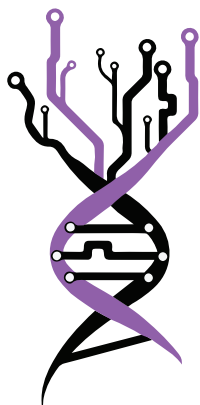


#BelBi2023 • Belgrade, Serbia

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

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|-------------------------|---|
| 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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Poster presentation

Methodology, performance and retrainability survey of intrinsic disorder predictors

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Intrinsically disordered proteins and regions are widely distributed within most proteomes. Recent studies show that they are associated with many essential biological processes and a broad range of human diseases. Given the prevalence of disordered proteins and the growing acknowledgement of their functional relevance, considerable effort has been made by the bioinformatics community to provide computational tools to predict protein disorder. To date, based on various characteristics of protein disorder, along with variety of diverse computational approaches, numerous disorder predictors have been developed. Over the past decade several review papers examining intrinsic disorder predictors have been published. All these papers have played a significant role in stimulating and greatly facilitating the development of this actively growing field by pinpointing the potential room for improvement. Inspired by these, in this work we aim to integrate the relevant information regarding the existing intrinsic disorder predictors from the corresponding research papers in a novel review, including latest prediction tools. In addition, for each disorder predictor, we examined the possibility of their retraining using different datasets. Here, we present an overview of 23 protein disorder prediction methods, including the thorough analysis of their advantages and weaknesses which derive from their different computational approaches. Regarding this, we precisely describe the methodology used for building the models and categorize them by different classification schemes. The performance of these models is presented by their scores from the most recent CAID competition. Additional contribution of this work is the models' retraining availability analysis. We describe in detail the predictors' implementation source code (if available) and propose a way around to overcome the obstacles with retraining procedure (if possible). This insight might be very useful, since older models were trained on significantly smaller datasets compared to the newer ones, due to the increase in the number of experimentally annotated disorder proteins with time. With respect to this, we discuss in detail the possibility of retraining the models on a different (bigger, novel) dataset in order to perform full-scale comparison of their expression power in delineating disorder in proteins.

Keywords: intrinsic disorder, predictors, review, categorization, retraining availability



ISBN: 978-86-82679-14-1