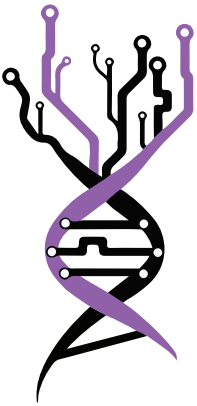
#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

HYBRID • 19 - 23 JUNE **2023**

EDITORS
Dr. Ivana Morić
Dr. Valentina Đorđević

ISBN: 978-86-82679-14-1

belbi.bg.ac.rs

Title 4th Belgrade Bioinformatics Conference
BOOK OF ABSTRACTS

Publisher Institute of Molecular Genetics and Genetic Engineering, University of Belgrade
Vojvode Stepe 444a, Belgrade, Serbia
https://www.imgge.bg.ac.rs/

Editors dr. Ivana Morić
dr. Valentina Đorđevic

Technical editor Dušan Radojević

ISBN **978-86-82679-14-1**

BelBi2023 Committees

International Advisory Board

Alessandro Treves,
International School for Advanced Studies, Trieste, Italy

Guanglan Zhang,
Health Informatics Lab, Metropolitan College, Boston University, Boston, USA

Konstantin Severinov,
Waksman Institute for Microbiology, Rutgers University, Piscataway, USA

Lou Chitkushev,
Health Informatics Lab, Metropolitan College, Boston University, Boston, USA

Milena Stevanović,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Belgrade, Serbia

Oxana Galzitskaya,
Institute of Protein Research, Russian Academy of Sciences, Moscow, Russia

Paul Sorba,
Laboratory of Theoretical Physics and CNRS, Annecy, France

Peter Tompa,
VIB Structural Biology Research Center, Flanders Institute for Biotechnology, Brussels, Belgium

Predrag Radivojac,
Khoury College of Computer Sciences, Northeastern University, Boston, SA

Sergey Volkov,
Bogolyubov Institute for Theoretical Physics, National Academy of Sciences, Kiev, Ukraine

Vladimir Brusić,
Li Dak Sum Chair Professor of Computer Science, University of Nottingham, Ningbo, China

Vladimir Uversky,
Department of Molecular Medicine, University of South Florida, Tampa, USA

Yuriy Orlov,
I.M. Sechenov First Moscow State Medical University, Moscow, Russia

Zoran Ognjanović,
Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade, Serbia

International Program Committee

Alexandre de Brevern,
INSERM, Université Paris Cité, Université de la Réunion, Paris, France

Branislava Gemović,
VINCA Institute of Nuclear Sciences, University of Belgrade, Serbia

Branka Zukić,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

Branko Dragovich,
Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade, Serbia

Dragan Matić,
Faculty of Sciences, Department of Mathematics and Informatics, University of Banja Luka, Bosnia and Herzegovina

George Patrinos,
Department of Pharmacy, University of Patras, Greece

Gordana Pavlović-Lazetić,
Faculty of Mathematics, University of Belgrade, Serbia

Hong-Yu OU,
Shanghai Jiao Tong University, The Microbial Bioinformatics Group, State Key Laboratory of Microbial Metabolism, Shanghai, China

Ivana Morić,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

Jelena Bojović,
Center for the Fourth Industrial Revolution, Belgrade, Serbia

Marko Đordević,
Faculty of Biology, University of Belgrade, Serbia

Mirjana Maljković,
Faculty of Mathematics,
University of Belgrade, Serbia

Nataša Kovacevic-Grujičić,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

Nataša Pržulj,
Catalan Institution for Research and Advanced Studies (ICREA), Spain;
Barcelona Supercomputing Center, Spain;
University College London, UK

Nenad Mitić,
Faculty of Mathematics,
University of Belgrade, Serbia

Nevena Veljković,
VINCA Institute of Nuclear Sciences,
University of Belgrade, Serbia

Predrag Radivojac,
Khoury College of Computer Sciences,
Northeastern University, Boston, USA

Saša Malkov,
Faculty of Mathematics,
University of Belgrade, Serbia

Sergei Kozyrev,
Department of Mathematical Physics,
Steklov Mathematical Institute RAS,
Moscow, Russia

Valentina Đorđević,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Serbia

Vladimir Babenko,
Institute of Cytology and Genetics,
Novosibirsk, Russia

Local Organizing Committee

Anđela Rodić,
Faculty of Biology, University of Belgrade

Branislava Gemović,
VINCA Institute of Nuclear Sciences,
University of Belgrade

Branko Dragovich,
Mathematical Institute, Serbian Academy of Sciences and Arts, Belgrade

Gordana Pavlović-Lazetić,
Faculty of Mathematics,
University of Belgrade

Ivana Morić,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade

Jovana Kovačević,
Faculty of Mathematics,
University of Belgrade

Marko Đorđević,
Faculty of Biology, University of Belgrade

Marko Živanović,
Bioengineering Research and Development Center

Nenad Filipović,
Faculty of Engineering, University of Kragujevac

Nenad Mitić,
Faculty of Mathematics,
University of Belgrade

Radoslav Davidović,
VINCA Institute of Nuclear Sciences,
University of Belgrade

Saša Malkov,
Faculty of Mathematics,
University of Belgrade

Valentina Đorđević,
Institute of Molecular Genetics and Genetic Engineering, University of Belgrade

Željko D. Popović,
Faculty of Sciences, University of Novi Sad

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
Organizing Committee

ORGANIZER

Institute of Molecular Genetics and Genetic Engineering, University of Belgrade

MAIN CO-ORGANIZERS

Faculty of Biology, University of Belgrade

Faculty of Mathematics, University of Belgrade

Mathematical Institute of SASA, Belgrade

Vinča Institute of Nuclear Sciences, University of Belgrade

Serbian Society for Bioinformatics and Computational Biology

CO-ORGANIZERS

Faculty of Sciences, University of Novi Sad

BioIRC - Bioengineering Research and Development Center

Faculty of Engineering, University of Kragujevac

Centre for the Fourth Industrial Revolution in Serbia

Serbian Society for Molecular Biology

Biophysical Society of Serbia

TABLE OF CONTENT

KEYNOTE LECTURES

INVITED LECTURES

ORAL PRESENTATION

POSTER PRESENTATION

Single cell 3' transcriptome profiling

Nevena Milivojević*[1], Uršula Prosenc Zmrzljak[2], Biljana Ljujić[3], Valentina Đorđević[4], Marina Gazdić Janković[3], Marko Živanović[1,5], Feđa Puač[6], Miloš Ivanović[7], and Nenad Filipović[5,8]

[1]Institute for Information Technologies, University of Kragujevac, Jovana Cvijića bb, 34000 Kragujevac, Serbia
[2]BIA Separations CRO Laboratory, Teslova ulica 30, 1000 Ljubljana, Slovenia
[3]Faculty of Medical Sciences, University of Kragujevac, Svetozara Markovića 69, 34000 Kragujevac, Serbia
[4]Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Vojvode Stepe 444a, 11042 Belgrade, Serbia
[5]BioIRC - Bioengineering Research and Development Center, University of Kragujevac, Prvoslava Stojanovića 6, 34000 Kragujevac, Serbia
[6]Labena d.o.o. Serbia, Bulevar Zorana Đinđića 123G, 11070 Belgrade, Serbia
[7]Faculty of Science, University of Kragujevac, Radoja Domanovića 12, 34000 Kragujevac, Serbia
[8]Faculty of Engineering, University of Kragujevac, Sestre Janjić 6, 34000 Kragujevac, Serbia

nevena_milivojevic@live.com

Whole 3' transcriptome profiling at the single cell level opens up new abilities for researchers to answer complex questions. Thousands of individual cells per sample are Barcoded separately to index the transcriptome of each cell individually. It is done by partitioning thousands of cells into nanoliter-scale Gel Beads-in-emulsion (GEMs), where cells are delivered at a limiting dilution, such that the majority (~90-99%) of generated GEMs contain no cell. The 16 bp 10x Barcode and 12 bp UMI are encoded in Read 1, while the poly(dT) primers are used in this protocol for generating Single Cell 3' Gene Expression libraries. After GEM generation, copartitioned cells are lysed and reverse transcription (RT) was performed after which all cDNA from single cell share a common Barcode. Full-length cDNA was amplified via PCR to generate sufficient mass for library construction. This is followed by enzymatic fragmentation and size selection to optimize the cDNA amplicon size. Library construction was finished via End Repair, A-tailing, Adaptor Ligation, and PCR. P5, P7, i7 and i5 sample index, and TruSeq Read 2 (read 2 primer sequence) were added. TruSeq Read 1 and TruSeq Read 2 are standard Illumina sequencing primer sites used in paired-end sequencing. The library prepared in this way, containing the P5 and P7 primers, is ready for Illumina amplification.

Keywords: single-cell analysis, mRNA, bioinformatics, transcriptome, sequencing

Acknowledgement: This research is funded by Labena Slovenia 10xGenomics Grant Challenge (Project title: Deciphering the effects of nanosized polystyrene particles using lab-on-chip technology and transcriptome profile). This research was supported by Labena Serbia, the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, contract number 451-03-47/2023-01/200378 (Institute for Information Technologies Kragujevac, University of Kragujevac), 451-03-47/2023-01/200111 (Faculty of Medical Sciences, University of Kragujevac), as well as Junior projects of Faculty of Medical Sciences, University of Kragujevac JP 25/19, JP 05/20, JP 06/20 and JP 24/20. This work is supported by the European Union's Horizon 2020 research and innovation program under grant agreement No 952603 (SGABU). This article reflects only the author's view. The Commission is not responsible for any use that may be made of the information it contains.

ISBN: 978-86-82679-14-1