

#BelBi2023 • Belgrade, Serbia

# BOOK OF ABSTRACTS



## 4th Belgrade Bioinformatics Conference

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EDITORS

**Dr. Ivana Morić**

**Dr. Valentina Đorđević**

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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 5<sup>th</sup> Belgrade Bioinformatics Conference.

Belgrade, July 2023

*Dr. Valentina Đorđević  
& Dr. Ivana Morić,*  
On behalf of BelBi2023  
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## Poster presentation

### The past, the present, and the future of RNA secondary structure prediction

Lazar Vasović<sup>1</sup>

<sup>1</sup>Faculty of Mathematics, University of Belgrade, Studentski trg 16,  
11000 Belgrade, Serbia

[pd212006@alas.matf.bg.ac.rs](mailto:pd212006@alas.matf.bg.ac.rs)

RNA is a biopolymer whose primary structure is a sequence of nucleobases. While messenger RNA is probably the most known, an increasing number of non-coding RNAs is being discovered. In order to become biologically active, ncRNA folds intramolecularly, thus forming segments of paired bases. This secondary structure largely determines the function of an ncRNA, so its prediction is important for newly discovered sequences. Owing to the strong link between the two structural levels, most predictors are data-driven and sequence-based.

The oldest and simplest algorithm was base pair maximization (BPM), which did not presume important structural features. Another approach exploited the fact that biophysics dictates RNA folding, so it searched for the thermodynamically optimal structure. Statistical learning was the base of the third group, with probabilistic context-free grammars (PCFGs) being the most influential. These were the state-of-the-art methods at the beginning of the century.

However, much has changed in the last years, since technological advancement allowed the widespread use of machine learning. Its use in the RNA structure prediction ranges from being the supplementary method (e.g., for estimating thermodynamical and statistical parameters of traditional methods) to encapsulating the whole prediction process. The highest success has been reported with transformers, recurrent, and convolutional neural networks (CNN).

This paper was designed as a review and aimed to compare several methods theoretically and assess them practically. As expected, model complexity was highly correlated with accuracy. On the subset of simply structured transfer RNA, for example, BPM predicted ~22% of pairings correctly, PCFG ~86%, and CNN ~99%. Other subsets, such as 16S ribosomal RNA, were more challenging, but deep learning always performed best. With the continued growth of computational power and the amount of annotated data, prediction accuracy is expected to get even closer to the experimental determination, while still maintaining a much lower cost.

**Keywords:** RNA structure prediction, review, machine learning

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