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List of Publications

Journal Articles

1. Zahra Tayebi, Sarwan Ali, and Murray Patterson. Robust representation and efficient feature selection allows for effective clustering of SARS-CoV-2 variants. *Algorithms*, 2021. doi:10.3390/a14120348.

2. Sarwan Ali, Simone Ciccolella, Lorenzo Lucarella, Gianluca Della Vedova, and Murray Patterson. Simpler and faster development of tumor phylogeny pipelines. *Journal of Computational Biology*, 28(11):1142–1155, 2021. doi:10.1089/cmb.2021.0271.

3. Andrew Melnyk, Fatemeh Mohebbi, Sergey Knyazev, Bikram Sahoo, Roya Hosseini, Pavel Skums, Alex Zelikovsky*, and Murray Patterson*. From alpha to zeta: Identifying variants and subtypes of SARS-CoV-2 via clustering. *Journal of Computational Biology*, 28(11):1113–1129, 2021. doi:10.1089/cmb.2021.0302.

4. Simone Ciccolella*, Murray Patterson*, Paola Bonizzoni, and Gianluca Della Vedova. Effective clustering for single cell sequencing cancer data. *IEEE Journal of Biomedical and Health Informatics*, 25(11):4068–4078, 2021. doi:10.1109/JBHI.2021.3081380.

5. Simone Ciccolella, Mauricio Soto, Murray D. Patterson, Gianluca Della Vedova, Iman Hajirasouliha, and Paola Bonizzoni. Gpps: An ILP-based approach for inferring cancer progression with mutation losses from single cell data. *BMC Bioinformatics*, 2020. doi:10.1186/s12859-020-03736-7.

6. Simone Ciccolella, Camir Ricketts, Mauricio Soto Gomez, Murray Patterson, Dana Silverbush, Paola Bonizzoni, Iman Hajirasouliha, and Gianluca Della Vedova. Inferring cancer progression from single-cell sequencing while allowing mutation losses. *Bioinformatics*, 2020. doi:10.1093/bioinformatics/btaa722.

7. Raffaella Rizzi, Stefano Beretta, Murray Patterson, Yuri Pirola, Marco Previtali, Gianluca Della Vedova, and Paola Bonizzoni. Overlap graphs and de Bruijn graphs: data structures for de novo genome assembly in the big data era. *Quantitative Biology*, 7(4):278–292, 2019. doi:10.1007/s40484-019-0181-x.

8. Stefano Beretta*, Murray Patterson*, Simone Zaccaria, Gianluca Della Vedova, and Paola Bonizzoni. HapCHAT: Adaptive haplotype assembly for efficiently leveraging high coverage in long reads. *BMC Bioinformatics*, 2018. doi:10.1186/s12859-018-2253-8.

9. Wandrille Duchemin, Yoann Anselmetti, Murray Patterson, Yann Ponty, Sèverine Bérard, Cedric Chauve, Celine Scornavacca, Vincent Daubin, and Eric Tannier. DeCoSTAR: Reconstructing the ancestral organization of genes or genomes using reconciled phylogenies. *Genome Biology and Evolution*, 9(5):1312–1319, 2017. doi:10.1093/gbe/evx069.

10. Andrea Bracciali, Marco Aldinucci, Murray Patterson, Tobias Marschall, Nadia Pisanti, Ivan Merelli, and Massimo Torquati. PWhatsHap: Efficient haplotyping for future generation sequencing. *BMC Bioinformatics*, 2016. doi:10.1186/s12859-016-1170-y.

11. Murray Patterson*, Tobias Marschall*, Nadia Pisanti, Leo van Iersel, Leen Stougie, Gunnar W. Klau[†], and Alexander Schonhuth[†]. WhatsHap: Weighted haplotype assembly for future-generation sequencing reads. *Journal of Computational Biology*, 22(6):498–509, 2015. doi:10.1089/cmb.2014.0157.

12. Murray Patterson, Gergely Szöllősi, Vincent Daubin, and Eric Tannier. Lateral gene transfer, rearrangement, reconciliation. *BMC Bioinformatics*, 2013. doi:10.1186/1471-2105-14-S15-S4.

13. Mohammed El-Kebir*, Tobias Marschall*, Inken Wohlers*, Murray Patterson, Jaap Heringa, Alexander Schönhuth, and Gunnar W. Klau. Mapping proteins in the presence of paralogs using units of coevolution. *BMC Bioinformatics*, 2013. doi:10.1186/1471-2105-14-S15-S18.

14. Ján Maňuch*, Murray Patterson*, Roland Wittler*, Cedric Chauve, and Eric Tannier. Linearization of ancestral multichromosomal genomes. *BMC Bioinformatics*, 2012. doi:10.1186/1471-2105-13-S19-S11.

15. Ján Maňuch*, Murray Patterson*, and Cedric Chauve. Hardness results on the gapped consecutive-ones property problem. *Discrete Applied Mathematics*, 160(18):2760–2768, 2012. doi:10.1016/j.dam.2012.03.019.

16. Ján Maňuch* and Murray Patterson*. The complexity of the gapped consecutive-ones property problem for matrices of bounded maximum degree. *Journal of Computational Biology*, 18(9):1243–1253, 2011. doi:10.1089/cmb.2011.0128.

17. Roland Wittler, Ján Maňuch*, Murray Patterson*, and Jens Stoye. Consistency of sequence-based gene clusters. *Journal of Computational Biology*, 18(9):1023–1039, 2011. doi:10.1089/cmb.2011.0083.

Conference Proceedings

18. Sarwan Ali, Bikram Sahoo, Naimat Ullah, Alex Zelikovsky, Murray Patterson*, and Imdadullah Khan. A k-mer based approach for SARS-CoV-2 variant identification. In *the 17th International Symposium on Bioinformatics Research and Applications (ISBRA, Shenzhen, China, 2021)*, volume 13064 of LNCS, 153–164. 2021. doi:10.1007/978-3-030-91415-8_14.

19. Brendan Smith, Cristian Navarro-Martinez, Rebecca Buonopane, S. Ashley Byun*, and Murray Patterson*. Correlated evolution in the small parsimony framework. In *the 17th International Symposium on Bioinformatics Research and Applications (ISBRA, Shenzhen, China, 2021)*, volume 13064 of LNCS, 608–619. 2021. doi:10.1007/978-3-030-91415-8_51.

20. Sarwan Ali and Murray Patterson. Spike2Vec: An efficient and scalable embedding approach for COVID-19 spike sequences. In *the 2021 IEEE International Conference on Big Data (IEEE BigData, Virtual Conference, 2021)*, 1533–1530. 2021. doi:10.1109/BigData52589.2021.9671848.

21. Sarwan Ali, Tamkanat-E-Ali, Muhammad Asad Khan, Imdadullah Khan, and Murray Patterson. Effective and scalable clustering of SARS-CoV-2 sequences. In *the 5th International Conference on Big Data Research (ICBDR, Virtual Conference, 2021)*. 2021. to appear.

22. Andrew Melnyk, Fatemeh Mohebbi, Sergey Knyazev, Bikram Sahoo, Roya Hosseini, Pavel Skums, Alex Zelikovsky*, and Murray Patterson*. Clustering based identification of SARS-CoV-2 subtypes. In *the 10th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS, Virtual Conference, 2020)*, volume 12686 of LNCS, 127–141. 2021. doi:10.1007/978-3-030-79290-9_11.

23. Simone Ciccolella*, Murray Patterson*, Paola Bonizzoni, and Gianluca Della Vedova. Effective clustering for single cell sequencing cancer data. In *the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB, Niagara Falls, NY, USA, 2019)*, ACM, 437–446. 2019. doi:10.1145/3307339.3342149.

24. Giulia Bernardini*, Paola Bonizzoni*, Gianluca Della Vedova*, and Murray Patterson*. A rearrangement distance for fully-labelled trees. In *the 30th Annual Symposium on Combinatorial Pattern Matching (CPM, Pisa, Italy, 2019)*, volume 128 of LIPIcs, 1–15. 2019. doi:10.4230/LIPIcs.CPM.2019.28.

25. Gianluca Della Vedova*, Murray Patterson*, Raffaella Rizzi*, and Mauricio Soto*. Character-based phylogeny construction and its application to tumor evolution. In *the 13th Conference on Computability in Europe (CiE, Turku, Finland, 2017)*, volume 10307 of LNCS, 3–13. 2017. doi:10.1007/978-3-319-58741-7_1.

26. Marco Aldinucci, Andrea Bracciali, Tobias Marschall, Murray Patterson, Nadia Pisanti, and Massimo Torquati. High-performance haplotype assembly. In *the 11th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics (CIBB, Cambridge, UK, 2014)*, volume 8623 of LNCS, 245–258. 2015. doi:10.1007/978-3-319-24462-4_21.

27. Murray Patterson*, Tobias Marschall*, Nadia Pisanti, Leo van Iersel, Leen Stougie, Gunnar W. Klau†, and Alexander Schönhuth†. WhatsHap: Haplotype assembly for future-generation sequencing reads. In *the 18th Annual International Conference on Research in Computational Molecular Biology (RECOMB, Pittsburgh PA, USA, 2014)*, volume 8394 of LNCS, 237–249. 2014. doi:10.1007/978-3-319-05269-4_19.

28. Cedric Chauve*, Murray Patterson*, and Ashok Rajaraman*. Hypergraph covering problems motivated by genome assembly questions. In *the International Workshop on Combinatorial Algorithms (IWOCA, Rouen, France, 2013)*, volume 8288 of LNCS, 428–432. 2013. doi:10.1007/978-3-642-45278-9_37.

29. Cedric Chauve*, Ján Maňuch*, Murray Patterson*, and Roland Wittler*. Tractability results for the consecutive-ones property with multiplicity. In *the 22nd Annual Symposium on Combinatorial Pattern Matching (CPM, Palermo, Italy, 2011)*, volume 6661 of LNCS, 90–103. 2011. doi:10.1007/978-3-642-21458-5_10.

30. Ján Maňuch*, Murray Patterson*, and Arvind Gupta. Towards a characterization of the generalized cladistic character compatibility problem for non-branching character trees. In *the 7th International Symposium on Bioinformatics Research and Applications (ISBRA, Changsha, China, 2011)*, volume 6674 of LNCS, 440–451. 2011.

31. Ján Maňuch*, Murray Patterson*, Sheung-Hung Poon*, and Chris Thachuk*. Complexity of finding non-planar rectilinear drawings of graphs. In *the 18th International Symposium on Graph Drawing (GD, Konstanz, Germany, 2010)*, volume 6502 of LNCS, 305–316. 2010. doi:10.1007/978-3-642-18469-7_28.

32. Cedric Chauve*, Ján Maňuch*, and Murray Patterson*. On the gapped consecutive-ones property. In *the European Conference on Combinatorics, Graph Theory and Applications (EuroComb, Bordeaux, France, 2009)*, volume 34 of ENDM, 121–125. 2009. doi:10.1016/j.endm.2009.07.020.

33. Ján Maňuch*, Murray Patterson*, and Arvind Gupta. On the generalised character compatibility problem for non-branching character trees. In *the 15th Annual International Computing and Combinatorics Conference (COCOON, Niagara Falls, USA, 2009)*, volume 5609 of LNCS, 268–276. 2009. doi:10.1007/978-3-642-02882-3_27.

34. Murray Patterson, Yongmei Liu, Eugenia Ternovska, and Arvind Gupta. Grounding for model expansion in k-guarded formulas with inductive definitions. In *the 20th International Joint Conferences on Artificial Intelligence (IJCAI, Hyderabad, India, 2007)*, 161–166. 2007.

note In any publication listing containing a *, this indicates that all authors whose names are followed by a * have contributed equally to this publication. In order to be consistent, this means that for papers that list the names of authors alphabetically (which is a common practice amongst computer science and theoretical bioinformatics papers), there is a * following every name.