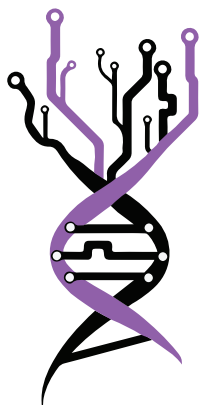


#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



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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 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

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

Machine learning-based data correlation between scanning electron microscopy images and energy-dispersive X-ray spectroscopy profiles

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Characterisation of organic and inorganic microparticles has long been an important topic in the field of environmental health sciences. Especially, combined analytical method of scanning electron microscopy (SEM) associated with energy-dispersive X-ray spectroscopy (EDX) is a commonly exploited approach to obtain extensive data on the size, morphological, and elemental information from the particulate specimens. Particulate matter (PM) is a representative atmospheric pollutant that may exert adverse effects on the human respiratory system, and SEM-EDX is a widely used tool for extracting PM analysis data, which can be subsequently utilised as physicochemical features for toxicological predictions.

In this presentation, we show a machine learning-based automation of SEM-EDX correlation of environmental PM data. First, we segment SEM images using WEKA trainable segmentation which is based on a random forest algorithm to classify pixels as foreground and background groups, followed by finding connected components (pixels that are foreground and connected vertically or horizontally). These regions are used to calculate PM shape parameters. Next, element maps are obtained from EDX using curve fitting with HyperSpy Python package. PM regions from SEM images are utilised to sum intensities in the same spatial location for the element maps to obtain elemental profiles. We finally build two models to predict PM elements: (1) Element maps from SEM-EDX data using image-to-image translation, and (2) regression to predict PM element percentages from shape features. Results from model 1 and 2 are then applied to extract PM elemental profiles associated with PM morphology information. Our results show how to efficiently predict EDX and element maps from SEM images with a high degree of accuracy. This method has a potential to significantly reduce time and labour required for environmental PM monitoring.

Keywords: Environmental health, particulate matter, SEM, EDX, automated data analysis, multiple output regression



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