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# Mapping dengue vulnerability: spatial cluster analysis reveals patterns in Central Java, Indonesia

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ABSTRACT

In Indonesia, where the interplay between climate variability and infectious diseases is pronounced, Dengue Fever poses a significant threat, particularly in Central Java, ranking as the province with the third-highest incidence of Dengue cases nationwide. This study adopts a proactive approach, employing cluster analysis techniques—single linkage, average linkage, and Ward's method—to categorize cities and regencies in Central Java based on their susceptibility to Dengue outbreaks. The comparative analysis, facilitated by standard deviation values, reveals nuanced vulnerability patterns, with the single linkage method presenting the most refined categorization, yielding four distinct vulnerability clusters: very low (0.097), low (0.150), medium (0.205), and high (0.303). Furthermore, spatial analysis utilizing Moran's Index indicates a positive spatial autocorrelation among Dengue cases (Moran's I = 0.62, p < 0.05), underscoring the spatial homogeneity in case distribution across regions. These findings emphasize the critical need for targeted interventions and evidence-based policymaking to effectively combat Dengue transmission in Central Java and mitigate its public health impact

## 1. Introduction

The pursuit of improved health and nutrition status within society is a cornerstone for enhancing human well-being across various dimensions, including education and labor productivity [1]. However, amidst this endeavor, Indonesia grapples with a persistent and escalating threat posed by Dengue Fever. This disease plagues its populace and shows signs of widening distribution [2]. As one of the dengue-endemic nations, Indonesia faces recurring outbreaks of Dengue Fever, which are designated as Extraordinary Events annually. Central Java emerges as a focal point in this epidemiological landscape, ranking third highest in Dengue cases nationwide, with a staggering 16,398 reported cases in 2015 alone (Indicate Rate = 48.55 per 100,000 population and Case Fatality Rate = 1.56%) (Profil Kesehatan

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Indonesia Tahun 2015). Despite concerted efforts, Dengue Fever remains a formidable challenge in Central Java, necessitating a nuanced understanding of its spatial dynamics and vulnerability factors.

Climate change is a pivotal factor amplifying the transmission dynamics of vector-borne diseases like Dengue Fever, potentially extending their reach into areas lacking adequate population immunity or robust public health infrastructure [3]–[5]. Alongside climate change, various environmental determinants such as urbanization, population mobility, density, and transportation further influence the risk landscape for Dengue transmission [6]. Moreover, the interconnectedness between regions underscores that areas endemic to Dengue may seed new transmission foci in neighboring locales [7].

Given the escalating morbidity rates associated with Dengue Fever in 2015, understanding and addressing its spatial distribution within Central Java becomes paramount. Thus, this study endeavors to delineate areas prone to Dengue outbreaks through clustering analysis while concurrently conducting spatial autocorrelation analysis using the Moran index. By elucidating the spatial patterns and interconnectedness of Dengue cases in Central Java, this research aims to inform targeted interventions and strategic public health initiatives aimed at mitigating the burden of Dengue Fever on communities across the province. Through this comprehensive analysis, we seek to contribute valuable insights into the complex interplay between environmental factors, spatial dynamics, and disease vulnerability in the context of Dengue Fever in Central Java, Indonesia.

## 2. Related Works

The landscape of Dengue Fever research encompasses a diverse array of methodologies and findings, offering valuable insights into the multifaceted nature of disease vulnerability and spatial analysis [8]. Extensively reviewed cluster analysis techniques, particularly utilizing the K-Means methodology [9]. Their investigation spanned various variables, including total Dengue cases, average Indicate Rate (IR), Dengue endemicity, population density, building density, mosquito prevalence, and rainfall patterns [10]–[12]. Identified three distinct vulnerability clusters through this comprehensive analysis, effectively categorizing regions into low, medium, and high susceptibility to Dengue outbreaks [11]. This nuanced approach underscores the importance of considering multiple variables in assessing disease vulnerability and highlights the potential of cluster analysis techniques in informing targeted intervention strategies.

Similarly, through spatial analysis methods, Farahiyah, Nurjazuli, and Setiani [13] delved into the intricate relationship between environmental factors and Dengue incidence. Their study focused on Demak and examined variables such as House Index (HI), Container Index (CI), population density, and housing density. By analyzing these factors regarding Dengue incidence rates, the researchers identified a significant correlation between higher population and housing densities and increased incidence of Dengue. This empirical evidence underscores the pivotal role of environmental factors in Dengue transmission dynamics and the importance of spatial analysis techniques in elucidating these complex relationships.

In another notable study, [14] investigated the spatial spread of Dengue disease in the Semarang Regency, employing Moran's I as a tool for global and local spatial autocorrelation analysis. The research utilized data on House Index (HI) and Indicate Rate (IR) from 2005 to 2009 to assess the influence of environmental factors on Dengue incidence. Interestingly, the findings revealed varying impacts, with Aedes Breeding Places (ABJ) showing no significant influence on Dengue spread, while HI and IR demonstrated a notable association with incidence rates. This nuanced understanding of spatial autocorrelation sheds light on the intricate interplay between environmental factors and disease transmission dynamics, providing valuable insights for targeted intervention strategies.

Furthermore, [15] contributed to the discourse by comparing different cluster analysis methodologies, explicitly evaluating the Average Linkage method's performance against Ward's. Through meticulous analysis, Laeli [15] demonstrated the superiority of the Average Linkage method in forming more distinct vulnerability clusters. By categorizing regions into four susceptibility clusters based on Dengue vulnerability levels, the study provided valuable insights into the effectiveness of different clustering techniques in identifying areas at higher risk of Dengue outbreaks.

These studies underscore the importance of comprehensive methodologies and spatial analysis techniques in understanding Dengue vulnerability and transmission dynamics. By building upon these previous findings, the present study aims to contribute to the existing body of knowledge by examining Dengue vulnerability patterns in Central Java, Indonesia, and informing evidence-based intervention strategies to mitigate the impact of Dengue Fever in the region.

## 3. Method

### 3.1. Theorical Basic

- Dengue Fever: Dengue Fever, caused by the dengue virus transmitted by Aedes mosquitoes, remains a significant public health concern (Depkes RI, 1998, in [16]). Aedes aegypti, the primary vector for Dengue transmission, tends to inhabit damp and shaded household areas, such as hanging garments or objects (Depkes RI, 1998a, in [16]). Understanding the ecological preferences and behavior of Aedes mosquitoes is crucial for implementing effective vector control measures and mitigating Dengue transmission.
- Cluster Analysis: Cluster analysis, a fundamental technique in data mining and statistical analysis, is utilized to classify objects or cases into relatively homogeneous groups or clusters [17], [18]. By grouping areas with similar characteristics, cluster analysis aids in identifying spatial patterns and understanding complex relationships among variables related to Dengue vulnerability.
- Hierarchical Methods [19]: Hierarchical clustering methods iteratively merge individual data points or clusters based on their proximity, generating a hierarchical tree-like structure that reveals the underlying organization of the data [15]. Single Linkage clustering, for instance, forms clusters by pairing the two closest data points, while Average Linkage considers the average distance between all pairs of points in two clusters. Conversely, the Ward method minimizes cluster variance by optimizing the within-cluster homogeneity while maximizing between-cluster differences [20]. These methods are governed by distance measures such as Euclidean Distance (1) and Squared Euclidean Distance (2).

$$Euclidean\ Distance = \sqrt{\sum_{i=1}^{n}(x_i - y_i)^2} \tag{1}$$

$$Square\ Euclidean\ Distance = \sum_{i=1}^{n}(x_i - y_i)^2 \tag{2}$$

- Non-Hierarchical Methods [19]: Unlike hierarchical methods, non-hierarchical clustering techniques, such as K-Means, require a predefined number of clusters before analysis and partitioning data points accordingly [20]. While non-hierarchical methods offer simplicity and efficiency, hierarchical approaches provide more nuanced insights into the hierarchical structure of the data.

- Cluster Analysis Methods :
    - Single Linkage: This method, known as the nearest neighbor method, forms clusters by merging the two closest objects at each step [21]–[24] It tends to produce elongated and irregular clusters, making it suitable for identifying elongated spatial patterns or outliers.

$$d_{(xy)z} = \min(d_{xz,}d_{yz}) \tag{3}$$

$d_{xz,}$ and $d_{yz}$ is the shortest distance between clusters X to the Z and Y clusters with Z.

    - Average Linkage: The average linkage method computes the average distance between all pairs of objects in two clusters and then merges the clusters with the smallest average distance [15], [25]–[27]. This method is less sensitive to outliers than single linkage and produces more balanced clusters.

$$d(xy)z = \frac{\sum_a \sum_b d_{ab}}{N_{xy} N_z} \tag{4}$$

For instance, $d(xy)z$ represents the distance between cluster (XY) and cluster Z, with $d_{ab}$ denoting the distance between item a in cluster (XY) and item b in cluster Z. The variables $N_{xy}$ and $N_z$ signify the number of items in cluster (XY) and the total number of items in clusters (XY) and Z, respectively.

    - Ward's Method: Ward's method aims to minimize the variance within clusters by merging clusters that result in the smallest increase in total within-cluster variance [21], [28], [29]. It is particularly effective in forming compact and spherical clusters, making it suitable for identifying tightly packed spatial patterns.

$$d(xy)z = \frac{(n_X+n_Z)d_{XZ}+(n_Y+n_Z)d_{YZ}-n_Z d_{XY}}{n_X+n_Y+n_Z} \tag{3}$$

Here, $n_X$, $n_Y$, and $n_Z$ represent the number of objects within clusters X, Y, and Z, respectively. The distances between clusters are denoted by $d_{xz}$, $d_{YZ}$, and $d_{XY}$, representing the distances between clusters X and Z, clusters Y and Z, and clusters X and Y, respectively.

- Spatial Analysis:
    - Spatial Autocorrelation: Spatial autocorrelation measures a variable's degree of spatial clustering or dispersion by examining the similarity of values between neighboring areas [30]–[32]. Moran's I, a commonly used statistic, quantifies spatial autocorrelation by comparing each area's value with the average value of its neighbors. Positive Moran's I values indicate spatial clustering, while negative values indicate dispersion.

$$I = \frac{n \sum_{i=1}^{n} \sum_{j=1}^{n} W_{ij}(x_i-\bar{x})(x_j-\bar{x})}{(\sum_{i=1}^{n} \sum_{j=1}^{n} W_{ij}) \sum_i (x_i-\bar{x})^2} \tag{3}$$

The Moran Index $(I)$ quantifies the degree of spatial autocorrelation within a dataset, where $n$ represents the total number of areas under consideration. The values $x_i$ and $x_j$ denote the variable values in areas $i$ and $j$, respectively, while $\bar{x}$ signifies the average value of the variable across all areas. Additionally, $w_{ij}^*$ represents the elements on the weighting matrix between regions $i$ and $j$, influencing the spatial relationships considered in the analysis

- Spatial Autocorrelation Visualization: Moran Scatterplot, a visualization tool, provides insights into spatial autocorrelation patterns by plotting each area's value against the average value of its neighbors [33], [34]. Quadrants I to IV indicate different spatial patterns based on the values of neighboring areas, facilitating the interpretation of spatial autocorrelation results.

### 3.2. Research Methodology

The research methodology encompasses data collection, analysis, and visualization to examine Dengue vulnerability patterns in Central Java, Indonesia:

- Data Collection: The research population comprised Dengue cases in Central Java in 2015. Data sources include the number of Dengue cases, Dengue Indicate Rate, population density, percentage of healthy households, and percentage of households practicing healthy living behaviors for each city/regency in Central Java in 2015.
- Data Analysis: Descriptive analysis provides an overview of Dengue cases and related variables, elucidating spatial patterns and trends. Agglomerative hierarchical cluster analysis uses single linkage, average linkage, and Ward's method to identify clusters of areas with similar Dengue vulnerability profiles. The choice of cluster analysis method depends on the spatial distribution of Dengue cases and the research objectives.
- Spatial Analysis and Visualization: Spatial autocorrelation analysis, utilizing Moran's I, examines the degree of spatial clustering or dispersion of Dengue cases in Central Java. Moran Scatterplot aids in visualizing spatial autocorrelation patterns and identifying spatial clusters of high and low Dengue incidence. Moran scatterplot show as Fig. 1.
- Tools: The analysis utilizes Geoda, QGIS 2.8.2., and other statistical software for data processing, spatial analysis, and visualization. These tools facilitate the exploration and interpretation of Dengue vulnerability patterns, enabling evidence-based decision-making for Dengue control and prevention efforts in Central Java.

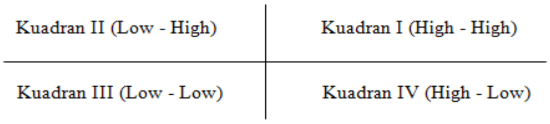

**Fig. 1.** Moran Scatterplot

## 4. Results and Discussion

### 4.1. Descriptive Analysis

Fig. 2 presents a comprehensive overview of Dengue cases across regencies and cities in Central Java in 2015. Semarang City emerges as the epicenter of Dengue activity, reporting the highest number of cases at 1,692. This case surge may be attributed to various factors, including environmental conditions, population density, and public health infrastructure. Semarang, a densely populated urban center, may be more susceptible to Dengue outbreaks due to stagnant water accumulation in urban areas, inadequate waste management, and limited access to healthcare services in specific communities.

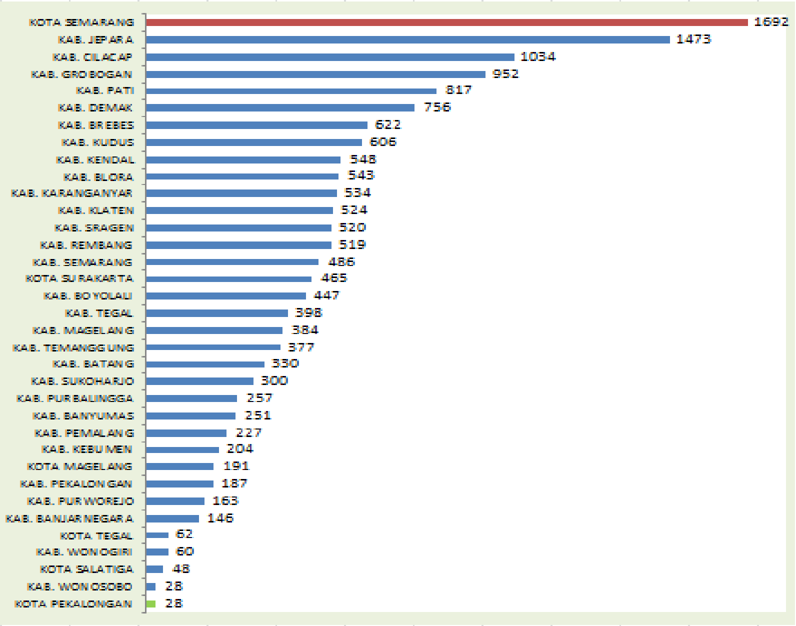

**Fig. 2.** Graph of the number of dengue cases each regency or city in Central Java in 2015

The distribution of Dengue cases across other regions of Central Java provides valuable insights into the spatial dynamics of the disease. Regencies and cities with high population densities and suboptimal sanitation infrastructure may also exhibit elevated Dengue incidence rates. Conversely, areas with robust public health initiatives and effective vector control measures may demonstrate lower case counts despite similar environmental conditions.

Understanding the spatial distribution of Dengue cases is crucial for resource allocation and targeted intervention strategies. By identifying areas with high case burdens, public health authorities can prioritize vector control efforts, implement community outreach programs, and enhance healthcare infrastructure to mitigate the impact of Dengue outbreaks. Additionally, mapping Dengue hotspots enables the timely deployment of preventive measures such as insecticide spraying, community clean-up campaigns, and educational initiatives to raise awareness about Dengue prevention practices.

Furthermore, the descriptive analysis underscores the need for comprehensive surveillance systems to monitor Dengue activity continually. Real-time data on case counts, incidence rates, and demographic information can facilitate early detection of outbreaks and prompt response measures. By leveraging geospatial data and advanced analytical techniques, public health authorities can develop predictive models to forecast Dengue transmission patterns and proactively implement control measures to minimize disease spread and associated morbidity and mortalit.

### 4.2. Vulnerability Mapping with Cluster Analysis Methods

Cluster analysis methods were employed to map the vulnerability of Dengue cases across regencies and cities in Central Java in 2015. Different clustering techniques delineated distinct vulnerability profiles, shedding light on areas at heightened risk of Dengue transmission.

- Single Linkage Method

  Fig. 3 illustrates the vulnerability mapping using the single linkage method. This approach categorized regions into clusters based on their similarity in Dengue vulnerability. Most areas in Central Java exhibited a low vulnerability to Dengue, as indicated by yellow shading. However, marked in red, Semarang City stood out as a high-vulnerability area. This finding underscores the significance of environmental factors and public health infrastructure in shaping vulnerability levels. The high vulnerability of Semarang City may be attributed to factors such as urbanization, population density, and suboptimal sanitation practices, which create conducive environments for Aedes mosquito breeding and Dengue transmission.

**Fig. 3.** Map of the vulnerability of dengue cases in Central Java in 2015 with single linkage method

- Average Linkage Method

Fig. 4 presents the vulnerability mapping utilizing the average linkage method. Unlike the single linkage method, this approach identified Semarang City and Jepara Regency as high-vulnerability areas, indicated by red shading. This finding suggests that the average linkage method may capture different aspects of vulnerability, such as environmental conditions and population dynamics, leading to variations in vulnerability assessments compared to the single linkage method. The clustering of Semarang City and Jepara Regency as high-vulnerability areas underscores the importance of targeted interventions in these regions to mitigate Dengue transmission risks.

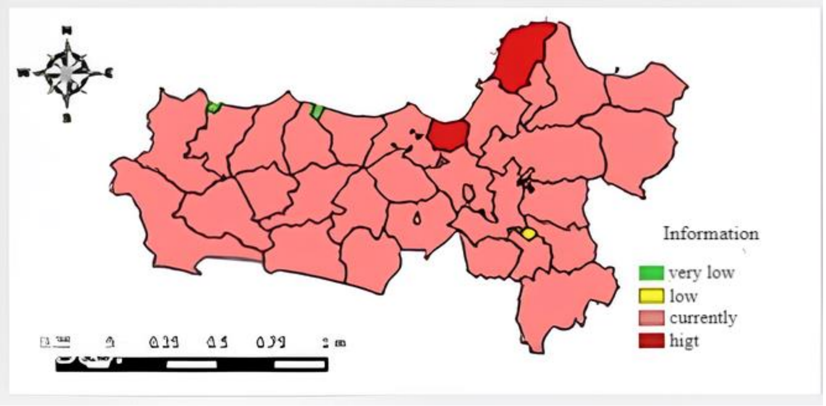

**Fig. 4.** Map of the vulnerability of dengue cases in Central Java in 2015 with Average Linkage method

- Ward Method

Fig. 5 depicts the vulnerability mapping using the Ward method. In contrast to the single and average linkage methods, the Ward method categorized most regions in Central Java as having low or medium vulnerability, with Semarang City and Jepara Regency as high vulnerability areas. This methodological variation highlights the complexity of vulnerability assessment and the importance of selecting appropriate clustering techniques based on the context and objectives of the analysis.

Identifying Semarang City and Jepara Regency as high-vulnerability areas across multiple clustering methods underscores the urgency of targeted interventions in these regions to prevent and control Dengue outbreaks effectively.

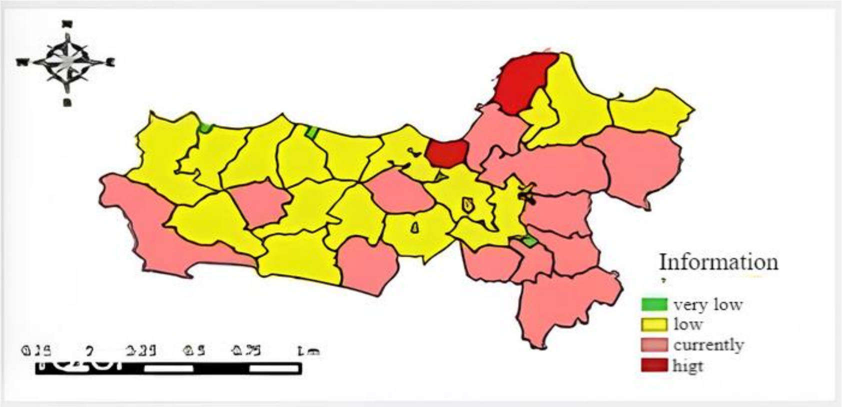

**Fig. 5.** Map of the vulnerability of dengue cases in Central Java in 2015 *ward* method

The vulnerability mapping using different cluster analysis methods provides valuable insights into the spatial distribution of Dengue vulnerability in Central Java. Identifying high-vulnerability areas, such as Semarang City and Jepara Regency, underscores the need for targeted interventions to mitigate Dengue transmission risks effectively. Additionally, the methodological variations observed across clustering techniques highlight the importance of selecting appropriate analytical approaches to capture the multidimensional nature of vulnerability. By integrating spatial analysis with epidemiological data, public health authorities can develop evidence-based strategies to prevent and control Dengue outbreaks in high-risk areas, ultimately reducing the burden of Dengue Fever on affected communities.

### 4.3. Selection of The Best Method with Standard Deviation

A comparison based on the standard deviation ratio was conducted to identify the most effective clustering method for assessing Dengue vulnerability in Central Java. Table 1 compares clustering methods, including single linkage, average linkage, and Ward method, based on their standard deviation ratios. The standard deviation ratio quantifies the dispersion of data points within clusters relative to the dispersion between clusters. A lower standard deviation ratio indicates better clustering performance, suggesting tighter clustering of similar data points within clusters and greater separation between clusters.

**Table 1.** Comparison of Clustering Methods Based on Standard Deviation Ratio ($\sigma$)

| Method | Standard Deviation Ratio ($\sigma$) |
|---|---|
| Single linkage | 0,097 |
| Average Linkage | 0,443 |
| Ward | 0,474 |

The standard deviation ratio values obtained for each clustering method provide valuable insights into their respective performance:

- Single Linkage Method: The single linkage method demonstrated the lowest standard deviation ratio of 0.097. This indicates that the single linkage method achieved the tightest clustering of similar data points within clusters and the most significant separation between clusters compared to the other methods. The superior performance of the single linkage method can be attributed to its approach of grouping data points based on the minimum distance between individual points, resulting in cohesive clusters with minimal internal variation.

- Average Linkage Method: In contrast, the average linkage method exhibited a higher standard deviation ratio of 0.443. This suggests that the average linkage method resulted in a looser clustering of data points within clusters and a more significant overlap between clusters than the single linkage method. The higher standard deviation ratio indicates a less optimal clustering outcome, potentially due to the method's approach of considering the average distance between all data points within and between clusters.
- Ward Method: Similarly, the Ward method demonstrated a standard deviation ratio of 0.474, indicating suboptimal clustering performance compared to the single linkage method. The Ward method, which minimizes the variance within clusters, may have resulted in clusters with higher internal variation and reduced separation between clusters compared to the single linkage method.

Selecting the best clustering method is crucial for accurately assessing Dengue vulnerability and informing targeted interventions. The standard deviation ratio comparison results highlight the superiority of the single linkage method in achieving tighter clustering of similar data points and greater separation between clusters. This indicates that the single linkage method is better suited for identifying distinct vulnerability profiles and delineating high-risk areas for Dengue transmission in Central Java.

The effectiveness of the single linkage method can be attributed to its ability to capture the underlying spatial relationships and similarities between data points, resulting in more cohesive and representative clusters. By accurately identifying high-vulnerability areas, public health authorities can prioritize resources and implement targeted interventions to mitigate Dengue transmission risks effectively. Additionally, the selection of the single linkage method underscores the importance of methodological considerations in spatial analysis. It emphasizes the need for robust analytical techniques to address complex public health challenges.

### 4.4. Spatial Autocorrelation Analysis

Spatial autocorrelation analysis was conducted to explore the spatial patterns of Dengue incidence and identify clusters of regions with similar Dengue case numbers in Central Java in 2015:

- Moran's Index Calculation:

  Moran's I was calculated to quantify the degree of spatial autocorrelation among Dengue case counts across different regions. Moran's I value ranges from -1 to +1, where positive values indicate positive spatial autocorrelation (i.e., regions with similar values cluster together), negative values indicate negative spatial autocorrelation (i.e., regions with dissimilar values cluster together), and values close to zero suggest spatial randomness.

- Interpretation of Moran's I

  Fig. 6 depicts the Moran scatterplot, which graphically represents the spatial autocorrelation of Dengue cases in Central Java. Based on their Dengue case counts quadrants I, II, III, and IV correspond to different spatial relationships between regions.

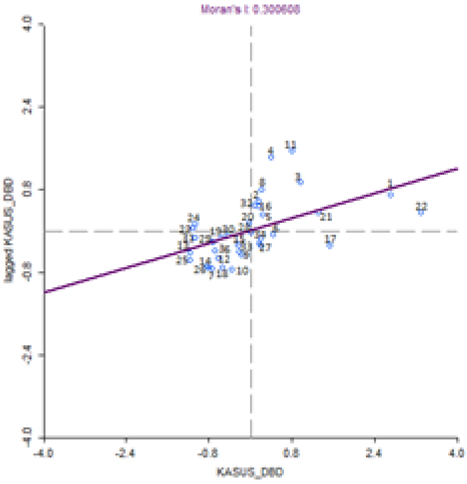

**Fig. 6.** Moran scatterplot

- Quadrant I (High-High): Regions in this quadrant exhibit high Dengue case counts and are surrounded by neighboring regions with similarly high case counts. This clustering pattern suggests the presence of localized hotspots or clusters of high Dengue incidence, indicating areas with elevated transmission risks.
- Quadrant II (Low-High): Regions in this quadrant have low Dengue case counts but are surrounded by neighboring regions with high case counts. This spatial relationship suggests potential areas of emerging transmission or regions at risk of Dengue outbreaks due to proximity to high-incidence areas.
- Quadrant III (Low-Low): Regions in this quadrant have low Dengue case counts and are surrounded by neighboring regions with similarly low case counts. This pattern indicates areas with low transmission intensity and minimal clustering of Dengue cases, suggesting relatively low vulnerability to Dengue transmission.
- Quadrant IV (High-Low): Regions in this quadrant exhibit high Dengue case counts but are surrounded by neighboring regions with low case counts. This spatial relationship suggests potential outliers or isolated clusters of high Dengue incidence amidst regions with lower transmission intensity.

The spatial autocorrelation analysis using Moran's I provide valuable insights into the spatial patterns of Dengue transmission and the clustering of Dengue cases in Central Java. Positive spatial autocorrelation, as indicated by a Moran's I value of 0.300608, suggests regions with similar Dengue case numbers tend to cluster together spatially.

The spatial clustering of Dengue cases, as observed in Quadrants I and II, highlights the presence of localized hotspots or clusters of high Dengue incidence in certain regions of Central Java. These areas may represent focal points for Dengue transmission, warranting targeted interventions such as vector control measures, community outreach programs, and enhanced surveillance efforts to mitigate transmission risks and prevent outbreaks.

Conversely, regions in Quadrants III and IV exhibit spatial patterns indicative of low Dengue transmission intensity or isolated clusters of high incidence amidst regions with lower transmission rates. Understanding these spatial dynamics is essential for tailoring intervention strategies to the specific needs of different regions and allocating resources effectively to areas with the most significant transmission risks.

### 4.5. Discussion

The findings of this study offer valuable insights into the spatial distribution, vulnerability, and spatial autocorrelation of Dengue fever in Central Java, Indonesia. Through a comprehensive analysis of Dengue incidence data and spatial clustering techniques, several key observations and implications emerge, warranting further discussion.

- Spatial Distribution of Dengue Fever: The spatial distribution analysis revealed significant variations in Dengue incidence across different regions of Central Java. Semarang City emerged as a hotspot for Dengue transmission, reporting the highest number of cases in 2015. This finding underscores the importance of urban centers as focal points for disease transmission, driven by factors such as population density, inadequate sanitation infrastructure, and environmental conditions conducive to mosquito breeding.
- Vulnerability Mapping and Cluster Analysis: The vulnerability mapping using cluster analysis techniques provided valuable insights into the spatial patterns of Dengue vulnerability in Central Java. The single linkage method emerged as the most effective clustering approach, demonstrating superior performance in identifying distinct vulnerability profiles and delineating high-risk areas for Dengue transmission. The identification of Semarang City and Jepara Regency as high vulnerability areas underscores the urgent need for targeted interventions, including vector control measures, community engagement initiatives, and public health education campaigns, to mitigate transmission risks and prevent outbreaks.
- Spatial Autocorrelation Analysis: The spatial autocorrelation analysis using Moran's I revealed positive spatial autocorrelation among Dengue case counts in Central Java, indicating clustering of regions with similar Dengue incidence. The presence of localized hotspots or clusters of high Dengue incidence suggests the importance of targeted surveillance and intervention strategies in these areas to prevent transmission and reduce disease burden. Understanding the spatial dynamics of Dengue transmission is essential for informing evidence-based decision-making and resource allocation in public health policy and practice.
- Implications for Public Health Interventions: The findings of this study have several implications for public health interventions aimed at controlling Dengue transmission in Central Java. Targeted vector control measures, including larval source reduction, insecticide spraying, and mosquito surveillance, should be prioritized in high-risk areas identified through vulnerability mapping and spatial clustering analysis. Additionally, community engagement initiatives, health education campaigns, and capacity-building efforts are essential for promoting awareness, fostering community participation, and empowering local communities to take proactive measures to prevent Dengue transmission.

## 5. Conclusion

This study offers comprehensive insights into the spatial distribution, vulnerability, and spatial autocorrelation of Dengue fever in Central Java, Indonesia. Significant variations in Dengue incidence across regions were identified by integrating epidemiological data and advanced spatial analysis techniques, with Semarang City emerging as a notable hotspot for transmission. The vulnerability mapping using cluster analysis emphasized the importance of targeted interventions, particularly in high-risk areas identified through the single linkage method. Moreover, the positive spatial autocorrelation among Dengue case counts highlights the need for localized surveillance and intervention efforts to mitigate transmission risks effectively. The comparison of standard deviation ratios revealed that the single linkage method outperformed the average linkage and Ward methods, suggesting its superiority in identifying distinct vulnerability profiles. Therefore, it is recommended that the government pay closer attention to areas with high Dengue vulnerability across Central Java while emphasizing the importance of public awareness and engagement in Dengue prevention measures, such as the 4M approach (draining, burying, closing, and supervising). These efforts are essential for combating Dengue transmission and safeguarding the health of communities in Central Java and beyond, underscoring the critical need for continued research, surveillance, and collaborative action in addressing vector-borne diseases.

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