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Milica Matavulj
University of Novi Sad, Faculty of Science, Department of Biology and Ecology,
Trg D. Obradovića 2, 21000 Novi Sad, Serbia, milica. matavulj @dbe.uns.ac.rs

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Department of Biology and Ecology
Faculty of Sciences
University of Novi Sad
Trg Dositeja Obradovića 2
21000 Novi Sad, Serbia
: +381 21 485 26 59
: +381 21 450 620
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+381/21/499-461, +381/21/499-088
sajnosns@gmail.com

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Department of Biology and Ecology
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University of Novi Sad

New age for alignment-free methods for sequence analyses

Vladimir Perovic, Branislava Gemovic and Nevena Veljkovic*

Laboratory for bioinformatics and computational chemistry, VINCA Institute of Nuclear Sciences, University of Belgrade, National Institute of the Republic of Serbia

Abstract:
Progress in a wide range of fields ranging from population genetics to precision medicine may be attributed to availability of big biological data. Alignment-free sequence comparison is the methodology of choice in data-intensive applications given that it is significantly faster and requires less resources compared to traditional sequence comparison based on pairwise or multiple sequence alignment.
The symbiosis of alignment-free methods with machine learning is a paradigm of new age in bioinformatics, as it ensures the much needed boost to quicken the complex predictions on large datasets, particularly of molecules with low sequence identity.
In this talk, I will present two stories in which I will describe approaches to predict functional consequences of gene variants and imperfect tandem repeats in protein sequences.

*Corresponding author, e-mail: