

# GIW 2000 Program

## Registration Garden Hall

December 18 : 9:00 -18:30

December 19 9:00 -17:00

## December 18, 2000 (Mon)

### Opening Address

9:20 -9:30 *A.Keith Dunker (Washington State University)*

### Session 1 Genome Analysis

9:30 -9:50 "Rice at the Forefront of Plant Genome Informatics "

*Bal A.Antonio, Katsumi Sakata, Takuji Sasaki*

9:50 -10:10 "An Integrated Analysis and Database System for Full-Length cDNA "

*Tetsuo Nishikawa, Katsuhiko Murakami, Naoyuki Harada, Toshio Ota,  
Tomoyasu Sugiyama, Keiichi Nagai, Ryotaro Irie, Hiroshii Matui,  
Makiko Suwa, Takao Isogai*

10:10 -10:30 "An Infrastructure for Comparative Genomics to Functionally  
Characterize Genes and Proteins "

*Clemens Suter-Crazzolara, Gunther Kurapkat*

10:30 -10:50 "Intelligent DNA Chips: Logical Operation of Gene Expression Profiles  
on DNA Computers "

*Yasubumi Sakakibara, Akira Suyama*

**Break 10:50-11:00**

**Invited Talk** "Whole Genome Assemblies of the Drosophila and Human Genomes "

11:00 -12:00 *Gene Myers (Celera Genomics)*

**Lunch Break 12:00 -13:20**

### Session 2 Intelligent Systems and Algorithms for Molecular Biology

13:20 -13:40 "Biological Sequence Compression Algorithms "

*Toshiko Matsumoto, Kunihiko Sadakane and Hiroshi Imai*

13:40 -14:00 "Sequencing by Hybridization in the Presence of Hybridization Errors "

*Koichiro Doi and Hiroshi Imai*

14:00 -14:20 "Visualization and Manipulation of Pedigree Diagrams "

*Limsoon Wong*

**14:20 -14:40** “Intelligent System for Topic Survey in MEDLINE by Keyword Recommendation and Learning Text Characteristics ”  
*Miyako Tanaka, Sanae Nakazono, Hiroshi Matsuno, Hideki Tsujimoto, Yasuhiko Kitamura, Satoru Miyano*

**JSBi Annual Meeting**

**14:40 -15:00** General Meeting  
**15:00 -17:00** One-Minute Talks for Poster &Software Demonstrations  
**17:00 -18:30** Poster &Software Demonstrations (Garden Hall Foyer)

**Social Events** **Award Ceremony &Banquet (Garden Hall Foyer)**  
**18:30 -21:00**

**December 19, 2000 (Tue)**

**Session 3** **Expression Profile Analyses**

**9:00 -9:20** “Correspondence Analysis of Genes and Tissue Types and Finding Genetic Links from Microarray Data ”  
*Hirohisa Kishino, Peter J. Waddell*

**9:20 -9:40** “Environmental Factor Dependent Maximum Likelihood Method for Association Study Targeted to Personalized Medicine ”  
*Tatsuhiko Tsunoda, Ryo Yamada, Toshihiro Tanaka, Youzo Ohnishi, Naoyuki Kamatani*

**9:40 -10:00** “Expression Profiles and Biological Function ”  
*Juan Carlos Oliveros, Christian Blaschke, Javier Herrero, Joaquin Dopazo, Alfonso Valencia*

**10:00 -10:20** “Inferring Genetic Networks from DNA Microarray Data by Multiple Regression Analysis ”  
*Mamoru Kato, Tatsuhiko Tsunoda, Toshihisa Takagi*

**10:20 -10:40** “Cluster Inference Methods and Graphical Models Evaluated on NCI60 Microarray Gene Expression Data ”  
*Peter J.Waddell, Hirohisa Kishino*

**Break** **10:40 -10:50**

**Invited Talk** “RIKEN Structural Genomics Initiative ”  
**10:50 -11:50** *Shigeyuki Yokoyama (RIKEN &University of Tokyo)*

**Lunch Break** **11:50-13:00**

**Poster and Software Demonstrations (JSBi Session,Garden Hall Foyer)**

**13:00 -14:30**

**Session 4 Protein Structure Analyses**

**14:30 -14:50** “Protein Sequence-Structure Alignment Based on Site-Alignment Probabilities ”

*Sanzo Miyazawa*

**14:50 -15:10** “Clustering and Averaging of Images in Single-Particle Analysis ”

*Kiyoshi Asai, Yutaka Ueno, Chikara Sato, Katsutoshi Takahashi*

**15:10 -15:30** “Intrinsic Protein Disorder in Complete Genomes ”

*A.Keith Dunker ,Zoran Obradovic, Pedro Romero, Ethan C.Garner, Celeste J. Brown*

**15:30 -15:50** “Comparing Predictors of Disordered Protein ”

*Xiaohong Li, Zoran Obradovic, Celeste J.Brown, Ethan C.Garner, A.Keith Dunker*

**Break**

**15:50-16:00**

**Session 5 Protein Interaction Simulation**

**16:00 -16:20** “Two-Phase Partition Method for Simulating a Biological System at an Extremely High Speed ”

*Hiroyuki Kurata, Kazunari Taira*

**16:20 -16:40** “ A Gene Network Inference Method from Continuous-Value Gene Expression Data of Wild-Type and Mutants ”

*Koji M.Kyoda, Mineo Morohashi, Shuichi Onami, Hiroaki Kitano*

**16:40 -17:00** “MIAX: A System for Assessment of Macromolecular Interaction. 3)A Parallel Hybrid GA for Flexible Protein Docking ”

*Carlos Adriel Del Carpio M., Atsushi Yoshimori*

**Closing**

**17:00 -17:10**