

#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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**Prediction of cell types using single-cell mRNA profiles**

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Single cell transcriptomics is a rapidly growing area with an urgent need for new analytical tools to complement and supersede unsupervised clustering. We defined a new method for deriving gene expression profiles from single-cell gene expression matrices. We named these profiles the "single-cell-derived-class" (SCDC) profiles. We developed SCDC profiles for multiple cell types and subtypes of peripheral blood mononuclear cells (PBMC) using the results of single cell transcriptomics (SCT) experiments. SCDC profiles represent characteristic patterns of gene expressions of the types and subtypes of healthy human PBMC. We studied the reproducibility of SCDC profiles, their robustness, and their applications in classifying healthy human PBMC types and subtypes. SCDC profiles are efficient and convenient tools for the analysis of SCT data derived from PBMC samples. These profiles are highly reproducible, even when derived from unrelated studies, provided that the sample processing steps are comparable and the same SCT technology is used. The classification accuracy of SCDC profiles is high. SCDC profiles can be used for supervised classification and the discovery of new subtypes of PBMC.





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