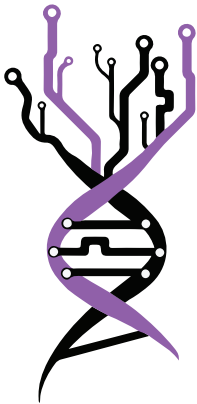


#BelBi2023 • Belgrade, Serbia

# BOOK OF ABSTRACTS



## 4th Belgrade Bioinformatics Conference

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EDITORS

**Dr. Ivana Morić**

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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 5<sup>th</sup> Belgrade Bioinformatics Conference.

Belgrade, July 2023

*Dr. Valentina Đorđević  
& Dr. Ivana Morić,*  
On behalf of BelBi2023  
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## Invited lectures

### Some Applications of Graph-Based Machine Learning Methods on Biological Data

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Machine learning has made considerable contributions to various fields, most notably by providing methods for predictive modeling and data analysis. Usually, different kinds of data are best modeled by specialized machine learning models, tailored to account for the specifics of the data at hand. Graphs are an expressive data representation most suited for representing relationships between objects. The relationships can be interactions, hierarchies, similarities, or others. Such structures can be found in different kinds of data, including biological ones. Luckily, machine learning toolbox abounds with methods suitable for handling these kinds of data and we consider several applications of such graph-based machine learning methods on biological data. First we discuss tree-like hierarchies over the target variable values and the ways to account for such hierarchies in learning. We consider enzyme classification as a suitable application. Then we discuss hierarchies over the target variable values corresponding to directed acyclic graphs and graph neural network as a suitable model for this kind of data. We consider protein function classification as a suitable application. Finally, we discuss construction of similarity graphs over tabular instances, based on autoencoders and graph representation learning ideas. We consider the application of such techniques to the exploratory analysis of biological data related to expression of schizophrenia.

**Keywords:** machine learning, graphs, biological data

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