

Hotspot Analysis of Dengue Hemorrhagic Fever Using Getis-Ord Statistic: Evidence from Ho Chi Minh City in the 32nd Epidemiological Week

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Abstract

Background: Dengue hemorrhagic fever (DHF) continues to pose a serious public health threat in Ho Chi Minh City, where recurrent outbreaks are sustained by complex socio-environmental and urban dynamics. Hotspot analysis of DHF is essential for guiding targeted interventions, as uniform citywide measures are often inefficient. This study applies spatial statistical techniques to detect hotspots of DHF during the 32nd epidemiological week of 2025.

Methods: Confirmed DHF cases aggregated at the ward level were analyzed using descriptive mapping, boxplot visualization, and scatter plots to explore spatial heterogeneity and the relationship with population density. The Getis-Ord G_i^* statistic was employed to identify statistically significant hotspots (high-high clusters) and coldspots (low-low clusters). Significance testing at multiple confidence levels (95%, 99%, 99.9%) was used to validate cluster strength.

Results: The descriptive analysis revealed a right-skewed distribution of DHF incidence, with most wards reporting low to moderate case numbers and a small subset exceeding 70 cases. The relationship between population density and case counts was weakly negative, indicating that density alone does not explain spatial variation. Hotspot analysis identified 20 wards as significant high-high clusters, concentrated in the central-northern urban core, and 13 wards as low-low coldspots in peripheral districts. Several wards showed highly significant clustering ($p \leq 0.01$), highlighting critical foci that disproportionately contributed to the epidemic burden.

Conclusions: Dengue hemorrhagic fever transmission in Ho Chi Minh City during Week 32, 2025, was characterized by localized hotspots embedded within a largely neutral background. These findings emphasize the utility of spatial statistics in detecting high-risk zones and provide actionable guidance for geographically targeted interventions. By prioritizing vector control, surveillance, and community engagement in hotspot wards, public health authorities can optimize resource allocation and enhance the effectiveness of dengue control programs.

Keywords: Dengue Hemorrhagic Fever; Hotspot analysis; Getis-Ord G_i^* statistic; Spatial Clustering; Ho Chi Minh City; Vietnam; Epidemiology

1. Introduction

Dengue hemorrhagic fever remains one of the most significant mosquito-borne viral diseases worldwide, causing recurrent outbreaks and posing a substantial public health burden, particularly in tropical and subtropical regions. The World Health Organization estimates that approximately 390 million dengue infections occur annually, of which about 96 million manifest clinically (1). Southeast Asia has been recognized as one of the most affected regions, where dengue

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continues to cause morbidity, mortality, and economic disruption (2). In Vietnam, dengue has become endemic in nearly all provinces, with the highest incidence recorded in southern urban areas such as Ho Chi Minh City. In Ho Chi Minh City, dengue outbreaks impose recurring pressures not only in terms of morbidity and mortality but also in economic and social burdens. For example, by mid-July 2025 (epidemiological week 28), over 15,500 dengue cases were reported in the city, marking an approximately 159.4% increase compared with the same period in 2024. Average treatment cost per case has been estimated at USD 61.36 in Ho Chi Minh City in some studies, while more comprehensive national estimates place the cost per case (all ages) at USD 139.2 ± 61.7 , representing a substantial financial burden for both health care systems and households. The rapid pace of urbanization, coupled with high population density and inadequate waste and water management, creates favorable breeding habitats for *Aedes aegypti*, the principal vector of dengue (3,4). Seasonal patterns driven by rainfall and temperature variability further exacerbate transmission dynamics, resulting in recurrent outbreaks that challenge the healthcare system (5).

Spatial epidemiology has emerged as an essential tool in understanding the geographical distribution of vector-borne diseases. Unlike conventional epidemiological analysis, spatial methods allow for the identification of localized high-risk areas, or “hotspots,” that may not be apparent in aggregate statistics (6). Among these approaches, local spatial autocorrelation techniques, such as the Getis-Ord G_i^* statistic, are particularly effective in detecting spatial clustering of disease cases (7). These methods provide valuable evidence for public health interventions by identifying areas where resources should be prioritized. Several studies have successfully applied spatial autocorrelation and hotspot analysis to vector-borne diseases. For example, research in Thailand and Indonesia has shown that dengue cases often cluster in urban neighborhoods, and these hotspots persist over time (8,9). In Brazil, hotspot analysis was used to identify persistent dengue transmission zones, guiding vector control strategies and targeted community engagement (10). Spatial autocorrelation methods have become essential for understanding the spatial dynamics of infectious diseases, including dengue. Traditional approaches such as Moran’s I provide valuable insights into global clustering but may overlook localized variations in disease risk (11,12). To capture these patterns, hotspot statistics like the Getis-Ord G_i^* have been increasingly employed to identify significant spatial concentrations of cases, distinguishing “hotspots” (areas of unusually high incidence) and “coldspots” (areas of low incidence) (12,13). Applications of Getis-Ord statistics in dengue research have expanded in recent years, with studies in Thailand, Indonesia, and the Philippines demonstrating the utility of hotspot analysis for identifying neighborhoods where socio-environmental and vector-related factors drive transmission (14–16). In Vietnam, research has shown that dengue distribution is strongly shaped by urban density, climate variability, and human mobility patterns (17). More recent work emphasizes that combining hotspot analysis with epidemiological data enhances the ability to inform spatially targeted interventions and optimize vector control strategies (18,19). The Getis-Ord G_i^* statistic offers clear advantages, particularly for public health planning, by providing a direct measure of clustering intensity and highlighting priority areas for intervention where the burden of dengue is highest (12,20). However, in Vietnam, applications of such advanced spatial statistics to dengue surveillance remain limited, despite the recurrent outbreaks and the availability of case-based surveillance data.

Therefore, this study applies the Getis-Ord G_i^* statistic to analyze dengue hemorrhagic fever cases reported during the 32nd epidemiological week in Ho Chi Minh City. The objective is to identify statistically significant hotspots and coldspots of dengue transmission, thereby providing evidence for more precise and effective control measures. The results are expected to contribute to strengthening spatially explicit dengue surveillance and to support decision-making in resource allocation for vector control.

2. Data used and methods

2.1. Data used

Data on confirmed dengue hemorrhagic fever cases were obtained from the Ho Chi Minh City Center for Disease Control (HCDC) for the 32nd epidemiological week of 2025. The dataset consisted of laboratory-confirmed cases aggregated at the ward level, covering all administrative wards across the city. To ensure comprehensive spatial representation, wards with zero reported cases were retained in the dataset. Population statistics for each ward were collected from the Ho Chi Minh City Statistical Office (2025) and used to calculate population density (persons per square kilometer). These data enabled assessment of the relationship between DHF incidence and demographic distribution across the city. Geospatial data, including administrative boundary shapefiles at the district and ward levels, were acquired from the Department of Land Administration, Ministry of Natural Resources and Environment of Vietnam. These shapefiles served as the spatial framework for mapping DHF cases and for constructing the spatial weights matrix required for hotspot analysis. Together, the epidemiological, demographic, and spatial datasets provided the basis for descriptive epidemiology, population density correlation analysis, and the Getis-Ord G_i^* hotspot analysis. This integration allowed for both visualization of case distribution and identification of statistically significant clusters of DHF transmission in Ho Chi Minh City.

2.2. Methods

Getis-Ord G_i^* statistic-based Hotspot Analysis

To detect hotspots of dengue hemorrhagic fever cases, this study employed the Getis-Ord G_i^* statistic, a widely used local spatial autocorrelation measure for hotspot analysis. Unlike global statistics that provide a single measure of spatial association across the study area, the Getis-Ord G_i^* statistic identifies localized clusters of high or low values, thereby highlighting areas of elevated or reduced transmission risk. The form of Getis-Ord G_i^* statistic is defined as follows (11):

$$G_i^* = \frac{\sum_{j=1}^N W_{ij} x_j - \bar{x} \sum_{j=1}^N W_{ij}}{S \sqrt{\frac{N \sum_{j=1}^N [W_{ij}^2 - (W_{ij})^2]}{N-1}}} \quad (1)$$

with:

$$\bar{x} = \frac{1}{N} \sum_{j=1}^N x_j \quad (2)$$

and:

$$S = \sqrt{\frac{\sum_{j=1}^N x_j^2}{N} - (\bar{x})^2} \quad (3)$$

Expectation:

$$E(G_i^*) = \frac{W_i^*}{n-1} \quad (4)$$

with:

$$W_i^* = \sum_{j=1}^n w_{ij}(d) \quad (5)$$

and variance:

$$\text{Var}(G_i^*) = \frac{W_i^*(n - W_i^*)Y_{i2}^*}{n^2(n-1)(Y_{i1}^*)^2} \quad (6)$$

with:

$$Y_{i1}^* = \frac{\sum_{j=1}^n x_j}{n}; \quad (7)$$

and:

$$Y_{i2}^* = \frac{\sum_{i=1}^n \sum_{j=1}^n (x_i x_j)^2}{n} - (Y_{i1}^*)^2; \quad (8)$$

where: the Getis-Ord G_i^* statistic is computed for the number of DHF cases at ward i ; x_i , x_j , \bar{x} , and W_{ij} are defined in equation (1); and N is the total number of neighborhood wards as defined in equation (2). W_{ij} can be constructed using

the methods of the first order and second of contiguity. In this study, adjacency to compute W_{ij} is defined using the first order of continuity.

The Getis-Ord G_i^* statistic generates a standardized Z-score for each ward, which indicates the degree to which observed case counts are higher or lower than would be expected under spatial randomness: high positive Z-scores ($p < 0.05$, 0.01, 0.001) indicate statistically significant hotspots (high-high clusters), low negative Z-scores indicate coldspots (low-low clusters), Non-significant Z-scores suggest random spatial distribution. To assess statistical significance, a 999-permutation Monte Carlo test was conducted, and p-values were adjusted to classify clusters at the 95%, 99%, and 99.9% confidence levels. Hotspot results were visualized using Getis-Ord G_i^* cluster maps and corresponding significance maps, which together delineated wards with significant clustering patterns. In addition, descriptive tools including percentile maps, boxplots, and scatter plots were used to contextualize the spatial statistics and provide a comprehensive picture of the epidemiological landscape during the study period.

2.3. Scatter plot analysis

In this study, to explore the relationship between DHF incidence and demographic factors, a scatter plot analysis was conducted using ward-level confirmed case counts and corresponding population density data. This method provides a simple yet informative way to visualize potential associations between disease burden and urban density. Population density (persons per km²) for each ward was calculated using ward population data from the Ho Chi Minh City Statistical Office (2025) and administrative boundary shapefiles. Confirmed DHF case counts from the 32nd epidemiological week of 2025 were then plotted against these density values. In the scatter plot, the x-axis represents population density, while the y-axis represents the number of confirmed DHF cases. A linear regression line was fitted to the data to assess the overall direction and strength of the relationship. The slope of the regression line indicates whether incidence tends to increase or decrease with population density, while the dispersion of points around the line reflects variability across wards. This analysis allowed for the identification of general trends such as positive or negative associations while also highlighting potential outliers, i.e., wards with unexpectedly high or low case counts relative to their population density. By comparing these patterns to results from the hotspot analysis, the scatter plot provides complementary insights into the extent to which urban density influences dengue risk in Ho Chi Minh City.

3. Results and discussion

3.1. Descriptive epidemiology

The spatial distribution of DHF confirmed cases during the 32nd epidemiological week in Ho Chi Minh City revealed substantial heterogeneity across wards (Figure 1, left). The percentile map illustrates that most wards fell within the middle range of incidence (10-50th and 50-90th percentiles), suggesting a broad distribution of moderate case numbers throughout the city. However, distinct high-incidence areas were detected, particularly in the central-northern wards, where two wards exceeded the 99th percentile, reporting between 72 and 77 confirmed cases. These locations represent the most intense transmission zones during the study week. Conversely, peripheral and less densely populated wards predominantly clustered within the lowest percentiles (<10%), reflecting relatively few reported cases. The spatial distribution of confirmed DHF cases in Ho Chi Minh City in the 32nd week of 2025 is heterogeneous rather than uniform. The choropleth map shows several contiguous, high-value polygons embedded within predominantly lower-value surroundings, indicating localized concentrations of transmission. By design quantiles, most polygons fall between the 10th-90th percentiles (≈ 13 -33 cases), while the upper tail is steep: 12 polygons lie in the 90th-99th percentile band (≈ 33 -72 cases), and two polygons exceed the 99th percentile ($\geq \sim 73$ cases). Conversely, a small set of polygons are at the bottom tail (<1st percentile; 2-3 cases).

Data from the boxplot in Figure 1 (right) provides additional insight into the distribution of confirmed DHF cases across wards. The box-and-whisker plot corroborates this right-skewed distribution: the interquartile range is tight (middle half clustered around the low-to-mid 20s), but numerous high outliers extend to the maximum (~ 77 cases). This pattern is consistent with focal amplification of transmission in a minority of places while most areas experience moderate counts. From a surveillance perspective, such dispersion implies that citywide averages mask substantial local burden. The median incidence was low compared to the maximum values, highlighting a right-skewed distribution. A substantial number of wards reported fewer than 20 cases, while a small set of wards recorded exceptionally high case counts, identified as statistical outliers above the upper whisker. These outliers correspond to the extreme high-incidence wards highlighted in the percentile map, indicating that dengue transmission during the study week was highly concentrated in localized hotspots rather than being uniformly spread across the city.

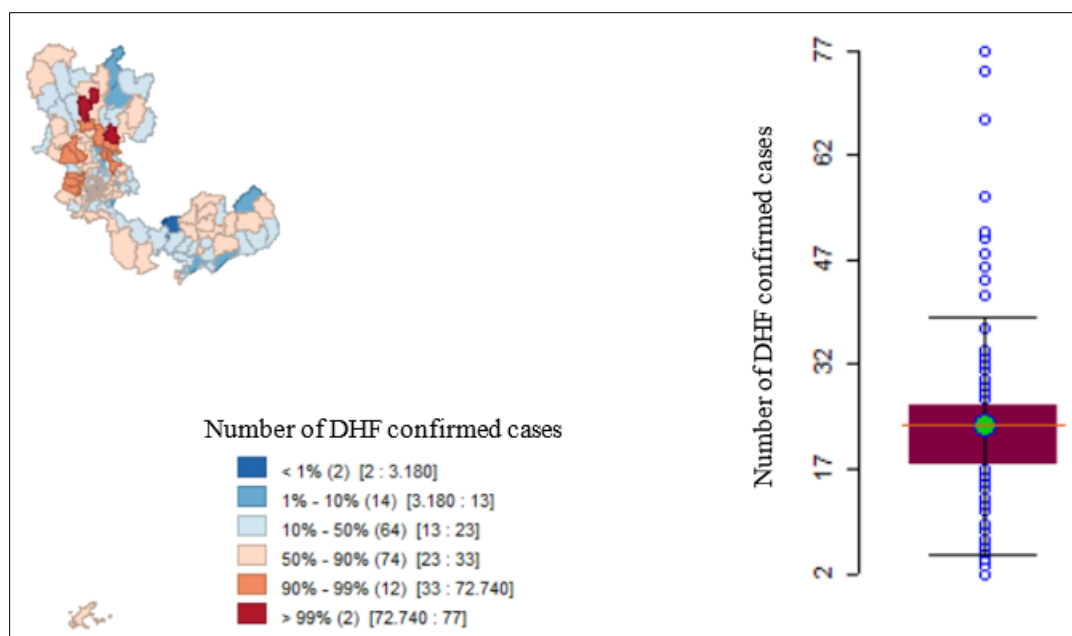


Figure 1 Percentile map (left) and boxplot (right) of DHF confirmed cases

3.2. Relationship between DHF cases and population density

The scatter plot of confirmed DHF cases against population density (Figure 2) reveals a weak and slightly negative association between the two variables. While it is generally expected that higher population density could facilitate dengue transmission due to increased human–vector contact, the observed pattern suggests that this relationship is not straightforward in Ho Chi Minh City. Most wards with very high case counts are concentrated within the lower to moderate ranges of population density, while wards with the highest densities (above 50,000 persons/km²) did not consistently report elevated case numbers. The regression line indicates a subtle downward trend, implying that increasing density alone does not predict higher DHF incidence during the 32nd week of 2025. This finding is consistent with earlier studies that emphasize the multifactorial nature of dengue transmission in urban areas. Although high-density environments create conditions for rapid spread, structural housing differences, water storage practices, and socioeconomic variability may either exacerbate or mitigate actual transmission intensity. In some high-density wards, improved infrastructure and routine control measures may offset the expected risk, while in moderately dense neighborhoods, inadequate waste management and water storage practices may amplify mosquito proliferation and drive case numbers upward.

The wide dispersion of data points around the regression line further underscores the heterogeneity of dengue epidemiology across the city. This pattern indicates that population density should not be considered in isolation but integrated with other determinants, including environmental conditions, socio-economic factors, and micro-scale habitat suitability for *Aedes* mosquitoes. Importantly, the weak overall correlation reinforces the need for spatially explicit approaches, such as hotspot analysis, which can better capture localized clustering patterns rather than relying solely on citywide density metrics. The coexistence of low-incidence peripheral wards and high-incidence urban wards points to the complex interplay of demographic, environmental, and infrastructural factors. These findings provide a strong foundation for subsequent hotspot analysis using the Getis-Ord G_i^* statistic, which evaluates the statistical significance of observed spatial clusters.

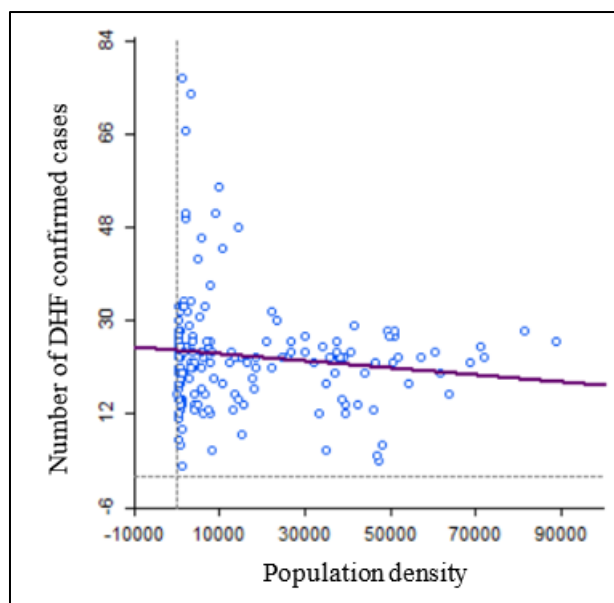


Figure 2 Scatter plot of DHF confirmed cases and population density

3.3. Hotspot analysis of dengue hemorrhagic fever

The Getis-Ord G_i^* statistic was applied to detect statistically significant clusters of DHF incidence across wards in Ho Chi Minh City. The spatial distribution of G_i^* values (Figure 3, left) highlights a clear concentration of hotspots in the central-northern and western parts of the city. These wards not only recorded high numbers of confirmed cases but also exhibited strong local spatial association, indicating that elevated incidence was not random but embedded within spatially reinforcing neighborhood effects. In contrast, several wards in the peripheral southern and eastern districts displayed very low G_i^* values (<0.002), suggesting coldspots with significantly lower DHF activity compared to their neighbors. The accompanying boxplot (Figure 3, right) illustrates the overall distribution of G_i^* values across wards. The median value was modest, reflecting the predominance of wards with weak clustering. However, a subset of wards emerged as statistical outliers in the upper range, confirming the existence of localized high-high clusters. This pattern reinforces the interpretation that dengue transmission during Week 32, 2025, was highly uneven, with a few wards disproportionately contributing to the citywide burden of disease. These results underscore the multifactorial drivers of dengue transmission in dense urban environments. High G_i^* clusters largely overlap with densely built environments characterized by inadequate waste management, abundant artificial water containers, and intense human mobility, which collectively create favorable conditions for *Aedes aegypti* proliferation. Conversely, the persistence of coldspots in peripheral zones may reflect lower human density, better housing structures, or more effective local vector control programs. Such contrasts highlight the importance of accounting for neighborhood-level environmental and infrastructural differences when designing intervention strategies.

From a public health perspective, hotspot identification using Getis-Ord G_i^* statistic provides actionable insights for resource allocation. Interventions such as targeted vector control campaigns, intensified case surveillance, and community-based awareness programs should be prioritized in the identified hotspot wards. By contrast, coldspot areas may require a more preventive approach aimed at sustaining low transmission levels and preventing potential resurgence. It is noteworthy that while the G_i^* statistic effectively delineates high- and low-risk zones, the analysis is limited by the temporal scope of a single epidemiological week. Hotspot dynamics may shift across weeks depending on rainfall patterns, population movement, and intervention coverage. Longitudinal hotspot monitoring would provide a more robust understanding of persistent versus transient clusters, thereby enhancing the capacity of local health authorities to implement timely and spatially targeted dengue control measures. In summary, the Getis-Ord G_i^* analysis confirms the presence of statistically significant dengue hotspots in central-northern Ho Chi Minh City during Week 32, 2025. These findings not only validate the descriptive epidemiology but also provide strong evidence for the utility of spatial statistics in guiding geographically focused public health interventions.

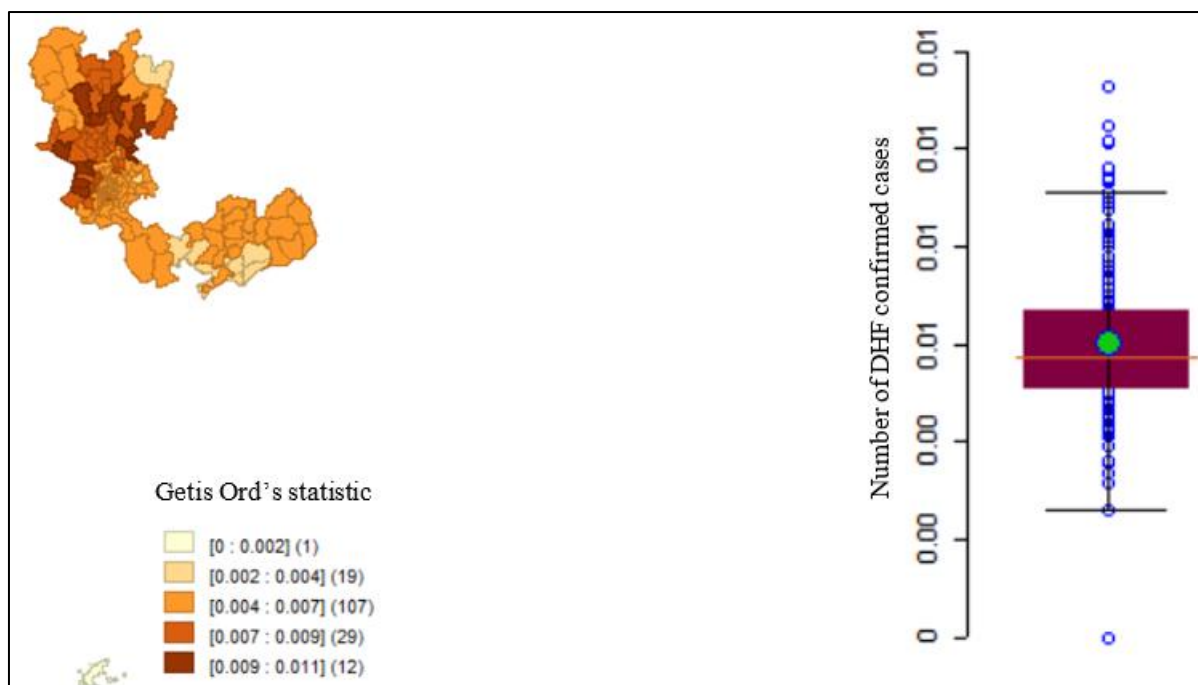


Figure 3 Map (left) and boxplot (right) of Getis-Ord G_i^* statistic obtained from DHF confirmed cases

The hotspot map derived from the Getis-Ord G_i^* statistic (Figure 4, left) reveals clear spatial clustering of dengue hemorrhagic fever (DHF) cases during the 32nd epidemiological week. A total of 20 wards were identified as statistically significant hotspots (high-high clusters), predominantly concentrated in the central and northern urban core of Ho Chi Minh City. These hotspots correspond closely with the high-incidence wards observed in the descriptive analysis, reinforcing the evidence that dengue transmission is strongly localized in specific high-risk neighborhoods. Conversely, 13 wards were classified as coldspots (low-low clusters), located mainly in peripheral and southern areas, reflecting significantly lower DHF activity compared to their surrounding wards. One ward was classified as neighborless due to its lack of spatial adjacency, highlighting the importance of geographic connectivity in local autocorrelation analysis.

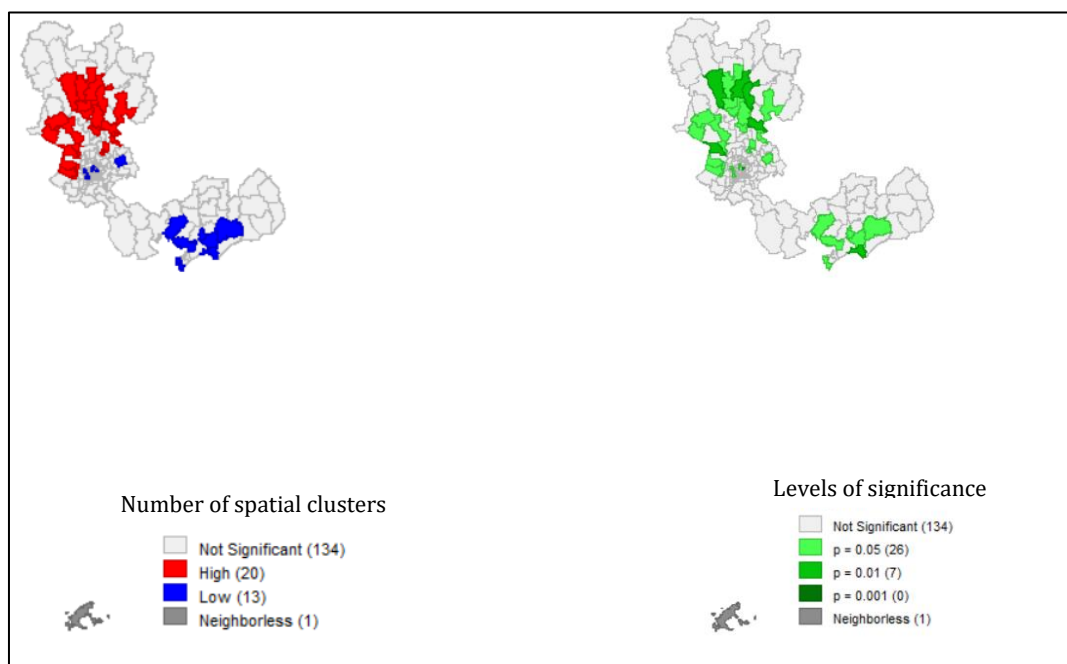


Figure 4 Hotspot (left) and significant (right) maps of DHF confirmed cases

The statistical significance map (Figure 4, right) provides further confidence in these patterns. Among the identified clusters, 26 wards reached significance at the 95% confidence level ($p \leq 0.05$), with seven wards at the 99% level ($p \leq 0.01$) and one ward at the 99.9% level ($p \leq 0.001$). The gradation of significance suggests that while most hotspots reflect robust clustering, a smaller subset of wards represents extremely strong clusters where dengue incidence is substantially higher than expected under random distribution. These highly significant wards can be considered critical foci of transmission requiring urgent and intensive public health interventions. Taken together, these findings demonstrate that dengue transmission in Ho Chi Minh City is characterized by spatial heterogeneity, with a small proportion of wards driving much of the epidemic burden. This pattern aligns with observations from other Southeast Asian megacities, where socio-environmental factors such as informal housing, water storage practices, waste accumulation, and high human mobility converge to sustain transmission in localized clusters. At the same time, the presence of coldspots suggests that not all densely populated areas are equally vulnerable, and that factors such as improved infrastructure, better drainage, or effective community-level interventions may mitigate risk.

From a practical standpoint, these hotspot and significance maps provide actionable intelligence for vector control and surveillance programs. Rather than dispersing resources uniformly across the city, health authorities can prioritize high-significance hotspot wards for targeted interventions such as indoor residual spraying, larval source reduction, and community awareness campaigns. Conversely, coldspot wards can be maintained under routine surveillance, ensuring that they do not transition into hotspots during subsequent weeks. In conclusion, the integration of hotspot mapping with statistical significance testing confirms the presence of localized, high-priority zones for dengue control in Ho Chi Minh City. This evidence highlights the utility of geospatial analytics in optimizing dengue surveillance and in guiding cost-effective, geographically targeted interventions.

4. Conclusion

This study applied spatial statistical techniques, particularly the Getis-Ord G_i^* statistic, to analyze the spatial distribution of dengue hemorrhagic fever cases in Ho Chi Minh City during the 32nd epidemiological week of 2025. The results consistently demonstrated that dengue transmission is spatially heterogeneous rather than uniformly distributed. Descriptive mapping and boxplot analysis revealed a right-skewed distribution of cases, with a small number of wards reporting disproportionately high incidence. The scatter plot analysis indicated that population density alone does not account for the observed distribution, underscoring the importance of other socio-environmental and infrastructural factors. Hotspot analysis confirmed the existence of statistically significant high-high clusters in the central-northern urban core, where localized conditions appear to facilitate sustained transmission. A smaller number of wards were classified as coldspots, reflecting areas of consistently lower incidence. The significance maps further highlighted a subset of wards with very strong clustering ($p \leq 0.01$), indicating critical foci that drive much of the epidemic burden. These findings align with global evidence that dengue outbreaks in megacities are driven by complex, neighborhood-level interactions among human population dynamics, urban infrastructure, and environmental conditions. However, a limitation of this study is that the analysis was restricted to a single epidemiological week, which provides only a snapshot of transmission dynamics. Temporal variability, seasonal factors, and longitudinal persistence of hotspots were not addressed. Future research should extend the analysis across multiple weeks or entire transmission seasons to identify persistent versus transient hotspots and strengthen the evidence base for long-term intervention planning.

Compliance with ethical standards

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Disclosure of conflict of interest

The authors declare no conflict of interest.

Statement of informed consent

Informed consent was obtained from all individual participants included in the study.

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