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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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Supervised Machine Learning Approach for Prediction of Occult Lymph Node Metastasis in T1-T2 Papillary Thyroid Carcinoma

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This study aimed to assess and compare four machine learning (ML) based classifiers in predicting occult cervical lymph node metastasis (LNM) in clinically node-negative (cNO), T1-T2 papillary thyroid carcinoma (PTC) patients.

The study cohort included 288 PTC patients who underwent total thyroidectomy and prophylactic central neck dissection with sentinel lymph node biopsy performed for lateral LNM identification. The classifiers, namely k-Nearest Neighbor (k-NN), Support Vector Machines, Decision Tree, and Logistic Regression were developed using patients' demographic and clinicopathological variables. Evaluation metrics such as area under the receiver operating characteristic curve (AUC), sensitivity, specificity, positive and negative predictive values (PPV and NPV), accuracy, and F1 and F2 scores were utilized for model comparison.

The final ML classifier was selected based on achieving the highest specificity and the lowest degree of overfitting while maintaining a sensitivity of 95%. Among the evaluated models, the k-NN emerged as the best-performing, demonstrating an AUC of 0.72. The sensitivity, specificity, PPV, NPV, F1, and F2 scores were 98%, 27%, 56%, 93%, 72%, and 85%, respectively. Furthermore, a web application was developed allowing users to predict the potential of cervical LNM and explore possibilities for further model development.

The k-NN classifier incorporating patients' clinicopathological information shows potential in predicting LNM. Improved prediction models are necessary to identify patients at higher risk of LNM, guiding appropriate postsurgical treatment for high-risk individuals while minimizing unnecessary interventions for low-risk patients.

Keywords: machine learning, papillary thyroid carcinoma, lymph node metastasis

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