

**GIW 2005**  
**The Sixteenth International Conference on Genome Informatics**  
**Pacifico Yokohama, Japan**  
**December 19–21, 2005**

**Scope**

GIW is the longest running international bioinformatics conference, which provides unique opportunities that bridge theory and experiments, academia and industry, and East and West. Its scope includes all work that is ultimately devoted to the computational understanding of biological systems on a molecular basis.

**Sponsored and Organized by**

Bioinformatics Center (Kyoto University)

Human Genome Center (University of Tokyo)

Systems Genomics Towards System-Level Understanding of Life (MEXT of Japan)

Japanese Society for Bioinformatics (JSBi)

**Steering Committee**

Minoru Kanehisa (Kyoto University)

Toshihisa Takagi (University of Tokyo)

Satoru Miyano (University of Tokyo)

# GIW 2005

The Sixteenth International Conference on Genome Informatics  
Pacifico Yokohama, Japan  
December 19–21, 2005

## Registration

Registration should be done at: <http://giw.ims.u-tokyo.ac.jp/giw2005/registration.html> until December 4, 2005. Registration fee includes a copy of Genome Informatics Vol. 16, No. 2 and coffee breaks. We offer registration fee discount for JSBi and ISCB members.

		until Dec. 4, 2005	after Dec. 4, 2005
Standard Registration	Standard	JPY15,000.-	JPY20,000.-
	ISCB Member	JPY14,000.-	JPY19,000.-
	JSBi Member	JPY8,000.-	JPY13,000.-
	JSBi & ISCB Member	JPY7,000.-	JPY12,000.-
Student Registration	Standard	JPY10,000.-	JPY15,000.-
	ISCB Member	JPY9,000.-	JPY14,000.-
	JSBi Member	JPY5,000.-	JPY10,000.-
	JSBi & ISCB Member	JPY4,000.-	JPY9,000.-

(Banquet on December 20 evening : JPY6,000.-)

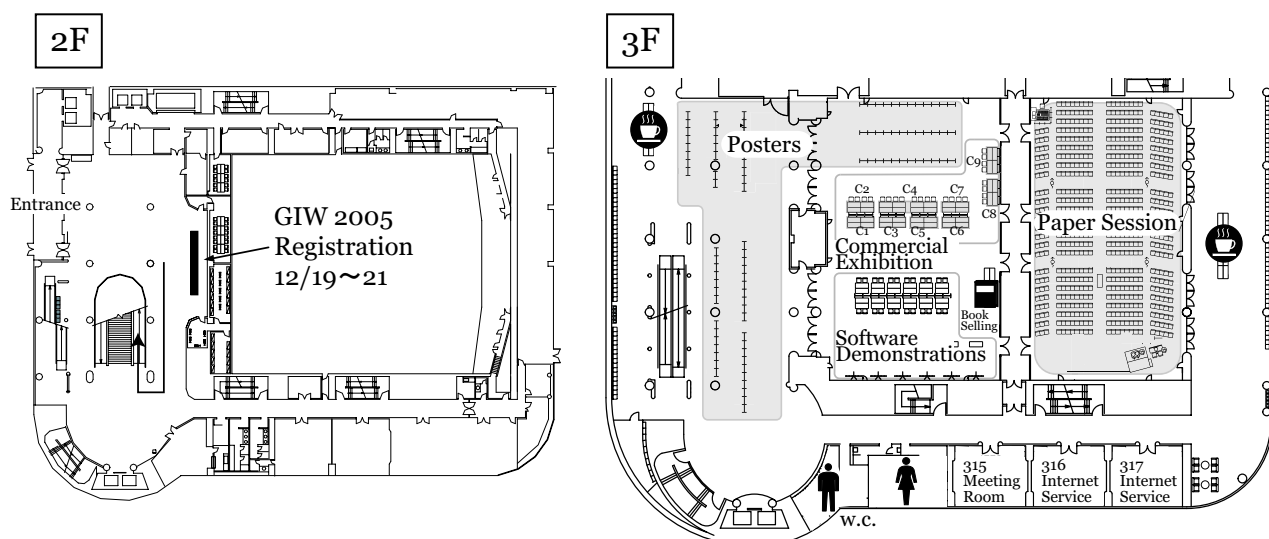
## Secretary and Local Arrangements

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/giw2005/index.html>

## Location

The conference will take place at PACIFICO YOKOHAMA. Please get off at Minato Mirai Station on the Minato Mirai Line (connecting from the Tokyu Toyoko Line). It takes about 3 minutes' walk from the Minato Mirai Station to Pacifico Yokohama.  
Address: 1-1-1, Minato Mirai, Nishi-ku, Yokohama 220-0012, Japan  
Tel: +81-45-221-2155  
URL: [http://www.pacifico.co.jp/index\\_e.html](http://www.pacifico.co.jp/index_e.html)

## Conference Center



# GIW 2005 Advanced Program

## Registration

December 19, 2005: 08:30 - 18:00

December 20, 2005: 08:00 - 18:00

December 21, 2005: 08:00 - 16:00

## Monday, December 19, 2005

### Opening Address

09:00 - 09:10 Reinhart Heinrich (Humboldt U.) and Hiroshi Mamitsuka (Kyoto U.)

### Paper Session 1

Chair: Tetsuo Shibuya (U.Tokyo)

09:10 - 09:35 Qualitatively Predicting Acetylation and Methylation Areas in DNA Sequences, *Tho Hoan Pham*<sup>1</sup>, *Dang Hung Tran*<sup>2</sup>, *Tu Bao Ho*<sup>2,3</sup>, *Kenji Satou*<sup>2,3</sup>, *Gabriel Valiente*<sup>4</sup> (<sup>1</sup>Hanoi U. Pedagogy, <sup>2</sup>JAIST, <sup>3</sup>JST, <sup>4</sup>Technical U. Catalonia)

09:35 - 10:00 Knowledge-Based Prediction of DNA Atomic Structure from Nucleic Sequence, *Marcos J. Araúzo-Bravo*, *Akinori Sarai* (U. Vermont)

10:00 - 10:25 Prediction of Functional Modules Based on Gene Distributions in Microbial Genomes, *Hongwei Wu*<sup>1,2</sup>, *Fenglou Mao*<sup>1</sup>, *Zhengchang Su*<sup>1,2</sup>, *Victor Olman*<sup>1</sup>, *Ying Xu*<sup>1,2</sup> (<sup>1</sup>U. Georgia, <sup>2</sup>Oak Ridge National Lab.)

10:25 - 11:00 Break

### Keynote Address

Chair: Hiroshi Mamitsuka (Kyoto U.)

11:00 - 12:00 Chemoinformatics, Drug Design, and Systems Biology, *Pierre Baldi* (UC Irvine)

12:00 - 13:30 Lunch

### Posters and Software Demonstrations Session 1

13:30 - 14:30 ( Odd Number )

### Paper Session 2

Chair: Oliver Ebenhöf (Humboldt U.)

14:30 - 14:55 Supporting the Curation of Biological Databases with Reusable Text Mining, *Olivo Miotto*<sup>1</sup>, *Tin Wee Tan*<sup>1</sup>, *Vladimir Brusilovskii*<sup>2,3</sup> (<sup>1</sup>National U. Singapore, <sup>2</sup>U. Queensland, <sup>3</sup>Inst. for Infocomm Res.)

14:55 - 15:20 Reconstruction of Phylogenetic Relationships from Metabolic Pathways Based on the Enzyme Hierarchy and the Gene Ontology, *José C. Clemente*<sup>1</sup>, *Kenji Satou*<sup>1</sup>, *Gabriel Valiente*<sup>2</sup> (<sup>1</sup>JAIST, <sup>2</sup>Technical U. Catalonia)

15:20 - 15:45 Mass Identification of Chloroplast Proteins of Endosymbiont Origin by Phylogenetic Profiling Based on Organism-Optimized Homologous Protein Groups, *Naoki Sato*, *Masayuki Ishikawa*, *Makoto Fujiwara*, *Kintake Sonoike* (U. Tokyo)

15:45 - 16:15 Break

### Paper Session 3

Chair: Limsoon Wong (Inst. Infocomm Res.)

16:15 - 16:40 Strategies for Genome Reduction in Microbial Genomes, *Kishore R. Sakharkar*, *Vincent T.K. Chow* (National U. Singapore)

16:40 - 17:05 Reassembly and Interfacing Neural Models Registered on Biological Model Databases, *Mihoko Otake*<sup>1,2</sup>, *Toshihisa Takagi*<sup>1</sup> (<sup>1</sup>U. Tokyo, <sup>2</sup>PRESTO, JST)

- 17:05 - 17:30 Objective Measurement of Spindle Orientation in Early *Caenorhabditis elegans* Embryo, *Shugo Hamahashi*<sup>1,2</sup>, *Shuichi Onami*<sup>1,2</sup> (<sup>1</sup>Keio U., <sup>2</sup>JST)
- 17:30 - 17:55 Evolution from Possible Primitive tRNA-Viroids to Early Poly-tRNA-Derived mRNAs: A New Approach from the Poly-tRNA Theory, *Koji Ohnishi*, *Madoka Ohshima*, *Naotaka Furuichi* (Niigata U.)

## Tuesday, December 20, 2005

- Paper Session 4** Chair: Ying Xu (U. Georgia)
- 09:00 - 09:25 A Study of Fragment-Based Protein Structure Prediction: Biased Fragment Replacement for Searching Low-Energy Conformation, *Sung-Joon Park* (Kobe U.)
- 09:25 - 09:50 Comparison of Protein Structures by Multi-Objective Optimization, *Lunan Chen*<sup>1</sup> *Ling-Yun Wu*<sup>2</sup>, *Ruiqi Wang*<sup>1</sup>, *Yong Wang*<sup>1</sup> *Shihua Zhang*<sup>2</sup>, *Xiang-Sun Zhang*<sup>2</sup> (<sup>1</sup>Osaka Sangyo U., <sup>2</sup>Chinese Acad. of Sci.)
- 09:50 - 10:15 Statistical Evaluation of a Bottom-Up Clustering for Single Particle Molecular Images, *Yutaka Ueno*<sup>1</sup>, *Katsunori Isono*<sup>1,2</sup>, *Katsutoshi Takahashi*<sup>1</sup>, *Yukio Shimonohara*<sup>1,3</sup>, *Kiyoshi Asai*<sup>1</sup> (<sup>1</sup>CBRC, <sup>2</sup>INTEC Web and Genome Informatics Corp., <sup>3</sup>Information and Mathematical Science Laboratory Inc.)
- 10:15 - 10:45 Break
- Paper Session 5** Chair: Koji Tsuda (CBRC)
- 10:45 - 11:10 Inter-Species Validation for Domain Combination Based Protein-Protein Interaction Prediction Method, *Woo-Hyuk Jang*<sup>1</sup>, *Dong-Soo Han*<sup>1,3</sup>, *Hong-Soog Kim*<sup>2</sup>, *Sung-Doke Lee*<sup>1</sup> (<sup>1</sup>Information & Communications U., <sup>2</sup>Electronics & Telecommunications Res. Inst., <sup>3</sup>Correspondence author)
- 11:10 - 11:35 A Graph Theoretical Approach for Analysis of Protein Flexibility Change at Protein Complex Formation, *Carlos A. Del Carpio M.*<sup>1</sup>, *Abdul Rajjak Shaikh*<sup>1</sup>, *Eichiro Ichiishi*<sup>1</sup>, *Michihisa Koyama*<sup>1</sup>, *Momoji Kubo*<sup>1,2</sup>, *Kazumi Nishijima*<sup>1,3</sup>, *Akira Miyamoto*<sup>1</sup> (<sup>1</sup>Tohoku University, <sup>2</sup>PRESTO, JST, <sup>3</sup>Mochida Pharmaceutical Co. Ltd.)
- 11:35 - 12:00 A Fast Protein-Protein Docking Algorithm Using Series Expansion in Terms of Spherical Basis Functions, *Kazuya Sumikoshi*, *Tohru Terada*, *Shugo Nakamura*, *Kentaro Shimizu* (U. Tokyo)
- 12:00 - 13:30 Lunch
- Keynote Address** Chair: Kenta Nakai (U. Tokyo)
- 13:30 - 14:30 Membrane Proteins in Vivo and in Silico: Getting the Best of Two Worlds, *Gunnar von Heijne* (Stockholm U.)
- Paper Session 6** Chair: Gabriel Valiente (Tech. U. Catalonia)
- 14:30 - 14:55 Viewing the Proteome from Oligopeptides and Prediction of Protein Function, *Hisayuki Horai*<sup>1,2</sup>, *Kowichi Doi*<sup>1</sup>, *Hirofumi Doi*<sup>1,2</sup> (<sup>1</sup>NAIST, <sup>2</sup>Celestar Lexico-Sciences, Inc.)
- 14:55 - 15:20 Mass Distributed Clustering: A New Algorithm for Repeated Measurements in Gene Expression Data, *Shinya Matsumoto*<sup>1</sup>, *Ken-ichi Aisaki*<sup>2</sup>, *Jun Kanno*<sup>2</sup> (<sup>1</sup>NCR Japan, Ltd., <sup>2</sup>NIHS)

15:20 - 15:45      Diagnosis of Early Relapse in Ovarian Cancer Using Serum Proteomic Profiling, *Jung Hun Oh*<sup>1</sup>, *Jean Gao*<sup>1</sup>, *Animesh Nandi*<sup>2</sup>, *Prem Gurnani*<sup>2</sup>, *Lynne Knowles*<sup>3</sup>, *John Schorge*<sup>3</sup>, *Kevin P. Rosenblatt*<sup>2</sup> (<sup>1</sup>U.Texas, <sup>2</sup>UT Southwestern Med. Center, Dallas)

15:45: - 16:00      Break

### JSBi Annual Meeting

16:00 - 16:30

### Posters and Software Demonstrations Session 2

16:30 - 18:00      ( Even Number )

### Banquet

18:30 - 20:30      Ballroom "Monaco" at Inter Continental The Grand Yokohama

## Wednesday, December 21, 2005

### Paper Session 7      Chair: Tatsuya Akutsu (Kyoto U.)

09:00 - 09:25      Reverse Engineering Genetic Networks Using Evolutionary Computation, *Nasimul Noman*, *Hitoshi Iba* (U. Tokyo)

09:25 - 09:50      Toward Integration of Systems Biology Formalism: The Gene Regulatory Networks Case, *Raffaella Gentilini* (U. Udine)

09:50 - 10:15      Reconstruction of Gene Regulatory Networks under the Finite State Linear Model, *Dace Ruklisa*<sup>1</sup>, *Alvis Brazma*<sup>2</sup>, *Juris Viksna*<sup>1</sup> (<sup>1</sup>U. Latvia, <sup>2</sup>EBI)

10:15 - 10:40      A Space-Efficient Algorithm for the Constrained Pairwise Sequence Alignment Problem, *Dan He*, *Abdullah N. Arslan* (U. Vermont)

### Posters and Software Demonstrations Session 3

10:40 - 12:00

12:00 - 13:30      Lunch

### Keynote Address      Chair: Reinhart Heinrich (Humboldt U.)

13:30 - 14:30      Cell-Cell Interaction Network That Generates the Skin Pattern of Animal, *Shigeru Kondo* (Nagoya U.)

### Paper Session 8      Chair:

14:30 - 14:55      Automatic Drawing of Biological Networks Using Cross Cost and Subcomponent Data, *Mitsuru Kato*, *Masao Nagasaki*, *Atsushi Doi*, *Satoru Miyano* (U. Tokyo)

14:55 - 15:20      Interaction Graph Mining for Protein Complexes Using Local Clique Merging, *Xiao-Li Li*<sup>1</sup>, *Soon-Heng Tan*<sup>1,2</sup>, *Chuan-Sheng Foo*<sup>1,3</sup>, *See-Kiong Ng*<sup>1</sup> (<sup>1</sup>Inst. for Infocomm Res., <sup>2</sup>National U. Singapore, <sup>3</sup>Stanford U.)

15:20 - 15:45      Topology of Mammalian Transcription Networks, *Anatolij P. Potapov*<sup>1</sup>, *Nico Voss*<sup>2</sup>, *Nicole Sasse*<sup>1</sup>, *Edgar Wingender*<sup>1,2</sup> (<sup>1</sup>U. Göttingen, <sup>2</sup>BIOBASE GmbH)

### Closing and Award Ceremony

15:45 - 16:00

## **Commercial Exhibitions**

- C1: Ryoka Systems Inc.
- C2: CTC Laboratory Systems Corporation
- C3: NABE International Corporation
- C4: SGI Japan, Ltd.
- C5: Mathematical Systems, Inc.
- C6: Pathway Solutions Inc.
- C7: HITACHI, LTD.
- C8: INFOCOM CORPORATION
- C9: HIT corporation Ltd.

## Software Demonstrations

- S01 Using the Approach of Comparative Proteomics and Systems Biology to Decipher the Human Protein Network, *Chung-Yen Lin, Fan-Kai Lin, Chi-Shyang Cho, Chieh-Hwa Lin, Li-Wei Lai, Chao A. Hsiung*
- S02 b-Src: A Source-Code Search Engine for Bioinformatics Open-Source Packages, *Mitsuteru Nakao, Paul Horton*
- S03 INOH: Pathways and Ontologies, *Noriko Sakai, Tatsuya Kushida, Satoko Yamamoto, Emi Hattori, Hiromi Nakamura, Yuki Yamagata, Yukiko Nakanishi, Toshihisa Takagi, Ken Ichiro Fukuda*
- S04 Fast Retrieval of Useful Information from Literature Database, *Hiroko Matsui, Shigeki Tanishima, Norihiro Akasaka, Takafumi Hayashi, Keiko Oketa, Keizoh Uehara*
- S05 VECT: The Visual Extraction and Conversion Tool, *Hui-Hsien Chou*
- S06 Toxicogenomics: Novel Computational Strategies for Prediction of Long Term Carcinogenicity, *Jochen Koenig, Claire Pallez, Hans Gmuender, Reinhard Doelz, Deepak Thakkar, Frank Staubli*
- S07 AlignScope : A System for Visualization and Analysis of Whole Genome Alignments, *Hee-Jeong Jin, Hye-Jung Kim, Hwan-Gue Cho*
- S08 KeyMolnet: An Integrated Platform for Analysis of Molecular Networks, *Atsushi Nogi, Hiromi Sato, Miki Fukuda, Makoto Shigetaka, Yohei Ozeki, Misa Ogura, Kyoko Nakanishi, Rie Taniguchi, Hisako Kuriki, Nakako Iwasaki, Yoko Inoue, Yoko Wakamatsu, Shizuka Homma, Mikiko Izumi, Yoshinobu Mizoguchi, Yuichi Kikushima, Takeshi Namba, Keiichi Ayabe, Nobuo Tomioka, Akiko Itai*
- S09 BioRuby+ChemRuby: An Exploratory Software Project, *Toshiaki Katayama, Mitsuteru C. Nakao, Naohisa Goto, Nobuya Tanaka*
- S10 Cell Illustrator 2.0: A Platform for Biopathway Modeling and Simulation, *Masao Nagasaki, Atsushi Doi, Satoru Miyano*
- S11 Tools for Supporting Computational Experiments on Genomic Object Net, *Toshinori Tanaka, Katsuyuki Harada, Hironori Kitakaze, Junkichi Yamanaka, Hiroshi Matsuno, Satoru Miyano*

## Posters

- P001 Systematic Analysis of Structure-Stability Relationship for Proteins and Mutants, *Noboru Furukawa, Yuko Takeno, Goran Neshich, Akinori Sarai*
- P002 Hierarchy of Metabolic Compounds Based on Their Synthesizing Capacity, *Thomas Handorf, Oliver Ebenhöf, Daniel Kahn, Reinhart Heinrich*
- P003 IBTS: An Extensible System for Integration of Bioinformatics Tools Allowing Cluster Computing, *Youngmahn Hahn, Yongseong Cho, Sang Joo Lee*
- P004 Virtual Drug Screening of Endothelin Receptor Ligands Using Active Learning, *Yukiko Fujiwara, Yoshiko Yamashita, Minoru Asogawa, Chiaki Fukushima, Masaaki Asao, Hideshi Shimadzu, Kazuya Nakao, Ryo Shimizu*
- P005 KAAS: KEGG Automatic Annotation Server, *Yuki Moriya, Masumi Itoh, Sujiro Okuda, Minoru Kanehisa*
- P006 Mining Implicit Biological Related Entities from Literature Using a Probabilistic Model, *Shanfeng Zhu, Yasushi Okuno, Gozoh Tsujimoto, Hiroshi Mamitsuka*
- P007 Constraints Based Dynamic Protein Interaction Network, *Dong-Soo Han, Suk-Hoon Jung, Woo-Hyuk Jang, Choon-Ho Lee*
- P008 New Features of *MutationView* : Implementation of Various Protein-Oriented Tools to Find out the Relation between Protein Function and Diseases, *Masafumi Ohtsubo, Takashi Kawamura, Susumu Mitsuyama, Nobuyoshi Shimizu, Shinsei Minoshima*
- P009 KEGG-Based Pathway Visualization Tool for Complex Omics Data, *Nobuaki Kono, Kazuharu Arakawa, Yohei Yamada, Hirotada Mori, Masaru Tomita*
- P010 Visualization of Gene Database on WEB Using Self Organizing Maps, *Yasuhiko Miyazaki, Hiroshi Dozono, Hisao Tokushima, Yoshio Noguchi*
- P011 Evolutionary Identifications of Functional Modules in Yeast Protein Interaction Network, *Soichi Ogishima, Yasuhiro Suzuki, Takashi Hase, So Nakagawa, Hiroshi Tanaka*
- P012 An Integrated Database and Knowledge-Base of Interaction between Human Proteins and Commonly Used Drugs, *Hiroyasu Shimada, Masashi Nemoto, Ken Horiuchi, Atsuko Yamaguchi, Motoi Tobita, Kenji Araki, Tetsuo Nishikawa*
- P013 Structural Annotation Viewer and Database for Splice-Variant Human cDNA Sequences, *Tetsuo Nishikawa, Kouichi Kimura, Jun-ichi Yamamoto, Ai Wakamatsu, Hiroshi Makita, Keiichi Nagai, Sumio Sugano, Nobuo Nomura, Takao Isogai*
- P014 PRIME: Platform for RIKEN Metabolomics, *Atsushi Fukushima, Miyako Kusano, Kenji Akiyama, Takeshi Obayashi, Takayuki Tohge, Masami Yokota Hirai, Shigehiko Kanaya, Masanori Arita, Yoko Shinbo, Kazuo Shinozaki, Tetsuya Sakurai, Kazuki Saito*
- P015 Construction of Reference Cis-Regulatory Module Database as a Tool for the Pattern Analysis of Cis-Regulatory Regions on Human Genome Sequence, *Eri Kibukawa, Yoshiaki Tanaka, Satoru Miyazaki*
- P016 BioTextLinker: Dynamic Informative Link Annotation for Biological Text over Heterogeneous Databases, *Hodong Lee, Jong C. Park*
- P017 MiDB: Mitochondrial Proteomics Database in Human Heart, *Hyun Joo, Taeho Kim, Jae Boum Youm, Nari Kim, Jin Han*
- P018 FAMSBASE of Human, Rat and Mouse Genomes with Model Quality Estimation, *Mitsuo Iwate, Kazuhiko Kanou, Genki Terashi, Mayuko Takeda-Shitaka, Hideaki Umeyama*
- P019 Framework Approach for a Search Platform on Biological Data, *Seok Jong Yu, Dan Bi Kim, Inae Hur, Sang Joo Lee*



- P020 PSE: A Tool for Browsing a Large Amount of PubMed Abstracts with Gene Names and Common Words as the Keywords, *Takashi Yoneya*
- P021 RPAIR: A Database of Chemical Transformation Patterns in Enzymatic Reactions, *Takuji Yamada, Masahiro Hattori, Min A. Oh, Susumu Goto, Minoru Kanehisa*
- P022 A Resource Discovery Service for Bioinformatics Applications in a Grid-Based Environment, *Xiujun Gong, Jitender Jit Singh Cheema, Kensuke Nakamura, Kei Yura, Nobuhiro Go*
- P023 Gene Annotation Using Proteomic Data, *Yoko Ishino, Hisaaki Taniguchi*
- P024 A Database for Comparative Analysis of Tunicate Promoter Sequences, *Nicolas Sierro, Takehiro Kusakabe, Keun-Joon Park, Riu Yamashita, Kengo Kinoshita, Kenta Nakai*
- P025 An Existence of Cooperative (*Clustered*) Genes in Coliphage $\phi$ k, *Eisei Takushi, Miyako Kawachi*
- P026 Evaluation Measures of ‘Marker Selection’ and ‘Genotype Membership’ in Large-Scale SNP Genotyping, *Eli Kaminuma, Hiroshi Masuya, Hiromi Motegi, K. Ryo Takahasi, Miki Nakazawa, Minami Matsui, Yoichi Gondo, Tetsuo Noda, Toshihiko Shiroishi, Shigeharu Wakana, Tetsuro Toyoda*
- P027 Finding Small and Resistance-Predictable Feature Sets for Bacterium Classification by Multi-Objective Optimization, *Hiroshi Yamakawa, Yoshio Nakao, Takahisa Suzuki, Yumiko Sanbongi, Takashi Ida*
- P028 Sensitizing GO Tools Using Multiple Ratio-Cutoffs for Gene Selection, *Kenichi Hirotani, Yoichi Yamada, Miyuki Onda, Ken-ichiro Muramoto, Kenji Satou, Takashi Ito*
- P029 Cell-Distance Networks: A Clue for Understanding of Cell Diversity, *Larisa Kiseleva, Paul Horton, Wataru Fujibuchi*
- P030 How Much We Know about Soluble Domains Existing in Loop Regions of Transmembrane Proteins?, *Syuuichi Yoshida, Masafumi Arai, Takuhiro Nishio, Toshio Shimizu*
- P031 Discovering Novel MicroRNAs from Small RNA Component of the Mouse Embryo Transcriptome, *Tatsuya Ando, Sachiko Okamoto, Masahiro Sato, Hiroyuki Izu, Masanori Takayama, Masanari Kitagawa, Junichi Mineno, Kiyozo Asada, Ikunoshin Kato*
- P032 Inferring Protein Interaction Network by Boosting Algorithm, *Yong Wang, Feng Bao, Jiadong Zhang, Luonan Chen*
- P033 Construction of Human Gene Catalogue by mRNA Using 1.4 Million of Full-Length cDNAs by Oligo-Capping Method, *Ai Wakamatsu, Jun-ichi Yamamoto, Kouichi Kimura, Keisuke Tsuchiya, Tetsuo Nishikawa, Sumio Sugano, Takao Isogai*
- P034 Genome Mapping Analysis of Splice Variant One-Pass Sequences of Human Full-Length cDNAs, *Kouichi Kimura, Tetsuo Nishikawa, Ai Wakamatsu, Jun-ichi Yamamoto, Keiichi Nagai, Nobuo Nomura, Sumio Sugano, Takao Isogai*
- P035 State Space Model with Markov Switching for Estimating Time-Dependent Gene Regulatory Networks from Time Series Microarray Experiments, *Ryo Yoshida, Seiya Imoto, Tomoyuki Higuchi, Satoru Miyano*
- P036 Knowledge Discovery Using Cross Database Search, *Asako Koike, Toshihisa Takagi*
- P037 Ontology Based Petri Net Modeling of Signaling Networks, *Takako Takai-Igarashi*
- P038 Discovering Reliable Protein Interactions Using Bayesian Networks, *Thanh Phuong Nguyen, Tu Bao Ho, Ngoc Binh Nguyen*
- P039 Cluster Analysis of Neutrophilic Differentiation by Using Fuzzy K-Means, *Akitsu Suga, Kazumi Hakamada, Chinatsu Arima, Masahiro Okamoto, Hitoshi Ichikawa, Taizo Hanai*

- P040 Validity Index for Fuzzy K-Means Clustering Using the Gap Statistic Method, *Chinatsu Arima, Kazumi Hakamada, Masahiro Okamoto, Taizo Hanai*
- P041 Validation of Mathematical Model Based Clustering by Using Time-Course Data, *Kazumi Hakamada, Masahiro Okamoto, Taizo Hanai*
- P042 Improvement in the Accuracy of Gene Prediction in Rice cDNA Sequences, *Fusano Todokoro, Takeshi Itoh, Chisato Yamasaki, Hiroaki Kawashima, Tadashi Imanishi, Takashi Gojobori*
- P043 Co-Expression Analysis Tool for Large Gene Expression Datasets, *Hajime Harada, Natalia Polouliakh, Wataru Fujibuchi, Paul Horton*
- P044 New Reliable Cancer Diagnosis Method Using Boosting and Projective Adaptive Resonance Theory, *Hiro Takahashi, Yasuyuki Murase, Hiroyuki Honda*
- P045 Classification Method for Prediction of Multifactorial Disease Development by Using Genetic and Environmental Factors, *Yasuyuki Tomita, Mitsuhiro Yokota, Hiroyuki Honda*
- P046 Ranking Metabolic Paths with Expression Similarities, *Ichigaku Takigawa, Hiroshi Mamitsuka*
- P047 Classifying Microarray Data Using Pairwise Similarity between Gene Profiles, *Raymond Wan, Ása M. Wheelock, Matthew J. Bartosiewicz, Hiroshi Mamitsuka*
- P048 A Selection Criterion for Robust Classifiers: Cancer Prognosis with Microarray Gene Expression, *Ikumi Suzuki, Shigeeyuki Oba, Shin Ishii*
- P049 Memory-Efficient Clustering Algorithms for Microarray Gene Expression Data, *Kazuyuki Numata, Hideo Bannai, Yoshinori Tamada, Michiel de Hoon, Seiya Imoto, Satoru Miyano*
- P050 Clustering Gene Expression Data with Stepwise Data Envelopment Analysis, *Masako Hoshino, Hiroshige Inazumi*
- P051 Effective Nearest Neighbor Methods for Multiclass Cancer Classification Using Microarray Data, *Satoshi Niijima, Satoru Kuhara*
- P052 Algorithm for Predicting Co-Expression Genes by Improvement of Path Consistency Algorithm, *Shigeru Saito, Sachiyo Aburatani, Katsuhisa Horimoto*
- P053 A New Method for Analyzing Large-Scale Microarray Data Using Biological Knowledge, *Shingo Tsuji, Kouji Nakayama, Masaru Sekijima, Shigeo Ihara, Hiroyuki Aburatani*
- P054 Non-Negative Matrix Factorization of Lung Adenocarcinoma Expression Profiles, *Takeshi Fujiwara, Shumpei Ishikawa, Yujin Hoshida, Kentaro Inamura, Takayuki Isagawa, Miyuki Shimane, Hiroyuki Aburatani, Yuichi Ishikawa, Hitoshi Nomura*
- P055 Classification of Cancer Data with Genetic Programming, *Topon Kumar Paul, Hitoshi Iba*
- P056 The Application of Cell Surface Marker DNA Microarray in the Search for Molecular Targets, *Tuoya, Koichi Hirayama, Yuh Sugii, Tadahiro Nagaoka, Takayuki Fukuda, Hiroko Tada, Hidenori Yamada, Yasaburo Matsuura, Heizo Tokutaka, Masaharu Seno*
- P057 Detection of Cluster Boundary in Microarray Data by Reference to MIPS Functional Catalogue Database, *Yoshifumi Okada, Takehiko Sahara, Satoru Ohgiya, Tomomasa Nagashima*
- P058 Multiplicative Decomposition of Time- and Dose-Dependent Gene Expression Changes, *Yukitaka Tani, Takeshi Kamimura, Takeshi Nagashima, Kaori Ide, Mariko Hatakeyama, Hidetoshi Shimodaira*
- P059 Species-Specific Variation of Alternative Splicing and Transcriptional Initiation in Six Eukaryotes, *Hideki Nagasaki, Masanori Arita, Tatsuya Nishizawa, Makiko Suwa, Osamu Gotoh*
- P060 The Requirements and Problems to Use Draft Sequencing Results in Comparative Genomics of Bacteria, *Hidetoshi Yamashita, Yuki Maruyama, Ryuta Komatsu, Toru Suzuki, Seiki Kuramitsu, Kiyozo Asada, Ikunoshin Kato, Masanari Kitagawa*

- P061 Comparative Sequence Analysis of Human and Promoter Regions, *Hirokazu Chiba, Riu Yamashita, Kengo Kinoshita, Kenta Nakai*
- P062 Comprehensive Analysis of Triplet Repeats in Vertebrate Genomes, *Shigeo Okada, Riu Yamashita, Kengo Kinoshita, Kenta Nakai*
- P063 A Maximum Likelihood Method for Inference of Spliceosomal Intron Evolution, *Hung Dinh Nguyen, Maki Yoshihama, Naoya Kenmochi*
- P064 Comparative Genomic Analysis of Transcription Regulation Elements in Higher Eukaryotes, *Natalia Polouliakh, Wataru Fujibuchi, Hajime Harada, Tohru Natsume, Paul Horton*
- P065 Comparative Analysis of Autocorrelations of Electric Charges in Amino Acid Sequences of *S. cerevisiae* and *E. coli*, *Runcong Ke, Shigeki Mitaku*
- P066 Seeking Genomic Duplication in Prokaryotic Genomes by Equivalent Tandem Repeats Distributions, *Satoshi Mizuta, Michimasa Koshino, Toshio Shimizu*
- P067 Statistical Characterization of Transcription Start Sites in Plant Genomes, *Shigeo Fujimori, Takanori Washio, Masaru Tomita*
- P068 A Scale-Free Prior over Graph Structures for Bayesian Inference of Gene Networks, *Takeshi Kamimura, Hidetoshi Shimodaira*
- P069 Physicochemical and Structural Characterization of Nonapeptides Targeted in Autoimmune Diseases, *Wataru Honda, Shuichi Kawashima, Minoru Kanehisa*
- P070 Genome-Wide Protein-Protein Interaction Network Prediction for *Oryza sativa*, *Chen-Yu Chen, Chen-hsiung Chan, Sheng-An Lee, Cheng-Yan Kao*
- P071 Dependence of the Accuracy of Protein Secondary Structure Prediction on Long-Range Interactions, *Daisuke Kihara*
- P072 Fast Protein-Protein Docking Algorithm Using Pre-Identified Binding Site Patches, *Daisuke Kihara, Sael Lee, Karthik Ramani, Srinivasan Turuvekere, Manish Agrawal, Bin Li*
- P073 Ligand Binding Sites Prediction with the Visibility Criteria, *Bin Li, Srinivasan Turuvekere, Manish Agrawal, Karthik Ramani, Daisuke Kihara*
- P074 A Weighting Profile Method for Protein-RNA Interaction Prediction, *Euna Jeong, Satoru Miyano*
- P075 Protein-Protein Docking by the Benzene Clusters Fitting, Grid Scoring and the Pairwise Interaction Potential in CAPRI Rounds 3-5, *Genki Terashi, Mayuko Takeda-Shitaka, Daisuke Takaya, Katsuichiro Komatsu, Hideaki Umeyama*
- P076 A Software for a New Methodology of Kinetics Analyses of Protein-Ligand Interaction, *Masaki Yamamura, Takuma Shiraki, Takashi S.Kodama, Tatsuo Nakagawa, Natsuhiro Ichinose, Osamu Gotoh*
- P077 Identifying Cooperative Transcriptional Regulations Using Protein-Protein Interactions, *Nobuyoshi Nagamine, Yuji Kawada, Yasubumi Sakakibara*
- P078 WoLF PSORT: Protein Localization Prediction Software, *Paul Horton, Keun-Joon Park, Takeshi Obayashi, Kenta Nakai*
- P079 Online Discrimination of  $\beta$ -Barrel Membrane Proteins from Amino Acid Sequence, *M. Michael Gromiha, Makiko Suwa*
- P080 Comparison of Prediction Methods for Protein-Protein Interactions Using Co-Evolutionary Information, *Tetsuya Sato, Yoshihiro Yamanishi, Hisako Ichihara, Minoru Kanehisa, Hiroyuki Toh*
- P081 Characterization of Secondary Structure Elements in Riboswitches, *Ai Muto, Masahiro Hattori, Minoru Kanehisa*

- P082 Identification of Clinical Data Effect on Aplastic Anemia Treatment Using Multilayer Fuzzy Neural Network, *Hironori Mutoh, Seiji Kojima, Hiroyuki Honda*
- P083 Reliability Index for 2-class Classification in Diagnosis of Disease:  $RI_{bin}$ , *Masahiro Nakatochi, Hiro Takahashi, Hiroyuki Honda*
- P084 Automatic Assignment of Full EC Numbers Based on Structural Changes of Chemical Compounds, *Nobuya Tanaka, Tadashi Kadowaki, Susumu Goto, Minoru Kanehisa*
- P085 Chemical Genomic Study of Endocrine Disrupting Chemicals in Metabolic Pathways, *Tadashi Kadowaki, Tetsuya Adachi, Shinobu Okamoto, Nobuya Tanaka, Koichiro Tonomura, Gozoh Tsujimoto, Minoru Kanehisa*
- P086 Development of a Method for Predicting Biological Functions of Compounds Using Support Vector Machine, *Tomohiro Sato, Yo Matsuo, Shigeyuki Yokoyama*
- P087 Modeling Tertiary Structure of Complementarity Determining Region of Antibodies, *Toru Hosokawa, Kenta Nakai, Kengo Kinoshita*
- P088 A New Perspective on an Old Tool: Extending the Coverage of Sequence Similarity-Based Function Prediction with PFP, *Troy Bartholomew Hawkins, Stanislav Luban, Daisuke Kihara*
- P089 AR( $n$ ) Models Applied in Estimation of Genetic Covariance Functions for QTL Mapping, *Yini Cui, Runqing Yang, Shaoqing Huang*
- P090 Direct Physical Mapping Method Based on Scanning Probe Microscope, *Yoshitaka Suetsugu, Kazumi Tsukamoto, Seigo Kuwazaki, Takeshi Yamauchi, Tomoyuki Yoshino, Motoharu Shichiri, Hirokazu Takahashi, Junko Narukawa, Shigeru Sugiyama, Kazuei Mita, Toshio Ohtani, Kimiko Yamamoto*
- P091 Comprehensive Promoter Analyses Using a Database of Transcription Start Sites, *Riu Yamashita, Katsuki Tsuritani, Yutaka Suzuki, Hiroyuki Wakaguri, Sumio Sugano, Kenta Nakai*
- P092 A Genome-Wide Analysis of p53 Binding Sites Using Tiling Arrays, *Shuichi Tsutsumi, Kiyofumi Kaneshiro, Shingo Tsuji, Hiroyuki Aburatani*
- P093 Discriminative Detection of Transcription Factor Binding Sites from Location Data, *Yuji Kawada, Yasubumi Sakakibara*
- P094 PPMuSA: PROSITE-Pattern Matcher Using Suffix Array, *Aki Hasegawa, Akihiko Konagaya*
- P095 Sequence-Based Analyses of Biosynthesis Rate Limiting Factors in Wheat Germ Cell-Free System, *Naoya Fujita, Motoaki Seki, Kazuo Shinozaki, Kengo Kinoshita, Tatsuya Sawasaki, Yaeta Endo, Kenta Nakai*
- P096 Machine Learning Prediction of Amino Acid Sequence Characterization in Protein N-Myristoylation, *Ryo Okada, Chigusa Miyakawa, Manabu Sugii, Hiroshi Matsuno, Satoru Miyano*
- P097 Prediction of Long Disorder Region Using Two-Step SVM, *Shuichi Hirose, Kana Shimizu, Satoru Kanai, Tamotsu Noguchi*
- P098 Large-Scale Analysis of Expressed Pseudogenes in Higher Eucaryotes, *Hayataro Kochi, Rintaro Saito, Masaru Tomita*
- P099 Development of Translational Signal Database and Analysis of Sequence-Activity Relationship, *Hayato Nishida, Alex. Kochetov, Akinori Sarai*
- P100 Genome Wide Analysis of the Alternative Splicing Based on Full-Length cDNA Data, *Hiroki Sakai, Yutaka Suzuki, Katsuhisa Horimoto, Sumio Sugano, Minoru Kanehisa*
- P101 An Unsupervised Diplotype Clustering Method to Improve Race-Based Medicine, *Junji Tanaka, Masato Inoue, Naoyuki Kamatani*
- P102 Toward Full-Automatic Derivation of P450 Gene Database –Performance of Familywise Applied to Plant Genomes–, *Makoto Hirohara, Daisuke Shibata, Osamu Gotoh*

- P103 Discovery of Protein Coding Genes Through Chromosome-to-Chromosome Sequence Comparison, *Osamu Gotoh, Masao Morita, Nobuyuki Ichiyoshi, Tetsushi Yada*
- P104 Development of a Primer Design Program for Multiplex PCR, *Seok Jong Yu, Yong Seong Cho, Byeong-Jin Jeong, Hyeon S. Son, Sang Joo Lee*
- P105 Watermark Embedding Techniques for DNA Sequences Using Codon Usage Bias Features, *Toshio Modegi*
- P106 Genome Analyze by Using Spherical SOM, *Yasaburo Matsuura, Toshimichi Ikemura, Takashi Abe, Heizo Tokutaka, Masaaki Ohkita*
- P107 The Identification of a Cancer Cell Gene by Using SOM, *Yasaburo Matsuura, Tuoya, Masaharu Seno, Heizo Tokutaka, Masaaki Ohkita*
- P108 Bioprocess Optimal Control Simulator Design and Development, *Jebrou Youssef, Masahiro Okamoto*
- P109 A System-Biological Approach to Interferon-Based Therapies, *Kazunori Miyazaki, Satoshi Itoh*
- P110 BAAQ: A Platform for Integrating Bioinformatics Tools and Sharing Knowledge, *Jitender Jit Singh Cheema, Xiujun Gong, Kensuke Nakamura, Kei Yura, Nobuhiro Go*
- P111 Simulation of Light-Induced Phase Response in Mammals with Hybrid Function Petri Net, *Yumi Harada, Natsumi Mito, Yasushi Fujii, Hiroshi Matsuno, Satoru Miyano, Sin-Ichi T. Inouye*
- P112 Expanding Large Scale Signal Transduction Networks, *Kosuke Hashimoto, Bernd Binder, Minoru Kanehisa, Oliver Ebenhoeh, Reinhart Heinrich*
- P113 Comprehensive Detection of TM Protein Genes which might be Associated with Febrile Seizure, *Yasuhito Inoue, Kazuaki Kanai, Satoshi Mizuta, Motohiro Okada, Sunao Kaneko, Toshio Shimizu*
- P114 CADLIVE: Computer-Aided Design of Living Systems, *Hiroyuki Kurata, Marie Kajiwara, Yuki Shimokawa,*
- P115 Petri Net Based Modeling of Signaling Pathways Including Inhibitory Function, *Chen Li, Shunichi Suzuki, Yoko Takeuchi, Qi-Wei Ge, Mitsuru Nakata, Hiroshi Matsuno, Satoru Miyano*
- P116 Interlocked Feedback Is Not the Best Choice for PER Oscillators, *Fumitaka Ohnishi, Hiroyuki Kurata*
- P117 Symbolic-Numeric Estimation of Kinetic Parameters in Biochemical Pathways by Quantifier Elimination, *Shigeo Orii, Hirokazu Anai, Katsuhisa Horimoto*
- P118 Developing Cardiac Cell Models (Kyoto model) on *simBio*, *Nobuaki Sarai, Satoshi Matsuoka, Akinori Noma*
- P119 A Modeling Tool for E-CELL System: Power-Law Model Generator Based on Time-Course Data, *Shigeru Sato, Yasuhiro Naito, Masaru Tomita*
- P120 Kinetic Modeling of Metabolic Pathways in Acetone-Butanol-Ethanol (ABE) Fermentation Using Novel Simulator, *Hideaki Shinto, Yukihiko Tashiro, Mayu Yamashita, Genta Kobayashi, Tatsuya Sekiguchi, Taizo Hanai, Masahiro Okamoto, Kenji Sonomoto*
- P121 Theoretical Research on Dynamics of the Genetic Toggle Switch, *Tomohiro Ushikubo, Wataru Inoue, Mitsumasa Yoda, Masaki Sasai*
- P122 Optimization of a Large-Scale Dynamic Model of the Cell Cycle Network Using Multi Objective GA, *Shunsuke Yamamichi, Hiroyuki Kurata*
- P123 Module Decomposition and Integration Optimizes Gene Regulatory and Metabolic Networks, *Keisuke Yoshida, Hiroyuki Kurata*

- P124 Structure-Based Analysis of Cooperativity in Protein-DNA Recognition, *Akinori Sarai, Satoshi Fujii, Marcos J. Araúzo-Bravo, Hidetoshi Kono*
- P125 Indirect Readout in Drug-DNA Complexes, *Marcos J. Araúzo-Bravo, Akinori Sarai*
- P126 Prediction of Pseudoknotted RNA Structure by a Structural Alignment Using Genetic Algorithm, *Akito Taneda*
- P127 A New Method of Computing Ligand-Based Pharmacophore Models for Flexible Chemical Compounds, *Atsuko Yamaguchi, Hiroyasu Shimada, Ken Horiuchi, Tetsuo Nishikawa*
- P128 Large Scale Protein Side-Chain Packing Based on Maximum Edge-Weight Clique Finding Algorithms, *Dukka Bahadur K. C., J. B. Brown, Etsuji Tomita, Jun'ichi Suzuki, Tatsuya Akutsu*
- P129 Thermal Adaptations of DNA-Binding Proteins, *Masashi Fujita, Minoru Kanehisa*
- P130 CCG-Based RNA Secondary Structure Prediction, *Hee-Jin Lee, Jong C. Park*
- P131 Comparisons between Dynamic Properties of Homologous Protein Structure in ProMode (Database of Normal Mode Analyses on Proteins), *Hiroshi Wako, Motohiro Otsuka, Yuhki Tomizawa, Masaki Kato, Shigeru Endo*
- P132 Genome-Wide Protein Structure Characterization of *Mycoplasma genitalium*, *Jun-Wei Hsu, Chen-hsiung Chan, Cheng-Yan Kao*
- P133 High Quality Protein Structure Prediction Server, SKE-FAMSD, *Kazuhiko Kanou, Mitsuo Iwadate, Genki Terashi, Daisuke Takaya, Mayuko Takeda-Shitaka, Hideaki Umeyama*
- P134 Computational Analysis of microRNA Recognition Site, *Keishin Nishida, Riu Yamashita, Kengo Kinoshita, Kenta Nakai*
- P135 RNA Structural Alignment with Conditional Random Fields, *Kengo Sato, Yasubumi Sakakibara*
- P136 Predicting Non-Coding RNAs Based on Free Energy Minimization by Means of Genetic Algorithms, *Kouichi Okada, Hitoshi Iba*
- P137 Sequence and Structural Analysis of Ligand Binding Sites in Membrane Proteins, *M. Xavier Suresh, M. Michael Gromiha, M. Suwa*
- P138 Homology Modeling in CASP6 (Critical Assessment of Techniques for Protein Structure Prediction) Using CHIMERA and FAMS, *Mayuko Takeda-Shitaka, Genki Terashi, Daisuke Takaya, Kazuhiko Kanou, Mitsuo Iwadate, Hideaki Umeyama*
- P139 Pareto-Optimal Motif for Predicting Peptide Binders, *Menaka Rajapakse, Bertil Schmidt, Vladimir Brusic*
- P140 Fold Recognition and Flexibility of the HIV-1 V3-Loop Crown Structure During the Course of Adaptation to a Host, *Teruaki Watabe, Hirohisa Kishino, Yasuhiro Kitazoe*
- P141 An Alignment Algorithm by Matching Fixed-Length Stem Fragments for Comparing RNA Sequences, *Yasuo Tabei, Koji Tsuda, Taishin Kin, Kiyoshi Asai*
- P142 Non-Arbitrary Judgment for Periodicity of Time-Series Data by an Information Criterion and Discrete Fourier Transform, *Daisuke Tominaga, Paul Horton*
- P143 Searching for Similar Gene Expression Profiles Across Platforms, *Wataru Fujibuchi, Larisa Kiseleva, Paul Horton*
- P144 Phenotype MicroArray Analysis of *Escherichia coli* K-12: An *in silico* Approach, *Hiroaki Gohara, Tomoya Baba, Md. Altaf-Ul-Amin, Masanori Arita, Ken Kurokawa, Shigehiko Kanaya, Hirotada Mori*
- P145 Inference Engine for Gene Expression by Bayesian Network, *Hirofumi Suzaki, Akinori Sarai*

- P146 A Hypothesis of Intrinsic Vital Volatility in Gene Expression, *Hiroto Yoshii, Hideki Takayasu*
- P147 Gene Duplication Models and Reconstruction of Network Evolution, *Juris Viksna, David Gilbert, Dace Ruklisa*
- P148 Efficient Method for Extracting Common Core Binomial Genetic Interactions, *Masahiko Nakatsui, Takanori Ueda, Isao Ono, Masahiro Okamoto*
- P149 Structural and Functional Analysis of Transiently Expressed Metabolic Networks, *Mina Oh, Wolfram Liebermeister, Minoru Kanehisa, Reinhart Heinrich, Oliver Ebenhöf*
- P150 Estimation of Gene Regulatory Network Using Stochastic Differential Equation Model, *Shinya Nabatame, Hitoshi Iba*
- P151 Comparative Study of State Space Models for Time-Course Gene Expression Data of Yeast, *Rui Yamaguchi, Tomoyuki Higuchi*
- P152 On Conditions for Morphogenetic Diversity of Multicellular Organisms, *Hiroshi Yoshida, Hirokazu Anai, Shigeo Orii, Katsuhisa Horimoto*
- P153 Orchestration of Gene Systems Inferred from Expression Profiles in Hepatocellular Carcinoma, *Katsuhisa Horimoto, Sachiyo Aburatani, Shigeru Saito, Masao Honda, Shu-ichi Kaneko*
- P154 Causal Inference of Gene Systems Network in Hepatocellular Carcinoma Progression by Graphical Chain Model, *Masao Honda, Shu-ichi Kaneko, Shigeru Saito, Sachiyo Aburatani, Katsuhisa Horimoto*
- P155 Evaluation of Inference Performance by ASIAN in Transcriptional Regulatory Relationships, *Ritsuko Onuki, Sachiyo Aburatani, Katsuhisa Horimoto, Minoru Kanehisa*
- P156 Inference of Cell Cycle-Regulatory Systems Network in *Saccharomyces cerevisiae*, *Sachiyo Aburatani, Shigeru Saito, Katsuhisa Horimoto*
- P157 Inferring Module-Based Gene Networks from Time Course Microarray Data by State Space Models, *Osamu Hirose, Ryo Yoshida, Seiya Imoto, Satoru Miyano*
- P158 Identification of Drug Active Pathways Based on Gene Networks Estimated by Bayesian Networks and Gene Expression Data, *Yoshinori Tamada, Seiya Imoto, Kousuke Tashiro, Satoru Kuhara, Satoru Miyano*
- P159 Scaling-Law and Fluctuation in Gene Expression, *Jose C. Nacher, Tomoshiro Ochiai, Tatsuya Akutsu*
- P160 Stochastic Fluctuation and Relaxation in a Genetic Feedback Loop, *Yurie Okabe, Yu Yagi, Masaki Sasai*
- P161 Effects of Disease-Associated Mutations and SNP on Protein Structures, *Akiyuki Koga, Hidetoshi Kono, Akinori Sarai*
- P162 Particle Simulation Approach for Cellular Level Spatio-Temporal Properties, *Ryuzo Azuma, Tetsuji Kitagawa, Hiroshi Kobayashi, Ryo Umetsu, Tomoyuki Yamamoto, Akihiko Konagaya*
- P163 Theoretical Analysis of Metabolic Networks: Attempt to Express Topological Position of Individual Atoms in a Given Network, *Jun Ohta*
- P164 Objective Distances for Transcriptome Analyses According to the Thermodynamic Model, *Tomokazu Konishi*
- P165 Elucidation of Xenobiotic Responsive and NR Mediated Pathways/Networks, *Tsuguchika Kaminuma, Masumi Yukawa, Naomi Komiyama, Tatsuya Nakano, Kotoko Nakata, Yoshitomo Tanaka, Hiroshi Tanaka*
- P166 Improvement of ASIAN Web Site, *Kousuke Goto, Shigeru Saito, Sachiyo Aburatani, Katsuhisa Horimoto*
- P167 Characteristic Chemical Transformation Patterns in Biodegradation Pathways, *Mina Oh, Masahiro Hattori, Susumu Goto, Minoru Kanehisa*

## Program Committee

Reinhart Heinrich (Humboldt U., Ger., PC Co-Chair)  
Hiroshi Mamitsuka (Kyoto U., JP, PC Co-Chair)  
Tatsuya Akutsu (Kyoto U., JP)  
Vladimir Brusic (U. Queensland, Austral.)  
Yi-Ping Phoebe Chen (Deakin U., Austral.)  
Stefan Hohmann (Goteborg U., Sweden)  
Minoru Kanehisa (Kyoto U., JP)  
Stefan Kramer (TUM, Ger.)  
Sang Yup Lee (KAIST, South Korea)  
Osamu Maruyama (Kyushu U., JP)  
Aleksandar Milosavljevic (BCM, USA)  
Gene W. Myers (UC Berkeley, USA)  
Haruki Nakamura (Osaka U., JP)  
William Stafford Noble (U. Washington, USA)  
Shoba Ranganathan (Macquarie U., Austral.)  
Tobias Scheffer (Humboldt U., Ger.)  
Tetsuo Shibuya (U. Tokyo, JP)  
Hideaki Sugawara (NIG, JP)  
Toshihisa Takagi (U. Tokyo, JP)  
Koji Tsuda (CBRC, JP)  
Alfonso Valencia (U. Autonoma, Spain)  
Jean-Philippe Vert (Ecole des Mines, France)  
Limsoon Wong (Inst. Infocomm Res., Singapore)  
Ying Xu (U. Georgia, USA)  
Søren Brunak (DTU, Den.)  
Oliver Ebenhöf (Humboldt U., Ger.)  
Darren R. Flower (EJIVR, UK)  
Katsuhisa Horimoto (U. Tokyo, JP)  
Edda Klipp (MOLGEN, MPG, Ger.)  
Richard Lathrop (UC Irvine, USA)  
Yixue Li (SIBS, China)  
Hideo Matsuda (Osaka U., JP)  
Satoru Miyano (U. Tokyo, JP)  
Kenta Nakai (U. Tokyo, JP)  
See-Kiong Ng (Inst. Infocomm Res., Singapore)  
Stephen Oliver (U. Manchester, UK)  
Kenji Satou (JAIST, JP)  
Christian Schönbach (RIKEN, JP)  
Jörg Stelling (ETH, Switzerland)  
Makiko Suwa (CBRC, JP)  
Hiroyuki Toh (Kyushu U., JP)  
Hiroki R. Ueda (RIKEN, JP)  
Gabriel Valiente (Tech. U. Catalonia, Spain)  
Hidemi Watanabe (Hokkaido U., JP)  
Eric P. Xing (Carnegie Mellon U., USA)  
Ueng-Cheng Yang (Nat. Yang-Ming U., Taiwan)