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SIMILARITY STUDIES OF VIRAL GENOME SEQUENCES

Abstract:

The aim of the research is to develop new bioinformatics methods known in the literature as Graphical Representation Methods [1]. The presented approach facilitates the construction of algorithms for calculating numerical values characterizing DNA/RNA sequences. It allows for the analysis of the similarity/dissimilarity of the considered objects. A method for comparing DNA/RNA sequences, which we called 3D-Dynamic Representation of DNA/RNA Sequences [2], was obtained as a generalization of our 2D approach [3]. The basic ideas are taken from classical mechanics: biological sequences are represented by sets of "material points" in 2D or 3D spaces. Using this non-standard approach, we achieved the highest possible accuracy: you can recognize the difference between sequences that differ by only one nucleobase. We can also indicate the type of this nucleobase and its approximate location. An example of the method's application is the characterization of the viral genome sequence. The classification diagrams obtained by this method create a new mathematical description of the time evolution of the Zika virus genome sequence [3].

References:

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computational biology, bioinformatics, graphical representation methods