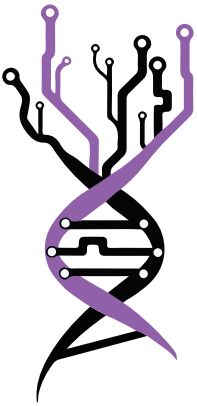
#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

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Dr. Ivana Morić
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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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Impact of different mapping tools on detection of small RNAs in bacterial outer membrane vesicles

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Bacterial small RNAs (sRNAs) represent a highly diverse RNA class ranging from 8 to 200 nucleotides in length, originating from the bacterial chromosome, plasmids or phages. After syntheses sRNAs can remain inside the bacterial cell, be secreted or packed into outer membrane vesicles (OMV), enabling various intra- and inter-kingdom interactions. Different sRNAs biotypes display differences in structure, mechanism of action and level of regulation (i.e. transcription, translation, mRNA stability, etc.), but could be broadly grouped in: *trans*-acting sRNAs (bind to target mRNAs) and *cis*-encoded sRNAs (or antisense RNA that may interact not only with mRNAs, but also with proteins and DNA).
Even though the advancement of high-throughput sequencing technology led to a burst of knowledge on small RNAs complexity and diversity, there are still specific challenges related to sRNA-seq data analysis that need to be resolved. Two main challenges, associated to short length of many bacterial sRNA biotypes, are: (i) to discriminate between functional sRNAs synthesized by bacterial cell and degradation fragments produced by sample preparation and (ii) to detect functional sRNAs displaying sequence variation. While loss of very small sized sRNAs could easily be overcome by cutting-off only the specific adapter sequences that were used in sRNA library preparation, providing a proper mapping still remains a strenuous task.
The aim of this study was to test five different mapping tools that are widely used in NGS data analysis (bbmap, bowtie2, bwa, minimap2 and segemehl) for their performances in mapping of bacterial OMV sRNA-seq data to bacterial reference genome. For this test publicly available NCBI sRNA-seq dataset from OMVs of *Aliivibrio fischeri* (PRJNA629425) was used, as it contained sRNAs of different length and biotype and because *A.fischeri* reference genome and annotation were available (PRJNA12986). We evaluated five mappers using alignment and assignment rates as well as computational time. Alignment rate was calculated as the ratio of aligned and input reads, while the assignment rate was calculated as the ratio of assigned and aligned reads. Finally, totals of detected sRNAs biotypes were compared between different mappers. The statistical analysis was performed in R (version 4.3.0) and performance metrics are discussed.

Keywords: small RNAs, outer membrane vesicles, mapping

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