns Using SCOPE, an Ensemble Learning Method Motif Finder

1:40pm~2:00pm 55: Tieming Ji, Desh Ranjan, Jeanne Curry and Mary O'Connell. Computational Identification of Cis-regulatory Elements Associated with Pungency of Chili Peppers

2:00pm~2:20pm 241: Yong Gao and Michael Henderson. Speeding Up Pairwise Sequence Alignments: A Scoring Scheme Reweighting Based Approach

2:20pm~2:40pm 186: Antonio de la Serna. Differential Scoring for Systolic Sequence Alignment

2:40pm~3:00pm 157: Paul Dan Cristea, Rudi Deklerck, Jan Cornelis, Rodica Tuduce, Iulian Nastac and Marius Andrei. Signal Representation and Processing of Nucleotide Sequences

3:00pm~3:20pm 114: Dan He, Abdullah N Arslan, Yu He and Xindong Wu. Iterative Refinement of Repeat Sequence Specification Using Constrained Pattern Matching

Break: 3:20pm - 3:25pm

Regular session paper Part II: 6 Bioengineering D – Biomedical Applications (120 min) 3:35pm-4:05pm(rest moved to Sunday)

Chair: Walker Land

3:25pm~3:45pm 338: Yong-Jie Ni, Chan-Hyun Youn, Byoung-Jin Kim, Young-Joo Han and Chang-Hee Han. *A PQRM-based PACS System for Advanced Medical Services under Grid Environment*

3:45pm~4:05pm 363: Sung-Huai Hsieh, Sheau-Ling Hsieh, Yung-Ching Weng, Tzuh-siang Yang, FeiPei Lai, P.H. Cheng, X.O. Ping, C.H. Peng, K.L. Ko, M.Y. Jan and L.W. Chiang. *Middleware based Inpatient Healthcare Information System*

4:05pm~4:25pm 6:597: Guo-Zheng Li, Jack Y. Yang, and Mary Qu Yang Support Vector Regression with Feature Selection for the Multivariate Calibration of Spectrofluorimetric Determination of Aromatic Amino Acids

Oct 16th, 2007, Tuesday Afternoon

Harvard Medical School New Research Building

Harvard Medical School Conference Center Room 214 :

Special Session (parallel session)

1pm-3:20pm

Special Session: Evolutionary Systems Biology (140 min)

Chairs: Dr. Xun Gu, Iowa State University

Dr. Yufeng Wang, The University of Texas at San Antonio

1:00pm~1:20pm Wen Zhou, Tian Xia, Jiansong Tong, Julie Dickerson, Bo Su and Xun Gu. Modeling protein interaction network and mechanisms in exocytosis

1:20pm~1:40pm Wenhai Chen, Tian Xia, Tianzi Jiang and Xun Gu. Toward a Realistic Model for Gene Network Evolution

1:40pm~2:00pm Pan Du, Haihui Wang, Simon Lin and Warren Kibbe. Application of Wavelet Transform to the MS-based Proteomics Data Preprocessing

2:00pm~2:20pm Jennifer Neary, Maribel Sanchez, Timothy Lilburn and Yufeng Wang. Pathway Complements of Four Yersinia

2:20pm~2:40pm zhang yi and Yanchun Liang. An Improved Ant Colony Optimization Algorithm Based on Route Optimization and Its Applications to Solving Travelling Salesman Problem

2:40pm~3:00pm James Courage, Saurabh Gupta and Yufeng Wang. Characterization of MYC expression in gefitinib versus Acute Myeloid Leukemia reveals novel therapeutic targets

3:00pm~3:20pm Misha Rajaram, Vladimir N. Minin, Marc A. Suchard and Karin Dorman. Hot and Cold: Spatial Fluctuation in HIV-1 Recombination Rates

Break: 3:20pm - 3:25pm

3:25pm-5:25pm

Special Session: DNA Microarray Data Analysis **(120min)**

Chair: Dr. Heng Huang, University of Texas at Arlington

3:25pm~3:45pm 146 Kenneth Bryan and Padraig Cunningham BALBOA: Extending Bicluster Analysis to Classify ORFs using Expression Data

3:45pm~4:05pm 170 Zhenyu Wang and Vasile Palade A Comprehensive Fuzzy-Based Framework for Cancer Microarray Data Gene Expression Analysis

4:05pm~4:25pm 187 Ángela Blanco, Manuel Martín-Merino and Javier De Las Rivas Ensemble of Support Vector Machines to Improve the Cancer Prediction Based on the Gene Expression Profiles

4:25pm~4:45pm 198 Teng Li and Laiwan Chan Mining Order Preserving Patterns in Microarray data by Finding Frequent Orders

4:45pm~5:05pm 382 Nha Nguyen, Heng Huang, Soontorn Oraintara and An Vo A New Smoothing Model for Analyzing Array CGH Data

5:05pm~5:25pm 385: Sheehyun Kim and Dongsup Kim. Inference of Gene Regulatory Networks Using Time Sliding Comparison and Transcriptional Lagging Time from Time Series Gene Expression Profiles

5:25pm~5:45pm: 414: Jack Y. Yang, Mary Qu Yang, Andrzej Niemierko, and Youping Deng. Non-Monotonic Radio-Sensitivity over Tumor Volumes on Adjuvant Radio Therapy

5:45pm~6:05pm: 166 Hyunsoo Kim, Haesun Park and Hongyuan Zha Distance Preserving Dimension Reduction Using the QR Factorization or the Cholesky Factorization

Oct 16th, 2007, Tuesday Afternoon

Harvard Medical School New Research Building

Harvard Medical School Conference Center Rotunda:

Special Session (parallel session) **1pm-3:20pm**

Special Session: Sequence Alignment and Phylogenetic Analysis (140 min)

Chair: Mark Clement, Brigham Young University

1:00pm~1:20pm 119: Kenneth Sundberg, Timothy O'Connor, Hyrum Carroll, Mark Clement and Quinn Snell. Using Parsimony to Guide Maximum Likelihood Searches

1:20pm~1:40pm 36: Xu Zhang and Tamer Kahveci. QOMA2: Optimizing the alignment of many sequences

1:40pm~2:00pm 24: Ken Nguyen and Yi Pan. A Reliable Metric for Quantifying Multiple Sequence Alignment

2:00pm~2:20pm 40: Ahmet Sacan and I. Hakki Toroslu. Amino acid substitution matrices based on 4-body Delaunay contact profiles

2:20pm~2:40pm 107 Feng Yue, Meng Zhang and Jijun Tang. A Heuristic for Phylogenetic Reconstruction Using Transposition

2:40pm~3:00pm 357: Abdullah N Arslan and Peyman Bizargity. Phylogeny By Top Down Clustering Using a Given Multiple Alignment

3:00pm~3:20pm 366: Patricia Buendia. Reconstructing Mutational Pathways from Serial Evolutionary Trees

Break: 3:20pm - 3:25pm

3:25pm-5:45pm

Special Session: Bio-Complexity (80 min)

Chairs: Drs. Matthias Dehmer, Frank Emmert-Streib University of Washington

3:25pm~3:45pm 312: ICHIM LORETTA and Radu Dobrescu. Fractal Dimension of Mie Scattering Spectra for the Appraisal of Infected HeLa Cells in Cultures

3:45pm~4:05pm 155: Jiejun Kong, Xiaoyan Hong, Dapeng Oliver Wu and Mario Gerla. Complexity-theoretic Modeling of Biological Cyanide Poisoning as Security Attack in Self-organizing Networks

4:05pm~4:25pm 43: Alessandro Abate, Yu Bai, Nathalie Sznajder, Carolyn Talcott and Ashish Tiwari. Quantitative and Probabilistic Modeling in Pathway Logic

4:25pm~4:45pm 268: Dimitrios Dakopoulos, Sanjay K**.** Boddhu and Nikolaos Bourbakis A 2D Vibration Array as an Assistive Device for Visually Impaired

Special Session: Pattern Recognition and Gene Discovery in Molecular Genetics (60min)

Chair**:** Sridhar Ramachandran, Wright State University

4:45pm~5:15pm ??

5:15m~5:35pm 294: Vandana Gummuluru and su-shing chen. An Intelligent System for Searching Genomic Sequences

5:35pm~5:55pm 369: Michael Blinov and Ion Moraru. *XML Encoding of Features Describing Rule-Based Modeling of Reaction Networks with Multi-Component Molecular Complexes*

5:55pm~6:15pm: 346: Krzysztof Malczewski and Ryszard Stasinski. HIGH RESOLUTION MRI IMAGE RECONSTRUCTION FROM A PROPELLER DATA SET OF SAMPLES

7:00am~7:50am: On-site Registrations and Registrations pick-up

Social Event: Museum of Fine Arts Boston http://www.mfa.org/ It is within walking distance from HMS and Free admission from 4pm–9:45 pm. If you need guidance, please ask at our registration desk.

Oct 17th, 2007, Wednesday morning three tracks:

Harvard Medical School New Research Building

Harvard Medical School Conference Center 214 Room: (parallel session)

Regular session paper Part I: 7: Sequence (120 min) 8am-10am

Chair: Dr. Jason T.L. Wang, New Jersey Institute of Technology

8:00am~8:20am 41: Xiaoyong Fang, Zhigang Luo, Bo Yuan and Zhenghua Wang. *Detecting and Assessing Conserved Stems for Accurate Structural Alignment of RNA Sequences*

8:20am~8:40am 353: Shibin Qiu and Terran Lane. *The RNA String Kernel for siRNA Efficacy Prediction*

8:40am~9:00am 86: Stephanie Jimenez Irausquin and Liangjiang Wang. *A Machine Learning Approach for Prediction of Lipid-Interacting Residues in Amino Acid Sequences*

9:00am~9:20am 140: Marina Barsky, Ulrike Stege, Alex Thomo and Chris Upton. Shortest Path Approaches for the Longest Common Subsequence of a Set of Strings

9:20am~9:40am 32: Jason Wang. *Constrained RNA Structural Alignment: Algorithms and Applications to Motif Detection in the Untranslated Regions of Trypanosoma Brucei mRNAs*

9:40am~10:00am 99: Huiru Zheng, Haiying Wang and Jinglu Hu. Clustering Analysis of Regulatory Sequences with a Log Likelihood Ratio Statistics-based Similarity Measure (short paper)

Break 10am~10:05am

Regular session paper Part I: 8 System Biology (100 min) 10:15am-11:55am

Chair: Gil Alterovitz MIT/Harvard

10:05am~10:25am 45: Young-Rae Cho, Woochang Hwang and Aidong Zhang. *Optimizing Flow-based Modularization by Iterative Centroid Search in Protein Interaction Networks*

10:25am~10:45am 383: Qiong Cheng, Alex Zelikovsky and Robert Harrison. *Optimal Homomorphic Mapping of a Multisource Tree to Digraph: Application to Metabolic Pathways*

10:45am~11:05am 112: Melissa Freedenberg, Chanchala Kaddi, Chang Quo and May D. Wang. Review of Systems Biology Simulation Tools for Translational Research

11:05am~11:25am 364: Juliette Blanchet and Matthieu Vignes. *Combined expression data with missing values and gene interaction network analysis: a Markovian integrated approach*

11:25am~11:45am 185: Gil Alterovitz, Taro Muso, Paresh Malalur and Marco Ramoni. A Systematic Approach to Quantifying Evolutionary Functional Trends Across the Universal Tree of Life

11:45am~12:05pm: 50: Yuhang Wang, Siling Wang and Andrew R. Zinn. *rSWTi: A Robust Stationary Wavelet Denoising Method for Array CGH Data* (microarray session)

Oct 17th, 2007, Wednesday morning

Harvard Medical School New Research Building

Harvard Medical School Conference Center 216 Room: (parallel session)

Regular session paper Part II: 7 Algorithms in Bioinformatics (120 min) 8am-10am

Chair: Mohammed Yeasin, University of Memphis

8:00am~8:30am

: Keynote Session on Metallobiochemistry of Alzheimer's Disease and Its Theranostic Agent Development

Plenary Keynote Lecturer: Dr. Xudong Huang (Harvard University, Harvard Medical School and Brigham and Women's Hospital, and Massachusetts Institute of Technology)

8:30am~8:50am

Ingenuity Talk

Deborah Riley, Karma Carrier, Ingenuity Pathways Analysis: enabling biologists to understand microarray, toxicogenomic, proteomic and metabolomics data and to facilitate biomarker discovery.

8:50am~9:10am 154: Juan Shan, yuxuan wang and Changhui Yan. Toward the recognition code of protein-DNA recognition

9:10am~9:30am 384: Dragos Trinca and Sanguthevar Rajasekaran. Self-Optimizing Parallel Algorithms for Haplotype Reconstruction and Their Evaluation on the JPT and CHB Genotype Data

9:30am~9:50am 373: Xiaolu Huang and Hesham Ali. Reducing folding scenario candidates in pseudoknots detection using highly sensitive PLMM_DPSS algorithm integrated with energy filters

9:50am~10:10am 377: Paulius Micikevicius and Narsingh Deo. Exploring Topological Properties of NMR Graphs

10:10am~10:30am 355: Jahangheer Shaik, George Ebenezer and Mohammed Yeasin. An Empirical CDF Approach to Estimate the Significance of Gene Ranking for Finding Differentially Expressed Genes (workshop Midwest)

Break 10:30am~10:35am

Regular session paper Part II: 8 Biological Networks (100 min) 10:15am-11:55am

Chair: Dr. Reda Alhajj, University of Calgary

10:35am~10:55am 28: Rui Chang. Consistent Modeling, Integration and Simulation of Molecular Interaction Networks in Space-Time Dimension

10:55am~11:15am 113: Reda Alhajj. Feature Reduction for Gene Regulatory Network Control

11:15am~11:35am 118: Martin Samuel Rao Paradesi, Doina Caragea and William H. Hsu. Structural Prediction of Protein-Protein Interactions in Saccharomyces cerevisiae

11:35am~11:55am 172: Mohieddine MISSAOUI, Cécile Militon, David HILL and Pierre PEYRET. Complete Backtranslation of Oligopeptides for Metabolic Pathways exploration of Complex Environments using Functional Microarrays

11:55am~12:15pm 345: Kazuyuki Numata, Seiya Imoto and Satoru Miyano. *A Structure Learning Algorithm for Inference of Gene Networks from Microarray Gene Expression Data Using Bayesian Networks*

12:15pm~12:35pm: 65: Yu-ting Huang, Shih-Fang Lin, Chung-Cheng Chiu, Hsiang-Yuan Yeh and Von-Wun Soo. Probability Analysis on Associations of Statistical Modeling for the Adverse Drug Events with Drug-Drug Interactions

Oct 17th, 2007, Wednesday morning

Fenway Room. Longwood Inn at Harvard Medical Campus (tentative place): (parallel session)

8am-9:40am

Special Session: Computational Intelligence in Medical Informatics (100 min)

Chairs: Dr. Jijun Tang, University of South Carolina

Dr. Jianlin Chen University of Missouri

8:00am~8:20am 38: Jacqueline Signorini and Patrick Greussay. Silent Killing: an Object-Oriented View of Hypertension and Kidney Failures - Part I

8:20am~8:40am 217: Wei Liu, Weidong Xu and Lihua Li. Medical Image Retrieval Based on Bidimensional Empirical Mode Decomposition

8:40am~9:00am 220: Jun Kong, Wenjing Lu, Yinghua Lu, Jianzhong Wang and Na Che. A Modified Fuzzy Kohonen's Competitive Learning Algorithms Incorporating

9:00am~9:20am 264: Siyuan Liu, Chao Liu, Chunzhe Zhao and Yu Liu. An Efficient Modeling and Simulation System on the Kidney Matching, Distribution and Exchange Problems

9:20am~9:40am 510 Welch Lonnie SiteSeeker – A Motif Discovery Tool (NP)

Special Session: Machine Learning Methods in Structural and Functional Genomics (100min)

Chair: Dr. Rui Kuang, University of Minnesota

9:40am~10:00am: 96: Leonardo Bobadilla, Fernando Nino, Edilberto Cepeda and Manuel Patarroyo. Characterizing and Predicting Catalytic Residues in Enzyme Active Sites Based on Local Properties. A Machine Learning Approach.

Break 10:00am~10:05am

10:05am-11:45am

10:05am~10:25am 196: Tapan Patel and Li Liao. Predicting Protein-Protein Interaction based on Fisher Scores Extracted from Domain Profiles

10:25am~10:45am 261: Majid Masso and Iosif Vaisman. A Novel Sequence-Structure Approach for Accurate Prediction of Resistance to HIV-1 Protease Inhibitors

Oct 17th, 2007, Wednesday afternoon two tracks:

Harvard Medical School New Research Building

Harvard Medical School Conference Center 214 Room:

Regular session paper Part I: 9 Sequence and Structure (140 min) 1pm-3:20pm

Chair: Dr. Chris Bailey-Kellogg, Dartmouth College

1:00pm~1:20pm 304: Bernard Chen, Stephen Pellicer, Phang C. Tai, Robert Harrison and Yi Pan. *Super Granular SVM Feature Elimination (Super GSVM-FE) Model for Protein Sequence Motif Information Extraction*

1:20pm~1:40pm 295: Gaofeng Huang and Peter Jeavons. *A Geometrical Model for the SNP Motif Identification Problem*

1:40pm~2:00pm 90: Fei Xiong and Chris Bailey-Kellogg. *A Hierarchical Grow-and-Match Algorithm for Backbone Resonance Assignment Given 3D Structure*

2:00pm~2:20pm 375: Xiang Chen, Si-Min He, Dong-Bo Bu, Run-Sheng Chen and Wen Gao. *A Flexible Stem-Based Local Search Algorithm for Predicting RNA Secondary Structures Including Pseudoknots*

2:20pm~2:40pm 325: Yu-Feng Huang, Yu-Shing Lin, Tian-Wei Hsu and Chien-Kang Huang. *Mining Conserved Structure of Enzymes from Functional Hierarchical Classification*

2:40pm~3:00pm 381: Kreshna Gopal, James Sacchettini and Thomas Ioerger. *Database Approaches and Data Representation in Structural Bioinformatics*

3:00pm~3:20pm 288: Tapani Utriainen and Graham Kemp. Using long fragments to reconstruct RNA backbones (short paper)

Break: 3:20pm - 3:25pm

Regular session paper Part I: 10 Bioinformatics Applications (140 min) 3:35pm-5:55pm

Chair: Dr. Siyuan Liu, Institute of Computing Technology, Chinese Academy of Sciences

3:25pm~3:45pm 324: Jung Hoon Woo, Tian Zheng and Ju Han Kim. *Identifying genomic regulators of set-wise co-expression*

3:45pm~4:05pm 105: Mingwu Zhang, Daisuke Kihara and Sunil Prabhakar. *Tracing Lineage in Multi-version Scientific Databases*

4:05pm~4:25pm 342: Kenneth Marx, ML Ujwal and Patrick Hoffman. A Machine Learning Approach to Pharmacological Profiling of the Quinone Scaffold in the NCI Database: Effective Against Melanoma and Leukemia Cell Lines

4:25pm~4:45pm 108: N. Yacoubi and Z. Lacroix. Resolving Scientific Service Interoperability With Schema Mapping

4:45pm~5:05pm 106: Eric R. Muir, Ibrahima J. Ndiour, Nolwenn A. Le Goasduff, Richard A. Moffitt, Ying Liu, M. Cameron Sullards, Alfred H. Merrill, Jr., Yanfeng Chen and May D. Wang. Multivariate Analysis of Imaging Mass Spectrometry Data

5:05pm~5:25pm 48: wen-ran zhang and Karl Peace. MentalSquares - An Equilibrium-Based System for Bipolar Neurobiological Pattern Classification and Analysis

5:25pm~5:45pm 303: FangXiang Wu and Jiarui Ding. A Framework for Mass Spectral Quality Assessment Without Prior Information

5:45pm~6:05pm: 102: Benjamin Kelly, Paul Anderson, Nicholas Reo, Nicholas DelRaso, Travis Doom and Michael Raymer. A Proposed Statistical Protocol for the Analysis of Metabolic Toxicological Data Derived from NMR Spectroscopy

Oct 17th, 2007, Wednesday afternoon

Harvard Medical School New Research Building

Harvard Medical School Conference Center 216 Room:

Regular session paper Part II: 9 Bioinformatics tools (140 min) 1pm-3:20pm

Chair: TBA

1:00pm~1:20pm 267: Jay Urbain, Nazli Goharian and Ophir Frieder. *Combining Semantics, Context, and Statistical Evidence in Genomics Literature Search*

1:20pm~1:40pm 82: Fan Wang, Gagan Agrawal, Ruoming Jin and Helen Piontkivska. *Graph and Topological Structure Mining on Scientific Articles*

1:40pm~2:00pm 293: Chen Lin, Wayne Mak, Pengyu Hong, Katharine Sepp and Norbert Perrimon. *Intelligent Interfaces for Mining Large-Scale RNAi-HCS Image Databases*

2:00pm~2:20pm 331: Neha Nahar, Lutz Hamel, Maria Poptsova and J. Peter Gogarten. *GPX: A Tool for the Exploration and Visualization of Genome Evolution*

2:20pm~2:40pm 358: Tom Milledge, Gaolin Zheng, Tim Mullins and Giri Narasimhan. SBLAST: Structural Basic Local Alignment Searching Tools using Geometric Hashing

2:40pm~3:00pm 168: Anuradha Roy, Jennifer Leopold and Anne Maglia. Alternative Splicing: Associating Frequency with Isoforms

3:00pm~3:20pm 179: Enis Afgan and Purushotham Bangalore. Performance Characterization of BLAST for the Grid

Break: 3:20pm - 3:25pm

Regular session paper Part II: 10 Protein (140 min) 3:35pm-5:55pm

Chair: TBA

3:25pm~3:45pm 30: Mudassir Fayyaz, Adnan Mujahid and Asifullah Khan Khan. G-protein Coupled Receptor Subfamilies Prediction Based on Nearest Neighbor Approach

3:45pm~4:05pm 344: Ionut Bebu, Francoise Seillier-Moiseiwitsch and Hongfang Liu. Semiparametric RMA Background-Correction for Oligonucleotide Arrays

4:05pm~4:25pm 68: Fiona Browne, Haiying Wang, Huiru Zheng and Francisco Azuaje. Supervised Statistical and Machine Learning Approaches to Inferring Pairwise and Module-Based Protein Interaction Networks

4:25pm~4:45pm 153: Jing Hu and Changhui Yan. Predicting Protein Subcelluar Localizations Using Weighted Euclidian Distance

4:45pm~5:05pm 51: Alireza Hadj Khodabakhshi, Mahdi Mirzazadeh and Arvind Gupta. An efficient data structure for applying multiple seeds in homology search

5:05pm~5:25pm 176: Ian MacDonald and George Berg. A Mixture of Experts Method for Predicting Domain Boundaries in Proteins

5:25pm~5:45pm 111: woochang Hwang, Taehyoung Kim, Young-Rae Cho, Aidong Zhang and Murali Ramanathan. SIGN: reliable protein interaction identification by integrating the Similarity In GO and the similarity in protein interaction Networks

5:45pm~6:05pm 141: Anjum Reyaz-Ahmed and Yanqing Zhang. Protein Secondary Structure Prediction Using Genetic Neural Support Vector Machines