Program (Preliminary)

- 03 October 2012
- 04 October 2012
- 05 October 2012
- 06 October 2012
- 07 October 2012

Keynote Lecture: 60 minutes((about 45 minutes for talk and 15 minutes for Q and A)
Invited Talk: 40 minutes (about 30 minutes for talk and 10 minutes for Q and A)
Main conference regular Paper: 25 minutes (about 20 minutes for talk and 5 minutes for Q and A)
Main conference short Paper: 20 minutes (about 16 minutes for talk and 4 minutes for Q and A)

03-Oct

4:00pm-20:30pm	Registration: **TBD**

04-Oct

08:00am-6:00pm	Registration: **TBD**
Venue:	*The ground floor of the conference venue*

08:30-12:30	Workshop 12	Workshop 2	Workshop 4	Workshop 5	Workshop 13	Workshop 11	Workshop 8	Tutorial 1
Session Chair:	Taesung Park	Jing He A. Shehu N. Hapel Brian Chen	Young Cho Pietro Guzzi	D. Cameron A. Sheth O. Bodenreider	Kaizhi Tang Xiong Liu	Illhoi Yoo	Rui Jiang Jane Zheng Zhongming Zhang	Jun Huan
Venue:	*TBD* *xxx*	*TBD*	*TBD* *xxx*	TBD xxx	*TBD*	*TBD*	*TBD*	*TBD* *xxx*

12:30-13:30 Lunch

Coffee: 10:00 – 10:20

Set up Poster Session (the poster authors could start their poster set-up and the posters will be displayed until Oct 7)

13:30-18:00	Industrial Session 1	Workshop 2	Workshop 3	Workshop 7	Workshop 10	Workshop 11	Workshop 8	Tutorial 2
Session Chair:	Anastasia Christianson Michael Liebman	Jing He A.Shehu N. Hapel Brian Chen	S. Kim L. Chen K. Horimoto	Dong Xu Guozheng Li Z. Liang	Dongxiao Zhu Steve Qin	Illhoi Yoo	Rui Jiang Jane Zheng Zhongming Zhang	Jalel Akaichi
Venue:	*TBD*	*TBD*	*TBD*	TBD	*TBD*	*TBD*	*TBD*	

Coffee: 16:00-16:20

05-Oct

08:00am-6:00pm	Registration: **TBD**
Venue:	*The ground floor of the conference venue*

08:15-8:45

Opening and Welcoming Speech:
Conference co-Chairs:
Lyle Ungar (University of Pennsylvania, USA)
Cathy Wu (University of Delaware, USA)
Program co-Chairs:
Jean Gao (University of Texas at Arlington, USA)
Reda Alhaij (University of Calgary, Canada)
Werner Dubitzky (University of Ulster, UK)
Industry Program co-Chairs:
Anastasia Christianson (AstraZenica, USA)
Michael Lieban (Strategic Medicine Inc., USA)
BIBM Steering Committee Chair:
Xiaohua Tony Hu (Drexel University)

Venue: *TBD*

8:45-9:45 Session Chair: Lyle Ungar

Keynote Lecture 1: The CellOrganizer Project: An Open Source System to Learn Image-derived Models of Subcellular Organization over Time and Space

	Dr. Robert Murphy, Lane Center for Computational Biology and Department of Biological Sciences, Carnegie Mellon University, USA				
Venue:	*TBD*				
9:45-10:05	Coffee				
10:05-12:00	Session 1	Session 2	Session 3	Industrial Workshop 1	Tutorial 3
Session Chair:	TBD	TBD	TBD	David Fenske Michael Liebman	Illhoi Yoo
Venue	*TBD*	*TBD*	*TBD*	*TBD*	*TBD*
12:00-13:15	Lunch Poster Session				
13:15-14:15	Session Chair: Cathy Wu Keynote Lecture 2: Protein 3D structure from genomic sequences and application to cancer genomics Dr. Chris Sander, Chair, Computational Biology Program, Sloan-Kettering Institute				
Venue:	*TBD*				
14:15-16:10	Session 4	Session 5	Session 6	Industrial Session 2	Workshop 11
speaker	TBD	TBD	TBD	Anastasia Christianson Michael Liebman	Illhoi Yoo
Session Chair:	TBD	TBD	TBD		
Venue	*TBD*	*TBD*	*TBD*	*TBD*	*TBD*
16:10-16:30	Coffee				
16:30-18:25	Session 7	Session 8	Session 9	Industrial Session 2	Workshop 11
Session Chair:	TBD	TBD	TBD	Anastasia Christianson Michael Liebman	Illhoi Yoo
Venue	*TBD*	*TBD*	*TBD*		*TBD*
18:30-20:30	Reception: TBD				

06-Oct					
08:00am-6:00pm	Registration: **TBD**				
Venue:	*The ground floor of the conference venue*				
8:30-9:30	Session Chai: Jean Gao Keynote Lecture 3: Obstacles and Options for Big-Data Applications in Biomedicine: The role of standards and normalizations Dr. Christopher G. Chute, MD, PH, Professor of Medical Informatics, Mayo Clinic College of Medicine, and IHI Fellow, University of Minnesota, MN				
Venue	*TBD*				
9:30-9:50	Coffee				
9:50-12:00	Session 10	Session 11	Session 12	Industrial Workshop 2	Workshop 9
Session Chair:	TBD	TBD	TBD	Sabrina Molinaro Michael Liebman	Fangxiang Wu Jianxing Wang
Venue	*TBD*	*TBD*	*TBD*	*TBD*	*TBD*
12:00-13:30	Lunch (provided by the conference) **Poster Session**				
13:30-14:30	Session Chair: Reda Alhaij Keynote Lecture 4: Protein Structure Determination on Demand Prof. Ming Li, Canada Research Chair in Bioinformatics, University of Waterloo				
14:35-15:15	Invited Talk1	Invited Talk 2	Invited Talk 3	Industrial Workshop 3	Workshop 9
Session Chair:	TBD	TBD	TBD	Aaron Kamauu Scott DuVall	Fangxiang Wu Jianxing Wang
Venue	*TBD*	*TBD*	*TBD*	*TBD*	*TBD*
15:15-15:30	Coffee				

15:30-17:25	Session 13	Session 14	Session 15	Industrial Workshop 3	Workshop 9
Session Chair:	TBD	TBD	TBD	Aaron Kamauu Scott DuVall	Fangxiang Wu Jianxing Wang
Venue	*TBD*	*TBD*	*TBD*	*TBD*	*TBD*
18:00-22:00	Banquet: TBD				

07-Oct				
08:00am-3:00pm	Registration: **TBD**			
Venue:	*The ground floor of the conference venue*			
8:15-10:10	Session 16	Session 17	Session 18	Workshop 6
Session Chair:	TBD	TBD	TBD	Ye Duan Yu-Ping Wang
Venue	*TBD*	*TBD*	*TBD*	*TBD*
10:10-10:30	Coffee			
10:30-12:25	Session 19	Session 20	Session 21	Workshop 6
Session Chair:	TBD	TBD	TBD	Ye Duan Yu-Ping Wang
Venue	*TBD*	*TBD*	*TBD*	*TBD*
12:25-13:30	Lunch			
13:30-15:25	Session 22	Session 23	Session 24	
Session Chair:	TBD	TBD	TBD	
Venue	*TBD*	*TBD*	*TBD*	

keynote Lectures: 4

Keynote 1: The CellOrganizer Project: An Open Source System to Learn Image-derived Models of Subcellular Organization over Time and Space, Dr. Robert Murphy , Lane Center for Computational Biology and Department of Biological Sciences, Carnegie Mellon University, USA

Keynote 2: Protein 3D structure from genomic sequences and application to cancer genomics, Dr. Chris Sander, Computational and

Systems Biolog Memorial Sloan-Kettering Cancer Center

Keynote 3: Obstacles and Options for Big-Data Applications in Biomedicine: The role of standards and normalizations, Dr. Christopher G. Chute, MD, PH, Professor of Medical Informatics, Mayo Clinic College of Medicine, and IHI Fellow, University of Minnesota, MN

Keynote 4: Protein Structure Determination on Demand, Prof. Ming Li, Canada Research Chair in Bioinformatics, School of Computer Science, University of Waterloo

Invited Talks: 6

Invited Talks 1: TBD

Invited Talks 2: TBD

Invited Talks 3: TBD

Session 1

Regular B211 "Manifold learning reveals nonlinear structure in metagenomic profiles"
Xingpeng Jiang, Xiaohua Hu, Huiyu Shen, and Tingting He
Regular B293 "LSH-Div: Species Diversity Estimation using Locality Sensitive Hashing"
Zeehasham Rasheed, Huzefa Rangwala, and Daniel Barbara
Short B207 "Extending the Ball-Histogram Method with Continuous Distributions and an Application to Prediction of DNA-Binding Proteins"
Ondrej Kuzelka, Andrea Szaboova, and Filip Zelezny
Short B218 "Pre-miRNA Classification via Combinatorial Feature Mining and Boosting"
Jason Wang, Ling Zhong, Dongrong Wen, and Bruce Shapiro
Short B249 "OWA-PSSM - A Position Specific Scoring Matrix based Method Integrated with OWA Weights for HLA-DR Peptide Binding Prediction"
Wen-Jun Shen and Hau-San Wong

Session 2

Regular B307 "Efficient Basin Hopping in the Protein Energy Surface"
Brian Olson and Amarda Shehu
Regular B366 "Improving Interacting Residue Prediction Using Long-Distance Information in Hidden Markov Models"
Colin Kern, Alvaro Gonzalez, Li Liao, and Vijay Shanker
Short B286 "Rotation Crossover and K-Site Move Mutation for Evolutionary Protein Folding in 3D FCC HP Model"
Shih-Chieh Su and Jyh-Jong Tsay
Short B288 "Identifying essential proteins via integration of protein interaction and gene expression data"
Xi-wei Tang, Jianxin Wang, and Yi Pan
Short B291 "Combining Homolog and Motif Similarity Data with Gene Ontology Relationships for Protein Function Prediction"
Hafeez ur Rehman, Alfredo Benso, Stefano Di Carlo, Gianfranco Politano, Alessandro Savino, and Prashanth Suravajhala

Session 3

Regular B481 "Estimating a gene's mutation burden by the number of observed synonymous base substitutions"
Perry Evans and Michael Krauthammer
Regular B498 "De-noise Biological Network from Heterogeneous Sources via Link Propagation"
Nan Du, Jing Gao, Vishrawas Gopalakrishna, and Aidong Zhang
Short B295 "Identifying enterotype in human microbiome by decomposing probabilistic topics into components"
Xingpeng Jiang, Dushoff Jonathan, Xin Chen, and Xiaohua Hu
Short B316 "A Basin Hopping Algorithm for Protein-protein Docking"
Irina Hashmi and Amarda Shehu
Short B330 "Not All Protein Complexes Exhibit Dense Structures in S. cerevisiae PPI Network"
Bolin Chen, Jinhong Shi, and Fang-Xiang Wu

Session 4

Regular B225 "Efficient Filtration for Similarity Search with Spaced k-mer Neighbors"
Weiming Li, Bin Ma, and Kaizhong Zhang
Regular B263 "A Log-Linear Graphical Model for Inferring Genetic Networks from High-Throughput Sequencing Data"
Genevera Allen and Zhandong Liu
Regular B285 "Prediction of Novel Systems Components in Cell Cycle Regulation in Malaria Parasite by Subnetwork Alignments"
Hong Cai, Changjin Hong, Jianying Gu, Timothy Lilburn, Rui Kuang, and Yufeng Wang
Short B240 "Drug-Target Network in Myocardial Infarction: a Structural Analysis"
Haiying Wang, Huiru Zheng, Francisco Azuaje, and Xing-Ming Zhao
Short B247 "A Model of Cellular Decision Making in Photodynamic Therapy of Cancer"
Ioannis Gkigkitzis and Xin Hua Hu

Session 5

Regular B298 "Significance Analysis by Minimizing False Discovery Rate"

	Yuanzhe Bei and Pengyu Hong
Regular	B299 "SiS: Significant Subnetworks in Massive Number of Network Topologies" Md Mahmudul Hasan, Yusuf Kavurucu, and Tamer Kahveci
Regular	B310 "Identifying Context-Specific Transcription Factor Targets from Prior Knowledge and Gene Expression Data" Elana J Fertig, Alexander V Favorov, and Michael F Ochs
Short	B252 "Similarity Analysis of Feature Ranking Techniques on Imbalanced DNA Microarray Datasets" David Dittman, Taghi Khoshgoftaar, Randall Wald, and Amri apolitano
Short	B277 "The Effect of Measurement Approach and Noise Level on Gene Selection Stability" Randall Wald, Taghi Khoshgoftaar, and Ahmad Abu Shanab

Session 6

Regular	B346 "Aligning protein-protein interaction networks using random neural networks" Hang Phan, Michael Sternberg, and Erol Gelenbe
Regular	B381 "Computation of biochemical pathway fluctuations beyond the linear noise approximation using iNA" Philipp Thomas, Hannes Matuschek, and Ramon Grima
Short	B353 "A Comparison Study on Protein-protein Interaction Network Models" Mingyu Shao, Yi Yang, Jihong Guan, and Shuigeng Zhou
Short	B296 "Modelling Non-Stationary Gene Regulatory Process with Hidden Markov Dynamic Bayesian Network" Shijia Zhu and Yadong Wang
Short	B409 "A Model to Predict and Analyze Protein-protein Interaction Types Using Electrostatic Energies" Gokul Vasudev and Luis Rueda

Session 7

Regular	B417 "Combining gene expression and function in a spatially localized approach" Evangelia Zacharaki, Angeliki Skoura, Li An, Desmond Smith, Scott Faro, and Vasileios Megalooikonomou
Regular	B440 "An Advanced Method for Identifying Protein-Protein Interaction by Analyzing TAP/MS Data" Xiaoyun Sun, Pengyu Hong, Meghana Kulkarni, Young Kwon, and Norbert Perrimon
Regular	B459 "A two-variable model for stochastic modelling of chemical events with multi-step reactions" Qianqian Wu, Kate Smith-Miles, and Tianhai Tian
Short	B338 "Accurate detection of SNPs using base-specific cleavage and mass spectrometry" Ruimin Sun, Xiang Gao, Nanyu Han, Qiong Wu, Yuguang Mu, Kai Tang, and Xin Chen
Short	B374 "An Efficient Algorithm for Clustering of Large-Scale Mass Spectrometry Data" Fahad Saeed, Trairak Pisitkun, Mark Knepper, and Jason Hoffert

Session 8

Regular	B463 "Identifying Protein Binding Functionality of Protein Family Sequences by Aligned Pattern Clusters" En-Shiun Annie Lee and Andrew K. C. Wong
Regular	B467 "A Weighted Hypergeometric Statistic for the Enrichment of Gene Sets" Rehman Qureshi and Ahmet Saçan
Regular	B468 "An adaptive feature selection method for microarray data analysis" Jie Cheng, Joel Greshock, Leming Shi, Jeff Painter, Xiwu Lin, Kwan Lee, Shu Zheng, Richard Wooster, Lajos Pusztai, and Alan Menius
Short	B377 "Robust RFCM Algorithm for Identification of Co-expressed miRNAs" Sushmita Paul and Pradipta Maji
Short	B415 "Using Gene Sets to Identify Putative Drugs for Breast Cancer" Tzu-Hung Hsiao, Hung-I Harry Chen, Yidong Chen, Yu-Heng Chen, and Eric Y. Chuang

Session 9

Regular	B475 "Fast Sparse Representation Approaches for the Classification of High-Dimensional Biological Data" Yifeng Li and Alioune Ngom

Regular B484 "A Discrete Bayesian Network Framework for Discrimination of Gene Expression Profiles"
Nikolay Balov

Regular B499 "A Link Prediction based Unsupervised Rank Aggregation Algorithm for Informative Gene Selection"
Kang Li, Nan Du, and Aidong Zhang

Short B419 "On the Design of Advanced Filters for Biological Networks using Graph Theoretic Properties"
Kathryn Dempsey, Tzu-Yi Chen, Sanjukta Bhowmick, and Hesham Ali

Short B464 "Stress induces biphasic-rewiring and modularization patterns in the metabolomic networks of Escherichia coli"
Fayez Aziz, Philemon Chan, Johan Osorio, Bushra Minhas, Vaisak Parekatt, and Gustavo Caetano-Anolles

Session 10

Regular B486 "A random walk based approach for improving protein-protein interaction network and protein complex prediction"
Chengwei Lei and Jianhua Ruan

Regular B492 "Unsupervised Kernel Parameter Estimation by Constrained Nonlinear Optimization for Clustering Nonlinear Biological Data"
Hyokyeong Lee and Rahul Singh

Short B470 "Inferring Fuzzy Cognitive Map Models for Gene Regulatory Networks from Gene Expression Data"
Ye Chen, Lawrence Mazlack, and Long Lu

Short B476 "Discovering Distal Regulatory Elements by Integrating Multiple Types of Chromatin State Maps"
Li Teng and Kai Tan

Short B494 "Drug-Drug Interaction Analysis Using Heterogeneous Biological Information Network"
Kyubum Lee, Sunwon Lee, Minji Jeon, Jaehoon Choi, and Jaewoo Kang

Session 11

Regular B385 "Data Driven Knowledge Acquisition Method for Domain Knowledge Enrichment in the Healthcare"
Sujan Perera, Cory Henson, Krishnaprasad Thirunarayan, Amit Sheth, and Suhas Nair

Short B255 "Bridging Encounter Forms and Electronic Medical Record Databases: Annotation
Yuan An, Ritu Khare, Xiaohua Hu, and Il-Yeol Song

Short B356 "Formalization of clinical trial eligibility criteria: Evaluation of a pattern-based approach"
Krystyna Milian, Anca Bucur, and Annette ten Teije

Short B379 "Skeleton Timed Up and Go"
Okko Lohmann, Thomas Luhmann, and Andreas Hein

Short B437 "Maps, Rates, and Fuzzy Mountains: Generating Meaningful Risk Maps"
Tamara Jimenez, Chetan Tiwari, Armin Mikler, and Marty O'Neill II

Session 12

Regular B258 "Integrating Protein Networks for Identifying Cooperative miRNA Activity in Disease Gene Signatures"
Mohammed Alshalalfa and Reda Alhajj

Regular B260 "PPIExtractor: A Protein-Protein Interaction Extractor for Biomedical Literature"
Zhihao Yang, Zhehuan Zhao, Yanpeng Li, Yuncui Hu, and Hongfei Lin

Regular B264 "Drug-induced QT Prolongation Prediction Using Co-regularized Multi-view Learning"
Jintao Zhang and Jun Huan

Short B458 "ENISI Visual, an agent-based simulator for modeling gut immunity"
Yongguo Mei, Raquel Hontecillas, Xiaoying Zhang, Keith Bisset, Stephen Eubank, Stefan Hoops, Madhav Marathe, and Josep Bassaganya-Riera

Short B372 "The e!DAL JAVA-API: Store, Share and Cite Primary Data in Life Sciences"
Daniel Arend, Matthias Lange, Christian Colmsee, Steffen Flemming, Jinbo Chen, and Uwe Scholz

Session 13

Regular B268 "MultiFacTV: Finding Modules from Higher-order Gene Expression Profiles with Time Dimension"

Xutao Li, Yunming Ye, Qingyao Wu, and Michael Ng

Regular B278 "Modeling Semantic Influence for Biomedical Research Topics using MeSH Hierarchy"
Dan He

Regular B297 "M-Finder: functional association mining from protein interaction networks weighted by semantic similarity"
Young-Rae Cho, Tak Chien Chiam, and Yanxin Lu

Short B411 "Building a Classifier for Identifying Sentences Pertaining to Disease-Drug Relationships in Tardive Dyskinesia"
Xia Bi, Hongzhan Huang, Sherri Matis-Mitchell, Peter McGarvey, Manabu Torii, Hagit Shatkay, and Cathy Wu

Short B439 "Composition of Bioinformatics Model Federations using Communication Aspects"
Keith Lee and David Stotts

Session 14

Regular B314 "Integration of Multiple Annotators by Aggregating Experts and Filtering Novices"
Ping Zhang and Zoran Obradovic

Regular B332 "An Efficient Sequential Pattern Mining Algorithm for Motifs with Gap Constraints"
Chiang-Chi Liao and Ming-Syan Chen

Regular B339 "Parallel Simulation of Apoptotic Receptor-Clustering on GPGPU Many-Core Architectures"
Claus Braun, Markus Daub, Alexander Schöll, Guido Schneider, and Hans-Joachim Wunderlich

Short B371 "CTGR-Span: Efficient Mining of Cross-Timepoint Gene Regulation Sequential Patterns from Microarray Datasets"
Chun-Pei Cheng, Yi-Lin Tsai, and Vincent S. Tseng

Short B496 "Placement of Unique Restriction Sites in Synthetic Genomes using Multi-Objective Optimization"
Mahfuza Sharmin and Sohel Rahman

Session 15

regular B343 "Using Similarity Learning to Improve Network-based Gene Function Prediction"
Ngo Phuong Nhung and Tu Minh Phuong

regular B388 "Identifying Protein Complexes Based on Local Fitness Method"
Jun Ren, Jianxin Wang, and Min Li

Regular B392 "iSimp: A Sentence Simplification System for Biomedical Text"
Yifan Peng, Catalina O. Tudor, Manabu Torii, Cathy H. Wu, and K. Vijay-Shanker

Short B311 "Linking and Querying Genomic Datasets Using Natural Language"
Bobby McKnight and Budak Arpinar

Short B362 "Personalized Semantic Assistance for the Curation of Biochemical Literature"
Fedor Bakalov, Marie-Jean Meurs, Birgitta König-Ries, Bahar Sateli, René Witte, Greg Butler, and Adrian Tsang

Session 16

Regular B422 "An Accurate Scalable Template-based Alignment Algorithm"
David Gardner, Weijia Xu, Jamie Cannone, Daniel Miranker, Stuart Ozer, and Robin Gutell

Regular B430 "PhylOnt: A Domain-Specific Ontology for Phylogeny Analysis"
Maryam Panahiazar, Ajith Ranabahu, Vahid Taslimitehrani, Hima Yalamanchili, Arlin Stoltzfus, Jim Leebens_Mack, and Amit Sheth

Regular B447 "A Novel Dynamic Graph-Based Computational Model for Predicting Salivary Gland Branching Morphogenesis"
Nimit Dhulekar, Lauren Bange, Abhirami Baskaran, Daniel Yuan, Basak Oztan, Bulent Yener, Shayoni Ray, and Melinda Larsen

Short B290 "Incorporating Semantic Similarity into Clustering Process for Identifying Protein Complexes from Affinity Purification/Mass Spectrometry Data"
Bingjing Cai, Haiying Wang, Huiru Zheng, and Hui Wang

Short B460 "A Neural Network Approach to the Identification of b-/y-ions in MS/MS Spectra"
James Cleveland and John Rose

Session 17

Regular B466 "Comprehensive human membrane protein database"
Min-sung Kim and Gwan-Su Yi

Regular B477 "Novel Features for Categorizing Biomedical Images"

	Jianqiang Sheng, Songhua Xu, Weicai Deng, and Xiaonan luo
Short	B251 "A Semi-Supervised Learning Method for Names of Traditional Chinese Prescriptions and Drugs Recognition" Dongfeng Cai, Changlin Ding, Junjun Zuo, and Yu Bai
Short	B271 "Using microenvironments to identify allosteric binding sites" Christopher Foley, Sana AlAzwari, Mark Dufton, and John Wilson
Short	B275 "The Effect of Unhealthy β-cells in Synchronized Insulin Secretion" Yang Pu, Saangho Lee, David Samuels, Layne Watson, and Yang Cao

Session 18

Regular	B479 "CWT-PLSR for Quantitative Analysis of Raman Spectrum" Shuo Li, Jean Gao, James Nyagilo, and Digant Dave
Short	B304 "A New Method for Computational Drug Repositioning Using Drug Pairwise Similarity" Jiao Li and Zhiyong Lu
Short	B202 "Keyword Annotation of Biomedical Documents with Graph-based Similarity Methods" Shuguang Wang and Milos Hauskrecht
Short	B237 "The Role of Eigen-matrix Translation in Classification of Biological Datasets" Hao Jiang and Wai-Ki Ching
Short	B242 "Immune System Simulation: Modeling the Mast Cell" Charles da Silva, Alcione Oliveira, Maurílio Possi, Fabio Cerqueira, Andreia Gomes, Rodrigo Siqueira-Batista, and Luiz Alberto Santana

Session 19

Regular	B233 "Robust Segmentation of Biomedical Figures Toward an Image-based Document Retrieval" Luis Lopez, Jingyi Yu, Catalina Tudor, Cecilia Arighi, Hongzhan Huang, K Vijay-Shanker, and Cathy Wu
Regular	B236 "Predicting distant metastasis in breast cancer using ensemble classifier based on context-specific miRNA regulation modules" Xionghui Zhou, Juan Liu, and Jianghui Xiong
Regular	B276 "Epileptic EEG Signal Analysis and Identification Based On Nonlinear Features" Yuedong Song
Short	B270 "Automatic Analysis Method of Protein Expression images based on Generalized Data Field" Shuliang Wang, Ying Li, Wenchen Tu, and Peng Wang
Short	B351 "An Automated Blood Vessel Extraction Algorithm in Fundus Images" Marwan Saleh and C. Eswaran

Session 20

Regular	B284 "A Monte Carlo Approach to Biomedical Time Series Search" Jonathan Woodbridge, Bobak Mortazavi, Majid Sarrafzadeh, and Alex Bui
Regular	B471 "Labor Contraction Prediction via Demographic and Obstetrical Information Analysis" Zifang Huang, Mei-Ling Shyu, James Tien, David Birnbach, and Michael Vigoda
Regular	B303 "Early Classification of Multivariate Time Series Using a Hybrid HMM/SVM model" Mohamed Ghalwash, Dusan Ramljak, and Zoran Obradovic
Short	B394 "Improved biomarker performance for the detection of hepatocellular carcinoma by inclusion of clinical parameters" Mengjun Wang, Timothy Block, Jorge Marrero, Adrian Di Bisceglie, Karthik Devarajan, and Anand Mehta
Short	B395 "Extracting BI-RADS Features from Portuguese Clinical Texts" Houssam Nassif, Filipe Cunha, Inês Moreira, Ricardo Cruz-Correia, Eliana Sousa, David Page, Elizabeth Burnside, and Inês Dutra

Session 21

Regular	B319 "Network-based Inferring Drug-Disease Associations from Chemical, Genomic and Phenotype Data" Yu-Fen Huang, Hsiang-Yuan Yeh, and Von-Wun Soo
Regular	B320 "A Data Mining Approach for Optimization of Acute Inflammation Therapy" Vladan Radosavljevic, Kosta Ristovski, and Zoran Obradovic
Regular	B364 "Prediction of Human Immunodeficiency Virus Type 1 Drug Resistance: Representation of Target Sequence Mutational Patterns via an n-Grams Approach" Majid Masso

Short	B456 "A Bayesian-based Prediction Model for Personalized Medical Health Care" Jiashu Zhao, Jimmy Xiangji Huang, Xiaohua Hu, Joseph Kurian, and William Melek
Short	B491 "Automated Wound Identification System Based on Image Segmentation and Artificial Neural Networks" Bo Song and Ahmet Sacan

Session 22

Regular	B378 "Improving Health Records Search Using Multiple Query Expansion Collections" Dongqing Zhu and Ben Carterette
Regular	B407 "Classification of Multicolor Fluorescence In-Situ Hybridization (M-FISH) Image Using Structure Based Sparse Representation Model" Jinyao Li and Yu-Ping Wang
Regular	B410 "Biomarker Identification for Diagnosis of Schizophrenia with Integrated Analysis of fMRI and SNPs" Hongbao Cao, Yu-Ping Wang, Dongdong Lin, Junbo Duan, and Vince Calhoun
Short	B483 "Predicting Viral Infection by Selecting Informative Biomarkers From Temporal High-Dimensional Gene Expression Data" Qiang Lou and Zoran Obradovic
Short	B489 "ForeTell - Facilitating doctor-patient conversation through interactive information visualization of risk prediction index" Pratibha Bhaskaran, Milind Kaduskar, Preeti Saluja, Smitha Tallimani, Sandip Bhaumik, and Sanghyun Yoo

Session 23

Regular	B446 "A Multi-Objective Program for Quantitative Subtyping of Clinically Relevant Phenotypes" Jiangwen Sun, Jinbo Bi, and Henry Kranzler
Short	B306 "Uncertain interactions affect degree distribution of biological networks" Andrei Todor, Alin Dobra, and Tamer Kahveci
Short	B342 "Systematic Measurement of Missmatch Effect for Designing Inter-Species Microarray" Fukuzaki Mutsumi, Masa-aki Yoshida, Atsushi Ogura, and Jun Sese
Short	B352 "Finding Genomic Features from Enriched Regions in ChIP-Seq Data" Iman Rezaeian and Luis Rueda
Short	B358 "Reconstructing Isoform Graphs from RNA-Seq data" Stefano Beretta, Paola Bonizzoni, Gianluca Della Vedova, and Raffaella Rizzi

Session 24

Regular	B289 "Multi-Instance Learning for Skin Biopsy Image Features Recognition" Gang Zhang, Xiangyang Shu, Zhaohui Liang, Yunting Liang, Shuyi Chen, and Jian Yin
Short	B393 "The Human Imprintome v1.0: Over 120 Imprinted Genes in the Human Genome Impose a Major Review on Previous Censuses" Samara Silva-Santiago, Ana Carolina Landim-Pacheco, Elton José Rosas-Vasconcelos, Samyra Maria Vieira-Brasil, Tereza Cristina L Rocha, Mônica Mor
Short	B427 "De Novo Co-Assembly of Bacterial Genomes from Multiple Single Cells" Narjes Movahedi, Elmirasadat Forouzmand, and Hamidreza Chitsaz
Short	B441 "MDAsim: a Multiple Displacement Amplification Simulator" Zeinab Taghavi and Sorin Draghici
Short	B478 "Aligning Ligand Binding Cavities by Optimizing Superposed Volume" Ruobing Chen, Katya Scheinberg, and Brian Chen
Short	B282 "Recognizing Drosha processing sites by a two-step prediction model with structure and sequence information" Xingchi Hu, Chuang Ma, and Yanhong Zhou

Workshops

1. Workshop on Multi-Level and Multi-Scale Modeling, Analysis, and Simulation in Biology *(Merged with Workshop 6)*

2. The 2012 Computational Structural Bioinformatics Workshop

3. Pharmaco-Informatics for Drug Discovery

4. The Fifth International Workshop on Biomolecular Network Analysis (IWBNA)

5. The First International Workshop on the role of Semantic Web in Literature-Based Discovery

6. International Workshop on Multiscale Biomedical Imaging Analysis(MBIA)

7. The Third International Workshop on Information Technology for Chinese Medicine (ITCM2012)

8. The Third Integrative Data Analysis in Systems Biology (IDASB 2012)

9. International Workshop on Computational Proteomics

10. Data-mining of Next-Generation Sequencing

11. The 2012 International Workshop on Biomedical and Health Informatics (BHI 2012)

12. The Third Workshop on Data mining from genomic variants and its application to genome-wide analysis

13. 2012 Workshop on Nanoinformatics for Biomedicine

14. Bioinformatics Strategies for Integrative Cancer Genomics *(Merged with Workshop 12*)

Industrial Track

Industrial Session 1:

Discovering breast cancer prognostic biomarkers using a novel feature selection tool, *Jie Cheng, Glaxo SmithKline*

A high-throughput analysis pipeline for large next generation DNA sequencing studies, *Zayed Albertyn and Jörg Hakenberg, Roche*

In Silico Target Portal: An Integrated Oncology Target Discovery Web Portal, *Ying Li, Roche*

Approach to Information Management in an Externalized Business Environment, *Bob O'Hara, ResultWorks*

Industrial Session 2:

Clinical Case: Enhancing medical monitoring with visualization and analytics, *Michael Farnum, Johnson and Johnson*

Click-ON: Methodologies and infrastucture supporting personalized medicine, Sabrina Molinaro, *Institute for Clinical Physiology, National Research Council of Italy*

Systematic Drug Repositioning: A new paradigm in Drug Discovery, *Vinod Kumar, Glaxo SmithKline*

New approaches for better decisions in Pharma R&D, *Anastasia Christianson, AstraZeneca*

Data-Driven Methods for Leveraging Electronic Health Records in support of Clinical Trials: Protocol Optimization, Site Selection and Patient Recruitment, *Aaron Kamauu, Anolinx LLC*

Industrial Workshop 1:

Title: Hindsight, Insight and Foresight - How to Optimize Industry Research by Measuring and Predicting Change Effects in Bioinformatics Applications

Workshop Organizers:
- David Fenske, Dean, iSchool, Drexel University
- Michael N. Liebman, PhD (Managing Director, Strategic Medicine, Inc)

Background:

This session will include perspectives from industry on collaborative efforts to bring next generation visual and decision support tools and techniques to enable decision makers in the bioinformatics industry to improve fundamentally the way an organization's information is analyzed, interpreted and used.

Objectives:
- Dean David Fenske and Dr Chaomei Chen will outline some of the ground-breaking research of the National Science Foundation Center for Visual and Decision Informatics, awarded this year to the *iSchool* at Drexel and the University of Louisiana at Lafayette. Industry and academic perspectives in this effort are integrated to probe research applications and deliver novel approaches to optimize industry research while cutting time and costs. Dr Fenske will describe examples of the Center's projects
- Dirk Husselman and Dr. Liebman will present examples of solutions into complex problem-solving from the user perspective back to the technology application

Program Outline:

1. National Science Foundation Center for Visual and Decision Informatics , an integration of industrial and academic perspectives on research needs(David Fenske, Dean, iSchool, Drexel University)
2. Tracking and modeling exploratory searches in a structure-function space, with application to drug discovery and compound optimization (Chaomei Chen, Professor, iSchool, Drexel University)
3. Risk, Challenges and Opportunities in Healthcare using Cloud-based solutions(Dirk Husselman, President, 2lemetry, Inc)
4. Optimizing Clinical Trial Success by Evaluating and Refining the Hypothesis (Michael Liebman, Managing Director, IPQ Analytics, LLC)
5. Panel discussion with a question and answer session.

Industrial Workshop 2:

Title: Data-mining: Issues and Challenges in Commercial Applications

Workshop Organizers:
- Sabrina Molinaro, PhD (Head, Division of Epidemiology and Health Research, National Research Council of Italy, Institute for Clinical Physiology, Pisa)
- Michael N. Liebman, PhD (Managing Director, Strategic Medicine, Inc)

Background:
Biomedicine is confronted with the challenges and opportunities presented by the evolving access to large data sets and the need to identify and create value from their contents. This workshop will focus on the development and application of methods for data-mining to resources ranging from genomic, proteomic and molecular data to clinical observations and data.

Objectives:
- To empower researchers with an understanding of the challenges and issues around data-mining in large, complex data repositories, virtual or integrated
- To familiarize attendees with available methods and tools.

Description:
The focus of the workshop will be to introduce issues and challenges in data-mining from virtual and/or integrated heterogeneous data and describe methodologies that are being used to develop value for commercial clients.

Program Outline:
1. Next generation in Technology for Advances in Biological data Analysis (Sultan Meghji, EVP, Appistry, Inc)
2. Fostering Computational Reasoning for Big Data by Non-mathematicians (Peter Schad, CSO, Digital Infuzion, Inc)
3. Applying Social Network Analysis for Data-mining in Complex Medical Data (Sabrina Molinaro,Head, Epidemiology and Health Research, ICP, CNR)
4. Network analysis of high throughput data for prediction of disease-related genes and identification of drug targets (Marina Bessarabova, Director Computational Biology & Bioinformatics ,Thomson Reuters)
5. (Ilya Mazo, Elsevier)
6. Panel discussion with a question and answer session.

Industrial Workshop 3:

Title: An Introduction to Natural Language Processing (NLP) Methods in Clinical Research

Workshop Presenters:
- Aaron Kamauu MD, MS, MPH (President, Anolinx LLC)
- Scott DuVall PhD (Associate Director of VINCI, VA Salt Lake City Health Care System)

Background:
As the use of natural language processing methods in preparing data for research continues to increase, researchers should understand the benefits and limitations of such a tool. While NLP is not a "solved" science, there are many tasks that NLP can do reliably. Extracting concepts (symptoms, diseases, medications) and values (lab values, vital signs) that are stored in the text is one example. More complex tasks, such as determining what caused an event of interest or why a patient discontinued a medication can also be addressed using the right tools. This workshop will introduce researchers to NLP and explore ways that NLP can support ongoing research.

Objectives:
- To empower researchers with knowledge of strengths and limitations of NLP methods.
- To familiarize attendees with available methods and tools.

Description:
The focus of the workshop will be to introduce the methodology of natural language processing (NLP) and demonstrate how it can be used in pharmacoepidemiological research.

Program Outline:
1. Explanation of what NLP is and discussion of the practical role it can play in pharmacoepidemiology (Aaron Kamauu)
2. Discussion of the different approaches for processing clinical text, including symbolic and statistical (Scott DuVall)
3. Practical demonstration of the interplay between clinical and technical teams to determine the relevant clinical concepts for training the NLP system (Aaron Kamauu and Scott DuVall)
4. Interactive walk-through of NLP tools on sample data (Scott DuVall and Aaron Kamauu)
5. Summary: Open discussion with a question and answer session.

Tutorials

Tutorial 1: Big Data in Drug Discovery: Opportunities and Challenges (4 hours)
Dr. Jun Huan, University of Kansas, USA
jhuan@ku.edu

Tutorial 2: Mobility data analysis to understand unknown diseases behavior: the case of facial paralysis (2 hours)
Dr. Jalel Akaichi, University of Sciences and Technologies of Lille, France
j.akaichi@gmail.com

Tutorial 3: Introduction to biomedical vocabularies and ontologies (2 hours, primer tutorial)
Dr. Illhoi Yoo, University of Missouri School of Medicine, USA
yooil@health.missouri.edu

Posters