Please note that many posters will be accompanied with additional ISMB’99 Software Demonstrations during the poster sessions.

Due to the different technical requirements, software demos will be given in two different rooms in five parallel sessions:

- the "Kammer-Musik-Saal"
- the Mail Room (behind the "Trübnersaal" on the second floor)

The numbers in the following time/room schedule correspond to the poster numbers in your poster abstract booklet and the numbers on the poster boards.

**Saturday, 07.08.1999, 16:30–19:30**

<table>
<thead>
<tr>
<th>Time</th>
<th>Kammer-Musik-Saal</th>
<th>Mail Room</th>
</tr>
</thead>
<tbody>
<tr>
<td>16:30–17:30</td>
<td>10 11 14</td>
<td>16 17</td>
</tr>
<tr>
<td>17:30–18:30</td>
<td>61 64 73</td>
<td>25 29</td>
</tr>
<tr>
<td>18:30–19:30</td>
<td>81 96 102</td>
<td>41 44</td>
</tr>
</tbody>
</table>

**Sunday, 08.08.1999, 16:30–18:30**

<table>
<thead>
<tr>
<th>Time</th>
<th>Kammer-Musik-Saal</th>
<th>Mail Room</th>
</tr>
</thead>
<tbody>
<tr>
<td>16:30–17:30</td>
<td>103 112 116</td>
<td>49 50</td>
</tr>
<tr>
<td>17:30–18:30</td>
<td>138 147 166</td>
<td>53 107</td>
</tr>
</tbody>
</table>

Several other posters will be demonstrated at booths of the industrial exhibitors in the Kammer-Musik-Saal during the whole conference, namely posters:

- 13 (InforMax booth),
- 98 (BIOTITAN booth), and
- 134 (SGI booth).
NOTE

- Due to the large number of posters and the short time available for the poster sessions, we encourage to have the posters on display during all of the conference days according to the following schedule: The posters of the first session are displayed from Sat, August 7, morning (poster session on Saturday evening 16:30-18:30) until Sunday, August 8, 12:00. The posters of the second session are displayed from Sunday, August 8, 12:00, (poster session Sunday evening 16:30-18:30) until the end of conference.

  If you are going to present a poster please stick to this schedule.

- The demonstration space and the machines may be available for additional demos at other times during the conference as well. Please approach the technical staff or the reception desk for information.

- If you are going to demonstrate software, please approach one of the technical staff in the scheduled room a little bit ahead of your scheduled time. You will be assigned a machine or space/monitor and the IP number for your demo. (Needless to say: If you bring your own laptop and want to hook it up to the internet, you should know how to set your IP number/broadcast mask in order to avoid delays.)
List of ISMB’99 Software Demonstrations:

Judith A. Blake, Joel E. Richardson, Lois J. Maltais, Richard M. Baldarelli, Ken S. Frazer, Martin Ringwald, Janan T. Eppig: Integration of Gene Family and Protein Family Information in the Mouse Genome Database 10

Christian Blaschke, Alfonso Valencia: Tools for the Extraction of Biological Information from Text 11


Bert-Oliver Böhmer: Vector NTI Suite: SSBM-Software solution for Bio-Medicine 14


Andreas Bohne, Elke Lang, Claus-W. von der Lieth: Carbohydrate Modeling by Internet: New Features of W3-SWEET 17


David Dahle, Mark Diekhans, Leslie Grate, Eric Rice, Richard Hughey: The UCSC Kestrel Sequence Analysis Server 29

Nir Friedman, Iftach Nachman, Dana Pe’er: From Bayesian Networks to Gene Networks: Understanding Expression Data 41

Terry Gaasterland, Bing Hai: Eukaryotic Functional Families based on Prokaryotic Genomic Neighborhoods 44

Terry Gaasterland, Gulriz Kurban: Target Selection for Structural Genomics 45

Terry Gaasterland, Alexander Sczyrba: Multigenome MAGPIE 46

David Gilbert, Juris Viksna: Pattern Discovery Methods for Protein Topology Diagrams 49

Christoph Gille, Andrean Goede, Robert Preissner, Kristian Rother, Cornelius Frömmel: Evolutionary Conservation of Interfaces of Secondary Structural Elements in Proteins shown for the Proteasomal Subunits 50

Ian Holmes, William J. Bruno: Handel Operatics for Alignment, Phylogeny and Profiling 61

Daniel H. Huson: New Software for Phylogenetic Analysis 64

M. Kieninger, J. Gohrke, T. Kämpfe, C. Sarkar: Large Scale Sequence Analysis with DoPrimer 73

Stefan Kurtz, Chris Schleiermacher: REPuter: Fast Computation of Maximal Repeats in Complete Genomes 81

Pedro Mendes: Gepasi - Numerical Simulation and Optimization of Biochemical Kinetics 96

Theo Mevissen, Friedrich Rippmann, Ralf Zimmer, Thomas Lengauer: Large Scale Genome Annotation with 123D using Multiprocessor Machines 98

Adam Moore, Peter Murray-Rust: XML and BioDOM - Structured Documents in Molecular Science 102

Juha Muilu, Patricia Rodriguez-Tomé, Alan Robinson: Genome Builder - Integrating External Applications and Databases using CORBA 103

Tamotsu Noguchi, Kentaro Onizuka, Yutaka Akiyama: PDB-REPRDB: An Interactive Database of Representative Protein Chains from the Protein Data Bank (PDB) 107

Marco Pagni, Thomas Junier: Dotlet: a Java Applet for Sequence Comparisons using the Dot Matrix Method 112

Marco Pagni, Elsa Schweiss: GiCAS: Towards a Web-based Integration of Bioinformatics Resources 113

Hans-Peter Pohle, Bernd Drescher: A Flexible Environment for Sequence Analysis and Visualisation 116

Roger A. Sayle, J. Scott Dixon: Virtual Network File Servers for Sequence Database Management and Bioinformatics Tool Integration 134

Philip Scordis, William Wright, Teresa K. Attwood: Intelligent Alternatives for Searching the PRINTS Database 138

Kouichi Takahashi, Kenta Hashimoto, Yusuke Saito, Tom Shimizu: The E-CELL Simulation System: Software Environment for Whole Cell Simulation 147

Golan Yona, Michael Levitt: A Unified Sequence-Structure Classification of Protein Sequences: Combining Sequence and Structure in a Map of Protein Space 166