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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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From protein-protein to isoform-isoform interactions: the toolkit to map alternative splicing to interactome

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Alternative splicing (AS) can impact protein structure and lead to protein-protein interaction (PPI) rewiring. Available PPI networks neglect alternative splicing isoforms: as interactions might happen only between a subset of isoforms, the PPI network contains both false-positive and false-negative interactions. Since it is not feasible to validate all isoform-isoform interactions experimentally, we present a set of tools to investigate AS on a network level: DIGGER to map splicing to the PPI network, as well as NEASE and Spycone to evaluate the functional consequences of network rewiring.

DIGGER (<https://exbio.wzw.tum.de/digger>) integrates PPIs, domain-domain, and residue-level interactions - the structures that might be spliced in or out and result in interaction gain or loss. Users can explore possible rewiring for an isoform or exon of interest and extract relevant subnetworks. NEASE (<https://github.com/louadi/NEASE>) identifies pathways that are significantly affected by network rewiring. NEASE extends classic gene set enrichment analysis by considering isoform-specific interactions affecting pathways. Spycone (<https://github.com/yollct/spycone>) addresses the time-course changes in AS. It searches for isoforms that demonstrate similar temporal splicing patterns and reflect the splicing co-regulation. Spycone further integrates gene set, network, and splicing-aware NEASE enrichment.

Overall, we offer a splicing-focused network analysis toolkit that allows for studying the mechanistic consequences of AS.

Keywords: bioinformatics, protein-protein interactions, alternative splicing, network enrichment, time series analysis



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