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Spatial Modeling of Climate Change Effects on Dengue Fever Incidence: A Case Study in East Nusa Tenggara

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ABSTRACT

This study analyzes the spatial correlation between climate variability and the incidence of dengue fever in East Nusa Tenggara (NTT) with 2022 data on 22 districts/cities. The climate data (temperature, humidity, and rainfall) and Euclidean distance data were obtained from the Meteorological, Climatological, and Geophysical Agency (BMKG), and data on dengue fever cases were obtained from the NTT Provincial Health Office. The study used the Queen Contiguity spatial weight matrix, Ordinary Least Squares (OLS), Moran's I test, and spatial error model (SEM). SEM was identified as the best model: $R^2=45.38\%$, AIC=285.235. Temperature was the most significant factor, with a coefficient of -75.934, which means a 1℃ decrease in temperature is associated with an estimated increase of 75 dengue cases. Though the p-value (0.08927), suggests weak statistical significance, this relationship is still relevant for understanding the epidemiological picture. Further, the spatial error coefficient ($\lambda=-0.217$, $p=0.481$) suggests there are potential spatial dependencies that have not been adequately contextualized and could be associated with unobserved mechanisms (e.g., human mobility, environmental characteristics of mosquito habitats). This study highlights the need to involve spatial analysis in the planning of public health interventions, particularly targeted vector control as these can be done in the cooler season. They recommend district-level early warning systems utilizing spatial and climate data to predict outbreaks. Future studies should incorporate other variables, including socio-economic factors and climate change projections, to improve the models' accuracy and inform health adaptation strategies in the long term.

1. INTRODUCTION

The impact that climate change is having on human life in general is one of the biggest threats to humankind today, and it touches on every aspect of human life, including public health. Dengue fever is the most widely distributed mosquito-borne viral infection, and increased transmission of vector-borne diseases (VBD) is one of the most disastrous effects of climate change. Approximately half of the world population is vulnerable to infection with the dengue virus DENV, leading to an estimated 50-100 million cases of DENV globally each year [1]. This figure has slowly increased from 2.4 million cases in 2010 to over 5.2 million cases in 2019, illustrating the durability of the global health burden caused by this one disease [2].

There is great variability in the geography of risk perceptions in terms of climate change and vector-borne diseases. In tropical and subtropical places where dengue is endemic, people tend to have a better sense of the risk because there are more frequent outbreaks. Awareness of dengue is also on the rise in still unaffected areas, including temperate regions, as the environmental conditions that favor the spread of the Aedes mosquitoes spread with increasing global temperatures [3]. Rising temperatures and changing rainfall patterns related to climate change are believed to cause more mosquitoes to survive in more humid or stormy regions and to expand their transmission season.

Studying how climate change affects dengue fever is thus critical not only for improving predictions of future health risks but also to inform responses to current challenges in preventing and controlling the disease. More detailed knowledge of the association between climate variables and dengue transmission is required to guide more effective public health interventions that may help prevent future outbreaks. This is all the more so in tropical and seasonal climates, as in East Nusa Tenggara, Indonesia, a province often affected by outbreaks of this disease and exacerbated by unstable weather patterns and extreme weather events.

Dengue fever is a viral disease, primarily passed on to humans through the bite of an infected Aedes mosquito, and the transmission dynamics of it heavily rely on climatic parameters. Climate determinants such as temperature, rainfall, and humidity impact the mosquito lifecycle, and there with its capacity to transmit the virus. For example, increasing temperature can accelerate mosquito development, increase its aggressiveness as well as shorten its incubation period in the mosquito [4], and rainfall creates breeding spaces for mosquitoes. The incidence and severity of dengue cases are highly influenced by these climatic conditions.

Global epidemiological and ecological theories suggest that climate change could modify environmental determinants dynamically relevant in disease transmission and, thus, those related to spatial distribution and magnitude of dengue outbreaks. Earlier studies that used process-based and statistical modeling approaches have revealed a strong association between increasing temperatures and increased dengue incidence, especially in tropical and subtropical areas [5]. But other studies have suggested that the association between climate change and transmission of dengue is nonlinear, with very high temperatures decreasing mosquito life span [6], and thus, the effect size on dengue incidence may vary by region.

While many studies have tried to demonstrate the link between climate change and dengue, insufficient local-level coverage has been done to understand these dynamics. Most of the studies have been conducted at the global or continental scale and generally have failed to account for local conditions (e.g., socioeconomic aspects, microclimates, and geographical features) that play a role in dengue transmission [7].

In this tropical region with high variability of climatic conditions in terms of rainfall and temperature, for instance, East Nusa Tenggara, it is vulnerable to the epidemiologic threat of dengue. Additionally, climate variability, largely driven by the El Niño and La Niña phenomena, has been shown to strongly affect the cyclic flow of dengue incidence in tropical regions [8]. Nonetheless, certain areas (especially rural/remote areas with limited access to health facilities) may be especially vulnerable to the effects of outbreaks driven by local environmental phenomena and/or limited healthcare infrastructure [9].

New sectors that are at risk of increased dengue cases, overexploitation of healthcare systems, and increased mortality rates are likely unless adequately modeled, creating opportunities to understand the role climate change plays in the transmission of dengue. This type of targeted approach requires understanding of high-risk areas, and local methods using comparable spatial data as that rudimentarily used in this study will be fundamental. Previous studies have demonstrated that, in tropical regions, disease transmission is also influenced by context characteristics such as urbanization, population density, and environmental factors [10].

This study intends to present a model to estimate the impact of climate change on the incidence of dengue fever in East Nusa Tenggara using spatial statistical methods. It hopes to determine how climate factors such as temperature, precipitation, and humidity are associated with dengue transmission, controlling for spatial dependencies among regions. Hence, several key approaches used in the spatial statistical modeling with strong relevance to the epidemiological data characteristics are employed to fulfill this objective.

This is done with the Queen Contiguity method in which a spatial weight matrix of W is defined so two regions are neighbors if they are adjacent either by border or vertex. Incorporating W in the model is crucial for modeling incorporated spatial interaction between different regions because it is likely to reflect the spatial distribution and intensity of the diffusion of the disease better [11, 12]. This is crucial in order to aid modeling of how the spatial patterns of disease transmission, and contributions of surrounding areas.

This study aims to find a model of the relationship between climate change and the incidence of dengue fever (DBD) in East Nusa Tenggara with the spatial statistical method. Such a method thus considers that data is not linear but rather relies upon spatial weight matrices to investigate assertive interregional interaction effects, an approach that has not been sufficiently pursued in prior work that instead has tended to ignore spatial characteristics. In this context, several research needs remain common, specifically the integration of the characteristics of climatic data with the epidemiological aspects of dengue and better spatial modeling to account for interregional interactions.

Urgent, the absence of context-specific climate data characteristics within the East Nusa Tenggara domain, suggests a highly relevant gap in this research. With the exception of relatively few approaches, most previous studies have only explored simple linear relationships between the climatic factors and the dengue incidence at specific locations, completely disregarding more complex spatial dynamics. The present study seeks to address this issue by deploying spatial weight matrices on the basis of the Queen Contiguity method, which is a more efficient method than the others, for the inter-regional spatio-temporal marker, as it identifies the relationship not only via regional boundaries but also via meeting points, and thus affords a more holistic representation of spatial interaction [13]. This matrix serves not only as an indication of which geographical areas interact directly with each other, but also leads to a more accurate description of the geographical distribution and intensity of a disease [14, 15]. We aim to use Queen County to reflect a high degree of relation between entities not yet well studied as in reference [5] used a similar approach to investigate the impact of climate on dengue dynamics but derived variable conclusions.

The data characteristics in our study are climatic variables with high temporal resolution and geo-climatic dengue epidemiological data with spatial granularity at the administrative region level. Previous work primarily applied climate and epidemiological data with a lower resolution, thus missing important aspects of spatial and temporal heterogeneity. This seems to extend the data of the study [16], who incorporated historical climate data in Brazil to model dengue dynamics without representing some spatial variability at the local scale [16]. This offers higher precision and predictive power, relevant to the actual context of the analysis, for instance, by incorporating the data derived from end-of-satellite high-temporal resolution climate data, such as daily rainfall and humidity, which have been proven to be closely associated with dengue distribution in similar environments.

To examine spatial dependencies, this research employs Moran's I statistic to assess spatial autocorrelation. This is essential to ascertain whether the spatial patterns of dengue incidence demonstrate a substantial similarity within certain regions. This method is the underlying basis of assumptions when using econometric spatial models such as the spatial lag model (SAR) and the spatial error model (SEM) [17]. SAR models are used to capture the direct effect from neighboring regions to dengue incidence, thus facilitating the understanding of interregional spatial interactions on the pathophysiology of the disease. In contrast, SEM models are used to capture spatial constraints in the error components that often represent unobservable factors contributing to the transmission dynamics. Results: The coupling of these models provides the flexibility and accuracy needed to better understand the mechanics of dengue transmission in areas with heterogeneous spatial attributes. The study [18] showed that semi-parametric spatial-based methods were better predictors of dengue distribution in Nepal.

Moreover, another innovation in this study refers to the use of advanced diagnostic strategies for selecting the best model. Model selection in many previous studies relied on conventional methods that did not account for the inherently complex nature of spatial data. This research uses AIC and BIC type approaches studying the spatial models. This method leads to a more solid basis for the decision in selecting the best model based on conditions of data and area of study. Early dengue predictions were yielded through integrating predictive modeling strategies with climate variables [19].

This study fills a gap in the literature on data-driven intervention strategies, including therapies that risk areas to prioritize where to target resources or designing high health campaigns targeting areas of high humidity that speed up the cycle of mosquitoes. In sum, findings from this research support informed decision-making and data-driven policies to implement effective interventions that can improve the health of a population with endemic infectious diseases like Chagas disease. Another case is the creation of climate-based risk maps to help local authorities plan mitigation actions-such as improving drainage systems in areas prone to flooding. This study highlights the use of spatial models for not only detecting high-risk areas but also deriving evidence-informed guidelines to assist in more targeted public health intervention planning.

2. METHODS

This study was conducted in the East Nusa Tenggara region. The research data consists of secondary data on climate change from database of Meteorological, Climatological, and Geophysical Agency (BMKG), meanwhile the data of dengue fever incidence in the NTT region, obtained from the NTT Provincial Health Office. The data collected is from the year 2022, based on 22 districts/cities.

Meanwhile, the research variables used in this study are detailed in Table 1.

In this study, the spatial weight matrix W used is the Queen Contiguity matrix. This matrix was selected because it considers that adjacent regions have a greater influence on each other. In the Queen Contiguity matrix, spatial units are defined as neighbours if they share a common side or vertex. The research was carried out following a series of methodical steps. First, exploratory spatial data analysis was applied to the research variables to understand the underlying patterns and relationships. This initial analysis helps in identifying spatial dependencies and distributions within the data. Next, the study involved constructing a model for regional investments in Indonesia using a spatial panel data approach. Digital map of East Nusa Tenggara Province is shown in Figure 1.

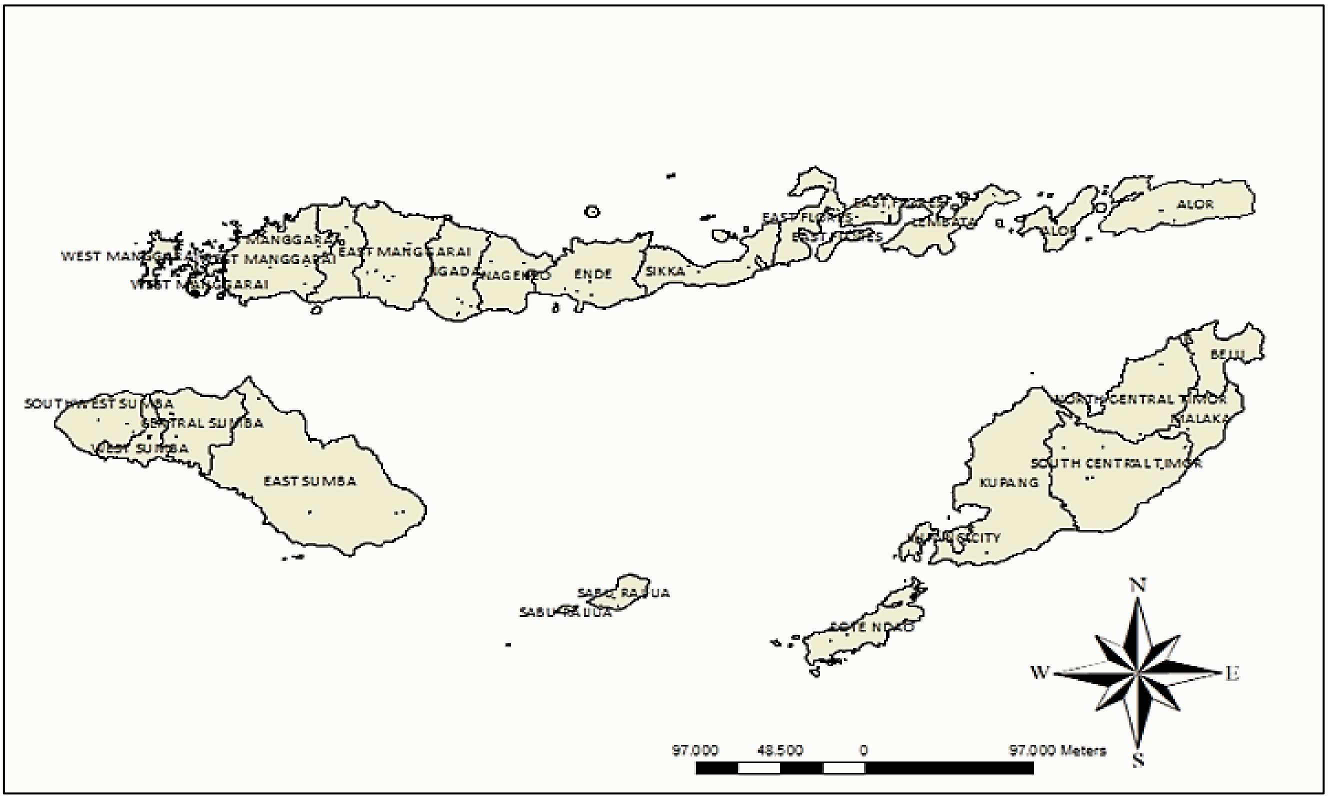

Figure 1. Digital map of East Nusa Tenggara Province

Table 1. Research variables

Variable	Variable's Name	Unit
Y	Dengue Fever	Case
X_1	Temperature	°C
X_2	Humidity	Percentage
X_3	Rainfall	Millimeter

2.1 Spatial weight matrix W

The spatial weight matrix W | n×n, with n being the number of regions or the number of observations that must be defined beforehand, is the basis point of the spatial econometric analysis as it describes the impact of the spatial interaction between the regions. It controls what happens in one area, as it is affected by what happens in neighboring areas, so the choice of matrix specification is a critical stage; formally, it can affect the analysis results. For example, the Queen Contiguity uses a matrix where regions that share borders or vertices are treated as neighbors, thus providing more flexibility for spatial definition. However, this method has weaknesses, especially in areas with sparse connections like an island area; sometimes, some regions remain unconnected [20].

The selection of the spatial weight matrix is a crucial aspect, as this plays a critical role in how spatial dependence is captured and the validity of the model. Although the Queen Contiguity matrix is common due to its straightforward interpretation, other approaches, such as distance-based or k-nearest neighbor matrices, may offer greater insights into spatial interactions. Distance-based matrices, for instance, consider geographical distances between sample points; hence, they are very useful in areas where spatial structures are unbalanced. Likewise, k-nearest neighbor matrices guarantee the number of neighbors for each region is a constant number, which is very helpful in solving the problem of isolation in sparsely connected or remote places [21].

The use of a Queen Contiguity matrix here is justifiable by the ability of this type of contiguity to get a direct spatial association at borders or the inclusion of either vertices or boundaries, whilst matching the administrative limit and geographical form of East Nusa Tenggara (NTT). Alternative approaches, such as distance-based matrices, were contemplated, but ultimately not adopted, as the region has a wide geographic scale, and establishing adequate distance thresholds in a heterogeneous topography is challenging.

Also, the selection of the Queen Contiguity matrix bears a direct impact on the outcomes of this research. It guarantees that spatial dependencies, such as spillover effects of climate variables, occur within districts that are close to each other. This decision affected how the spatial error model (SEM) performed, enabling the SEM to detect spatially correlated errors associated with unobserved elements, like endogenous population movement or local characteristics of mosquito habitat. Nonetheless, it should be noted that this matrix does not capture long-distance interactions or spatial dependence beyond immediate neighbors, which may result in underestimating spatial effects that act more globally.

The results also suggest the exploration of alternative matrices, like hybrid matrices that integrate contiguity and distance, in future research to give researchers a more nuanced understanding of how spatial relationships interact. The hybrid matrices can represent both direct and indirect interactions between regions and produce better results in geography that is complicated like NTT. This would improve knowledge of the local drivers of dengue fever transmission and form a robust basis for targeted public health action.

The matrix is defined as:

$$w_{ij} = \begin{cases} 1, & \text{if regions } i \text{ and } j \text{ are neighbors} \\ 0, & \text{otherwise} \end{cases}$$

To ensure consistency across regions, w is row-standardized, meaning that each row of w sums to one. This standardization transforms the weights to:

$$w_{ij}^{*} = \frac{w_{ij}}{\sum_{j=1}^{N} w_{ij}} \tag{1}$$

where, w_{ij}^{*} represents the standardized spatial weight for neighboring region pairs.

2.2 Basic regression model

We start with the basic Ordinary Least Squares (OLS) model that explains the relationship between the independent variables and the dependent variable, ignoring any spatial effects.

$$Y_i = \alpha + \sum_{k=1}^{3} \beta_k X_{ik} + \epsilon_i \tag{2}$$

where,

Y_i is the observed value of the dependent variable (dengue fever cases) for region i.

X_{ik} represents the independent variables for region i, including temperature (X_1), humidity (X_2), and rainfall (X_3).

α is the intercept term.

β_k are the coefficients for the independent variables.

ϵ_i is the error term for region i.

2.3 Testing for spatial autocorrelation: Moran's I

To determine whether to accommodate spatial effects in the model, we test for spatial autocorrelation in the residuals from the OLS model with Moran's I, a common test of spatial autocorrelation based upon a statistic that demonstrates whether similar values group in the space. A strong Moran's I statistic indicates that the residuals are spatially autocorrelated, which means that there are significant spatial dependencies in the data and the use of standard OLS regression is not an appropriate technique. This is illustrated by the presence of spatial autocorrelation, whereby not only are observations in neighboring regions not independent, but rather the relationships between variables may cross spatial boundaries [18]. This can be done by incorporating spatial effects in traditional econometric models, such as spatial autoregressive (SAR) or spatial error models (SEM) [22].

$$I = \frac{N \sum_{i=1}^{N} \sum_{j=1}^{N} w_{ij} (Y_i - \bar{Y})(Y_j - \bar{Y})}{\sum_{i=1}^{N} (Y_i - \bar{Y})^2 \sum_{i=1}^{N} \sum_{j=1}^{N} w_{ij}} \tag{3}$$

where,

N is the total number of regions.

$\bar{Y}$ is the mean value of Y.

w_{ij} denotes the spatial weight between regions i and j. A significant Moran's I statistic indicates spatial autocorrelation in the data, suggesting that the standard OLS model is inadequate and a spatial econometric model is necessary.

2.4 Spatial econometric model development

Since Moran's I suggests that there are spatial autocorrelations, we extend the OLS model by incorporating spatial effects. The dependence of observations on other observations can be included in two main ways, via the spatial lag of the dependent variable or the spatial autocorrelation in the error term.

Step 1: Implementing the spatial lag model (SAR)

The first extension adds a spatially lagged dependent variable. This method shows the impact of the other regions on the active region. The equation is:

$$Y_i = \rho \sum_{j=1}^{N} w_{ij} Y_j + \alpha + \sum_{k=1}^{3} \beta_k X_{ik} + \epsilon_i \tag{4}$$

where,

ρ is the spatial autoregressive coefficient, indicating the strength of the spatial dependence.

$\sum_{j=1}^{N} w_{ij} Y_j$ represents the spatially lagged dependent variable that accounts for average values of adjacent areas.

The SAR model is obtained by incorporating the term ρWY into the OLS model, thus making Eq. (1) into Eq. (4), where the spatial influence is explicitly involved.

Step 2: Spatial error model (SEM)

Or it can be modeled as spatial dependence in the error term. In this model, known as the spatial error model (SEM), spatial correlation is specified in the residuals, which also means that unobserved variables that affect the incidence of dengue fever are spatially correlated between regions. The SEM is represented as:

$$Y_i = \alpha + \sum_{k=1}^{3} \beta_k X_{ik} + \epsilon_i \tag{5}$$

$$\epsilon_i = \lambda \sum_{j=1}^{N} w_{ij} \epsilon_j + u_i \tag{6}$$

where,

λ is the spatial autoregressive parameter for the error term.

u_i is an independent error term that follows a normal distribution.

In this model, the error term ϵ_i is influenced by the spatially lagged error from neighboring regions $\sum_{j=1}^{N} w_{ij} \epsilon_j$. This approach assumes that the spatial effects originate from the unobserved variables rather than the observed variables.

2.5 Model selection criteria

Selecting the appropriate spatial econometric model (SAR vs. SEM) is a key element of spatial data analysis. This choice has a major impact on capturing spatial dependencies correctly, which ultimately leads to accurate and interpretable information about the data. While torque is used by-group in almost all statistical models, researchers often test their data with a variety of model evaluation criteria to make sure that their selection is consistent with their data.

The most popular tests to achieve this are the Lagrange Multiplier (LM) tests, the LM Lag Test, and the LM Error Test. Assessment of how the spatial dependencies are embedded in the data. The LM Lag Test examines the parameter of nominal spatial lag (ρ) to determine if there are direct spatial interactions that may influence the dependent variable. A substantial result means spatial effects have a direct influence on the dependent variable, making the SAR model more adequate. Note that the LM Error Test checks the spatial error parameter (λ) to determine spatial autocorrelation in the residuals. If the result of the LM Error Test is significant, the SEM is preferred because it incorporates this type of spatial dependency better [14].

As a consequence, the results of these tests often seem to make the decision cut and dry. If the LM Lag Test is significant and the LM Error Test is not, a SAR model better captures spatial interdependence since it focuses on such interactions in the dependent variable. In contrast, if the LM Error Test is significant while the LM Lag Test is not, then SEM is more appropriate, since it aims at capturing spatial correlations in the residuals. Spationomic models have the advantage that researchers can adjust their models to the realistic spatial structure of the data [17].

Still, ambiguity may arise if both tests yield significant results, which indicates spatial dependencies can exist for both the dependent variable and residuals. When this is the case, researchers frequently resort to robust variants of the LM tests, which account for possible overlaps between the two types of spatial effects. Also, model selection criteria (e.g., Akaike Information Criterion (AIC); Bayesian Information Criterion (BIC)) can assist in the decision-making process. These criteria are designed to evaluate the fit of the model while applying a penalty for developing complex models [23].

Finally, the decision of whether to use SAR or SEM depends on statistical tests, model fit indices, and the nature of spatial dependencies present in the data. Combining these techniques gives researchers the ability to have robust results while capturing the complexities of the spatial relationships. This process is essential for estimating spatial econometric models that are explicitly meaningful and practically useful.

2.6 Model estimation techniques

Spatial econometric models, including the spatial autoregressive (SAR) and spatial error models (SEM), utilize robust estimation techniques to model the spatial dependencies inherent in the data. There are two common approaches to estimating the model parameters, including the spatial autoregressive coefficient (ρ), spatial error coefficient (λ), and regression coefficients (βk): Maximum Likelihood Estimation (MLE) and Generalized Method of Moments (GMM). The choice of method depends on the whisker of the data and what the analysis should achieve. MLE is a technique that maximizes the likelihood function of the observed data conditioned on a certain distribution of the error term. When the assumptions of normality and homoscedasticity are satisfied, this is a very efficient way of doing it. Under such conditions, it yields uniform and efficient estimates of the function parameters. However, MLE provides computational challenges, specifically with matrix inversion of the form (I−ρW), which can be computationally intensive in cases of large data set or complex spatial structures. Generally, such approaches require sophisticated computational resources to guarantee the applicability of the method [22]. GMM is a more flexible approach where we do not need strong assumptions on the error term distribution. Instead, it uses population moment conditions that can be obtained from the model to estimate parameters. Its flexibility also makes it particularly appropriate for situations where the data exhibits heteroskedasticity or departures from normality. In addition, GMM has lower computational costs than MLE, since it does not require the direct inversion of large spatial matrices.

Already established empirical studies have shown that GMM offers a stable performance in the spatial econometric context, even more with data sets with highly spatially varying data [24]. In contrast, MLE's advantage remains for datasets for which the error structure conforms to normality assumptions, as it yields highly-efficient and accurate parameter estimates [25]. When it comes to deciding which estimation technique to use, it should be based on the question we want to answer and the data we have. MLE, on the other hand, is more suitable for applications that emphasize estimation accuracy from correctly specified distributions, whereas GMM offers more flexibility and resilience when data is problematic, like heteroskedasticity or non-standard distributional errors. These contrasting properties reflect the complementary functions of MLE and GMM within the scope of spatial econometric analysis. Both MLE and GMM are critical for SAR and SEM models.

2.7 Diagnostic checks and interpretation

Once you fit a spatial econometric model, it is important to conduct diagnostic checks for the model and multicollinearity. Hence, those checks would also indicate that something went wrong-if any were going wrong-e.g., in case of multicollinearity, non-normality of the residuals, presence of the residuals' spatial autocorrelation, et cetera. These diagnostics guarantee the robustness of results when analyzing complex phenomena such as dengue fever incidence in East Nusa Tenggara.

The first step in a diagnostic process is to check multicollinearity in the independent variables. This phenomenon in multiple regression is known as multicollinearity, whereby two or more predictors are highly correlated, leading to inflated estimates of their coefficients and making the causal relationships harder to interpret. Tools such as Variance Inflation Factor (VIF) are often used to check for this problem. Flagging high VIF scores indicates that some collinearity issue exists and that we should prepare to address it by either merging correlated variables or dropping the redundant ones. This applies to climate variables, like temperature and rainfall, that may inherently have interdependence.

Another important diagnostic of whether or not the standard linear regression assumptions hold true is checking the normality of the residuals. Residual normality is an assumption of many spatial econometric models, especially those implemented using Maximum Likelihood Estimation. Violations of normality can lead to inaccurate parameter estimates and invalid tests of inference. Tests such as the Shapiro-Wilk test can be conducted to assess residual normality, or residuals can be observed graphically with quantile-quantile (Q-Q) plots. Transformations or robust estimation techniques may be necessary if the residuals do not conform strictly to normality [26].

The third key diagnostic is used to check for remaining spatial autocorrelation in the residuals. Just like in traveling salesman problems, if residuals are still spatially correlated, it means your solution has not found optimal parameters for your model to capture spatial dimensions. Moran's I statistic is a classic tool to investigate the spatial autocorrelation of residuals. However, the identification of spatial dependence implies the necessity for model improvement, for example, through additional spatial lags or error terms. In the context of a dengue fever model, for instance, failing to address spatial dependencies likely indicates missing factors (e.g., population density, healthcare access within the area) affecting the distribution of the cases [14].

With careful execution of these diagnostic checks and addressing any issues, the spatial econometric model is a potent vehicle for insight into complex dynamics. In the case of dengue fever, such a model could help show how the climate factors interact with the spatial dependencies to create patterns of disease. For example, increased rainfall may not only favor local mosquito breeding but also induce "spillover effects" in adjacent regions via human or vector mobility. Addressing all diagnostic issues ensures that researchers will provide more robust and useful knowledge to shape public health efforts.

Diagnostic checks are critical to validating spatial econometric models. Through steps like addressing multicollinearity, ensuring the normality of residuals, and accounting for spatial autocorrelation, researchers can develop more nuanced models and provide findings that accurately reflect the spatial dynamics highlighted in their data.

2.8 Latest research in the field of climate change and dengue transmission

Climate change has become an increasingly critical factor driving the emergence and reemergence of vector-borne diseases (VBDs), such as dengue fever, over the past decades. The link between climate change and the global proliferation of these diseases is well-documented. The study [27] emphasizes that global warming, when coupled with urbanization and rising greenhouse gas emissions, has facilitated the expansion of mosquito populations into regions previously unsuitable for their survival. Changing weather patterns such as variations in temperature, precipitation, and humidity play a pivotal role in shaping the habitats and breeding cycles of these vectors, thereby amplifying the risks of dengue transmission.

To address the challenges posed by the spatial and temporal dimensions of dengue transmission, researchers have employed a variety of modelling techniques. The study [28] utilized geostatistical methods, including binomial kriging, to map the prevalence of dengue fever in Khyber Pakhtunkhwa, Pakistan. Their findings revealed that dengue outbreaks were particularly concentrated in low-altitude regions, with Peshawar experiencing the highest burden of cases. The study identified critical risk factors such as population density, proximity to roads, and vector distribution, which provided valuable insights for targeted public health interventions in the region.

The relationship between climatic factors and dengue incidence has also been explored through geographical information system (GIS)-based approaches. For example, the study [29] analysed the spatial and temporal distribution of dengue cases in Sri Lanka from 2009 to 2014, discovering a significant positive correlation between rainfall and dengue incidence. Interestingly, their study did not find a similar correlation for temperature or humidity. Similarly, the study [30] investigated the epidemiology of dengue in Bangkok, Thailand, focusing on seasonal patterns and their association with climatic factors. Through Spearman correlation and multivariate Poisson regression analyses, the study demonstrated that humidity and rainfall were significant contributors to dengue transmission. A 1% increase in rainfall was associated with a 3.3% rise in dengue cases, underscoring the critical role of weather variables in the region's dengue dynamics.

In Pakistan, the study [31] used GIS mapping and generalized linear modeling (GLM) to study the spatial intensity and significant factors associated with dengue outbreaks. The results showed that rainfall, temperature, and access to healthcare facilities were significant determinants of dengue prevalence. The study also revealed that 2011 was the most devastating year during the 2006–2017 study period, with 290 fatalities attributed to dengue in Pakistan. This highlights the potential of spatial models to identify high-risk areas and improve resource allocation for disease control.

In the meantime, Bayesian approaches have further advanced the understanding of dengue fever dynamics by incorporating both spatial and temporal autocorrelations. The study [32] reviewed the use of Bayesian spatial and spatio-temporal models for dengue, emphasizing their superiority over frequentist methods in handling complex data structures and uncertainties. The study [33] applied these methods to study dengue risk in Puerto Rico, revealing significant lagged effects of temperature and precipitation on dengue incidence, with delays of up to four and three months, respectively. Their work provided actionable insights for designing targeted interventions. Similarly, the study [34] explored the effects of forest loss, precipitation, and temperature on dengue in Mexico, finding that a 1% decrease in forest cover was linked to a 16.9% increase in dengue risk. The study [35] expanded this focus by using downscaled climate models to predict spatial and temporal shifts in dengue transmission suitability under future climate scenarios in Pakistan. Their findings highlighted the need for adaptive strategies as climate change alters the landscape of dengue risk.

Expanding the scope of analysis, the study [36] incorporated both environmental and socioeconomic factors into a generalized additive model (GAM) to examine the spatiotemporal patterns of dengue fever. The study demonstrated that while environmental factors, such as temperature and precipitation, exhibited slight variations across regions, socioeconomic variables like population density, land use, and road density played a more pronounced role in determining the incidence of dengue fever. Zheng et al. [36] concluded that resources for prevention and control should be allocated based on the spatial patterns of primary influencing factors to maximize the effectiveness of interventions.

In the context of East Nusa Tenggara, this study seeks to understand the spatial relationship between climatic factors and dengue incidence using spatial regression modeling. This method provides a simpler yet effective framework for analyzing spatial dependencies and understanding how climatic factors influence disease transmission.

3. RESULT AND DISCUSSION

3.1 Spatial interpolation using universal kriging on climate variable data

Universal Kriging is a method of spatial interpolation used to predict values at non-measured sites, considering the presence of trends or systematic changes in value across the measured area. As opposed to Ordinary Kriging, where a constant value is assumed across the area, Universal Kriging allows for global changes of trends-for example, due to geographical or environmental reasons-using polynomial functions to describe those global structures. Since in NTT not all districts have weather stations, this method is used to obtain data for the unmeasured districts, taking into account the global spatial trend or variation in areas of research (Figures 2-4).

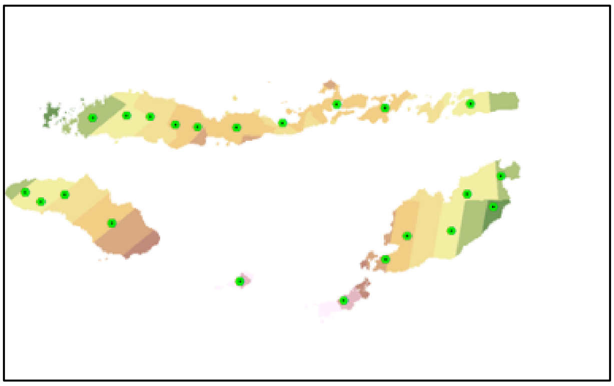

Figure 2. Universal Kriging on temperature data

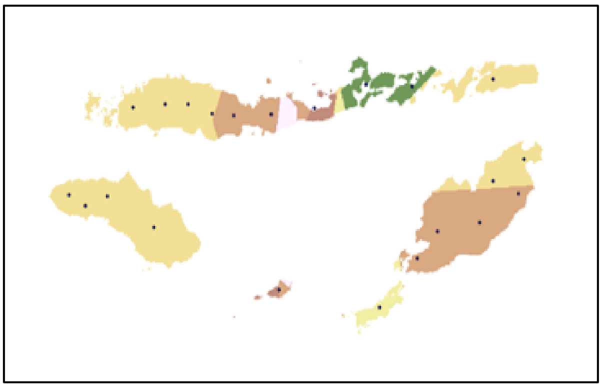

Figure 3. Universal Kriging on humidity data

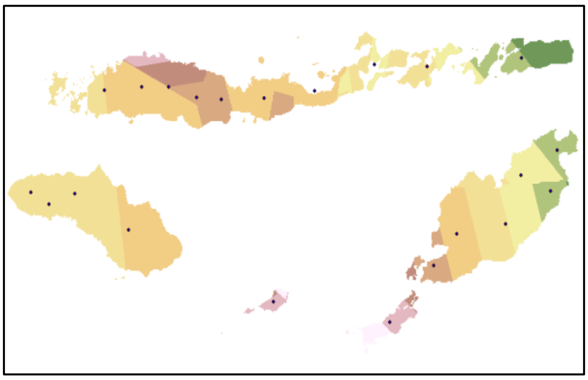

Figure 4. Universal Kriging on rainfall data

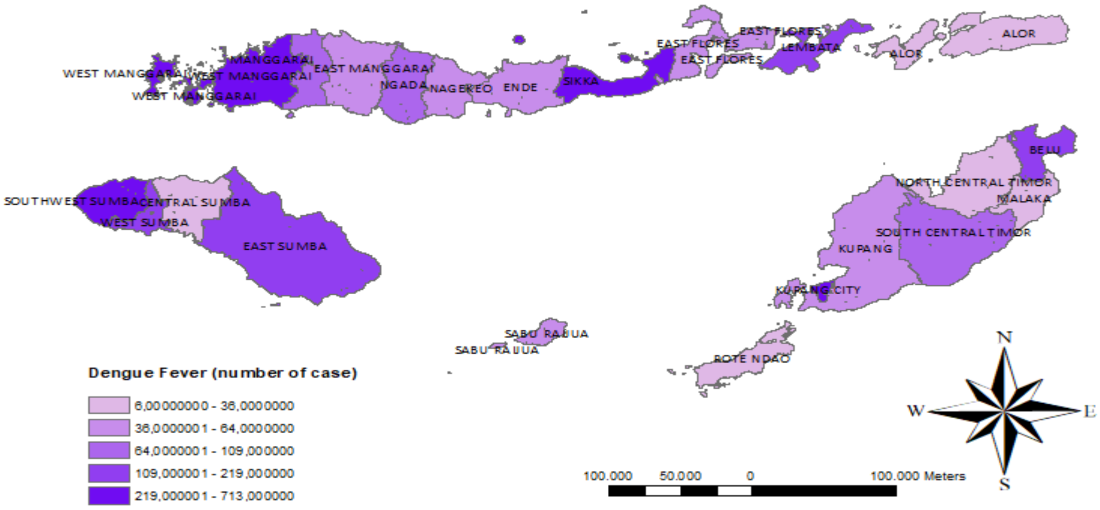

Figure 5. Distribution of dengue fever based on regency in East Nusa Tenggara Province in 2022

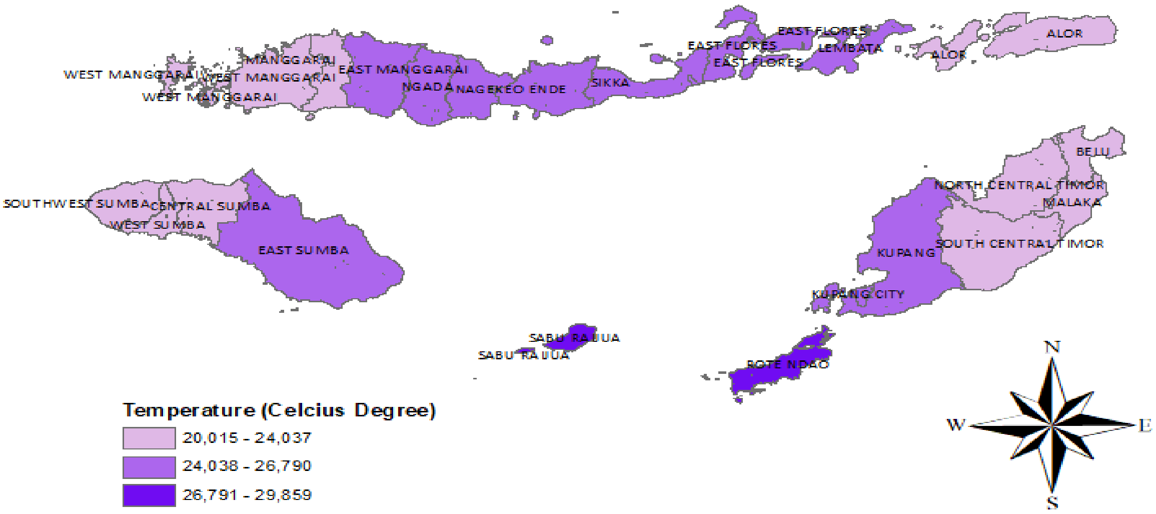

Figure 6. Distribution of temperature based on regency in East Nusa Tenggara Province in 2022

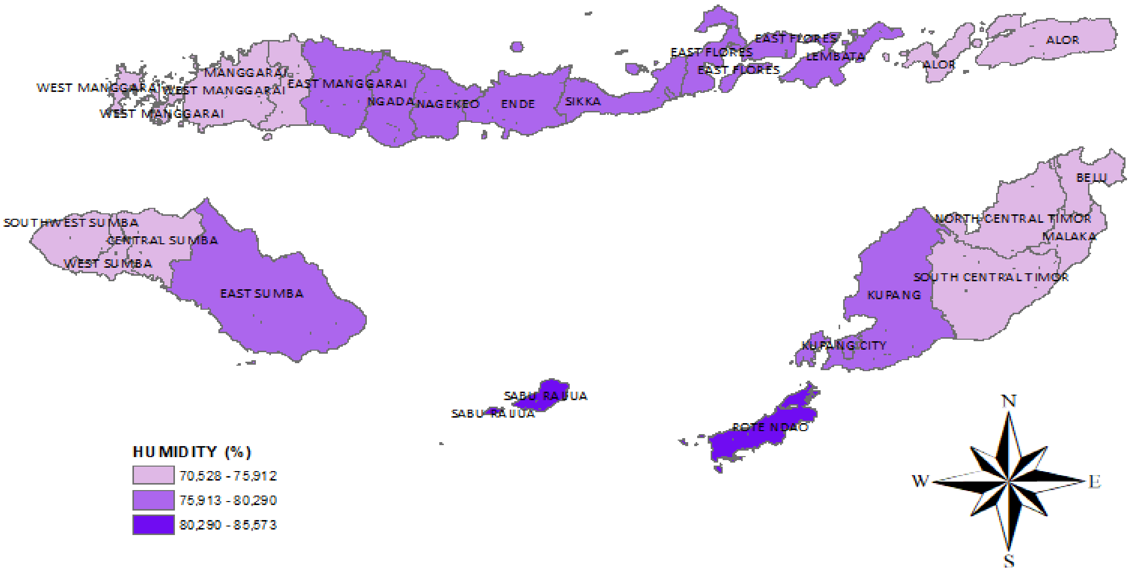

Figure 7. Distribution of humidity based on regency in East Nusa Tenggara Province in 2022

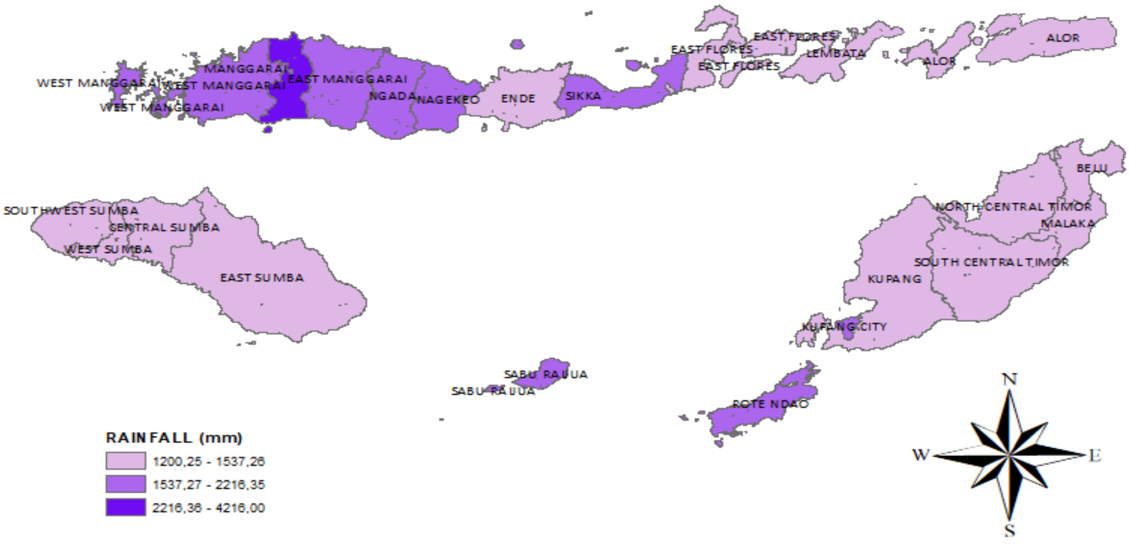

Figure 8. distribution of rainfall based on regency in East Nusa Tenggara Province in 2022

Figures 5-8 show the spread of dengue fever, temperature, humidity, and rainfall in the NTT region in 2022. Based on the color gradation, the darker the color gradation indicates the higher the value of these variables.

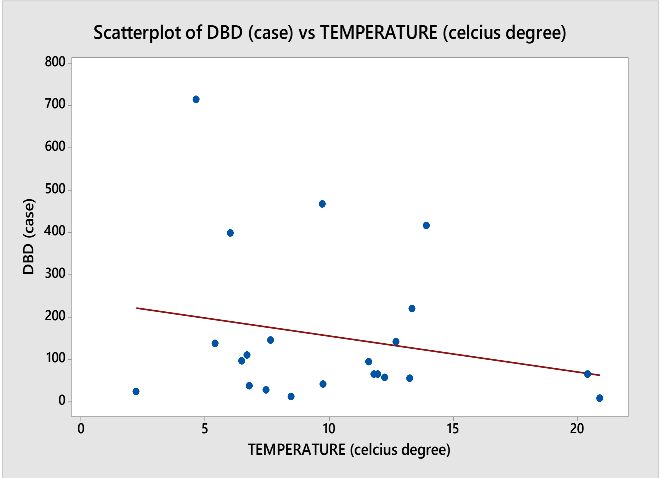

Figure 9. Scatterplot dengue fever vs. temperature

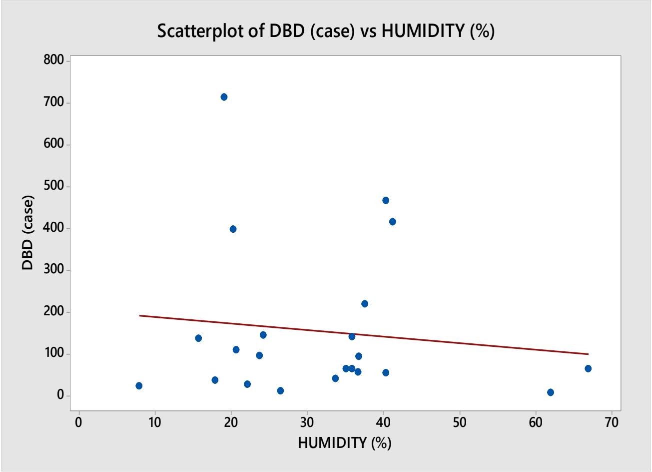

Figure 10. Scatterplot dengue fever vs. humidity

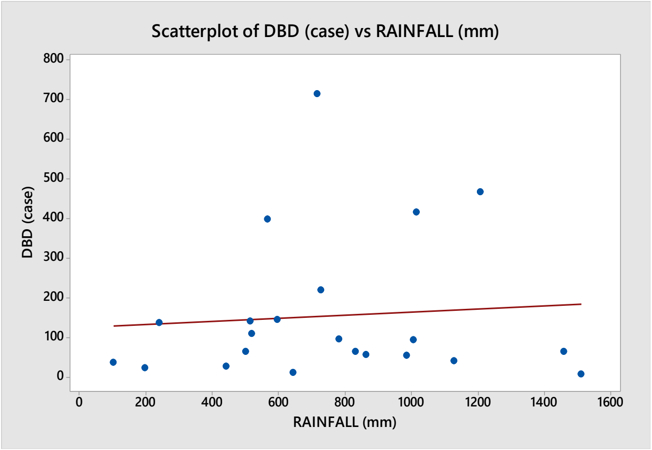

Figure 11. Scatterplot dengue fever vs. rainfall

3.2 Characteristics of dengue fever

Increasing temperatures can be associated with increased case numbers for Dengue Fever (DBD) cases, as shown in Figure 9, which illustrates the relationship between temperature and DBD case numbers in the NTT (Nusa Tenggara Timur) province. Essentially, colder temperatures correlate with a rise in DBD cases for a given area, as demonstrated in Figure 10, where humidity levels, which tend to be higher at reduced temperatures, create an ideal environment for the Aedes aegypti mosquito, the primary vector for DBD, to reproduce and live longer. This extended lifespan raises the risk of DBD transmission.

Moreover, Figure 11 depicts the relationship between rainfall and DBD cases, suggesting that seasonal rainfall may further contribute to creating breeding grounds for mosquitoes. Lower temperatures can lengthen the mosquito's life cycle, allowing them more time to transmit the virus before dying. The seasonal trends in the NTT region, as evidenced in these figures, indicate a direct correlation between temperature, humidity, rainfall, and the incidence of DBD cases. These findings underscore the importance of considering climate conditions in efforts to prevent this disease.

3.3 Regression spatial analysis

As reported in Table 2, the Moran's I ρ-value (0.08089) provides statistical circumspect of H0 (reject H0 at α=10%), yielding evidence for spatial dependence in OLS regression errors. This is what we mean by spatial dependence: the values of neighboring regions are not independent but rather exhibit patterns by proximity (residuals in one area depend on residuals in neighboring areas). The residuals clearly indicate that the model fitted does not suffice to explain the behavior of the studied phenomenon as the residuals are not cooperating. Moran's I gives only a first hint of the spatial structure in the data, but more testing is needed to determine the exact form of this spatial dependence.

Besides detecting spatial dependence by means of Moran's I, we use the Lagrange Multiplier (LM) test to determine more specific types of spatial dependence (lag, error, or both (lag and error). 'lag' refers to the influence of dengue incidence in surroundings on a region's dengue rates, and 'error' captures spatial correlation in unobserved processes affecting dengue incidence across regions. Table 2 displays the results of these tests, which underscore through p-values the degree of importance of different spatial dependency tests and their respective interpretations.

For the Lagrange Multiplier-error test, p-value obtained =0.059768<α=10%, which leads to rejection of H0. This finding indicates spatial error dependence, meaning that factors not captured by this model that affect dengue incidence are correlated over spatial proximity. Potential examples of these unobserved factors may include variations in access to healthcare that are only relevant at the individual care level, unrecognized environmental variables (e.g., within a city: microclimates), or behavioral variations (e.g., community-wide adherence to mosquito control measures). This result requires immediate attention via the spatial error model (SEM), which caters to the spatial correlation between the error terms, subsequently having the likelihood of increasing the explanatory strength and infallibility of the model.

Also, the Robust LM-lag test provides ρ-value=0.047827, which is significant at α=10% (ρ-value <α=10%). This reflects H0 rejection while indicating the existence of spatial lag dependence. Spatial lag dependence means that the incidence of dengue in a given area is affected by that in the neighboring sectors. An example of one is high incidence in one city may expose nearby areas to risk as infected individuals or mosquitoes cross borders, also showing how interconnected disease people are. This outcome suggests analyzing the results further with the Spatial Autoregressive Model (SAR), which incorporates space interaction effect explicitly in the dependent variable.

On the other hand, the Lagrange Multiplier (lag) test and Robust LM-error test show p-values 0.759683 and 0.406930, which are not significant at α=10% level. These results reflect the non-rejection of H0 in the sense of no spatial lag or spatial error dependence (in these tests). In addition, the Lagrange Multiplier (SARMA) test to check simultaneously for spatial lag and error has a p-value of 0.676611, which also confirms there exists not so dominant form of spatial dependence in the data in the context of spatial lag and error combined.

From the analysis in Table 2, the significant spatial lag and spatial error found under certain conditions indicate that differing spatial dependency structure is present in the data. Together, these results underscore the need to utilize both SAR and SEM models in subsequent analyses to better capture the spatial dynamics that drive dengue incidence. Since the incidence of dengue in one area can directly affect the neighboring areas, the SAR model highlights the transmission effect through the spatial interaction. On the other hand, the SEM model aims at adjusting for unobserved factors that are spatio-temporally correlated and contained in the error term, thus preventing external factors such as unobserved environmental or socio-economic factors from biasing the results. By using both models together, we get a more holistic view of the mechanics behind how spatial patterns as well as externalities influence disease transmission. The models attempted to be generated by taking care of both spatial lag and spatial error effects are expected to shed light on a more nuanced perspective regarding the spatial mechanism at work regarding disease transmission, thus allowing for better-guided targeted public health interventions.

Thereby, according to Table 3, the lag parameter coefficient (ρ) p-value shows p-value >α=10% (p-value=0.742). It means that the spatial lag parameter is non-significant in the spatial autoregressive model. This also implies that due to the small value of the spatial lag coefficient, one can say that it had little or no effect on the model, indicating that the lag effect on the spatial relationship of regions is not significant in explaining dengue variation. This suggests the spread of dengue is driven more directly by local factors, including environmental context and direct human-mosquito interactions, than transmission between adjacent areas. There was no significant lag effect, indicating that these interventions should be of local level control measures and not of interactions between regions.

Similarly, the constant term has a p-value (0.029) significant at α=5%, suggesting that even in the absence of the explanatory variables, there is a "base incidence" of dengue (possibly linked with factors other than β). For meteorological variables, temperature has a negative coefficient (-67.801), but it was not statistically significant (p-value=0.130). So, it means that higher temperatures may have some capacity to reduce the incidence of dengue, but not enough to be conclusive. Scientifically, this may mean that temperature effects on vector competency and virus spread may also interact with other unmeasured factors, such as population density or mosquito control efforts, which may weaken its sole effect. For instance, temperatures may facilitate mosquito activity, but this could be neutralized in densely inhabited urban regions where vector control programs, such as fogging or larvicidal administration, are more robust. On the contrary, such effects could be pronounced in rural areas with low control measures, showing a space questioning on localized interactions into the observations.

Likewise, for humidity (17.7414, p-value=0.354) and rainfall (0.11539, p-value=0.649), the coefficients are positive, but they are not statistically significant. These findings are congruous with the results of some previous studies in which climatic variables such as humidity and rainfall showed weak or non-significant associations with dengue incidence when analyzed at aggregated spatial scales. Does this mean that these variables do not matter for arboviral transmission and/or breeding habitats for mosquitoes? However, research has recently demonstrated that these variables also play an important role in arboviral transmission dynamics, suggesting localized or seasonal variation might be important in understanding transmission and its impact on mosquito breeding habitats. Thus, after carrying out multicollinearity diagnostics, we found that humidity and rainfall do not significantly influence incidence in the present spatial autoregressive model. The absence of significance may thus also be explained in terms of scale, as microclimatic differences or other local environmental factors may affect these variables in ways that the model does not convey.

The R²=0.4193 indicates that 0.42 of the variances in dengue incidence is explained by the model. The unexplained 58% presumably incorporates microclimatic variation, unobserved demographic effects, or aspects of behavior like the community-level adherence to mosquito control efforts. Also, social or economic factors such as health care infrastructure or urbanization may be very influential. These include aspects like improved treatment of input features, interaction terms, or using additional features that the model can build on to provide better interpretations of the results. This average R² indicates that while the model captures some of the dynamics, a large part of the variability is not captured by the model. Statistically, this would indicate possible multicollinearity or omitted variable bias. Furthermore, the moderate Akaike Information Criterion (AIC) value of 294.52 reflects this need for model improvement.

Adding new variables that might be relevant to the disease, such as socioeconomic factors (e.g., access to healthcare, tropo-urban environments), vector control measures, or even more fine-resolution climate data (e.g., daily or weekly) could lead to improvements, both statistically and scientifically, in the model. Alternatively, exploring different modeling strategies, such as the spatial error model (SEM), may help account for unobserved spatial effects, as the model presented here may not adequately model for correlated errors that could be impacting dengue transmission patterns. The SEM is particularly useful for correcting for spatially correlated error terms that can occur from omitted variables that correlate with the regions, such as variations in health infrastructure or localized mosquito control efforts. Climate variables would also provide opportunities for exploring interactions between climate variables (for instance, those of temperature and humidity) to understand the overall influence on vector ecology and disease dynamics.

Table 2. Results of spatial effect testing with Queen Contiguity

No.	Spatial Dependency Test	Value	p-value	Result
1	Moran's I (error)	0.1498	0.08089	Reject H_0
2	Lagrange Multiplier (lag)	0.0936	0.759683	Failed to reject H_0
	Robust LM (lag)	0.5028	0.047827	Reject H_0
3	Lagrange Multiplier (error)	0.2785	0.059768	Reject H_0
4	Robust LM (error)	0.6877	0.406930	Failed to reject H_0
5	Lagrange Multiplier (SARMA)	0.7813	0.676611	Failed to reject H_0

Table 3. Parameter estimation using spatial autoregressive model with Queen Contiguity

Parameter	Coefficient	Std. Error	z-value	Probability
ρ	-0.0950	0.2893	-0.328	0.742
Constant	206.011	94.769	2.173	0.029
Temperature	-67.801	44.835	-1.512	0.130
Humidity	17.7414	19.160	0.925	0.354
Rainfall	0.11539	0.2539	0.454	0.649
R^2		**0,4193**		
AIC		**294.52**		

Table 4. Parameter estimation using spatial error model with Queen Contiguity

Parameter	Coefficients	Std. Error	z-value	Probability
λ	-0.217	0.308	-0.704	0.481
Constant	186.8	72.167	2.588	0.00964
Temperature	-75.934	44.687	-1.699	0.08927
Humidity	21.235	18.859	1.125	0.26017
Rainfall	0.0867	0.240	0.361	0.71806
R^2		**0,4538**		
AIC		**285.235**		

Table 5. Comparison of R^2 and AIC values from several models

No.	Model	R^2	AIC
1	Classical regression (OLS)	0.3572	294.623
2	Spatial Autoregressive Model (SAR)	0.4193	294.52
3	Spatial Error Model (SEM)	0.4538	285.235

Result α=10% level (p-value=0.08927), only the temperature variable has a significant result on the spread of dengue fever in the NTT region as presented in Table 4. This may imply a target on temperature-associated interventions, such as targeted climate adaptation policies or localized systems for temperature adjustments. This knowledge could inform mitigation efforts during the transmission season; for example, reductions in mosquito populations through targeted habitat modification or increased larval control during periods of increased temperature could be effective at reducing transmission rates. This indicates that temperature significantly influences the transmission dynamics of dengue fever, probably because temperature affects the breeding, activity, and survival of the vector (Aedes mosquitoes) of the disease. In particular, increased (or reduced) temperatures can directly influence the mosquito life cycle, as well as the extrinsic incubation period of the dengue virus in the vector.

The spatial error dependence coefficient (λ) is not significant (p=0.481). Because of the lack of significance of the Gaussian Process term, this indicates that unmeasured spatially correlated variables do not explain any large portion of the uncertainty in dengue cases in this analysis. This research may be consistent with findings in other areas where local environmental or socioeconomic factors drive dengue transmission more strongly than broader spatial patterns. On the other hand, it may simply mean that the spatial structure in this dataset is captured better by other variables or models, which would deserve investigation. These results indicate that unobserved spatial factors do not account for much of the residual variation in the number of dengue cases from the SEM. As a result, the model's explanatory power mainly arises from climate variables rather than unmeasured spatially correlated factors.

Humidity (p-value=0.26017) and rainfall (p-value=0.71806) coefficients are positive but not statistically significant. However, these factors can still affect dengue transmission because they affect mosquito breeding and the conditions for their survival. The absence of them in the model could be explained by the pooled nature, which could dampen local variations in these climatic variables or in time. Moreover, interactions with other unmeasured factors, including vegetation density, water storage habits, or drainage infrastructure, could dilute the direct effect of climate variables on dengue incidence. This is congruent with the results of the Spatial Autoregressive Model (SAR), where it suggests that these variables have little effect on the incidence of dengue in this specific context or are subject to other mediating factors that we do not have the data for in this model.

This means that with an R^2 of 0.4538, the SEM explains around 45% of the variability of dengue incidence. The remaining 55% of unexplained variation might be explained by unmeasurable factors such as local socioeconomic conditions, heterogeneous healthcare infrastructure, human behavioral alterations limiting mosquito exposure, and microclimates not measured in the dataset. There may also be the influence of undocumented interventions, like unsupervised vector control initiatives: community action could come into play. Future models should consider the incorporation of these drivers, as they influence dynamics and may enhance our understanding of dengue transmission. This shows an improvement from the SAR model and suggests that accounting for spatial error improves the fit for the data. Also, the value of AIC for the SEM (285.235<SAR=294.52) shows that the SEM represents the data better, making it a parsimonious and statistically sound explanation of the underlying factors.

These findings underscore the environmental temperature as a major driver of dengue transmission, but also expose the necessity for further model refinements to include more explanatory variables or different choices of spatial driver structure. Future studies might also investigate interactions of climatic and socioeconomic variables or higher spatial resolution data to improve model performance and predictive power. In particular, socioeconomic factors such as income, health service coverage, level of urbanization, and knowledge about vector control strategies can also be incorporated. National health surveys, census data, and geospatial databases related to infrastructure and land use, for example, could be used as inputs to improve the accuracy and relevance of these models. The results can be seen in Table 5.

Based on Table 5, the smaller the AIC values, the better the modeling that has been carried out. The SEM model is the best model when compared to the classical regression and SAR models because it has a larger R^2, namely 0.4538 and the smallest AIC, namely 285.235. The spatial error model means that for every onedegree Celsius decrease in temperature where other variables are considered constant, the spread of dengue fever will increase by 75 cases. The general SEM model is as follows:

$$\hat{y}_i = 186.8 - 75.935X_{1i} + u_i \tag{7}$$

$$u_i = -0.217 \sum_{j=1, i\neq j}^{n} w_{ij}u_j + \varepsilon_i$$

where,

$\hat{y}_i$: the i -th number of dengue fever of districts/cities.

X_{1i}: the i -th temperature of districts/cities of districts/cities.

W_{ij}: the spatial weighting matrix element at the i -th row and j -th column.

u_i: spatial residual of the i-th district/city.

ε_i: residual of the i-th district/city.

It should be noted that each district and city have a different form of spatial error model (SEM) because it is influenced by the Queen Contiguity weighting matrix that is adjacent to one region and another region as the object of observation. The spatial regression modeling that is formed will consist of a number of n observations, namely SEM models. The following is an example of a spatial error model for TTS district where the location of this district intersects with Kupang, TTU and Malaka districts.

$$\begin{aligned}\hat{y}_{KabTTS} = 186.8 - 0.217(&w_{TTSKabKupang} * u_{kabkupang} \\ &+ w_{TTSTTU} * u_{TTU} + w_{TTSMalaka} \\ &* w_{Malaka}) - 75.935X_{1i}\end{aligned} \tag{8}$$

The Spatial Error Model (SEM) is a sophisticated approach used to understand the spatial relationships and dependencies inherent in regional data. The SEM employed here provides a structured framework for analyzing the spread of dengue fever across districts, with specific emphasis on the influence of temperature and the residual spatial interactions between neighboring districts. The model consists of two main components: the structural equation for the predicted outcome (dengue fever cases) $\hat{y}_i$, and the spatial error equation (u_i), which accounts for unobserved spatial influences. By incorporating spatial residuals weighted by the Queen Contiguity matrix, the model provides an advanced means to capture both observed and latent spatial effects.

The first component of the model $\hat{y}_i = 186.8 - 75.935X_{1i} + u_i$, quantifies the relationship between temperature X_{1i} and the number of dengue cases in a given district. The negative coefficient (−75.935) indicates that a unit decrease in temperature correlates with an increase of approximately 75 dengue cases, holding other factors constant. This finding underscores the significant role of temperature in dengue dynamics, consistent with known biological mechanisms: mosquito activity, breeding rates, and virus replication are temperature-dependent. Lower temperatures within a suitable range can prolong mosquito survival and increase the extrinsic incubation period, thereby facilitating disease transmission.

The second component of the SEM is the spatial error term, $u_i = -0.217 \sum_{j=1,i\neq j}^{n} W_{ij}\, u_j + \varepsilon_i$. The first equation includes the spatial residuals (u_j) of the neighboring districts, weighted by the Queen Contiguity matrix (W_{ij}). A coefficient (−0.217-0.217) indicates excess residuals in adjacent districts correspond to fewer predicted dengue cases in the district itself. Spatial dynamics have been demonstrated as interconnected up until now, as the negative effects on unobserved elements in one area might even affect the neighboring regions due to the network of spatial associations. For example, the actual risk of transmission may be lessened due to effective public health interventions in a neighboring district, while underreporting or different surveillance systems may distort observed spatial patterns. W_{ij} is the spatial weights matrix, a central element of the SEM that shows how much the example from district interacts with the sample from district A, additionally shows how much sample A interacts with sample amount based on geographical proximity. The Queen Contiguity matrix assumes all directly neighboring districts are equally influential. This is a good first approach but can be an oversimplification of real-world interactions. As an illustrative example, if distance decay with respect to the influence of specific features is not uniformly distributed (e.g., travel patterns, population density, environmental constraints, etc.), our current understanding of spatial interaction may not be truly reflective of underlying processes. Furthermore, incorporating other spatial weighting schemes alternative to Queen Contiguity weights, such as based on distance or on travel networks, may allow for a more nuanced interpretation of these spatial dependencies.

The SEM applied specifically to the TTS district provides additional insights into localized dynamics. The spatial error term for TTS includes contributions from neighboring districts-Kupang, TTU, and Malaka-weighted by their spatial relationships. The model, $\hat{y}_{KabTTS} = 186.8 - 0.217(w_{TTSKabKupang} * u_{kabkupang} + w_{TTSTTU} * u_{TTU} + w_{TTSMalaka} * w_{Malaka}) - 75.935X_{1i}$, how the interactions of spatial residuals and temperature affect dengue incidence. This negative coefficient for spatial residuals (−0.217) implies that unaccounted influences in the Kupang, TTU, and Malaka regions reduce the number of predicted cases in TTS. This may result from differences in intervention effectiveness, access to health care, or accuracy of reporting. SEM is concerned in that, from a modeling perspective, it enables the effects that can be observed (e.g., temperature) to be deconstructed from unobserved spatial processes.

The residual spatial autocorrelation captured by the model indicates that there are other factors, not captured within the model, that are significant predictors of the density of dengue cases, going above and beyond temperature as a predictor. This implies that other unmeasured factors, like socioeconomic circumstances, vector control strategies, or climate-outliers, could be contributing to the trends seen. Future iterations may use more variables or non-linear relationships to fill in these gaps.

The meaning of the temperature coefficient (−75.935) also has to be based on a balance of the potential limitations of the assumption of linearity. Dengue transmission is characterized by threshold effects, such that both very low and high temperatures suppress mosquito cathexis and virus survival. The negative coefficient here likely indicates low range condition. Adding nonlinear terms or piecewise regression models may result in a more accurate representation of the relationship between temperature and dengue cases, especially in areas with high climate variation.

Yet another reason for the caveat is the model's use of the Queen Contiguity matrix. Although it reflects direct adjacency, it does not consider differences in connectivity between districts. For example, towns that have frequent human exchange of people or the use of infrastructure may have stronger spatial dependencies than towns that are close by. Adopting a hybrid spatial weights matrix based on socioeconomic and geographic interactions might increase the explanatory power of the model.

The negative residual spatial effects (−0.217) are counterintuitive and warrant further investigation. It might be a result of exposure to external interventions, such as targeted efforts to control vector-borne diseases or locally delivered healthcare, that lower dengue in one district and have perceived spillover effects on nearby locations. Or it might reflect differences in data reporting or rate any underreporting of cases in some districts. This trend emphasizes the importance of strong data collection and surveillance systems to inform models.

Estimation of the spatial and climatic drivers of dengue fever. The model illustrates how temperature impacts this type of data while also highlighting complex spatial dependencies that need to be investigated further. Further studies are needed to enhance these models by overcoming the limitations of existing spatial weights, nonlinear relationships, and unobserved variables to better understand the multidimensional nature of the drivers of dengue transmission. These results highlight the need for spatial analysis to be included in public health strategies that pave the way for local strategies to control diseases in specific areas.

4. DISCUSSION OF RESEARCH FINDINGS

The Universal Kriging method employed in this study enables the estimation of climate variables in Nusa Tenggara Timur (NTT) at a given location based on observations from surrounding locations while accounting for global trends or systematic variations. Universal Kriging explicitly accounts for spatial trends, allowing it to estimate for unmeasured districts in a region with extensive gaps in weather stations. Studies in mountain areas found Universal Kriging to improve significantly upon the interpolation of temperature and rainfall data and allow for more accurate assessments of climatic effects on the local ecosystem. This is important in areas with heterogeneous climate conditions, where localized microclimates can have a large impact on disease transmission dynamics [37]. The consideration of spatial variability and trend in the summary of climate data is more meaningful to represent whether climatic conditions are related to the spread of DBD compared with simple interpolation methods that would fail to capture such a relationship.

Example or evidence, in a study comparing Universal Kriging with other interpolation methods [38-40] the authors reported that Universal Kriging performed better both in terms of minimizing interpolation errors and capturing the spatial trends, especially in regions where the topography is complex or the climate is heterogeneous. Differences in temperature, humidity, and rainfall throughout NTT are correlated to the diversity of dengue fever cases found across the region, the study found. Other studies reported that there is a negative correlation between temperature and incidence of dengue.

This mirrors patterns of dengue globally, in other tropical regions where cooler temperatures are associated with extended mosquito life cycles as well as greater virus survivability. Yet the study did not establish precise temperature thresholds, suggesting one potential direction for future studies would be to delineate specific ranges that have substantial effects on transmission dynamics.

This is in line with findings in other tropical areas, in which decreased temperature has been associated with increased incidence of dengue due to prolonged longevity of mosquitoes and higher survival. Lower temperatures, however, may also result in higher humidity, leading to ideal breeding conditions for the Aedes mosquito. Similar results have been observed in studies conducted in Thailand and Brazil, indicating that the relative humidity and temperature should be cool and wet for better survival and reproduction of mosquitoes [41].

The sensitivity of the study between humidity and dengue incidence is weak, due to the impact of other environmental factors, that hit harder than humidity. Although high humidity is often understood to correlate to optimal conditions for mosquitoes, temperature fluctuations, rainfall variability, and socio-environmental dynamics (e.g., urban density, water management practices, and waste disposal systems) might exert a stronger influence on dengue transmission. However, poor water storage and drainage lead to abundant ideal breeding conditions resulting in increased mosquito populations irrespective of humidity level. Studies in Malaysia and Singapore indicate that while humidity facilitates mosquito life cycle development, temperature and rainfall patterns exert a larger influence on mosquito population dynamics and transmission rates of the virus itself. Socio-economic factors like urban planning and housing density are also crucial in this aspect. Poor waste disposal and a lack of proper urban drainage can worsen conditions for mosquito breeding, even in humid highland areas. Thus, although humidity is conducive to mosquito propagation, it might not be the most important factor associated with dengue incidence in NTT.

In contrast, rainfall did not correlate well with the distribution of dengue cases. Another interesting note about why these areas may not face such high mosquito breeding rates could be related to better drainage systems or local practices related to vector control aimed at limiting standing water that leads to elevated breeding rates of mosquitoes. Moreover, heterogeneities in infrastructure and public health interventions may mask the expected impact of rainfall on dengue transmission.

Several previous studies reported that rainfall contributes to breeding sites for mosquitoes, but the overall spatial distribution of dengue cases may correlate with other factors better than rainfall, such as temperature, population density, and local environmental conditions. Similar observations have been made in Colombia [42], where areas with higher rainfall were not necessarily places with a higher number of dengue cases, possibly as a result of differences in vector control strategies and local environmental determinants. Particular approaches like the frequent application of larvicide, desirable drainage maintenance, and the implementation of community-based mosquito source reduction programs could determine whether high rainfalls can be avoided, increasing the risk of dengue transmission.

Results of our spatial regression analysis, which included Moran's I and Lagrange Multiplier tests, showed that we had spatial dependencies in our data that called for the use of spatial econometric models. The strong spatial error dependence indicates that unobserved factors that influence dengue cases have spatial dependence. Unmeasured covariates may include sociodemographic conditions, such as income levels and housing quality, accessibility to health services, or undocumented local measures such as community-led vector control programs or environmental management practices. Incorporating and recognizing such variables could help improve the strength of spatial models. As derived from the Akaike Information Criterion (AIC) value and R^2 statistics, the well-performing model was the spatial error model (SEM) over Ordinary Least Squares (OLS) and Spatial Autoregressive Model (SAR). The comparative AIC and R^2 values for each of the four models are summarized in visual representation of the analytical data from Table 1, which was drawn from using R. This finding is consistent with other studies that have preferred to use SEM for modeling health outcomes influenced by environmental exposures where residual spatial autocorrelation needs to be taken into account [43].

Temperature was negatively associated with dengue incidence, meaning that dengue incidence in NTT increased as temperatures decreased. This conclusion fits with the observations from other tropical regions with cooler temperatures, which also elongate the lifespans of mosquitoes and also lengthen the period between infection and transmission of a virus. The specific geographic and climatic traits in NTT with its numerous microclimates and large climatic oscillation may enhance this relationship differently compared to other places. Although this relationship was noted in other studies, which find that cooler temperatures extend mosquito life expectancy and therefore also the extrinsic incubation period of the virus, thus increasing potential for transmission [44]. Our findings are in line with these observations and indicate that effective temperature control measures would likely be central to break dengue transmission in the cooler regions of NTT.

The low value of the spatial lag parameter in the SAR model indicates that the impact of cases in neighboring districts on those in a given district is small. The unique geographical characteristics of NTT islands, the distance between islands, and their diverse topography, could be one of the contributing factors to the continuity of its decentralized development as this led to limited connectivity and human mobility between districts. Moreover, socio-political aspects such as differing levels of expenditure for vector control and public health measures may indirectly lead to this lack of effective influence by fostering discrepancies in dengue prevention between districts. These findings suggest that dengue transmission may be more spatially localized and driven by predictors unique to the level of querying districts (local environmental conditions, population density, and health interventions) than those from neighboring districts. Similar conclusions have been drawn from studies conducted in Mexico and Vietnam, where localized factors had a greater influence on dengue transmission than spatial spillover effects.

We conclude that based on this study's results that the SEM is the most appropriate model used to obtain spatial distribution on dengue cases in NTT. From the comparison of the OLS, SAR, and SEM models, it was proven that SEM is the model that best suits the analysis of the spatial distribution of dengue cases in East Nusa Tenggara (NTT) proven by the lowest AIC value and the highest R^2. Table 2 provides a summary of the comparative AIC and R^2 values across the models, visually reaffirming the superior performance and applicability of SEM to spatial analysis for this study. Thus, the minimum AIC value points out that SEM fitted best to the data without being overfitted while maximum R^2 shows its superior capability of explaining the variance of dengue cases by some climatic and spatial factors. This indicates the ability of SEM to handle cross-spatial relations that are missed by simpler models like Ordinary Least Squares (OLS) and even the Spatial Autoregressive Model (SAR).

This field relevance may also be supported by the spatial autocorrelation of the OLS model residual spatial analysis and the results of the Moran's I test. This suggests that unobserved factors such as breeding habitat, population density, or environmental management may not be accounted for with OLS or SAR. This spatial dependency is accommodated in a spatial error component model (SEM), which thus provides for superior robustness and accuracy of the estimates [43]. This result is consistent with earlier studies highlighting the utility of SEMs for modeling spatially autocorrelated environmentally mediated health outcomes [14, 43].

The results of the comparison between OLS and the two spatial regression models (SAR and SEM) also showed that the SEM was the most appropriate model to assess the spatial distribution of cases in NTT, as reflected in the lowest AIC and the highest R^2. Additionally, the SEM model, due to this spatial error dependence, indicates that dengue management would need to be tailored around the peculiarities of those specific districts. In this study, for example, low temperatures were positively significantly associated with dengue cases. The association underscores the importance of implementing targeted interventions in districts with low temperatures during the colder months, where the conditions prolong mosquito lifespan and prolong the extrinsic incubation period of the virus [44]. Along the same lines, cooler and wetter climate conditions clinically increased dengue transmission in Thailand and Brazil as increased Aedes aegypti mosquito survival and proliferation [41].

On the contrary, the performance of the SAR model is not better than SEM in this study. In contrast, the spatial lag parameter in SAR had a minuscule effect, indicating that the distribution of dengue cases is less dependent on direct spillover effects of dengue from neighboring districts and more dependent on local factors. This pattern indicates that dengue transmission in NTT is more influenced by local processes (i.e., microclimatic differences and water management practices) than by regional-level scatterings and interaction. Interestingly, in studies from Vietnam and Mexico, local socio-economic and environmental characteristics were found to be more influential in shaping patterns of dengue transmission than effects of spatial spillover [42].

Thus, the implementation of SEM within this work has important implications for public health approaches. The SEM model's capacity to control for spatial error dependence underscores the importance of targeting interventions based on district-specific features that increase the risk of dengue. Some types of interventions include the targeted delivery of vector control, including insecticide spraying and larvicide application in high-risk districts, or social sector interventions/health infrastructure improvements, such as drainage enhancement to mitigate standing water. These measures can be adapted depending on the specific environmental and socio-economic conditions of each district. Districts with lower temperatures, for instance, need to ramp up vector control activities during cooler months. Localized interventions are crucial in breaking the transmission cycle and limiting the potential for dengue outbreaks. These recommendations are consistent with those from other studies in Southeast Asia, which highlight the need for localized dengue control strategies based on district-specific conditions [45].

This study shows that the SEM model is the best choice for modeling the spatial pattern of NTT dengue cases. Based on the AIC effect and R^2 comparison of OLS, SAR, and SEM, it was found that SEM is the most appropriate model to see the spatial distribution of dengue cases in NTT. SEM reveals additional localized insights into dengue transmission drivers, pointing towards the necessity of district-specific interventions as it accurately captures spatial error dependence. These results are consistent with more extensive investigations that highlight the importance of spatial models for elucidating the role of climatic, spatial, and socio-environmental parameters in determining the risk of diseases [14]. This use of SEM not only deepens the understanding of the complex dynamics of dengue fever transmission in geographically diverse regions such as NTT but also provides a framework for guiding public health interventions at local, provincial, and national levels.

The spatial error model (SEM) is a statistical model that is used to analyze spatial dependencies between regions in a dataset. This method was applied in this study to analyze directly and indirectly how temperature affects the transmission of dengue fever in East Nusa Tenggara (NTT). While the p-value for temperature (0.08927) indicates that temperature is weakly statistically significant, it is the practical significance of temperature that should not be neglected. For the primary vector of dengue fever, the Aedes aegypti mosquito, temperature is an important determinant of its lifecycle. It also affects how mosquitoes reproduce and how the virus develops inside a mosquito. Temperature is a key predictor of disease risk in a context like NTT with high climate variability.

The coefficient for spatial error ($\lambda=-0.217$, $p=0.481$) in SEM indicates the absence of statistically significant spatial dependencies. This indicates that the regional interconnections that previously facilitated the spread of dengue cases, as measured using this model, do not have a significant impact on those previously observed data, or that other factors not measured were influencing the spread. Spatial dependencies may account for factors such as human movement between districts or differences in environmental characteristics such as open pools of stagnant water or amounts of vegetation, both of which are critical for mosquito breeding. Due to the diverse landscape and unequal infrastructure crisis in NTT, the risk of disease is usually unequal in the region.

The poor model temperature-case relationship might also suggest that the model is missing important variables, such as rainfall, humidity, or socio-economic variables. NTT has seasonal rainfall patterns which lead to formations of breeding sites for mosquitoes. And, in cooler times, the mosquito lifecycle may slow but the efficiency with which the virus spreads in the mosquito may actually increase, highlighting the complexity of the temperature-disease relationship. Even with weak statistical significance aside, temperature is an important consideration in assessing the risk of dengue in the region.

The study underlines the need for the use of data in making decisions that work towards averting the risks of dengue with district-level early warning systems that involve climate and spatial data. For instance, in cooler or wetter times, aerosol insecticide spraying or source reduction campaigns could be emphasized in high-risk areas. Future studies should also include variables such as poverty levels, population density, and access to clean water in order to increase model accuracy. Including projections of climate change could also help to understand how the risks of dengue may change over time. This will not only provide a depth of analysis but also an actionable insight that can feed into planning for health on the ground to formulate a mechanism to live up to vector-borne diseases in NTT more dynamically.

The results of this study highlight the importance of temperature in the determination of dengue incidence in NTT. This is especially important as climate change has been predicted to amplify temperature fluctuations, potentially leading to more days of vulnerability and more instances of dengue outbreaks. This finding helps to explain the observed association between cooler temperatures and greater dengue incidence and suggests that health authorities should consider implementing targeted interventions during cooler periods to reduce dengue risk. This method could, for example, facilitate enhanced vector control measures in the lead-up to and throughout the cooler months to reduce the abundance of mosquitoes and interrupt the transmission cycle.

The weak correlation of humidity and rainfall and distribution of dengue case in the current study indicates that while those factors help to create breeding grounds, the two variables may not act as good predictors for outbreaks, which is also true in the case of a previous study conducted in NTT [46]. These results are consistent with findings from tropical areas such as Colombia and India, showing that rainfall did not predict outbreaks alone, as drainage systems, and locally delineated vector control measures were effective. Yet, the distinctive climatic and geographic characteristics of NTT, including its marked microclimates and uneven infrastructure, may further modulate the influence of these factors, necessitating region-specific analysis. This result aligns with previous analyses that have found temperature to be a more significant driver of dengue risk than humidity and precipitation. Thus, the monitoring and controlling of temperature should be a priority of public health interventions so that the changes in dengue risk could be predicted and properly addressed.

While these findings offer valuable insights into the spatial dynamics of dengue fever in NTT, there are some limitations that need to be acknowledged. The interpolation of climate data could be affected by the scarcity of weather stations, thus influencing the accuracy of the Universal Kriging method. In order to overcome this limitation, additional data sources, such as satellite-based calculated climate data or reanalysis datasets, could be incorporated. These sources provide higher spatial and temporal resolution to better interpolate climate variables and assess their influence on dengue transmission. In addition, these findings must be interpreted carefully as they represent probabilistic and not deterministic relations. This level was statistically significant but may not sufficiently describe the relationships between the many factors that drive dengue incidence. The use of incomplete or incomplete spatial data is also known to influence the prediction accuracy of climate-influenced diseases [47].

Socio-economic factors (such as income level, housing conditions, and access to healthcare services) and mobility/migration patterns can be potential confounders. They are considered to influence the vulnerability and exposure of populations to vector-borne diseases. For example, one study shows that areas with limited access to healthcare facilities and congested living conditions have a high vulnerability to dengue fever offenses [48]. Furthermore, high mobility results in the potential dispersal of infected individuals or vectors between areas [49]. Furthermore, inequitable socio-economic factors also affect the utility of vector control programs, and it is shown that under-resourced communities are less likely to benefit from interventions.

Local vector control practices, which were not accounted for in this analysis, are also a key factor that modulates the dynamics of dengue transmission. Community engagement has also shown to be beneficial for vector control programs with a case study in the developing world exemplifying that there is a reliance on community support for vector control efforts and the sustainability of interventions [50].

Further studies should have more holistic and robust spatial models by incorporating socio-economic factors, mobility trends, and local actions. Potential data sources may include census data with data on socio-economic variables such as income and housing quality, health facility access records, migration measures from transport or cellphone network data. Integrating these data would greatly improve the predictive power and contextual relevance of the models. Such analysis would not only improve our predictive models but also better inform the drivers of dengue disease burden in this location. These results reinforce the importance of a multidimensional approach to studying vector-borne diseases in tropical regions [23]. Additionally, future research could delve into the application of other spatial econometric frameworks, including Geographically Weighted Regression (GWRs), to acknowledge potential non-stationary spatial interdependencies across diverse administrative units. GWR could say more about the socio-environmental variables that contribute to dengue transmission that are specific to a given dataset, and therefore help direct more localized interventions. In addition, the incorporation of climate projections into the models can help inform our understanding of how climate change can impact dengue transmission and support longer-term public health planning.

Results showed that temperature is the main weather determinant of dengue transmission in NTT, while humidity and rainfall have minimal variable significance. These results signify the necessity of place-specific interventions and suggest that spatial dependencies could be captured using a spatial error model, which was found to be the best performing model in this context. These results help to better explain dengue dynamics in the region and ensure that spatial heterogeneity is better accounted for in disease prevention strategies.

This study's findings indicate that climate change, especially temperature and precipitation changes, have a significant effect on the spread of dengue fever in East Nusa Tenggara (NTT). These environmental factors affect the lifecycle of the Aedes aegypti mosquito, including its reproduction rate and the ability for the virus to thrive in the mosquito. Considering these results, community-based public health approaches are vital in mitigating the effects of climate change on dengue fever. Such strategies must prioritize early warning systems, environmental management, and community awareness to build understanding of the links between climate change and health risks.

Perhaps the most effective one is to establish a climatically based early warning system to alert when dengue fever is likely to outbreak. Using data about temperature, precipitation, and humidity, the authorities can now identify periods of heightened risk in advance, enabling them to take preventive measures. For instance, such an information system can help guide the timing of insecticide spraying campaigns, community clean-up drives, or the distribution of protective measures such as mosquito nets in areas at risk for an outbreak. Early warning also helps disseminate information to the public on measures they can take to prevent mosquito breeding, such as covering containers where water is stored or clearing stagnant water near their households.

Another preventive strategy is environmental management to minimize the risk of dengue as more rain and stagnant water rise due to climate change. Building an efficient drainage system and improving waste management infrastructure can help eliminate potential mosquito breeding sites. Community participation is critical in this initiative, which includes periodic clean-up drives to remove potential breeding habitats such as used containers and to desilt blocked drains. Ensuring that communities are empowered to manage and monitor their environments means that efforts to control mosquito habitats will be sustainable and effective.

Public awareness is essential for the success of these strategies. Teaching communities how climate change worsens dengue outbreaks can help them understand the need for preventive measures. Health education campaigns in culturally diverse areas such as NTT should be adapted to local practices and traditions. Using community leaders, health volunteers, and women’s groups, the messaging will reach all levels of society. Practical tips, including the use of natural larvicides, covering water tanks, mosquito screens, etc., can be localized and presented on platforms where people can relate to them and adapt them easily.

Lastly, a long-term method is required to react to the evolving dangers of climate change. The strategy is to draft risk maps by integrating climate and environmental data into epidemiological data to gain insight into the areas in NTT that are at highest risk. There are already tools in place to assist in the integration and visualization of these data layers, such as Geographic Information System (GIS) platforms, which can assist in more accurately targeting and allocating meaningful interventions and resources. These maps can help policymakers decide where resources or funds flow to where they are needed most. Incorporating climate projections into the health planning process also enables authorities to forecast future patterns of disease spread and develop adaptive strategies accordingly. Combining both these approaches helps mitigate immediate harm and simultaneously builds the capacity of communities in NTT to withstand the health consequences of climate change.

5. CONCLUSIONS

Based on these results, this study concludes that the Spatial Error Model (SEM) provides the most appropriate spatial regression model to analyze climate variables and DBD cases in NTT because, compared with OLS or SAR, which ignore strict spatial correlations, SEM is able to consider spatial dependence in the residuals or unobserved occurrence factors that might include dengue dynamic factors in NTT. The SEM provides the best fit to the data, according to an R^2 statistic of 0.4538 and an Akaike Information Criterion (AIC) statistic of 285.235, the latter being the lowest of those compared. Only temperature is statistically significant (coefficient=-75.934, p-value=0.08927 at α=0.10), indicating that for a 1°C decrease in temperature, the average number of dengue cases increases by 75. These results highlight the critical need for tailored interventions in the cooler districts during peak seasons for high-prevalence arboviruses, such as the scale-up of vector control measures (e.g., fogging, larvicide application) and public education campaigns to minimize mosquito breeding sites in these micro-climatic settings. The model's lambda (λ=-0.217, p-value =0.481) suggests spatial dependencies in the residuals, implying that there are spatial patterns in the distribution of DBD that are not solely attributable to temperature effects.

The results suggest that cooler temperatures provide favorable conditions for mosquito survival and transmission of the pathogens they carry, possibly because longer mosquito lifespans and higher humidity are seen with cooler weather. The observation suggests potential for targeted vector control measures during cooler periods when the risks of dengue transmission are greater. The SEM identified commonalities in the spatial dependencies of the districts, which highlights that localized contributors to dengue dynamics offer an essential layer of insights for the effective design of district-specific interventions in areas such as comprehensive and targeted fogging operations, improved drainage systems to mitigate mosquito breeding sites, and community-led clean-up activities to remove standing water sources. Using organizations that monitor the climate in real-time combined with predictive modeling, early warning systems could issue real-time alerts for when and where cycling is riskier.

More parameters to be added to future analyses include socio-economic and ecological variables. Some of these features may be mobility data to capture how humans move around, housing conditions to measure vulnerability to exposure to mosquitoes, and sites of healthcare services to see how quickly people can react. These environmental variables would greatly improve the model's predictive performance and their ability to be contextualized. Although temperature is important, factors such as urbanization, access to health care, and social conditions may improve the model's explanatory power. Alternatives such as Geographically Weighted Regression (GWR) when used as spatial modeling tools can also be beneficial to explore spatial heterogeneity in each district.

Since East Nusa Tenggara (NTT) has different climatic and socio-environmental challenges, particular public health strategies need to be taken by each region to reduce climate change's influence on dengue fever (DBD) incidence. One important aspect is the strengthening of locally adapted vector control programs that target the local drivers of DBD transmission. That includes larviciding and fogging campaigns during peak mosquito breeding seasons, mapped out with predictive climate models. In high-risk areas, these interventions can be scaled up to directly reduce the populations of the vector mosquitoes and break the transmission cycle.

Another common approach is the development of early warning systems targeting DBD outbreaks. These systems can combine real-time climate data-including temperature, rainfall, and humidity-with spatial regression models to predict times and places of increased risk. By spreading this information through community health networks, mobile apps, and local media, it helps ensure both the public and health authorities can respond in a timely manner. Not only do such systems allow action to be taken pre-emptively to keep the mosquito population under control, they also allow medical resources to be allocated to those districts where outbreaks are most likely.

The third aspect is infrastructure development, which is a vital part of the war on DBD in NTT. Water stagnation is a prime breeding ground for Aedes mosquitoes, especially during downpours, and building or improving drainage systems can prevent this. Moreover, these measures can reduce discarded containers and other man-made areas that provide ideal breeding conditions for mosquitoes through efficient waste management systems. These improvements in infrastructure are interactive, addressing the root causes of mosquito proliferation, thus reducing the risk of DBD outbreaks.

The DBD mitigation strategies also hinge on public knowledge regarding DBDs as well as community involvement. Dengue education campaigns are culturally tailored and promote preventive practices, including covering water storage containers, using insecticide-treated bed nets, and aiding in the recognition of initial dengue symptoms. Training and resourcing community health workers to monitor and respond to climate-driven DBD risks will ensure that interventions are sustainable and suitable to the local context.

Another essential approach is the allocation of resources according to detailed DBD risk maps. Spatial modeling and climate data can help pinpoint districts with the greatest disease burden, allowing for targeted interventions like specific vector control measures, increased access to healthcare, and enhanced emergency preparedness for high-risk periods. These maps could also assist in long-term planning and allocation of supplies to regions experiencing recurrent DBD hotspots.

Lastly, the integration of climate change projections into public health planning remains crucial to ensure we effectively tackle the evolving epidemiology of DBD transmission. Climate change could reshape the spatial layout of dengue by expanding mosquito habitat or extending transmission seasons into cooler areas. For example, adaptive vector control programs and seasonal interventions during cooler months are proactive strategies that can mitigate changes to the entomological setting. This simulation helps capture the evolutionary dynamics of DBD in NTT and keep public health planning on the right path through a secure mechanism of connecting climate data to public health planning. These public health strategies combined can form a multi-faceted approach in reducing the increasing impact of climate change on this disease in the region.

The major challenge of this study is the quality of data used for climate variables and dengue fever cases. In the case of East Nusa Tenggara (NTT), where the number of available weather stations is limited, the climate people used interpolation methods, like Universal Kriging, for estimating the effective climate data in these unmeasured regions. Even though this method contributes to closing data gaps, it has some assumed biases that can result in actual inaccuracies in areas where climatic conditions are highly heterogeneous. Additionally, the dengue fever case data used may not completely reflect the actual burden of disease considering potential under-reporting or misdiagnosis, especially within remote areas where healthcare access is constrained. Such limitations could be addressed in future work by integrating high-resolution climate information (e.g., derived from satellite observations), along with enhanced disease surveillance systems that provide increasingly accurate and insightful data.

Diffusion of interview bias, another important limitation is unmeasured factors that can also affect the transmission of dengue fever. Socioeconomic conditions, population density, migration patterns, and access to healthcare services (all known to have a significant impact) were not considered in this analysis. As a result, the study may overstate climatic influences and overlook the social and environmental determinants. Future studies should consider these variables in concert to more fully elucidate dengue transmission dynamics, thereby allowing for more integrative public health efforts.

Another limitation with regard to methodology includes the statistical models used. Although the SEM worked well to account for spatial dependencies, it might not fully explain nonlinear relationships or complex interactions between climatic and social factors. Furthermore, the model ignores spatial relationships that vary regionally. In the future, explore advanced GWR based on the above model that can analyze highly localized spatial relationships. Implementing time-series analysis techniques may also uncover seasonal patterns and lagged relationships, providing more nuanced insight into how climate variables drive dengue incidences temporally.

For future research, a multi-scale analysis that combines investigations at local, district, and regional levels should be considered whenever possible. This would allow the determination of key drivers of dengue fever transmission at multiple scales. Moreover, incorporating climate change projections and consideration of microclimate data could improve prediction, informing long-term public health planning. However, some limitations must be addressed in future studies, and studies along these lines will further strengthen the findings of this study along with other findings by contributing to robust strategies to mitigate the impacts of climate change on dengue fever in East Nusa Tenggara.

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