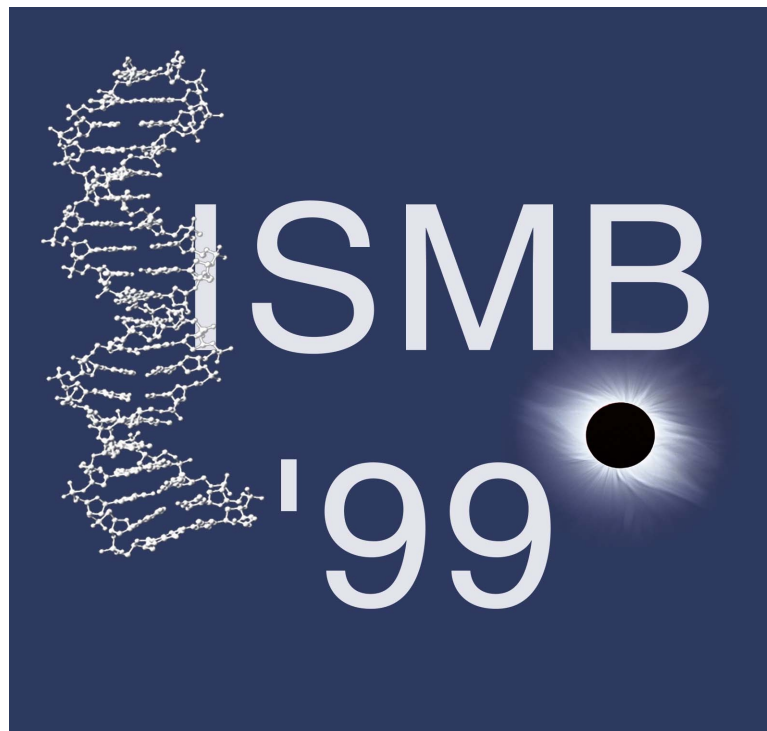


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**Welcome to ISMB 99  
August 6 – 10, 1999  
Heidelberg, Germany**



**The Seventh International Conference on  
Intelligent Systems for Molecular Biology**

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**Final Program and Detailed Schedule**

# Friday, August 6, 1999

## Tutorial Day

The tutorials will take place in the following rooms:

### 8:30 – 12:30 (Coffee break around 10:30)

|                    |                        |                              |   |
|--------------------|------------------------|------------------------------|---|
| <b>Tutorial #1</b> | Trübnersaal            | Piere Baldi                  | Probabilistic graphical models  |
| <b>Tutorial #2</b> | Robert-Schumann-Zimmer | Douglas L. Brutlag           | Bioinformatics and Molecular Biology  |
| <b>Tutorial #3</b> | Ballsaal               | Martin Reese                 | The challenge of annotating a complete eukaryotic genome:<br>A case study in <i>Drosophila melanogaster</i> |
| <b>Tutorial #4</b> | Gustav-Mahler-Zimmer   | Tandy Warnow<br>Junhyong Kim | Computational and statistical challenges involved in reconstructing evolutionary trees                      |
| <b>Tutorial #5</b> | Sebastian-Münster-Saal | Thomas Werner                | The biology and bioinformatics of regulatory regions in genomes   |

**Lunch (on this day served in "Grosser Saal" on the ground floor)**

### 13:30 – 17:30 (Coffee break around 15:30)

|                      |                        |   |   |
|----------------------|------------------------|---|---|
| <b>Tutorial #6</b>   | Sebastian-Münster-Saal | Rob Miller<br>Alan Christoffels<br>Winston Hide     | EST Clustering  |
| <b>Tutorial #7</b>   | Trübnersaal            | Kevin Karplus<br>Melissa Cline<br>Christian Barrett | Getting the most out of hidden Markov models                                    |
| <b>Tutorial #8</b>   | Robert-Schumann-Zimmer | Arthur Lesk   | Sequence-structure relationships and evolutionary structure changes in proteins |
| <b>Tutorial #9</b>   | Gustav-Mahler-Zimmer   | David States<br>Brian Dunford<br>Shore              | PERL abstractions for databases and distributed computing                       |
| <b>Tutorial # 10</b> | Ballsaal               | Zoltan Szallasi                                     | Genetic network analysis - From the lab bench to computers and back             |

Trübnersaal is located on the second floor, please follow signs in the hallway.

**18:00 Welcome reception in the Stadthalle Foyer**

# Saturday, August 7, 1999

9:00 Chair: Thomas Lengauer

## Conference Opening

### Opening address

Uwe Thomas  
State Secretary  
German Federal Ministry of Education and Research

9:50

### Keynote

#### The Origin of Biological Information

Manfred Eigen  
Max-Planck-Institut für Biophysikalische Chemie, Göttingen, Germany

10:40

## Coffee Break

### Session: Protein Structures I

Chair: Rick Lathrop

11:00

### Keynote

#### Exploiting Protein Structure in the Post-genome Era

Michael J. E. Sternberg  
Imperial Cancer Research Fund, London, UK

11:50

TEXTAL: A Pattern Recognition System for Interpreting Electron Density Maps  
*Thomas R. Ioerger, Thomas Holton, Jon A. Christopher, James C. Sacchettini*  
Texas A&M University, TX, USA

12:15

### Crystallographic Threading

*A. Ableson, J.I. Glasgow*  
Queen's University, Kingston, Canada

12:40

## Lunch

14:00 Chair: Peer Bork

**Keynote**

**Comparative Genomics: Is it Changing the Paradigm of Evolutionary Biology?**

Eugene V. Koonin

National Center for Biotechnology Information, NIH, Bethesda, MD, USA

**Session: Protein Structures II**

Chair: Janice Glasgow

- 14:50 Multiple Structural Alignment and Core Detection by Geometric Hashing  
*Nathaniel Leibowitz, Zipora Y. Fligelman, Ruth Nussinov, Haim J. Wolfson*  
Tel Aviv University, Israel & Lab. of Experimental and Computational Biology,  
NCI, Frederick, MD, USA
- 15:15 Using Sequence Motifs for Enhanced Neural Network Prediction of Protein  
Distance Constraints  
*Jan Gorodkin, Ole Lund, Claus A. Andersen, Soren Brunak*  
The Technical University of Denmark, Lyngby, Denmark &  
University of Aarhus, Denmark
- 15:40 Nearest Neighbor Classification in 3D Protein Databases  
*Mihael Ankerst, Gabi Kastenmueller, Hans-Peter Kriegel, Thomas Seidl*  
University of Munich, Germany & Max Planck Institute for Biochemistry,  
Munich, Germany
- 16:05 A Data Base of Minimally Frustrated Alpha-Helical Segments Extracted from  
Proteins According to an Entropy Criterion  
*Rita Casadio, Mario Compiani, Piero Fariselli, Pier Luigi Martelli*  
University of Bologna, Italy & University of Camerino, Italy
- 16:30 **Coffee Break**
- 16:50 **Posters and Demos**
- 18:30 **End of Scientific Day**

# Sunday, August 8, 1999

## Session: Arrays and Expression Patterns

Chair: Reinhard Schneider

- 9:00      **Keynote**  
**Genes, Chips and Genomes**  
David Balaban  
Affymetrix, Inc., Santa Clara, CA, USA
- 9:50      Pharmaceutical Target Discovery using Guilt-by-Association:  
Schizophrenia and Parkinson's Disease Genes  
*Michael G. Walker, Wayne Volkmoth, Tod M. Klingler*  
Incyte Pharmaceuticals, Palo Alto, CA, USA
- 10:15     Fidelity Probes for DNA Arrays  
*Earl Hubbell, Pavel A. Pevzner*  
University of Southern California, Los Angeles, CA, USA & Affymetrix, Santa  
Clara, CA, USA
- 10:40     **Coffee Break**

## Session: Remote Homologies

Chair: Ralf Zimmer

- 11:00     Database Search Based on Bayesian Alignment  
*Jun Zhu, Roland Luethy, Charles E. Lawrence*  
Amgen, Inc., Thousand Oaks, CA, USA & Wadsworth Center, Albany, NY,  
USA
- 11:25     Using the Fisher Kernel Method to Detect Remote Protein Homologies  
*Tommi Jaakkola, Mark Diekhans, David Haussler*  
University of California, Santa Cruz, CA, USA
- 11:50     Protein Fold Class Prediction: New Methods of Statistical Classification  
*J. Grassmann, M. Reczko, S. Suhai, L. Edler*  
Stanford University, Palo Alto, CA, USA & Synaptic Ltd., Acharnai, Greece &  
German Cancer Research Center, Heidelberg, Germany
- 12:15     **Lunch**

Chair: Thomas Lengauer

14:00 **Keynote**  
**Combinatorial Problems in Gene Expression Analysis Using DNA Microarrays**  
Richard M. Karp  
University of Washington, Seattle, WA, USA

**Session: Sequence Analysis Algorithms**

Chair: Chris Rawlings

14:50 A Linear Time Algorithm for Finding All Maximal Scoring Subsequences  
*Walter L. Ruzzo, Martin Tompa*  
University of Washington, Seattle, WA, USA

15:15 Rapid Assessment of Extremal Statistics for Local Alignment With Gaps  
*Rolf Olsen, Ralf Bundschuh, Terence Hwa*  
University of California at San Diego, La Jolla, CA, USA

15:40 Metrics and Similarity Measures for Hidden Markov Models  
*Rune B. Lyngsø, Christian N. S. Pedersen, Henrik Nielsen*  
University of Aarhus, Denmark & Technical University of Denmark

16:05 An Exact Method for Finding Short Motifs in Sequences with Application to the Ribosome Binding Site Problem  
*Martin Tompa*  
University of Washington, Seattle, WA, USA

16:30 **Coffee Break**

16:50 **Posters and Demos**

18:30 **End of Scientific Day**

20:00 **ISCB Plenary Meeting**

# Monday, August 9, 1999

## Session: Databases

Chair: Peter Karp

- 9:00      **Keynote**  
**SWISS-PROT in the 21st Century !**  
Amos Bairoch  
University of Geneva, Switzerland
- 9:50      Automatic extraction of biological information from Scientific text: protein-protein interactions  
*Christian Blaschke, Miguel A. Andrade, Christos Ouzounis, Alfonso Valencia*  
CNB-CSIC, Madrid, Spain & EMBL Heidelberg, Germany & EBI, Cambridge, UK
- 10:50     Constructing Biological Knowledge Bases by Extracting Information from Text Sources  
*Mark Craven, Johan Kumlien*  
Carnegie Mellon University, Pittsburgh, PA, USA
- 10:40     **Coffee Break**

## Session: Systems and Networks

Chair: Peer Bork

- 11:00     Identify by Descent Genome Segmentation Based on Single Nucleotide Polymorphism Distributions  
*Thomas W. Blackwell, Eric Rouchka, David J. States*  
Washington University, St. Louis, MO, USA
- 11:25     Spatio-temporal Registration of the Expression Patterns of Drosophila Segmentation Genes  
*Ekaterina M. Myasnikova, David Kosman, John Reinitz, Maria G. Samsonova*  
Institute of High Performance Computing and Data Bases, St. Petersburg, Russia, Mount Sinai School of Medicine, New York, NY, USA
- 11:50     Seamless Integration of Biological Applications into a Database Framework  
*Thodoros Topaloglou, Anthony Kosky, Victor Markowitz*  
Gene Logic Inc., Berkeley, CA, USA
- 12:15     **Lunch**

14:00

**Solar Eclipse Lecture**

Thomas Lengauer, GMD-SCAI, Sankt Augustin, Germany

15:30

**Excursion**



# Tuesday, August 10, 1999

## Session: Whole Genome Analysis

Chair: Hans-Werner Mewes

- 9:00 **Keynote**  
**Computational Genomics: Biological Discovery in Complete Genomes**  
Anthony R. Kerlavage  
Celera Genomics Corporation, Rockville, MD, USA
- 9:50 Building Dictionaries Of 1D and 3D Motifs By Mining The Unaligned 1D Sequences Of 17 Archeal and Bacterial Genomes  
*Isidore Rigoutsos, Yuan Gao, Aris Floratos, Laxmi Parida*  
IBM TJ Watson Research Center, Yorktown Heights, NY, USA & University of Memphis, TN, USA
- 10:15 Position-Specific Annotation of Protein Function Based on Multiple Homologs  
*Miguel A. Andrade*  
EMBL, Heidelberg, Germany
- 10:40 **Coffee Break**

## Session: Molecular Interactions

Chair: Douglas Brutlag

- 11:00 A Motion Planning Approach to Flexible Ligand Binding  
*Amit P. Singh, Jean-Claude Latombe, Douglas L. Brutlag*  
Stanford University, CA, USA
- 11:25 Database Screening for HIV Protease Ligands: The Influence of Binding-Site Conformation and Representation  
*Volker Schneck, Leslie A. Kuhn*  
Michigan State University, East Lansing, MI, USA,
- 11:50 INTERACT: An Object Oriented Protein-Protein Interaction Database  
*Karen Eilbeck, Andy Brass, Norman Paton, Charlie Hodgman*  
University of Manchester, UK & Glaxo Wellcome Research and Development, Stevenage, UK
- 12:15 Quantitative, Scalable Discrete-Event Simulation of Metabolic Pathways  
*Peter Meric, Michael Wise*  
University of Sydney, Australia
- 12:40 **Lunch**

Chair: Peer Bork

- 14:00 **Keynote**  
**Gene Function via the Mass Spectrometric Analysis of Multi-Protein Complexes**  
Matthias Mann  
Odense University, Denmark

### **DNA Sequencing, Mapping, ESTs**

Chair: Martin Vingron

- 14:50 An Algorithm Combining Discrete and Continuous Methods for Optical Mapping  
*R.M. Karp, I. Pe'er, R. Shamir*  
University of Washington, Seattle, WA, USA, Tel Aviv University, Israel
- 15:15 Genomics via Optical Mapping III: Contigging Genomic DNA and Variations  
*Thomas Anantharaman, Bud Mishra, David Schwartz*  
New York University, NY, USA
- 15:40 A Dataset Generator for Whole Genome Shotgun Sequencing  
*Gene Myers*  
Celera Genomics, Rockville, MD, USA
- 16:05 ESTScan: a program for detecting, evaluating, and reconstructing potential coding regions in EST sequences  
*Christian Iseli, C. Victor Jongeneel, Philipp Bucher*  
Swiss Institute of Bioinformatics, Epalinges, Switzerland

- 16:30 **Coffee Break**

### **Session: Phylogenetic Analysis and Clustering**

Chair: Gary Stormo

- 16:50 Solving Large Scale Phylogenetic Problems using DCM2  
*Daniel H. Huson, Lisa Vawter, Tandy J. Warnow*  
Princeton University, NJ, USA & Smithkline Beecham, King of Prussia, PA, USA & University of Arizona, Tucson, AZ, USA
- 17:15 A Phylogenetic Approach to Molecular Structure Prediction  
*Viatcheslav R. Akmaev, Scott T. Kelley, Gary D. Stormo*  
University of Colorado, Boulder, CO, USA
- 17:40 Reconstructing the Duplication History of a Tandem Repeat  
*Gary Benson, Lan Dong*  
Mount Sinai School of Medicine, New York, NY, USA

18:05 Analysis of ribosomal RNA sequences by combinatorial clustering  
*Poe Xing, Casimir Kulikowski, Ilya Muchnik, Inna Dubchak, Denise Wolf, Sylvia Spengler, Manfred Zorn*  
Rutgers University, Piscataway, NJ, USA, Lawrence Berkeley National Laboratory, Berkeley, CA, USA

18:30 **Conferral of the SGI-Outstanding ISMB'99 Paper Award**  
**Closing Remarks**

19:00 **End of Conference**

# **SGI-Outstanding ISMB'99 Paper Award !**

**SGI will donate an award for an outstanding paper presented during the ISMB'99 Conference.**

Out of all the presented papers, among the top ranking papers according to the review process five will be chosen by the organizing committee as nominees. (Papers with participation from the groups of the organizing committee are excluded.)

During the conference the organizing committee will listen to the respective presentations and decide on the award winner. The final decision criteria will be a balance of: novelty of the work, significance of the work, age of the author (juniors are preferred) and presentation style.

The winner will be announced at the end of the conference. The winner will receive an SGI 320 - the new Pentium-based NT desktop machine from SGI that combines SGI's graphics technology with the standard Intel platform.

## **SGI-ISMB'99 Crunch Contest !**

**Win 120 hours of time on a 128 CPU SGI Origin 2000!**

Submit your crunch idea at the SGI booth during the meeting. The organizing committee will select the winning idea and will announce the winner on the last day of the conference.

The winner will work with SGI HPC Bioinformatics specialists to perform the crunch project. Resulting data will become property of the winner.

# MISCELLANEOUS

## Location

All events will take place at Stadthalle Heidelberg. The rooms mentioned in this program are all located in the Stadthalle. A large floorplan of the Stadthalle pointing to the various rooms will be posted at the meeting.

## Registration

The registration and conference office will open on Friday, August 6 and on Saturday, August 7 at 7:30 a.m. On the remaining conference days the office will open at 8:30 a.m. During opening hours the conference office can be reached under the telephone number +49 6221 14 22 804.

## Public Transport

Transfer to the Conference Site "Stadthalle": from the Marriott Hotel, please take bus line # 35 from the Betriebshof (3 minutes walking distance from the Marriott). The bus runs every 10 minutes and stops right in front of the Stadthalle. From the IBIS Hotel take bus line #35, 41 or 42 to the Stadthalle. The bus runs every 10 minutes.

Prices: single trip: DM 3.40, 5-trip-ticket: DM 13.50, 3-day ticket: DM 20.00.

All other hotels are within walking distance (10-15 minutes), although the Marriott and the IBIS are also within walking distance (20 minutes).

## Parking

Parking is available at the park garages: Kongresshaus P6 and P8.

## **Mail Room**

There are 20 computers available for your personal use. They are located in the room behind "Trübnersaal" on the second floor.

These computers are generously sponsored by SGI.

## **Awards**

There may be other paper and poster awards, besides SGI award, offered. Look for details on these awards at the meeting.

## **Poster Sessions**

The number in the poster book corresponds to the number of the poster stand.

## **Software Demonstrations**

During the Poster Session, there will also be Software Demonstrations. There is separate material in your conference bags informing you about this program item.

## **Industrial Exhibition**

There is an industrial exhibition at ISMB'99. There is separate material in your conference bags informing you about this program item.

**PLEASE WEAR YOUR BADGE AT ALL TIMES, YOU WILL NEED IT TO BE ADMITTED TO THE "GROSSER SAAL" AND TO OBTAIN MEALS.**

# ORGANIZATIONAL DETAILS

On Friday, August 6, lunch will be served in "Grosser Saal".

On the other conference days, lunch will be served in the Restaurant at the back of the Stadthalle and "Ballsaal" located on the first floor.

NOTE: Due to the large number of participants we ask you to please vacate your table after you finish eating and take your coffee outside the dining area (e.g. terrace, exhibition hall, foyer).

Speakers can check their slides in the slide-check-room "Tagungsbüro" located on the ground floor.

Invited speakers and tutorial speakers are asked to come to the registration desk for organizational purposes.

Messages for other participants can be placed on a board next to the registration desk.

Should you wish to take a shared limousine to Frankfurt airport on the day of your departure, please inform the personnel at the registration desk at least 48 hours in advance. The shuttle service costs DM 70,- per person (two people is DM 110,- and so on) and needs to be paid to the driver. A regular taxi costs approx. DM 150,-.

You can also take the Lufthansa shuttle service bus, which leaves from the Marriott Hotel approximately every hour. The cost is DM 36,- per person.

Trains leave from the Heidelberg train station approximately every half hour.

# SOCIAL EVENTS

## **Friday evening, 18:00 – 20:00**

Reception for all conference participants (Snacks and drinks will be served)

## **Sunday evening, 20:00 – 22:00**

ISCB Plenary Meeting open to all the participants (Drinks will be available)

# EXCURSIONS

## **Excursion to Neckarsteinach on Monday, August 9**

Neckarsteinach is a very nice old town close to Heidelberg. It is known as the 4-castle-city.

On August 9, we will leave by boat from Heidelberg Stadthalle at **15:30** to Neckarsteinach. The trip will take 1 1/2 hours and will take you along the Neckar River. You will be able to see the 4 castles on your way up the river.

In Neckarsteinach you will have 1 1/2 hours to visit the beautiful town. You will receive a short guide to Neckarsteinach in English.

The boat will take you back to Heidelberg leaving Neckarsteinach at **18:30**. On the trip a buffet with local specialties will be offered which is included in the price. Drinks can be bought at your own expense on the boat. (Please be on time. This is the last boat).

## **Solar Eclipse Excursion on Wednesday, August 11**

We will leave Heidelberg by bus at 9:00 on August 11. We will drive to the Castle Neipperg. From the wonderful castle grounds you will be able to follow the solar eclipse accompanied by a buffet with local specialties. After the solar eclipse there will be a wine tasting including local wines as well as wines from the regions the path of totality of the solar eclipse has touched.

We will leave the castle around 16:00.

After the eclipse tour, we will arrange for a bus to go from the Castle Neipperg via Heidelberg to Frankfurt airport (if sufficiently many people sign up). You can bring your luggage in the morning and leave it on the bus. The price depends on the number of people signing up (approx. DM 20,-). If we leave the castle at 16:00, it takes one hour to Heidelberg. From there it takes another hour to get to Frankfurt. Allowing for heavy traffic on the Autobahn, you should reach Frankfurt around 19:00 (no guarantees).