

Contents

BicNET: Efficient Biclustering of Biological Networks to Unravel Non-Trivial Modules	1
<i>Rui Henriques and Sara C. Madeira</i>	
Simultaneous Optimization of both Node and Edge Conservation in Network Alignment via WAVE	16
<i>Yihan Sun, Joseph Crawford, Jie Tang, and Tijana Milenković</i>	
The Topological Profile of a Model of Protein Network Evolution Can Direct Model Improvement.	40
<i>Todd A. Gibson and Debra S. Goldberg</i>	
Algorithms for Regular Tree Grammar Network Search and Their Application to Mining Human-Viral Infection Patterns.	53
<i>Ilan Smoly, Amir Carmel, Yonat Shemer-Avni, Esti Yeager-Lotem, and Michal Ziv-Ukelson</i>	
Orthology Relation and Gene Tree Correction: Complexity Results	66
<i>Manuel Lafond and Nadia El-Mabrouk</i>	
Finding a Perfect Phylogeny from Mixed Tumor Samples	80
<i>Ademir Hujdurović, Urša Kačar, Martin Milanič, Bernard Ries, and Alexandru I. Tomescu</i>	
A Sub-quadratic Time and Space Complexity Solution for the Dated Tree Reconciliation Problem for Select Tree Topologies	93
<i>Benjamin Drinkwater and Michael A. Charleston</i>	
Maximum Parsimony Analysis of Gene Copy Number Changes	108
<i>Jun Zhou, Yu Lin, Vaibhav Rajan, William Hoskins, and Jijun Tang</i>	
Multiple-Ancestor Localization for Recently Admixed Individuals.	121
<i>Yaron Margalit, Yael Baran, and Eran Halperin</i>	
Association Mapping for Compound Heterozygous Traits Using Phenotypic Distance and Integer Programming	136
<i>Dan Gusfield and Rasmus Nielsen</i>	
Semi-nonparametric Modeling of Topological Domain Formation from Epigenetic Data	148
<i>Emre Sefer and Carl Kingsford</i>	

Scribe: Ultra-Accurate Error-Correction of Pooled Sequenced Reads.	162
<i>Denise Duma, Francesca Cordero, Marco Beccuti, Gianfranco Ciardo, Timothy J. Close, and Stefano Lonardi</i>	
Jabba: Hybrid Error Correction for Long Sequencing Reads Using Maximal Exact Matches	175
<i>Giles Miclotte, Mahdi Heydari, Piet Demeester, Pieter Audenaert, and Jan Fostier</i>	
Optimizing Read Reversals for Sequence Compression: (Extended Abstract)	189
<i>Zhong Sichen, Lu Zhao, Yan Liang, Mohammadzaman Zamani, Rob Patro, Rezaul Chowdhury, Esther M. Arkin, Joseph S.B. Mitchell, and Steven Skiena</i>	
Circular Sequence Comparison with q -grams	203
<i>Roberto Grossi, Costas S. Iliopoulos, Robert Mercas, Nadia Pisanti, Solon P. Pissis, Ahmad Retha, and Fatima Vayani</i>	
Bloom Filter Trie – A Data Structure for Pan-Genome Storage	217
<i>Guillaume Holley, Roland Wittler, and Jens Stoye</i>	
A Filtering Approach for Alignment-Free Biosequences Comparison with Mismatches	231
<i>Cinzia Pizzi</i>	
Models and Algorithms for Genome Rearrangement with Positional Constraints	243
<i>Krister M. Swenson and Mathieu Blanchette</i>	
Sparse RNA Folding Revisited: Space-Efficient Minimum Free Energy Prediction.	257
<i>Sebastian Will and Hosna Jabbari</i>	
A Sparsified Four-Russian Algorithm for RNA Folding	271
<i>Yelena Frid and Dan Gusfield</i>	
Higher Classification Accuracy of Short Metagenomic Reads by Discriminative Spaced k -mers	286
<i>Rachid Ounit and Stefano Lonardi</i>	
Graph-Theoretic Modelling of the Domain Chaining Problem.	296
<i>Poly H. da Silva, Simone Dantas, Chunfang Zheng, and David Sankoff</i>	
Efficient Design of Compact Unstructured RNA Libraries Covering All k -mers	308
<i>Yaron Orenstein and Bonnie Berger</i>	
Author Index	327