

GIW 2001 Advanced Program

December 17, Monday, The Garden Hall

Opening Address

14:00 - 14:10 Limsoon Wong (KRDL)

Session 1

Gene Expression

Chair: Satoru Kuhara (Kyushu U.)

14:10 - 14:35 *Emerging Patterns and Gene Expression Data*, Jinyan Li, Limsoon Wong (Kent Ridge Digital Lab.)

14:35 - 15:00 *Selecting Informative Genes with Parallel Genetic Algorithms in Tissue Classification*, Juan Liu^{*†}, Hitoshi Iba[†], Mitsuru Ishizuka[†] (*Wuhan U., [†]U. Tokyo)

15:00 - 15:25 *Minimum Spanning Trees for Gene Expression Data Clustering*, Ying Xu, Victor Olman, Dong Xu (Oak Ridge Nat'l Lab.)

15:25 - 15:50 *Characterizing the Relationship between Protein-Fusion and Gene Co-Expression*, Cary S. Gunther, Terry Gaasterland (Rockefeller U.)

Break 15:50 - 16:05

Session 2

Pathway Analysis

Co-chair: Terry Gaasterland (Rockefeller U.)

Susumu Goto (Kyoto U.)

16:05 - 16:30 *Extraction of Correlated Gene Clusters by Multiple Graph Comparison*, Akihiro Nakaya, Susumu Goto, Minoru Kanehisa (Kyoto U.)

16:30 - 16:55 *XML Documentation of Biopathways and Their Simulations in Genomic Object Net*, Hiroshi Matsuno^{*}, Atsushi Doi^{*}, Yuichi Hirata[†], Satoru Miyano[†] (*Yamaguchi U., [†]U. Tokyo)

16:55 - 17:20 *Estimation of Bidirectional Metabolic Fluxes from MS and NMR Data Using Positional Representations*, Marcos J. Araúzo-Bravo, Kazuyuki Shimizu (Kyushu Inst. of Tech.)

December 18, Tuesday, The Garden Hall

Session 3 Protein Sequence and Structure

Co-chair: Akihiko Konagaya (JAIST)
Richard Lathrop (UC Irvine)

- 9:00 - 9:25 *A Multi-Queue Branch-and-Bound Algorithm For Anytime Optimal Search With Biological Applications*, Richard H. Lathrop, Anton Sazhin, Ye Sun, Nick Steffen, Sandra S. Irani (UC Irvine)
- 9:25 - 9:50 *Local Multiple Alignment of Numerical Sequences: Detection of Subtle Motifs from Protein Sequences and Structures*, Tatsuya Akutsu (Kyoto U.), Katsuhisa Horimoto (Saga Med. Sch.)
- 9:50 - 10:15 *A Graph-Based Clustering Method for a Large Set of Sequences Using a Graph Partitioning Algorithm*, Hideya Kawaji*[†], Yosuke Yamaguchi*, Hideo Matsuda*, Akihiro Hashimoto* (*Osaka U., [†]NTT Software Corp.)
- 10:15 - 10:40 *Prediction of Subcellular Localizations Using Amino Acid Composition and Order*, Yukiko Fujiwara, Minoru Asogawa (NEC Corp.)

Break 10:40 - 10:55

Invited Talk Chair: Limsoon Wong (KRDL)

- 10:55 - 11:55 *New Data Driven Research Paradigm for the Post Genome Era*
Charles Lawrence (Wadsworth Center)

Lunch Break 11:55 - 13:30

Invited Talk Chair: Takashi Ito (Kanazawa U.)

- 13:30 - 14:30 *Protein Interactions*
David Eisenberg (UCLA)

Break 14:30 - 14:45

Session 4 Protein Interaction

Chair: Makiko Suwa (CBRC)

- 14:45 - 15:10 *Automatic Epitope Recognition in Proteins Oriented to the System for Macromolecular Interaction Assessment MIAx*, Atsushi Yoshimori, Carlos A. Del Carpio (Toyohashi U. of Tech.)
- 15:10 - 15:35 *The Potential Use of SUISEKI as a Protein Interaction Discovery*, Christian Blaschke, Alfonso Valencia (CNB/CSIC)
- 15:35 - 16:00 *Conservation of Protein Interaction Network in Evolution*, Jong Park, Dan Bolser (Cambridge U.)

JSBi Annual Meeting

- 16:00 - 16:30 General Meeting

Poster & Software Demonstrations Session 1

- 16:30 - 18:30 JSBi Session (The Garden Hall Foyer)
Poster Session: The Garden Hall Foyer
Software Demonstrations: The GardenHall

Social Events Award Ceremony and Banquet

- 18:30 - 21:00 The Garden Room

December 19, Wednesday, The Garden Hall

Session 5 **Molecular Phylogeny**

Chair: Hideo Matsuda (Osaka U.)

9:00 - 9:25 *A Phylogenetic Foundation for Comparative Mammalian Genomics*, Peter J. Waddell*, Hirohisa Kishino[†], Rissa Ota[‡] (*U. South Carolina, [†]U. Tokyo, [‡]Massey U.)

9:25 - 9:50 *Bacterial Molecular Phylogeny Using Supertree Approach*, Vincent Daubin, Manolo Gouy, Guy Perrière (UCBL)

Break 9:50 - 10:05

Poster & Software Demonstrations Session 2

10:05 - 12:05 JSBi Session (The Garden Hall Foyer)
 Poster Session: The Garden Hall Foyer
 Software Demonstrations: The Garden Hall

Lunch Break 12:05 - 13:35

Session 6 **Genome Analysis**

Co-chair: Tatsuya Akutsu (Kyoto U)
 Gene Myers (Celera Genomics)

13:35 - 14:00 *Optimally Separating Sequences*, Gene Myers (Celera Genomics)

14:00 - 14:25 *Indexing Huge Genome Sequences for Solving Various Problems*, Kunihiro Sadakane*, Tetsuo Shibuya[†] (*Tohoku U., [†]IBM Tokyo Res. Lab.)

14:25 - 14:50 *A Mini-Greedy Algorithm for Faster Structural RNA Stem-Loop Search*, Jan Gorodkin*, Rune B. Lyngsø[†], Gary D. Stormo[‡] (*U. Aarhus, [†]UC Santa Cruz, [‡]Washington U.)

Break 14:50 - 15:05

- 15:05 - 15:30 *High-Throughput Identification, Database Storage and Analysis of SNPs in EST Sequences*, Francisco José Useche*, Guang Gao*, Mike Hanafey[†], Antoni Rafalski[†] (*U. Delaware, [†]DuPont Crop Genetics)
- 15:30 - 15:55 *Bioinformatics Issues for Automating the Annotation of Genomic Sequences*, Kim Carter*, Akira Oka[†], Gen Tamiya[†], Matthew I. Bellgard* (*Murdoch U., [†]Tokai U.)
- 15:55 - 16:20 *DNAinsight: A Web Based Image Processing System for Large Scale RLGS Analysis*, Katsutoshi Takahashi*, Masayuki Nakazawa[†], Yasuo Watanabe (*CBRC, [†]Kanazawa Tech. Coll, [‡]Kanazawa Inst. of Tech.)

Closing

- 16:20 - 16:30 Kenta Nakai (U. Tokyo)