

Chapter 55

The Diagnosis of Dengue Disease: An Evaluation of Three Machine Learning Approaches

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ABSTRACT

This article describes how Dengue fever is a fatal and hazardous disease resulting from the bite of several species of the female mosquito (principally, Aedes aegypti). Symptoms of the dengue fever mimic those of a number of other infectious and/or mosquito-borne tropical diseases such as Viral flu, Chikungunya, and Zika fever. Yet, with dengue fever, human life can be more at risk due to severe depletion of blood platelets. Thus, early detection of dengue disease can ensure saving lives; furthermore, it can help in making a preventive move before the disease progresses to epidemic proportion. Hence, the target of this article is to propose a model for an early detection and precise diagnosis of dengue disease. In this article, three prevalent machine learning methodologies, including, Artificial Neural Network (ANN), Decision Tree (DT) and Naive Bayes (NB) are evaluated for designing a diagnostic model. The performance of these models is assessed utilizing available dengue datasets. Results comparing and contrasting performance of diagnostic models utilizing accuracy, sensitivity, specificity and error rate parameters showed that ANN-based diagnostic model appears to yield better performance measures over both the DT and NB models.

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1. INTRODUCTION

Dengue is a mosquito-infected viral disease that can spread quickly under tropical climatic conditions. Principally communicated actively through the bite of female mosquitoes named '*Aedes aegypti*', dengue growing prevalence is primarily due to variations in rainfall, temperature, and unplanned rapid urbanization. Today, dengue cases have proliferated around the globe; notwithstanding, the real number of dengue cases are either never or sometimes inaccurately disseminated.

As per World Health Organization (WHO) report (Bhatt et al., 2013), about 390 million dengue cases have been noted worldwide each year; out of this, 96 million are clinically defined and revealed with the severity of disease. Another source on the occurrence of dengue disease indicates that dengue viruses can infect upward of 3.9 billion people across 128 countries (Brady et al., 2012). Importantly, the number of registered dengue cases has grown from 2.2 million (in 2010) to 3.2 million (in 2015). To date, it is considered among one of the most lethal viral diseases on the planet; undeniably, one of a tropical virus infections with significant morbidity and fatality rate (Bubler, 1998). Dengue, in and of its own, has been perceived to be endemic in India for over two centuries as a benign and self-limited disease. More recently, the contamination moved its course to show up as a real sort of dengue hemorrhagic fever (DHF) with repeats of similar extended scenes (Gupta, Dar, Kapoor, & Broor, 2006). Dengue disease in a formerly non-invulnerable host creates a key reaction of antibodies described by a moderate and low-titer counteracting agent reaction. The IgM counteracting agent is the vital immunoglobulin Isotype to appear. Recent infection is often suggested by the presence of anti-dengue IgM antibodies inspeculated dengue cases. Anti-dengue IgM detection utilizing an enzyme-linked immunosorbent assay (ELISA) stands out as amongst the most vital advances, which has become a telling method for routine dengue diagnosis (Hati, 2006).

Lately, various decision support systems (DSS) and diagnostic models have been deployed for enhancing encounters and capacities of physicians for more precise detection and diagnosis of various diseases. Among the more popular methodologies include multilayer neural networks (MLNNs) to replace conventional pattern recognition methods for the disease diagnosis and training of available data sources (Temurtas, 2009); machine learning (Sengur, 2008) and specialized algorithms for different disease diagnosis (Sengur, 2008), including Naive Bayes (NB), J48 (an open source Java implementation of the C4.5 algorithm) and OneR (one rule classification) approaches (Soman, & Bobbie, 2005). More recently, dengue disease has been a focus for a growing research community with the emergence of an expert system (ES) for the precise sensing and diagnosis of the disease. Symptoms of the dengue fever mimic those of a number of other infectious and/or mosquito-borne tropical diseases such as Viral flu, Chikungunya, and Zika fever. Yet, with dengue fever, human life can be at more risk due to severe depletion of blood platelets. Thus, the motivation for this work is to search for a fitting diagnostic model for early detection and more precise diagnosis of dengue disease. To fulfill this mandate, dengue disease related data samples are being gathered from the different hospitals in the Delhi region in 2016. A total of 110 data samples were collected, out of which 85 data samples have been classified as dengue positive and the rest as dengue negative. The specific contribution of this study to the research community is highlighted in *section 1.1*.

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