

#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

HYBRID • 19 - 23 JUNE 2023

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ISBN: 978-86-82679-14-1

belbi.bg.ac.rs

Title	4 th Belgrade Bioinformatics Conference BOOK OF ABSTRACTS
Publisher	Institute of Molecular Genetics and Genetic Engineering, University of Belgrade Vojvode Stepe 444a, Belgrade, Serbia https://www.imgge.bg.ac.rs/
Editors	dr. Ivana Morić dr. Valentina Đorđević
Technical editor	Dušan Radojević
ISBN	978-86-82679-14-1
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FOREWORD

Dear colleagues and friends,

The 4th Belgrade Bioinformatics Conference - BelBi2023, where many high-quality scientific contributions were presented, has just ended. With great thanks to all participants, we now proudly present a book of abstracts that both reflects the scientific abundance and diversity of the conference and serves as a reminder of a memorable event.

Several research institutions, faculties, and scientific societies from Serbia joined forces in organizing this international conference, which covered numerous topics in computational biology, bioinformatics, and biomedical and health informatics. The main goal of BelBi2023 was to foster contact between scientists, both early stage career and senior researchers, allowing them to share experiences and latest advances in their fields. We sincerely hope that BelBi2023 has served as a platform for researchers from around the world to meet, initiate new collaborations, and expand professional contacts, and that all of you would become a part of the growing BelBi community.

We are grateful and proud to have welcomed more than 250 researchers from 21 countries. We have had 28 scientific sessions, consisting of more than 60 lectures (including eight Keynote talks), 47 presented posters, as well as three workshops and one satellite event – COST action. We have also organized seven industry lectures, including the NGS Challenge,

two Meet the Expert Sessions, and one Business Coffee Break where ten start-up companies took part. And finally, the future BIO4 campus was presented and first panel on Serbia's resources for storage and analyses of genetic data was organized.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help in making this event a success. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, SAIGE project, and UNDP-Serbia for their support. Finally, the Local Organizing Committee is very grateful to all the sponsors of the conference - BGI, Illumina & Elta'90MS, PacBio & East Diagnostics, ThermoFisher Scientific & Vivogen, Huawei, Labena, DSP Chromatography, RNIDS, Telekom Srbija, Alfa Genetics, Kefo and Superlab, hoping that they will stay with us for many years to come.

Looking forward to seeing you again at the 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

Dr. Valentina Đorđević
& *Dr. Ivana Morić,*
On behalf of BelBi2023
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Oral presentation

Machine learning approach in inferring main population-level COVID-19 risk factors

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Machine-learning methods have become indispensable in scientific research as the amount of available data has grown exponentially in recent years. It is, thus, necessary to employ various unsupervised and supervised machine learning methods to uncover the main determinants of COVID-19 transmissibility and severity in the population. Upon introducing appropriate disease transmissibility and severity measures and gathering relevant socio-demographic, environmental, and health-related data for the countries with obtained said measures, we implement several machine-learning-based approaches to select the most prominent drivers of disease transmissibility and severity. These approaches include regularization-based linear regression models and more advanced Random Forest and Gradient Boost methods, which are not limited to the linear relationships between the features and the response. Principal component analysis was used for preselection to avoid overfitting, where numerous features were considered for a relatively small number of observations (i.e., countries/states). As a result, a broad range of potential COVID-19 risk factors was reduced to several prominent features, selected robustly by different methods - we further untangle how they, directly or indirectly, contribute to the transmissibility and severity of the disease. Our results underscore the evolving nature of COVID-19, from the severity experienced during the first wave to the emergence of new, highly transmissible variants like Omicron. These insights can guide public health interventions, vaccine strategies, and policies aimed at reducing the burden of COVID-19 and effectively managing future waves and emerging variants.

Keywords: COVID-19, machine learning, ecological regression analysis, epidemiological modeling, outburst risk factors

Acknowledgment: This work is supported by the Ministry of Science, Technological Development, and Innovation of the Republic of Serbia.



ISBN: 978-86-82679-14-1