New applications of the 2D-Dynamic Representation of DNA/RNA Sequences

Damian Panas[1], Piotr Wąż[2], Dorota Bielińska-Wąż[1]

[1] Department of Radiological Informatics and Statistics, Medical University of Gdańsk, Tuwima 15, 80-210 Gdańsk, Poland
dpanas@gumed.edu.pl, djwaz@gumed.edu.pl

[2] Department of Nuclear Medicine, Medical University of Gdańsk, Tuwima 15, 80-210 Gdańsk, Poland
phwaz@gumed.edu.pl

Keywords: alignment-free methods, similarity analysis of DNA/RNA sequences.

New applications of the 2D-dynamic representation of DNA/RNA sequences are presented [1, 2]. The method provides simple yet powerful tool in genomic analysis. Its core idea consists on mapping nucleobases to unit vectors. Cytosine, for example, is mapped to (0,1), adenine to (-1,0), guanine to (1,0) and thymine to (0,-1). The sequence is represented by a set of material points in a 2D-space, called by us 2D-dynamic graph. The main idea of the method is borrowed from the classical mechanics: we treat the 2D-dynamic graph as a rigid body and characterize it by the quantities met in this area, such as the coordinates of the centers of mass or the moments of inertia.

The method has been applied to the characterization of the Zika virus [1] and to the influenza viruses [2].

In particular, the conclusion is that the descriptors i.e. numerical values characterizing the graph, can be also applied in predictive analysis (with over 90% accuracy of predicting subtype of the influenza A virus) [2]. One can therefore find 2D-dynamic representation efficient and easy to apply, even to ambitious challenges such as the identification of unknown viruses.

References

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[2] D. Panas, P. Wąż, D. Bielińska-Wąż, A. Nandy, S.C Basak, An application of the 2D-Dynamic Representation of DNA/RNA Sequences to the prediction of influenza A virus subtypes, under review.