

# Bibliografia

- [1] Christina Boucher et al. *Computing the original eBWT faster, simpler, and with less memory*. 2021. arXiv: 2106.11191 [cs.DS]. URL: <https://arxiv.org/abs/2106.11191>.
- [2] Christina Boucher et al. “PFP Compressed Suffix Trees”. In: *Proceedings of the SIAM Symposium on Algorithm Engineering and Experiments (ALENEX)*. 2021.
- [3] Christina Boucher et al. “Prefix-free parsing for building big BWTs”. In: *Algorithms for Molecular Biology* 14.1 (mag. 2019), p. 13. ISSN: 1748-7188. DOI: 10.1186/s13015-019-0148-5. URL: <https://doi.org/10.1186/s13015-019-0148-5>.
- [4] Michael Burrows et al. “A Block-sorting Lossless Data Compression Algorithm”. In: 1994. URL: <https://api.semanticscholar.org/CorpusID:2167441>.
- [5] Davide Cenzato e Massimiliano Rossi. *PFP-eBWT*. 2021. URL: <https://github.com/davidecenzato/PFP-eBWT>.
- [6] Madeline A. Crosby et al. “FlyBase: genomes by the dozen”. In: *Nucleic Acids Research* 35.suppl\_1 (nov. 2006), pp. D486–D491. ISSN: 0305-1048. DOI: 10.1093/nar/gkl827. eprint: [https://academic.oup.com/nar/article-pdf/35/suppl\\_1/D486/3834834/gkl827.pdf](https://academic.oup.com/nar/article-pdf/35/suppl_1/D486/3834834/gkl827.pdf). URL: <https://doi.org/10.1093/nar/gkl827>.
- [7] Paolo Ferragina e Giovanni Manzini. “Indexing compressed text”. In: *Journal of the ACM (JACM)* 52.4 (2005), pp. 552–581.
- [8] Christoph Fischer et al. “Complete Mitochondrial DNA Sequences of the Threadfin Cichlid (*Petrochromis trewavasae*) and the Blunthead Cichlid (*Tropheus moorii*) and Patterns of Mitochondrial Genome Evolution in Cichlid Fishes”. In: *PloS one* 8 (ago. 2013), e67048. DOI: 10.1371/journal.pone.0067048.
- [9] Travis Gagie, Gonzalo Navarro e Nicola Prezza. “Fully functional suffix trees and optimal text searching in BWT-runs bounded space”. In: *Journal of the ACM (JACM)* 67.1 (2020), pp. 1–54.

- [10] Travis Gagie, Gonzalo Navarro e Nicola Prezza. “Optimal-time text indexing in BWT-runs bounded space”. In: *Proceedings of the Twenty-Ninth Annual ACM-SIAM Symposium on Discrete Algorithms*. SIAM. 2018, pp. 1459–1477.
- [11] Veronica Guerrini, Felipe A. Louza e Giovanna Rosone. “Metagenomic analysis through the extended Burrows-Wheeler transform”. In: *BMC Bioinformatics* 21.8 (2020), p. 299. ISSN: 1471-2105. DOI: 10.1186/s12859-020-03628-w. URL: <https://doi.org/10.1186/s12859-020-03628-w>.
- [12] Veronica Guerrini et al. “phyBWT2: phylogeny reconstruction via eBWT positional clustering”. In: *Algorithms for Molecular Biology* 18.1 (ago. 2023), p. 11.
- [13] Ivica Letunic e Peer Bork. “Interactive Tree of Life (iTOL) v6: recent updates to the phylogenetic tree display and annotation tool”. In: *Nucleic Acids Research* 52.W1 (apr. 2024), W78–W82. ISSN: 0305-1048. DOI: 10.1093/nar/gkae268. eprint: <https://academic.oup.com/nar/article-pdf/52/W1/W78/58435928/gkae268.pdf>. URL: <https://doi.org/10.1093/nar/gkae268>.
- [14] Felipe A. Louza, Simon Gog e Guilherme P. Telles. “Inducing enhanced suffix arrays for string collections”. In: *Theoretical Computer Science* 678 (2017), pp. 22–39. ISSN: 0304-3975. DOI: <https://doi.org/10.1016/j.tcs.2017.03.039>. URL: <https://www.sciencedirect.com/science/article/pii/S0304397517302621>.
- [15] S Mantaci et al. “A New Combinatorial Approach to Sequence Comparison”. In: *Theory of Computing Systems* 42.3 (apr. 2008), pp. 411–429.
- [16] S. Mantaci et al. “An extension of the Burrows–Wheeler Transform”. In: *Theoretical Computer Science* 387.3 (2007). The Burrows-Wheeler Transform, pp. 298–312. ISSN: 0304-3975. DOI: <https://doi.org/10.1016/j.tcs.2007.07.014>. URL: <https://www.sciencedirect.com/science/article/pii/S0304397507005282>.
- [17] Sabrina Mantaci, Antonio Restivo e Marinella Sciortino. “Distance measures for biological sequences: Some recent approaches”. In: *International Journal of Approximate Reasoning* 47.1 (2008). Approximate Reasoning and Machine Learning for Bioinformatics, pp. 109–124. ISSN: 0888-613X. DOI: <https://doi.org/10.1016/j.ijar.2007.03.011>. URL: <https://www.sciencedirect.com/science/article/pii/S0888613X07000382>.
- [18] Sabrina Mantaci et al. “An Extension of the Burrows Wheeler Transform and Applications to Sequence Comparison and Data Compression”. In: *Combinatorial Pattern Matching*. A cura di Alberto Apostolico, Maxime Crochemore e Kunsoo Park. Berlin, Heidelberg: Springer Berlin Heidelberg, 2005, pp. 178–189. ISBN: 978-3-540-31562-9.

- [19] Ge Nong. “Practical Linear-Time  $O(1)$ -Workspace Suffix Sorting for Constant Alphabets”. In: *ACM Transactions on Information Systems (TOIS)* 31 (lug. 2013). DOI: 10.1145/2493175.2493180.
- [20] Ge Nong, Sen Zhang e Wai Hong Chan. “Two Efficient Algorithms for Linear Time Suffix Array Construction”. In: *IEEE Transactions on Computers* 60.10 (2011), pp. 1471–1484. DOI: 10.1109/TC.2010.188.
- [21] *PHYLIP*. URL: <https://phylipweb.github.io/phylip/> (visitato il giorno 12/09/2024).
- [22] N Saitou e M Nei. “The neighbor-joining method: a new method for reconstructing phylogenetic trees.” In: *Molecular Biology and Evolution* 4.4 (lug. 1987), pp. 406–425. ISSN: 0737-4038. DOI: 10.1093/oxfordjournals.molbev.a040454. eprint: <https://academic.oup.com/mbe/article-pdf/4/4/406/11167444/7sait.pdf>. URL: <https://doi.org/10.1093/oxfordjournals.molbev.a040454>.
- [23] Martin Simonsen. *rapidNJ*. 2020. URL: <https://github.com/somme89/rapidNJ>.
- [24] Xiaomeng Wu et al. “Nucleotide composition string selection in HIV-1 subtyping using whole genomes”. In: *Bioinformatics* 23.14 (mag. 2007), pp. 1744–1752. ISSN: 1367-4803. DOI: 10.1093/bioinformatics/btm248. eprint: [https://academic.oup.com/bioinformatics/article-pdf/23/14/1744/49813204/bioinformatics\\\_23\\\_14\\\_1744.pdf](https://academic.oup.com/bioinformatics/article-pdf/23/14/1744/49813204/bioinformatics\_23\_14\_1744.pdf). URL: <https://doi.org/10.1093/bioinformatics/btm248>.
- [25] Lianping Yang, Xiangde Zhang e Tianming Wang. “The Burrows–Wheeler similarity distribution between biological sequences based on Burrows–Wheeler transform”. In: *Journal of Theoretical Biology* 262.4 (2010), pp. 742–749. ISSN: 0022-5193. DOI: <https://doi.org/10.1016/j.jtbi.2009.10.033>. URL: <https://www.sciencedirect.com/science/article/pii/S0022519309005220>.
- [26] Andrzej Zielezinski et al. “Alignment-free sequence comparison: benefits, applications, and tools”. In: *Genome Biology* 18.1 (ott. 2017), p. 186.
- [27] Andrzej Zielezinski et al. “Benchmarking of alignment-free sequence comparison methods”. In: *Genome Biology* 20.1 (2019), p. 144. ISSN: 1474-760X. DOI: 10.1186/s13059-019-1755-7. URL: <https://doi.org/10.1186/s13059-019-1755-7>.