Sunday, January 4, 2009

5:00-7:00pm   *Registration*   Ballroom Prefunction

Monday, January 5, 2009

7:00-9:30   *Registration*   Ballroom Prefunction
11:00-2:00   *Registration*   Ballroom Prefunction
4:30-7:30   *Registration*   Ballroom Prefunction

9:00-12:00 **Workshop:** Open Science: Developing tools and   Plaza Ballroom
                approaches to facilitate open exchange between
                scientists and data
9:00-9:50   **Tutorial:** Biomolecular Networks: From analysis to synthesis   Salon 2&3
10:00-10:50 **Tutorial:** Computational Challenges in Comparative Genomics: Salon 2&3
                Gene evolution, ancestral genome reconstruction and
                applications human genetics
11:00-11:50 **Tutorial:** Dynamics of biological networks   Salon 2&3

12:00-1:30   ***Lunch on Own***

1:30-4:30   **Workshop:** Post-transcriptional gene regulation: RNA-protein   Plaza Ballroom
                interactions, RNA processing, mRNA stability and
                localization
1:30-2:20   **Tutorial:** Emerging challenges in multi-scale modeling in biology   Salon 2&3
2:30-3:20   **Tutorial:** Knowledge-driven analysis and data integration for high   Salon 2&3
                throughput biological data
3:30-4:20   **Tutorial:** Molecular bioinformatics for diseases   Salon 2&3

4:30   ***Dinner on Own***

Tuesday, January 6, 2009

7:30-9:00   *Registration*   Ballroom Prefunction
10:30-11:30   *Registration*   Ballroom Prefunction
1:30-2:30   *Registration*   Ballroom Prefunction

7:30-8:30   ***Breakfast***   Ballroom Courtyard

8:30-8:40   **Welcome – Teri Klein**   Salon 2&3

8:40-8:50   **DYNAMICS OF BIOLOGICAL NETWORKS**   Salon 2&3
                   Tanya Berger-Wolf, Teresa Przytycka, and Mona Singh

    8:50-9:10   Invited Talk – Trey Ideker
    9:10-9:30   Dense Graphlet Statistics of Protein Interaction and Random Networks
                       R. Colak, F. Hormozdiari, F. Moser, A. Schonhuth, J. Holman, M.
                       Ester and S.C. Sahinalp
    9:30-9:50   Reverse Engineering the Evolution of Protein Interaction Networks
                       Todd A. Gibson and Debra S. Goldberg

9:50-10:10   Identifying Dynamic Network Modules with Temporal and Spatial Constraints
> *Ruoming Jin, Scott Mccallen, Chun-Chi Liu, Yang Xiang, Eivind Almaas, and Xianghong Jasmine Zhou*

10:10-10:30   Break

10:30-10:50   Efficient and Robust Prediction Algorithms for Protein Complexes Using Gomory-Hu Trees
> *A. Mitrofanova, M. Farach-Colton, and B. Mishra*

10:50-11:10   Unraveling Dynamic Activities of Autocrine Pathways that Control Drug-Response Transcriptome Networks
> *Yoshinori Tamada, Hiromitsu Araki, Seiya Imoto, Masao Nagasaki, Atsushi Doi, Yukiko Nakanishi, Yuki Tomiyasu, Kaori Yasuda, Ben Dunmore, Deborah Sanders, Sally Humphreys, Cristin Print, D. Stephen Charnock-Jones, Kousuke Tashiro, Satoru Kuhara, and Satoru Miyano*

11:10-11:30   Dissecting the Interface Between Signaling and Transcriptional Regulation in Human B Cells
> *Kai Wang, Mariano J. Alvarez, Brygida C. Bisikirska, Rune Linding, Katia Basso, Riccardo Dalla Favera, and Andrea Califano*

11:30-12:00   Break

12:00-1:00   Keynote Lecture – Introduction (Russ Altman)   Salon 2&3
Post-Synthesis Genetics & Engineering Biological Simplicity
> *Drew Endy*

1:00-2:30   Lunch on Own

2:30-2:40   COMPUTATIONAL CHALLENGES IN COMPARATIVE   Salon 2&3
GENOMICS: GENE FAMILY EVOLUTION, ANCESTRAL GENOME
RECONSTRUCTION, AND APPLICATIONS to HUMAN GENETICS
> *Webb Miller, Bernard Moret, Pavel Pevzner, David Sankoff*

2:40-3:00   Identifying Parent-Daughter Relationships Among Duplicated Genes
> *Mira V. Han And Matthew W. Hahn*

3:00-3:20   A Parsimony Approach to Analysis of Human Segmental Duplications
> *Crystal L. Kahn and Benjamin J. Raphael*

3:20-3:40   An Exact Solver for the DCJ Median Problem
> *Meng Zhang, William Arndt, and Jijun Tang*

3:40-4:00   Inferring Genome-Wide Mosaic Structure
> *Qi Zhang, Wei Wang, Leonard Mcmillan, Fernando Pardo-Manuel De Villena, and David Threadgill*

4:00-5:00   **Discussion Session:** Dynamics of biological networks   Salon 2&3

4:00-5:00   **Discussion Session:** Computational Challenges in Comparative Genomics: Gene family evolution, ancestral genome reconstruction, and applications to human genetics   Plaza III

5:00-5:30   **ISCB Open Business Meeting**   Salon 2&3

5:30   ***Dinner and Evening on Own***

Wednesday, January 7, 2009

7:30-9:00   *Registration*   Ballroom Prefunction
12:00-2:00   *Registration*   Ballroom Prefunction

7:30-8:30   ***Breakfast***   Ballroom Courtyard

8:30-8:40   **Morning Announcements – Russ Altman**   Salon 2&3

8:40-8:50   **BIOMOLECULAR NETWORKS: FROM ANALYSIS TO SYNTHESIS** Salon2&3
                                Gil Alterovitz, Marco Ramoni

   8:50-9:10   Stochastic Transient Analysis of Biochemical Systems and Its Application
                        to the Design of Biochemical Logic Gates
                                Bin Cheng and Marc Riedel
   9:10-9:30   Identification of Discriminating Biomarkers for Human Disease Using
                        Integrative Network Biology
                                Joel T. Dudley and Atul J. Butte
   9:30-9:50   Learning the Structure of Protein-Protein Interaction Networks
                                Oleksii Kuchaiev and Natasa Przulj
   9:50-10:10   Inference of Functional Networks of Condition-Specific Response--A
                        Case Study of Quiescence in Yeast
                                *Sushmita Roy, Terran Lane, Margaret Werner-Washburne, and
                                Diego Martinez*

10:10-10:30   ***Break***

   10:30-10:50   Learning Cyclic Signaling Pathway Structures While Minimizing Data
                        Requirements
                                *K. Sachs, S. Itani, J. Fitzgerald, L. Wille, B. Schoeberl, M.A.
                                Dahleh, And G.P. Nolan*
   10:50-11:10   Querying Parse Tree Database of Medline Text to Synthesize User-
                        Specific Biomolecular Networks
                                Luis Tari, Jorg Hakenberg, Graciela Gonzalez, Chitta Baral
   11:10-11:30   Pairwise Alignment of Interaction Networks by Fast Identification of
                        Maximal Conserved Patterns
                                Wenhong Tian and Nagiza F. Samatova

11:30-12:30   ***Discussion Session***: Biomolecular Networks: From   Salon 2&3
                        Analysis to Synthesis

12:30-2:30   ***Poster Session #1 with Finger Food Lunch***   Salon 1 & Ballroom Courtyard
                        (A-L, last name of the first author presents)

2:30-2:40   **MOLECULAR BIOINFORMATICS FOR DISEASE**   Salon 2&3
        Atul Butte, Maricel Kann, Yves Lussier, Yanay Ofran, Predrag Radivojac

    2:40-3:00   Invited Talk – Andrea Califano
    3:00-3:20   Supervised Classification of Array CGH Data with HMM-Based Feature
                Selection
                      Anneleen Daemen, Olivier Gevaert, Karin Leunen, Eric Legius,
                      Ignace Vergote, and Bart De Moor
    3:20-3:40   Prediction of Interactions Between HIV-1 and Human Proteins by
                  Information Integration
                      Oznur Tastan, Yanjun Qi, Jaime G. Carbonell, and Judith
                      Kleinseetharaman
    3:40-4:00   FastChi: An Efficient Algorithm for Analyzing Gene-Gene Interactions
                      Xiang Zhang, Fei Zou, and Wei Wang

4:00-5:00   **Discussion Session:** Molecular Bioinformatics for Disease   Salon 2&3

5:30-7:30   *Dinner Beach Party*   Coconut Grove

7:30-9:00   **Dessert & Keynote Lecture**   Salon 2&3 and Ballroom Courtyard
                Introduction (Larry Hunter)
                      "DNA Don't Lie": How Bioinformatics freed some of my best friends,
                      and sent the guilty to prison
                      Greg Hampikian

Thursday, January 8, 2009

7:30-8:30   *Breakfast*   Ballroom Courtyard

8:30-8:40   **Morning Announcements – Keith Dunker**   Salon 2&3

8:40-8:50   **EMERGING CHALLENGES IN MULTI-SCALE MODELING IN BIOLOGY**
                Peter Arzberger, James Bassingthwaighte, Roy Kerckhoffs, Jeff Reinbolt

    8:50-9:10   Invited Talk – Duane Malcolm
    9:10-9:30   Advances in Semantic Representation for Multiscale Biosimulation: A
                  Case Study in Merging Models
                      Maxwell Lewis Neal, John H. Gennari, Theo Arts, and Daniel L.
                      Cook
    9:30-9:50   Integration of Angiogenesis Modules at Multiple Scales: From Molecular
                  to Tissue
                      Amina A. Qutub, Gang Liu, Prakash Vempati, and Aleksander S.
                      Popel
    9:50-10:10   Towards Computational Modeling of Excitation-Contraction Coupling in
                  Cardiac Myocytes: Reconstruction of Structures and Proteins from
                  Confocal Imaging
                      Frank B. Sachse, Eleonora Savio-Galimberti, Joshua I.
                      Goldhaber, and John H. B. Bridge

10:10-10:30   A Multiscale Approach to Sampling Nascent Peptide Chains in the Ribosomal Exit Tunnel
V. A. Voelz, P. Petrone, and V. S. Pande

10:30-11:00   Break

11:00-12:00   *Discussion Session*: Emerging Challenges in Multi-Scale   Salon 2&3
Modeling in Biology

12:00-2:00   *Poster Session #2 with Finger Food Lunch*   Salon 1 & Ballroom Courtyard
(M-Z, last name of the first author presents)

2:00-2:30   Workshop Highlights: Salon 2&3
Open Science: Developing tools and approaches to facilitate open exchange between scientists and data
Cameron Neylon and Shirley Wu

2:30-3:00   Workshop Highlights: Salon 2&3
Post-transcriptional gene regulation: RNA-protein interactions, RNA processing, mRNA stability and localization
Benjamin Blencowe, Steven Brenner, Timothy Hughes, Quaid Morris

3:00   *Afternoon and Dinner on Own*

Friday, January 9, 2009

7:30-8:30   *Breakfast*   Ballroom Courtyard

8:30-8:40   Closing – Larry Hunter   Salon 2&3

8:40-8:50   KNOWLEDGE-DRIVEN ANALYSIS AND DATA   Salon 2&3
INTEGRATION FOR HIGH-THROUGHPUT BIOLOGICAL DATA
Michael Ochs, John Quackenbush, Ramana Davuluri, Habtom Ressom

8:50-9:10   Invited Talk – Olga Troyanskaya
9:10-9:30   Characterization of Unknown Adult Stem Cell Samples by Large Scale Data Integration and Artificial Neural Networks
G. Bidaut and C.J. Stoeckert Jr.
9:30-9:50   Biofilter: A Knowledge-Integration System for the Multi-Locus Analysis of Genome-Wide Association Studies
William S. Bush, Scott M. Dudek, and Marylyn D. Ritchie
9:50-10:10   Interpreting Genetics Of Gene Expression: Integrative Architecture In Bioconductor
V. J. Carey and R. Gentleman

10:10-10:30   Break

10:30-10:50   High Throughput Interaction Data Reveals Degree Conservation of Hub Proteins
A. Fox, D. Taylor, and D. K. Slonim

10:50-11:10   Unison: An Integrated Platform for Computational Biology Discovery
                Reece K. Hart and Kiran Mukhyala
11:10-11:30   TreeQA: Quantitative Genome Wide Association Mapping Using Local
              Perfect Phylogeny Trees
                *Feng Pan, Leonard Mcmillan, Fernando Pardo-Manuel De Villena,
                David Threadgill, and Wei Wang*
11:30-11:50   Improving the Efficiency of Biomarker Identification Using Biological
              Knowledge
                *John H. Phan, Qiqin Yin-Goen, Andrew N. Young, and May D.
                Wang*

11:50-1:00   *Lunch on Own*

1:00-1:20   Towards a Cytokine-Cell Interaction Knowledgebase of the Adaptive
              Immune System
                *Shai S. Shen-Orr, Ofir Goldberger, Yael Garten, Yael Rosenberg-
                Hasson, Patricia A. Lovelace, David L. Hirschberg, Russ B.
                Altman, Mark M. Davis, and Atul J. Butte*
1:20-1:40   A Bayesian Integration Model of High-Throughput Proteomics and
              Metabolomics Data for Improved Early Detection of Microbial Infections
                *Bobbie-Jo M. Webb-Robertson, Lee Ann Mccue, Nathanial
                Beagley, Jason E. Mcdermott, David S. Wunschel, Susan M.
                Varnum, Jian Zhi Hu, Nancy G. Isern, Garry W. Buchko, Kathleen
                Mcateer, and Joel G. Pounds*

1:40-2:40   Discussion Session: Knowledge-Driven Analysis and   Salon 2&3
              Data Integration for High-Throughput Biological Data

PSB over--see you next year!