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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 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

Dr. Valentina Đorđević
& *Dr. Ivana Morić,*
On behalf of BelBi2023
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Poster presentation

Developing bioinformatics pipeline for processing environmental DNA metabarcoding sequencing data

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Environmental DNA (eDNA) is DNA present in an environmental sample, originating from any biological material released from organisms living in that environment. This DNA can be isolated, amplified, sequenced, and analyzed in order to examine the taxonomic richness and abundance of different organism groups in the targeted environment. Methods of eDNA metabarcoding thus offer a unique opportunity to systematically streamline and scale-up regular biological assessments across many different environments of interest. Recently, as a part of the project funded by European structural and investment funds, Labena d.o.o. company established a modern laboratory in Zagreb focused on the research and provision of services in the field of eDNA. In collaboration with the Institute Ruđer Bošković we have been working on developing tests for analysis of water quality based on the eDNA and, as part of the standardization and optimization of sample-to-results eDNA analysis process, we developed a custom bioinformatics pipeline to facilitate efficient and effective eDNA sequencing data analysis.

The pipeline was written in Bash and utilizes several different algorithms to filter, trim, merge, denoise and classify targeted eDNA sequences. Python-based scripts which allow automatically download, filter, and format the data available on various online platforms were included in the pipeline to facilitate the curation of custom reference databases needed for taxonomic classification of targeted organism groups. User-friendly and interactive pipeline report generation, comprised of both wet- and dry-lab step-by-step sample statistics and graphical representations of the main results, is supported using Rmarkdown and Plotly and DataTables libraries. The pipeline is containerized in Docker, allowing for easier environment building and pipeline deployment.

Keywords: environmental DNA, pipeline, reference databases, containerization



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