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## DENGUE MODELING USING MULTIPLE REGRESSION IN BANDAR LAMPUNG PROVINCE, INDONESIA

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**Abstract** || Dengue Hemorrhagic Fever remains a significant global concern, with its complex distribution influenced by geographic and demographic factors. Indonesia, particularly the city of Bandar Lampung, is an endemic area for Dengue Hemorrhagic Fever. Factors such as population density, area, and geographical coordinates are believed to influence the spread of the disease. Bandar Lampung, which has the highest population density in the region, has recorded a high population growth rate. In this context, multiple linear regression analysis is an effective approach to understanding the relationship between dependent and independent variables, including population density, area, longitude, and latitude. These factors play a crucial role in the transmission of the dengue virus, with high population density increasing human-mosquito interactions. This analysis is expected to provide comprehensive insights to design more effective and targeted intervention strategies for preventing and controlling the spread of Dengue Hemorrhagic Fever at both geographic and demographic levels.

**Keywords** || Modeling; Dengue Hemorrhagic Fever (DHF); Regression

**Abstrak** || Penyakit Demam Berdarah Dengue terus menjadi perhatian global dengan penyebarannya yang kompleks dipengaruhi oleh faktor geografis dan demografis. Indonesia, khususnya Kota Bandar Lampung, merupakan daerah endemi Demam Berdarah Dengue. Kepadatan penduduk, Luas wilayah dan koordinat geografis diyakini memengaruhi penyebaran Demam Berdarah Dengue. Bandar Lampung, sebagai kota dengan kepadatan penduduk tertinggi, mencatat laju pertumbuhan penduduk tinggi. Dalam konteks ini, analisis regresi linier berganda menjadi pendekatan efektif untuk memahami hubungan antara variabel dependen dan independen (kepadatan penduduk, luas wilayah, longitude, latitude). Faktor-faktor ini memainkan peran penting dalam penyebaran virus dengue, dengan kepadatan penduduk tinggi meningkatkan interaksi manusia-nyamuk. Analisis ini diharapkan memberikan wawasan holistik untuk merancang strategi intervensi yang lebih efektif dan tepat sasaran dalam mencegah dan mengendalikan penyebaran Demam Berdarah Dengue di tingkat geografis dan demografis.

**Katakunci** || Pemodelan; Demam Berdarah Dengue (DBD); Regresi

## Introduction

Dengue fever is a disease that continues to be a serious concern in various parts of the world. The spread of dengue fever is complex and influenced by numerous factors, including the geographic and demographic characteristics of a region. Therefore, a comprehensive analysis is required to understand the factors contributing to the number of dengue fever cases. The cause of dengue fever is the dengue virus, which is transmitted by mosquitoes in tropical areas (Lembang et al., 2019; Rahayu K et al., 2012). Dengue Hemorrhagic Fever (DHF) is a tropical disease that frequently occurs in Indonesia, creating endemic conditions. An endemic is when a disease becomes common in a specific area. The city of Bandar Lampung is part of this endemic region.

In 2020, the Indonesian Ministry of Health reported 103,781 cases of dengue fever in Indonesia. Several researchers have shown that mobility, population density, and human behavior towards the environment can influence the spread of dengue fever (Beyer et al., 2006). In the city of Bandar Lampung, there are 20 sub-districts affected by the dengue virus, with the number of cases ranging from 16 to 149. This situation illustrates the complexity of the disease's spread (Rifai et al., 2022).

In 2020, the population of Lampung reached 9,007,848 people, with varying population densities across its 15 districts. Bandar Lampung is the city with the highest population density, reaching 6,361 people per square kilometer (Rifai et al., 2022). Data from the Central Statistics Agency in 2021 supports that Bandar Lampung recorded the highest population growth rate from 2010 to 2021 (Bappeda Kota Kupang, 2013). The rapid spread of the Dengue Hemorrhagic Fever virus between regions can occur due to short distances and high population density. The basic principle in the law of geography states that everything is related to everything else, but near things are more related than distant things (Waters, 2017; Zheng et al., 2023). In this context, statistical techniques such as regression analysis can be utilized to study the distribution pattern of Dengue Hemorrhagic Fever cases.

Regression analysis is a method for identifying patterns of relationships between dependent and independent variables (Uyanık & Güler, 2013). The linear regression model is a type of model in regression analysis that assumes the linearity of parameters (S.-W. Kim et al., 2021). Linear regression models include simple linear regression

and multiple linear regression, distinguished by the number of independent variables involved (Bangdiwala, 2018). In this context, using multiple linear regression becomes an effective approach to analyze the relationship between the dependent variable and several carefully selected independent variables. In analyzing dengue cases, population density, area size, and geographic coordinates (longitude and latitude) will be considered as independent variables.

High population density may significantly influence the spread of dengue due to increased interactions between humans and virus-carrying mosquitoes (Ispriyanti et al., 2018; Nurdiansyah & Sulistiawan, 2023). Area size can impact the spread of mosquitoes and the environmental conditions that support the breeding of *Aedes aegypti* mosquitoes (Jayanti et al., 2017). Longitude and latitude, as spatial variables, can provide additional insights into the geographic distribution of dengue cases (Kusuma & Sukendra, 2016). These factors may include climate, topography, and ecological variability, which contribute to conditions favorable for mosquito reproduction (Anwar & Ariati, 2014).

Multiple linear regression analysis will help identify the extent to which each independent variable contributes to dengue cases. By understanding these relationships, authorities can design more effective and targeted intervention strategies to prevent and control the spread of dengue fever. Thus, analyzing dengue cases using multiple linear regression by considering factors such as population density, area size, and geographic coordinates provides a comprehensive approach to understanding the dynamics of this disease at geographic and demographic levels.

## Methodology

This research utilizes data from 2020 published by the Lampung Province Statistical Bureau (BPS) and the Indonesian Ministry of Health. The research employs an associative quantitative approach, aiming to determine the relationships between two or more variables. The dependent variable is the number of dengue fever cases (Y). The independent variables include Population Density (X1), Area Size (X2), and Geographic Coordinates (X4). According to Draper & Smith (1998); Rawlings et al. (1998), the multiple linear regression model is generally formulated as follows:

$$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \dots + \beta_p X_{pi} + \varepsilon_i,$$

The linear regression model in matrix notation is represented as follows:

$$\begin{aligned}
 \underset{n \times 1}{y} &= \underset{n \times k}{X} \underset{k \times 1}{\beta} + \underset{n \times 1}{\varepsilon} \\
 \underset{n \times 1}{\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix}} &= \underset{n \times k}{\begin{bmatrix} 1 & X_{11} & \cdots & X_{1(k-1)} \\ 1 & X_{21} & \cdots & X_{2(k-1)} \\ \vdots & \vdots & \ddots & \vdots \\ 1 & X_{n1} & \cdots & X_{n(k-1)} \end{bmatrix}} \underset{k \times 1}{\begin{bmatrix} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_{k-1} \end{bmatrix}} + \underset{n \times 1}{\begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{bmatrix}}
 \end{aligned}$$

Here,  $y$  is an  $n \times 1$  column matrix containing the dependent variable, and  $\varepsilon$  represents the errors or deviations between the actual and predicted values (Jayanti et al., 2017). Theoretically, the use of multiple linear regression analysis will produce valid parameter estimates if the classical assumptions are met. The classical assumptions for regression are as follows (Mardiatmoko, 2020):

### *Normality Test*

The normality test is an essential assumption in research. It is used to determine whether the data are normally distributed. In this study, the Shapiro-Wilk test was employed with the following hypotheses:

- H0 : Data are normally distributed
- H1 : Data are not normally distributed

### *Homogeneity Test*

Homogeneity testing can be conducted using the Breusch-Pagan test with the following hypotheses:

- H0 :  $\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_n^2 = 0$  (no heterogeneity)
- H1 : there is at least one  $\sigma_i^2 \neq \sigma^2$  (heterogeneity exists)
- Decision-making : Reject H0 if  $BP > x_p^2$  or if the p-value is less than  $\alpha$

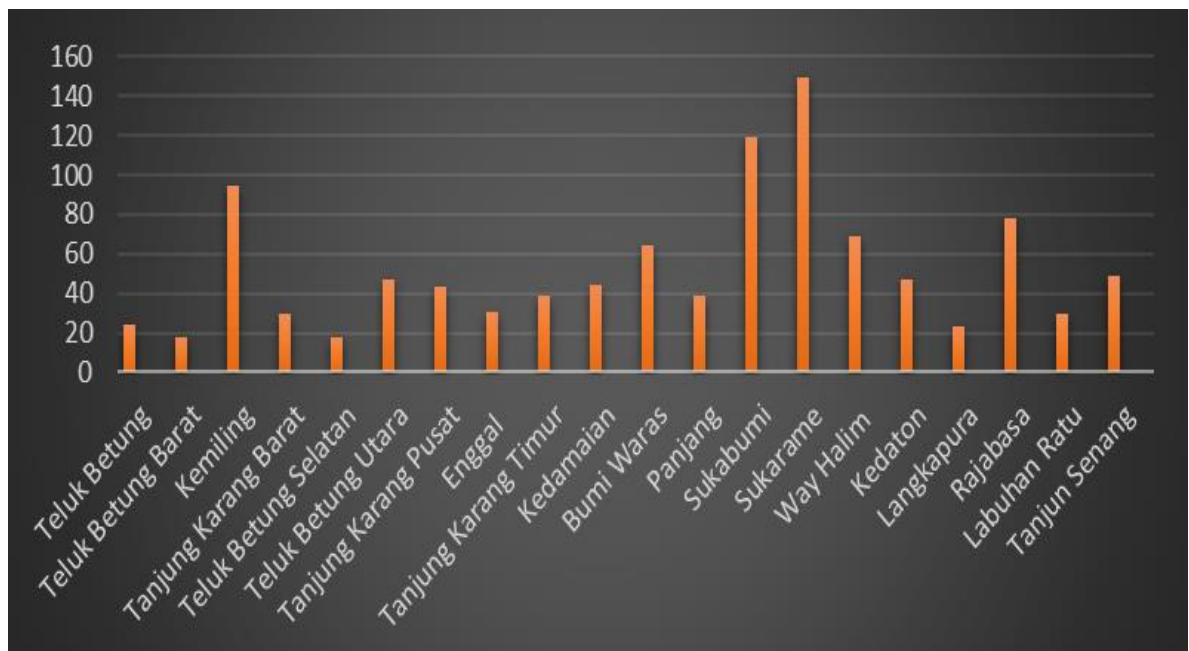
### *Multicollinearity Test*

The multicollinearity test aims to determine whether a correlation exists between the independent variables in the regression model. A good regression model should have no correlation between the independent variables. Multicollinearity can be detected by examining the Variance

Inflation Factor (VIF) and tolerance values. If  $VIF < 10$  and tolerance  $> 0.1$ , then multicollinearity does not occur. However, if  $VIF > 10$  and tolerance  $> 0.1$ , then multicollinearity is present.

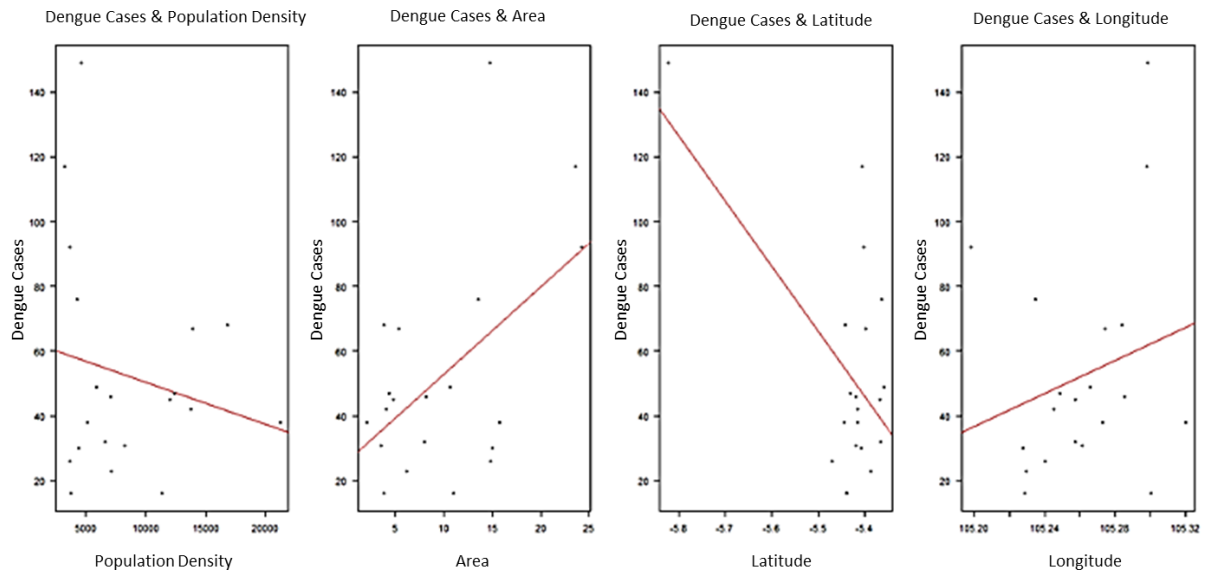
## Analysis and Discussion

This research was conducted in Bandar Lampung City, with the observation units being the 20 sub-districts within the city. In 2020, two sub-districts in Bandar Lampung, Sukarame and Sukabumi, Indonesia had notably high numbers of dengue cases. Figure 1 illustrates the distribution of dengue fever cases in Bandar Lampung City. According to Figure 1, the highest number of dengue cases recorded was 149, while the lowest was 16.



**Figure 1.** 2020's Dengue cases recorded in Bandar Lampung, Indonesia

As shown in Figure 2, there is a positive relationship between the dependent variable (Y) and all independent variables (X). This indicates that as the value of the Y variable increases, the values of the X variables also increase. Conversely, if the value of the Y variable decreases, the values of the X variables decrease as well:



**Figure 2.** Pattern of relationship between variables Y and X

### *Multiple Regression Model*

The parameter estimates for the multiple linear regression model were obtained using *Ordinary Least Squares* (OLS) estimation. Below is an estimate of the multiple linear regression parameters between the dependent variable and the independent variables. The parameter estimation results from the multiple linear regression model are presented in Table 1.

**Table 1.** An estimate of the multiple linear regression parameters

| Variables        | Coefficient | P-value |
|------------------|-------------|---------|
| <i>Intercept</i> | -9,299      | 0,65028 |
| X <sub>1</sub>   | 0,003556    | 0,05226 |
| X <sub>2</sub>   | 4,501       | 0,00326 |
| X <sub>3</sub>   | -1,696      | 0,01308 |
| X <sub>4</sub>   | 7,938       | 0,68536 |
| R <sup>2</sup>   | 54,03%      |         |

Table 1 presents the parameter estimates from the multiple linear regression analysis. Based on the p-value, it can be concluded that the independent variables, specifically X<sub>1</sub>, have a significance level ( $\alpha$ ) of 0.68536. The resulting multiple linear regression equation is:

$$y = -9.299 + 0.003556x_1 + 4.501x_2 - 1.696x_3 + 7.938x_4$$

This equation can be interpreted as follows: the expected number of dengue hemorrhagic fever cases is -9.299 when there is no influence from other factors. If population density X<sub>1</sub> increases by one person, dengue hemorrhagic fever cases increase by 0.003556, assuming other

variables remain constant. If the area  $X_2$  increases by 1 km<sup>2</sup>, dengue hemorrhagic fever cases increase by 4.501, assuming other variables remain constant. If the latitude coordinate  $X_3$  increases by one unit, dengue hemorrhagic fever cases decrease by 1.696, assuming other variables remain constant. If the longitude coordinate  $X_4$  increases by one unit, dengue hemorrhagic fever cases increase by 7.938, assuming other variables remain constant. The  $R^2$  value of this model is 54.03%, indicating that the model explains 54.03% of the variance in dengue fever cases, while the remaining 45.97% is explained by variables outside the model.

**Table 2.** Normality test results

| <i>Shapiro Wilk Test</i> |         |         |
|--------------------------|---------|---------|
|                          | W       | P-value |
| Data                     | 0,80328 | 0,0309  |

For the multiple linear regression model, it is essential to meet the classical assumptions, which include the normality test, linearity test, homogeneity test, autocorrelation test, and multicollinearity test. The normality test in this modeling uses the Shapiro-Wilk test. The results of the normality test are presented in Table 2. Based on Table 2, the p-value is greater than ( $\alpha$ ) ( $0.0309 > 0.05$ ), supporting the rejection of the null hypothesis ( $H_0$ ). This indicates that the residuals are normally distributed. Therefore, it can be concluded that the assumption of normally distributed residuals has been fulfilled.

**Table 3.** Linearity test results

| <i>Harvey-Collier (HC) Test</i> |         |
|---------------------------------|---------|
| HC                              | p-value |
| 2,8978                          | 0,01169 |

Next, we conducted a linearity test to ensure that the relationship between the independent variables and the dependent variable is linear. Based on the results presented in Table 3, we used the Harvey-Collier test to evaluate this assumption. The test results show that the p-value obtained is 0.01169. This value is greater than the predetermined significance level ( $\alpha$ ), which is 0.01. In other words, the p-value of 0.01169 is greater than ( $\alpha$ ). This indicates that we cannot reject the null hypothesis, which states that the relationship between the independent variables and the dependent variable is linear. Therefore, it can be concluded that the relationship between these variables meets the linearity assumption, validating the regression model used to describe this linear relationship.

**Table 4.** Homogeneity test results

| <i>Breusch Pagan (BP) Test</i> |                |
|--------------------------------|----------------|
| BP Value                       | <i>p-value</i> |
| 3,911                          | 0,4182         |

In this modeling, we performed a homogeneity test to ensure that the variance of the regression model error is constant. This test was conducted using the Breusch-Pagan test, which is designed to detect the presence of heteroscedasticity in the regression model. The results of this homogeneity test are presented in Table 4. According to the data displayed in the table, the Breusch-Pagan test results indicate that the p-value obtained is 0.4182. This value is greater than the predetermined significance level ( $\alpha$ ) (e.g., 0.05 or 0.01). In other words, the p-value of 0.4182 is greater than ( $\alpha$ ).

Based on the Breusch-Pagan test, we do not have sufficient evidence to reject the null hypothesis, which states that the error variance is homogeneous or constant. Therefore, it can be concluded that there is no heteroscedasticity in this regression model, meaning that the error variance remains constant across the range of the independent variables. This indicates that the regression model used meets the assumption of homogeneity of variance, which is a crucial prerequisite in regression analysis to ensure the validity and reliability of the results obtained.

**Table 5.** Autocorrelation test results

| <i>Durbin Watson (DW)</i> |                |
|---------------------------|----------------|
| DW                        | <i>p-value</i> |
| 1,508                     | 0,09188        |

In this modeling, we conducted an autocorrelation test to ensure that the residuals or errors from the regression model do not exhibit patterns that are correlated with each other. This autocorrelation test was performed using the Durbin-Watson test, specifically designed to detect autocorrelation in residual data. The results of the autocorrelation test are presented in Table 5. According to the data provided in this table, the Durbin-Watson test yielded a p-value of 0.09188. This value exceeds the predetermined significance level ( $\alpha$ ), such as 0.05.

In other words, the p-value of 0.09188 is greater than 0.05. This implies that we lack sufficient evidence to reject the null hypothesis, which suggests the absence of autocorrelation in the residuals of the regression model. Thus, it can be concluded that there is no

autocorrelation in this regression model. This observation indicates that the assumption of residual independence has been satisfied, which is an essential prerequisite in regression analysis to ensure the accuracy and unbiasedness of the model's results.

**Table 6.** Multicollinearity test results

| Variables      | VIF Value |
|----------------|-----------|
| X <sub>1</sub> | 2,622917  |
| X <sub>2</sub> | 2,539249  |
| X <sub>3</sub> | 1,199308  |
| X <sub>4</sub> | 1,228726  |

The detailed results of the multicollinearity test on the independent variables in this model are presented in Table 7. According to the data provided in Table 6, the results of the multicollinearity assumption test indicate that the Variance Inflation Factor (VIF) values for each independent variable, namely X<sub>1</sub> through all of them, are less than 10. VIF values below 10 suggest the absence of significant multicollinearity among the independent variables.

Multicollinearity refers to a condition in which one independent variable in a regression model is highly correlated with one or more other independent variables, potentially leading to challenges in accurately estimating regression coefficients (Shrestha, 2020). In this context, a low VIF value signifies that the independent variables are not strongly correlated with each other. Consequently, there is no substantial relationship between the independent variables that could impact the results of the regression analysis. Therefore, it can be concluded that the regression model used satisfies the assumption of no multicollinearity. As a result, the independent variables included in the model can be considered independent of each other, thereby providing more precise and reliable estimates.

Following a series of classical assumption tests on the multiple linear regression model, it was observed that there was a violation of the multicollinearity assumption. This was evidenced by the Variance Inflation Factor (VIF) value exceeding 10 for variables X<sub>2</sub> and X<sub>3</sub>. Specifically, a VIF value exceeding 10 indicates a strong correlation between the independent variables in the model, namely X<sub>2</sub> and X<sub>3</sub>.

This multicollinearity issue arises due to a significant relationship between the two independent variables. When two independent variables exhibit a close relationship, the estimated regression coefficient becomes unstable, leading to potentially inaccurate results

(J. H. Kim, 2019). Violation of this assumption results in biased and unreliable parameter estimates (Daoud, 2017).

The implication of violating the multicollinearity assumption is that the constructed regression model fails to meet the criteria for effective modeling. An ideal model should be devoid of multicollinearity to ensure that each independent variable contributes uniquely and independently to the dependent variable. Therefore, it is imperative to undertake further remedial measures, such as eliminating one of the highly correlated variables or employing a regression technique capable of addressing multicollinearity. This ensures that the regression model adheres to classical assumptions and yields valid and dependable estimates.

## Conclusion

Through multiple linear regression analysis, it was determined that population density, area, and latitude significantly impact the spread of dengue cases, whereas longitude does not exhibit a significant influence on dengue case spread. When conducting statistical analysis, precision and attentiveness are paramount in employing each available analytical method. Each statistical technique necessitates meeting specific assumptions to yield accurate and reliable results. The multiple linear regression model generated an  $R^2$  value of 54.03%, signifying that the model elucidated 54.03% of the variance in dengue fever cases, with the remaining 45.97% attributed to unaccounted variables. The formulated model employs the following multiple linear regression equation:

$$y = -9.299 + 0.003556x^1 + 4.501x^2 - 1.696x^3 + 7.938x^4$$

As for recommendations, the author could suggest further research avenues. Future investigations may explore ridge regression and logistic regression models as extensions of this study. Additionally, subsequent research endeavors could incorporate a broader range of variables that influence the spread of dengue fever.

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