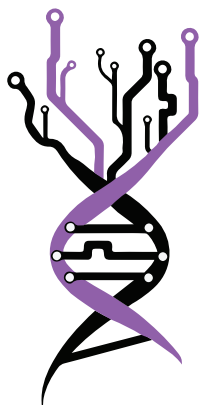


#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



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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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Oral presentation

The use of Active Machine Learning for Protospacer-Adjacent Motif recovery in Class 2 CRISPR-Cas systems

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The recognition of target DNA sequences during the interference phase of prokaryotic CRISPR-Cas immunity relies on Protospacer-Adjacent Motif (PAM) sequences, specific for each Cas effector. PAM identification is a laborious and time consuming process that requires multiple stages including *in vitro* and *in vivo* cleavage assays followed by Next Generation Sequencing of targets that withstood cleavage. Determining PAM is an essential step of characterisation of any novel Cas9 ortholog and determines the likelihood of its potential use. This study investigates the potential of machine learning to predict PAM sequences for a given Cas9 ortholog based on the results of cleavage experiments and employing an Active Learning process akin to Reinforcement Learning with Human Feedback. Machine learning-facilitated PAM identification would streamline and accelerate existing pipelines for describing novel Cas proteins. We demonstrate that simple models with a small amount of data are sufficient for confident PAM predictions when training is effectively orchestrated.

Keywords: bioinformatics, CRISPR, machine learning



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