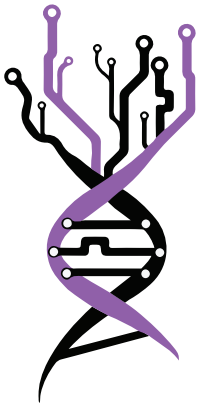


#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



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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 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

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

Can we use biobanks to study infectious diseases?

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Understanding the molecular and environmental basis of diseases in order to improve diagnosis and treatment represent a top priority for researchers. Much of the progress occurred following the growth of various omics technologies and the IT progress in developing large electronic databases capable of storing huge amounts of data. Biobanks represents the most valuable resource for personalized medicine as these are the large collection of various patient samples with well-annotated clinical data which strive to identify possible links between genetic predisposition and disease. A significant step forward are biobanks that are linked to the electronic health records of each participant enabling up-to-date source of relevant medical information and those “deeply phenotyped” for various other omics data, such as microbiome, epigenome, transcriptome, metabolome and proteome.

Since infectious diseases still represent a huge threat to global human health, and host genetic factors have been implied as determining risk factors for observed variations in disease susceptibility, severity, and outcome, during this lecture we will discuss challenges and opportunities of using biobanks as a potential source to study infectious diseases based on the case example of isolated population-based longitudinal biobank “10,001 Dalmatians”. Results of a genome-wide association meta-analyses of 14 different infectious-related phenotypes identified 29 infection-related genetic associations, most belonging to rare variants, all of which have a role in immune response. These findings support the concept that host genetic susceptibility to bacterial and viral infections in adults is polygenic, where common variations have very low explained variance and/or “unfortunate” combinations of numerous rare variants. Expanding our understanding of rare variants may help in the construction of genetic panels which might predict an individual’s lifetime vulnerability to major infectious diseases. Furthermore, longitudinal biobanks are a valuable source of data for discovering host genetic variations involved in infectious disease susceptibility and severity. Because infectious diseases continue to exert selective pressure on our genomes, a global network of biobanks with access to genetic and environmental data is required to further explain complicated mechanisms underlying host-pathogen interactions and infectious disease vulnerability.

Keywords: biobanks, “10,001 Dalmatians”, genome-wide association studies, rare variants, infectious diseases



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