

GIW '98

The Ninth Workshop on Genome Informatics

Yebisu Garden Hall
Yebisu Garden Place, Tokyo, Japan

December 10-11, 1998

The Ninth Workshop on Genome Informatics (GIW '98) 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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Newest Information

<http://www.hgc.ims.u-tokyo.ac.jp/giw98>

Program Committee

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Advanced Registration

The registration fee is **free** except the banquet (6,000 Yen; 3,000 Yen for student) and the workshop book (3,000 Yen).

Registration to GIW '98 can be done at the above URL site, or please send your name, affiliation, email address, phone number, fax number, banquet attendance, to the secretary.

GIW '98 Advanced Program

Registration

From 9:00 at Yebisu Garden Hall on December 10 and 11. (Registration Desk is open from through the workshop.)

December 10, Thursday

Opening Address

9:50 - 10:00 Toshihisa Takagi (Univ. Tokyo)

Session 1

Chair: Kenta Nakai (Osaka Univ.)

10:00 - 10:20 *Genomic Analysis of the Genes Encoding Ribosomal Proteins in Eight Eubacterial Species and Saccharomyces cerevisiae*, Katsutoshi Fujita*, Tomoya Baba[†], Katsumi Isono* (*Kobe Univ., [†]STAFF)

10:20 - 10:40 *Construction of the gyrB Database for the Identification and Classification of Bacteria*, Hiroaki Kasai*, Kanako Watanabe*, Elizabeth Gasteiger[†], Amos Bairoch[†], Katsumi Isono[‡], Satoshi Yamamoto[§], Shigeaki Harayama* (*Marine Biotech. Inst., [†]Univ. Geneva, Switz., [‡]Kobe Univ., [§]Nichirei Corp.)

10:40 - 11:00 *Phylogenetic Invariants for Metazoan Mitochondrial Genome Evolution*, David Sankoff* and Mathieu Blanchette[†] (*Univ. Montreal, Canada, [†]Univ. Washington, USA)

11:00 - 11:20 *Systematic Prediction of Orthologous Units of Genes in the Complete Genomes*, Hidemasa Bono, Susumu Goto, Wataru Fujibuchi, Hiroyuki Ogata, Minoru Kanehisa (Kyoto Univ.)

11:20 - 11:40 *Comprehensive Sequence Analyses of 5' Flanking Regions of Primate Alu elements*, Yoshimi Toda, Rintaro Saito, Masaru Tomita (Keio Univ.)

11:40 - 12:00 *Evidence of Limited Structural Organization in Globin Intron Sequences of Messenger RNA*, Wayne Dawson and Kenji Yamamoto (Univ. Tokyo)

- Lunch Break 12:00 - 13:30
- Invited Talk** Chair: Hiroshi Imai (Univ. Tokyo)
 13:30 - 14:30 *Information Geometry and Neural Networks*, Shun-ichi Amari (RIKEN Brain Science Institute)
- Coffee Break 14:30 - 14:40
- Session 2** Chair: Christos Ouzounis (EMBL-EBI, UK)
- 14:40 - 15:00 *Identifying the Interaction between Genes and Gene Products Based on Frequently Seen Verbs in Medline Abstracts*, Takeshi Sekimizu, Hyun S. Park, Jun'ichi Tsujii (Univ. Tokyo)
- 15:00 - 15:20 *Detecting Gene Symbols and Names in Biological Texts : A First Step toward Pertinent Information Extraction*, Denys Proux*, François Rechenmann†, Laurent Julliard*, Violaine Pillet‡, Bernard Jacq§ (*Xerox Research Centre Europe, France, †INRIA Rhône-Alpes, France, ‡CRRM, France, §LGPD, France)
- 15:20 - 15:40 *Developing NLP Tools for Genome Informatics: An Information Extraction Perspective*, Teruyoshi Hishiki, Nigel Collier, Chikashi Nobata, Tomoko Okazaki-Ohta, Norihiro Ogata, Takeshi Sekimizu, Roland Steiner, Hyun S. Park, Jun'ichi Tsujii (Univ. Tokyo)
- 15:40 - 16:00 *A Machine Learning Approach to Reducing the Work of Experts in Article Selection from Database: A Case Study for Regulatory Relations of S. cerevisiae Genes in MEDLINE*, Shin-ichi Usuzaka*, Kim Lan Sim†, Miyako Tanaka‡, Hiroshi Matsuno*, Satoru Miyano† (*Yamaguchi Univ., †Univ. Tokyo, ‡Ube Natl. Coll. of Tech.)

Posters & Software Demonstrations

Chair: Shigeki Mitaku (Tokyo Univ. of
Agriculture and Tech.)
16:00 - 18:30

Banquet 18:30 - 21:00
Foyer, Garden Hall

December 11, Friday

Session 3

Chair: Hideo Matsuda (Osaka Univ.)

9:30 - 9:50 *Using Kleisli to Bring Out Features in BLASTP Results*, Jing Chen, Daphna Strauss, Limsoon Wong (Kent Ridge Digital Lab., Singapore)

9:50 - 10:10 *MUSCA: An Algorithm for Constrained Alignment of Multiple Data Sequences*, Laxmi Parida, Aris Floratos, Isidore Rigoutsos (IBM T.J.Watson Research Center, USA)

10:10 - 10:30 *Improvement of the A* Algorithm for Multiple Sequence Alignment*, Hirotada Kobayashi and Hiroshi Imai (Univ. Tokyo)

10:30 - 10:50 *Parallel Protein Information Analysis (PAPIA) System Running on a 64-Node PC Cluster*, Yutaka Akiyama, Kentaro Onizuka, Tamotsu Noguchi, Makoto Ando (RWCP)

Coffee Break 10:50 - 11:00

Invited Talk

Chair: Naotake Ogasawara (AIST-Nara)

11:00 - 12:00 *Comparative Genomics: Is It Changing the Paradigm of Evolutionary Biology?*, Eugene V. Koonin (NIH, USA)

Lunch Break 12:00 - 13:00

Posters & Software Demonstrations

13:30 - 15:00

Session 4	Chair: Takashi Ito (Univ. Tokyo)
15:00 - 15:20	<i>Finding Genetic Network from Experiments by Weighted Network Model</i> , Kiyoshi Noda*, Ayumi Shinohara*, Masayuki Takeda*, Satoshi Matsumoto [†] , Satoru Miyano [‡] , Satoru Kuhara* (*Kyushu Univ. [†] Tokai Univ. [‡] Univ. Tokyo)
15:20 - 15:40	<i>A System for Identifying Genetic Networks from Gene Expression Patterns Produced by Gene Disruptions and Overexpressions</i> , Tatsuya Akutsu*, Satoru Kuhara [†] , Osamu Maruyama*, Satoru Miyano* (*Univ. Tokyo [†] Kyushu Univ.)
15:40 - 16:00	<i>Fully-Automated Spot Recognition and Matching Algorithms for 2-D Gel Electrophoretogram of Genomic DNA</i> , Katsutoshi Takahashi*, Masayuki Nakazawa [†] , Yasuo Watanabe [‡] , Akihiko Konagaya* (*JAIST, [†] IPC, [‡] Kanazawa Inst. of Tech.)
Coffee Break	16:00 - 16:20

Session 5	Chair: Satoru Kuhara (Kyushu Univ.)
16:20 - 16:40	<i>Hunting TPR Domains Using Kleisli</i> , Kui Lin*, Anthony E. Ting†, Jiren Wang‡, Limsoon Wong‡, (*National Univ. of Singapore, †Inst. of Molecular & Cell Biol., Singapore, ‡Kent Ridge Digital Labs., Singapore)
16:40 - 17:00	<i>Low Identity, Low Similarity Protein Sequences: Independent Modeling of the Ordered-Series-of-Motifs and Motif-Intervening-Regions</i> , Marcella A. McClure, Julianna Hudak, John Kowalski (UNLV, USA)
17:00 - 17:20	<i>The Sequence Attribute Method for Determining Relationships Between Sequence and Protein Disorder</i> , Qian Xie*, Gregory E. Arnold†, Pedro Romero*, Zoran Obradovic*, Ethan Garner*, A. Keith Dunker* (*Washington State Univ., USA, †Biol. Info. Tech., USA)
17:20 - 17:40	<i>Predicting Disordered Regions from Amino Acid Sequence: Common Themes Despite Differing Structural Characterization</i> , Ethan Garner, Paul Cannon, Pedro Romero, Zoran Obradovic, A. Keith Dunker (Washington State Univ., USA)
Closing	17:40 - 17:50
Remarks	Kiyoshi Asai (ETL)

Software Demonstrations

- S1: *Mobile Agent System for Animal Genome Database*, Yasuhiko Wada*, Hirohisa Kishino[†], Nobuhisa Kashiwagi[‡], Hiroshi Yasue*, (*NIAI, [†]Inst. of Statistical Math., [‡]Univ. Tokyo)
- S2: *A Sample Tracking Tool for Rice Genome Sequencing*, Katsumi Sakata*, Kazunori Waki*, Takuji Sasaki*, Michihiko Shimomura[†], Masaki Kise[†] (*NIAR/STAFF, [†]Mitsubishi Space Software Co., Ltd.)
- S3: *NEXTDB: The Expression Pattern Map Database for C. elegans*, Tadasu Shin-i, Yuji Kohara (NIG)
- S4: *Constructing and Annotating GENES Database in KEGG*, Susumu Goto*, Kotaro Shiraishi[†], Kayo Okamoto*, Hiroko Ishida*, Sanae Asanuma*, Hidemasa Bono*, Hiroyuki Ogata*, Wataru Fujibuchi*, Minoru Kanehisa* (*Kyoto Univ., [†]Fujitsu Kyushu System Eng.)
- S5: *ORI-GENE: A Tool for Gene Classification Based on Evolutional Tree*, Hideaki Mizuno*, Yoshimasa Tanaka*, Yoshihiro Ugawa[†], Akinori Sarai[‡] (*Univ. of Tsukuba, [†]NIAR, [‡]RIKEN)
- S6: *Genome-Scale Gene Expression Profiles Mapped onto the Pathway and Genome Maps in KEGG*, Mitsuteru Nakao*, Kazushige Sato[†], Tomomi Kamiya*, Yoshiko Kimura*, Minoru Kanehisa* (*Kyoto Univ., [†]Nihon SiliconGraphics K.K.)
- S7: *Virtual Drosophila Project: Simulation of Drosophila Leg Formation*, Koji Kyoda*, Hiroaki Kitano[†] (*Keio Univ., [†]Sony Computer Sci. Lab., Inc.)
- S8: *KMeyeDB: Keio Mutation Database for Eye Disease Genes Constructed on a Graphical Distributed Database System Mutation View*, Shinsei Minoshima, Susumu Mitsuyama, Saho Ohno, Takashi Kawamura, Nobuyoshi Shimizu (Keio Univ.)
- S9: *GeneWeb II: Sequence Analysis Tools on Web Server Using Java API*, Ken Kurokawa*, Kenichi Kawashima[†], Toshiyuki Okumura[†], Tatsuya Takagi*, Teruo Yasunaga* (*Osaka Univ., [†]Senri Life Sci. Center)
- S10: *Parallelized Knowledge Discovery System: An Enhancement to BONSAI*, Hideo Bannai*, Toshio Masuda[†], Masao Nagasaki*, Tomohiro Yasuda*, Osamu Maruyama*, Satoru Miyano* (*Univ. Tokyo, [†]Graduate School of Electro-Comm.)

Posters

- P01: *Annotation of PDB with respect to “Disordered Regions” in Proteins*, Meeta Rani*, Pedro Romero[†], Zoran Obradovic[†], A. Keith Dunker[†] (*Natl. Univ. Singapore, [†]Washington State Univ., USA)
- P02: *E-CELL Project Overview: Towards Integrative Simulation of Cellular Processes*, Masaru Tomita, Kenta Hashimoto, Kouichi Takahashi, Yuri Matsuzaki, Ryo Matsushima, Kanako Saito, Katsuyuki Yugi, Fumihiko Miyoshi, Hisako Nakano, Sakura Tanida, Thomas S. Shimizu (Keio Univ.)
- P03: *Modeling of Transcription and DNA Replication Using the E-CELL Simulation System*, Kenta Hashimoto, Fumihiko Miyoshi, Thomas S. Shimizu, Takeshi Satoyoshi, Masaru Tomita (Keio Univ.)
- P04: *Modeling of Signal Transduction for Bacterial Chemotaxis Using the E-CELL Simulation System*, Yuri Matsuzaki, Kanako Saito, Tom Shimizu, Masaru Tomita (Keio Univ.)
- P05: *Modeling of Human Red Blood Cell Using the E-CELL Simulation System*, Riou Matsushima, Akiko Kawase, Naoko Watanabe, Hisako Nakano, Kanako Saito, Masaru Tomita (Keio Univ.)
- P06: *Modeling Theory and Software Architecture of the E-CELL Simulation System*, Kouichi Takahashi, Tom Shimizu, Katsuyuki Yugi, Masaru Tomita (Keio Univ.)
- P07: *Multivariate Time Series Analysis of Metabolic Network Using the E-CELL Simulation System*, Yusuke Saito, Kouichi Takahashi, Masaru Tomita (Keio Univ.)
- P08: *Evolution of Overlapping Genes: Comparative Genomics of Mycoplasma genitalium and Mycoplasma pneumoniae*, Yoko Fukuda, Takanori Washio, Masaru Tomita (Keio Univ.)
- P09: *On Periodicity of Adenine-Adenine Dinucleotides in Bacterial Genomes*, Masahiko Wada, Yukihiro Kawashima, Masaru Tomita (Keio Univ.)
- P10: *Computer Analysis of Base Pairing Free-Energy between Shine-Dalgarno Sequence and 16S rRNA in Various Prokaryotes*, Yuko Osada, Rintaro Saito, Masaru Tomita (Keio Univ.)
- P11: *On Low Frequency of CpG Dinucleotides in Bacterial Genomes*, Mami Goto, Takanori Washio, Masaru Tomita (Keio University)
- P12: *Analysis of Translation Initiation Sites in the Complete Genome of Mycoplasma genitalium Suggests That This Bacterium Uses Alternative Signal for Translation Initiation*, Rintaro Saito, Masaru Tomita (Keio Univ.)
- P13: *Expression Frequency of the Human Immunoglobulin λ Light Chain Genes and the Roles of Their Recombination Signal and Spacer Sequences*, Taku Okada, Masaru Tomita, Kazuhiko Kawasaki, Shinsei Minoshima, Nobuyoshi Shimizu (Keio Univ.)
- P14: *Assessment of Utility of ESTs for Nucleotide Diversity Using Available Assembled Alignments from dbEST, STACK 2.0 and STACK-INDEX*, Brian Karlak, Winston Hide (Univ. of the Western Cape, South Africa)

- P15: *A Genome-Level Search for Bacterial Genes on Which Positive Selection May Operate: A Means for Identifying Possible Virulence Factors?*, Junaid Gamiel-dien, Winston Hide (Univ. of the Western Cape, South Africa)
- P16: *A Statistical Model for Prokaryotic Promoter Prediction*, Joseph Oppon, Winston Hide (Univ. of the Western Cape, South Africa)
- P17: *Algorithms for Inference of Genetic Networks (AIGNET)*, Shoji Watanabe*, Yukihiko Maki*, Yukihiko Eguchi*, Daisuke Tominaga†, Masahiro Okamoto† (*Mitsui Knowledge Ind. Co., Ltd., †Kyushu Inst. of Tech.)
- P18: *An Educational Tool for Visualize DNA Structures in vivo*, Shigehiro Fukase*, Masato Wayama† (*Hitachi Software Eng. Co., Ltd., †Biz. Service Corp.)
- P19: *Extended Sequence Alignment Method for Protein Secondary Structure Prediction*, Susumu Hiraoka (Hitachi, Ltd.)
- P20: *Detection of Frame-Shift Error in the Yeast Genome Sequences*, Naoko Kasahara, Naoyuki Harada, Keiichi Nagai (Hitachi, Ltd.)
- P21: *Clustering and Detection of 5'Splice Sites of mRNA by k Weight Matrix Model*, Katsuhiko Murakami*, Toshihisa Takagi† (*Hitachi, Ltd., †Univ. Tokyo)
- P22: *Automated Metabolic Reconstruction at the Molecular Level*, Masanori Arita (Univ. Tokyo)
- P23: *Correlation between Exon and Dispersed Repetitive DNA Distributions on the Human Genome*, Yoshiaki Hojo, Ikuo Uchiyama, Yataro Daigo, Yusuke Nakamura, Toshihisa Takagi (Univ. Tokyo)
- P24: *Automatic Construction of Biological Abbreviation Dictionary from Abstracts of Biomedical Papers*, Mikio Yoshida, Kenichiro Fukuda, Toshihisa Takagi (Univ. Tokyo)
- P25: *A Workbench for Systematic Construction of Signal Transduction Pathways: Ontologies and Architectures*, Kenichiro Fukuda, Mikio Yoshida, Toshihisa Takagi (Univ. Tokyo)
- P26: *Development of Information Extraction Tool: Toward Construction of Protein-Protein Interaction Database*, Tomoko Okazaki-Oota, Toshihisa Takagi (Univ. Tokyo)
- P27: *Palindrome Analysis: Distribution of Complete-Matched Inverted Repeats with a Moderate Length Spacer*, Masao Fukagawa, Tatsuhiko Tsunoda, Toshihisa Takagi (Univ. Tokyo)
- P28: *Construction of Ortholog/Paralog Group Table for PTS*, Takeaki Taniguchi, Minoru Kanehisa (Kyoto Univ.)
- P29: *A Library of Protein-Ligand Interaction Sites for de novo Ligand Design*, Kiminobu Sato, Minoru Kanehisa (Kyoto Univ.)
- P30: *Automatic Detection of Gene Clusters by P-Quasi Complete Linkage Grouping*, Wataru Fujibuchi*, Hiroyuki Ogata*, Hideo Matsuda†, Minoru Kanehisa* (*Kyoto Univ., †Osaka Univ.)
- P31: *The Construction of the Knowledge Base of Immune System*, Yoshinobu Igarashi, Minoru Kanehisa (Kyoto Univ.)

- P32: *Detection of Co-regulated Genes by Comparative Analysis of Microbial Genomes*, Hiroyuki Ogata, Wataru Fujibuchi, Minoru Kanehisa (Kyoto Univ.)
- P33: *Extracting Regulatory Signals from the Upstream Region of Co-expressed Genes Derived from DNA Microarray Experiments*, Shuichi Kawashima, Hiroyuki Ogata, Minoru Kanehisa (Kyoto Univ.)
- P34: *Protein Folding Simulation and Self-Consistent Potential Functions*, Fumi Takazawa, Masaki Sasaki, Minoru Kanehisa (Kyoto Univ.)
- P35: *Systematic Classification of B. subtilis Genes and Construction of a Knowledge Base to Represent Functional Information*, Atsushi Ogiwara (Natl. Inst. for Basic Biol.)
- P36: *Search Pathways for Secondary Metabolites Based on Genome Analysis and Chemical Knowledge on Metabolism*, Takaaki Nishioka*, Kimito Funatsu[†] (*Kyoto Univ., [†]Toyohashi Univ. of Tech.)
- P37: *A Method for Querying Complete Genomes by Viewing Them as Structured Documents*, Aaron J. Stokes, Hideo Matsuda, Akihiro Hashimoto (Osaka Univ.)
- P38: *Maintenance of Transcription Factor DataBase TFDB by TFDB Maintenance System*, Masako Kaizawa*, Satoru Watanabe*, Takahiro Nobukuni*, Masami Horikoshi[†], Hiroshi Handa[‡], Yoshiyuki Kuchino*, Takao Sekiya*, Hiroshi Mizushima* (*NCCRI, [†]Exploratory Research for Advanced Tech., [‡]Grad. School of Biosci. & Biotech.)
- P39: *ALIS: Data Management Systems for Human Genome Sequencing*, Mika Hirakawa, Kensaku Imai, Hiroko Yamaguchi, Junko Shimada, Kazuo Takehana, Katsuji Matsumura, Takehiko Itoh, Masako Kuroda (JST)
- P40: *Automatic cDNA classification System for Mouse Genome Project*, Yoshifumi Fukunishi, Hideaki Konno, Yoshihide Hayashizaki (RIKEN)
- P41: *Automated cDNA Information System for Large Scale cDNA Project*, Hideaki Konno, Yuichi Sugahara, Yoshifumi Fukunishi, Kazuhiro Shibata, Yoshihide Hayashizaki (RIKEN)
- P42: *Application of the RLGS Image Analysis Tool (RAT) to the Construction of a Genetic Linkage Map of Recombinant Inbred Strain SMXA*, Yuichi Sugahara, Yoshihide Hayashizaki (RIKEN, JST)
- P43: *3DinSight: An Integrated Database and Search Tool for Structure, Function and Property of Biomolecules*, Jianghong An*, Takao Nakama[†], Yasushi Kubota[†], Akinori Sarai* (*RIKEN, [†]Advanced Tech. Inst. Inc.)
- P44: *ProTherm: Thermodynamic Database for Proteins and Mutants*, M. Michael Gromiha, Jianghong An, Hidetoshi Kono, Motohisa Oobatake, Hatsuho Uedaira, Akinori Sarai (RIKEN)
- P45: *Prediction of DNA target Sites by Regulatory Proteins Based on Structure-Derived Potential*, Hidetoshi Kono, Akinori Sarai (RIKEN)
- P46: *Genomic Hypothesis Creator: A Multi-Strategic View Creator for Sequences*, Osamu Maruyama*, Tomoyuki Uchida[†], Takayoshi Shoudai[‡], Satoru Miyano* (*Univ. Tokyo, [†]Hiroshima City Univ., [‡]Kyushu Univ.)

- P47: *Development of Web Interface of Image Analysis System DDGEL for 2D Gel Electrophoresis*, Kyotetsu Kanaya*, Akira Ohyama*, Tatsuya Akutsu[†], Asao Fujiyama[‡] (*Mitsui Knowledge Industry Co., Ltd., [†]Tokyo Univ., [‡]NIG)
- P48: *Subcubic Time Algorithms for RNA Secondary Structure Prediction*, Tatsuya Akutsu (Univ. Tokyo)
- P49: *ThreeTree: A New Method to Reconstruct Phylogenetic Trees*, Satoshi Oota (NIG)
- P50: *Efficiency of Model-Based Complexity Method for Estimating Unrooted Multifurcate Phylogenetic Tree*, Fengrong Ren, Hiroshi Tanaka (Tokyo Medical and Dent. Univ.)
- P51: *Secondary Structure Prediction Based on Statistical Mechanics*, Yukio Kobayashi*, Nobuhiko Saitô[†] (*Soka Univ., [†]Waseda Univ.)
- P52: *Integrating Multiple Evidences by Hidden Markov Models*, Kiyoshi Asai*, Katunobu Itou*, Tetsushi Yada[†] (*ETL, [†]Mitsubishi Research Inst.)
- P53: *Modeling Transcriptional Units of E. coli Genes Using HMM*, Tetsushi Yada*, Mitsuteru Nakao[†], Yasushi Totoki[‡], Takahiro Ishii[§], Kenta Nakai[§] (*Mitsubishi Research Inst., [†]Kyoto Univ., [‡]Info. & Math. Sci. Lab., Inc., [§]Osaka Univ.)
- P54: *A Database of B. subtilis Promoters and Transcription Factors*, Takahiro Ishii, Kenta Nakai (Osaka Univ.)
- P55: *A Study Using Sequence Comparison to Investigate the Molecular Evolution of Mitochondrial tRNA Genes*, Jun-Ichi Sagara, Shugo Nakamura, Mitsunori Ikeguchi, Kentaro Shimizu (Univ. Tokyo)
- P56: *Prediction of Initiation Codons in cDNA Fragments Using Statistical Information and Similarity with Protein Sequences*, Tetsuo Nishikawa, Toshio Ota, Takao Isogai (Helix Research Inst.)
- P57: *Genome Analysis: Assigning Protein Coding Regions to 3D Structures*, Asaf A. Salamov*, Makiko Suwa*, Christine A. Orengo[†], Mark B. Swindells* (*Helix Research Inst., [†]Univ. Coll. London, UK)
- P58: *A Novel Application of GeneMark-RC to the Analysis of Prokaryotic Genomes and Human cDNAs: Sequence Data with Statistical Deviations Are Rich in Important Biological Information*, Makoto Hirose*, Osamu Ohara*, Katsumi Isono[†] (*Kazusa DNA Research Inst., [†]Kobe Univ.)
- P59: *Annotation and Presentation Systems for Arabidopsis Genome Sequencing Project at Kazusa DNA Research Institute*, Yasukazu Nakamura, Shusei Sato, Satoshi Tabata (Kazusa DNA Research Inst.)
- P60: *Charge Distribution of Signal Peptides and Signal Anchor Type II*, Masahiro Gomi, Takatsugu Hirokawa, Shigeki Mitaku (Tokyo Univ. of Agriculture & Tech.)
- P61: *Topology Prediction of Membrane Proteins Based on a Modified "Positive-Inside" Rule*, Koji Kadota, Hiroyuki Sasamoto, Takatsugu Hirokawa, Shigeki Mitaku (Tokyo Univ. of Agriculture & Tech.)
- P62: *Classification of Membrane Proteins by Types of Transmembrane Helices Using SOSUI System*, Shigeki Mitaku, Takatsugu Hirokawa, Mitsuo Ono (Tokyo Univ. of Agriculture & Tech.)

- P63: *Gene Classification by Self-Organization Mapping of Codon Usage in Bacteria with Completely Sequenced Genome*, Shigehiko Kanaya*, Yoshihiro Kudo*, Takashi Abe*, Takanori Okazaki*, Carlos Del Carpio[†], Toshimichi Ikemura[‡] (*Yamagata Univ., [†]Toyohashi Univ. of Tech., [‡]NIG)
- P64: *GAFLEX: A Hybrid GA Engine for Mapping the Configuration Hyper-Space of Organic Compounds in Solution*, Carlos A. Del Carpio (Toyohashi Univ. of Tech.)
- P65: *DYNAX: A New System for Biomolecular Dynamics Simulation in Solution*, Atsushi Yoshimori, Carlos A. Del Carpio (Toyohashi Univ. of Tech.)
- P66: *Development of an Antibacterial MAP Homologous to a Loop Region in Human Lactoferrin*, Masachika Azuma, Taiki Kojima, Masaki Kobayashi, Carlos Adriel Del Carpio (Toyohashi Univ. of Tech.)
- P67: *MOLDEX: A Computer System for Drug Design. 4) A Combined Electro-Geometric Method for the Identification of Pharmacophoric Structural Patterns in Drugs*, Hiromi Nakatake, Carlos Adriel Del Carpio (Toyohashi Univ. of Tech.)
- P68: *A Simulated Annealing Algorithm for Geometrical Assessment of Macromolecular Hydrophobic Interaction*, Tomoko Hara, Carlos Adriel Del Carpio (Toyohashi Univ. of Tech.)
- P69: *A Genetic Programming Based System for the Prediction of Secondary and Tertiary Structures of RNA*, Katsuhisa Yamaguchi, Carlos Adriel Del Carpio (Toyohashi Univ. of Tech.)
- P70: *Detailed Sequence Analysis of the Distal Down Syndrome Critical Region and the SOD1/AML1 Region on Chromosome 21*, Todd Taylor*, Masahira Hattori*, Kiyoteru Noguchi[†], Tomomi Shobu*, Kazuo Ishii*, Atsushi Toyoda*, Yoshiyuki Sakaki* (*Univ. Tokyo, [†]Hitachi, Ltd.)
- P71: *Genome Wide Survey of the Entire C. elegans alpha-Tubulin Gene Family: cDNA Cloning, Expression, and Structure-Function Analysis*, Camelia B. Gogonea*, M. Y. Ali*, Tetsunari Fukushige[†], M. Afaq Shakir[‡], Takashi Matsuo*, Shahid S. Siddiqui* (*Toyohashi Univ. Tech., [†]Univ. Caigary, Canada, [‡]Mass. Gen. Hosp., USA)
- P72: *Gene Has Its Inherent Significantly Repetitive Tuples*, Nobuyuki Uchikoga, Akira Suyama (Univ. Tokyo)
- P73: *Nucleotide Sequence of a Gene Encodes Characteristic Features of an Organism as Well as an Amino Acid Sequence*, Hiroshi Nakashima*, Motonori Ota[†], Ken Nishikawa[†], Tatsuo Ooi[‡] (*Kanazawa Univ., [†]NIG, [‡]Kyoto Women's Univ.)
- P74: *Application Computer Software in Mapping Quantitative Trait Loci*, Chindo Hicks, Eiji Kobayashi, Masahiro Satoh, Kazuo Ishii, Tsutomu Furukawa (NIAI)
- P75: *Phosphoglycerate-transporter Protein B as a Most Primitive Protein Predicted by the Poly-tRNA Theory*, Koji Ohnishi (Niigata Univ.)
- P76: *Sequence Analysis of the IRES-Loop III Region of Hepatitis C Virus*, Takayoshi Sasano, Jun-Ichi Sagara, Shugo Nakamura, Mitsunori Ikeguchi, Kentaro Shimizu (Univ. Tokyo)

P77: *ORF Clustering Analysis of 17 Complete Genomes*, Kenji Suzuki*, Takeshi Ara*, Hideo Matsuda†, Hirotada Mori* (*AIST-NARA, †Osaka Univ.) [P77 is not included in the book because the final manuscript was not in time for publication but included in CD-ROM.]

Commercial Exhibitions

- C1: Nihon SiliconGraphics K.K.
- C2: Ryoka Systems Inc.
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- C5: CTC LABORATORY SYSTEMS CORP.
- C6: Teijin Systems Technology Ltd.
- C7: Hitachi, Ltd.
- C8: Sumisho Electronics Co.
- C9: Perkin-Elmer Japan Co., Ltd.
- C10: Paracel Inc.

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/visa>
(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.