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DOROTA BIELIŃSKA-WĄŻ

Medical University of Gdańsk, Poland

PIOTR WĄŻ

Medical University of Gdańsk, Poland

NON-STANDARD BIOINFORMATICS ANALYSIS OF SARS-COV-2 VIRUS

Abstract:

A broad branch of bioinformatics are "alignment-free" computational methods combining ideas from various fields of science [1]. They often offer graphical and numerical tools for comparing biological sequences. The applications of alignment-free methods are wide. Each method reveals different aspects of sequence similarity. A variety of accurate approaches are of particular potential importance in medical sciences, for example in the bioinformatics characterization of viruses. In this work, we review the method we introduced, called 4D-Dynamic Representations of DNA/RNA Sequences [2,3]. This approach implements concepts and ideas originally developed in classical dynamics. The distribution of point clusters that appeared on our classification maps supports the hypothesis that SARS-CoV-2 virus could have originated from a bat and a pangolin [2].

References:

- [1]. N. Ramanathan, J. Ramamurthy, G. Natarajan, Numerical Characterization of DNA Sequences for Alignment-free Sequence Comparison - A Review, *Combinatorial Chemistry & High Throughput Screening* 25 (2022), pp. 365-380.
- [2]. D. Bielińska-Wąż, P. Wąż, Non-standard bioinformatics characterization of SARS-CoV-2, *Computers in Biology and Medicine* 131 (2021) Art. No. 104247.
- [3]. D. Bielińska-Wąż, P. Wąż, A. Lass, J. Karamon, 4D-Dynamic Representation of DNA/RNA Sequences: Studies on Genetic Diversity of *Echinococcus Multilocularis* in Red Foxes in Poland, *Life* 12 (2022) Art. No. 877.

Keywords:

Bioinformatics, Alignment-free methods, SARS-CoV-2