

are described. The first one, denoted eBWT, is defined on multisets of strings and allows to establish a bijection between the multiset of conjugacy classes of strings and all the strings on a given alphabet, with interesting theoretical and applicative implications. The second variant, denoted ABWT, uses a different order (called alternating order) to sort the cyclic rotations of a string. It is interesting to note that the ABWT preserves many combinatorial and mathematical properties of the BWT and it can be used as a compressed index in the same way as the BWT.

3.11 BWT / eBWT similarity

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Joint work of Giovanna Rosone, Veronica Guerrini, Sabrina Mantaci, Marinella Sciortino, Antonio Restivo

Main reference Sabrina Mantaci, Antonio Restivo, Giovanna Rosone, Marinella Sciortino: “A New Combinatorial Approach to Sequence Comparison”, *Theory Comput. Syst.*, Vol. 42(3), pp. 411–429, 2008.

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Sequence comparison has become a very essential tool in modern molecular biology. In fact, in biomolecular sequences high similarity usually implies significant functional or structural similarity. Traditional approaches use techniques that are based on sequence alignment able to measure character level differences. Here, we describe some similarity measures, alignment-free, based on the Burrows-Wheeler transform with several application in bioinformatics, such as the metagenomic problem.

3.12 Searching Patterns in the Bijective BWT

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Joint work of Hideo Bannai, Juha Kärkkäinen, Dominik Köppl, Marcin Piatkowski

Main reference Hideo Bannai, Juha Kärkkäinen, Dominik Köppl, Marcin Piatkowski: “Indexing the Bijective BWT”, in *Proc. of the 30th Annual Symposium on Combinatorial Pattern Matching, CPM 2019*, June 18-20, 2019, Pisa, Italy., *LIPICs*, Vol. 128, pp. 17:1–17:14, Schloss Dagstuhl – Leibniz-Zentrum fuer Informatik, 2019.

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We present an index data structure for the bijective Burrows-Wheeler transform [1]. The index data structure is based on the FM index [2]. Like the FM index, it reports the suffix array interval of all pattern occurrences by means of backward searches.

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