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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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Exploration of Pharmacogenomic Biomarkers in Chronic Immune Diseases Using Single-Cell RNA Sequencing

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Biological therapies have revolutionized management of the severe cases of Chronic Immune Diseases refractory to the standard therapies. However, many patients do not respond to the selected biological therapy, loose response over time, or develop adverse effects. A personalized approach to treatment of these patients, based on reliable biomarkers is thus clearly needed.

Non-invasive approaches, such as use of the peripheral blood immune cells, are favored for novel biomarker discovery. However, the attention has shifted away from the bulk immune cells and towards specific immune cell sub-populations. Thus, the single-cell RNA sequencing (scRNA-seq) can prove highly valuable. By simultaneously capturing and profiling all the cells in a sample, scRNA-seq allows the analysis of cellular heterogeneity and gene expression in all immune cell sub-populations, targeted or adversely affected by the biological treatment.

In our ongoing research, scRNA-seq was utilized to analyze samples from Inflammatory Bowel Disease and Childhood Asthma patients with varied response to the biological therapy. Confounding effects of disease conditions and (biological) therapies on marker genes were eliminated using computational integration in order to identify conserved marker genes across all states. It turned out, that a reliable identification of the different immune cell sub-populations in this setting is quite challenging due to subjective cell-landscape clustering resolution. Several resolutions and automated annotation approaches were subsequently tested and validated.

Oral presentation

A reference-based approach (Seurat-Azimuth) combined with manual cluster validation proved superior. Alas, manual cluster validation is time consuming. Annotation validation is important, especially to provide additional insights into unidentified clusters, which are essential for the identification of predictive biomarkers for personalized therapies in the vast heterogeneity of immune cell landscapes residing behind pathophysiology of chronic immune diseases.

Keywords: precision medicine, chronic immune diseases, biological therapy, Single-Cell RNA Sequencing, identification of cell sub-populations

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