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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IBM
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Organized by
Human Genome Center

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. Dančík, 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: Pseudonknots 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. Shimozono 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`
      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-ariport.or.jp/airport_e/index_e.html`