

#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

HYBRID • 19 - 23 JUNE 2023

EDITORS

Dr. Ivana Morić

Dr. Valentina Đorđević

ISBN: 978-86-82679-14-1

belbi.bg.ac.rs

Title	4 th Belgrade Bioinformatics Conference BOOK OF ABSTRACTS
Publisher	Institute of Molecular Genetics and Genetic Engineering, University of Belgrade Vojvode Stepe 444a, Belgrade, Serbia https://www.imgge.bg.ac.rs/
Editors	dr. Ivana Morić dr. Valentina Đorđević
Technical editor	Dušan Radojević
ISBN	978-86-82679-14-1
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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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Circular Codes in the Genetic Information

Elena Fimmel¹ and Lutz Strümgmann¹

¹Mannheim University of Applied Sciences,
Paul-Wittsack Str. 10, 68163 Mannheim, Germany

l.struengmann@hs-mannheim.de

e.fimmel@hs-mannheim.de

Codes are the sets of words over arbitrary alphabets with the property of unique decipherability.

Circular codes are a special class of codes. They are the sets of words with the property of unique recognition of the reading frame for any sequence composed of them and written on a circle. They were introduced by Golomb and Gordon in the 60s under the name of codes with bounded synchronization delay, because they have a strong property of synchronization. For this reason, they play an important role in problems of error correction.

In the middle 90's such a circular code X was identified in the genes of bacteria, eukaryotes, plasmids, and viruses by a comprehensive statistical investigation. The code X contained the 20 trinucleotides that appeared to be the codons that had the highest preference for the correct reading frame compared to frames 1 and 2. Since then intensive research on circular codes in the genetic information and their potential role in maintaining the correct reading frame during the translation process in the ribosome has been done by various authors. In particular, X -motifs were identified in (i) genes "universally" (ii) tRNAs of prokaryotes and eukaryotes; (iii) rRNAs of prokaryotes (16S) and eukaryotes (18S), in particular in the ribosome decoding center where the universally conserved nucleotides G530, A1492, and A1493 are included in the X -motif; and (iv) genomes (non-coding regions of eukaryotes). Circular codes have a highly complex structure and the ones found in genes possess additional properties like e.g. self-complementarity that reflect their biological nature.

In our talk we give a short introduction to the theory of circular codes and an overview on the methods from mathematics, statistics and bioinformatics to explore their properties and their biological role. Finally, a possible model of the evolution of the genetic code from the perspective of circular code theory is presented.

Keywords: Circular Codes, Genetic Code, Frame-Shift, Translation



ISBN: 978-86-82679-14-1