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Constructing Orthogonal De Bruijn and Kautz Sequences and Applications

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Abstract : A de Bruijn graph of order k is a graph whose vertices representing all length-k sequences with edges joining pairs of vertices whose sequences have maximum possible overlap (length k−1). Every Hamiltonian cycle of this graph defines a distinct, minimum length de Bruijn sequence containing all k-mers exactly once. A Kautz sequence is the minimal generating sequence so as the sequence of minimal length that produces all possible length-k sequences with the restriction that every two consecutive alphabets in the sequences must be different. A collection of de Bruijn/Kautz sequences are orthogonal if any two sequences are of maximally differ in sequence composition; that is, the maximum length of their common substring is k. In this paper, we discuss how such a collection of (maximal) orthogonal de Bruijn/Kautz sequences can be made and use the algorithm to build up a web application service for the synthesized DNA and other related biomolecular sequences.

Keywords : biomolecular sequence synthesis, de Bruijn sequences, Eulerian cycle, Hamiltonian cycle, Kautz sequences, orthogonal sequences
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