Platform for monitoring arboviruses

Subjects: Computer Science, Artificial Intelligence Contributor: Patricia Takako Endo, Sebastião Rogério

As part of SDG, the members of the UN aim to end epidemics of neglected tropical diseases by 2030. These include wide range communicable diseases that prevail in tropical and subtropical conditions. These diseases are present in over 149 countries worldwide and are a significant burden on health systems and economies. One major category of neglected tropical disease are arthropod-borne viruses or arboviruses including West Nile virus, yellow fever, dengue, chikungunya and Zika. Arboviruses spread rapidly and as they present very similar symptoms, it is hard to diagnose and select the best treatment. The use of machine learning for the diagnosis and prognosis of these diseases has become increasingly common however there is a paucity of research on deep learning and associated decision support platforms for frontline staff.

Keywords: arbovirus ; deep learning ; classification

Introduction

In 2015, all United Nations (UN) member states adopted Agenda 2030 for Sustainable Development comprising 17 sustainable development goals (SDGs) "*to end poverty, protect the planet and improve the lives and prospects of everyone, everywhere*" by 2030. <u>SDG 3</u> (Health and Wellbeing) includes ending epidemics of neglected tropical diseases (NTDs). NTDs are a wide range of communicable diseases that prevail in tropical and subtropical conditions in 149 countries and affect one billion people every year^[1].

One major NTD category are arthropod-borne viruses or arboviruses. While over 100 mosquito-transmitted viruses are known that can infect humans, the two most important vectors of arboviral diseases are *Aedes aegypti* and *Aedes albopictus*; these are vectors for dengue (DENV), chikungunya (CHIKV), Zika (ZIKV), and Yellow Fever amongst others. Arborviral diseases have become a worldwide health problem due to a variety of factors influencing the global distribution of disease vectors not least globalization, climate change, habitat modification, and increased human and animal populations and their movement^[2]. The ability of arborvirus disease vectors, and in particular *Aedes aegypti*, to thrive in urban and semi-urban areas enables infected mosquitoes access large urban populations^[3]. As poor quality housing and neglected peri-domestic environments are significant risk factors in the transmission of these viruses, the poor are disproportionately affected^[4]. This is not to say these diseases are restricted to poorer nations; there are nearly 3,000 cases of West Nile Virus (WNV) in the US each year^[5] and arboviruses have expanded in to traditionally naive areas across Europe^[6]. These diseases have a significant economic burden resulting from both morbidity and mortality including the costs of vector control, case management, reduced workforce, and less tourism in endemic areas^[4].

Arboviruses are a particular public health risk in Brazil due to a convergence of transmission factors including disordered urban growth, population migration (both internally and from other countries), social, economic, environmental, and climatic conditions. In addition to endemic viruses, a number of arboviruses have recently emerged in Brazil e.g. WNV in 2009, CHIKV in 2014, and ZIKV in 2015^[Z]. The impact and economic burden of these diseases in Brazil cannot be underestimated. Up to September 2019, 1,439,471 probable cases of DENV were registered in Brazil, 110,627 of CHIKV and 9,813 of ZIKV^[8]; neither CHIKV nor ZIKV existed in Brazil before 2014.

Accurate reporting of arbovirus cases in Brazil is a significant challenge. For example, of the 56,300 DENV notifications in Pernambuco in 2019, only 17,810 were confirmed; of the 7,562 notifications of CHIKV, 700 were confirmed; and of the 3,524 notifications of ZIKV, only 106 were confirmed^[9]. These variances can be explained by the concurrent circulation of several arboviruses which present similar symptoms; inaccurate serologic tests resulting from cross-reaction; and co-infection with other arboviruses^[2]. The concurrent circulation of different arboviruses in Brazil combined with the associated epidemiological challenges in traditional analysis and associated financial cost, particularly where there are competing pressures for funding (e.g. COVID19 and malaria interventions), requires novel approaches to differential diagnosis of arboviruses for both entomological and epidemiological surveillance.

Given the operational challenges and limitations related to diagnostic confirmation in Brazil, and particularly in epidemic and pandemic periods, and for areas with restricted access, the development of computational models for monitoring and diagnostic classification based on clinical data, symptoms and laboratory tests presents itself as a low-cost solution that can contribute to improving the accurate recording of confirmed cases of DENV, CHIKV, ZIKV, WNV and other arboviruses.

Machine learning has been widely used for the classification of events in entomology and epidemiology due its capacity to process large volumes of data, suitability for outcomes with multiple categories, as well as the need for few premises. In recent years, studies have explored the use of deep learning to recognize the *Aedes aegypti* mosquito through images to detect disease outbreaks^{[10][11][12][13]}. Chakraborty et al.^[14] investigated the use of hybrid machine learning to predict DENV epidemics and assist health authorities to better target available resources in areas most prone to such epidemics. Unlike extant works, our study focuses on the classification seeks to support the clinical diagnosis of arboviruses based on cases of febrile and/or exanthematic syndromes in concomitant arbovirus scenarios.

Proposal

Figure 1 presents a high level architecture of the initial platform for monitoring and clinical diagnosis of arboviruses using machine learning models. There are three main modules decision support, monitoring, and graphical interface.

Figure 1. Proposed Monitoring and Clinical Diagnosis Platform for Arboviruses using Computational Models [15]

The decision support module uses the data available in Brazilian health databases. These databases are characterised by inconsistencies, maintenance, and integration issues. Deep learning models are proposed for the classification and prediction of arbovirus epidemics. The selection of predictors must be driven by and validated by a health professional to avoid possible bias in the results. Similarly, in advance of the model design, Exploratory Data Analysis (EDA) of the historical data is required to identify patterns, and thus assist in selecting the most appropriate best deep learning techniques. The monitoring module will monitor data from the available databases and generate inputs for the graphical interface, such as epidemic alerts.

Since the results of this work intend to improve the classification capacity of the different existing arboviruses, this research can contribute to improved entomological and epidemiological surveillance, vector control and disease mitigation, more effective clinical management and patient treatment, and more efficient turnaround of timely data-driven recommendations to policymakers.

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