Title: ***Stacked Ensemble Model With Explainable AI for Early Detection of Heart Disease***

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Abastact: Autophagy is an important cell process that may be critical for various physiological activities as well as maintenance of the cellular bioenergetic and metabolic homeostasis. Identifying the proteins involved in autophagy is essential for understanding autophagy pathways and developing treatments for autophagy-related disorders. This work introduces an innovative approach to the prediction of autophagy proteins that involves the integration of stacking classifiers with the feature fusion of Amphiphilic Pseudo Amino Acid Composition and Amino Acid Composition. Initially, protein sequences are used to extract Amphiphilic Pseudo Amino Acid Composition and Amino Acid Composition features. The complementary data collected by Amphiphilic Pseudo Amino Acid Composition and Amino Acid Composition are then integrated using a feature fusion technique. Stacking classifiers combines multiple base classifiers to improve predictive performance, using the fused features as input. The proposed method proves its efficacy in the identification of autophagy proteins by achieving an impressive accuracy of 0.9606 and the Matthews correlation coefficient (MCC) of 0.9241 on the independent test. Further, our methodology is better than the standard methods in terms of predictive accuracy, as evidenced through comparative analysis. Overall, the current study provides a realistic model for the prediction of autophagy proteins with prospects for use in the protein prediction field as well as the field of bioinformatics and biomedical to enhance future research directions.

Keywords: Autophagy protein Ensemble learning Machine learning Feature extraction StackAPP model

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