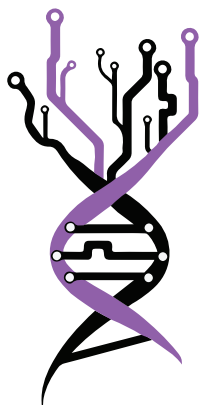


#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



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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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Analysis of Long COVID Phenotypes and their Impact on Mental Health and Daily Functioning: Insights from Twitter

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In this study, we conducted an investigation into Long COVID from a user perspective, utilizing Twitter social media data. Prior to analysis, the data underwent preprocessing to obtain raw text per tweet. Our analysis commenced with basic statistical analysis and subsequently expanded to identify characteristic periods for the phenotypes based on dynamic timelines. We also explored the relationships between the phenotypes, as well as the interdependence between phenotypes and geolocation.

In the context of this research, an analysis was conducted on a collection of tweets that encompassed the timeframe from March 2020 to March 2022. The dataset consisted of approximately 1.9 million tweets. In order to concentrate on word phrases, extraneous elements such as mentions, emoticons, links, and hashtags were eliminated. Subsequently, a process of lemmatization was performed. For the purpose of reducing the number of distinct phenotypes under investigation and facilitating the presentation of results, the collected data was categorized into five overarching groups: Cardiovascular, Respiratory, Daily Living, Neurological and Mental Health, and Other.

The statistical data regarding the most commonly used words by individuals describing their experiences during the Long COVID period are as follows: "Ampicillin" was tweeted 125,295 times, "Death" was tweeted 121,156 times, "Suffer" was tweeted 125,113 times, and "Vaccine" was tweeted 108,968 times. We observe distinct patterns in the emergence of certain phenotypes during this period, particularly in relation to the quality of life. On August 1, 2020, the term "quality of life" was mentioned in only 223 tweets, whereas one year later, during the same month, this phenotype garnered 1,663 tweets.

Our findings reveal that the occurrence of Long COVID phenotypes is influenced by both temporal and geographical factors. The analysis shows a clear and notable trend within the dataset. Specifically, it is observed that neurological symptoms, along with symptoms that impede individuals' daily functioning, exhibit the highest prevalence, particularly during the latter half of the analyzed tweet period. This period corresponds to a time when an increasing number of individuals have recovered from COVID-19 and are reporting their experiences with Long COVID. Notably, fatigue, depression, stress, and anxiety emerge as the most prevalent phenotypes.

This scientific investigation of the complex interactions between Long COVID phenotypes, mental health, and the manifestation of diverse symptoms is offering insights into the profound consequences on individuals' lives. These findings shed light on the significant burden posed by Long COVID and its cascading effects on various aspects of individuals' well-being and society at large.

Keywords: Long COVID, data mining, computer science, nlp



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