

**GIW 2003**  
**The Fourteenth International Conference on Genome Informatics**  
**Pacifico Yokohama, Japan**  
**December 14-17, 2003**

**Registration**

Registration should be done at: <http://giw.ims.u-tokyo.ac.jp/giw2003/registration.html>  
 until November 30, 2003. Registration fee includes a copy of Genome Informatics Vol.14 and coffee breaks. We offer registration fee discount for JSBi and ISCB members.

		until Nov. 30, 2003	after Nov. 30, 2003
<b>Standard Registration</b>	<b>Standard</b>	JPY12,000.-	JPY15,000.-
	<b>ISCB Member</b>	JPY11,000.-	JPY14,000.-
	<b>JSBi Member</b>	JPY8,000.-	JPY11,000.-
	<b>JSBi &amp; ISCB Member</b>	JPY7,000.-	JPY10,000.-
<b>Student Registration</b>	<b>Standard</b>	JPY8,000.-	JPY11,000.-
	<b>ISCB Member</b>	JPY7,000.-	JPY10,000.-
	<b>JSBi Member</b>	JPY5,000.-	JPY8,000.-
	<b>JSBi &amp; ISCB Member</b>	JPY4,000.-	JPY7,000.-

(Banquet on December 16 evening : JPY6,000.-)

**Secretary and Local Arrangements**

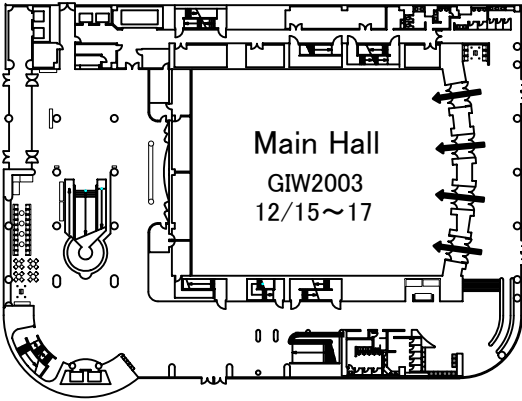
Human Genome Center, Institute of Medical Science, University of Tokyo  
 4-6-1 Shirokanedai, Minato-ku, Tokyo 108-8639, Japan  
 Tel: +81-3-5449-5615 / Fax: +81-3-5449-5442  
 E-mail: [giw@ims.u-tokyo.ac.jp](mailto:giw@ims.u-tokyo.ac.jp)  
 URL: <http://giw.ims.u-tokyo.ac.jp/giw2003/index.html>

**Location**

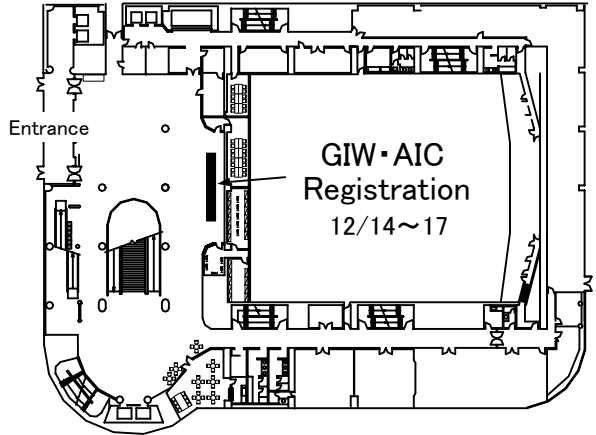
The conference will take place at *PACIFICO YOKOHAMA*. Please get off at JR Sakuragicho Station or Sakuragicho Station on the Tokyu Toyoko Line. It takes about 12 minutes' walk from the JR Sakuragicho station to Pacifico Yokohama via Moving Walkway.  
 Address: 1-1-1, Minato Mirai, Nishi-ku, Yokohama 220-0012, Japan  
 Tel:+81-45-221-2155  
[http://www.pacifico.co.jp/index\\_e.html](http://www.pacifico.co.jp/index_e.html)

# Conference Center

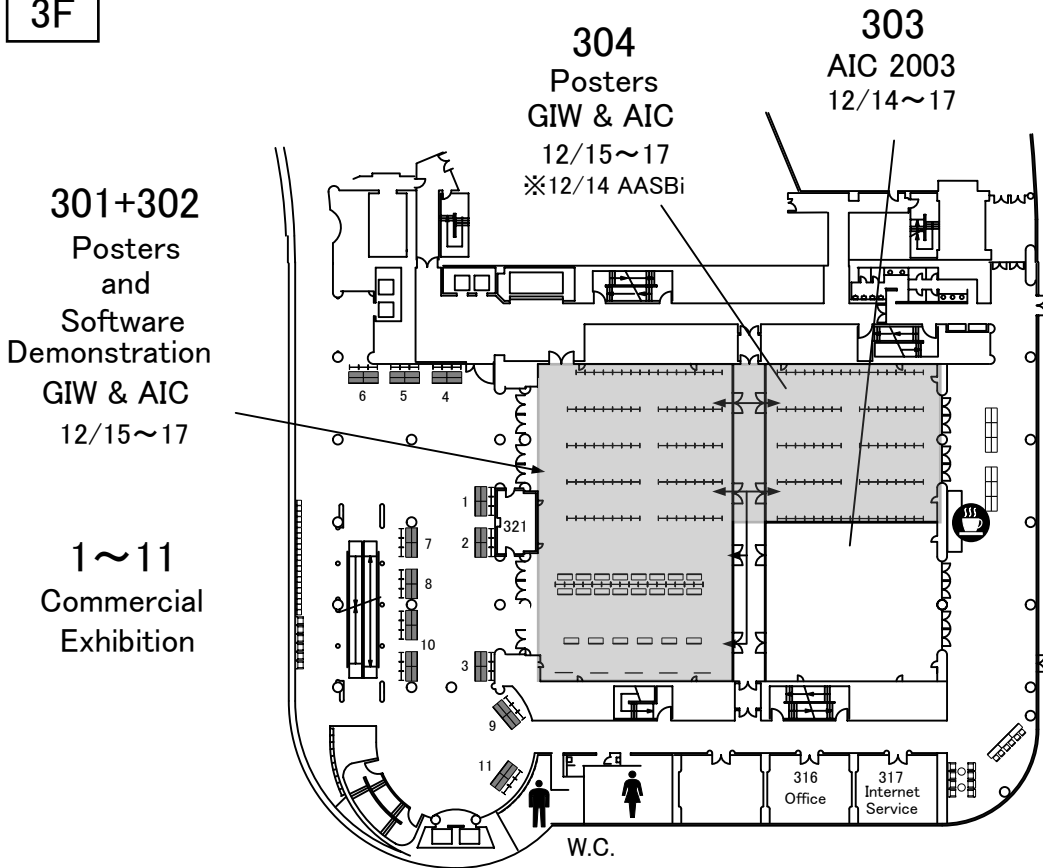
1F



2F



3F



# GIW 2003 Advanced Program

## Registration

December 14, 2003: 10:00 - 17:45  
December 15, 2003: 08:30 - 17:30  
December 16, 2003: 08:30 - 18:00  
December 17, 2003: 08:30 - 16:20

## Monday, December 15, 2003

### Opening Address

09:00 - 09:10 Minoru Kanehisa (Kyoto U.)

### Paper Session 1

09:10 - 09:35 Chair: Eberhard Voit (USC)  
Computational Inference of Regulatory Pathways in Microbes: an Application to Phosphorus Assimilation Pathways in *Synechococcus sp.* WH8102, *Zhengchang Su*<sup>1</sup>, *Phuongan Dam*<sup>1</sup>, *Xin Chen*<sup>2</sup>, *Victor Olman*<sup>1</sup>, *Tao Jiang*<sup>2</sup>, *Brian Palenik*<sup>2</sup>, *Ying Xu*<sup>1</sup> (<sup>1</sup>U. Georgia, <sup>2</sup>U. California)

09:35 - 10:00 A Case Study of Object-Oriented Bio-Chemistry: A Unified Specification of the Coagulation Cascade, *Jacqueline Signorini*, *Patrick Greussay* (U. Paris)

10:00 - 10:25 MetaFluxNet, a Program Package for Metabolic Pathway Construction and Analysis, and Its Use in Large-Scale Metabolic Flux Analysis of *Escherichia coli*, *Sang Yup Lee*, *Dong-Yup Lee*, *Soon Ho Hong*, *Tae Yong Kim*, *Hongsoek Yun*, *Young-Gyun Oh*, *Sunwon Park* (KAIST)

### ISCB Address

10:25 - 10:40 Michael Gribskov (UCSD)  
10:40 - 11:00 Break

### Keynote Address

11:00 - 12:00 Chair: Genshiro Kitagawa (ISM)  
On the Art of Modeling; Illustrated with the Analysis of the Golf Swing Motion, *Hirotsugu Akaike* (ISM)

12:00 - 13:30 Lunch

### Posters and Software Demonstrations Session 1

13:30 - 15:00

### Paper Session 2

15:00 - 15:25 Chair: Vladimir Brusic (Inst. Infocomm Res.)  
Reducing False Positives in Molecular Pattern Recognition, *Xijin Ge*, *Shuichi Tsutsumi*, *Hiroyuki Aburatani*, *Shuichi Iwata* (U. Tokyo)

15:25 - 15:50 On Combining Multiple Microarray Studies for Improved Functional Classification by Whole-Dataset Feature Selection, *See-Kiong Ng*<sup>1</sup>, *Soon-Heng Tan*<sup>1</sup>, *V.S. Sundararajan*<sup>1,2</sup> (<sup>1</sup>I2R, <sup>2</sup>Nat'l U. Singapore)

15:50 - 16:15 Statistical Inference Methods for Detecting Altered Gene Associations, *Sang-Heon Yoon*, *Je-Suk Kim*, *Hae-Hiang Song* (Cath. U. Korea)

### Paper Session 3

16:15 - 16:40 Chair: Kenta Nakai (U. Tokyo)  
Splice Site Detection with a Higher-Order Markov Model Implemented on a Neural Network, *Loi Sy Ho*, *Jagath C. Rajapakse* (Nanyang Tech U)

16:40 - 17:05 On Selecting Features from Splice Junctions: An Analysis Using Information Theoretic and Machine Learning Approaches, *Christina L. Zheng*, *Virginia R. de Sa*, *Michael Gribskov*, *T. Murtidharan Nair* (U. California)

17:05 - 17:30 An *In-Silico* Method for Prediction of Polyadenylation Signals in Human Sequences, *Huiqing Liu*, *Hao Han*, *Jinyan Li*, *Limsoon Wong* (I2R)

## Tuesday, December 16, 2003

- Paper Session 4** Chair: Ueng-Cheng Yang (Yang Ming U.)  
09:00 - 09:25 Construction of Genetic Network Using Evolutionary Algorithm and Combined Fitness Function, *Ando Shin, Hitoshi Iba* (U. Tokyo)  
09:25 - 09:50 Layout Search of a Gene Regulatory Network for 3-D Visualization, *Naoki Hosoyama, Noman Nasimul, Hitoshi Iba* (U. Tokyo)  
09:50 - 10:15 Neural-Network-Based Parameter Estimation in S-System Models of Biological Networks, *Jonas S. Almeida, Eberhard O. Voit* (U. South Carolina)  
10:15 - 10:40 Finding Optimal Gene Networks Using Biological Constraints, *Sascha Ott, Satoru Miyano* (U. Tokyo)  
10:40 - 11:00 Break

- Keynote Address** Chair: Michael Gribskov (UCSD)  
11:00 - 12:00 Predicting Nucleic Acid Hybridization and Melting Profiles, *Michael Zuker* (Rensselaer Polytechnic Inst.)  
12:00 - 13:30 Lunch

- Keynote Address** Chair: Minoru Kanehisa (Kyoto U.)  
13:30 - 14:30 Orthologous Sets of Functional Networks: Inference, Mining and Visualization, *Charles DeLisi* (Boston U.)

- Paper Session 5** Chair: Mark Ragan (U. Queensland)  
14:30 - 14:55 Efficient Tree-Matching Methods for Accurate Carbohydrate Database Queries, *Kiyoko F. Aoki, Atsuko Yamaguchi, Yasushi Okuno, Tatsuya Akutsu, Nobuhisa Ueda, Minoru Kanehisa, Hiroshi Mamitsuka* (Kyoto U.)  
14:55 - 15:20 Heuristics for Chemical Compound Matching, *Masahiro Hattori, Yasushi Okuno, Susumu Goto, Minoru Kanehisa* (Kyoto U.)  
15:20 - 15:45 Processing Sequence Annotation Data Using the Lua Programming Language, *Yutaka Ueno<sup>1</sup>, Masanori Arita<sup>1,2</sup>, Toshitaka Kumagai<sup>1</sup>, Kiyoshi Asai<sup>1,2</sup>* (<sup>1</sup>AIST, <sup>2</sup>U Tokyo)

### JSBi Annual Meeting

16:00 - 16:30

### Posters and Software Demonstrations Session 2

16:30 - 18:00

### Banquet

18:00 - 21:00

## Wednesday, December 17, 2003

- Paper Session 6** Chair: Shinichi Morishita (U. Tokyo)  
09:00 - 09:25 PatternHunter II: Highly Sensitive and Fast Homology Search, *Ming Li<sup>1</sup>, Bin Ma<sup>2</sup>, Derek Kisman<sup>3</sup>, John Tromp<sup>4</sup>* (<sup>1</sup>U Waterloo, <sup>2</sup>U Western Ontario, <sup>3</sup>Bioinformatics Solutions Inc, <sup>4</sup>CWI)  
09:25 - 09:50 On Half Gapped Seed, *Wei Chen, Wing-kin Sung* (Nat'l U Singapore)  
09:50 - 10:15 Clone-Array Pooled Shotgun Mapping and Sequencing: Design and Analysis of Experiments, *Miklós Csűrös<sup>1</sup>, Bingshan Li<sup>2</sup>, Aleksandar Milosavljevic<sup>2</sup>* (<sup>1</sup>U Montréal, <sup>2</sup>Baylor Col Med)

### Posters and Software Demonstrations Session 3

10:15 - 12:00

12:00 - 13:30 Lunch

- Paper Session 7** Chair: Kiyoshi Asai (U. Tokyo)
- 13:30 - 13:55 Prediction and Analysis of  $\beta$ -Turns in Proteins by Support Vector Machine, *Tho Hoan Pham*<sup>1</sup>, *Kenji Satou*<sup>1,2</sup>, *Tu Bao Ho*<sup>1</sup> (<sup>1</sup>JAIST, <sup>2</sup>JST)
- 13:55 - 14:20 Multi-Class Protein Fold Classification Using a New Ensemble Machine Learning Approach, *Aik Choon Tan*<sup>1</sup>, *David Gilbert*<sup>1</sup>, *Yves Deville*<sup>2</sup> (<sup>1</sup>U Glasgow, <sup>2</sup>U cath Louvain)
- 14:20 - 14:45 Multi-Class Support Vector Machines for Protein Secondary Structure Prediction, *Minh N. Nguyen*, *Jagath C. Rajapakse* (Nanyang Tech U)
- 14:45 - 15:05 Break
- Paper Session 8** Chair: Satoru Miyano (U. Tokyo)
- 15:05 - 15:30 Development of an *ab initio* Protein Structure Prediction System ABLE, *Takashi Ishida*, *Takeshi Nishimura*, *Makoto Nozaki*, *Tsuyoshi Inoue*, *Tohru Terada*, *Shugo Nakamura*, *Kentaro Shimizu* (U Tokyo)
- 15:30 - 15:55 Docking Unbound Proteins with MIAX: A Novel Algorithm for Protein-Protein Soft Docking, *Carlos A. Del Carpio Muñoz*<sup>1,2</sup>, *Tobias Peissker*<sup>3,4</sup>, *Atsushi Yoshimori*<sup>3</sup>, *Eiichiro Ichishi*<sup>1</sup> (<sup>1</sup>Tohoku U, <sup>2</sup>U Católica St Moria, <sup>3</sup>Toyohashi U Tech, <sup>4</sup>Zwickau U App Sci)
- 15:55 - 16:20 A Domain Combination Based Probabilistic Framework for Protein-Protein Interaction Prediction, *Dongsoo Han*, *Hong-Soog Kim*, *Jungmin Seo*, *Woohyuk Jang* (Info and Comm U)
- Closing and Award Ceremony**
- 16:20 - 16:35

## Commercial Exhibitions

- C1: Silicon Genetics
- C2: NABE International Corp.
- C3: Ryoka Systems Inc.
- C4: TOMY DIGITAL BIOLOGY Co., Ltd.
- C5: Hitachi, Ltd.
- C6: INFOCOM Corp.
- C7: Mitsui Knowledge Industry Co., Ltd.
- C8: Mathematical Systems Inc.
- C9: Hitachi High-Technologies Corp.
- C10: SGI Japan, Ltd.
- C11: Bioinformatics Center, Institute for Chemical Research, Kyoto University

## Software Demonstrations

- S01 CADLIVE System: Map-Based Dynamic Simulation of Biochemical Networks, *Hiroyuki Kurata*, *Rei Iwasaki*, *Kouichi Masaki*, *Takayuki Tanaka*, *Kouji Mitsukiyo*, *Yoshiyuki Sumida* (Kyushu Inst. Tech.)
- S02 Selection of Causal Gene Sets from Gene Expression Profiles Using GeneFis<sup>®</sup>, New Software Based on FNN, *Hiroyuki Honda*, *Takeshi Kobayashi* (Nagoya U.)
- S03 Development of an Integrated System for Genetic Network Analysis and Microarray Data Management, *Ji-Hung Kim*, *Kyung-Shin Lee*, *Pan-Gyu Kim*, *Hwan-Gue Cho* (Pusan Nat. U.)
- S04 An Open Source Client-Server System for the Analysis of Affymetrix Microarray Data, *Lars Martin Jakt*, *Mitsuhiro Okada*, *Shin-Ichi Nishikawa* (RIKEN)
- S05 ASIAN: A Web Site for Network Inference, *Katsuhisa Horimoto*<sup>1</sup>, *Hiroyuki Toh*<sup>2</sup>, *Sachiyo Aburatani*<sup>1</sup>, *Nobuyoshi Sugaya*<sup>1</sup>, *Hiroo Murakami*<sup>1</sup>, *Makihiko Sato*<sup>3</sup>, *Shigeru Saito*<sup>3</sup>, *Kousuke Goto*<sup>3</sup>, *Masaki Fumoto*<sup>3</sup> (<sup>1</sup>U. Tokyo, <sup>2</sup>Kyoto U., <sup>3</sup>Mitsui Sumitomo Insurance Co., Ltd.)
- S06 Netview: Application Software for Constructing and Visually Exploring Phylogenetic Networks, *Kirill Kryukov*, *Naruya Saitou* (SOKENDAI)

- S07 Integrated System for Inference of Gene Expression Network, *Masahiko Nakatsui, Takanori Ueda, Masahiro Okamoto* (Kyusyu U.)
- S08 *MutationView*: An Integrated Knowledge Base for Mutations and Polymorphisms in Human Disease Genes - Automatic Extraction of Disease-Associated Knowledge -, *Masafumi Ohtsubo<sup>1</sup>, Susumu Mitsuyama<sup>1</sup>, Takashi Kawamura<sup>1</sup>, Nobuyoshi Shimizu<sup>1</sup>, Shinsei Minoshima<sup>2</sup>* (<sup>1</sup>Keio U., <sup>2</sup>Hamamatsu U.)
- S09 BirdsAnts: Bringing Informative Rules from a Database System, Aimed at Novel Targets Search, *Motoi Tobita, Ken Horiuchi, Kenji Araki, Masashi Nemoto, Tetsuo Nishikawa* (REPRORI Co., Ltd.)
- S10 Ecell2d : Distributed E-CELL2, *Andrew Stubbings<sup>1,4</sup>, Naota Ishikawa<sup>2</sup>, Takashi Yamazaki<sup>1,4</sup>, Ariya Fujita<sup>3</sup>, Iriko Kaneko<sup>2</sup>, Yoshinari Fukui<sup>2</sup>, Toshikazu Ebisuzaki<sup>2</sup>* (<sup>1</sup>Grid Res. Inc., <sup>2</sup>RIKEN, <sup>3</sup>Swimmy Software, Inc, <sup>4</sup>Best Systems Inc.)
- S11 Integrated Distributed Computing Environment on the G-Language GAE v.2, *Ryo Hattori, Kazuharu Arakawa, Hayataro Kouchi, Masaru Tomita* (Keio U.)
- S12 SuperNORM: A Computer Program for the Parametric Normalization of Microarray Data, *Tomokazu Konishi<sup>1</sup>, Masanori Yoshida<sup>2</sup>, Kenya Shibahara<sup>2</sup>* (<sup>1</sup>Akita Prefectural U., <sup>2</sup>Skylight-Biotech Inc.)
- S13 E-CELL System Version 3: A Software Platform for Integrative Computational Biology, *Kowichi Takahashi<sup>1</sup>, Takeshi Sakurada<sup>1</sup>, Kazunari Kaizu<sup>1</sup>, Tomoya Kitayama<sup>1</sup>, Satya Arjunan<sup>1</sup>, Tatsuya Ishida<sup>1</sup>, Gabor Bereczki<sup>1</sup>, Daiki Ito<sup>1</sup>, Masahiro Sugimoto<sup>1,2</sup>, Takashi Komori<sup>3</sup>, Ohta Seiji<sup>4</sup>, Masaru Tomita<sup>1</sup>* (<sup>1</sup>Keio U., <sup>2</sup>Mitsubishi Space Software Co., Ltd., <sup>3</sup>W&G, <sup>4</sup>Mitsui Knowledge Industry Co.,Ltd.)
- S14 BPE: Biopathway Executer for Large-Scale Biopathway Modeling and Simulation, *Masao Nagasaki<sup>1</sup>, Atsushi Doi<sup>2</sup>, Kazuko Ueno<sup>1</sup>, Eri Torikai<sup>1</sup>, Hiroshi Matsuno<sup>2</sup>, Satoru Miyano<sup>1</sup>* (<sup>1</sup>U. Tokyo, <sup>2</sup>Yamaguchi U.)
- S15 Bioinformatics and Computational Biology with Biopython, *Michiel J.L. de Hoon<sup>1</sup>, Brad Chapman<sup>2</sup>, Iddo Friedberg<sup>3</sup>* (<sup>1</sup>U. Tokyo, <sup>2</sup>U. Georgia, <sup>3</sup>The Burnham Inst.)
- S16 Representing Metabolic Networks by the Substrate-Product Relationships, *Masanori Arita<sup>1,2,3</sup>* (<sup>1</sup>U. Tokyo, <sup>2</sup>CBRC, <sup>3</sup>Keio U.)

## Posters

- P001 Comprehensive Analysis of Delay in Transcriptional Regulation Using Expression Profiles, *Koji Ota, Takuji Yamada, Yoshihiro Yamanishi, Susumu Goto, Minoru Kanehisa* (Kyoto U)
- P002 Prediction of Glycan Structures from Glycosyltransferase Expression Profiles, *Shin Kawano<sup>1</sup>, Yasushi Okuno<sup>1</sup>, Kosuke Hashimoto<sup>1</sup>, Harumi Yamamoto<sup>2</sup>, Hiromu Takematsu<sup>1</sup>, Yasunori Kozutsumi<sup>1,2</sup>, Susumu Goto<sup>1</sup>, Minoru Kanehisa<sup>1</sup>* (<sup>1</sup>Kyoto U, <sup>2</sup>RIKEN)
- P003 Statistical Analysis of the Relationship between Gene Expression and Location, *Sachiyo Aburatani<sup>1</sup>, Nobuyoshi Sugaya<sup>1</sup>, Hiroo Murakami<sup>1</sup>, Makihiko Sato<sup>1,2</sup>, Katsuhisa Horimoto<sup>1</sup>* (<sup>1</sup>U Tokyo, <sup>2</sup>Fujitsu)
- P004 Detection of Genes with Tissue-Specific Patterns Using Akaike's Information Criterion, *Koji Kadota, Katsutoshi Takahashi* (AIST)
- P005 Operon Prediction by DNA Microarray: An Approach with a Bayesian Network Model, *Hitoshi Shimizu, Shigeyuki Oba, Shin Ishii* (NAIST)
- P006 Automatic Extraction of Expression-Related Features Shared by a Given Group of Genes, *Takuya Oyama<sup>1,5</sup>, Mikio Yoshida<sup>1,5</sup>, Satoshi Kamegai<sup>1,5</sup>, Kagehiko Kitano<sup>1,5</sup>, Fumihito Miura<sup>2</sup>, Noriko Kawaguchi<sup>3,5</sup>, Miyuki Onda<sup>3</sup>, Kenji Satou<sup>4,5</sup>, Takashi Ito<sup>2,3,5</sup>* (<sup>1</sup>INTEC W&G Info Corp, <sup>2</sup>U Tokyo, <sup>3</sup>Kanazawa U, <sup>4</sup>JAIST, <sup>5</sup>JST)
- P007 Dynamics of Repressilator: From Noise to Coherent Oscillation, *Tomohiro Ushikubo, Wataru Inoue, Masaki Sasai* (Nagoya U.)
- P008 Gene Expression Analysis Refining System (GEARS) via Statistical Approach: A Preliminary Report, *Chen-Hsin Chen<sup>1</sup>, Henry Horng-Shing Lu<sup>2</sup>, Chen-Tuo Liao<sup>3</sup>, Chun-houh Chen<sup>1</sup>, Ueng-Cheng Yang<sup>4</sup>, Yun-Shien Lee<sup>5</sup>* (<sup>1</sup>Acad Sinica, <sup>2</sup>Nat'l Chiao Tung U, <sup>3</sup>Nat'l Taiwan U, <sup>4</sup>Nat'l Yang-Ming U, <sup>5</sup>Chang Gung U)
- P009 CAPIES: DNA Microarray-Based Class Prediction System for Computational Diagnostics, *Sung Geun Lee<sup>1</sup>, Bonghee Seo<sup>1</sup>, Yang Seok Kim<sup>1,2</sup>* (<sup>1</sup>ISTECH Inc, <sup>2</sup>Yonsei U)
- P010 Gene Screening Method for Prognostic Prediction Using Projective ART Model, *Hiro Takahashi, Takeshi Kobayashi, Hiroyuki Honda* (Nagoya U)
- P011 Features of Gene Extraction by Nonlinear Support Vector Machines in Gene Expression Analysis, *Daisuke Komura, Hiroshi Nakamura, Shuichi Tsutsumi, Hiroyuki Aburatani, Sigeo Ihara* (U Tokyo)

- P012 Prognosis Prediction by Microarray Gene Expression Using Support Vector Machine, *Chihoko Tago, Taizo Hanai, Masahiro Okamoto* (Kyushu U)
- P013 Automatically Finding Good Clusters with Seed K-Means, *Miyoung Shin, Eun Mi Kang, Seon Hee Park* (ETRI)
- P014 Analysis of DNA Microarray Data by Using Self-Organizing Maps, *Tomoyuki Kato, Kikuo Fujimura, Heizo Tokutaka, Yasushi Kawata, Masaaki Ohkita* (Tottori U)
- P015 Clustering Method Based on Onset and Cessation of Gene Expression, *Kazumi Hakamada, Taizo Hanai, Masahiro Okamoto* (Kyushu U)
- P016 Significance Test of Clusters in Gene Expression Profile Data, *Natsuko Kawase, Shigeyuki Oba, Shin Ishii* (NAIST)
- P017 Gene Expression Analysis Using Fuzzy K-Means Clustering, *Chinatsu Arima, Taizo Hanai, Masahiro Okamoto* (Kyushu U)
- P018 A Method for Normalization of Gene Expression Data, *Makoto Kano<sup>1</sup>, Hisashi Kashima<sup>1</sup>, Tetsuo Shibuya<sup>1</sup>, Kaori Ide<sup>2</sup>, Aiko Kashihara<sup>2</sup>, Noriko Nakagawa<sup>2,3</sup>, Mariko Hatakeyama<sup>2</sup>, Seiki Kuramitsu<sup>2,3</sup>, Akihiko Konagaya<sup>2</sup>* (<sup>1</sup>IBM, <sup>2</sup>Riken, <sup>3</sup>Osaka U)
- P019 Normalization of Target Fluorescence Using Reference Fluorescence for cDNA Microarray Method, *Yu Suzuki, Kenji Hatano, Shigehiko Kanaya, Shunsuke Uemura* (NAIST)
- P020 A System for Visualizing Gene Expressions Using Metabolic Networks, *Ryoko Tamaru, Toshiyuki Amagasa, Shigehiko Kanaya, Shunsuke Uemura* (NAIST)
- P021 Image Preprocessing for cDNA Microarray Using Deconvolution Method, *Hyo Jung Ban<sup>1</sup>, Myungguen Chung<sup>1,2</sup>, Yong Sung Lee<sup>1</sup>, Jin Hyuk Kim<sup>1</sup>, Young Seek Lee<sup>1</sup>* (<sup>1</sup>Han-yang U, <sup>2</sup>ETRI)
- P022 On Visualization, Screening, and Classification of Cell Cycle-Regulated Genes in Yeast, *Henry Horng-Shing Lu<sup>1</sup>, Han-Ming Wu<sup>2</sup>* (<sup>1</sup>Nat'l Chiao-Tung U, <sup>2</sup>Acad Sinica)
- P023 A PCA Based Method of Gene Expression Visual Analysis, *Kunihiro Nishimura, Koji Abe, Shumpei Ishikawa, Shuichi Tsutsumi, Koichi Hirota, Hiroyuki Aburatani, Michitaka Hirose* (U Tokyo)
- P024 Bioinformatics for Oncogenomic Target Identification, *Masaru Katoh* (NCC)
- P025 Multiscale Bootstrap Analysis of Gene Networks Based on Bayesian Networks and Nonparametric Regression, *Takeshi Kamimura<sup>1</sup>, Hidetoshi Shimodaira<sup>1</sup>, Seiya Imoto<sup>2</sup>, SunYong Kim<sup>2</sup>, Kousuke Tashiro<sup>3</sup>, Satoru Kuhara<sup>3</sup>, Satoru Miyano<sup>2</sup>* (<sup>1</sup>Tokyo Inst Tech, <sup>2</sup>U Tokyo, <sup>3</sup>Kyushu U)
- P026 Combining Gene Expression Data with DNA Sequence Information for Estimating Gene Networks Using Bayesian Network Model, *Yoshinori Tamada<sup>1</sup>, SunYong Kim<sup>2</sup>, Hideo Bannai<sup>2</sup>, Seiya Imoto<sup>2</sup>, Kousuke Tashiro<sup>3</sup>, Satoru Kuhara<sup>3</sup>, Satoru Miyano<sup>2</sup>* (<sup>1</sup>Kyoto U, <sup>2</sup>U Tokyo, <sup>3</sup>Kyushu U)
- P027 Enumeration of Likely Gene Networks and Network Motif Extraction for Large Gene Networks, *Sascha Ott, Satoru Miyano* (U Tokyo)
- P028 Genetic Networks with Stochastic Fluctuations, *Luonan Chen<sup>1</sup>, Ruiqi Wang<sup>1</sup>, Kazuyuki Aihara<sup>2</sup>* (<sup>1</sup>Osaka Sangyo U, <sup>2</sup>U Tokyo)
- P029 Integrative Method for Identifying Combinatorial Regulation of Transcription Factors, *Mamoru Kato<sup>1,2</sup>, Naoya Hata<sup>2</sup>, Nila Banerjee<sup>2</sup>, Michael Q. Zhang<sup>2</sup>* (<sup>1</sup>CSSL, <sup>2</sup>RIKEN)
- P030 Pathways/Networks to Syndrome X, *Tsuguchika Kaminuma<sup>1</sup>, Masumi Yukawa<sup>2</sup>, Naomi Komiyama<sup>2</sup>, Kotoko Nakata<sup>3</sup>, Hiroki Momose<sup>4</sup>, Yoshitomo Tanaka<sup>4</sup>, Hiroshi Tanaka<sup>4</sup>* (<sup>1</sup>Biodynamics Inc., <sup>2</sup>CBI, <sup>3</sup>NIHS, <sup>4</sup>Tokyo Med & Dent U)
- P031 Identification of Regulation Networks of Lipid Metabolism by Nuclear Receptors, *Yoshitomo Tanaka<sup>1</sup>, Tsuguchika Kaminuma<sup>2</sup>, Hiroki Momose<sup>1</sup>, Kotoko Nakata<sup>3</sup>, Hiroshi Tanaka<sup>1</sup>* (<sup>1</sup>Tokyo Med&Dent U, <sup>2</sup>Biodynamics Inc., <sup>3</sup>NIHS)
- P032 Analysis of Gene Regulation Network by Nuclear Receptor PPAR, *Hiroki Momose<sup>1</sup>, Tsuguchika Kaminuma<sup>2</sup>, Yoshitomo Tanaka<sup>1</sup>, Kotoko Nakata<sup>3</sup>, Hiroshi Tanaka<sup>1</sup>* (<sup>1</sup>Tokyo Med&Dent U, <sup>2</sup>Biodynamics Inc., <sup>3</sup>NIHS)
- P033 Analysis of Reactive Modules in the Metabolic Pathways, *Masaaki Kotera, Masahiro Hattori, Susumu Goto, Minoru Kanehisa* (Kyoto U)
- P034 Metabolic Pathway Reconstruction for Malaria Parasite *Plasmodium falciparum*, *Vachiranee Limviphu-vadh<sup>1</sup>, Yasushi Okuno<sup>1</sup>, Toshiaki Katayama<sup>2</sup>, Susumu Goto<sup>1</sup>, Akiyasu C. Yoshizawa<sup>1</sup>, Minoru Kanehisa<sup>1</sup>* (<sup>1</sup>Kyoto U, <sup>2</sup>U Tokyo)
- P035 Extraction of a Thermodynamic Property for Biochemical Reactions in the Metabolic Pathway, *Michihiro Tanaka<sup>1</sup>, Yasushi Okuno<sup>2</sup>, Takuji Yamada<sup>2</sup>, Susumu Goto<sup>2</sup>, Shunsuke Uemura<sup>1</sup>, Minoru Kanehisa<sup>2</sup>* (<sup>1</sup>NAIST, <sup>2</sup>Kyoto U)
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