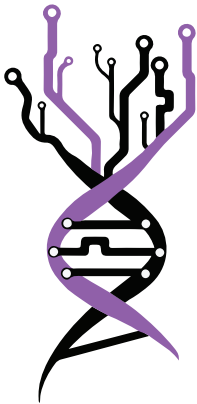


#BelBi2023 • Belgrade, Serbia

# 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

### **The complete solution and interpretation algorithms for large field-of-view and high-resolution spatial transcriptomics**

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The large field-of-view and high-resolution spatial transcriptomics technology can reveal and answer scientific questions that cannot be discovered or elucidated by low-resolution spatial transcriptomics. Obtaining expression profiles at the single-cell level from high-resolution spatial transcriptomics requires sophisticated data processing and interpretation strategies, including extensive image data processing, transcriptome data processing, integration analysis. At the same time, the introduction of spatial information helps with the annotation of single cells at the tissue level and the study of tissue structure and function, while cell clustering and cell annotation are important foundations for subsequent in-depth analysis. Cell annotation can be divided into clustering and re-annotation based on marker genes and end-to-end cell annotation based on reference datasets. The choice between the two depends on whether markers are easier to obtain or whether reference datasets with consistent data backgrounds are easier to obtain. The algorithm team at BGI Research Institute has conducted extensive algorithm research and development on data interpretation strategies, cell clustering algorithms, and cell annotation algorithms for large field-of-view and high-resolution spatial transcriptomics technology, with the aim of providing comprehensive, efficient, and highly reliable data analysis algorithms, tools and platform support.





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