

GIW '99

The Tenth Anniversary Workshop on Genome Informatics

Yebisu Garden Hall
Yebisu Garden Place, Tokyo, Japan
December 14–15, 1999

Yebisu Garden Room
The Anniversary Event
December 13, 1999

The Tenth Workshop on Genome Informatics (GIW '99) is a forum for researchers, practitioners and users working on various aspects of Genome Informatics. The aim is to present recent research results (theory/practice), to demonstrate systems, and to explore directions for future research and new applications related to Genome Science.

Steering Committee

Minoru Kanehisa (Chair, Kyoto University)
Toshihisa Takagi (University of Tokyo)
Satoru Miyano (University of Tokyo)

Sponsored by

Human Genome Center, University of Tokyo
Grant-in-Aid for Scientific Research on Priority Areas
“GENOME SCIENCE” from MESSC of Japan

Secretary and Local Arrangements

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Institute of Medical Science, University of Tokyo
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Newest Information

<http://giw.ims.u-tokyo.ac.jp/giw99>

Program Committee

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Registration

Registration should be done at

<http://giw.ims.u-tokyo.ac.jp/giw99/>

until November 30, 1999.

Until November 30, 1999: (Japan time)

Registration	Free
Banquet on December 14	JPY6,000.-
(Student)	(JPY3,000)
A copy of workshop book	JPY3,000.-
Reception Party on December 13	Free

After November 30, 1999: (Japan time)

Registration	Free
Banquet on December 14	JPY7,000.-
(Student)	(JPY4,000)
A copy of workshop book	JPY4,000.-
Reception Party on December 13	Free

GIW '99 Advanced Program

Registration

Dec. 13:	16:30 - 18:30	Garden Room
Dec. 14:	9:00 - 18:30	Garden Hall
Dec. 15:	9:00 - 18:00	Garden Hall

December 13, Monday, Garden Room

The Anniversary Event

16:30 - 18:30	Registration at Garden Room
17:30 - 18:00	Event Presented by Japanese Society for Bioinformatics
18:00 - 18:30	Event Presented by International Society for Computational Biology
18:30 - 21:00	Reception Party and General Meeting

December 14, Tuesday, Garden Hall

Opening Address

9:20 - 9:30	Kiyoshi Asai (ETL)
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Session 1

	Chair: A. Keith Dunker (Washington State University)
9:30 - 9:50	<i>MIAX: A Novel System for Assessment of Macromolecular Interaction in Condensed Phases. 1) Description of the Interaction Model and Simulation Algorithm</i> , Carlos A. Del Carpio Munoz, Atsushi Yoshimori (Toyohashi University of Technology)
9:50 - 10:10	<i>A Generic Criterion for Gene Recongnitions in Genomic Sequences</i> , Chungfan Kim*, Akihiko Konagaya*, Kiyoshi Asai [†] , (*Japan Advanced Institute of Science and Technology, [†] ETL)
10:10 - 10:30	<i>Protein Threading Based on Multiple Protein Structure Alignment</i> , Tatsuya Akutsu, Kim Lan Sim (Univ. of Tokyo)

Session 2	Chair: Akihiko Konagaya (JAIST)
10:30 - 10:50	<i>Predicting Protein Disorder for N-, C-, and Internal Regions</i> , Xiaohong Li, Pedro Romero, Meeta Rani, A. Keith Dunker, Zoran Obradovic (Washington State Univ.)
10:50 - 11:10	<i>Predicting Binding Regions within Disordered Proteins</i> , Ethan Garner, Pedro Romero, A. Keith Dunker, Celeste Brown, Zoran Obradovic (Washington State Univ.)
Break	11:10 - 11:20
Invited Talk	Chair: Kiyoshi Asai (ETL)
11:20 - 12:20	<i>Computational Analysis of High-throughput Genomics Data Using Hidden Markov Models and Support Vector Machines</i> , David Haussler (UC Santa Cruz)
Lunch Break	12:20 - 14:00
Session 3	Chair: Matsuda Hideo (Osaka Univ.)
14:00 - 14:20	<i>A Compression Algorithm for DNA Sequences and Its Applications in Genome Comparison</i> , Xin Chen*, Sam Kwong [†] , Ming Li [‡] (*Univ.of Hong Kong, [†] Peking Univ. [‡] Univ.of Waterloo)
14:20 - 14:40	<i>An EM-type Algorithm for Ordered Restriction Map Alignment</i> , Hirotada Kobayashi, Hiroshi Imai (Univ.of Tokyo)
14:40 - 15:00	<i>A Greedy Algorithm for Minimizing the Number of Primers in Multiple PCR Experiments</i> , Koichiro Doi, Hiroshi Imai (Univ.of Tokyo)
15:00 - 15:20	<i>On the Reconstruction of Ancient Doubled Circular Genomes Using Minimum Reversals</i> , Nadia El-Mabrouk, David Sankoff (Université de Montréal)
Message from International Society for Computational Biology (ISCB)	
15:20 - 15:30	A. Keith Dunker (Board of Director, ISCB)

One-Minute Talks for Posters & Software Demonstrations

Chair: Shigeki Mitaku

(Tokyo Univ. of Agric. and Tech.)

15:30 - 17:00

Posters & Software Demonstrations

17:00 - 18:30

Banquet 18:30 - 21:00

Foyer, Garden Hall

December 15, Wednesday, Garden Hall

Session 4	Chair: Satoru Kuhara (Kyushu Univ.)
9:40 - 10:10	<i>Genome-scale Gene Expression Analysis and Pathway Reconstruction in KEGG</i> , Mitsuteru Nakao, Hidemasa Bono, Shuichi Kawashima, Tomomi Kamiya, Kazushige Sato, Susumu Goto, Minoru Kanehisa (Kyoto Univ.)
10:00 - 10:20	<i>Toward Routine Automatic Pathway Discovery from On-line Scientific Text Abstracts</i> , See-Kiong Ng*, Marie Wong [†] (*Kent Ridge Digital Labs, [†] Natl. Univ. Singapore)
10:20 - 10:40	<i>Finding Precursor Compounds in Secondary Metabolism</i> , Masanori Arita*, Kiyoshi Asai*, Takaaki Nishioka [†] (*ETL, [†] Kyoto Univ.)
Coffee Break	10:40 - 11:00
Invited Talk	Chair: Toshihisa Takagi (Univ. Tokyo)
11:00 - 12:00	<i>Human Genome Analysis and Medicine in the 21st Century</i> , Yusuke Nakamura (Director, Human Genome Center, Univ. Tokyo)
Lunch Break	12:00 - 13:30
Posters & Software Demonstrations	13:30 - 15:00

Session 5	Chair: Susumu Goto (Kyoto Univ.)
15:00 - 15:20	<i>Automated Processing of 2-D Gel Electrophoretograms of Genomic DNA for Hunting Pathogenic DNA Molec- ular Changes</i> , Katsutoshi Takahashi*, Masayuki Nakazawa [†] , Yasuo Watanabe [‡] Akihiko Konagaya* (*JAIST, [†] Kanazawa Technical College, [‡] Kanazawa Institute of Technology)
15:20 - 15:40	<i>Bio-calculus: Its Concept and Molecular Interaction</i> , Masao Nagsaki* [‡] , Shuichi Onami [‡] , Satoru Miyano* [‡] , Hiroaki Kitano ^{†‡} (*Univ. Tokyo, [†] SONY CSL, [‡] ERATO)
15:40 - 16:00	<i>Towards Automatic Construction of Cell- Lineage of C.elegans from Nomarski DIC Microscope Images</i> , Tomohiro Yasuda* [‡] , Hideo Bannai* [‡] , Shuichi Onami [‡] , Satoru Miyano* [‡] , Hiroaki Kitano ^{†‡} (*Univ. Tokyo, [†] SONY CSL, [‡] ERATO)
Coffee Break	16:00 - 16:20

Session 6	Chair: Kenta Nakai (Univ. Tokyo)
16:20 - 16:40	<i>Tracing Synergetic Behavior of the QTLs Affecting Oral Glucose Tolerance in the OLETF Rat</i> , Akihiro Nakaya*, Haretugu Hishigaki [†] , Shinichi Morishita* (*Univ.of Tokyo, [†] Otsuka GEN Research Institute)
16:40 - 17:00	<i>Integrating Application Programs for Bioinformatics Using a web Browser</i> , Yutaka Ueno, Kiyoshi Asai, Masanori Arita (ETL)
17:00 - 17:20	<i>Making High-level Queries on Diverse Genome Data: A Structured Genome Document Database System Based on GXML and GQL</i> , Aaron Stokes*, Hideo Matsuda [†] , Akihiro Hashimoto [†] (*JST, [†] Osaka Univ.)
17:20 - 17:40	<i>A System to Find Genetic Networks using Weighted Network Model</i> , Tomohiro Moriyama*, Ayumi Shinohara*, Masayuki Takeda*, Osamu Maruyama [†] , Takao Goto [†] , Satoru Miyano [†] , Satoru Kuhara [‡] (*Kyushu Univ., [†] Univ.of Tokyo, [‡] Graduate School of Genetic Resources Technology, Kyushu Univ.)
Best Paper Award Ceremony	17:40 - 17:50
Closing Remarks	17:50 - 18:00 Akihiko Konagaya (JAIST)

Software Demonstrations

- S01: *PAPIA (Parallel Protein Information Analysis) System and MolTreC Parallel Molecular Dynamics Simulator Running on a Compact 8-node Linux PC Cluster*, Yutaka Akiyama*, Tamotsu Noguchi*, Kentaro Onizuka*[†], Makoto Ando*[‡]
(*RWCP, [†]Matsushita Research Inst., [‡]NKK Corp.)
- S02: *Ortholog Identifiers for Integration of Genomic and Pathway Information in KEGG*, Susumu Goto*, Kotaro Shiraishi[†], Kayo Okamoto*, Hiroko Ishida*, Toshi Nakatani*, Tomoko Deno*, Minoru Kanehisa*
(*Kyoto Univ., [†]Fujitsu Kyushu System Ltd.)
- S03: *A Keyword Recommendation System for GenBank*, Yasuhiko Kitamura, Tetsuro Nanbu, Shoji Tatsumi (Osaka City Univ.)
- S04: *GeneAlign: Java Application Software for Multiple Sequence Alignment Editor*, Ken Kurokawa*, Yoshitaka Hasegawa*, Kenichi Kawashima[†], Toshiyuki Okumura[†], Tatsuya Takagi*, Teruo Yasunaga* (*Osaka Univ., [†]Net Navi)
- S05: *KMDB: Keio Mutation Database for Human Disease Gene*, Shinsei Minoshima, Susumu Mitsuyama, Saho Ohno, Takashi Kawamura, Nobuyoshi Shimizu (Keio Univ.)
- S06: *NEXTDB: The Expression Pattern Map Database for C. elegans*, Tadasu Shin-i*, Yuji Kohara[†]
(*CREST, JST, [†]NIG)
- S07: *ViewDesigner: A Tool for Designing Viewscopes in Discovery System HypothesisCreator*, Yoshinori Tamada*, Satoshi Matsumoto*, Osamu Maruyama[†], Satoru Miyano[†]
(*Tokai Univ., [†]Univ. Tokyo)
- S08: *Protein Dynamics Observations of Lambda Phage by Hybrid Petri Net*, Atsuhiko Doi*, Rainer Drath[†], Masao Nagasaki[‡], Hiroshi Matsuno* Satoru Miyano[‡]
(*Yamaguchi Univ., [†]Technical Univ. of Ilmenau, [‡]Univ. Tokyo)
- S09: *An Intelligent Tool for Selecting Abstracts in MEDLINE*, Miyako Tanaka*, Sanae Nakazono[†], Hiroshi Matsuno[†], Satoru Miyano[‡] (*Ube Natl. Coll. of Tech., [†]Yamaguchi Univ., [‡]Univ. Tokyo)

Posters

- P01: *Development of an Efficient Data Processing Method for cDNA Microarray and Its Application to Tissue Expression Profiling*, Koji Kadota^{*†}, Rika Miki^{*‡}, Yasushi Okazaki^{*§}, Kentaro Shimizu[†], Yoshihide Hayashizaki^{*‡§} (*RIKEN, [†]Univ. Tokyo, [‡]Tsukuba Univ., [§]CREST, JST)
- P02: *DDGEL/DDCHIP: Web-Based Systems for Analysis of 2-D Gel Electrophoresis Images and DNA Macro/Micro Array Images*, Kyotetsu Kanaya^{*}, Akira Ohyama^{*}, Tatsuya Akutsu[†], Asao Fujiyama[‡] (*Mitsui Knowledge Ind. Co., Ltd., [†]Univ. Tokyo, [‡]NIG)
- P03: *Probe Design for DNA Chip*, Ken-ichi Kurata, Akira Suyama (Univ. Tokyo)
- P04: *Discrimination of Drug Sensitivity of Cancer Using cDNA Microarray and Multivariate Statistical Analysis*, Tatsuhiko Tsunoda^{*}, Yoshiaki Hojo[†], Chikashi Kihara^{*}, Norihiko Shiraishi^{*}, Osamu Kitahara^{*}, Kenji Ono^{*}, Toshihiro Tanaka^{*}, Toshihisa Takagi^{*}, Yusuke Nakamura^{*} (*Univ. Tokyo, [†]Hitachi, Ltd.)
- P05: *Construction of an Integrated Environment for Sequence, Structure, Property and Function Analysis of Proteins*, Jianghong An^{*}, Takao Nakama[†], Yasushi Kubota[†], Hiroshi Wako[‡], Akinori Sarai^{*} (*RIKEN, [†]Advanced Tech. Inst. Inc., [‡]Waseda Univ.)
- P06: *Recent Improvements in the Automatic System for Protein Tertiary Structure Prediction GAX*, Carlos Adriel Del Carpio Munoz (Toyohashi Univ. of Tech.)
- P07: *Development of an Automated Identification Program for Three-Dimensional Protein Motifs*, Hiroaki Kato, Yoshimasa Takahashi, Hidetsugu Abe (Toyohashi Univ. of Tech.)
- P08: *Genius: System for Assigning Protein Coding Regions to 3D Structures*, Makiko Suwa^{*}, Henrik T. Yudate^{*}, Yasuhiko Masuho^{*}, Asaf A. Salamov[†], Christine A. Orengo[‡], Mark B. Swindells[§] (*Helix Research Inst., [†]The Sanger Centre, [‡]Univ. Coll. London, UK, [§]Inpharmatica, Ltd.)
- P09: *A System for Displaying Protein Structure Information Based on Sequence Fragment Similarity*, Shouji Tatsumoto, Kenji Satou (JAIST)

- P10: *An Automated Structure Prediction System by Lattice Model for Seven-Helix-Type Membrane Proteins*, Junichi Uechi*, Takatsugu Hirokawa[†], Makiko Suwa[‡], Shigeki Mitaku* (*Tokyo Univ. of Agric. & Tech., [†]Ryoka Systems Inc., [‡]Helix Research Inst.)
- P11: *BESPA: Software Tools for 3D Structure Reconstruction from Single Particle Images of Proteins*, Yutaka Ueno*, Katsutoshi Takahashi[†], Kiyoshi Asai*, Chikara Sato* (*ETL, [†]JAIST)
- P12: *Chemical Knowledge for Predicting Biosynthetic Pathways of Secondary Metabolites*, Takaaki Nishioka*, Kimito Funatsu[†] (*Kyoto Univ., [†]Toyohashi Univ. of Tech.)
- P13: *Prediction of Secondary Metabolism Pathways from Genomic Information and Compounds Data*, Atsushi Ogiwara (Glaxo Wellcome)
- P14: *Methods for Predicting Target Sites of Transcription Factors*, Akinori Sarai*, Hidetoshi Kono[†], Michael Gromiha*, Fabio Pichierri*, Kenji Sayano[‡], Misako Aida[§] (*RIKEN, [†]Univ. of Pennsylvania, [‡]ETL, [§]Hiroshima Univ.)
- P15: *Evaluation of a Method for Predicting Transcription Factors*, Goro Terai*, Takeshi Mizuno*, Toshihisa Takagi[†] (*INTEC Inc., [†]Univ. Tokyo)
- P16: *Prediction of Cooperative Binding Sites for Multiple Transcription Factors*, Yifei Wang, Akinori Sarai (RIKEN)
- P17: *AIGNET: A System That Infers Large Scale Genetic Networks*, Yukihiro Maki*, Shoji Watanabe*, Yukihiro Eguchi*, Daisuke Tominaga[†], Masahiro Okamoto[†] (*Mitsui Knowledge Industry Co., Ltd., [†]Kyushu Inst. of Tech.)
- P18: *Coherent Structural Prediction of a Set of Paralogous Genes on a Eukaryotic Genome*, Osamu Gotoh (Saitama Cancer Center Research Inst.)
- P19: *Interaction-based Analysis of Protein Function and Network*, Haretsugu Hishigaki*[†], Toshihide Ono[†], Akira Tanigami[†], Toshihisa Takagi* (*Univ. Tokyo, [†]OTSUKA Pharmaceutical Co., Ltd.)
- P20: *Prediction of MHC Class II-Peptide Interaction Using Fuzzy Neural Network*, Hideki Noguchi, Taizo Hanai, Hiroyuki Honda, Takeshi Kobayashi (Nagoya Univ.)

- P21: *Prediction of Nuclear Localization Signals by HMM*,
Keun-Joon Park, Minoru Kanehisa (Kyoto Univ.)
- P22: *A Novel System for Assessment of Macromolecular
Interaction in Condensed Phases. 2) Interaction Site
Inference by Molecular Shape and Electrostatic
Complementarity*, Atsushi Yoshimori, Carlos Adriel
Del Carpio Munoz (Toyohashi Univ. of Tech.)
- P23: *Progress of ProTherm: Thermodynamic Database
for Proteins and Mutants*, Michael Gromiha*,
Jianghong An*, Hidetoshi Kono*, Motohisa Oobatake*[†],
Hatsuho Uedaira*, P. Prabakaran*, Akinori Sarai*
(*RIKEN, [†] Meijo Univ.)
- P24: *Detection of Apoptotic Domains against KEGG
Database by the HMM Search*,
Masahiro Hattori, Minoru Kanehisa (Kyoto Univ.)
- P25: *Maintenance of Transcription Factor DataBase TFDB*,
Masako Kaizawa*, Satoru Watanabe*,
Takahiro Nobukuni*, Masami Horikoshi[†], Hiroshi Handa[‡],
Yoshiyuki Kuchino*, Takao Sekiya*, Hiroshi Mizushima*
(*NCCRI, [†]Exploratory Research for Advanced Tech.,
[‡]Tokyo Institute of Tech.)
- P26: *A Database System for the Management and
Karyotype Analysis of Chromosome Image Data*,
Akihiro Kawaguchi, Kenji Satou (JAIST)
- P27: *MAGEST: ESTs and Gene Expression Pattern Database
for *Halocynthia roretzi* Maternal cDNA*,
Shuichi Kawashima*, Takeshi Kawashima*,
Hiroki Nishida[†], Kazuhiro W. Makabe*,
Minoru Kanehisa* (*Kyoto Univ., [†]Tokyo Inst. of
Tech.)
- P28: *INE: The Rice Genome Sequence Database*, Yoshiyuki
Mukai*, Hideki Nagasaki*, Baltazar A. Antonio*,
Katsumi Sakata*, Yasumichi Sakai[†], Takuji Sasaki*
(*NIAR/STAFF, [†]Mitsubishi Space Software Co., Ltd.)
- P29: *Receptor Database (RDB) in 1999*, Kotoko Nakata,
Takako Takai, Tsuguchika Kaminuma (Natl. Inst. of
Health Sciences)
- P30: *Thermodynamic Database for Protein-Nucleic Acid
Interactions*, P. Prabakaran*, Jianghong An*,
Michael Gromiha*, S. Selvaraj*, Hatsuho Uedaira*,
Hidetoshi Kono[†], Akinori Sarai* (*RIKEN, [†]Univ.
of Pennsylvania)
- P31: *SLAD - An Integrated Swine MHC Database: A
Case Study of Data Warehousing in Molecular*

Immunology, Christian Schönbach, Vladimir Brusic,
Judice L.Y. Koh (Kent Ridge Digital Labs)

- P32: *PDB-DO:Database of Disorder*, Kim Lan Sim*,
Tomoyuki Uchida[†], Satoru Miyano* (*Univ. Tokyo,
[†]Hiroshima City Univ.)
- P33: *An Aberrant Splicing Database for Finding Rules of
Splice-Site Selection*, Takashi Yamanaka*,
Tetsushi Yada[†], Kenta Nakai* (*Univ. Tokyo, [†]RIKEN)
- P34: *Construction and Application of Mouse Full-length
cDNA Database*, Hideaki Konno*,
Yoshifumi Fukunishi*[†], Toshinori Endo*,
Yoshihide Hayashizaki* (*RIKEN[†]CREST, JST)
- P35: *Classification of MEDLINE Abstracts*,
Katsutoshi Ibushi, Nigel Collier, Jun'ichi Tsujii
(Univ. Tokyo)
- P36: *A Combined Query Expansion Approach for
Information Retrieval*, Hisao Imai, Nigel Collier,
Jun'ichi Tsujii (Univ. Tokyo)
- P37: *A Semantically Annotated Corpus from MEDLINE
Abstracts*, Tomoko Ohta, Yuka Tateisi, Nigel Collier,
Chikashi Nobata, Katsutoshi Ibushi,
Jun'ichi Tsujii (Univ. Tokyo)
- P38: *Automatic Extraction of Information on
Protein-Protein Interaction from Scientific Literature*,
Toshihide Ono*, Haretsugu Hishigaki*[†], Akira Tanigami*,
Toshihisa Takagi[†] (*OTSUKA Pharmaceutical. Co.,
Ltd., [†]Univ. Tokyo)
- P39: *An Ontology for Biological Reaction Events*, Yuka
Tateisi, Tomoko Ohta, Takako Takai, Jun'ichi Tsujii
(Univ. Tokyo)
- P40: *An Object-Protocol Model Multidatabase Query
System for Rice and Maize*, Bal A. Antonio*,
Zhiwei Fang[†], Hector Sanchez[†], Mary Polacco[†],
Su-Shing Chen[†], Katsumi Sakata*, Isamu Ohta*,
Yoshiyuki Mukai*, Ed Coe, Jr.[†], Takuji Sasaki*
(*NIAR/STAFF [†]Univ. of Missouri-Columbia)
- P41: *A Preliminary Study in Data Management and
Visualization of Signal Transduction Pathway
Data – Viewing Interaction Data*,
Ken-ichiro Fukuda, Toshihisa Takagi (Univ. Tokyo)
- P42: *Toward a Data Mining Service from Large and
Heterogeneous Genome Databases in GenomeNet*,
Yoshiki Fuseda, Kenji Satou (JAIST)

- P43: *Cross Database Visualization*, David P. Hansen*, Thure Etzold*, Guenther Kurapkat[†]
(*LION Bioscience Ltd., [†]LION Bioscience AG)
- P44: *A Full-Text Search System Covering the Whole GenomeNet*, Takao Kataoka, Kenji Satou (JAIST)
- P45: *WEB Based GENOME Analysis Tools in ALIS Project*, Kazuo Takehana*, Takehiko Ito[†], Tetsushi Yada[‡], Mika Hirakawa*, Hiroko Yamaguchi*, Junko Shimada*, Katsuji Matsumura*, Masako Kuroda*
(*JST, [†]Mitsubishi Research Inst., [‡]RIKEN)
- P46: *Global Integration of Gene Databases by Eigen-ID Method*, Tetsuro Toyoda and Akiko Itai
(Inst. of Medicinal Molecular Design)
- P47: *Gene Classification Method Based on Batch-Learning SOM*, Takashi Abe*, Shigehiko Kanaya*[§], Makoto Kinouchi*, Yoshihiro Kudo*, Hirotada Mori^{§¶}, Hideo Matsuda^{§||}, Carlos Del Carpio[†], Toshimichi Ikemura[‡] (*Yamagata Univ., [†]Toyohashi Univ. of Tech., [‡]NIG, [§]CREST, JST, [¶]Nara Inst. of Sci. & Tech., ^{||}Osaka Univ.)
- P48: *Synonymous Codon Usage Based on Codon-Anticodon Interaction Energy and Gene Expression Level*, Mamoru Kato, Akira Suyama (Univ. Tokyo)
- P49: *Analysis of Molecular Evolution in Mitochondrial tRNA Gene Sequences*, Jun-Ichi Sagara, Kentaro Shimizu (Univ. Tokyo)
- P50: *Unit-Based de novo Drug Design Using a Library of Protein-Ligand Interaction Sites*, Kiminobu X. Sato, Susumu Goto, Minoru Kanehisa (Kyoto Univ.)
- P51: *Characterization and Classification of Splicing Patterns*, Yumi Tamada, Toshio Shimizu (Hiroshima Univ.)
- P52: *Application to Gene Cluster Analysis of Inductive Inference of Languages over Patterns with Conceptual Hierarchy*, Yukako Tohsato, Hideo Matsuda, Akihiro Hashimoto (Osaka Univ.)
- P53: *Distribution of Species Specific Gene Family in Microorganisms*, Takeshi Ara*, Kenji Suzuki[†], Hideo Matuda*[‡], Hirotada Mori*[§] (*CREST, JST, [†]Kyoto Univ., [‡]Osaka Univ., [§]Nara Inst. of Sci. & Tech.)
- P54: *Differences of Translation Termination Sites among the Three Stop Codons*, Yosuke Ozawa, Satoshi Hanaoka, Rintaro Saito, Masaru Tomita (Keio Univ.)

- P55: *Fop Values, Start Codons, SD Sequence Conservation, and Their Correlation to Gene Expression Level*, Hiroaki Sakai, Chiaki Imamura, Hiroshi Ohno, Takanori Washio, Masaru Tomita (Keio Univ.)
- P56: *Computational Analysis of χ Sequences*, Reina Uno, Yoichi Nakayama, Kenji Yotsutani, Takehito Mogami, Kazuharu Arakawa, Masaru Tomita (Keio Univ.)
- P57: *Zipf-Scaling Description in the DNA Sequences*, Yasuo Yonezawa, Hiroyuki Motohasi (Ibaraki Univ.)
- P58: *Toward Full 3D Structural Investigation of Intron Splicing in Human Cytochrome P450 2D6 pre-mRNA*, Wayne Dawson^{*†}, Kenji Yamamoto^{*} (^{*}Univ. Tokyo, [†]Kitasato Univ.)
- P59: *Systematic Analyses on Mouse Encyclopedia*, Toshinori Endo^{*}, Yoshifumi Fukunishi^{*†}, Hideaki Konno^{*†}, Harukazu Suzuki^{*}, Yasuhiro Ozawa^{*}, Masayasu Yoshino^{*}, Kazuhiro Shibata^{*}, Masayoshi Itoh^{*}, Piero Carninci^{*}, Yasushi Okazaki^{*}, Yoshihide Hayashizaki^{*} (^{*}RIKEN, [†]CREST, JST)
- P60: *Sequence Analysis for Discrimination of Signal Peptides and Signal Anchor Sequences*, Masahiro Gomi, Shigeki Mitaku (Tokyo Univ. of Agric. & Tech.)
- P61: *Pairwise Alignment on the Loop Structured Computer*, Zhongmin Li, Yoshio Yoshioka, Toshio Shimizu (Hirosaki Univ.)
- P62: *A High-throughput Gene Discovery System for Arabidopsis Genome Sequencing Project*, Yasukazu Nakamura, Satoshi Tabata (Kazusa DNA Research Inst.)
- P63: *Insertion with Long Target Duplication: A Novel Mechanism for Bacterial Gene Mobility Suggested from Genome Comparison*, Ayaka Nobusato^{*}, Ikuo Uchiyama[†], Seishi Ohashi^{*}, Ichizo Kobayashi^{*} (^{*}Univ. Tokyo, [†]Okazaki Natl. Research Inst.)
- P64: *Evolutionary Emergence of Early-Peptide-Synthesizing RNA Machines by Means of Hierarchical Sociogenesis of tRNA-riboorganisms*, Koji Ohnishi, Shoken Hokari (Niigata Univ.)
- P65: *Distances between Completely Matched Tuples in the Modern Gene Sequences*, Nobuyuki Uchikoga, Akira Suyama (Univ. Tokyo)
- P66: *Synthesis and Analysis of a Biological System*, Hiroyuki Kurata^{*}, Kazunari Taira^{*}, Hiroaki Kitano[†] (^{*}Univ. Tokyo, [†]ERATO, JST)

- P67: *BioDRIVE: Simulator for Biochemical and Genetic Networks*, Koji M. Kyoda^{*†}, Michiko Muraki^{*‡}, Shugo Hamahashi^{*†}, Mineo Morohashi^{*‡}, Shuichi Onami^{*}, Hiroaki Kitano^{*§} (*ERATO, JST, [†]Keio Univ., [‡]Tokyo Med. & Dent. Univ., [§]Sony CSL)
- P68: *Generic Gene Expression System for Modeling Complex Gene Regulation Network Using E-CELL System*, Kenta Hashimoto, Fumihiko Miyoshi, Sae Seno, Masaru Tomita (Keio Univ.)
- P69: *Parameter Estimation Mechanism of E-CELL Simulation Environment*, Yusuke Saito, Kouichi Takahashi, Tomoharu Iwata, Tomohiko Aikawa, Masaru Tomita (Keio Univ.)
- P70: *Pathological Analyses of Enzyme Deficiency in Human Erythrocyte Using E-CELL System*, Ryo Matsushima, Yoichi Nakayama, Natsumi Noguchi, Hironori Tanaka, Ayako Kinoshita, Masaru Tomita (Keio Univ.)
- P71: *Towards Kinetic Modeling of DNA Replication Using the E-CELL System*, Fumihiko Miyoshi, Kenta Hashimoto, Yuki Fujita, Reina Matsuo, Youhei Yamada, Masaru Tomita (Keio Univ.)
- P72: *Computer Simulation of Human Erythrocyte Using the E-CELL System*, Yoichi Nakayama, Ryo Matsushima, Masaru Tomita (Keio Univ.)
- P73: *Mathematical Analysis of Metabolic Networks Using the E-CELL Simulation Environment*, Masayuki Okayama, Motohiro Yoneda, Yusuke Saito, Kouichi Takahashi, Masaru Tomita (Keio Univ.)
- P74: *Kinetic Modelling of Energy Metabolism in Mitochondria*, Katsuyuki Yugi, Yuko Kanai, Masaru Tomita (Keio Univ.)

Commercial Exhibitions

- C1: CTC LABORATORY SYSTEMS CORP.
- C2: Ryoka Systems Inc.
- C3: Mitsubishi Space Software Ltd.
- C4: Mitsui Knowledge Industry Co., Ltd.
- C5: Nihon SiliconGraphics K.K.
- C6: Hitachi, Ltd.
- C7: Teijin Systems Technology Ltd.
- C8: PE Biosystems Japan Ltd.

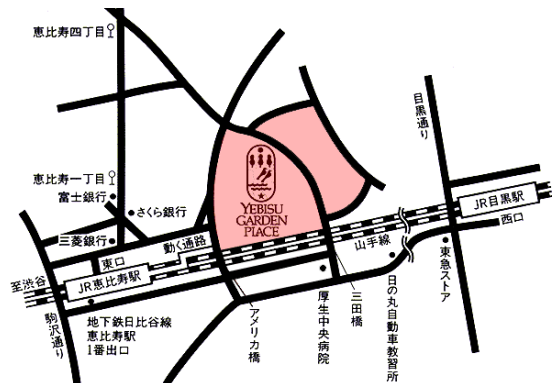
Location

The workshop will take place at the *Garden Hall* which is located in the Yebisu Garden Place. Please get off at JR Ebisu Station or Ebisu Station on the Eidan Subway Hibiya Line. It takes about 5 minutes walk from the east exit JR EBISU station to Yebisu Garden Place if you use the “Yebisu Skywalk” covered moving walkway. The address/TEL/FAX of Yebisu Garden Place are as follows:

1-13-2 Mita, Meguro-ku, Tokyo 153-0062, Japan

TEL: +81-3-5424-0111 FAX: +81-3-5424-1444

URL: <http://www.sgi.co.jp/YGP/> (Japanese)



Getting There

Tokyo is the capital city of Japan. There are direct flights to Narita International Airport from many countries. You can take trains from the airport.

After arriving in Narita International Airport, take a train (either JR line or Keisei line) from the airport station:

1. JR line:

Using Express (Narita Express) train, it takes about 1 hour from the airport station to JR Tokyo station. From JR Tokyo station to JR Ebisu station, take JR Yamanote line to the direction of Shinagawa and Shibuya. It takes about 30 minutes.

2. Keisei line:

Using Express (Skyliner) train, it takes about 1 hour from the airport station to Keisei Ueno station. It takes about 5 minutes walk from Keisei Ueno station to JR Ueno station. From JR Ueno station to JR Ebisu station, take JR Yamanote line to the direction of Tokyo and Shinagawa. It takes about 40 minutes.

Go along the Sky Walk from the east exit of JR Ebisu station. After 5 minutes walk, you will find the entrance to the Yebisu Garden Place.

Passport and Visa Requirements

All overseas visitors wishing to enter Japan require a valid Passport. Visa will also be required for participants coming from the countries without visa exemption agreements with Japan.

Entry into Japan for 90 days is very easy to obtain a Visa. Participants requiring visas should apply well in advance to Japanese consular offices or diplomatic missions in their countries prior to making final travel arrangements with a travel agent.

For more information about visa, please see

http://www.mofa.go.jp/j_info/visit/visa/index.html
(The Ministry of Foreign affairs, Japan)

If you require a letter advising your registration for the conference, please E-mail : giw@ims.u-tokyo.ac.jp.

