References

[1] Ali Bashir, Qing Lu, Dennis Carson, Benjamin Raphael, Yu-Tsueng Liu, and Vineet Bafna. Optimizing pcr assays for dna based cancer diagnostics. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 220–235. Springer-Verlag, Berlin-Heidelberg, 2009.

[2] Sharon Bruckner, Falk Hüffner, Richard M. Karp, Ron Shamir, and Roded Sharan. Topology-free querying of protein interaction networks. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 74–89. Springer-Verlag, Berlin-Heidelberg, 2009.

[3] Cedric Chauve and Nadia El-Mabrouk. New perspectives on gene family evolution: Losses in reconciliation and a link with supertrees. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 46–58. Springer-Verlag, Berlin-Heidelberg, 2009.

[4] Constantinos Daskalakis, Elchanan Mossel, and Sebastien Roch. Phylogenies without branch bounds: Contracting the short, pruning the deep. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 451–465. Springer-Verlag, Berlin-Heidelberg, 2009.

[5] Alexandre Donzé, Gilles Clermont, Axel Legay, and Christopher J. Langmead. Parameter synthesis in nonlinear dynamical systems: Application to systems biology. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 155–169. Springer-Verlag, Berlin-Heidelberg, 2009.

[6] Banu Dost, Nuno Bandeira, Xiangqian Li, Zhouxin Shen, Steve Briggs, and Vineet Bafna. Shared peptides in mass spectrometry based pro-

tein quantification. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 356–371. Springer-Verlag, Berlin-Heidelberg, 2009.

[7] Dan Gusfield. The multi-state perfect phylogeny problem with missing and removable data: Solutions via integer-programming and chordal graph theory. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 236–252. Springer-Verlag, Berlin-Heidelberg, 2009.

[8] Zengyou He, Chao Yang, Can Yang, Robert Z. Qi, Jason Po-Ming Tam, and Weichuan Yu. Optimization-based peptide mass fingerprinting for protein mixture identification. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 16–30. Springer-Verlag, Berlin-Heidelberg, 2009.

[9] Benjamin J. Hescott, Mark D.M. Leiserson, Lenore J. Cowen, and Donna K. Slonim. Evaluating between-pathway models with expression data. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 372–385. Springer-Verlag, Berlin-Heidelberg, 2009.

[10] Fereydoun Hormozdiari, Can Alkan, Evan E. Eichler, and S. Cenk Sahinalp. Combinatorial algorithms for structural variation detection in high throughput sequenced genomes. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 218–219. Springer-Verlag, Berlin-Heidelberg, 2009.

[11] Rami Jaschek and Amos Tanay. Spatial clustering of multivariate genomic and epigenomic information. In Serafim Batzoglu, editor, *Proceed-*

ings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009), volume 5541 of *LNCS/LNBI*, pages 170–183. Springer-Verlag, Berlin-Heidelberg, 2009.

[12] Eun Yong Kang, Ilya Shpitser, Chun Ye, and Eleazar Eskin. Detecting the presence and absence of causal relationships between expression of yeast genes with very few samples. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 466–481. Springer-Verlag, Berlin-Heidelberg, 2009.

[13] Hyun Min Kang, Noah A. Zaitlen, Buhm Han, and Eleazar Eskin. An adaptive and memory efficient algorithm for genotype imputation. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 482–495. Springer-Verlag, Berlin-Heidelberg, 2009.

[14] Eagu Kim, Travis Wheeler, and John Kececioglu. Learning models for aligning protein sequences with predicted secondary structure. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 512–531. Springer-Verlag, Berlin-Heidelberg, 2009.

[15] Bonnie Kirkpatrick, Javier Rosa, Eran Halperin, and Richard M. Karp. Haplotype inference in complex pedigrees. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 108–120. Springer-Verlag, Berlin-Heidelberg, 2009.

[16] Mathieu Lavallée-Adam, Benoit Coulombe, and Mathieu Blanchette. Detection of locally over-represented go terms in protein-protein interaction networks. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*,

volume 5541 of *LNCS/LNBI*, pages 302–320. Springer-Verlag, Berlin-Heidelberg, 2009.

[17] Yong Lu, Roni Rosenfeld, Gerard J. Nau, and Ziv Bar-Joseph. Cross species expression analysis of innate immune response. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 90–107. Springer-Verlag, Berlin-Heidelberg, 2009.

[18] Veli Mäkinen, Gonzalo Navarro, Jouni Sirén, and Niko Välimäki. Storage and retrieval of individual genomes. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 121–137. Springer-Verlag, Berlin-Heidelberg, 2009.

[19] Mathias Möhl, Sebastian Will, and Rolf Backofen. Lifting prediction to alignment of rna pseudoknots. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 285–301. Springer-Verlag, Berlin-Heidelberg, 2009.

[20] Saket Navlakha, James White, Niranjan Nagarajan, Mihai Pop, and Carl Kingsford. Finding biologically accurate clusterings in hierarchical tree decompositions using the variation of information. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 400–417. Springer-Verlag, Berlin-Heidelberg, 2009.

[21] Nicholas D. Pattengale, Masoud Alipour, Olaf R.P. Bininda-Emonds, Bernard M.E. Moret, and Alexandros Stamatakis. How many bootstrap replicates are necessary? In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 184–200. Springer-Verlag, Berlin-Heidelberg, 2009.

[22] Jian Peng and Jinbo Xu. Boosting protein threading accuracy. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 31–45. Springer-Verlag, Berlin-Heidelberg, 2009.

[23] Snehit Prabhu and Itsik Pe'er. Overlapping pools for high throughput targeted resequencing. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 270–270. Springer-Verlag, Berlin-Heidelberg, 2009.

[24] Arvind Ramanathan, Pratul K. Agarwal, Maria Kurnikova, and Christopher J. Langmead. An online approach for mining collective behaviors from molecular dynamics simulations. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 138–154. Springer-Verlag, Berlin-Heidelberg, 2009.

[25] Tali Raveh-Sadka, Michal Levo, and Eran Segal. Incorporating nucleosomes into thermodynamic models of transcription regulation. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 217–217. Springer-Verlag, Berlin-Heidelberg, 2009.

[26] Sheila M. Reynolds, Jeff A. Bilmes, and William Stafford Noble. On the relationship between dna periodicity and local chromatin structure. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 434–450. Springer-Verlag, Berlin-Heidelberg, 2009.

[27] Itai Sharon, Amrita Pati, Victor M. Markowitz, and Ron Y. Pinter. A statistical framework for the functional analysis of metagenomes. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RE-*

COMB'2009 (Tucson, AZ, USA, May 18-21, 2009), volume 5541 of *LNCS/LNBI*, pages 496–511. Springer-Verlag, Berlin-Heidelberg, 2009.

[28] Tetsuo Shibuya. Searching protein 3-d structures in linear time. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 1–15. Springer-Verlag, Berlin-Heidelberg, 2009.

[29] Suzanne S. Sindi and Benjamin J. Raphael. Identification and frequency estimation of inversion polymorphisms from haplotype data. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 418–433. Springer-Verlag, Berlin-Heidelberg, 2009.

[30] Oliver Stegle, Katherine Denby, David L. Wild, Zoubin Ghahramani, and Karsten M. Borgwardt. A robust bayesian two-sample test for detecting intervals of differential gene expression in microarray time series. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 201–216. Springer-Verlag, Berlin-Heidelberg, 2009.

[31] Krister M. Swenson, Vaibhav Rajan, Yu Lin, and Bernard M.E. Moret. Sorting signed permutations by inversions in $o(n \log n)$ time. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 386–399. Springer-Verlag, Berlin-Heidelberg, 2009.

[32] Jérôme Waldispühl, Charles W. O'Donnell, Sebastian Will, Srinivas Devadas, Rolf Backofen, and Bonnie Berger. Simultaneous alignment and folding of protein sequences. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 339–355. Springer-Verlag, Berlin-Heidelberg, 2009.

[33] Osvaldo Zagordi, Lukas Geyrhofer, Volker Roth, and Niko Beerenwinkel. Deep sequencing of a genetically heterogeneous sample: Local haplotype reconstruction and read error correction. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 271–284. Springer-Verlag, Berlin-Heidelberg, 2009.

[34] Xiang Zhang, Feng Pan, Yuying Xie, Fei Zou, and Wei Wang. Coe: A general approach for efficient genome-wide two-locus epistasis test in disease association study. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 253–269. Springer-Verlag, Berlin-Heidelberg, 2009.

[35] Feng Zhao, Jian Peng, Joe DeBartolo, Karl F. Freed, Tobin R. Sosnick, and Jinbo Xu. A probabilistic graphical model for ab initio folding. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 59–73. Springer-Verlag, Berlin-Heidelberg, 2009.

[36] Wei Zheng, Karl E. Griswold, and Chris Bailey-Kellogg. Protein fragment swapping: A method for asymmetric, selective site-directed recombination. In Serafim Batzoglu, editor, *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2009 (Tucson, AZ, USA, May 18-21, 2009)*, volume 5541 of *LNCS/LNBI*, pages 321–338. Springer-Verlag, Berlin-Heidelberg, 2009.