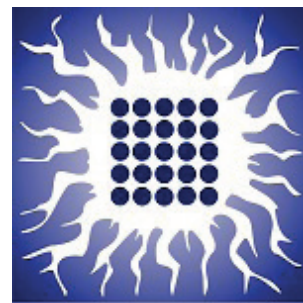


# Biologia Serbica

Department of Biology and Ecology,  
Faculty of Sciences, University of Novi Sad, Serbia



**BELBI 2021**



Book of Abstracts  
Belgrade Bioinformatics Conference 2021  
21-25 June 2021, Vinča, Serbia

# Biologia Serbica

JUNE 2021

Vol. 43 - No. 1 Special Edition

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Biologia Serbica is formerly Review of Research, Faculty of Sciences, Biology Series (1971-2004), published by Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia

## Aim and Scope

Biologia Serbica (BS) is an international scientific, peer-reviewed, open access journal that publishes original research articles, review articles, and short communications in all areas of biology.

## Publisher

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Faculty of Sciences  
University of Novi Sad  
Trg Dositeja Obradovića 2  
21000 Novi Sad, Serbia

☎: +381 21 485 26 59

☎: +381 21 450 620

www.dbe.uns.ac.rs

Biologia Serbica is published biannually.

## Printed by

"Sajnos"

Momčila Tapavice 2,  
21000 Novi Sad  
+381/21/499-461, +381/21/499-088  
sajnosns@gmail.com

Date of publication: June 2018.

## Subscription rates

Instructions available at  
[http://ojs.pmf.uns.ac.rs/index.php/dbe\\_serbica/index](http://ojs.pmf.uns.ac.rs/index.php/dbe_serbica/index)

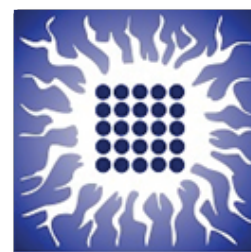
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# Biologia Serbica

Book of Abstracts  
Belgrade BioInformatics Conference 2021

Volume 43 - No. 1  
(Special Edition)  
2021



Department of Biology and Ecology  
Faculty of Sciences  
University of Novi Sad

## New age for alignment-free methods for sequence analyses

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### **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.

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