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)
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GIW 2006
The Seventeenth International Conference on Genome Informatics
Pacifico Yokohama, Japan
December 18–20, 2006

Registration
Registration should be done at: http://giw.ims.u-tokyo.ac.jp/giw2006/registration.html until December 3, 2006. Registration fee includes a copy of Genome Informatics Vol. 17, No. 2 and coffee breaks. We offer registration fee discount for JSBi and ISCB members.

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(Banquet on December 19 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: giw2006@ims.u-tokyo.ac.jp
URL: http://giw.ims.u-tokyo.ac.jp/giw2006/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
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2F
Registration Desk
Entrance

3F
GIW 2006 Advanced Program

Registration
December 18, 2006: 08:30 - 17:30
December 19, 2006: 08:30 - 18:00
December 20, 2006: 08:30 - 15:30

Monday, December 18, 2006

Opening Address
09:00 - 09:10 Yasubumi Sakakibara (Keio U.) and Temple F. Smith (Boston U.)

Paper Session 1
Chair: Byoung-Tak Zhang (Seoul National U.)
09:10 - 09:35 Hybrid Gibbs-Sampling Algorithm for Challenging Motif Discovery: GibbsDST, Kazuhiro Shida
09:35 - 10:00 Computational Annotation of Transcription Factor Binding Sites in D. Melanogaster Developmental Genes, Vipin Narang, Wing-Kin Sung, Ankush Mittal
10:00 - 10:25 A Gram Distribution Kernel Applied to Glycan Classification and Motif Extraction, Tetsuji Kuboyama, Kouichi Hirata, Kiyoko F. Aoki-Kinoshita, Hisashi Kashima, Hiroshi Yasuda
10:25 - 11:00 Break

Keynote Address
Chair: Yasubumi Sakakibara (Keio U.)
11:00 - 12:00 RNAs Everywhere: Genome-Wide Annotation of Structured RNAs, Ivo L Hofacker (University of Vienna)

12:00 - 13:30 Lunch

Posters and Software Demonstrations Session 1
13:30 - 14:30 ( Odd Number )

Paper Session 2
Chair: Masanori Arita (U. Tokyo)
14:30 - 14:55 Discovering Signal Transduction Networks Using Signaling Domain-Domain Interactions, Thanh Phuong Nguyen, Tu Bao Ho
14:55 - 15:20 Finding Conserved and Non-Conserved Reactions Using a Metabolic Pathway Alignment Algorithm, José C. Clemente, Kenji Satou, Gabriel Valiente
15:20 - 15:45 A Function-Centric Approach to the Biological Interpretation of Microarray Time-Series, Pablo Minguez, Fátima Al-Shahrour, Joaquín Dopazo
15:45 - 16:15 Break

Paper Session 3
Chair: Katsuhisa Horimoto (CBRC)
16:15 - 16:40 RaPiDS: An Algorithm for Rapid Expression Profile Database Search, Paul B. Horton, Larisa Kiseleva, Wataru Fujibuchi
16:40 - 17:05 Development of an Approach for Ab Initio Estimation of Compound-Induced Liver Injury Based on Global Gene Transcriptional Profiles, Xudong Dai, Yudong D. He, Hongyue Dai, Yek Y. Lam, Christopher J. Roberts, Jeffrey F. Waring, Roger G. Ulrich
17:05 - 17:30 The Distribution and Deposition Algorithm for Multiple Oligo Nucleotide Arrays, Kang Ning, Hon Wai Leong
17:30 - 17:55 Detection and Restoration of Hybridization Problems in Affymetrix GeneChip Data by Parametric Scanning, Tomokazu Konishi
**Tuesday, December 19, 2006**

**Paper Session 4**
- **Chair**: Kenji Satou (JAIST)
- **09:00 - 09:25** Gene Ontology Annotation by Density and Gravitation Models, *Wen-Juan Hou, Kevin Hsin-Yih Lin, Hsin-Hsi Chen*
- **09:25 - 09:50** Text Mining and Protein Annotations: the Construction and Use of Protein Description Sentences, *Martin Krallinger, Rainer Malik, Alfonso Valencia*
- **09:50 - 10:15** Assessing Clustering Results with Reference Taxonomies, *Gabriel Valiente*
- **10:15 - 10:45** Break

**Paper Session 5**
- **Chair**: Tetsuo Shibuya (U.Tokyo)
- **10:45 - 11:10** Pairwise Alignment with Rearrangements, *Le Sy Vinh, Andrés Varón, Ward C. Wheeler*
- **11:10 - 11:35** Techniques for Multi-Genome Synteny Analysis to Overcome Assembly Limitations, *Arjun Bhutkar, Susan Russo, Temple F. Smith, William M. Geibart*
- **11:35 - 12:00** A Markov Chain Model for Haplotype Assembly from SNP Fragments, *Rui-Sheng Wang, Ling-Yun Wu, Xiang-Sun Zhang, Luonan Chen*
- **12:00 - 13:30** Lunch

**Keynote Address**
- **Chair**: Temple F. Smith (Boston U.)
- **13:30 - 14:30** The New Phase of Transcriptome Analysis, *Yoshihide Hayashizaki* (RIKEN,GSC)

**Paper Session 6**
- **Chair**: Hiroyuki Toh (Kyushu U.)
- **14:30 - 14:55** MetaClustering: Discovery of The Different Sample Clusterings in Gene Expression Data, *David Venet, Hugues Bersini, Hitoshi Iba*
- **14:55 - 15:20** Biomarkers for Epithelial Ovarian Cancers, *Pritha Mahata*
- **15:20 - 15:45** PepSOM: An Algorithm for Peptide Identification by Tandem Mass Spectrometry Based on SOM, *Kang Ning, Hoong Kee Ng, Hon Wai Leong*
- **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 “Pacific” at Inter Continental The Grand Yokohama
Wednesday, December 20, 2006

**Paper Session 7**
Chair: Gabriel Valiente (Tech.U.Catalonia)

09:00 - 09:25 DAPID: A 3D-Domain Annotated Protein-Protein Interaction Database, Yung-Chiang Chen, Heng-Chu Chen, Jinn-Moon Yang

09:25 - 09:50 A Method to Detect Important Residues Using Protein Binding Site Comparison, Keunwan Park, Dongsup Kim


10:15 - 10:40 A Large-Scale Computational Approach to Drug Repositioning, Yvonne Y. Li, Jianghong An, Steven J.M. Jones

**Posters and Software Demonstrations Session 3**
10:40 - 12:00 (Even and Odd Number)

12:00 - 13:30 Lunch

**Keynote Address**
Chair: Hiroshi Mamitsuka (Kyoto U.)

13:30 - 14:30 Increasing Confidence of Protein-Protein Interactomes, Limsoon Wong (National University of Singapore)

**Paper Session 8**
Chair: Tatsuya Akutsu(Kyoto U.)


14:55 - 15:20 Protein Topology Classification Using Two-Stage Support Vector Machines, Jayavardhana Gubbi, Alistair Shilton, Michael Parker, Marimuthu Palaniswami

15:20 - 15:45 Robotic Path Planning and Protein Complex Modeling Considering Low Frequency Intra-Molecular Loop and Domain Motions, Carlos A. Del Carpio, Pei Qiang, Eiichiro Ichiishi, Hideyuki Tsuboi, Michihisa Koyama, Nozomu Hatakeyama, Akira Endou, Hiromitsu Takaba, Momoji Kubo, Akira Miyamoto

**Closing and Award Ceremony**
15:45 - 16:00
Commercial Exhibitions
C1: Ryoka Systems Inc.
C2: NABE International Corporation
C3: Mathematical Systems, Inc.
C4: Pathway Solutions Inc.
C5: SGI Japan, Ltd.
C6: Active Motif, Inc.
C7: SCRUM Inc.
C8: HITACHI, LTD
C9: BIOBASE GmbH

Software Demonstrations
S01 Mass Spectral Database for Metabolome Analysis, Hisayuki Horai, Kazuhiro Suwa, Masanori Arita, Yoshito Nihei, Takaaki Nishioka
S02 CADLIVE: Integration for Large-Scale Network Data, Yuki Shimokawa, Kazuhiro Maeda, Ken-taro Inoue, Hiroyuki Kurata
S03 RIKEN Natural Products Depository (RIKEN NPDepo), Hideaki Konno, Takeshi Tomiki, Tomio Saito, Masashi Ueki, Takeo Asaoka, Ryuichiro Suzuki, Masakazu Uramoto, Hideaki Kakeya, Hiroyuki Osada
S04 PreSPI: Prediction System for Protein Interaction, Woo-Hyuk Jang, Choon-Oh Lee, Dong-Soo Han
S05 Construction of Candida Albicans Protein Network from Yeast Protein Interactions in System Biology, Chung-Yen Lin, Chieh-Hwa Lin, Chi-Shiang Cho, Fan-Kai Lin, Shu-Hwa Chen, Chao A. Hsiung
S06 ExPlain: Causal Analysis of Gene Expression Data from Promoter Models to Signaling Pathways, Alexander Kel, Holger Karas, Nico Voss, Tagir Waleev, Edgar Wingender
S07 Cell Illustrator3.0: A Platform for Biopathway Modeling and Simulation, Masao Nagasaki, Atsushi Doi, Ayumu Saito, Emi Ikeda, Kazuko Ueno, Euna Jeong, Christopher J. Savoie, Satoru Miyano
S08 Ajax for Networks and Ontologies, Kinya Okada, Takahisa Furukawa, Kiyoshi Asai
Posters

P001 Serial Regulation on Cell Cycle System in *S.cerevisiae*, Sachiyo Aburatani, Katsuhisa Horimoto

P002 Efficient Inferring Method for Extracting Reliable Interactions from Time Series of Gene Expression Profile, Masahiko Nakatsu, Takanori Ueda, Maki Yukihiro, Isao Ono, Masahiro Okamoto

P003 Emerging Needs for Restructuring Biomedical Knowledge and Education System, Tsuguchika Kamimura, Masumi Yukawa, Yoshitomo Tanaka, Takako Takai-Igarashi, Yoshihiro Takemoto, Hiroshi Tanaka

P004 Relation between Cell Division and Gene Expression by Using Single Cell Tracking System, Kazumi Hakamada, Satoshi Fujita, Jun Miyake

P005 Identification of Apoptosis-Induced Gene Networks from Time Course Expression Profiles with Replicated Measurements, Osamu Hirose, Ryo Yoshida, Seiya Imoto, Satoru Miyano

P006 p53 Pathways to Simulate the p53 Transcriptional Activity, Atsushi Doi, Masao Nagasaki, Kazuko Ueno, Hiroshi Matsuno, Satoru Miyano

P007 An S-System Application for Mammalian Circadian Clock System, Daisuke Tominaga, Katsuhisa Horimoto

P008 Noise-Induced Robust Synchronization in a Multicellular System, Ruiqi Wang, Luonan Chen, Kazuyuki Akahara

P009 Mathematical Modeling of G1/S Phase in the Cell Cycle with Involving the p53/Mdm2 Network, Kazunari Iwamoto, Yoshihiro Tashima, Hiroyuki Hamada, Yoshihiro Eguchi, Masahiro Okamoto

P010 Sensitivity Analysis for the *E.coli* Nitrogen Assimilation System, Koichi Masaki, Hiroyuki Kurata

P011 Analysis for the Conflict between G2/M Phase Arrest in the Cell Cycle and Apoptosis Induction, Yoshihiro Tashima, Yu Kisaka, Hiroyuki Hamada, Taizo Hanai, Yoshihiro Eguchi, Masahiro Okamoto

P012 Spatio-Temporal Dynamics of Molecules on the Cell Surface Studied by Particle Simulation, Ryuzo Azuma, Hiroshi Kobayashi, Tomoyuki Yamamoto, Akihiko Konagaya

P013 Consistency of the Transition Theory in Computer Simulation of a Genetic Toggle Switch, Tomohiro Ushikubo, Masaki Sasai

P014 Regulation of Metabolic Networks By Small Molecule Metabolites, Alex Gutteridge, Minoru Kanehisa, Susumu Goto

P015 The Finitely Numerable Effect in the Coupled Molecular Motor Model, Kazunari Mouri, Tetsuya Shimokawa

P016 A Steady-State Approximation-Based Solver for Stiff Biochemical Models, Emi Shiraishi, Hiroyuki Kurata

P017 Genomic Data Assimization for a Hybrid Functional Petri Net Model of Circadian Rhythm with Time Course Gene Expression Data, Masao Nagasaki, Rui Yamaguchi, Ryo Yoshida, Seiya Imoto, Atsushi Doi, Yoshinori Tamada, Hiroshi Matsuno, Satoru Miyano, Tomoyuki Higuchi

P018 Cell Fate Simulation of ASE Cell in *Caenorhabditis elegans* Using Hybrid Functional Petri Net with Extension, Ayumu Saito, Masao Nagasaki, Atsushi Doi, Kazuko Ueno, Satoru Miyano

P019 A Cluster Identification Method without Using a Threshold of Correlation Coefficient in Hierarchical Cluster Analysis, Yuki Miyata, Yoichi Yamada, Ken-ichiro Muramoto

P020 Cluster Analysis of Transcription Factor Binding Sites in the Promoter Regions of Cardiac Genes in Failing Hearts, Masaharu Nakayama, Hiroko Tada, Yasuhide Asaumi, Hiroaki Shimokawa
Module Discovery in Gene Expression Data Using Closed Itemset Mining Algorithm, Yoshi-fumi Okada, Wataru Fujibuchi, Paul Horton

A Gene Clustering Method Using Gene Expression Data and Gene Networks, Motoki Shiga, Ichigaku Takigawa, Hiroshi Mamitsuka

Applying Gaussian Distribution-Dependent Criteria to Decision Trees for High-Dimensional Microarray Data, Raymond Wan, Ichigaku Takigawa, Hiroshi Mamitsuka

Computational Analysis of Global Expression Profiles in Mouse Natural Antisense Transcripts, Yuki Okada, Koji Numata, Rintaro Saito, Hidenori Kiyosawa, Akio Kanai, Masaru Tomita

Quantitative Control of Early Transcription by ERK and Akt Signal Transduction, Takashi Nakakuki, Kaori Ide, Takeshi Nagashima, Kaoru Takahashi, Noriko Yamoto, Mariko Hatakeyama

Prediction of Ligand- and ErbB Receptor-Specific Transcription Factors from Time-Course Gene Expression Data of Cancer Cells, Takeshi Nagashima, Jun Horiuchi, Kenji Nakano, Kaori Ide, Kaoru Takahashi, Mariko Hatakeyama

Modeling of Extracellular Matrix Degradation Processes in Cancer Metastasis Using Covariance Structure Analysis, Akiko Hatano, Kaoru Mogushi, Hiroshi Tanaka

Gene Expression Profiling of Hepatocellular Carcinoma Using Independent Component Analysis, Satoshi Nagae, Kaoru Mogushi, Hiroshi Tanaka

ROKU: An Improved Method for the Detection of Tissue-Specific Expression Patterns, Koji Kadota, Jiazhen Ye, Yuji Nakai, Tohru Terada, Kentaro Shimizu

Identification of Tissue Specific Transcription Factors Using Microarray Gene Expression Data, Larisa Kiseleva, Ekaterina Shelest, Edgar Wingender, Paul Horton

Profiling Prostate Cancer Signatures by Statistical Analysis of mRNA Isoform Expression, T.Murlidharan Nair, Hai-Ri Li, Xiang-Dong Fu

A Comparative Study of Exploratory Analysis versus Statistical Analysis for Oligo-DNA Microarrays, Kenichiro Kanda, Kaoru Azumi, Nori Satoh, Sorin V. Sabau

Genome-Wide Detection of Human Copy Number Variations Using High-Density DNA Oligonucleotide Arrays, Daizuke Komura, Shumpei Ishikawa, Fan Shen, Kunihiro Nishimura, Sigeo Ibara, Hiroshi Nakamura, Keith W. Jones, Jing Huang, Hiroyuki Aburatani

Experimental Design for Time-Series Microarray Analysis, Ryosuke Ito, Hiroki Takahashi, Taku Oshima, Naotaka Ogasawara, Md. Altaf-Ul-Amin, Ken Kurokawa, Shigehiko Kanaya

New Gene Filtering Method Using S2N’ Based on the Concept of PART Filtering Method, Hiro Takahashi, Hiroyuki Honda

Gene Alignment for Cell Division Cycle Microarray Experiments without Sinusoidal Fittings, Y-h. Taguchi

Power Spectra of Bird-Influenza A Virus (BIV) ssRNA Base Sequences : Possibility of Cooperative Genes or Interferences, Eisei Takushi, Hiroyuki Sakamoto, Mitsuhiro Seino

Gene Finding for Microbial Metagenomics, Jungho Park, Hideki Noguchi, Toshihisa Takagi

Conservation of Regulation Systems in Firmicutes, Nicolas Sierro, Kenta Nakai

Comprehensive Detection of Terminal Oligo-Pyrimidine (TOP) Genes in the Human Genome, Riu Yamashita, Yutaka Suzuki, Hiroyuki Wakaguri, Sumio Sugano, Kenta Nakai

Autoimmune Diseases and Evolutionary Trace of the T-Cell Epitopes, Wataru Honda, Shuichi Kawashima, Minoru Kanehisa
Combining Molecular Dynamics Simulation with a Graph Theoretical Approach to Study Protein Complex Flexibility, AbdulRajjak Shaikh, Mohamed Ismael, Pei Qiang, Hideyuki Tsuboi, Michihisa Koyama, Nozomu Hatakeyama, Akira Endou, Hiromitsu Takaba, Momoji Kubo, Eiichiro Ichiishi, Carlos A. Del Carpio, Akira Miyamoto

Inferring Domain Combination Pattern and Its Biological Meaning via Association Rules, Sukhoon Jung, Dong-soo Han, Sung-doke Lee

A Novel Method to Determine the Assembling Space between Two Protein Subunits, Miki Maeda, Hiroya Nobori

Biomolecular Computations toward Enzyme-Catalyzed Transformations of Non-Natural Organic Compounds: Ab initio Fragment Molecular Orbital Calculations, Takahisa Tanaka, Takatomo Kimura, Yoschiro Yagi, Yoshinobu Naoshima

Can Brownian Dynamics be a Useful Tool for Structure-Based Drug Design?, Akifumi Oda, H糸uo Matsuzaki, Noriyuki Yamaotsu, Shuichi Hirono

A Benchmark Study of the “Soft Docking” Module of MIAx, Using a Set of Unbound Proteins, Pei Qiang, Mohamed Ismael, Abdul Rajjak Shaikh, Hideyuki Tsuboi, Michihisa Koyama, Nozomu Hatakeyama, Akira Endou, Hiromitsu Takaba, Momoji Kubo, Eiichiro Ichiishi, Carlos A. Del Carpio, Akira Miyamoto

Supervised Consensus Scoring Methods for Structure-Based Drug Design, Reiji Teramoto, Hiroaki Fukunishi

Scoring Analysis of DNA Binding Sites of DNA Binding Proteins, Reika Okihara, Yukako Sakatsuji, Ayumi Suzuki, Ichiro Yamato, Satoru Miyazaki

Classification of Protein-DNA Complexes Based on Structural Descriptors, Ponraj Prabakaran, Shandar Ahmad, M. Michael Gromiha, Maria G. Singarayan, Akinori Sarai

Comparative Analysis of Amino Acid Residues and Structures between RNase HII and Argonaute Proteins from Pyrococcus furiosus, Sayaka Kitamura, Kosuke Fujishima, Asako Sato, Arun Krishnan, Masaru Tomita, Akio Kanai

Murlet: A Practical Multiple Alignment Tool for Structural RNA Sequences, Hisanori Kiryu, Yasuo Tabei, Taishin Kin, Kiyoshi Asai

fRNAdb: A Platform for Mining/Annotating Functional RNA Candidates from Non-Coding RNA Sequences, Taishin Kin, Kouichirou Yamada, Goro Tera, Hiroaki Okida, Yasuhiro Yoshi-nari, Yukiteru Ono, Aya Kojima, Takashi Komori, Kiyoshi Asai

RNAmine: Frequent Stem Pattern Miner from RNAs, Michiaki Hamada, Koji Tsuda, Taku Kudo, Taishin Kin, Kiyoshi Asai


Comprehensive Analysis of miRNA Effect to the Transcripts, Keishin Nishida, Riu Yamashita, Kengo Kinoshita, Kenta Nakai

Multiple Alignment of RNAs by Maximizing the Sum of the Matching Probability of Stem Fragments, Yasuo Tabei, Hisanori Kiryu, Taishin Kin, Kiyoshi Asai

Phylogenetic Analysis of Essential Genes by Using ORI-GENE, Hirotoshi Kawano, Hideaki Mizuno, Akinori Sarai

Evidence for Introns-Late from Intron Phase Distribution, Hung Dinh Nguyen, Maki Yoshihama, Naoya Kenmochi

Algebraic Evolution of the Genetic Code, Takashi Kawamura
P082 Distance Structure of Homologous Gene Cluster in *Cyanobacteria*, Naobumi Sasaki, Naoki Sato

P083 Tracing Back Xenobiotic Responsive and NR Mediated Pathways/Networks, Yoshitomo Tanaka, Masumi Yukawa, Hiroshi Tanaka, Tsuguchika Kaminuma

P084 Analyses of the Nutrient Dependency of Parasites to Hosts Using KEGG Database, Ai Muto, Masahiro Hattori, Wataru Honda, Minoru Kanehisa

P085 Identification of Novel Types of Prokaryotic Retroelements Based on Gene Neighborhood and Protein Architecture, Kenji K. Kojima, Minoru Kanehisa

P086 Comprehensive Analysis of Domain Architectures of Transmembrane Proteins, Syu-uchi Yoshida, Yoshihiro Yamazaki, Takahiro Nishio, Sunao Kaneko, Toshio Shimizu

P087 Gene Expression Profile Analysis for Circadian Promoter Activities of Cyanobacterial Bioluminescent Reporter Strains Using Non-Metric Multidimensional Scaling, Tokitaka Oyama, Hiroshi Ito, Takao Kondo, Y-h. Taguchi

P088 Comparative Sequence between Human and Mouse: Promoter Conservation and Protein Conservation, Hiroyasu Chiba, Ri Ri Yamashita, Kengo Kinoshita, Kenta Nakai

P089 Whole-Genome Functional Linkage Network Construction in the Domain Level by Probabilistic Model, Yong Wang, Ruei-Sheng Wang, Xiang-Sun Zhang, Luonan Chen

P090 Systematic Analysis of Functional SNP with Type 2 Diabetes Mellitus (T2DM) in the Korean Population, Hyo-Jeong Ban, Kwan-Joon Park, Ji-Hong Kim, Hyun-Woo Han

P091 Analysis of Disease-Associated Mutations and SNP in Relationship with Protein Structure, Taku Ashikari, Hitoshi Kono, Akinori Sarai

P092 Adaptive Threshold for Detecting Significant Fold Changes in Microarray Data, Hidenori Inaoka, Yutaka Fukuoka

P093 Precise Correlation between MLV Integration Sites and Transcription Start Sites in the Human Genome, Yoshiaki Tanaka, Ri Yamashita, Kengo Kinoshita, Kenta Nakai

P094 Hierarchical Bayes Approach to Array CGH Data Normalization, Shigeo Oba, Shin Ishii

P095 Development of a Platform for Functional Genomics under the Generation Challenge Programme (GCP), Masaru Takeya, Kohji Suzuki, Koji Doi, Shoshi Kikuchi, Richard Bruskewich

P096 Annotating Genes with Labelled and Unlabelled Data, Xing-Ming Zhao, Luonan Chen, Kazuyuki Aihara

P097 Developing SVM Classifier for GPI-(Like)-Anchored Proteins Prediction, Wei Cao, Shugo Nakamura, Kentaro Shimizu

P098 Enrichment of Protein Utilization in Protein-Protein Interaction Prediction by Adjusting e-value of InterProScan and Using Gene Ontology, Woo-Hyuk Jang, Hee-Young Hur, Dong-So Han

P099 An Approach to Identify Unknown Gene Function through Higher Order Correlations for Gene Clusters, Akira Funae, Daisuke Komura, Hiroshi Nakamura, Sigeo Ihara

P100 Proposal of Graphical Assessment Method of Attribute Significance for Comprehensive Combination Analysis, Masahiro Nakatomi, Hiroyuki Honda

P101 Predicting Types of Protein-Protein Interactions Using Various Multiple-Instance Learning Algorithms, Hiroshi Yamakawa, Koji Maruhashi, Yoshiro Nakao

P102 Relationship between Data Size and Accuracy of Prediction of Protein-Protein Interactions by Co-Evolutionary Information, Tetsuya Sato, Yoshihiro Yamamishi, Hisako Ichihara, Keiichi Kuma, Minoru Kanehisa, Hiroyuki Toh

P103 Prediction Accuracy Evaluation of Domain and Domain Combination Based Prediction Methods for Protein-Protein Interaction, Dong-So Han, Woo-Hyuk Jang
P104 Protein Feature Prediction Using Chi-Square in PPI Networks, YongHo Lee, JaeHun Choi, JongMin Park, SunLee Bang, SooJun Park

P105 Predicting Ligand Binding Sites of Uncharacterized Protein, Mizuki Morita, Shugo Nakamura, Kentaro Shimizu


P107 Comparison of the Prediction Abilities of FBA, MOMA and ROOM for a pykF Mutant of E. coli, Quanyu Zhao, Hiroyuki Kurata

P108 DNA Repair Recognition via Support Vector Machines, J.B. Brown, Tatsuya Akutsu


P110 Prediction of Protein-Protein Interaction Sites with Two-Stage Support Vector Machine, Masanori Kukita, Kentaro Shimizu

P111 Prediction of Mucin-Type O-Glycosylation by Layered Neural Networks and Support Vector Machines, Ikue Nouno, Hirotaka Sakamoto, Takeshi Iritani, Kazutoshi Sakakibara, Ikuko Nishikawa, Masahiro Ito

P112 Computational Prediction of Drosophila MicroRNA Targets and Analysis of their Negative Feedback Control, Yuka Watanabe, Nozomu Yachie, Masaru Tomita, Akio Kanai

P113 Detection of Transcription Units Based on Integration of Non-Targeted Analyses, Hirokazu Kobayashi, Yoshiaki Kiura, Kazuo Kobayashi, Md. Altaf-Ul-Amin, Naotake Ogasawara, Shigehiko Kanaya, Ken Kurokawa

P114 Prediction of Glycosphingolipid Chemical Structure from MALDI-TOF MS Data, Yuki Matsumuro, Saki Itonori, Mutsumi Sugita, Masahiro Ito

P115 An Expectation-Maximization Algorithm for Reconstructing Heterogeneous Gene-Content Evolution, Wataru Iwasaki, Toshihisa Takagi

P116 From Function Prediction to Pathway Prediction: A New Pipeline Based on KAAS and GENIES, Yuki Moriya, Yoshihiro Yamamishi, Masumi Itoh, Shinobu Okamoto, Minoru Kachisasa

P117 Proposal of PART (Projective Adaptive Resonance Theory) for Analysis of Gene Expression Data with Small Samples, Takashi Kawamura, Hiro Takahashi, Hiroyuki Honda

P118 Prediction of Glycan Structures from Gene Expression Data Based on Improved Scoring Scheme, Akitsugu Suga, Yoshihiro Yamamishi, Kosuke Hashimoto, Minoru Kachisasa

P119 Integrative Estimation of Gene Regulatory Network by Means of AdaBoost, Shinya Nabatame, Hitoshi Iba

P120 Analysis and Discrimination of Ligand Binding Membrane Proteins Using a Simple Statistical Approach, M.Xavier Suresh, M.Michael Gromiha, Makiko Suwa

P121 Prediction of Protein Subcellular Localization Using an Artificial Neural Network, Anton Kratz, Rintaro Saito, Arun Krishnan, Masaru Tomita

P122 A Statistical Framework for Genome Wide Discovery of Biomarker Splice Variations with GeneChip Human Exon 1.0 ST Arrays, Ryo Yoshida, Kazuyuki Numata, Seiya Imoto, Masao Nagasaki, Atsushi Doi, Kazuko Ueno, Satoru Miyano

P123 A Calibration Technique for Single-Dimensional Distribution of Local GC Content, Tomoyuki Fujimoto, Tadao Sugiura, Takeshi Nagaya, Tetsuo Sato, Kotaro Minato

P124 Nonmetric Distances for Barcode of Life, Hisamitsu Akiba, Y-h. Taguchi
modEst: A GMOD-Based Framework for Integrating Partial Polyploid Transcripts into Closely-Related Genomes, Aaron Chuah, Richard Bartfai, Laszlo Orban, Alan Christo®els

In Silico Functional Profiling of Small Molecules for Assessing their Physiological Effects, Tomohiro Sato, Yo Matsuo, Shigeyuki Yokoyama

Probabilistic Ranking for Analyzing Transcriptional Response Variations of Metabolic Gene Paths, Ichigaku Takigawa, Hiroshi Mamitsuka

Interpreting Patterns of Gene Expression with spherical Self-Organizing Maps (sSOM): Application to Search for Cell Surface Markers, Tuoya, Yuh Sugii, Tadayoshi Nagaoka, Takayuki Fukuda, Hioko Tada, Hidenori Yamada, Yasaburo Matsuura, Heizo Tokutaka, Masaharu Seno

Gene Subset Selection for Kernel-Based Classifiers, Satoshi Niijima, Satoru Kuhara

Improvement of a Gene Network Discovery Method via Frequent Subtree Mining, Alexandre Terrier, Yoshinori Tamada, Kazuyuki Numata, Seiya Imoto, Takashi Washio, Tomoyuki Higuchi

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Pathway Mapping Web-Service Based on KEGG and SVG, Nobuaki Kono, Kazuharu Arakawa, Masaru Tomita

14
P146 Visualization of Metabolic Networks as Networks of Atoms by Pajek: An Application of Connectivity Matrix Method, Jun Ohta

P147 A Hub-Seeded Multilevel Algorithm for Fast Layout of Protein-Protein Interaction Networks, SunLee Bang, JaeHun Choi, JongMin Park, SooJun Park


P149 Correlation Analysis of Sequence and Activity Based on Translation Signal Database, TRSIG, Takahiro Ishimoto, Alex V. Kochetov, Akinori Sarai

P150 New Features of MutationView: A Module to Search for Disease-Causing Genes from Protein Functional Domain, Masafumi Ohtsubo, Takashi Kawamura, Susumu Mitsuyama, Nobuyoshi Shimizu, Shinsei Minoshima

P151 Construction of Biomolecular Network in Structurome and Analysis of Cooperativity, Mitsunobu Sekitou, Akinori Sarai

P152 INOH Pathway Data Ontologies, Noriko Sakai, Satoko Yamamoto, Hiromi Nakamura, Yukiko Nakanishi, Toshihisa Takagi, KenIchiro Fukuda

P153 Application of AI-Based Database Methods in Purification of Traditional Chinese Pharmacy Recipes, Yini Cui

P154 Restauro-G: A Rapid Genome Re-Annotation System, Satoshi Tamaki, Kazuharu Arakawa, Nobuaki Kono, Masaru Tomita

P155 A Web-Based Resource for Glycome Informatics, Kiyoko F. Aoki-Kinoshita, Masao Ichikawa, Shuichi Ikeda, Kouichi Yamada, Takako Yamaguchi

P156 Gclust Server: Phylogenetic Profiling with Pre-Defined Organism Sets, Naoki Sato

P157 TACT: Transcriptome Auto-Annotation Conducting Tool of H-InvDB, Chisato Yamasaki, Hiroaki Kawashima, Fusano Todokoro, Yasuhiro Imamizu, Makoto Ogawa, Motohiko Tanino, Takeshi Itoh, Takashi Gojobori, Tadashi Imanishi
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