

#BelBi2023 • Belgrade, Serbia

# BOOK OF ABSTRACTS



## 4th Belgrade Bioinformatics Conference

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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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## Keynote lectures

### **A tale of two stories: data-driven precision medicine and precision public health**

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Big Data offers opportunities in health care to refine individuals' characterization and thus complement traditional precision medicine approaches toward individual-targeted prevention, diagnosis and treatment management. Not surprisingly, network theory plays a vital role in modelling Big Data: the higher the number of measurements, the higher the number of potential relationships or dependencies among them. Recent developments have shown the complementary value of personalizing population-based networks for individuals (Menche et al. 2017, Dimitrakopoulos et al. 2018) or deriving individual-specific networks via populations of cells (Gosak et al. 2018, Li et al. 2023).

Individual-specific networks do not necessarily require repeated measurements over time or in space. Reverse-engineered individual-specific networks (Kuijjer et al. 2019) from an aggregate network (hereafter referred to as ISNs) allow for investigating the impact of individual-level network wirings, paths or connectivity on medical decision-making in the individual's interest. Wondering about the utility of these ISNs, we illustrate by example from microbiome and gene co-expression experiments how ISNs give complementary insights in dynamic network biomarker identification and can reveal (genetic modifiers of) co-eQTLs as direct or indirect regulators of gene co-expression.

**Keywords:** individual-specific networks, precision medicine, precision public health, Big Data science

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