Dengue Hotspot Detection in Bangi, Selangor, Malaysia

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Abstract. Dengue fever has increased dramatically in Malaysia in recent decades and has triggered tremendous public health concerns. This paper addresses the spatial and temporal aspects of Dengue epidemics in Selangor, Bangi. This study aimed to examine spatial diffusion trends and to recognize hotspots in recorded dengue cases. The study used the Malaysia Ministry of Health epidemiological data for dengue cases reported in 2016-2019. These data have been processed and converted into GIS format. The geospatial spread pattern of the 2016, 2017, 2018, and 2019 dengue outbreak was investigated and mapped. The hotspot analysis is shown as points on a map and refers to dengue cases locations in the study area and measures the Getis-Ord Gi statistics for dengue cases in 2016-2019. The related z-scores and p-values are shown spatially in the Bangi region with either a cluster of high or low values. The map produced from data range between -3 (cold spot -99% confidence level) to 3 (hotspot – 99% confidence level) is classified into very low, low, very high, and high dengue fever clustered in the urban area.

Keywords: spatial-temporal, hotspot, dengue, urban

1. Introduction

Dengue is a disease caused by a virus transmitted by bites of mosquitoes. This is an Aedes aegypti mosquito-borne viral disease. Dengue Fever is a significant cause of illness and death in tropical and subtropical areas, and more than a third of the global population lives in vulnerable regions [1]. Dengue disease ranges from the hemorrhagic fever that is mild to dengue. Most of the dengue vector distribution varies depending on the rainfall [2]. In Southeast Asia, dengue is a rapidly developing pandemic-prone viral disease. There is also a dengue outbreak in the Philippines, Thailand, Laos, Vietnam, Singapore and, Indonesia, as well as in Malaysia.

WHO has confirmed that from January to 16 November 2019, there were 114,745 cases, including 158 killed. This is higher than the 66,570 cases reported with 111 deaths in the same timeframe in 2018 [3]. Increasing dengue cases are causing acute health care and concern among stakeholders and government agencies in Malaysia. There were no specific anti-viral therapies, however, and the vaccine licensed was concerned about the increased risk of hospitalization [4]. The rapid spread is continuing despite considerable efforts in research and control methods, resulting in a significant concern in Malaysia.

Elements of dengue transmission are involved, including viruses, vectors, and hosts. Several factors such as climatic factors (temperature, precipitation, wind, and relative humidity), human movement and
behavior, sociological, cultural, demographic, and ecological factors influence these parameters (virus, vector, and human host) [5].

The Dengue vector breeding environment, Aedes mosquitoes, has triggered rapid urban growth with extensive land-uses processes through the construction of new cities and services and population growth needs [6]. The rapid spread of dengue cases in many countries is due to globalization, rapid unplanned urban development, poor water storage, and inadequate sanitation. Climate change also contributes to the spread of dengue virus in Malaysia over the past four decades, such as rising temperatures, increased rainfall, and increased humidity [7]. A more profound comprehension of the dynamics of time and dengue area can help to establish mitigation strategies to prevent disease and also to protect dengue-risk countries' lives and economic costs. Researchers have previously collaborated with an academic analysis of dengue surveillance to evaluate dengue transmission through predictive statistical analysis and space-time analysis of mosquito distribution and sites. The analysis of outbreak transmission using GIS mapping is, therefore, becoming increasingly relevant for disease control and management [8-10,12].

GIS has played a significant role in mosquito-borne disease monitoring and control in recent years. Having maps which are useful to classify areas with an inevitably serious dengue danger is critical to controlled the mitigation level and to consider the disease connected to the vector. In addition to providing an opportunity to improve our knowledge of dengue transmission trends, GIS can also provide an environmentally and socially conscious forum for developing elements of a dengue control and prevention early warning system [1].

2. Material and method

2.1. The study area

This study is located in the city of Bangi, in the district of Hulu Langat, Malaysia. With coordinates of 2°55'20.6"N and 101°46'50.6"E, Bangi is situated 38 km south of Kuala Lumpur. Bangi is of a town in Hulu Langat, Selangor's southern district. Located between the towns of Kajang and Putrajaya, it is becoming increasingly popular with hunters of property. Kajang, Putrajaya, Cyberjaya, Nilai, and Seremban's neighboring townships are a catchment area of approximately 1.2 million residents.
Bangi via Kajang to Kuala-Lumpur. It is also linked by the KTM train, and soon by the new Sungai Buloh-Kajang (SBK Line) Mass Rapid Transit (MRT). The growth of infrastructure, settlement, and road networks increases the density of the population in Bangi [13]. Despite urbanization, mosquito-borne viral disease in the study area has increased rapidly. Bangi developed rapidly towards urbanization, with a total population of 4811.

2.2. Methodology

2.2.1. Data Collection

Dengue fever details from the Malaysian Minister for Health have been recorded from the Ministry of Health in 2016-2019 in both government and private hospitals in Bangi by hospital patients. Over the city of Bangi, there are 4507 positive cases of dengue. Patient position coordinates are derived from the ArcMap10.5 info.

2.2.2. Spatiotemporal analysis

Statistical analysis is essential for evaluating dengue spatial distribution and for understanding the factors that may be correlated with the frequency of the cases [11]. The spatial distribution of dengue cases in the Bangi region has been mapped and analyzed using ArcGIS 10.5 spatial statistical tools. The point pattern analysis was used to assess whether there is significant clustering of points in a specific area. The ArcGIS10.5 software tool used in the analysis was the Spatial Autocorrelation and Getis-Ord Gi* (Getis-Ord Gi* statistics (pronounced G-i-star) measured in Hot Spot Analysis. This approach offered an intuitive visual presentation of results related to the spread of infections and spatial clusters at various stages of outbreaks in dengue history. The numerical value of Getis-Ord Gi* was measured using this method, and z-scores and p-values were determined to test the null random distribution hypothesis of the attribute being evaluated. Such findings were used to determine whether the cases of dengue were distributed across the entire study region in a statistically significant manner.

The Getis-Ord local statistic is given as:

\[ G^*_i = \frac{\sum_{j=1}^{n} w_{i,j} x_j - \bar{X} \sum_{j=1}^{n} w_{i,j}}{\sqrt{n \sum_{j=1}^{n} w_{i,j}^2 - \left( \sum_{j=1}^{n} w_{i,j} \right)^2}} \]

If the value of \( x_j \) for function \( j \) is, \( w_{i,j} \) is the spatial weight between \( i \) and \( j \), \( n \) is equal to the total number of functions and:

\[ \bar{X} = \frac{\sum_{j=1}^{n} x_j}{n} \]

\[ S = \sqrt{\frac{\sum_{j=1}^{n} x_j^2}{n} - \left( \bar{X} \right)^2} \]

The \( Gi \) statistics are a z-score; therefore no further calculations are required

3. Result
The outcome of the hot spot analysis is three values, which are the Nearest Neighbor (NN), z-scores, and p-value. The distribution of dengue cases in Bangi was generally found to be spatially clustered with significant z-scores and low p-value. The z-scores are a statistically significant indicator of whether to reject the null hypothesis or not. The null hypothesis in this study claimed that there is no spatial trend in Bangi among dengue cases.

Figure 2. Hot spot cluster map (2016)

Figure 3. Hot spot cluster map (2017)
Figure 4. Hot spot cluster map (2018)

Figure 5. Hot spot cluster map (2019)

The dengue cases are spatially clustered with strong $z$-scores and the null hypothesis is rejected. The main hot spot was categorized by association type as: yellow (high) and red (very high) indicating high spatial clusters, pink (low) and blue (very low) indicating low spatial clusters. The overall distribution of dengue hot spot within Bangi is high in 2017 ($NN = 750; z$-scores = 12.75; $p$-value < 0.8), 2016 ($NN$
= 253; z-scores = 12.19; p-value < 0.9), 2019 (NN = 199; z-scores = 9.14; p-value < 0.9) and 2018 (NN = 127; z-scores = 6.75; p-value < 0.9).

Dengue hot spot maps have been used to gain a better understanding of the spatial trend and pattern of vulnerabilities in dengue cases. In 2017, the hot spot with the highest dengue cases was clustered and concentrated in the northeastern district of Bangi. The results are similar to 2016, which clustered in the northern part of Bangi as well. In 2018, the hot spot map showed that dengue cases are highly concentrated in the south and east of the study area. Though, the hot spot dengue maps were focused on the northeast in 2019, close to those of 2016 and 2017. This is demonstrated by the high incidence of dengue cases in urban areas such as Kajang and Bandar Baru Bangi.

4. Discussion

Spatial research has a long history of epidemiology, but GIS epidemiological studies have only emerged in the last decade. GIS is becoming more prominent in disease control with the development of computer technology and spatial analysis methods. Monitoring and preparing for dengue have recently become crucial to the prevention of outbreaks of disease. Therefore, this article aimed to provide useful information on dengue incidences and to map their diffusion patterns and dynamics. Analysis of spatial tools is another platform for the analysis and proof of changes in spatial patterns over time. The study found that the location is critical for mosquito breeding. Urban areas provide habitats for the breeding of Aedes mosquitoes with appropriate weather and precipitation.

Dengue is an infectious disease highly transmissible due to its mosquito vector Aedes aegypti, which is well suited to the urban environment [15]. This rapid economic development over the past 15 years and the associated rising urbanization, as well as the growing population mix made possible by the country’s new transport network, could have led to increased homogeneity in the threat of dengue between urban areas over time [16]. Urban growth provides suitable breeding spaces and locations. In contrast, the Aedes mosquitoes are provided with good food sources and vector by a higher population of humans and animals. This is the critical point as the hotspot area is located in the north and east parts of Bangi. In addition to the increase in growth in the district of Bangi, dengue epidemiology needs to be monitored to ensure that its urban residents are free of the fear of health problems in the city, driving human migration into their urban areas [17].

5. Conclusion

Within the area of research, dengue case epidemiology, spatial statistical distribution, and trend analysis play a crucial role. This is how specific processes derive spatial distribution and trends. Hotspot analysis shows that the dengue cases in the years 2016-2019 are clustered and concentrated at the main urban area of the study site. Dengue is now spreading globally through potential urbanization, globalization, climate, human behavior, and lack of vector control. Therefore, if rapid population growth and continued urbanization continue as predicted, the rate, frequency, geographical distribution, and severity of dengue epidemics will increase gradually in the future.

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