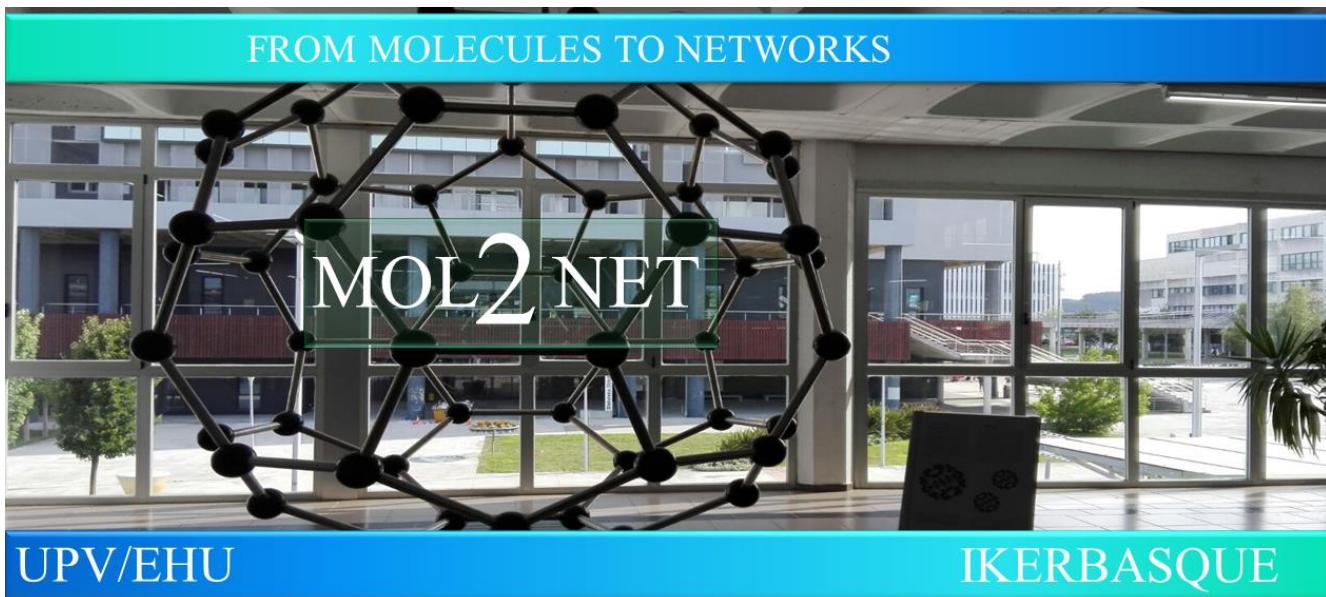




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Predicting Antimalarial Activity using Atomic Weight Vectors and Machine Learning

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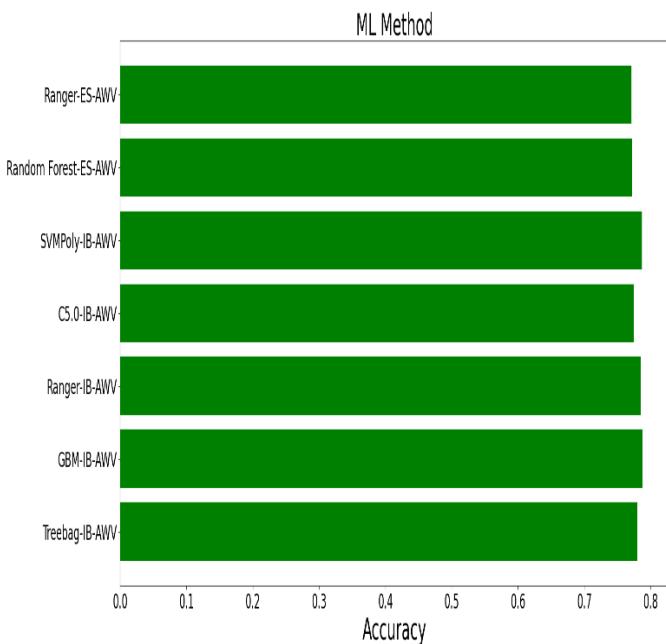
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Graphical Abstract



Abstract.

Malaria is a disease caused by the Plasmodium parasite, which is transmitted through the bites of infected mosquitos. Only the Anopheles genus of mosquito can transmit malaria. The symptoms of this disease can include fever, vomiting, and headache. As millions of people are exposed to the threat of the Plasmodium parasite, it leads to millions of deaths annually. Therefore, there is a need to develop models for predicting compounds that can counteract this disease.

Objective: The primary objective of this research was to employ different techniques of machine learning on molecular descriptors obtained from Atomic Weight Vectors (AWV) and MD-LOVIs tool to predict the activity of potential antimalarial compounds.

Methods: Several machine learning techniques such as Ranger-ES-AWV (accuracy = 0.7714), Random Forest-ES-AWV (accuracy = 0.7718), SVMPoly-IB-AWV (accuracy = 0.787), C5.0-IB-AWV (accuracy = 0.7746), Ranger-IB-AWV (accuracy = 0.7854), GBM-IB-AWV (accuracy = 0.7882), and Treebag-IB-AWV (accuracy = 0.7798) were applied to predict the activity of antimalarial compounds.

Results: The results showed that the models obtained using machine learning techniques can be a powerful tool for predicting the activity of antimalarial compounds.

Conclusion: This study demonstrates the potential of machine learning techniques for predicting the activity of antimalarial compounds. These models can be used to identify new compounds with antimalarial properties and contribute to reducing the number of malaria-related deaths worldwide. The experiment file and dataset can be downloaded at: https://github.com/cybervalient/DeepMD_AWV/blob/main/malaria.ipynb and https://github.com/cybervalient/DeepMD_AWV/blob/main/MD-Malaria.zip

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