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Assessment of cutting-edge machine learning models to significantly enhance predictions of Lassa fever outbreaks using whole genome sequencing

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Introduction

Lassa fever is a serious and often debilitating viral hemorrhagic illness endemic to some areas of West Africa, presenting a significant public health challenge. This disease is primarily transmitted through exposure to the excreta of infected rodents, highlighting the need for local communities to be aware of potential risks. Timely detection and accurate diagnosis are vital for mitigating mortality rates and effectively controlling outbreaks, as any delays can lead to severe health consequences. In recent years, machine learning (ML) has emerged as a promising approach to enhancing disease prediction and improving diagnostic accuracy in various medical conditions.

Methods

This study rigorously evaluates the performance of several ML models—Logistic Regression, K-Nearest Neighbors, Support Vector Machine, and Naïve Bayes—in predicting Lassa fever infections. The models were meticulously trained and tested using a comprehensive dataset that included diverse clinical and demographic features from patients exhibiting symptoms. Key evaluation metrics were adopted to assess the efficacy of each model, including accuracy, precision, recall (sensitivity), F1-score, macro average, and weighted average

Results

Among these models, the Support Vector Machine (SVM) delivered outstanding performance, achieving an impressive 95% accuracy, 93% precision, 97% recall, and 95% F1-score. These remarkable results emphasize the SVM model's potential as an effective diagnostic tool for Lassa fever, providing an essential resource for healthcare providers in resource-limited settings

Conclusion

This study's findings demonstrate machine learning's effectiveness in addressing public health challenges and lay the groundwork for future research. It is crucial to explore the integration of more diverse datasets and to include additional clinical parameters, which could further refine and enhance the accuracy of predictive models, ultimately leading to better health outcomes for communities affected by Lassa fever.