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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 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

*Dr. Valentina Đorđević
& Dr. Ivana Morić,*
On behalf of BelBi2023
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Invited lectures

Exploiting the linear organisation of omics network embedding spaces

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We are increasingly accumulating large-scale biological omics data that describe different aspects of cellular functioning. These datasets are typically modelled and analyzed as networks. To ease the downstream analyses, recent approaches embed the nodes of a network into a low-dimensional space by using a skip-gram neural network (e.g. DeepWalk, LINE and node2vec). These methods are implicitly factorizing a positive pointwise mutual information (PPMI) matrix, which could be explicitly factorized with Non-negative Matrix Tri-Factorization (NMTF). Importantly, in Natural Language Processing (NLP), word embeddings obtained by using similar approaches showed linear algebraic structures, which allows for answering analogy questions by using simple linear vector operations. Thus, we investigate if we can obtain and exploit similar linear embedding spaces for the biological omics networks.

We initiate the use of the PPMI matrices to capture the neighborhood relationship or the structural (topological) similarities of nodes in the network. By embedding the human Protein-Protein Interaction (PPI) network by factorizing its PPMI matrix representations with NMTF, we demonstrate that the embedding vectors of genes having different Gene Ontology (GO) annotations are linearly separated in the PPI embedding space.

Then, in analogy to the embedding vector of a sentence being obtained as the sum (average) of the embedding vectors of its constituent words in NLP, we show that the embedding vectors of biological functions and of protein complexes can be obtained by averaging the embedding vectors of the genes that participate in them, and that these embeddings can be used to predict protein complex memberships and cancer genes.

Finally, we investigate the embeddings of cancer and control tissue specific PPI networks and show that simple subtractions allow for identifying cancer altered biological functions and cancer genes.

Keywords: bioinformatics, molecular omics networks, network data mining, network embedding

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