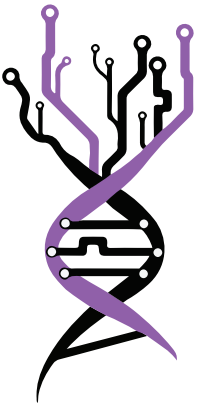
#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

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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 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

Dr. Valentina Đorđević
& Dr. Ivana Morić,
On behalf of BelBi2023
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Complexity driven evolution of Alternative splicing

Vladimir Babenko*[1] and Timophey Boltunov[1]

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Based on the animal model of agonistic interactions, we observed co-varied (linked) alternative exons (LEs) in the genes with alternative splicing phenotype in brain. As a result, we have found 263 positively co-varied pairs, and 26 pairs with negative co-variation. To ascertain the data consistency, we employed three organisms cross-validation: human, mouse and rat with available hippocampus brain region SRA repositories, which supported the co-varied effect of the corresponding exons.

From 142 genes with LE events the maximum LE pairs were observed in insulin – related *Sorbs1* (Sorbin And SH3 Domain Containing 1; 18 LE AS events), and synaptic *Nrcam* (12 LE events). 104 genes maintain only 1 LE pair and 36 genes maintain 2-7 LE pairs. Notably there is a mode at 3 LE pairs per gene (14 genes) in genes vs LE events distribution. GO analysis reveals that the majority of genes maintaining LE events have belong to the synaptic genes, RNA-splicing machinery, and chromatin remodeling.

The 'complexity' (entropic) measure of gene is calculated as $-\sum_{i=1,n}\psi \log 2(\psi)$,

where (Ψ) psi is a percent inclusion rate of a particular AS exon, *n* – number of AS exons in the gene. It is evident that linked AS exons decrease gene complexity rate [3], allowing coordinated splicing in high splicing dynamics rate genes, such as synaptic, RNA processing, chromatin remodeling genes. Herein we speculate if LE AS events are of evolutionary advantage for the high splicing turnover genes working in homeostasis equilibrium.

Next step of the work is to elucidate features providing the linking phenomenon, including mRNA secondary structure, the splicing factor binding sites within and around the corresponding exons.

We will present the results on the issue featuring some complex interactions between exons.

Keywords: alternative splicing, entropy, evolution

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