References

[1] Max A. Alekseyev and Pavel A. Pevzner. Limited lifespan of fragile regions in mammalian evolution. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 198–215. Springer-Verlag, Berlin-Heidelberg, 2010.

[2] Stéphane Aris-Brosou. A simple measure of the dynamics of segmented genomes: An application to influenza. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 149–160. Springer-Verlag, Berlin-Heidelberg, 2010.

[3] Ghada Badr, Krister M. Swenson, and David Sankoff. Listing all parsimonious reversal sequences: New algorithms and perspectives. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 39–49. Springer-Verlag, Berlin-Heidelberg, 2010.

[4] Mukul S. Bansal, J. Peter Gogarten, and Ron Shamir. Detecting highways of horizontal gene transfer. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 109–120. Springer-Verlag, Berlin-Heidelberg, 2010.

[5] Marília D.V. Braga. On sorting genomes with dcj and indels. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 62–73. Springer-Verlag, Berlin-Heidelberg, 2010.

[6] Hugo Devillers, Hélène Chiapello, Sophie Schbath, and Meriem El Karoui. Assessing the robustness of complete bacterial genome segmentations. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 173–187. Springer-Verlag, Berlin-Heidelberg, 2010.

[7] Ulisses Dias, Zanoni Dias, and João C. Setubal. A simulation tool for the study of symmetric inversions in bacterial genomes. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 240–251. Springer-Verlag, Berlin-Heidelberg, 2010.

[8] Jean-Philippe Doyon, Celine Scornavacca, K.Yu. Gorbunov, Gergely J. Szöllősi, Vincent Ranwez, and Vincent Berry. An efficient algorithm for gene/species trees parsimonious reconciliation with losses, duplications and transfers. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 93–108. Springer-Verlag, Berlin-Heidelberg, 2010.

[9] Yves Gagnon, Olivier Tremblay Savard, Denis Bertrand, and Nadia El-Mabrouk. Advances on genome duplication distances. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 25–38. Springer-Verlag, Berlin-Heidelberg, 2010.

[10] Katharina Jahn. Efficient computation of approximate gene clusters based on reference occurrences. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 264–277. Springer-Verlag, Berlin-Heidelberg, 2010.

[11] Haitao Jiang, Chunfang Zheng, David Sankoff, and Binhai Zhu. Scaffold filling under the breakpoint distance. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 83–92. Springer-Verlag, Berlin-Heidelberg, 2010.

[12] Minghui Jiang. The zero exemplar distance problem. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 74–82. Springer-Verlag, Berlin-Heidelberg, 2010.

[13] Jakub Kováč, Marília D.V. Braga, and Jens Stoye. The problem of chromosome reincorporation in dcj sorting and halving. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 13–24. Springer-Verlag, Berlin-Heidelberg, 2010.

[14] Yu Lin and Bernard M.E. Moret. A new genomic evolutionary model for rearrangements, duplications, and losses that applies across eukaryotes and prokaryotes. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 228–239. Springer-Verlag, Berlin-Heidelberg, 2010.

[15] Yu Lin, Vaibhav Rajan, and Bernard M.E. Moret. Fast and accurate phylogenetic reconstruction from high-resolution whole-genome data and a novel robustness estimator. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 137–148. Springer-Verlag, Berlin-Heidelberg, 2010.

[16] Ján Maňuch and Murray Patterson. The complexity of the gapped consecutive-ones property problem for matrices of bounded maximum degree. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 278–289. Springer-Verlag, Berlin-Heidelberg, 2010.

[17] Atheer A. Matroud, Michael D. Hendy, and Christopher P. Tuffley. An algorithm to solve the motif alignment problem for approximate nested tandem repeats. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 188–197. Springer-Verlag, Berlin-Heidelberg, 2010.

[18] Emmanuel Mongin, Ken Dewar, and Mathieu Blanchette. Mapping association between long-range cis-regulatory regions and their target genes using comparative genomics. In Eric Tannier, editor, *Proceedings*

of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010), volume 6398 of *LNCS/LNBI*, pages 216–227. Springer-Verlag, Berlin-Heidelberg, 2010.

[19] Aïda Ouangraoua, Anne Bergeron, and Krister M. Swenson. Ultra-perfect sorting scenarios. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 50–61. Springer-Verlag, Berlin-Heidelberg, 2010.

[20] Aïda Ouangraoua, Krister M. Swenson, and Cedric Chauve. An approximation algorithm for computing a parsimonious first speciation in the gene duplication model. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 290–301. Springer-Verlag, Berlin-Heidelberg, 2010.

[21] Raluca Uricaru, Alban Mancheron, and Eric Rivals. Novel definition and algorithm for chaining fragments with proportional overlaps. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 161–172. Springer-Verlag, Berlin-Heidelberg, 2010.

[22] Robert Warren and David Sankoff. Genome aliquoting revisited. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 1–12. Springer-Verlag, Berlin-Heidelberg, 2010.

[23] Roland Wittler and Jens Stoye. Consistency of sequence-based gene clusters. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada, October 9-11, 2010)*, volume 6398 of *LNCS/LNBI*, pages 252–263. Springer-Verlag, Berlin-Heidelberg, 2010.

[24] Andrew Wei Xu. On exploring genome rearrangement phylogenetic patterns. In Eric Tannier, editor, *Proceedings of the International Workshop on Comparative Genomics, RECOMB-CG'2010 (Ottawa, Canada,*

October 9-11, 2010), volume 6398 of *LNCS/LNBI*, pages 121–136. Springer-Verlag, Berlin-Heidelberg, 2010.