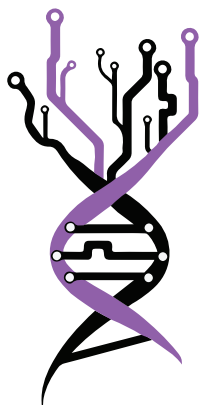


#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



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Dr. Ivana Morić

Dr. Valentina Đorđević

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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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Advancing Genomics with OrthoDB, BUSCO, and the LEM Framework

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The rapid growth of genomics data necessitates continuous advancements in bioinformatics tools. This presentation highlights the latest updates to our toolbox, including OrthoDB v11, BUSCO v5, and the LEM benchmarking framework.

OrthoDB (<https://www.orthodb.org>) is a leading resource for gene orthology and functional annotations across diverse eukaryotes, prokaryotes, and viruses. Orthology facilitates precise bridging of gene function knowledge within the genomics sphere. OrthoDB v11 encompasses over 100 million genes from 18,000 prokaryotes and nearly 2,000 eukaryotes, providing extensive species coverage. The open-source OrthoLogger software (<https://orthologer.ezlab.org>) allows mapping of novel gene sets to precomputed orthologs, linking them to relevant annotations.

BUSCO (<https://busco.ezlab.org>) serves as a standard tool for assessing the completeness of genome assemblies, transcriptomes, and predicted gene sets, complementing assembly contiguity measures like N50 values. A spin-off of OrthoDB, BUSCO evaluates the presence and coverage of marker genes, offering an evolutionarily-grounded expectation of gene content completeness. BUSCO v5 now automatically selects the most suitable dataset for evaluation, outperforming the popular CheckM tool. Its efficiency is particularly evident in large eukaryotic genomes, and it is uniquely capable of assessing both eukaryotic and prokaryotic species, making it applicable to metagenome-assembled genomes of unknown origin.

The LEMMI (<https://lemmi.ezlab.org>) benchmarking framework, now in version 2, facilitates informed software tool selection. This Live Evaluation of Methods (LEM) for Metagenome Investigation uses a container-based approach for continuous benchmarking and effective end-user distribution. The versatile framework can be extended to other procedures, such as gene orthology inference with LEMOrtho (<https://lemortho.ezlab.org>). The LEM benchmarking approach aims to become a community-driven effort, allowing developers to showcase novel methods and users to access standardized, easy-to-use software. We encourage researchers to apply this framework in their domain and welcome feedback.

Keywords: genomics, genomes, orthologs, genes, continuous benchmarking



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