Vol. 43 - No. 1 Special Edition 2021

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

http://ojs.pmf.uns.ac.rs/index.php/dbe_serbica/index

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

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
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 od publication: June 2018.

Subscription rates

Instructions available at
http://ojs.pmf.uns.ac.rs/index.php/dbe_serbica/index

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ISSN 2334-6590

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

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PREFACE

The Belgrade Bioinformatics conference is a biennial event since 2016. This year, we are hosting the third **Belgrade Bioinformatics 2021 conference – BelBI2021**. The aim of the BelBI2021 is to provide a forum for exchange of knowledge and new ideas between scientists in the field, as well as, to include young scientists in this process and provide educational opportunities for them. Previously, we had the pleasure to welcome participants in Belgrade, but the situation with COVID-19 pandemia during 2020. made us postpone our conference and hold it this year as a virtual event. Nevertheless, the research presented in the abstracts available in this book is outstanding and it was an honor to edit it.

Several research institutions, faculties and scientific societies from Serbia have joined their forces to organize this international conference focused on different aspects of bioinformatics. Four Universities participated in the organization – Universities of Belgrade, Novi Sad, Niš and Kragujevac. The Conference is organized by the Vinča Institute of Nuclear Sciences – National Institute of the Republic of Serbia, University of Belgrade, as the the main organizer, and Faculty of Mathematics, University of Belgrade, Faculty of Biology, University of Belgrade, Institute of Molecular Genetics and Genetic Engineering University of Belgrade, Mathematical Institute of SASA and Serbian Society for Bioinformatics and Computational Biology, as co-organizing institutions, in cooperation with several other institutions and societies from Serbia.

This Book of Abstracts covers a wide range of various topics in bioinformatics, including Big data analytics, Machine learning in biological data analysis, Biological networks, Data mining methods and their applications in biology and medicine, Protein structure and function prediction, and much more. Special session of the BelBI2021 is dedicated to the bioinformatics in the field of COVID-19 analysis, which emerged as an immensely important research topic during the previous year, and these abstracts are also included in this book.

The Book of Abstract is printed as a Special Issue of Biologia Serbica, a journal published by the Faculty of Sciences, Department of Biology, University of Novi Sad, one of the Conference co-organizes, and thus, I would like to thank Prof. Željko D. Popović, Managing Editor, for all his effort to bring this enormous work successfully to the finish.

I would like to thank all members of the International Advisory, the International Program and the Local Organizing Committees for their efforts and help to make this event successful. Also, on behalf of the Local Organizing Committee, I would like to express my deepest gratitude to all attendees, and especially to all presenters for their interesting and much appreciated talks. In addition, we owe many thanks to the Ministry of Education, Science and Technological Development of the Republic of Serbia, as well as to the International Centre for Genetic Engineering and Biotechnology (ICGEB) that supported attendance of many students and early stage researchers. Also, the Local Organizing Committee is very grateful to all Conference's sponsors and donors, especially Factory World Wide d.o.o. and Seven Bridges Genomics, with the hope that they will be with us for many years to come.

This book contains 101 abstracts of presentations at the third Belgrade Bioinformatics 2021 conference – BelBI2021. Authors from 21 countries from almost all continents will present their work at the conference. There will be six keynote lectures, forty one invited lectures, twenty seven contributed talks and thirty two poster presentations.

Belgrade, June 2021.
Branislava Gemović
On behalf of BelBI2021

Bioinformatics analysis of eukaryotic positively oriented single stranded RNA viruses

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Abstract

Positively oriented single stranded RNA viruses [ssRNA(+)] persistently affect health and well-being of all eukaryotes, including plants, animals and humans (i.e. SARS-CoV-2, yellow fever, hepatitis C, zika, West Nile, pepper mild mottle virus, etc.). How come these viruses are so wide spread and hard to eradicate? Besides their high changeability, another major reason is their ability to mimic host processes upon entering the host. Only recently it was revealed that ssRNA(+) viruses undergo methylation inside the host in the process that is similar to the methylation of the hosts' own mRNAs. Such process may enable or disable virus to avoid some of the host's defense mechanisms, but it inevitably impacts viral stability and fitness.

Studies on this topic have only started, opening even more questions, with major ones being: how ssRNA(+) methylation, that occurs in the host, impacts viral pathogenicity and are these methylation patterns different in different hosts and for different ssRNA(+) viruses or do these viral methylomes share more universal pattern in concordance with their similar genome organization? Among numerous different methylation patterns of RNA, this research focused on N6-methyladenosine (m6A), as the most common and abundant methylation in eukaryotes, which was confirmed to be present in ssRNA(+) viruses as well.

This study searched for patterns in the primary sequences and secondary structures of ssRNA(+) that are associated to m6A methylation sites relying on the experimentally obtained m6A datasets for eukaryotes and eukaryotic ssRNA(+) viruses. The results are discussed in view of datasets characteristics and study approach.

Keywords:

bioinformatics, m6A, methylome pattern, single stranded RNA viruses, ssRNA(+)

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CIP – Каталогизација у публикацији
Библиотека Матице српске, Нови Сад 57
BIOLOGIA Serbica / editor-in chief Milica Matavulj. –
Vol. 34, no. ½ (dec. 2012) - . – Novi Sad : Faculty of Sciences, Department of Biology and Ecology, 2012-. –
Ilustr. ; 28 cm
Dva puta godišnje. – Je nastavak: Зборник радова Природно-математичког факултета. Серија за биологију = ISSN 0352 – 1788
ISSN 2334 – 6590 = Biologia Serbica
COBISS.SR – ID 275725831

ISSN 2334-6590

2021
Vol. 43 - No. 1 Special Edition

Biologia Serbica

ISSN 2334-6590