#BelBi2024 • Belgrade, Serbia

BOOK OF ABSTRACTS

5th Belgrade Bioinformatics Conference

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FOREWORD

We are pleased to announce the successful conclusion of the 5th Belgrade Bioinformatics Conference - BelBi2024, where numerous high-quality scientific contributions were presented. We sincerely thank all participants and proudly present a book of abstracts that not only reflects the scientific richness and diversity of the conference, but also serves as a lasting memento of this remarkable event.

This international conference was jointly organized by several research institutions, faculties, and scientific societies from Serbia. It covered a wide range of topics from the fields of computational biology, bioinformatics, biomedical informatics, and health informatics. The main goal of BelBi 2024 was to promote contacts between scientists of all levels, provide a platform for the exchange of experiences and present the latest advances in their fields. We hope that BelBi2024 was a valuable platform for researchers from all over the world to meet, build new collaborations and expand professional networks.

We are grateful and proud that we were able to welcome over 250 researchers from 21 countries from three continents. The conference included 24 scientific sessions with more than 68 oral presentations (including eight keynote lectures), 54 poster presentations, three hands-on workshops and three satellite events – the MICOS-EU competition, the TranSYS final conference and Shere the IDEA session. We also organized two industry presentations and two panel discussions - "Building Skills for the Future: Masters 4.0 in Bioinformatics" and "BIO4 Campus: Transforming Science into Business". We also presented the first BelBi art exhibition inspired by scientific discoveries, entitled "IMGGE Magnificent Cell Dance". And finally, we are particularly proud of the "Future Keynote Speakers" program, which enabled students from faculties across Serbia to attend this year's keynote lectures and panel discussions for free.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help that contributed to the success of this event. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, the SAIGE project and the Chamber of Commerce and Industry of Serbia for their support. Finally, the local organizing committee is very grateful to all sponsors of the conference - BGI & MGI, Elta'90MS, PacBio & East Diagnostics, Alfa Genetics, Vivogen, LKB, Altium, Telekom Srbija, Labena, AlphaMed, Galen Fokus, Superlab, Kefo, RNIDS, Danau Lab Beograd, RTC and Biomedica, and we hope that they will stay with us for many years to come.

Thank you once again to all who contributed to the success of BelBi2024. We look forward to seeing you at future conferences.

Warm regards,
Belgrade, July 2024

Dr. Valentina Đorđević
& Dr. Ivana Morić,
On behalf of BelBi2024
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The danger of powerful mitochondria: life-history traits shape the evolution of bird mtDNA

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A>G mutation in the mitochondria heavy chain is one of the most discussed types of mutational signatures: previous studies prove its association with mtDNA chemical damage, caused by elevated energy production level. Here we study A>G mutation patterns in birds - creatures with highest energy consumption in the world. We demonstrate a highly expected excess of A>G mutation frequency in birds compared to mammals. In order to understand biochemical mechanisms, which govern A>G mutations in birds, we describe a list of associations between A>G mutation frequencies and life history traits of birds.First, we show that unlike mammals, birds demonstrate no connection between frequency of A>G mutations and most obvious chemical damage correlates: body mass, lifespan or basal metabolic rate (BMR). It is a surprising result, which we interpret as a sign of a highly optimized electron-transport chain, which produces a very stable level of chemical damage agents in a wide range of "regular" conditions. However, according to our results, there is a list of "irregular" conditions, which cause significant change of A>G mutation frequencies. Decrease of A>G mutation is caused by loss of flight: this change is in line with drastic decrease of energy consumption. We have found an increase of A>G mutation rate in diving birds (diving hypoxia is known to produce chemical damage) and in long range migrators (which are known for outstanding peak metabolism levels). The results are significant after phylogenetic generalized least squares correction and show strong phylogenetic inertia.

Keywords: mitochondria, mtDNA, birds, evolution, mutagenesis

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