BAREKENG: Journal of Mathematics and Its Applications
March 2026 Volume 20 Issue 1 Page 0493–0508
P-ISSN: 1978-7227 E-ISSN: 2615-3017
https://doi.org/10.30598/barekengvol20iss1pp0493-0508

BIVARIATE POISSON LOG-NORMAL REGRESSION MODELING ON THE NUMBER OF LEPROSY CASES IN INDONESIA

Nasrah Sirajang[1*], **Salsabila Rahmadhani S**[2], **Siswanto Siswanto**[3]

[1,2,3]*Department of Statistics, Faculty of Mathematics and Natural Sciences, Universitas Hasanuddin*
Jln. Perintis Kemerdekaan Km 10, Makassar, 90245, Indonesia

*Corresponding author's e-mail: * **nas.sirajang@gmail.com***

Article Info

Article History:

Received: 15th April 2025
Revised: 2nd June 2025
Accepted: 13th June 2025
Available online: 24th November 2025

Keywords:

Bivariate Poisson log-normal regression;
Maximum likelihood estimation;
MB leprosy;
PB leprosy;
Overdispersion.

ABSTRACT

Bivariate Poisson regression is a method for modeling two correlated count response variables. However, standard Poisson models often assume equidispersion, which is frequently violated in real-world data due to overdispersion. To address this issue, the Bivariate Poisson Log-Normal Regression (BPLNR) model is employed, which incorporates random effects to account for variability beyond that captured by the Poisson distribution. This study applies the BPLNR model to analyze the number of leprosy cases in Indonesia in 2021, categorized by the World Health Organization (WHO) into Paucibacillary (PB) and Multibacillary (MB). These two types are known to be correlated and exhibit overdispersion, rendering standard Bivariate Poisson models inadequate. This research contributes by applying BPLNR to leprosy data in Indonesia—an area that has been underexplored in prior studies, which largely employed univariate or standard Poisson approaches and ignored the correlation and overdispersion structure. Data were obtained from the 2021 Indonesian Health Profile and the Central Statistics Agency. Parameter estimation was conducted using Maximum Likelihood Estimation (MLE) with the Newton-Raphson algorithm, and hypothesis testing was performed using the Maximum Likelihood Ratio Test (MLRT). The results confirm that BPLNR effectively models the joint distribution of PB and MB cases while accounting for overdispersion. Key factors influencing both types of leprosy include population density, poverty rate, access to proper sanitation and drinking water, and availability of medical personnel and health facilities. A limitation of this study is the use of aggregate provincial-level data, which may obscure local variation and spatial effects. Future research could integrate spatial modeling techniques or individual-level data to enhance inference.

How to cite this article:

N. Sirajang, S. Rahmadhani S, and S. Siswanto, "BIVARIATE POISSON LOG-NORMAL REGRESSION MODELING ON THE NUMBER OF LEPROSY CASES IN INDONESIA," *BAREKENG: J. Math. & App.*, vol. 20, iss. 1, pp. 0493-0508, Mar, 2026.

Journal homepage: *https://ojs3.unpatti.ac.id/index.php/barekeng/*
Journal e-mail: *barekeng.math@yahoo.com; barekeng.journal@mail.unpatti.ac.id*

Research Article · **Open Access**

1. INTRODUCTION

Poisson regression is a method that aims to model response variables in the form of discrete data and the Poisson distribution. Data that is distributed Poisson is data that has a small probability and depends on a certain time interval or area, with observations in the form of discrete variables, and between variables are mutually independent [1]. Discrete response variables distributed Poisson can be modeled using the Poisson regression approach, while two discrete data that are distributed Poisson and correlated can be modeled using Bivariate Poisson regression. In Poisson regression, there is an assumption that must be met, namely equidispersion.

Equidispersion is a condition of data that has the same mean and variance values. However, in many cases, the equidispersion assumption is not met. Some cases that are often encountered have data conditions where the variance value is greater than the mean value, or referred to as overdispersion [2]. The problem of overdispersion can cause an underestimation of the standard error of parameter estimates, which results in errors in concluding [3]. A method to get around the overdispersion issue is to utilize a mixed Poisson distribution, which combines a continuous distribution and the Poisson distribution. A combination of the Poisson and Log-Normal distributions, the Poisson Log-Normal distribution is one of the mixed Poisson distributions. When a distribution is converted to a normal distribution using the natural logarithm, it is known as the Log-Normal distribution [4].

One of the data assumed to be distributed Poisson is data on the number of leprosy cases, which is a chronic disease caused by infection with the bacteria Mycobacterium Leprae. There are two types of leprosy, namely Paucibacillary (PB), which is characterized by the presence of five or fewer skin lesions without bacteria visible on microscopic examination, and Multibacillary (MB), which is characterized by more than five skin lesions and the presence of bacteria that can be seen on microscopic examination. However, classifying leprosy solely based on the number of skin lesions is inadequate, as it can result in misidentifying many multibacillary (MB) cases as paucibacillary (PB), leading to incorrect treatment approaches. Hence, a thorough clinicobacteriological evaluation of each leprosy case is essential to accurately determine the bacillary status, ensure appropriate treatment, and help prevent under-treatment and the development of drug resistance [5]. Based on a report from the World Health Organization (WHO) in the Weekly Epidemiological Record (WER) in 2021, Indonesia is in third place as the country with the highest number of leprosy cases in the world, after India and Brazil [6]. In 2021, Indonesia reported 10,876 new cases of leprosy. Leprosy is influenced by several socio-economic aspects, environmental aspects, demographic aspects, and behavioral aspects [7]. In addition, aspects of health facilities also affect the occurrence of leprosy [8]. The socio-economic aspect includes the poor and households with dirt floors. Environmental aspects include healthy houses and healthy toilets. Demographic aspects include population density, behavioral aspects include PHBS households, and clean water facilities. While health facility aspects include many public health aspects and the number of medical personnel.

Data on the number of leprosy cases in Indonesia in 2021 is discrete data that has a small probability of occurrence, so the data is distributed Poisson. PB and MB leprosy data have dependent variables that are correlated with each other, so the Bivariate Poisson model can be applied. In addition, the 2021 leprosy data experienced overdispersion, which could result in invalid conclusions. To overcome this problem, the Poisson method was used. Log-Normal by introducing the Log-Normal distribution on the model parameters. By combining these approaches, the Bivariate Poisson Log-Normal Regression method was developed in the analysis of PB and MB leprosy data in Indonesia in 2021.

2. RESEARCH METHODS

2.1 Data

The data in this research is a case study in Indonesia with research units throughout the provinces. Thus, the total number of observations in this study consists of 34 provinces across Indonesia. The research utilizes secondary data sourced from the Indonesian Health Profile Report published by the Ministry of Health of the Republic of Indonesia. (Kemenkes RI) which can be accessed on the kemkes.go.id website and the Central Statistics Agency (BPS) publication, which can be accessed on the bps.go.id website in Indonesia for the 2021 period.

2.2 Leprosy

Leprosy is a long-term infectious illness brought on by the bacterium Mycobacterium leprae. This disease mainly attacks the skin, peripheral nerves, and mucosa of the upper respiratory tract, which, in the long term, causes some of the sufferer's body parts to not function properly. Leprosy consists of two types, namely Paucibacillary (PB) and Multibacillary (MB). PB type leprosy is a type of leprosy that is not contagious and is also called dry leprosy, while MB leprosy, or wet leprosy, is a very contagious leprosy. Based on the number of skin lesions and the results of bacteriological examination, PB leprosy is characterized by the presence of five or fewer skin lesions without bacteria visible on microscopic examination, while MB leprosy is characterized by more than five skin lesions and the presence of bacteria that can be seen on microscopic examination [9]. The main signs of leprosy are skin abnormalities such as white spots, reddish spots spread on the skin, there are parts of the body that do not sweat and are numb, and experience changes in skin color to lighter or darker [10] Leprosy is spread through prolonged direct contact with the skin and respiratory tract. Effective multidrug therapy is available, and with early detection and treatment, leprosy can be cured, but treatment of the disease can be complicated by immune-mediated reactions, which can cause permanent nerve damage and lead to lifelong disability associated with stigma and discrimination [11]. Other poor leprosy management can result in disability in the eyes, hands, and feet [5]. Risk factors for leprosy include household contact with leprosy sufferers, the presence of leprosy sufferers in the neighborhood, and poor personal hygiene conditions [12]. Other factors suspected of triggering leprosy are family economic conditions, personal hygiene, the physical environment of the residence, and the density of residents [13].

2.2 Risk Factors for Leprosy

2.2.1 Cleanliness Aspect

Clean and healthy living behaviors are essential for maintaining and improving health. Leprosy can be transmitted through the respiratory tract and skin. To prevent leprosy, it is important to adopt a clean and healthy lifestyle in the home environment, so that the number of disease-causing microorganisms can be minimized, which can enter through the skin and respiratory tract. Some preventive measures that can be taken are wearing long clothes, not sharing towels, bathing at least twice a day, and early detection and treatment with MDT (Multi Drug Therapy) if diagnosed with leprosy. It is also important to improve the home environment, such as cleaning the floor, opening windows every day, and maintaining personal hygiene by not sharing towels and using clean water for bathing, to reduce the potential growth of bacteria that cause leprosy [14].

2.2.2 Residential Density Aspect

A person who has a densely populated category in the home environment can be at risk the hazard of their associated household contacts developing leprosy increases by 3.14 times ($p < 0.001$) than someone who has a non-densely populated home category. This happens because the condition of a densely populated home environment will facilitate the transmission of leprosy to others through direct or indirect interaction. The main risk factor for leprosy growth within a household is the index case's slit skin smear positivity. Household contact examinations and case detection are essential to leprosy control [15].

2.2.3 Poverty Aspects

The rising incidence of leprosy among the poor can be attributed to several factors. Limited access to clean water, proper sanitation, and adequate nutrition makes them more susceptible to the disease. Additionally, despite needing medical care, many are hesitant to seek treatment due to a significant disconnect with healthcare providers, scarce resources to cover basic necessities, and a lack of knowledge about how to manage and respond to illness [6].

2.2.4 Health Facilities and Services Aspects

In order to stop the spread of leprosy and avoid long-term impairments, early identification and treatment are essential. The availability and skills of healthcare professionals at all levels are critical to the success of early detection and treatment. However, even though they could administer multidrug therapy

(MDT) at no cost, many healthcare facilities are unable to provide leprosy services, even though they are accessible to patients and have willing staff [16].

2.3 Log-Normal Poisson Regression

An approach to modeling overdispersed discrete data sets. The equidispersion assumption, a fundamental tenet of Poisson regression, states that the response variable's mean and variance must be equal. However, in many cases, this assumption is often not met. If the variance of the data is greater than the mean value in the Poisson model ($Var(Y) > E(Y)$), then this case can be overcome by Poisson Log-Normal regression from the Poisson Log-Normal distribution [2]. An alternative to the mixed Poisson distribution is the Poisson Log-Normal distribution, which combines the Poisson and Log-Normal distributions. Two British mathematicians, Donald McAlister and Franics Galton, first proposed the Log-Normal distribution in 1879. When a distribution is converted to a normal distribution using the natural logarithm, it is known as the Log-Normal distribution [6]. The characteristics of the Log-Normal distribution are positive non-zero values, positive skewness, and inconsistent variance (heteroscedasticity) [17]. A random variable with a V Log-Normal distribution is denoted by $V \sim LN(\lambda, \tau^2)$, and has a probability density function in Eq. (1).

$$g(v|\lambda,\tau^2) = \frac{1}{\sqrt{2\pi\tau v}} \exp\left(\frac{(\ln(v)-\lambda)^2}{2\tau^2}\right), v > 0;\ -\infty \le \lambda \le \infty, \tau^2 > 0, \tag{1}$$

with λ is a scale parameter and τ^2 is a location parameter. The mean and variance of the distribution are $E(V) = \exp\left(\lambda + \frac{\tau^2}{2}\right)$ and $Var(V) = \exp(2\lambda + \tau^2)[\exp(\tau^2) - 1]$. If given a random variable Y that follows the Poisson Log-Normal distribution (μ, τ) then the probability density function Y can be expressed in integral form in Eq. (2) [18].

$$f(y;\mu,\tau) = \int_0^\infty \frac{e^{-\mu v}(\mu v)^y}{y!} g(v)dv\,, \tag{2}$$

with $g(v)$ is the probability density function for $V \sim LN(\lambda, \tau^2)$ Eq. (1).

If the probability density function of a random variable with a Log-Normal distribution in Eq. (1) is substituted into Eq. (2), then the Poisson Log-Normal probability density function is obtained in Eq. (3).

$$f(y;\mu,\tau) = \int_0^\infty \frac{e^{-\mu v}(\mu v)^y}{y!} \frac{1}{\sqrt{2\pi\tau v}} \exp\left(-\frac{(\ln(v)-\lambda)^2}{2\tau^2}\right) dv\,; y \ge 0. \tag{3}$$

Poisson Log-Normal regression model with parameters μ connected to predictor variables using a link function $\ln(\cdot)$ is in Eq. (4) [19].

$$\begin{aligned} \ln(\mu_i) &= \left(\boldsymbol{x}_i^T \boldsymbol{\beta}\right) \\ \mu_i &= \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}\right) \end{aligned} \tag{4}$$

With μ_i is the mean of the Poisson-distributed response variable, $\boldsymbol{x}_i^T = [1 \quad x_{i1} \quad x_{i2} \quad \dots \quad x_{ik}]$ denotes a vector $1 \times (k+1)$ of the predictor variables, and $\boldsymbol{\beta} = [\beta_0 \quad \beta_1 \quad \beta_2 \quad \dots \quad \beta_k]^T$ denotes a vector $(k+1) \times 1$ of the regression parameters.

2.4 Bivariate Poisson Log-Normal Regression

Bivariate Poisson Log-Normal (BPLN) regression is used to determine the relationship between two responses in the form of discrete data. These are correlated with several predictor variables that are suspected of having an influence on the two response variables. The conditions for BPLN regression to be used are that both response variables experience overdispersion and are positively correlated. The two random variables (Y_1, Y_2) are distributed Poisson and are independent, with mean $E(Y_j) = v\mu_j$ and variance $Var(Y_j) = \mu_j + \mu_j^2, \tau; j = 1,2$. If the random variable V is distributed Log-Normal, then the joint probability density function Y_1 and Y_2 are shown in Eq. (5) [20].

$$f(y_j;\mu_j,\tau)=\int_0^{\infty}\prod_{j=1}^{2}\frac{\exp(-\mu_j v)\,(\mu_j v)^{y}}{y_j!}\,g(v)\,dv;\; y_j\geq 0\,, \tag{5}$$

with $g(v)$ is the probability density function for $V\sim LN(\lambda,\tau^2)$ in Eq. (2). If the probability density function of the random variable with a Log-Normal distribution in Eq. (1) is substituted into Eq. (5), then the probability density function of BPLN is obtained in Eq. (6).

$$f(y_j;\mu_j,\tau;j=1,2)=\int_0^{\infty}\prod_{j=1}^{2}\frac{\exp(-v\mu_j)\,(v\mu_j)^{y_j}}{y_j!}\frac{1}{\sqrt{2\pi\tau v}}\exp\left(-\frac{\left(\ln(v)+\frac{\tau^2}{2}\right)^2}{2\tau^2}\right)dv\,. \tag{6}$$

The parameters μ_j are connected to the predictor variables using a link function so that the $\ln(\cdot)$. The BPLN regression model is as in Eq. (7) [21].

$$\begin{aligned}\ln(\mu_{ij})&=(\boldsymbol{x}_i^T\boldsymbol{\beta}_j)\\ \mu_{ij}&=\exp(\boldsymbol{x}_i^T\boldsymbol{\beta}_j)\,;\; j=1,2\end{aligned} \tag{7}$$

With μ_i is the mean of the j-th response variable, which is distributed Poisson, $\boldsymbol{x}_i^T=[1\quad x_{i1}\quad x_{i2}\quad \dots\quad x_{ik}]$ which denotes a vector of sizes $1\times(k+1)$ of the predictor variables, and which $\boldsymbol{\beta}_j=[\beta_{0j}\quad \beta_{1j}\quad \beta_{2j}\quad \dots\quad \beta_{kj}\,]^T$ denotes a vector of the sizes $(k+1)\times 1$ of the regression parameters.

2.5 Model Evaluation

Testing the significance of the BPLNR model parameters is carried out with two tests, namely simultaneous and partial testing. Simultaneous significance testing of the BPLN regression model parameters uses the Maximum Likelihood Ratio Test (MLRT) method. With the hypothesis:

H_0: $\beta_{j1}=\beta_{j2}=\cdots=\beta_{jk}=0$, $j=1,2$ and $\tau=0$ (the predictor variables together do not influence the response variable).
H_1: At least there are $\beta_{jk}\neq 0$, $j=1,2\,;k=1,2,\dots,p$ and $\tau\neq 0$ (the predictor variables together influence the response variable).

The test statistics used are formulated in Eq. 8 as follows:

$$\begin{aligned}G^2_{BPLNR}&=-2\ln\left(\frac{L(\hat{\omega}_{BPLNR})}{L(\hat{\Omega}_{BPLNR})}\right)\\&=2\left(\ln L(\hat{\Omega}_{BPLNR})-\ln L(\hat{\omega}_{BPLNR})\right),\end{aligned} \tag{8}$$

With $L(\hat{\Omega})$ is the maximum likelihood function for the model involving predictor variables, and $L(\omega)$ is the maximum likelihood function for the model without involving predictor variables, with the test criterion of H_0 rejecting if $G^2_{BPLNR}>X^2_{(\alpha,db)}$ with db is the degree of freedom obtained from $n(\Omega_{BPLNR})-n(\omega_{BPLNR})$, meaning that the predictor variables together influence the response variable [22]. Partial testing of the BPLN regression model with covariance as a function of the predictor variables is used to test whether the parameters β_{kj} and τ affect the model. Significance testing is carried out using the hypothesis:

H_0: $\beta_{kj}=0;k=1,2,\dots,p;j=1,2$ (no significant effect)
H_1: $\beta_{kj}\neq 0$ (There is a significant effect).

The test statistics using the Wald test are formulated in Eq. 9 as follows.

$$Z_{BPLNR}=\frac{\hat{\beta}_{kj}}{\sqrt{Var(\hat{\beta}_{kj})}}, \tag{9}$$

with $Var(\hat{\beta}_{kj})$: the main diagonal elements of the variance-covariance matrix, $Cov(\widehat{\boldsymbol{\theta}}_{\boldsymbol{\Omega}_{BPLNR}})$: the variance-covariance matrix with $Cov(\widehat{\boldsymbol{\theta}}_{\boldsymbol{\Omega}_{BPLNR}})=-\hat{E}\left(\boldsymbol{H}^{-1}\left((\widehat{\boldsymbol{\theta}}_{\boldsymbol{\Omega}_{BPLNR}})\right)\right)=$

$-\boldsymbol{H}^{-1}\left(\left(\widehat{\boldsymbol{\theta}}_{\boldsymbol{\Omega}_{BPLNR}}\right)\right)$ corresponds to $\widehat{\boldsymbol{\theta}}_{\boldsymbol{\Omega}_{BPLNR}} = \left[\widehat{\boldsymbol{\beta}}_{1\boldsymbol{\Omega}_{BPLNR}} \quad \widehat{\boldsymbol{\beta}}_{2\boldsymbol{\Omega}_{BPLNR}} \quad \widehat{\boldsymbol{\tau}}_{\boldsymbol{\Omega}_{BPLNR}}\right]^{\boldsymbol{T}}$. With the test criterion rejecting H_0 if $|z_{BPLNR}| > z_{\alpha/2}$ with α is the level of significance.

2.6 Analysis Steps

The data analysis procedure conducted in this study is outlined as follows:

2.6.1 Parameter Estimation of Bivariate Poisson Log-Normal Regression Model.

The stages of analysis to estimate the parameters of the Bivariate Poisson Log-Normal Regression model are as follows:

1. Form a likelihood function for the *i*-th observation based on the Bivariate Poisson Log-Normal regression probability mass function in Eq. (6).
2. Determine the natural logarithm likelihood function for the *i*-th observation in Step 1.
3. Determine each estimated parameter's first derivative of the ln likelihood function, then set it equal to zero. The maximum value of $L(\boldsymbol{\theta}_{BPLNR})$ will be obtained if $\frac{\partial l(\boldsymbol{\theta}_{BPLNR})}{\partial \boldsymbol{\theta}_{BPLNR}} = 0$, If the first derivative of each parameter leads to an implicit form, parameter estimation is carried out using the Newton-Raphson algorithm.

2.6.2 Factors Affecting the Number of Leprosy Cases in Indonesia Using the Bivariate Poisson Log-Normal Regression Model

Developing a Bivariate Poisson Log-Normal Regression model to determine the variables influencing the number of leprosy cases in Indonesia involves the following analytical steps:

1. Describe the response and predictor variables using descriptive statistics.
2. Test the Bivariate Poisson distribution on the response variables Y_1 and Y_2 using the index of dispersion test.
3. Testing the correlation between the response variables Y_1 and Y_2 using the Pearson correlation test.
4. Testing the assumption of non-multicollinearity in the predictor variables using the VIF value.
5. Checking overdispersion with the Deviance test.
6. Estimating the BPLN regression model parameters with the MLE method.
7. Interpret the model obtained and draw conclusions.

3. RESULTS AND DISCUSSION

3.1 Parameter Estimation of Bivariate Poisson Log-Normal Regression Model

Model parameter estimation BPLNR is performed using the MLE method. The estimated parameters are $\boldsymbol{\beta}_1, \boldsymbol{\beta}_2$ and τ. The MLE method is performed by maximizing the likelihood function of the probability density function $Y_{i1}, Y_{i2} \sim BPLN(\mu_{i1}, \mu_{i2}, \tau)$. The likelihood function formed from Eq. (10) is as follows.

$$L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau) = \prod_{i=1}^{n}\left(f(y_1, y_2; \mu_{i1}, \mu_{i2}, \tau)\right)$$

$$= \prod_{i=1}^{n}\left(\int_0^{\infty}\prod_{j=1}^{2}\frac{\exp(-v_i\mu_j)\,(v_i\mu_j)^{y_{ij}}}{y_{ij}!}\frac{1}{\sqrt{2\pi\tau v_i}}\exp\left(-\frac{\left(\ln(v_i)+\frac{\tau^2}{2}\right)^2}{2\tau^2}\right)dv_i\right). \qquad (10)$$

The likelihood function is then transformed into a natural logarithm, and the ln likelihood function is obtained as follows.

$$\ln L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau) = \ln\left(\prod_{i=1}^{n}\left(f(y_1, y_2; \mu_{i1}, \mu_{i2}, \tau)\right)\right)$$

$$= \ln\left(\prod_{i=n}^{n}\left(\int_0^{\infty}\prod_{j=1}^{2}\frac{\exp(-v_i\mu_j)\,(v_i\mu_j)^{y_{ij}}}{y_{ij}!}\frac{1}{\sqrt{2\pi\tau v_i}}\exp\left(-\frac{\left(\ln(v_i)+\frac{\tau^2}{2}\right)^2}{2\tau^2}\right)dv_i\right)\right)$$

$$= \sum_{i=1}^{n}\sum_{j=1}^{2}\left(\ln\left(\exp(-v_i\mu_j)\,(v_i\mu_j)^{y_{ij}}\right) - \left(ln(y_{ij}!)\right)\right) + \sum_{i=1}^{n}\left(\ln\left(\frac{1}{\sqrt{2\pi\tau v_i}}\right)\right)$$
$$+ \ln\left(\exp\left(-\frac{\left(\ln(v_i)+\frac{\tau^2}{2}\right)^2}{2\tau^2}\right)\right)$$

$$= \sum_{i=1}^{n}\sum_{j=1}^{2}\left(-v_i\mu_j + y_{ij}\ln(v_i\mu_j) - \ln(y_{ij}!)\right)$$
$$+ \sum_{i=1}^{n}(\ln(2\pi\tau v_i)^{-\frac{1}{2}} + \sum_{i=1}^{n}\left(\ln\left(\exp\left(-\frac{\left(\ln(v_i)+\frac{\tau^2}{2}\right)^2}{2\tau^2}\right)\right)\right)$$

$$= \sum_{i=1}^{n}\sum_{j=1}^{2}\left(-v_i\mu_j + y_{ij}\ln(v_i\mu_j) - \ln(y_{ij}!)\right) + \sum_{i=1}^{n}(-\frac{1}{2}\ln(2\pi\tau v_i))$$
$$+ \sum_{i=1}^{n}\left(-\frac{\left(\ln(v_i)+\frac{\tau^2}{2}\right)^2}{2\tau^2}\right)$$

$$= \sum_{i=1}^{n}\sum_{j=1}^{2}\left(-v_i\mu_j + y_{ij}\ln(v_i\mu_j) - \ln(y_{ij}!)\right) - \frac{n}{2}\ln(2\pi) - \frac{n}{2}\ln(\tau) - \frac{1}{2}\sum_{i=1}^{n}v_i$$
$$+ \sum_{i=1}^{n}\left(-\frac{\left(\ln(v_i)+\frac{\tau^2}{2}\right)^2}{2\tau^2}\right)$$

Because $\mu_j = \exp(\boldsymbol{x}_i^T\boldsymbol{\beta}_j)$ then,

$$\ln L(\boldsymbol{\beta_1}, \boldsymbol{\beta_2}, \tau) = \sum_{i=1}^{n}\sum_{j=1}^{2}\left[-v_i\exp(\boldsymbol{x}_i^T\boldsymbol{\beta}_j) + y_{ij}\ln(v_i\exp(\boldsymbol{x}_i^T\boldsymbol{\beta}_j)) - \ln(y_{ij}!)\right]$$
$$-\frac{n}{2}\ln(2\pi) - \frac{n}{2}\ln(\tau) - \frac{1}{2}\sum_{i=1}^{n}v_i + \sum_{i=1}^{n}\left(-\frac{\left(\ln(v_i)+\frac{\tau^2}{2}\right)^2}{2\tau^2}\right)$$

$$\ln L(\boldsymbol{\beta_1}, \boldsymbol{\beta_2}, \tau) = \sum_{i=1}^{n}\left[\left(-v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_1\right) + y_{i1} \ln\left(v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_1\right)\right) - \ln(y_{i1}!)\right)\right.$$
$$\left. + \left(-v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_2\right) + y_{i2} \ln\left(v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_2\right)\right) - \ln(y_{i2}!)\right)\right] - \frac{n}{2}\ln(2\pi) - \frac{n}{2}\ln(\tau) - \frac{1}{2}\sum_{i=1}^{n} v_i$$
$$+ \sum_{i=1}^{n}\left(-\frac{\left(\ln(v_i) + \frac{\tau^2}{2}\right)^2}{2\tau^2}\right)$$

The ln likelihood function in the equation above is derived from $\boldsymbol{\beta}_1, \boldsymbol{\beta}_2$, and τ, and equated to zero to obtain the parameter estimates of the BPLNR model. The first derivative of the function $\ln L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau)$ with respect to $\boldsymbol{\beta}_1$ is as follows.

$$\frac{\partial \ln L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau)}{\partial \boldsymbol{\beta}_1}$$
$$= \frac{\partial}{\partial \boldsymbol{\beta}_1}\sum_{i=1}^{n}\left[\left(-v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_1\right) + y_{i1} \ln\left(v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_1\right)\right) - \ln(y_{i1}!)\right)\right.$$
$$\left. + \left(-v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_2\right) + y_{i2} \ln\left(v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_2\right)\right) - \ln(y_{i2}!)\right)\right] - \frac{n}{2}\ln(2\pi) - \frac{n}{2}\ln(\tau) - \frac{1}{2}\sum_{i=1}^{n} v_i$$
$$+ \sum_{i=1}^{n}\left(-\frac{\left(\ln(v_i) + \frac{\tau^2}{2}\right)^2}{2\tau^2}\right)$$
$$= \sum_{i=1}^{n}\left(-v_i \boldsymbol{x}^T \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_1\right) + y_{i1}\boldsymbol{x}^T\right)$$

The first derivative of the function $\ln L(\boldsymbol{\beta_1}, \boldsymbol{\beta_2}, \tau)$ with respect to $\boldsymbol{\beta}_2$ is as follows.

$$\frac{\partial \ln L(\boldsymbol{\beta_1}, \boldsymbol{\beta_2}, \tau)}{\partial \boldsymbol{\beta}_2}$$
$$= \frac{\partial}{\partial \boldsymbol{\beta}_2}\sum_{i=1}^{n}\left[\left(-v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_1\right) + y_{i1} \ln\left(v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_1\right)\right) - \ln(y_{i1}!)\right)\right.$$
$$\left. + \left(-v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_2\right) + y_{i2} \ln\left(v_i \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_2\right)\right) - \ln(y_{i2}!)\right)\right] - \frac{n}{2}\ln(2\pi) - \ln(\tau) - \frac{1}{2}\sum_{i=1}^{n} v_i$$
$$+ \sum_{i=1}^{n}\left(-\frac{\left(\ln(v_i) + \frac{\tau^2}{2}\right)^2}{2\tau^2}\right)$$
$$= \sum_{i=1}^{n}\left(-v_i \boldsymbol{x}^T \exp\left(\boldsymbol{x}_i^T \boldsymbol{\beta}_2\right) + y_{i2}\boldsymbol{x}^T\right)$$

The first derivative of the function $\ln L(\boldsymbol{\beta_1}, \boldsymbol{\beta_2}, \tau)$ with respect to τ is as follows.

$$\frac{\partial \ln L(\boldsymbol{\beta_1}, \boldsymbol{\beta_2}, \tau)}{\partial \tau}$$

$$= \frac{\partial}{\partial \tau} \sum_{i=1}^{n} [(-v_i \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_1) + y_{i1} \ln(v_i \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_1)) - \ln(y_{i1}!))$$

$$+ (-v_i \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_2) + y_{i2} \ln(v_i \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_2)) - \ln(y_{i2}!))] - \frac{n}{2}\ln(2\pi) - \frac{n}{2}\ln(\tau) - \frac{1}{2}\sum_{i=1}^{n} v_i$$

$$+ \sum_{i=1}^{n} \left(- \frac{\left(\ln(v_i) + \frac{\tau^2}{2}\right)^2}{2\tau^2} \right)$$

$$= -\frac{n}{2\tau} + \sum_{i=1}^{n} \frac{-\tau^2 \left(\ln(v_i) + \frac{\tau^2}{2}\right) - \left(\ln(v_i) + \frac{\tau^2}{2}\right)^2}{\tau^3}$$

When equated to zero, the first derivative of the ln likelihood function with respect to the parameters $\boldsymbol{\beta_1}, \boldsymbol{\beta_2}$, and τ yields an implicit equation. The Newton-Raphson algorithm is then used to estimate the parameters, yielding the following Eqs. (11), (12), and (13).

$$\boldsymbol{\beta}_1^{(s+1)} = \boldsymbol{\beta}_1^{(s)} - \boldsymbol{H}_1 \left(\boldsymbol{\beta}_1^{(s)}\right)^{-1} \boldsymbol{g}\left(\boldsymbol{\beta}_1^{(s)}\right) \tag{11}$$

$$\boldsymbol{\beta}_2^{(s+1)} = \boldsymbol{\beta}_2^{(s)} - \boldsymbol{H}_2 \left(\boldsymbol{\beta}_2^{(s)}\right)^{-1} \boldsymbol{g}\left(\boldsymbol{\beta}_2^{(s)}\right) \tag{12}$$

$$\tau^{(s+1)} = \tau^{(s)} - \boldsymbol{H}_3(\tau^{(s)})^{-1} \boldsymbol{g}(\tau^{(s)}) \tag{13}$$

With:

$s = 0,1,2, \ldots q$

$\boldsymbol{g}\left(\boldsymbol{\beta}_1^{(s)}\right) = \frac{\partial \ln L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau)}{\partial \boldsymbol{\beta}_1}$

$\boldsymbol{g}\left(\boldsymbol{\beta}_2^{(s)}\right) = \frac{\partial \ln L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau)}{\partial \boldsymbol{\beta}_2}$

$\boldsymbol{g}(\tau^{(s)}) = \frac{\partial \ln L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau)}{\partial \tau}$

$\boldsymbol{H}_1\left(\boldsymbol{\beta}_1^{(s)}\right) = \frac{\partial^2 \ln L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau)}{\partial \boldsymbol{\beta}_1 \partial \boldsymbol{\beta}_1^T}$

$= -\sum_{i=1}^{n} (v_i \boldsymbol{x}^T \boldsymbol{x}^T \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_1)$

$\boldsymbol{H}_2\left(\boldsymbol{\beta}_2^{(s)}\right) = \frac{\partial^2 \ln L(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \tau)}{\partial \boldsymbol{\beta}_2 \partial \boldsymbol{\beta}_2^T}$

$= -\sum_{i=1}^{n} (v_i \boldsymbol{x}^T \boldsymbol{x}^T \exp(\boldsymbol{x}_i^T \boldsymbol{\beta}_2)$

$\boldsymbol{H}_3(\tau^{(s)}) = \frac{\partial^2 \ln L(\boldsymbol{\beta_1}, \boldsymbol{\beta_2}, \tau)}{\partial \tau^2}$

$= \sum_{i=1}^{n} \left(\frac{3 \ln^2(v_i)}{\tau^4} + \frac{2 \ln(v_i) + \frac{1}{2}}{\tau^2} - \frac{3}{4} \right)$

3.2 Factors Influencing Indonesia's Leprosy Case Count Using the Bivariate Poisson Log-Normal Regression Model

1. Descriptive Analysis. The number of MB and PB leprosy cases in Indonesia in 2021 served as the study's response variables. Table 1 displays descriptive statistics for leprosy case data.

Table 1. Descriptive Statistics of Leprosy Data

Variables	N	Minimum	Maximum	Mean	Standard Deviation
PB Leprosy (Y_1)	34	1	250	36.15	56.43
MB Leprosy (Y_2)	34	13	1606	283.74	354.82
Population density (X_1)	34	9	15978	744.26	2721.06
Percentage of Poor Population (X_2)	34	4.56	27.38	10.43	5.41
Percentage of Households Having Access to Adequate Sanitation Services (X_3)	34	40.81	97.12	80.97	9.93
Number of Health Facilities (X_4)	34	67	1474	393.29	346.15
Number of Medical Personnel (X_5)	34	385	14784	3126.94	4011.11
Percentage of Households Having Access to Clean Drinking Water Source Services (X_6)	34	64.92	99.860	86.67	8.46

In Table 1, data are presented for two types of response variables, namely PB leprosy (Y_1) and MB leprosy (Y_2), each based on 34 observations. The average number of PB leprosy cases in Indonesia is 36 cases. The highest number of PB leprosy cases in Indonesia is 250 cases in Papua Province. The main factor causing the high number of PB leprosy cases in Papua Province is the lack of public understanding about the prevention and treatment of this disease. Many Papuans consider leprosy to be a mild skin problem, especially when the symptoms first appear as spots, which are often mistaken for tinea versicolor. As a result, they tend to postpone visits to health facilities until the disease reaches a severe stage, such as nerve paralysis, ulcers, or even amputation. In addition, the negative stigma against leprosy means that only a few sufferers voluntarily seek treatment, while most others must be visited to ensure they get the necessary care.

2. Assumption Test. Before carrying out the model formation process, there are assumptions that must be met, namely, the response variable is distributed Bivariate Poisson, the correlation test between response variables, the multicollinearity test, and the overdispersion detection test.

Before modeling the data, it is necessary to conduct a test to identify whether the response variables Y_1 and Y_2 follow the Bivariate Poisson distribution or not. Table 2 is a Bivariate Poisson distribution test using the index of dispersion test approach.

Table 2. Index Of Dispersion Test

I_B	χ^2
66.838	84.820

a. Hypothesis
$H_0 : F(x) = F_0(x)$ for Y_1 and Y_2 (response variables Y_1 and Y_2 follow a bivariate Poisson distribution).
$H_1 : F(x) \neq F_0(x)$ for Y_1 and Y_2 (response variables Y_1 and Y_2 do not follow a bivariate Poisson distribution).

b. Test statistics
Based on the results obtained in Table 2, the known value of $I_B = 66.838$ and $\chi^2 = 84.82$.

c. Test criteria
Reject H_0 if $|I_B| > \chi^2_{(0.05;65)}$ at the level of significance α.

d. Decision
Based on the results obtained in Table 2, the known value of $I_B = 66.838$ and $\chi^2 = 84.820$, which means the value $|I_B| < \chi^2_{(0.05;65)}$. Therefore, it is decided that H_0 it is accepted and H_1 rejected.

e. Conclusion
Thus, it is concluded that the data on the number of PB and MB leprosy in 2021 follows the Bivariate Poisson distribution.

The Bivariate Poisson Log-Normal Regression (BPLNR) model is a development of the univariate PLNR model with two response variables in the form of discrete data that are correlated with each other. Correlation testing of the response variables needs to be done as a requirement in the BPLNR model. Table 3 shows the Pearson Correlation test value.

Table 3. Pearson Correlation Test

t_{count}	t_{table}
4.701	2.037

a. Hypothesis
H_0 : There is no correlation between Y_1 and Y_2.
H_1 : There is a correlation between Y_1 and Y_2.

b. Test statistics
Based on the results obtained in Table 3, the value is known $t_{count} = 4.7009$ and $t_{(0.025;32)} = 2.0370$.

c. Test criteria
Reject H_0 if $|t_{count}| > t_{(0.025;32)}$ at the level of significance $\alpha = 0.05$.

d. Decision
Based on the results obtained in Table 3, the value is known $t_{count} = 4.7009$ and $t_{(0.025;32)} = 2.0370$, which means value $|t_{count}| > t_{(0.025;32)}$ That is, it was decided that H_0 it was rejected and accepted.

e. Conclusion
Thus H_1, the number of MB and PB leprosy cases in Indonesia in 2021 is found to be correlated.

Multicollinearity detection is carried out to determine whether there is a correlation between predictor variables. In this study, the VIF value criteria are used to detect multicollinearity cases, and the results of the multicollinearity test can be seen in Table 4.

Table 4. VIF Values

Variables	X_1	X_2	X_3	X_4	X_5	X_6
VIF Value	1.428	1.999	2.569	6.897	8.538	1.781

a. Hypothesis
$H_0 : VIF < 10$ (There are no symptoms of multicollinearity in the predictor variables).
$H_1 : VIF \geq 10$ (There are symptoms of multicollinearity in the predictor variables).

b. Test statistics
Based on the results obtained in Table 4, the known value VIF on all predictor variables is less than 10.

c. Test criteria
Reject H_0 if VIF ≥10 at the significance level α.

d. Decision
Based on the results obtained in Table 4, the known value VIF on all predictor variables is less than 10. which means the VIF value is <10. This means that it is decided to H_0 be accepted and H_1 rejected.

e. Conclusion
Consequently, it is determined that there are no signs of multicollinearity among the predictor variables.

Before modeling data with the BPLNR model, it is necessary to detect and test for overdispersion. Overdispersion occurs when the variance value of the response variable is greater than the mean value. Overdispersion testing is carried out using the deviance test. The results of the overdispersion test can be seen in Table 5.

Table 5. Overdispersion Test

Variables	D/db
PB Leprosy (Y_1)	73.76
MB Leprosy (Y_2)	421.23

a. Hypothesis
H_0 : There is no overdispersion in the Poisson regression model.
H_1 : There is overdispersion in the Poisson regression model.

b. Test statistics
According to the results obtained in Table 5, the known value for (Y_1), $D = 73.76$ and for (Y_2), $D = 421.23$.

c. Test criteria
Reject H_0 if $D/(28) > 1$ at the level of significance $\alpha = 0.05$

d. Decision
According to the results obtained in Table 5, the known value for (Y_1), $D = 73.76$ and for (Y_2), $D = 421.23$, which means the value of. That is, $D/(28) > 1$ it is decided that H_0 rejected and H_1 accepted.

e. Conclusion
Thus, it is concluded that there is a case of overdispersion in the response variable. Therefore, the data on the number of PB leprosy and MB leprosy in 2021 can be modeled using BPLN regression.

Parameter Estimation of Bivariate Poisson Log-Normal Regression Model. BPLNR modeling on the number of PB leprosy and MB leprosy cases in Indonesia produces global parameter estimates, meaning that the influencing factors are considered the same in each province. The parameter estimation results can be seen in Table 6.

Table 6. Overdispersion Test

Parameters	Estimation	Standard Error	Z	*p-value*
β_{01}	1.483486	0.000006	260982.290263	0.000000*
β_{11}	0.000016	0.000004	4.035241	0.000055*
β_{21}	0.105809	0.001148	92.182021	0.000000*
β_{31}	-0.022786	0.000625	-36.437231	0.000000*
β_{41}	0.000151	0.000055	2.746945	0.006015*
β_{51}	0.000086	0.000006	14.903874	0.000000*
β_{61}	0.015534	0.000666	23.331793	0.000000*
β_{02}	1.076462	0.000001	725860.188300	0.000000*
β_{12}	0.000117	0.000001	112.411500	0.000000*
β_{22}	0.044410	0.000299	148.295700	0.000000*
β_{32}	-0.033763	0.000163	-206.943500	0.000000*
β_{42}	0.002878	0.000014	200.055400	0.000000*
β_{52}	-0.000152	0.000002	-100.644100	0.000000*
β_{62}	0.062651	0.000174	360.680600	0.000000*
τ	0.001647	0.000001	1715.348000	0.000000*

*) Significant in $p - value < 0.05$

According to Table 6, every predictor variable including population density, the proportion of the population living in poverty, the proportion of households with access to adequate sanitation, the number of health facilities, the number of medical personnel, and the proportion of households with access to clean drinking water—has a significant impact on the number of PB and MB leprosy cases in Indonesia in 2021.

Furthermore, partial hypothesis testing of the dispersion parameter (τ). Based on Table 6, the estimated value of the dispersion parameter is $\exp(0.001647) = 1.001648$ with $p - value = 0.000000 < \alpha = 0.05$. This shows that the BPLNR model accommodates overdispersion in the data on the number of PB and MB leprosy cases in Indonesia in 2021.

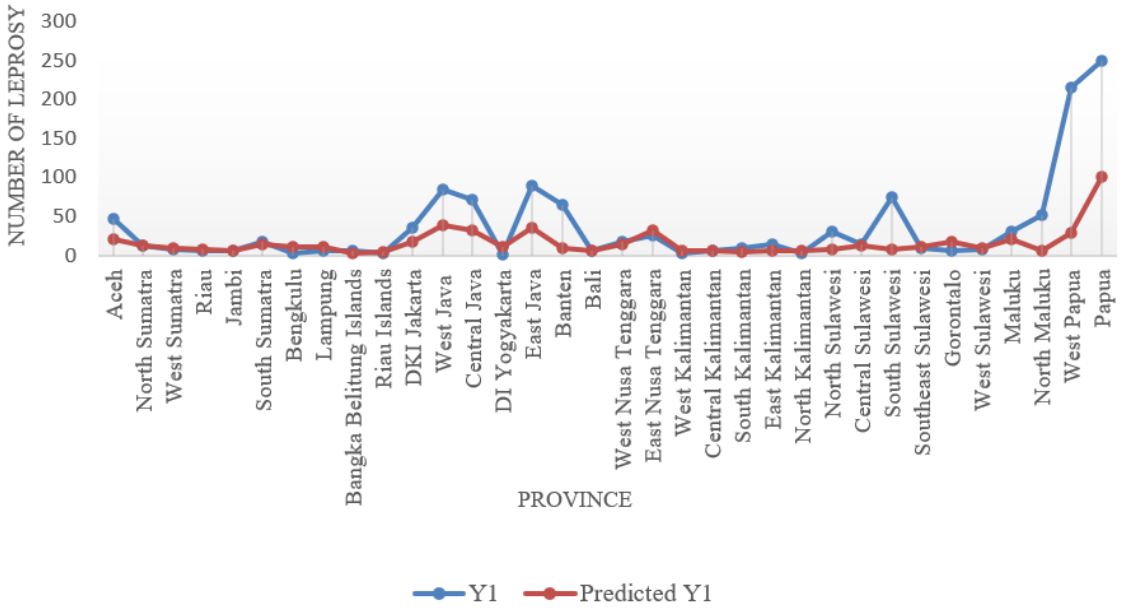

Figure 1. Plot of Actual VS Predicted Y1 on PB Leprosy in Indonesia in 2021

The plot comparing the predicted and actual values for PB leprosy cases, which are closely aligned, is shown in Fig. 1. This indicates that the BPLNR model performs well in modeling and predicting PB leprosy cases in Indonesia in 2021.

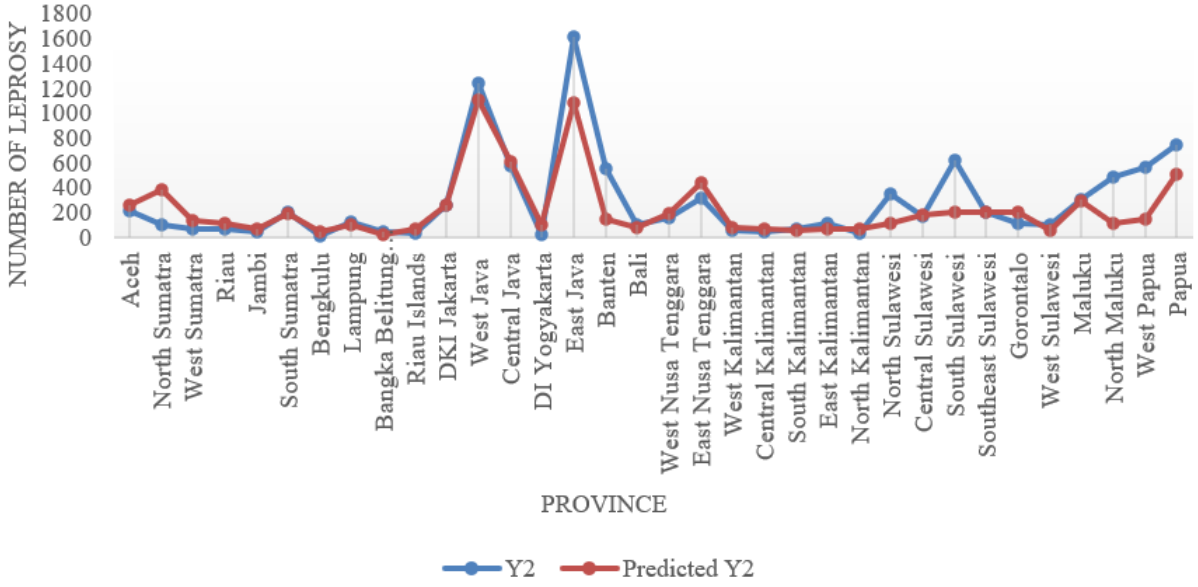

Figure 2. Plot of Actual VS Predicted Y2 on MB Leprosy in Indonesia in 2021

The plot comparing the predicted and actual values for MB leprosy cases, which are closely aligned, is presented in Fig. 2. This indicates that the BPLNR model performs well in modeling and predicting MB leprosy cases in Indonesia in 2021.

Table 7. BPLNR Model

Response	BPLNR Model
Y_1	$\hat{\mu}_{i1} = \exp(1.483486 + 0.000016x_{11} + 0{,}105809x_{21} - 0.022786x_{31} + 0.000151x_{41} + 0.000086x_{51} + 0.015534x_{61})$
Y_2	$\hat{\mu}_{i2} = \exp(1.076462 + 0.000117x_{12} + 0.044410x_{22} - 0.033763x_{32} + 0.002878x_{42} - 0.000152x_{52} + 0.062651x_{62})$

Based on Table 7, it is obtained that all variables that have a significant effect on the number of PB and MB leprosy cases, with the interpretation, every increase in population density of 1 person/km^{2,} the number of PB leprosy cases increases by $\exp(0.000016) = 1.000016$ times and the number of MB leprosy

cases increases by $\exp(0.000117) = 1.000117$ times, assuming other variables are constant. A person who has a densely populated category in the home environment can be at risk the hazard of their associated household contacts developing leprosy increases by 3.14 times ($p < 0.001$) than someone who has a non-densely populated home category. This happens because the condition of a densely populated home environment will facilitate the transmission of leprosy to others through direct or indirect interaction. Household contact examinations and case detection are critical aspects of control.

For every 1% increase in the percentage of poor people, the number of PB leprosy cases increases by $\exp(0.105809) = 1.111609$ times and the number of MB leprosy cases increases by $\exp(0.044410) = 1.045410$ times, assuming other variables are constant. Leprosy is becoming increasingly common among the impoverished, in part because they have less access to sanitary facilities, clean water, and a healthy diet, making them more susceptible to the illness. Due to a lack of health personnel, a lack of money to address basic requirements, and a lack of understanding about how to handle illness outbreaks, the impoverished often hesitate to seek care, even when they truly need it.

For every 1% increase in the percentage of households with access to proper sanitation, the number of PB leprosy cases will decrease by $\exp(-0.022786) = 0.977472$ times and the number of MB leprosy cases will decrease by $\exp(-0.033763) = 0.966801$ times, assuming other variables are constant. Clean behavior is behavior related to efforts to maintain and improve health. Transmission of leprosy is closely related to the respiratory tract and skin. Efforts to prevent leprosy can be done by implementing clean and healthy living behavior in households, so as to minimize the number of microorganisms that cause leprosy that can easily enter through the skin and respiratory tract.

For every increase in the number of health facilities by 1 unit, the number of PB leprosy cases increases by $\exp(0.000151) = 1.000152$ times and the number of MB leprosy cases increases by $\exp(0.002878) = 1.002882$ times, assuming other variables are constant. The increase in the number of leprosy even though there is an increase in the number of health facilities is due to the number of health facilities whose distribution is not evenly distributed. The phenomenon that occurs in several regions in Indonesia, the detection of Mycobacterium leprae bacteria, the cause of leprosy, is relatively slow due to limited facilities in several health facilities in remote areas of Indonesia.

For every increase in the number of medical personnel by 1 individual, the number of PB leprosy cases increases by $\exp(0.00086) = 1.00086$ times and the number of MB leprosy cases decreases by $\exp(-0.000152) = 0.999848$ times, assuming other variables are constant. In Indonesia, the number of medical personnel shows an increase. The difference in the increase in the number of cases between PB and MB leprosy is due to the quality and distribution of medical personnel, which are not optimal. The phenomenon that occurs in several regions in Indonesia, where medical personnel are not evenly distributed based on the phenomenon of several health centers lacking medical personnel, is one of the reasons why there is a difference in the increase in the number of leprosy cases.

For every 1% increase in the percentage of households with access to clean drinking water, the number of PB leprosy cases will increase by $\exp(0.015534) = 1.015655$ times and the number of MB leprosy cases will increase by $\exp(0.062651) = 1.064656$ times, assuming other variables are constant. The clean water supply system is a complex network involving various professionals, including policy makers, city planners, engineers, chemists, and regulators, who work together to ensure that clean water is available on time to people who need it. This system is supported by financial resources, data, and moral responsibility, with monitoring and demand from users to ensure that the government and service providers are responsible for meeting clean water needs. An increase in leprosy, in this case, means that there is an inability by the people involved in carrying out these responsibilities.

4. CONCLUSION

The modeling analysis of PB and MB leprosy cases in Indonesia in 2021 using the BPLNR model successfully achieved the objectives of this study. This research offers a novel application of the BPLNR model to leprosy case modeling, which has not been widely explored in the context of Indonesia. The estimation of model parameters using the Maximum Likelihood Estimation (MLE) method leads to implicit equations that require numerical iteration, for which the Newton-Raphson method was employed. The BPLNR model effectively identifies key influencing factors, including population density, poverty rate,

access to sanitation, number of health facilities, number of medical personnel, and access to clean drinking water, that affect the incidence of PB and MB leprosy.

However, this study is limited by the assumption of spatial independence and the potential sensitivity of the Newton-Raphson method to initial values. For future research, incorporating spatial modeling approaches, such as spatial autoregressive models or geographically weighted regression, may offer more comprehensive insights into the geographic distribution and spatial dependency of leprosy cases across regions in Indonesia.

However, this study is limited by the assumption of spatial independence and the potential sensitivity of the Newton-Raphson method to initial values. For future research, incorporating spatial modeling approaches, such as spatial autoregressive models or geographically weighted regression, may offer more comprehensive insights into the geographic distribution and spatial dependency of leprosy cases across regions in Indonesia.

Author Contributions

Nasrah Sirajang: Funding acquisition, Supervision, Writing - original draft; Salsabila Rahmadhani S: Data curation, Resources, Software, Visualization; Siswanto Siswanto: Formal analysis, Methodology, Validation, Writing - review & editing. All authors discussed the results and contributed to the final manuscript.

Funding Statement

This research received no funding from any public agency.

Acknowledgment

The authors would like to express their sincere gratitude to the Department of Statistics, Universitas Hasanuddin, for the guidance and support provided throughout the completion of this research.

Declarations

The authors declare no conflicts of interest to report study.

REFERENCES

[1] A. Prahutama, S. Suparti, D. A. Munawaroh, and T. W. Utami, "MODELING BIVARIATE POISSON REGRESSION FOR MATERNAL AND INFANT MORTALITY IN CENTRAL JAVA," *AIP Conf. Proc.*, vol. 2329, no. 1, 2021. doi: https://doi.org/10.1063/5.0042142

[2] P. McCullagh and J. Nelder, *GENERALIZED LINEAR MODELS*, Routledge, 2019. doi: https://doi.org/10.1201/9780203753736

[3] J. M. Hilbe, *MODEL COUNT DATA*, Cambridge University Press, 2014.

[4] R. E. Walpole, R. H. Myers, S. L. Myers, and K. Ye, *PROBABILITY AND STATISTICS FOR ENGINEERS AND SCIENTISTS*, Prentice Hall, Macmillan, New York, 2016.

[5] A. S. Ansari *et al*., "CLINICOBACTERIOLOGICAL EVALUATION OF LEPROSY PATIENTS WITH 1–5 SKIN LESIONS," *Int. J. Mycobacteriology*, vol. 9, no. 2, pp. 209–211, 2020.

[6] World Health Organization, "GLOBAL LEPROSY (HANSEN DISEASE) UPDATE, 2021: MOVING TOWARDS INTERRUPTION OF TRANSMISSION," 2021. doi: https://doi.org/10.4103/ijmy.ijmy_7_20

[7] S. C. Kurane and P. Dani, "CLINICAL AND SOCIODEMOGRAPHIC CHARACTERISTICS OF RECENTLY IDENTIFIED LEPROSY PATIENTS IN SANGLI DISTRICT OF MAHARASHTRA," *Journal of Neonatal Surgery*, vol. 14, no. 21s, 2025.

[8] V. E. M. de Araújo, G. A. Veloso, L. R. F. S. Kerr, J. M. Pescarini, L. D. M. Cardoso, M. Naghavi, and D. C. Malta, "LEPROSY IN BRAZIL: AN ANALYSIS OF THE GLOBAL BURDEN OF DISEASE ESTIMATES BETWEEN 1990 AND 2019," *Public Health*, vol. 236, pp. 307–314, 2024. doi: https://doi.org/10.1016/j.puhe.2024.07.035

[9] C. S. Smith *et al*., "MULTIDRUG THERAPY FOR LEPROSY: A GAME CHANGER ON THE PATH TO ELIMINATION," *Lancet Infect. Dis.*, vol. 17, no. 9, pp. e293–e297, 2017. doi: https://doi.org/10.1016/S1473-3099(17)30418-8

[10] I. Karunarathna, S. Rajapaksha, U. Ekanayake, and K. De Alvis, "FROM CLINICAL SYMPTOMS TO DIAGNOSIS: A GUIDE TO IDENTIFYING LEPROSY," 2024.

[11] Y. Pieter and M. L. Grijsen, "PICTURING HEALTH: THE BURDEN OF LEPROSY IN EASTERN INDONESIA," *Lancet*, vol. 399, no. 10335, pp. 1588–1599, 2022. doi: https://doi.org/10.1016/S0140-6736(22)00699-7

[12] S. Siswanti and Y. Wijayanti, "ENVIRONMENTAL RISK FACTORS FOR LEPROSY INCIDENCE," *HIGEIA (J. Public Health Res. Dev.)*, vol. 2, no. 3, pp. 352–362, 2018.

[13] I. Aisyah, A. V. W. Taufiq, and D. H. Apriliana, "DESCRIPTIVE EPIDEMIOLOGY OF HOUSEHOLD CONTACTS WITH LEPROSY PATIENTS IN LOMBOK BARAT AND LOMBOK TENGAH DISTRICTS, NUSA TENGGARA BARAT," in *Proc. Int. Conf. Public Health*, vol. 8, no. 1, pp. 152–166, Sep. 2023.

[14] J. L. S. Siagian, S. Pangaribuan, and A. S. Ulimpa, "RISK FACTORS FOR LEPROSY AT BAINGKETE MAKBON DISTRICT SORONG REGENCY," *Science Midwifery*, vol. 10, no. 5, pp. 4211–4218, 2022. doi: https://doi.org/10.35335/midwifery.v10i5.985

[15] E. E. Quilter *et al.*, "PATIENTS WITH SKIN SMEAR POSITIVE LEPROSY IN BANGLADESH ARE THE MAIN RISK FACTOR FOR LEPROSY DEVELOPMENT: 21-YEAR FOLLOW-UP IN THE HOUSEHOLD CONTACT STUDY (COCOA)," *PLoS Negl. Trop. Dis.*, vol. 14, no. 10, 2020. doi: https://doi.org/10.1371/journal.pntd.0008687

[16] T. Dahiru *et al.*, "LEPROSY CAPACITY IN HEALTH FACILITIES AND AMONG HEALTH WORKERS: A BASELINE SURVEY IN NIGERIA," *Leprosy Rev.*, vol. 94, no. 4, pp. 317–331, 2023. doi: https://doi.org/10.47276/lr.94.4.317

[17] S. Gustavsson, *EVALUATION OF REGRESSION METHODS FOR LOG-NORMAL DATA*, University of Gothenburg, Gothenburg, 2015.

[18] S. H. Ong, W. J. Lee, and Y. C. Low, "A GENERAL METHOD OF COMPUTING MIXED POISSON PROBABILITIES BY MONTE CARLO SAMPLING," *Math. Comput. Simul.*, vol. 170, pp. 98–106, 2020. doi: https://doi.org/10.1016/j.matcom.2019.09.003

[19] M. L. Hazelton and L. Najim, "USING TRAFFIC ASSIGNMENT MODELS TO ASSIST BAYESIAN INFERENCE FOR ORIGIN–DESTINATION MATRICES," *Transp. Res. Part B: Methodol.*, vol. 186, p. 103019, 2024. doi: https://doi.org/10.1016/j.trb.2024.103019

[20] S. Nadarajah and J. Lyu, "NEW BIVARIATE AND MULTIVARIATE LOG-NORMAL DISTRIBUTIONS AS MODELS FOR INSURANCE DATA," *Results Appl. Math.*, vol. 14, 2022. doi: https://doi.org/10.1016/j.rinam.2022.100246

[21] G. Tzougas and A. P. di Cerchiara, "BIVARIATE MIXED POISSON REGRESSION MODELS WITH VARYING DISPERSION," *North Am. Actuar. J.*, vol. 27, no. 2, pp. 211–241, 2023. doi: https://doi.org/10.1080/10920277.2021.1978850

[22] S. Mardalena, J. T. D. Purnomo, and D. D. Prastyo, "BIVARIATE POISSON INVERSE GAUSSIAN REGRESSION MODEL WITH EXPOSURE VARIABLE: INFANT AND MATERNAL DEATH CASE STUDY," *J. Phys.: Conf. Ser.*, vol. 1752, no. 1, 012016, 2021. doi: https://doi.org/10.1088/1742-6596/1752/1/012016