

# Table of Contents

An Improved Model for Statistical Alignment . . . . .	1
<i>István Miklós, Zoltán Toroczka</i>	
Improving Profile-Profile Alignments via Log Average Scoring . . . . .	11
<i>Niklas von Öhsen, Ralf Zimmer</i>	
False Positives in Genomic Map Assembly and Sequence Validation . . . . .	27
<i>Thomas Anantharaman, Bud Mishra</i>	
Boosting EM for Radiation Hybrid and Genetic Mapping . . . . .	41
<i>Thomas Schier, Patrick Chabrier, Martin Bouchez, Denis Milan</i>	
Placing Probes along the Genome Using Pairwise Distance Data . . . . .	52
<i>Will Casey, Bud Mishra, Mike Wigler</i>	
Comparing a Hidden Markov Model and a Stochastic Context-Free Grammar . . . . .	69
<i>Arun Jagota, Rune B. Lyngsø, Christian N.S. Pedersen</i>	
Assessing the Statistical Significance of Overrepresented Oligonucleotides . . . . .	85
<i>Alain Denise, Mireille Régnier, Mathias Vandenbogaert</i>	
Pattern Matching and Pattern Discovery Algorithms for Protein Topologies . . . . .	98
<i>Juris Veksna, David Gilbert</i>	
Computing Linking Numbers of a Filtration . . . . .	112
<i>Herbert Edelsbrunner, Afra Zomorodian</i>	
Side Chain-Positioning as an Integer Programming Problem . . . . .	128
<i>Olivia Eriksson, Yishao Zhou, Arne Elofsson</i>	
A Chemical-Distance-Based Test for Positive Darwinian Selection . . . . .	142
<i>Tal Pupko, Roded Sharan, Masami Hasegawa, Ron Shamir, Dan Graur</i>	
Finding a Maximum Compatible Tree for a Bounded Number of Trees with Bounded Degree Is Solvable in Polynomial Time . . . . .	156
<i>Ganeshkumar Ganapathysaravanabavan, Tandy Warnow</i>	
Experiments in Computing Sequences of Reversals . . . . .	164
<i>Anne Bergeron, François Strasbourg</i>	
Exact-IEBP: A New Technique for Estimating Evolutionary Distances between Whole Genomes . . . . .	175
<i>Li-San Wang</i>	
Finding an Optimal Inversion Median: Experimental Results . . . . .	189
<i>Adam C. Siepel, Bernard M.E. Moret</i>	

Analytic Solutions for Three-Taxon $ML_{MC}$ Trees with Variable Rates Across Sites .....	204
<i>Benny Chor, Michael Hendy, David Penny</i>	
The Performance of Phylogenetic Methods on Trees of Bounded Diameter .	214
<i>Luay Nakhleh, Usman Roshan, Katherine St. John, Jerry Sun, Tandy Warnow</i>	
$(1+\epsilon)$ -Approximation of Sorting by Reversals and Transpositions .....	227
<i>Niklas Eriksen</i>	
On the Practical Solution of the Reversal Median Problem .....	238
<i>Alberto Caprara</i>	
Algorithms for Finding Gene Clusters .....	252
<i>Steffen Heber, Jens Stoye</i>	
Determination of Binding Amino Acids Based on Random Peptide Array Screening Data .....	264
<i>Peter J. van der Veen, L.F.A. Wessels, J.W. Slootstra, R.H. Melen, M.J.T. Reinders, J. Hellendoorn</i>	
A Simple Hyper-Geometric Approach for Discovering Putative Transcription Factor Binding Sites .....	278
<i>Yoseph Barash, Gill Bejerano, Nir Friedman</i>	
Comparing Assemblies Using Fragments and Mate-Pairs .....	294
<i>Daniel H. Huson, Aaron L. Halpern, Zhongwu Lai, Eugene W. Myers, Knut Reinert, Granger G. Sutton</i>	
<b>Author Index</b> .....	307

Algorithms in Bioinformatics

First International Workshop, WABI 2001, Aarhus,  
Denmark, August 28-31, 2001, Proceedings

Gascuel, O.; Moret, B.M.E. (Eds.)

2001, X, 314 p., Softcover

ISBN: 978-3-540-42516-8