



Univeristy of Niš, Serbia Faculty Of Science and Mathematics Department of Biology and Ecology







Al and Molecular Taxonomy: A Comprehensive Approach to Aquatic Macroinvertebrate Identification and Genetic Diversity in the Balkans

Ana Samardžić University of Niš, Serbia



Al and Molecular Taxonomy: A Comprehensive Approach to Aquatic Macroinvertebrate Identification and Genetic Diversity in the Balkans

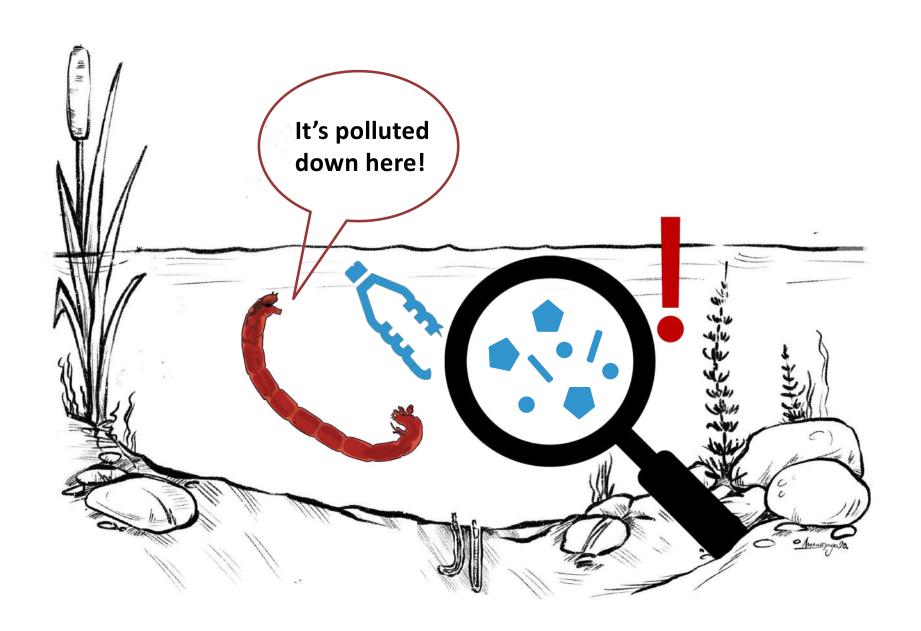
Dimitrija Savić-Zdravković¹, <u>Ana Samardžić*¹</u>, Aleksandar Milosavljević², Katarina Stojanović³, Bratislav Predić², Milena Radenković⁴, Predrag Simović⁴, Djuradj Milošević¹

*¹ Department of Biology and Ecology, Faculty of Sciences and Mathematics, University of Niš, Višegradska 33, 18000 Niš, Serbia

²Faculty of Electronic Engineering, University of Niš, Aleksandra Medvedeva 14, 18000 Niš, Serbia

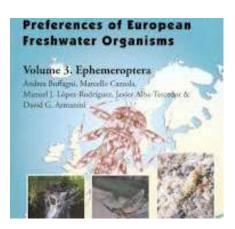
³Department of Biology and Ecology, Faculty of Science, University of Kragujevac, Radoja Domanovi 12, 34000 Kragujevac, Serbia

⁴Department of Zoology, Faculty of Biology, University of Belgrade, Studentski trg 16, Belgrade, Serbia

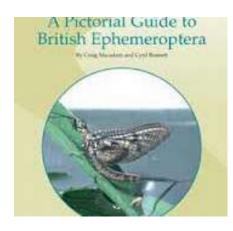


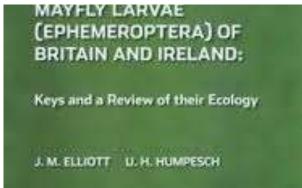
CHALLENGE

Improve the efficiency of species monitoring which will increase the costeffectiveness of biodiversity and aquatic ecosystem quality assessment





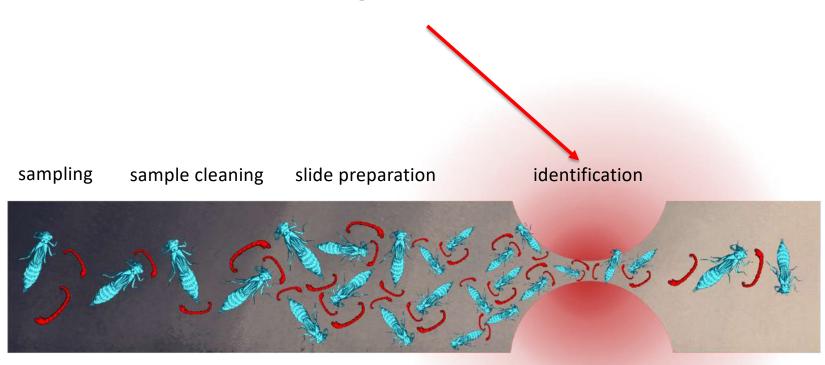




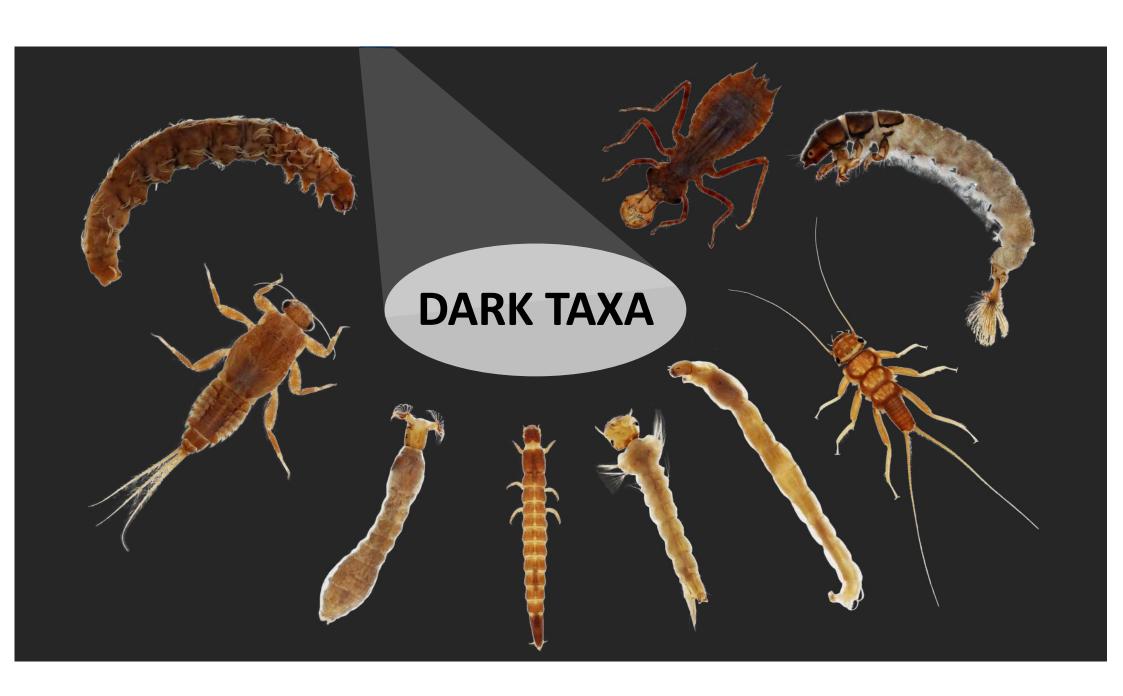




PROBLEM!



TAXONOMIST SHORTAGE

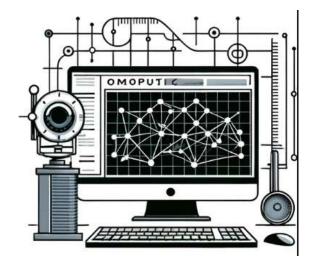


To develop an **automatic identifier** for aquatic macroinvertebrates (MI) by combining artificial intelligence (AI), molecular taxonomy and morphological approaches.

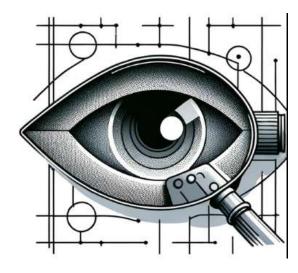
Investigate the application of deep learning to increase the efficiency and taxonomic resolution of biomonitoring programs.

To establish a comprehensive database of macroinvertebrate sequences, which can serve as a foundational resource for further research.

Deep learning



Computer vision





Methods in species monitoring

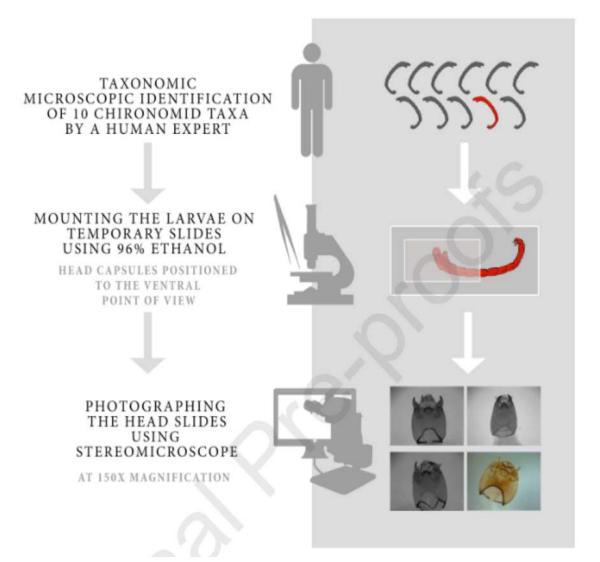




IMAGE ACQUISITION

LAB-BASED IMAGE ACQUISITION PROTOCOL

CNN MODEL DEVELOPMENT

2 STAGE TRAINING AND VALIDATION PROCESS

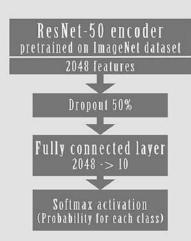
VISUALIZATION OF

GRADIENT-WEIGHTED CLASS ACTIVATION MAPPING (GRAD-CAM)

IDENTIFICATION PROCESS

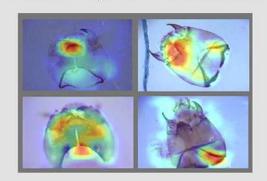
1846 SPECIMENS 10 SPECIES, 5 GENERA, 2 SUBFAMILIES





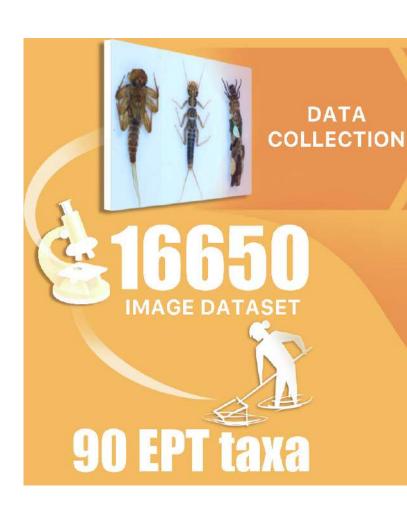
MENTUM, VENROMENTAL PLATES, MANDIBLES, SUBMENTUM, POSTOCCIPITAL MARGIN

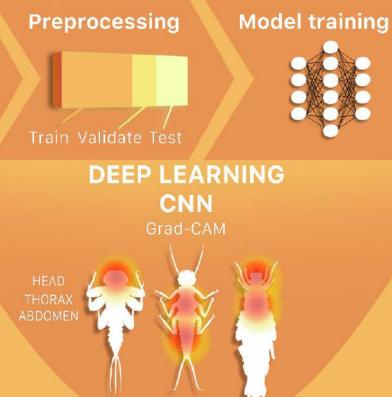
AUTOMATIC SPECIES IDENTIFIER-IMPROVED BIOMONITORING





RESULTS AND DISCUSSION





98.7% CLASSIFICATION

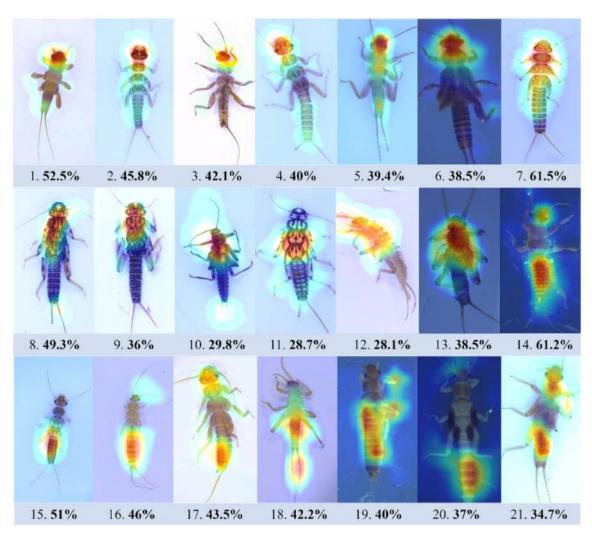
AUTOMATED

IDENTIFICATION

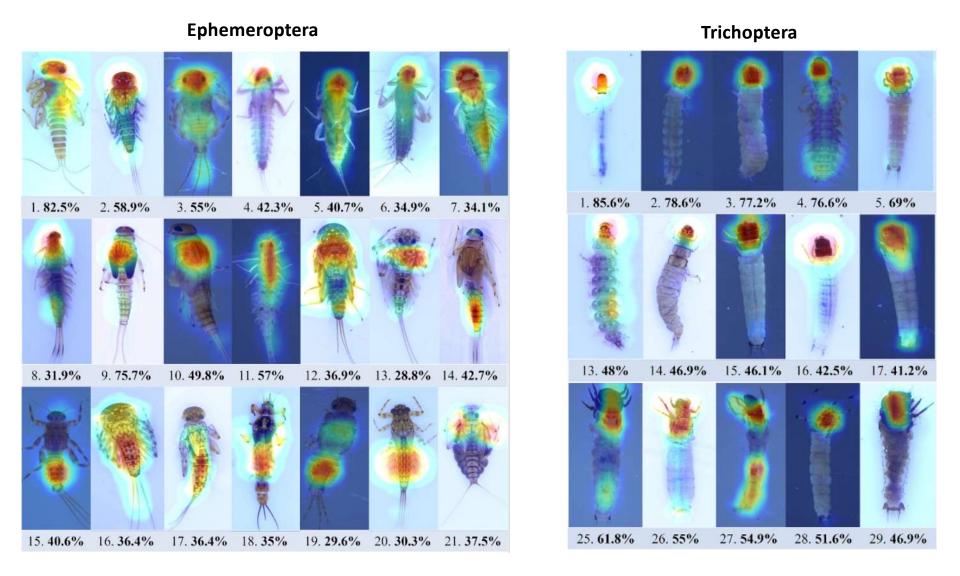


Deep Learning Outcomes

- Using Convolutional Neural Networks
 (CNNs), we classified over 90 taxa,
 including Ephemeroptera, Plecoptera and
 Trichoptera (EPT), with 98.7% accuracy
 and 100% precision for major taxa groups.
- For chironomids, we achieved 92.3% accuracy.
- Gradient-weighted Class Activation
 Mapping (Grad-CAM) highlighted the
 importance of specific morphological
 features, such as the head for EPT and the
 mentum and mandibles for chironomids.



Plecoptera

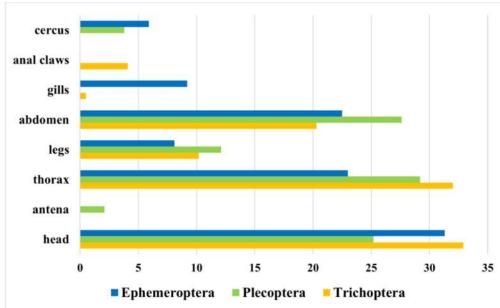


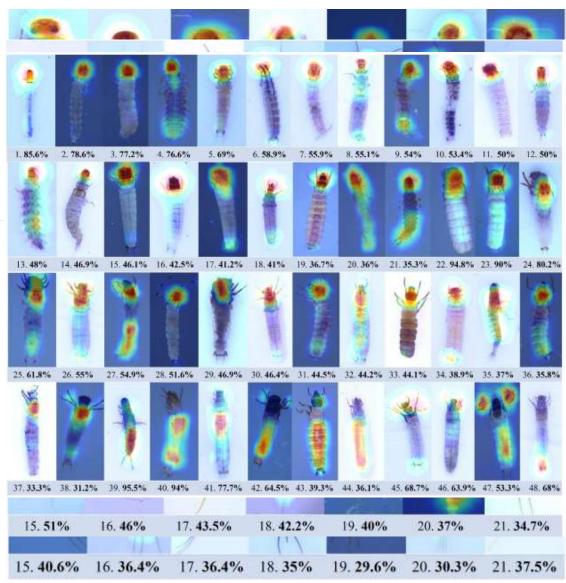
The alpha version of the standalone application is available on GitHub (Imagelytics).

RESULTS

EPT classification accuracy

98.7%



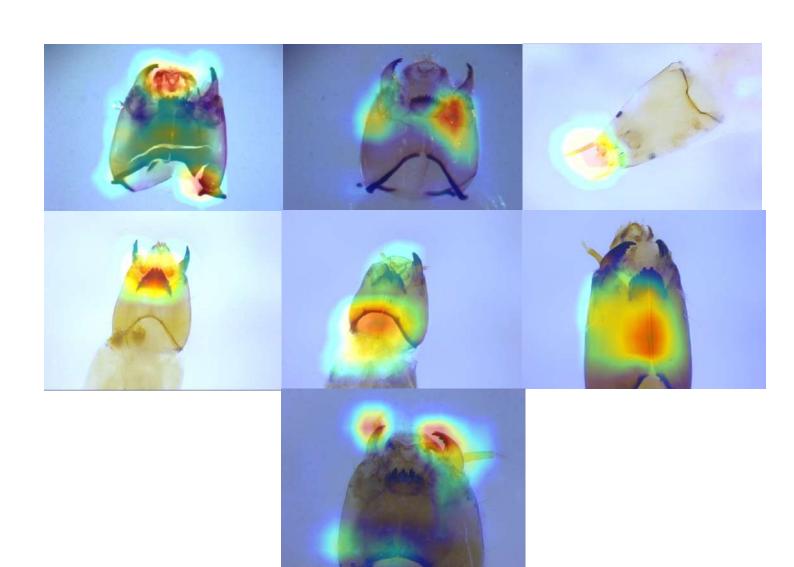


RESULTS

Chironomidae classification accuracy

92.3%

Based on mappings of the mentum, submentum and mandibles.



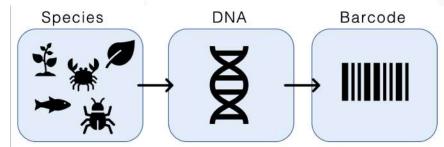
Gene sequencing

4

- Molecular validation of MI taxa was achieved through DNA barcoding.
- Deposition of over 100 gene sequences in the BOLD Gene Bank (https://v3.boldsystems.org/index.php/MAS_Management_UserConsole)
- Sequences, the **first-ever from Serbia and the Balkans**, provide foundational data for future research on population genetics, inbreeding management and evolutionary studies.
- Our findings underscore the necessity of integrating traditional morphological, molecular and AI-based tools for comprehensive species identification and biodiversity applications.









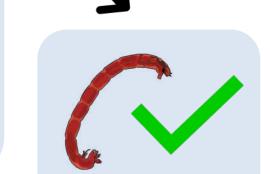
Unknown taxon

ATAAAGTATTGGAACATTATATTTTT GGAGCCTGATCAGGTATAGTGGAACTTCCC TAAGAATTCTAATTCGAGCTGAATTGGACA **TGCCGGTTCTTTAATTGGTGATGACCAAAT TTATAATGTAATTGTTACAGCTCATGCTTTT** AATTGAGGTTTTGGAAACTGATTAGTTCCT TTAATATTAGGGGCCCCAGATATAGCTTTC **CCTCGAATAAATAATATAAGTTTTTGAATA** TTACCTCCTTCTTTAACATTATTGTTATCTAG ATCTATTGTGAAAACGGAGCTGGGACAGG **ATGAACTGTTTACCCTCCTCTATCTTCTGGA GCTATTTTTCTTTACATTTAGCAGAATTTC** TTCTATTTTAGGAGCTGTAATTTTATTACTA **CTGTAATTAATATACGATCAAATGGAATTA** CTTTAGACCAAATACCTTTATTTTTTGATCT **GTTATTACTGCCGTTTTATTGTTACTTTC TTTACCCGT**

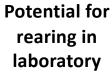


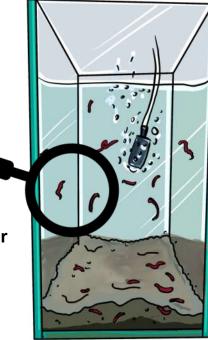


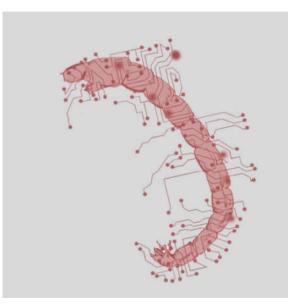
BOLD Gene Bank



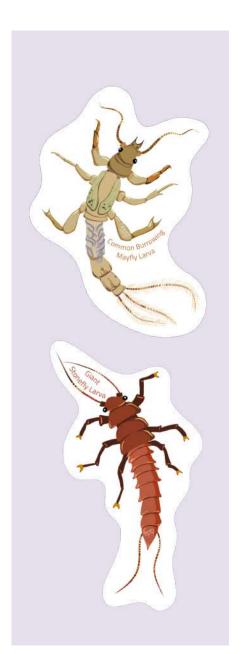








CONCLUSIONS



Our results demonstrate that deep learning can significantly enhance bioassessment by improving the identification of macroinvertebrates.

This approach addresses long-standing challenges in ecology and biodiversity research while tackling critical issues in biomonitoring.

These findings provide valuable insights into ecosystem health and highlight the potential of these taxa to be used as model organisms in future laboratory studies, given their role as bioindicators of environmental changes.

By integrating these methodologies and databases, this study not only improves taxonomic resolution but also establishes a framework for future research on Balkan taxa.



Any questions?

You can find me at

ana.samardzic@pmf.edu.rs

Linked with:











Djuradi Milošević Principal Investigator University of Nis







This research was conducted under the AIAQUAMI project number 7751676 awarded to D.M. funded by the Science Fund of the Republic of Serbia through the programme IDEJE PN; provided from the budget of the Republic of Serbia and the World Bank project - the Serbia Accelerating Innovation and Entrepreneurship Project (SAIGE).

You can find out more at: https://aiaquami.elfak.ni.ac.rs/







Katarina Stojanović University of Belgrade Faculty of Biology



Dimitrija Savić-Zdravković University of Nis-Faculty of Sciences and Mathematics



Predrag Simović University of Kragujevac Faculty of Sciences and Mathematics



University of Niš Faculty of Sciences and Mathematics

Ana Samardžić



We acknowledge the financial support of the COST Action 22140, Insect-IMP: Improved Knowledge Transfer for Sustainable Insect Breeding



