

# RECOMB 2000 Program

The Fourth Annual International Conference  
on Computational Molecular Biology  
Tokyo, Japan

April 8 - 11, 2000

Sponsored by  
ACM-SIGACT



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US Department of Energy  
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Organized by  
Human Genome Center



Institute of Medical Science, University of Tokyo

## Friday, April 7, 2000

- 16:00 – 19:00 **Welcome and Registration**  
(Tokyo Bay Ariake Washington Hotel, 3F, “IRIS”)  
18:00 – 20:00 **Reception**  
(Tokyo Bay Ariake Washington Hotel, 3F, “IRIS”)

## Saturday, April 8, 2000

(Tokyo Big Sight, The Tower Building, 6F, Room 607 & 608)

- 9:00** **Opening Remarks**  
Ron Shamir, RECOMB 2000 Program Chair  
Satoru Miyano, RECOMB 2000 Organizing Committee Chair  
Thomas Lengauer, RECOMB 2001 Program Chair

### Session Chair: Sorin Istrail

- 9:15-10:15** **The Stanislaw Ulam Computational Biology Address**  
*Minoru Kanehisa*  
**Sequence Comparison to Graph Comparison – A New Generation of Algorithms for Network Analysis of Interacting Molecules**

- 10:15-10:20** Short Break

- 10:20-10:45** S. Batzoglou, L. Pachter, J. P. Mesirov, B. Berger, E. S. Lander:  
Comparative Analysis of Mouse and Human DNA and Applications  
to Exon Prediction

- 10:45-11:10** P. Pevzner, V. Dančák, C. L. Tang: Mutation-Tolerant Protein  
Identification by Mass-Spectrometry

- 11:10-11:40** **Break**

### Session Chair: Steve Skiena

- 11:40-12:05** N. Friedman, M. Linial, I. Nachman, D. Pe’er: Using Bayesian  
Networks to Analyze Expression Data

- 12:05-12:30** A. Ben-Dor, L. Bruhn, N. Friedman, I. Nachman, M. Schummer,  
Z. Yakhini: Tissue Classification with Gene Expression Profiles

- 12:30-12:55** D. K. Slonim, P. Tamayo, J. P. Mesirov, T. R. Golub, E. S. Lander:  
Class Prediction and Discovery Using Gene Expression Data

- 12:55-14:15** **Lunch at Cafe-Restaurant New Tokyo, The Tower Building, 1F**  
(Poster Setup Period: Room 605 & 606)

**Session Chair: Thomas Lengauer**

**14:15-15:15 Keynote Lecture**

*Hans Lehrach*

**A Data-Analysis Pipeline for Large-Scale Gene Expression Analysis**

**15:15-15:20 Short Break**

**15:20-15:45** C. Bailey-Kellogg, A. Widge, J. J. Kelley, M. J. Berardi, J. H. Bushweller, B. R. Donald: The NOESY Jigsaw: Automated Protein Secondary Structure and Main-Chain Assignment from Sparse, Unassigned NMR Data

**15:45-16:10** J. M. Sorenson, T. Head-Gordon: Matching Simulation and Experiment: A New Simplified Model for Simulating Protein Folding

**16:10-16:40 Break**

**Session Chair: David Sankoff**

**16:40-17:40 Keynote Lecture**

*Svante Pääbo*

**DNA Sequence Variation among Humans and Apes**

**17:40-17:45 Short Break**

**17:45-18:10** A. Zien, R. Zimmer, T. Lengauer: A Simple Iterative Approach to Parameter Optimization

**18:20-20:00 Business Meeting**

*(Room 607 & 608)*

**Sunday, April 9, 2000**

**Session Chair: Andrea Califano**

**9:00-10:00 Keynote Lecture**

*Eric Davidson*

**Computational Analyses of Developmental cis-Regulatory Control Systems**

**10:00-10:05** Short Break

**10:05-10:30** T. Akutsu, S. Miyano, S. Kuhara: Algorithms for Identifying Boolean Networks and Related Biological Networks Based on Matrix Multiplication and Fingerprint Function

**10:30-10:55** M. Tomita, K. Hashimoto, K. Takahashi, Y. Matsuzaki, R. Matsushima, K. Yugi, F. Miyoshi, H. Nakano, Y. Saito, S. Shimizu, Y. Nakayama: The E-CELL Project: Towards Integrative Simulation of Cellular Processes

**10:55-11:25** Break

**Session Chair: Jadwiga Bienkowska**

**11:25-11:50** A. Liwo, J. Pillardy, C. Czaplewski, J. Lee, D. R. Ripoll, M. Groth, S. Rodziewicz-Motowidlo, R. Kaźmierkiewicz, R. J. Wawak, S. Oldziej, H. A. Scheraga: UNRES – a United-Residue Force Field for Energy-Based Prediction of Protein Structure – Origin and Significance of Multibody Terms

**11:50-12:15** Y. Z. Ohkubo, G. M. Crippen: Determining Contact Energy Function for Continuous State Models of Globular Protein Conformations

**12:15-15:00** **Poster Session and Lunch (odd numbered posters standby)**  
(Room 605 & 606. Lunch box will be served.)

**Session Chair: Satoru Miyano**

**15:00-16:00 Keynote Lecture**

*Takashi Gojobori*

**Evolutionary Features of Genomes as Disclosed by Comparative Analysis of Complete Genome Sequences**

**16:00-16:05** Short Break

**16:05-16:30** B. Chor, M. D. Hendy, B. R. Holland, D. Penny: Multiple Maxima of Likelihood in Phylogenetic Trees: An Analytic Approach

**16:30-16:55** R. Desper, M. Vingron: Tree Fitting: an Algebraic Approach Using Profile Distances

**16:55-17:25 Break**

**Session Chair: John Kececioglu**

**17:25-17:50** D. Sankoff, D. Bryant, M. Deneault, B. F. Lang, G. Burger: Early Eukaryote Evolution Based on Mitochondrial Gene Order Breakpoints

**17:50-18:15** K. Chen, D. Durand, M. Farach-Colton: Notung: Dating Gene Duplications using Gene Family Trees

**Session Chair: Pavel Pevzner**

**18:30-21:30 Distinguished Biology Lecture and Banquet  
at Tokyo Bay Ariake Washington Hotel, 3F, "IRIS"**

*Walter Gilbert*

**Introns and Modules in Ancient Conserved Genes**

# Monday, April 10, 2000

**Session Chair: Ron Shamir**

**9:00-10:00 Distinguished New Technologies Lecture**

*Leroy Hood*

**Computing Life and Global Technologies**

**10:00-10:05** Short Break

**10:05-10:30** A. Ben-Dor, R. M. Karp, B. Schwikowski, Z. Yakhini: Universal DNA Tag Systems: A Combinatorial Design Scheme

**10:30-10:55** F. P. Preparata, E. Upfal: Sequencing-by-Hybridization at the Information-Theory Bound: An Optimal Algorithm

**10:55-11:25** Break

**Session Chair: Lusheng Wang**

**11:25-11:50** R. B. Lyngsø, C. N. S. Pederson: Pseudoknots in RNA Secondary Structures

**11:50-12:15** Y. Xu, D. Xu, O. H. Crawford, J. R. Einstein, E. Serpersu: Protein Structure Determination using Protein Threading and Sparse NMR Data

**12:15-12:40** E. Althaus, O. Kohlbacher, H. P. Lenhof, P. Müller: A Combinatorial Approach to Protein Docking with Flexible Side-Chains

**12:40-14:00** Lunch at Cafe-Restaurant New Tokyo, The Tower Building, 1F

**Session Chair: Nir Friedman**

**14:00-15:00** Keynote Lecture

*Yusuke Nakamura*

**Human Genome Analysis and Medicine in the 21st Century**

**15:00-15:05** Short Break

**15:05-15:30** R. Bundschuh: An Analytic Approach to Significance Assessment in Local Sequence Alignment with Gaps

**15:30-15:55** T. Akutsu, H. Arimura, S. Shimozone On Approximation Algorithms for Local Multiple Alignment

**15:55-16:25** Break

**Session Chair: Dannie Durand**

**16:25-16:50** M. Kann, R. A. Goldstein: Optimizing for Success: A New Score Function For Distantly Related Protein Sequence Comparison

**16:50-17:15** S. A. Teichmann, C. Chothia, G. M. Church, J. Park: PDB\_ISL: an Intermediate Sequence Library for Protein Structures to Sequences

**17:15-17:40** J. R. Bieńkowska, L. Yu, S. Zarakhovich, R. G. Rogers, T. F. Smith: Comprehensive Statistical Method for Protein Fold Recognition

**17:40-19:40** **Poster Session (even numbered posters standby)**  
(Room 605 & 606)

# Tuesday, April 11, 2000

## Session Chair: Donna Slonim

- 9:00-9:25** S. Batzoglou, B. Berger, J. P. Mesirov, E. S. Lander: Sequencing a Genome by Walking with Clone-end Sequences: A Mathematical Analysis
- 9:25-9:50** M. T. Hallett, J. Lagergren: New Algorithms for the Duplication-Loss Model
- 9:55-10:20** S. Heber, J. Stoye, J. Hoheisel, M. Vingron: Contig Selection in Physical Mapping
- 10:20-10:45** J. Kececioglu, S. Shete, J. Arnold: Reconstructing Distances in Physical Maps of Chromosomes with Nonoverlapping Probes
- 10:45-11:15** **Break**

## Session Chair: Alberto Apostolico

- 11:15-11:40** L. Marsan, M.-F. Sagot: Extracting Structured Motifs Using a Suffix Tree – Algorithms and Application to Promoter Consensus Identification
- 11:40-12:05** X. Chen, S. Kwong, M. Li: A Compression Algorithm for DNA Sequences and Its Applications in Genome Comparison
- 12:05-12:30** R. Hart, A. K. Royyuru, G. Stolovitzky, A. Califano: Systematic and Automated Discovery of Patterns in PROSITE Families
- 12:30-14:00** **Lunch box will be served in Room 607 & 608**

## Session Chair: Tatsuya Akutsu

- 14:00-14:25** E. Portugaly, M. Linial: Probabilities for Having a New Fold on the Basis of a Map of All Protein Sequences
- 14:25-14:50** G. Yona, M. Levitt: A Unified Sequence-Structure Classification of Protein Sequences: Combining Sequence and Structure in a Map of the Protein Space
- 14:50-15:15** A. Apostolico, G. Bejerano: Optimal Amnesic Probabilistic Automata or How to Learn and Classify Proteins in Linear Time and Space
- 15:15** **End of Conference**
- 17:00** **Sightseeing Tour: Boat Ride and Dinner (Optional)**  
(Advanced reservation required)



# Commercial Exhibitions

Room 605 & 6-6

C1 SGI Japan, Ltd.

MineSet

C2 CTC Laboratory Systems Corporation

bioSCOUT/array SCOUT (LION)

Digital Genome (Molecular Ware)

SBd-Base (SBI)

Knowledge Library (Proteome)

Spotfire (Spotfire)

C3 Ryoka Systems, Inc.

Molecular Modeling Software

C4 Mitsui Knowledge Industry Co., Ltd.

GCG Wisconsin Package

Bio XL/P

Genome Gambler

C5 Teijin Systems Technology Ltd.

Gene Lime

C6 Hitachi, Ltd.

Super Technical Server SR8000

# Event Location Map

- **Welcome, Registration and Reception on April 7**  
Tokyo Bay Ariake Washington Hotel, 3F, “IRIS”
- **Distinguished Biology Lecture and Banquet on April 9**  
Tokyo Bay Ariake Washington Hotel, 3F, “IRIS”
- **Registration and Slide Registration on April 8 - 11**  
Tokyo Big Sight, The Tower Building, 6F, Registration Desk
- **Oral Presentation on April 7 - 11**  
Tokyo Big Sight, The Tower Building, 6F, Room 607 & 608
- **Poster Session on April 9 and 10**  
Tokyo Big Sight, The Tower Building, 6F, Room 605 & 606
- **Lunch**
  - April 8 and 10: **Cafe-Restaurant New Tokyo**  
Tokyo Big Sight, The Tower Building, 1F  
(See “**TOKYO BIG SIGHT – Guide to Facilities**”)
  - April 9 and 11: Lunch box will be served in Room 607 & 608.
- **Commercial Exhibitions**  
Tokyo Big Sight, The Tower Building, 6F, Room 605 & 606
- **Internet Service**  
Tokyo Big Sight, The Tower Building, 6F, Room 605 & 606
- **RECOMB 2000 Secretary Office**  
Tokyo Big Sight, The Tower Building, 6F, Room 621

## Optional Tour on April 11, 2000

OP-1: Yakata-bune (Houseboat) dinner cruise

Date: April 11, Tuesday 17:00 - 21:30

Fare: JPY 14,500 per person

Advanced reservation required

Itinerary: Assemble at Tokyo Big Site

Enjoy Yakata-bune cruise on Sumida River. The interior of the Yakata-bune, or Japanese style houseboat, is designed so that one may eat and drink seated on tatami mat while enjoying the outdoor scenery.

## Remarks

- **No Smoking**

# Transportation

- From **Tokyo Bay Ariake Washington Hotel** to **Tokyo/Narita Airport**

- By **Airport Limousine Bus**

[http://www.nairta-airport.or.jp/limousine/index\\_e.html](http://www.nairta-airport.or.jp/limousine/index_e.html)

About 65 minutes

Fee: JPY2,700.- / person (one way)

Departure Time from Tokyo Bay Ariake Washington Hotel (TBAWH)

Time : 07:20, 09:20, 12:15, 14:20, 15:50

- By **Train**

1st Step	From TBAWH to Kokusaitenjijo Station	on foot (5 min.)	
2nd Step	From Kokusaitenjijo Station to Shin-bashi Station	by Yurikamome Line (21 min.)	JPY370.-
3rd Step	From Shin-bashi Station to Tokyo Station	by JR Yamanote Line (4 min.)	JPY130.-
4th Step	From Tokyo Station to Narita Airport	by JR NARITA EXPRESS (N'EX) (53 min.)	JPY2,940.-

- See **“TOKYO BIG SIGHT – Guide to Facilities”** for further information.

<http://www.bigsight.or.jp/english/bigsight/index.html>

- See **NARITA AIRPORT-ACCESS**.

[http://www.narita-airport.or.jp/airport\\_e/index\\_e.html](http://www.narita-airport.or.jp/airport_e/index_e.html)