

GIW 2004
The Fifteenth International Conference on Genome Informatics
Pacifico Yokohama, Japan
December 13–15, 2004

Registration

Registration should be done at: <http://giw.ims.u-tokyo.ac.jp/giw2004/registration.html> until November 30, 2004. Registration fee includes a copy of Genome Informatics Vol. 15, No. 2 and coffee breaks. We offer registration fee discount for JSBi and ISCB members.

		until Nov. 30, 2004	after Nov. 30, 2004
Standard Registration	Standard	JPY12,000.-	JPY15,000.-
	ISCB Member	JPY11,000.-	JPY14,000.-
	JSBi Member	JPY8,000.-	JPY11,000.-
	JSBi & ISCB Member	JPY7,000.-	JPY10,000.-
Student Registration	Standard	JPY8,000.-	JPY11,000.-
	ISCB Member	JPY7,000.-	JPY10,000.-
	JSBi Member	JPY5,000.-	JPY8,000.-
	JSBi & ISCB Member	JPY4,000.-	JPY7,000.-

(Banquet on December 14 evening : JPY6,000.-)

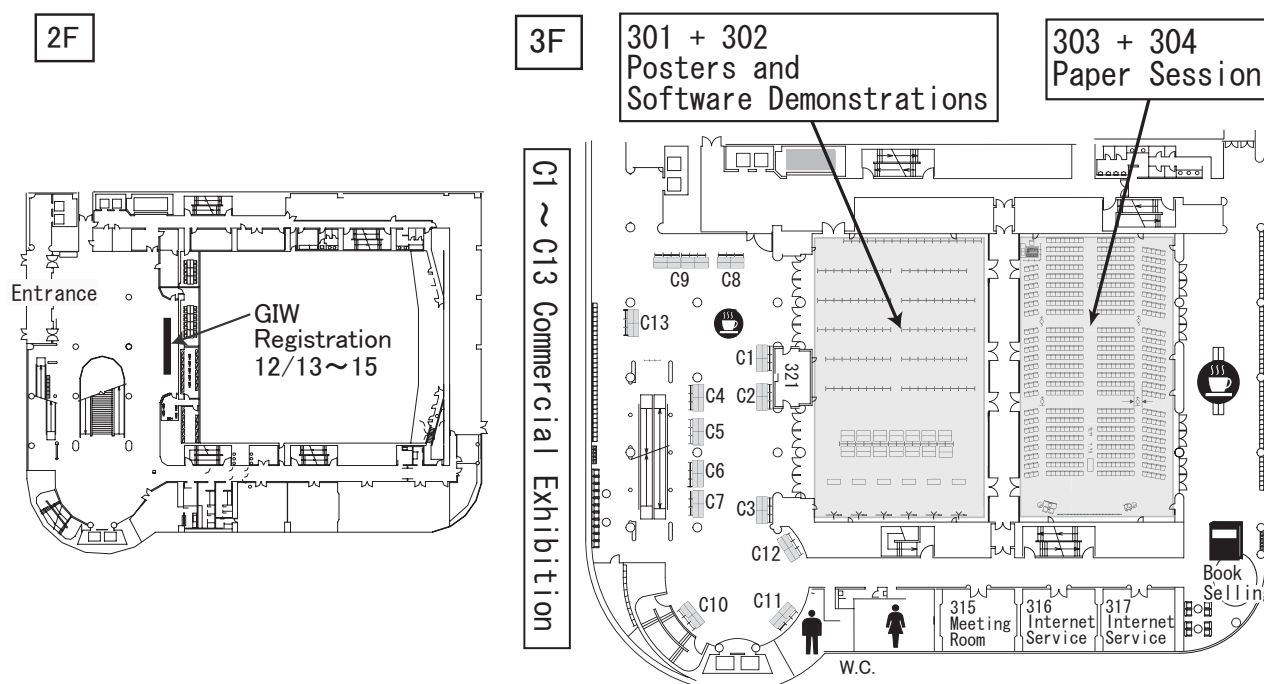
Secretary and Local Arrangements

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 E-mail: giw@ims.u-tokyo.ac.jp
 URL: <http://giw.ims.u-tokyo.ac.jp/giw2004/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

Conference Center



GIW 2004 Advanced Program

Registration

December 13, 2004: 08:30 - 18:00

December 14, 2004: 08:30 - 18:00

December 15, 2004: 08:30 - 15:00

Monday, December 13, 2004

Opening Address

09:00 - 09:10 Tatsuya Akutsu (Kyoto U.) and Vladimir Brusic (Inst. Infocomm Res.)

Paper Session 1

09:10 - 09:35 Chair: Limsoon Wong (Inst. Infocomm Res.)
Architecture of a Grid-Enabled Research Platform with Location-Transparency for Bioinformatics, *Yoshiyuki Kido*¹, *Susumu Date*², *Shingo Takeda*², *Shoji Hatano*³, *Juncai Ma*³, *Shinji Shimojo*², *Hideo Matsuda*² (¹Mitsui Knowledge Industry Co., Ltd., ²Osaka U., ³IMCAS)

09:35 - 10:00 Splicing Profile Based Protein Categorization between Human and Mouse Genomes by Use of the DDBJ Web Services, *Åke Västermark*^{1,2}, *Yasumasa Shigemoto*³, *Takashi Abe*¹, *Hideaki Sugawara*¹ (¹NIG, ²U. Oxford, ³Fujitsu Ltd.)

10:00 - 10:25 Computational Methods for the Analysis of Differential Conservation in Groups of Similar DNA Sequences, *Nikola Stojanovic* (U. Texas)

10:25 - 10:50 Comprehensive Identification of “Druggable” Protein Ligand Binding Sites, *Jianghong An*¹, *Maxim Totrov*², *Ruben Abagyan*¹ (¹The Scripps Res. Inst., ²Molsoft, LLC)

10:50: - 11:10 Break

Keynote Address

11:10 - 12:10 Chair: Vladimir Brusic (Inst. Infocomm Res.)
The Immune Epitope Database and Analysis Resource: From Vision to Blueprint, *Alessandro Sette* (La Jolla Institute for Allergy and Immunology)

12:10 - 13:30 Lunch

Posters and Software Demonstrations Session 1

13:30 - 14:30

Paper Session 2

14:30 - 14:55 Chair: Yixue Li (Shanghai Inst. Biol. Sci.)
General-Purpose Search Techniques for Genomic Text, *Abhijit Chattaraj*, *Hugh E. Williams*, *Adam Cannane* (RMIT U.)

14:55 - 15:20 Graphical Approach to Weak Motif Recognition, *Xiao Yang*, *Jagath C. Rajapakse* (Nanyang Tech. U.)

15:20 - 15:45 An Extension and Novel Solution to the (l,d) -Motif Challenge Problem, *Mark P Styczynski*¹, *Kyle L Jensen*¹, *Isidore Rigoutsos*², *Gregory N Stephanopoulos*¹ (¹MIT, ²IBM, USA),

15:45 - 16:10 Domain Discovery Method for Topological Profile Searches in Protein Structures, *Juris Viksna*^{1,2}, *David Gilbert*², *Gilleain Torrance*² (¹U. Latvia, ²U. Glasgow)

16:10: - 16:30 Break

Paper Session 3

16:30 - 16:55 Chair: Christian Schönbach (RIKEN)
A Novel Graph-Based Similarity Measure for 2D Chemical Structures, *Si Quang Le*¹, *Tu Bao Ho*¹, *T.T Hang Phan*² (¹JAIST, ²Ube Nat. Coll. Tech.)

16:55 - 17:20 IRIS: Intermolecular RNA Interaction Search, *Dmitri D. Pervouchine*^{1,2} (¹Boston U., ²Moscow State U.)

- 17:20 - 17:45 StructMiner: A Tool for Alignment and Detection of Conserved Secondary Structure, *Qian Yang, Mathieu Blanchette* (McGill U.)
- 17:45 - 18:10 RNA 3D Structure Prediction: (1) Assessing RNA 3D Structure Similarity from 2D Structure Similarity, *Jaime E. Barreda DC¹, Yoshimitsu Shigenobu², Eiichiro Ichiishi³, Carlos A. Del Carpio M.^{1,3}* (¹The Cath. U. Santa Maria, ²Toyohashi U. Tech., ³Tohoku U.)

Tuesday, December 14, 2004

- Paper Session 4** Chair: Tetsuo Shibuya (U. Tokyo)
- 09:00 - 09:25 Inference of Gene Regulatory Networks by Means of Dynamic Differential Bayesian Networks and Nonparametric Regression, *Naoya Sugimoto, Hitoshi Iba* (U. Tokyo)
- 09:25 - 09:50 Recovering Genetic Regulatory Networks from Micro-Array Data and Location Analysis Data, *Fan Li, Yiming Yang* (Carnegie Mellon U.)
- 09:50 - 10:15 Increasing Feasibility of Optimal Gene Network Estimation, *Annika Hansen, Sascha Ott, Georgy Koentges* (U. London)
- 10:15 - 10:35 Break
- Paper Session 5** Chair: Sang Yup Lee (KAIST)
- 10:35 - 11:00 A Method for Clustering Gene Expression Data Based on Graph Structure, *Shigeto Seno¹, Reiji Teramoto², Yoichi Takenaka¹, Hideo Matsuda¹* (¹Osaka U., ²Sumitomo Pharmaceuticals Co., Ltd.)
- 11:00 - 11:25 Statistical and Integrative Approach for Constructing Biological Network Maps, *Hiroyuki Kurata, Natsumi Shimizu, Kanako Misumi* (Kyushu Inst. Tech.)
- 11:25 - 11:50 PreSPI: Design and Implementation of Protein-Protein Interaction Prediction Service System, *Dong-Soo Han¹, Hong-Soog Kim¹, Woo-Hyuk Jang¹, Sung-Doke Lee¹, Jung Keun Suh²* (¹Info. Comm. U., ²LG Life Sci. R&D)
- 11:50 - 13:30 Lunch
- Keynote Address** Chair: Satoru Miyano (U. Tokyo)
- 13:30 - 14:30 Revealing the Structure and Dynamics of *Cis*-Regulation Using Heterogeneous, Genome-Wide, Multi-Species Data, *Ron Shamir* (Tel Aviv U.)
- Paper Session 6** Chair: Hiroshi Mamitsuka (Kyoto U.)
- 14:30 - 14:55 Predicting Protein Secondary Structure by a Support Vector Machine Based on a New Coding Scheme, *Long-Hui Wang, Juan Liu, Yan-Fu Li, Huai-Bei Zhou* (Wuhan U.)
- 14:55 - 15:20 Support Vector Machines with Profile-Based Kernels for Remote Protein Homology Detection, *Steven Busuttill¹, John Abela², Gordon J. Pace²* (¹U. London, ²U. Malta)
- 15:20 - 15:45 Kernel Mixture Survival Models for Identifying Cancer Subtypes, Predicting Patient's Cancer Types and Survival Probabilities, *Tomohiro Ando, Seiya Imoto, Satoru Miyano* (U. Tokyo)
- JSBi Annual Meeting**
- 16:00 - 16:30
- Posters and Software Demonstrations Session 2**
- 16:30 - 18:00
- Banquet**
- 18:30 - 21:00

Wednesday, December 15, 2004

Paper Session 7 Chair: Kenji Satou (JAIST)

- 09:00 - 09:25 Computational Prediction of Operons in *Synechococcus sp.* WH8102, *Xin Chen*¹, *Zhengchang Su*², *Ying Xu*², *Tao Jiang*¹ (¹UCR, ²UGA)
- 09:25 - 09:50 Intercellular Communications Induced by Random Fluctuations, *Tianshou Zhou*¹, *Luonan Chen*², *Ruiqi Wang*², *Kazuyuki Aihara*³ (¹Tsinghua U., ²Osaka Sangyo U., ³U. Tokyo)
- 09:50 - 10:15 Knowledge Representation Model for Systems-Level Analysis of Signal Transduction Networks, *Dong-Yup Lee*¹, *Ralf Zimmer*², *Sang-Yup Lee*¹, *Daniel Hanisch*³, *Sunwon Park*¹ (¹KAIST, ²Ludwig-Maximilians-Universität München, ³SCAI, Germany)
- 10:15 - 10:40 Consistent Re-Modeling of Signaling Pathways and Its Implementation in the TRANSPATH Database, *Claudia Choi*¹, *Torsten Crass*², *Alexander Kel*¹, *Olga Kel-Margoulis*¹, *Mathias Krull*¹, *Susanne Pistor*¹, *Anatolij Potapov*^{1,2}, *Nico Voss*¹, *Edgar Wingender*^{1,2} (¹BIOBASE, ²U. Göttingen)
- 10:40 - 11:05 Ontological Integration of Data Models for Cell Signaling Pathways by Defining a Factor of Causality Called 'Signal', *Takako Takai-Igarashi*¹, *Richiro Mizoguchi*² (¹U. Tokyo, ²Osaka U.)

Posters and Software Demonstrations Session 3

- 11:05 - 12:15
12:15 - 13:30 Lunch

Keynote Address Chair: Tatsuya Akutsu (Kyoto U.)

- 13:30 - 14:30 Orthologous Sets of Functional Networks: Inference, Mining and Visualization, *Charles DeLisi* (Boston U.)
- 14:30 - 14:50 Break

Paper Session 8 Chair: Kenta Nakai (U. Tokyo)

- 14:50 - 15:15 Using Protein Motif Combinations to Update KEGG Pathway Maps and Orthologue Tables, *Frédéric Nikitin*^{1,4}, *Bastien Rance*², *Masumi Itoh*³, *Minoru Kanehisa*³, *Frédérique Lisacek*^{1,4,5} (¹Geneva Bioinfo., ²U. Paris XI, ³U. Kyoto, ⁴Swiss Inst. Bioinfo., ⁵Génome & Informatique)
- 15:15 - 15:40 Systematic DNA-Binding Domain Classification of Transcription Factors, *Philip Stegmaier*¹, *Alexander E. Kel*¹, *Edgar Wingender*^{1,2} (¹BIOBASE, ²U. Göttingen)
- 15:40 - 16:05 Mining Yeast Transcriptional Regulatory Modules from Factor DNA-Binding Sites and Gene Expression Data, *Tho Hoan Pham*¹, *Kenji Satou*^{1,2}, *Tu Bao Ho*¹ (¹JAIST, ²JST)

Closing and Award Ceremony

- 16:05 - 16:20

Commercial Exhibitions

- C1: SILICON GENETICS / Yokokawa Analytical Systems Inc.
C2: Ryoka Systems Inc.
C3: NABE International Corporation
C4: INFOCOM CORPORATION
C5: BIOBASE GmbH

- C6: Cybernet Systems Co., Ltd.
- C7: HITACHI, LTD.
- C8: Pathway Solutions Inc.
- C9: SGI Japan, Ltd.
- C10: Hitachi High-Technologies Corporation
- C11: Mitsui Knowledge Industry Co., Ltd.
- C12: Sun Microsystems K.K.
- C13: Mathematical Systems, Inc.

Software Demonstrations

- S01 MPSS: an integrated database system for surveying multitudinous proteins, *Pei Hao, Wei-zhong He, Yi-Xue Li*
- S02 ASIAN on Personal Computer, *Shigeru Saito, Kousuke Goto, Sachiyo Aburatani, Katsuhisa Horimoto*
- S03 Reflection of Knowledge Information in ProMode (A Database of Normal Mode Analyses on Proteins), *Hiroshi Wako, Motohiro Otsuka, Yuhki Tomizawa, Masaki Kato, Shigeru Endo*
- S04 *MyGPS_client* A Genome Browser Integrating Client-side Private Data and Server-side Large-scale Public Annotations, *Katsura Hirosawa, Atsushi Moroda, Yoshikazu Hasegawa, Naohiko Heida, Yoshiki Mochizuki, Tetsuro Toyoda*
- S05 CADLIVE: New Modules for Domain Expansions and Topological Analysis, *Hiroyuki Kurata, Yuki Shimokawa, Tomoko Noguchi, Natsumi Shimizu*
- S06 Visualization and Cluster Analysis using Spherical SOM, *Daisuke Nakatsuka, Heizo Tokutaka*
- S07 *MutationView*: Addition of an enhanced search system for the clinical description in the OMIM based on a new algorithm, *Masafumi Ohtsubo, Katsue Daicho, Kouichi Kawaguchi, Susumu Mitsuyama, Takashi Kawamura, Tomoyoshi Horisawa, Nobuyoshi Shimizu, Shinsei Minoshima*
- S08 Studying the molecular evolution of the SARS-coronavirus on the the DiscoveryNet Environment, *Pei Hao, Yuan-Yuan Li, Wei-zhong He, Yi-Xue Li, Vasa Curcin, Moustafa Ghanem, Yike Guo*
- S09 GEDA-C: Gene Expression Data Analysis - Clustering based-on seed method, *Ho-Youl Jung, Miyoung Shin, Seon-Hee Park*
- S10 Care-free Metabolic Map Editor - From Pathways to Maps -, *Masanori Arita*
- S11 Bioinformatics Recipes with BioRuby, *Mitsuteru Nakao, Naohisa Goto, Toshiaki Katayama*
- S12 “Piment” and “Macaroni”: Nervous System Protein Database, *Takeshi Tomiki, Naruya Saitou*
- S13 HiGet: High Performance Database Entry Retrieval System, *Kazutomo Ushijima, Chiharu Kawagoe, Kenta Nakai, Shuichi Kawashima, Hideo Bannai, Toshiaki Katayama*
- S14 Genomic Object Net 1.5: A Platform for Biopathway Modeling and Simulation, *Masao Nagasaki, Atsushi Doi, Satoru Miyano*

Posters

- P001 Prediction of Debacle Parts for Robustness in a Cell by using Recurrent Neural Networks, *Hironori Kitakaze, Ryuhei Noda, Hiroshi Matsuno, Nobuhiko Ikeda, Satoru Miyano*
- P002 Modeling and Simulation of Cyanobacterial Circadian Clock Mechanism by Hybrid Functional Petri Net, *Mao Yamaji, Hideo Iwasaki, Hiroshi Matsuno, Satoru Miyano*
- P003 A New Regulatory Interactions Suggested by Simulations for Circadian Genetic Control Mechanism in Mammals, *Yasushi Fujii, Yasuki Okitsu, Hiroshi Matsuno, Satoru Miyano, Shin-Ichi T. Inouye*
- P004 A New Petri Net Modeling Method for Signaling Pathways with a Focus on Enzyme, *Chen Li, Qi-Wei Ge, Mitsuru Nakata, Hiroshi Matsuno, Satoru Miyano*

- P005 CellDesigner2.0: A Process Diagram Editor for Gene-regulatory and Biochemical Networks, *Akira Funahashi, Naoki Tanimura, Yukiko Matsuoka, Naritosi Yosinaga, Hiroaki Kitano*
- P006 Optimization and System Analysis of the Heat Shock Response by CADLIVE, *Kouji Mitsukiyo, Marie Kajiwara, Hiroyuki Kurata*
- P007 A Large-Scale Dynamic Model of the Yeast Cell Cycle, *Shunsuke Yamamichi, Hiroyuki Kurata*
- P008 Control Aspect of Common Interactions Extracted from Inferred Network Candidates of Gene Expression, *Masahiko Nakatsui, Takanori Ueda, Isao Ono, Masahiro Okamoto*
- P009 Simulation for detailed mathematical model of G1-to-S cell cycle phase transition, *Yoshihiko Tashima, Taizo Hanai, Hiroyuki Hamada, Masahiro Okamoto*
- P010 BAAQ: A Grid-based Infrastructure for Integrating Bioinformatics Applications, *Xiujun Gong, Kei Yura, Nobuhiro Go*
- P011 Simulation of Circadian Rhythms Using Grid Computing, *Takayuki Tanaka, Hiroyuki Kurata*
- P012 Development of a computer simulation system for particle-level molecular interactions, *Ryuzo Azuma, Yoshiki Yamaguchi, Tetsuji Kitagawa, Tomoyuki Yamamoto, Akihiko Konagaya*
- P013 The Molecular Dynamics Simulation of Prion Protein, *Masakazu Sekijima, Chie Motono, Tamotsu Noguchi, Tamotsu Noguchi, Kiyotoshi Kaneko, Yutaka Akiyama*
- P014 Symbolic-Numeric Optimization for Biological Kinetics by Quantifier Elimination, *Shigeo Orii, Hirokazu Anai, Katsuhisa Horimoto*
- P015 Equilibrium Model of DNA Chip Hybridization Error, *John A. Rose, Masami Hagiya, Akira Suyama*
- P016 An Analysis Tool Library for Biochemical Modeling on E-Cell System Version 3, *Kazunari Kaizu, Fumihiko Miyoshi, Yoichi Nakayama, Masaru Tomita*
- P017 Development of Integrated Modeling Environment for E-Cell3 System, *Gabor Bereczki, Kouichi Takahashi, Takeshi Sakurada, Ng Yan Hong, Masaru Tomita*
- P018 Development of E-Cell kinetic model interoperability environment, *Tatsuya Ishida, Takeshi Sakurada, Tomoya Kitayama, Masaru Tomita*
- P019 Development of Distributed Cell Simulations Middleware with E-Cell System, *Masahiro Sugimoto, Kouichi Takahashi, Daniel, Muhammad Nurazhar Bin Taher, Lu Yaomin, Novia Siswanto Be, Tracy Wong, Ng Yan Hong, Masaru Tomita*
- P020 Modeling Gene Networks Utilizing Evolutionary Information Using Bayesian Network Models, *Yoshinori Tamada, Hideo Bannai, Seiya Imoto, Toshiaki Katayama, Minoru Kanehisa, Satoru Miyano*
- P021 Estimating Regulatory Networks from DNA Microarrays and Protein-Protein Interactions, *Naoki Nariai, Yoshinori Tamada, Seiya Imoto, Satoru Miyano*
- P022 Estimating Gene Networks from Expression Data and Binding Location Data via Boolean Network, *Osamu Hirose, Naoki Nariai, Yoshinori Tamada, Hideo Bannai, Seiya Imoto, Satoru Miyano*
- P023 Multiscale Bootstrap Analysis of Gene Networks Based on Graphical Gaussian Modeling, *Takeshi Kamimura, Hidetoshi Shimodaira*
- P024 Systematic Identification of Weak Connections between Clusters in Biological Network, *Hiroki Sakai, Katsuhisa Horimoto, Minoru Kanehisa*
- P025 Genetic Network Reconstruction in Tryptophan Metabolism from Gene Expression Profiles, *Akira Imaizumi, Hisashi Yasueda, Sachiyo Aburatani, Katsuhisa Horimoto*

- P026 Selective Integration of Multiple Genomic Data for Biological Network Inference, *Tsuyoshi Kato, Koji Tsuda, Kiyoshi Asai*
- P027 Effective Procedures for the Estimation of Large-scale S-system Parameters, *Yukihiro Maki, Takanori Ueda, Masahiro Okamoto*
- P028 Correlations Between Scale-free Genetic Regulatory Model Networks and Dynamical Properties, *Chikoo Oosawa, Kazuhiro Takemoto, Genki Hanano*
- P029 Periodic Oscillation in Gene Networks Modelled by Cyclic Feedback Systems, *Ruiqi Wang, Luonan Chen*
- P030 A Gibbs Sampling Approach to Detection of Tree Motifs, *Lidio Marx Carvalho Meireles, Tatsuya Akutsu*
- P031 QSAR Analysis with Support Vector Machines and Graph Kernels, *Pierre Mahé, Nobuhisa Ueda, Tatsuya Akutsu, Jean-Luc Perret, Jean-Philippe Vert*
- P032 Stable Stochastic Dynamics in Yeast Cell Cycle , *Yurie Okabe, Masaki Sasai*
- P033 Comparative Analysis of Conditional Regulation Across the Yeast Genomes, *Koji Ota, Susumu Goto, Minoru Kanehisa*
- P034 An application of multiscale bootstrap resampling to hierarchical clustering of microarray data: How accurate are these clusters?, *Ryota Suzuki, Hidetoshi Shimodaira*
- P035 Mixed Factors Analysis for Identifying Transcriptional Modules and Clusters on Microarray Experiments, *Ryo Yoshida, Tomoyuki Higuchi, Seiya Imoto*
- P036 Incorporating prior knowledge into clustering of gene expression profiles, *Daisuke Komura, Hiroshi Nakamura, Shuichi Tsutsumi, Hiroyuki Aburatani, Sigeo Ihara*
- P037 Mathematical Model Based Clustering of Gene Expression, *Kazumi Hakamada, Taizo Hanai, Masahiro Okamoto*
- P038 Cleaning Microarray Expression Data with Markov Random Fields Based on Profile Similarity, *Raymond Wan, Hiroshi Mamitsuka*
- P039 A practical system for the detection of chromosomal aberration in tumor cells by array CGH, *Junya Futagawa, Tomohiro Isobe, Atsushi Moroda, Nobutaka Mitsunashi, Ken Aoshima, Yasuhito Arai, Fumie Hosoda, Misao Ohki, Issei Imoto, Johji Inazawa, Tokuki Sakiyama*
- P040 Statistical Analysis of Gene Expression in Repair Mechanism under UV Irradiation, *Sachiyo Aburatani, Nobuyoshi Sugaya, Hiroo Murakami, Katsuhisa Horimoto*
- P041 Integrated Analysis of Gene Expression Profile and Metabolite Quantity Data of *Arabidopsis thaliana* Using BL-SOM, *Yukiko Nakamura, Ryoko Morioka, Yoko Shinbo, Masami Yokota Hirai, Md. Altaf-Ul-Amin, Ken Kurokawa, Kotaro Minato, Kazuki Saito, Shigehiko Kanaya*
- P042 Analysis for time-course profiles of transcription arrays, *Daisuke Tominaga, Paul Horton*
- P043 A Step Towards Substructure Exploration from Gene Expression Patterns, *Masako Hoshino, Hiroshige Inazumi*
- P044 Markov Property and Scale-free Organization of Gene Expression, *Tomoshiro Ochiai, Jose C. Nacher, Tatsuya Akutsu*
- P045 Expression Analysis of Glycosyltransferase Genes in Human, Mouse, and Rat, *Takashi Miyama, Shin Kawano, Minoru Kanehisa*
- P046 Yeast Gene Classification based on Relevant Biological Functions for Gene Expression Data Analysis, *Satoshi Kamegai, Takuya Oyama, Mikio Yoshida, Fumihito Miura, Kenji Satou, Takashi Ito*

- P047 Rational Design for Molecular Breeding of Industrially Useful Strains Based on Bioinformatic Data in *Saccharomyces cerevisiae*, *Takashi Hirasawa, Katsunori Yoshikawa, Kengo Ashitani, Keisuke Nagahisa, Chikara Furusawa, Yoshio Katakura, Hiroshi Shimizu, Suteaki Shioya*
- P048 On-chip selection of DNA ligands using a method for generating point mutations, *Ryoichi Asai, Shin I. Nishimura, Takuyo Aita, Katsutoshi Takahashi*
- P049 Automatic generation of KEGG OC (Ortholog Cluster) and its assignment to draft genomes, *Yuki Moriya, Toshiaki Katayama, Akihiro Nakaya, Masumi Itoh, Akiyasu C. Yoshizawa, Shujiro Okuda, Minoru Kanehisa*
- P050 Functional Categorization of Multiple Genomes using KEGG OC in the Genome Indices, *Shujiro Okuda, Akiyasu C. Yoshizawa, Yuki Moriya, Masumi Itoh, Toshiaki Katayama, Susumu Goto, Minoru Kanehisa*
- P051 Gene-Transpositions on Functional Categories in Prokaryotic Genomes, *Nobuyoshi Sugaya, Hiroo Murakami, Sachiyo Aburatani, Kunio Shimizu, Katsuhisa Horimoto*
- P052 Prediction of DNA-binding sites in proteins using evolutionary profiles, *Shandar Ahmad, Akinori Sarai*
- P053 Method for finding p53 binding sites using tiling array, *Shingo Tsuji, Kiyofumi Kaneshiro, Shuichi Tsutsumi, Sigeo Ihara, Hiroyuki Aburatani*
- P054 Correlation between signal transduction domains and habitats in cyanobacteria, *Shinobu Okamoto, Shuichi Kawashima, Rei Narikawa, Minoru Kanehisa*
- P055 Transmembrane regions prediction for G-protein-coupled receptors by hidden Markov model, *Kayo Narukawa, Tadashi Kadowaki, Gozoh Tsujimoto*
- P056 GPCR and G-protein Coupling Selectivity Prediction Based on SVM with Physico-Chemical Parameters, *Makiko Suwa, Yukimitsu Yabuki, Takahiko Muramatsu, Takatsugu Hirokawa, Hidetoshi Mukai*
- P057 GLIDA : GPCR and Ligand Database, *Jiyeon Yang, Yasushi Okuno, Gozoh Tsujimoto*
- P058 3DMET: A Database of Three-Dimensional Structures of Natural Metabolites, *Miki Maeda*
- P059 Graph Theoretic Analysis of Chemical Compounds in Biological Pathways, *Atsuko Yamaguchi, Yasushi Okuno, Hiroshi Mamitsuka*
- P060 Prediction of Glycosyltransferases Synthesizing Glycoconjugates Using Variable-length N-gram Model, *Yeon-Dae Kwon, Shougo Shimizu, Hisashi Narimatsu*
- P061 An algorithm for graph isomorphism and its application to KEGG Compound Search, *Nobuya Tanaka, Susumu Goto, Minoru Kanehisa*
- P062 RPAIR: a reactant-pair database representing chemical changes in enzymatic reactions, *Masaaki Kotera, Masahiro Hattori, Min-A Oh, Rumiko Yamamoto, Tomoko Komeno, Junko Yabuzaki, Koichiro Tonomura, Susumu Goto, Minoru Kanehisa*
- P063 Glycan Linkage Substitution Matrix Rooted on Tree Alignments, *Kiyoko F. Aoki, Hiroshi Mamitsuka, Minoru Kanehisa*
- P064 Classification and Motif Extraction of Glycans in Bloods, *Yoshiyuki Hizukuri, Yoshihiro Yamanishi, Osamu Nakamura, Fumio Yagi, Susumu Goto, Minoru Kanehisa*
- P065 Integrated Quantification and Multivariate Analysis Workbench System for Phospholipids, *Kaoru Mogushi, Katsutoshi Takahashi*
- P066 Power-law Correlations of Connectivities in Biomolecular Networks, *Kazuhiro Takemoto, Chikoo Oosawa*
- P067 A method for estimation of enzyme kinetics in metabolic pathways using GMA, *Tomoya Kitayama, Ayako Kinoshita, Yoichi Nakayama, Masaru Tomita*

- P068 A method for customized cross-species metabolic pathway comparison, *Eric Lo, Takuji Yamada, Michihiro Tanaka, Masahiro Hattori, Susumu Goto, Chuan-Hsiung Chang, Minoru Kanehisa*
- P069 Decomposition of kinetically feasible metabolic flux distributions onto elementary modes, *Jean-Marc Schwartz, Minoru Kanehisa*
- P070 Global Tree of Known Carbohydrate Structures to Analyze Biosynthetic Pathways, *Kosuke Hashimoto, Shin Kawano, Yasushi Okuno, Minoru Kanehisa*
- P071 Comparative analysis of enzymatic reactions reveals phylogenetic evolution of metabolic pathways, *Michihiro Tanaka, Naoki Nariai, Thomas Handorf, Oliver Ebenhöf, Satoru Miyano, Minoru Kanehisa, Reinhart Heinrich*
- P072 Functional Enzyme Exploration combining SIMPLEX screening assisted with Fuzzy Neural Network, *Ryuji Kato, Hiroyuki Konishi, Yuichi Koga, Tsuneo Yamane, Takeshi Kobayashi, Hideo Nakano, Hiroyuki Honda*
- P073 Fold-Function Relationship of PLP-Dependent Enzymes, *Keiko Matsuda, Takaaki Nishioka, Kengo Kinoshita, Nobuhiro Go*
- P074 A novel classification of enzyme catalytic reactions, *Nozomi Nagano*
- P075 Phylogenetic Comparison of Human and Mouse Promoter Regions and Visualization of a Variety of Conserved Elements, *Hirokazu Chiba, Kenta Nakai*
- P076 Conservation of Physicochemical Properties during Protein Evolution, *Masashi Fujita, Masumi Itoh, Minoru Kanehisa*
- P077 A method for comparing microarray data of different species, *Kenji Hagimoto, Jun Miyazaki, Shigehiko Kanaya, Naotake Ogasawara, Toshiyuki Amagasa, Shunsuke Uemura*
- P078 Chromosome Profiling: A Clue to Trace The Genome Evolution, *Ayumu Saito, Koichi Nishigaki*
- P079 Searching for *cis*-elements in Mouse-Human Orthologous Promoter Regions, *Natalia Polouliakh, Wataru Fujibuchi, Tohru Natsume, Paul Horton*
- P080 Tandem Repeats in 44 Prokaryotic Genomes and Genome Evolution, *Satoshi Mizuta, Hikaru Munakata, Abulimiti Aimaiti, Kenji Oosawa, Toshio Shimizu*
- P081 An approximate maximum likelihood method for phylogenetic tree analysis based on high-temperature Markov Chain Monte Carlo, *Ryota Suzuki, Tomoya Taniguchi, Hidetoshi Shimodaira*
- P082 Extension of Prn: implementation of a doubly nested randomized iterative refinement strategy under a piecewise linear gap cost, *Shinsuke Yamada, Osamu Gotoh, Hayato Yamana*
- P083 Sequence Alignment Tool of Membrane Protein, *Takahiko Muramatsu, Makiko Suwa*
- P084 A Rapid peptide based Alignment -free method to construct Genome trees Independent of sequence annotation, *Vikash Kumar, Sunil Kumar*
- P085 Fast Homology Search using Categorisation Profiles, *Abhijit Chattaraj, Hugh E. Williams, Adam Cannane*
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