## References

- [1] Nuno Bandeira, Julio Ng, Dario Meluzzi, Roger G. Linington, Pieter Dorrestein, and Pavel A. Pevzner. De novo sequencing of nonribosomal peptides. In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 181–195. Springer-Verlag, Berlin-Heidelberg, 2008.
- [2] Michael Baym, Chris Bakal, Norbert Perrimon, and Bonnie Berger. High-resolution modeling of cellular signaling networks. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 257–271. Springer-Verlag, Berlin-Heidelberg, 2008.
- [3] Sivan Bercovici, Dan Geiger, Liran Shlush, Karl Skorecki, and Alan Templeton. Panel construction for mapping in admixed populations via expected mutual information. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 435–449. Springer-Verlag, Berlin-Heidelberg, 2008.
- [4] Sebastian Böcker, Katharina Jahn, Julia Mixtacki, and Jens Stoye. Computation of median gene clusters. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 331–345. Springer-Verlag, Berlin-Heidelberg, 2008.
- [5] J. Gordon Burleigh, Mukul S. Bansal, Andre Wehe, and Oliver Eulenstein. Locating multiple gene duplications through reconciled trees. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 273–284. Springer-Verlag, Berlin-Heidelberg, 2008.

- [6] Howard Cedar. Orchestration of dna methylation. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RE-COMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 65–65. Springer-Verlag, Berlin-Heidelberg, 2008.
- [7] Sourav Chatterji, Ichitaro Yamazaki, Zhaojun Bai, and Jonathan A. Eisen. Compostbin: A dna composition-based algorithm for binning environmental shotgun reads. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 17–28. Springer-Verlag, Berlin-Heidelberg, 2008.
- [8] Suzanne Cory. Bcl-2: From translocation to therapy. In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 346–346. Springer-Verlag, Berlin-Heidelberg, 2008.
- [9] Ritendra Datta and Marshall Bern. Spectrum fusion: Using multiple mass spectra for de novo peptide sequencing. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 140–153. Springer-Verlag, Berlin-Heidelberg, 2008.
- [10] Christophe Dessimoz, Daniel Margadant, and Gaston H. Gonnet. Dlight lateral gene transfer detection using pairwise evolutionary distances in a statistical framework. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 315–330. Springer-Verlag, Berlin-Heidelberg, 2008.
- [11] Delbert Dueck, Brendan J. Frey, Nebojsa Jojic, Vladimir Jojic, Guri Giaever, Andrew Emili, Gabe Musso, and Robert Hegele. Constructing treatment portfolios using affinity propagation. In Martin Vingron

- and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RE-COMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 360–371. Springer-Verlag, Berlin-Heidelberg, 2008.
- [12] Eleazar Eskin. Increasing power in association studies by using linkage disequilibrium structure and molecular function as prior information. In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 434–434. Springer-Verlag, Berlin-Heidelberg, 2008.
- [13] Jason Flannick, Antal Novak, Chuong B. Do, Balaji S. Srinivasan, and Serafim Batzoglou. Automatic parameter learning for multiple network alignment. In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 214–231. Springer-Verlag, Berlin-Heidelberg, 2008.
- [14] Caroline C. Friedel, Jan Krumsiek, and Ralf Zimmer. Bootstrapping the interactome: Unsupervised identification of protein complexes in yeast. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 3–16. Springer-Verlag, Berlin-Heidelberg, 2008.
- [15] Raluca Gordân, Leelavati Narlikar, and Alexander J. Hartemink. A fast, alignment-free, conservation-based method for transcription factor binding site discovery. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 98–111. Springer-Verlag, Berlin-Heidelberg, 2008.
- [16] John Hawkins and Timothy L. Bailey. The statistical power of phylogenetic motif models. In Martin Vingron and Limsoon Wong, ed-

- itors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 112–126. Springer-Verlag, Berlin-Heidelberg, 2008.
- [17] Maxim Kalaev, Vineet Bafna, and Roded Sharan. Fast and accurate alignment of multiple protein networks. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 246–256. Springer-Verlag, Berlin-Heidelberg, 2008.
- [18] Mustafa Kirac and Gultekin Ozsoyoglu. Protein function prediction based on patterns in biological networks. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RE-COMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 197–213. Springer-Verlag, Berlin-Heidelberg, 2008.
- [19] Sang Yup Lee. Systems metabolic engineering. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RE-COMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 196–196. Springer-Verlag, Berlin-Heidelberg, 2008.
- [20] Yong Fuga Li, Randy J. Arnold, Yixue Li, Predrag Radivojac, Quanhu Sheng, and Haixu Tang. A bayesian approach to protein inference problem in shotgun proteomics. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 167–180. Springer-Verlag, Berlin-Heidelberg, 2008.
- [21] Tien-ho Lin, Pradipta Ray, Geir K. Sandve, Selen Uguroglu, and Eric P. Xing. Baycis: A bayesian hierarchical hmm for cis-regulatory module decoding in metazoan genomes. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 66–81. Springer-Verlag, Berlin-Heidelberg, 2008.

- [22] Yu Lin, Yantao Qiao, Shiwei Sun, Chungong Yu, Gongjin Dong, and Dongbo Bu. A fragmentation event model for peptide identification by mass spectrometry. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 154–166. Springer-Verlag, Berlin-Heidelberg, 2008.
- [23] Fuhui Long, Hanchuan Peng, Xiao Liu, Stuart Kim, and Gene Myers. Automatic recognition of cells (arc) for 3d images of c. elegans. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 128–139. Springer-Verlag, Berlin-Heidelberg, 2008.
- [24] Andrei Lupas. At the origin of life: How did folded proteins evolve? In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 272–272. Springer-Verlag, Berlin-Heidelberg, 2008.
- [25] Rune B. Lyngsø, Yun S. Song, and Jotun Hein. Accurate computation of likelihoods in the coalescent with recombination via parsimony. In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 463–477. Springer-Verlag, Berlin-Heidelberg, 2008.
- [26] Bin Ma and Xiaoming Sun. More efficient algorithms for closest string and substring problems. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 396–409. Springer-Verlag, Berlin-Heidelberg, 2008.
- [27] Paul Medvedev and Michael Brudno. Ab initio whole genome shotgun assembly with mated short reads. In Martin Vingron and Limsoon

- Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 50–64. Springer-Verlag, Berlin-Heidelberg, 2008.
- [28] Michael R. Mehan, Juan Nunez-Iglesias, Mrinal Kalakrishnan, Michael S. Waterman, and Xianghong Jasmine Zhou. An integrative network approach to map the transcriptome to the phenome. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 232–245. Springer-Verlag, Berlin-Heidelberg, 2008.
- [29] Michael Sammeth, Gabriel Valiente, and Roderic Guigó. Bubbles: Alternative splicing events of arbitrary dimension in splicing graphs. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 372–395. Springer-Verlag, Berlin-Heidelberg, 2008.
- [30] Sriram Sankararaman, Gad Kimmel, Eran Halperin, and Michael I. Jordan. On the inference of ancestries in admixed populations. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 424–433. Springer-Verlag, Berlin-Heidelberg, 2008.
- [31] Yanxin Shi, Itamar Simon, Tom Mitchell, and Ziv Bar-Joseph. A combined expression-interaction model for inferring the temporal activity of transcription factors. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 82–97. Springer-Verlag, Berlin-Heidelberg, 2008.
- [32] Denis Smirnov and Vivian G. Cheung. Disruption of a transcriptional regulatory pathway contributes to phenotypes in carriers of ataxia

- telangiectasia. In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 410–410. Springer-Verlag, Berlin-Heidelberg, 2008.
- [33] Temple F. Smith. Computational biology: Its challenges past, present, and future. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 1–2. Springer-Verlag, Berlin-Heidelberg, 2008.
- [34] Oliver Stegle, Anitha Kannan, Richard Durbin, and John Winn. Accounting for non-genetic factors improves the power of eqtl studies. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 411–422. Springer-Verlag, Berlin-Heidelberg, 2008.
- [35] Andreas Sundquist, Eugene Fratkin, Chuong B. Do, and Serafim Batzoglou. Effects of genetic divergence in identifying ancestral origin using hapaa. In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 423–423. Springer-Verlag, Berlin-Heidelberg, 2008.
- [36] Igor Ulitsky, Richard M. Karp, and Ron Shamir. Detecting disease-specific dysregulated pathways via analysis of clinical expression profiles. In Martin Vingron and Limsoon Wong, editors, *Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008)*, volume 4955 of *LNCS/LNBI*, pages 347–359. Springer-Verlag, Berlin-Heidelberg, 2008.
- [37] Leo van Iersel, Judith Keijsper, Steven Kelk, Leen Stougie, Ferry Hagen, and Teun Boekhout. Constructing level-2 phylogenetic networks from

- triplets. In Martin Vingron and Limsoon Wong, editors, *Proceedings* of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 450–462. Springer-Verlag, Berlin-Heidelberg, 2008.
- [38] Jing Zhang, Xin Gao, Jinbo Xu, and Ming Li. Rapid and accurate protein side chain prediction with local backbone information. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 285–299. Springer-Verlag, Berlin-Heidelberg, 2008.
- [39] Yu Zhang, Giltae Song, Tomáš Vinař, Eric D. Green, Adam Siepel, and Webb Miller. Reconstructing the evolutionary history of complex human gene clusters. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 April 2, 2008), volume 4955 of LNCS/LNBI, pages 29–49. Springer-Verlag, Berlin-Heidelberg, 2008.
- [40] Wei Zheng, Alan M. Friedman, and Chris Bailey-Kellogg. Algorithms for joint optimization of stability and diversity in planning combinatorial libraries of chimeric proteins. In Martin Vingron and Limsoon Wong, editors, Proceedings of the 12th Annual International Conference on Research in Computational Molecular Biology, RECOMB'2007 (Singapore, March 30 - April 2, 2008), volume 4955 of LNCS/LNBI, pages 300-314. Springer-Verlag, Berlin-Heidelberg, 2008.