An Autonomous Cycle of Dengue Clinical Management Data Analysis Tasks

Riya Goyal*

Editorial office, Annals of Experimental Biology, Uxbridge, United Kingdom

***Corresponding Author:** Dr. Riya Goyal, Editorial office, Annals of Experimental Biology, Uxbridge, United*

E-mail: info@scholarsresearchlibrary

ABSTRACT

The most common vector-borne illness in the world is dengue. Medical experts' primary goal is to reduce mortality rates by promptly diagnosing and treating dengue. In this study, we suggest an autonomous cycle that combines data analytic activities to aid in clinical dengue management decision-making. The autonomous cycle supports the diagnosis and treatment of dengue in particular. Artificial neural networks and support vector machines were used in the construction of the suggested system for classification tasks, while a genetic algorithm was used in evolutionary computing for prescription tasks (treatment). With the aid of dengue patient datasets submitted by healthcare facilities, the system was statistically assessed. We used qualitative criteria to evaluate our technology against earlier research. The suggested system can categorize a patient's clinical profile and suggest the most effective course of therapy. A genetic algorithm specifically recommends treatment options for specific patients and classifies dengue with 98% accuracy. Finally, the adaptability and flexibility of our system will enable the addition of new tasks for dengue analysis.

Keywords: Clinical Management, Dengue

INTRODUCTION

Aedes mosquitoes, particularly *Aedes aegypti* and *Aedes albopictus*, are the principal vectors of the arthropod-borne virus disease dengue. As of right now, this illness is thought to be the most significant arbovirosis in terms of morbidity, death, and economic effect worldwide. Dengue cases in the Americas region were reported during epidemiological weeks 1 and 49 of 2021, with a total incidence rate of 118 cases per 100,000 people. The Southern Cone subregion experienced a cumulative incidence of 323 cases per 100,000 residents during this time, whereas the Andean subregion experienced 89 cases per 100,000 residents. Colombia ranks third in the Andean subregion with an incidence of 95 cases per 100,000 people, trailing only Peru and Ecuador, which have rates of 140 and 108 occurrences per 100,000 people, respectively.

World Health Organization (WHO) guidelines for dengue diagnosis, treatment, prevention, and control were published in 2009. Currently, medical professionals utilize these guidelines for the clinical care of dengue, from patient diagnosis to treatment, to prevent complications that could result in fatalities. The disease's diagnosis and treatment are still challenging, though. The key challenge with these two dengue-related topics is the volume of data that the medical team must quickly sort through to choose the best course of action for each patient. This data relates to demographic, clinical, and laboratory aspects like age, symptoms, and indications that a dengue patient might exhibit.

To lower dengue death rates, clinical care of the disease is crucial. To prevent complications that could result in mortality, diagnosis and treatment must be accurate and swift. We set out to create an ACODAT to assist with the clinical treatment of dengue decision-making. Our concept kept track of the quality of the data and fixed any inaccuracies that might have occurred due to missing information, incorrect patient classification, or an imbalance in the dengue categories. The data quality has a significant impact on the models' quality. The superior caliber of the classification models attained in task 2 of ACODAT speaks highly of the caliber of

the training data. Despite the rise of data-driven solutions in recent years, modeling in medicine still faces difficulties with this element.

In this paper, an ACODAT-based clinical DSS for dengue was proposed. The goal was to create a system that enables data processing, patient classification based on dengue type, and suggestion of the best treatment option from a list of possible medications based on this final attribute. The developed ACODAT can process the data and get it ready for the subsequent activity in the cycle. The AI methods SVM and ANN employed can accurately categorize patients with high performance. According to symptoms, indicators, and laboratory tests, the GA utilized in the final task of the cycle has the potential to recommend (prescribe) the optimal treatment option. The collaborative usage of data analysis tasks in a cycle provided significant advantages over independent methods. It's time to diagnose one of them. The suggested method makes it possible to automatically diagnose and suggest patient treatment. This is particularly significant since catching dengue at an early stage can prevent complications and patient death. To the best of our knowledge, this is the first study to support the clinical therapy of dengue using an autonomic strategy. The prescriptive paradigm for the clinical management of this condition is also being proposed for the first time in this work. There are a few restrictions to this study. First, some variables that were crucial to the medical professional's entire assessment process were not available for inclusion in the models' implementation. The lack of cohort datasets (before/after) to confirm whether the suggested treatment had a positive impact on the patient's health is the second issue. It is necessary to validate the study's findings in actual hospital settings to achieve the latter.

CONCLUSION

The goal of future research should be to enhance the models used with common laboratory tests including white blood cell counts, blood levels of liver enzymes, and cytokines. Additionally, because these conditions have an impact on how severe dengue is, the inclusion of comorbidities like diabetes and arterial hypertension may enhance the performance of the models. To validate the outcomes of prescriptive models, it would be helpful to provide datasets including prescriptive or treatment factors.