Title: StackAMP: Stacking-Based Ensemble Classifier for Antimicrobial Peptide Identification.

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Abstract: Antimicrobial peptides (AMPs) play a vital role in the immune defence systems of various organisms and have garnered significant attention for their potential applications in biotechnology and medicine. There are several approaches to identifying AMPs including clinical isolation and characterization, functional genomics, microbiology techniques, and others. However, these methods are mostly expensive, time-consuming, and require well-equipped labs. To overcome these challenges, machine learning models are a potential solution due to their robustness and high predictive capability with less time and cost. In this study, we explored the efficacy of stacking-based ensemble machine-learning techniques to identify AMPs with higher accuracy and precision. Five distinct feature extraction methods, namely amino acid composition, dipeptide composition, moran autocorrelation, geary autocorrelation, and pseudoamino acid composition, were employed to represent the sequence characteristics of peptides. To build robust predictive models, different traditional machine learning algorithms were applied. Additionally, we developed a novel stacking classifier, aptly named StackAMP, to harness the collective power of these algorithms. Our results demonstrated the exceptional performance of the proposed StackAMP ensemble method in AMP identification, achieving an accuracy of 99.97%, 99.93% specificity, and 100% sensitivity. This high accuracy underscores the effectiveness of our approach, which has promising outcomes for the rapid and accurate identification of AMPs in various biological contexts. This study not only contributes to the growing body of knowledge in the field of AMP recognition but also offers a practical tool with potential applications in drug discovery, biotechnology, and disease prevention.

Keyword: Antimicrobials, Feature Extraction Techniques, Microbial Treatments, Stacking Classifiers.

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