

#BelBi2023 • Belgrade, Serbia

# BOOK OF ABSTRACTS



## 4th Belgrade Bioinformatics Conference

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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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## Oral presentation

### Zero- and Few-Shot Machine Learning for Named Entity Recognition in Biomedical Texts

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Named entity recognition (NER) is an NLP that involves identifying and classifying named entities in text. Token classification is a crucial subtask of NER that assumes assigning labels to individual tokens within a text, indicating the named entity category to which they belong. Fine-tuning large language models (LLMs) on labeled domain datasets has emerged as a powerful technique for improving NER performance. By training a pre-trained LLM such as BERT on domain-specific labeled data, the model learns to recognize named entities specific to that domain with high accuracy. This approach has been applied to a wide range of domains including biomedical and has demonstrated significant improvements in NER accuracy.

Still, data for fine-tuning pre-trained LLMs is large and labeling is a time-consuming and expensive process that requires expert domain knowledge. Also, domains with an open set of classes yield difficulties in traditional machine learning approaches since the number of classes to predict needs to be pre-defined.

Our solution to the two mentioned problems is based on data transformation for factorizing the initial multiple classification problem into a binary one and applying cross-encoder-based BERT architecture for zero- and few-shot learning.

To create our dataset, we transformed six widely used biomedical datasets that contain various biomedical entities such as genes, drugs, diseases, adverse events, chemicals, etc., into a uniform format. This transformation process enabled us to merge the datasets into a single cohesive dataset of 26 different named entity classes.

We then fine-tuned two pre-trained language models: BioBERT and PubMedBERT for the NER task in zero- and few-shot settings. The results of the experiment for 9 classes in zero-shot mode are promising for semantically similar classes and improve significantly after providing only a few supporting examples for almost all classes. The best results were obtained using a fine-tuned PubMedBERT model, with average F1 scores of 35.44%, 50.10%, 69.94%, and 79.51% for zero-shot, one-shot, 10-shot, and 100-shot NER respectively.

**Keywords:** zero-shot learning, machine learning, deep learning, natural language processing, biomedical named entity recognition





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