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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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Oral presentation

Deciphering key regulatory networks and drug repurposing candidates through scRNAseq data analysis using SCANet

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Differences in co-expression networks between two or multiple cell (sub)types across conditions is a pressing problem in single-cell RNA sequencing (scRNA-seq). A key challenge is to define those co-variations that differ between or among cell types and/or conditions and phenotypes to examine small regulatory networks that can explain mechanistic differences. To this end, we developed SCANet, an all-in-one Python package that uses state-of-the-art algorithms to facilitate the workflow of a combined single-cell GCN and GRN pipeline including inference of gene co-expression modules from scRNA-seq, followed by trait and cell type associations, hub gene detection, co-regulatory networks, and drug-gene interactions. To illustrate the power of SCANet, we examined data from two studies. First, we identify the drivers of the mechanotype of a cytokine storm associated with increased mortality in patients with acute respiratory illness. Secondly, we find 20 drugs for 8 potential pharmacological targets in cellular driver mechanisms in the intestinal stem cells of obese mice. SCANet is available as a free, open source, and user-friendly Python package that can be easily integrated in systems biology pipelines.

Keywords: small single cell networks, GRN, GCN, mechanotyping, drug repurposing



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