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EXPLICIT MEAN PARAMETERIZATION AND BHHH-BASED ESTIMATION IN THE PGIG REGRESSION MODEL

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ABSTRACT

Modeling dispersed count data remains a substantial challenge in applied research, especially when traditional models struggle to capture complex dispersion structures or yield interpretable results. In this study, we introduce and evaluate the Poisson Generalized Inverse Gaussian Regression (PGIGR) model, which offers a flexible four-parameter framework with explicit mean parameterization. The model is applied to 2023 maternal mortality data from 38 cities and municipalities in East Java, Indonesia. The response variable was the number of maternal deaths, while the six predictors were the percentage of pregnant women receiving nutritional tablets, the percentage of malnourished pregnant women, contraceptive use, antenatal care coverage, healthcare professional availability, and access to proper sanitation. The results indicate that higher nutritional tablet coverage among pregnant women and greater antenatal care coverage are significantly associated with lower maternal mortality. In contrast, higher percentages of malnourished pregnant women, contraceptive users, healthcare professionals, and households with access to proper sanitation are significantly associated with higher maternal mortality. The unexpected positive associations observed for contraceptive use, healthcare professional availability, and proper sanitation may reflect differences in regional health needs, service allocation, reporting practices, or other unobserved factors and therefore require further investigation. Goodness-of-fit testing confirms the suitability of the PGIGR model for the data, and the maximum likelihood estimation procedure—supported by the BHHH optimization algorithm—yields statistically significant parameter estimates. This research underlines the applicability of the PGIGR model for modeling count data characterized by dispersion, while maintaining interpretability of the regression parameters. Such a framework can support informed decision-making in public health management and the strategic allocation of healthcare resources. The data on maternal mortality were obtained from the 2023 Health Profile of East Java Province, published by the East Java Provincial Health Office.

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1. INTRODUCTION

Count data commonly arise in experimental and observational studies and consist of non-negative integer observations. A standard approach for modeling such data is the Poisson distribution, which assumes that the mean equals the variance, yielding a variance-to-mean ratio (VMR) of 1. Under this assumption, the Poisson model adequately represents the stochastic nature of count outcomes [1].

Poisson regression extends this distribution to a regression framework, allowing the mean of the response variable to depend on a set of explanatory variables [2]. Nevertheless, empirical count data frequently violate the equidispersion assumption. In many cases, the variance may exceed the mean (overdispersion) or fall below it (underdispersion). Ignoring these dispersion patterns may lead to underestimated standard errors and consequently unreliable statistical inference in hypothesis testing [3].

To overcome these limitations, several modifications to the Poisson model have been proposed. The Generalized Poisson model, for instance, incorporates an additional parameter to flexibly account for varying levels of dispersion, though it may not perform well in cases of extreme underdispersion [4]. Another approach, the hurdle model, addresses zero counts separately from positive counts, which allows for more tailored modeling. However, it can be difficult to interpret and may not perform optimally when overdispersion or underdispersion is substantial [5]. Similarly, the zero-inflated model blends a Poisson component with an added mechanism for excess zeros. While useful for handling data with many zero counts, it becomes unnecessarily complex and inefficient if excessive zeros are not a prominent feature of the data [6]. Another commonly employed method for addressing dispersion in count data is the quasi-likelihood approach. Rather than relying on a complete probability distribution, it models the relationship between the mean and variance by introducing a dispersion parameter to flexibly handle overdispersion. Despite its adaptability, the lack of a defined likelihood function restricts its usefulness in certain inferential tasks, such as formal hypothesis testing [7].

An alternative strategy involves mixed Poisson distributions, which enhance the Poisson model by incorporating other distributions to better reflect variability. For example, the Poisson-Normal model is relatively simple but lacks the capability to adjust variance responsively, limiting its performance with highly variable data. The Poisson-Gamma model, also known as the Negative Binomial model, is more effective in managing overdispersion and yields robust estimates. However, it relies on the validity of the Poisson-Gamma mixture assumption, which must be assessed for each application. Moreover, it is not well suited to underdispersed data due to its structural limitations [8].

Advanced models such as the Conway-Maxwell-Poisson (CMP) and Tweedie-Poisson distributions can accommodate both over- and underdispersion. Nevertheless, these models typically require complex numerical techniques for parameter estimation, which increases computational demands and is often hindered by limited software availability [9], [10]. The Gamma Count model also involves challenging estimation procedures and tends to perform poorly when the data include a large number of zero counts [11]–[13]. this study, we propose an extension to the mixed Poisson framework by utilizing the Sichel distribution, as suggested by [14]. This model treats the mixing distribution as a Generalized Inverse Gaussian (GIG), resulting in the Poisson–Generalized Inverse Gaussian (PGIG) model. As a mixed Poisson model with a GIG mixing distribution, the PGIG distribution naturally accommodates overdispersion (and approaches equidispersion in limiting cases). We explicitly derive $E(Y)$, $Var(Y)$, and the variance-to-mean ratio (VMR) to clarify the dispersion behavior [15]. One of the standard objectives of the study is to introduce a novel parameterization of the Poisson Generalized Inverse Gaussian (PGIG) distribution that is both interpretable and directly applicable within regression frameworks. Existing parameterizations, such as those proposed by [16], are limited in scope, being applicable only to overdispersed data—and lack flexibility due to constraints on one or more of their parameters. Similarly, the formulation in [17] struggles with datasets that contain zero-valued response variables, limiting its practical utility. In this work, we define a class of mixed Poisson distributions in which the mean parameter λ is explicitly incorporated into the structure of the distribution. This explicit parameterization enhances interpretability within regression models, particularly when the focus is on modeling λ as a function of covariates, and provides a more orthogonal configuration of parameters, reducing confounding between mean and dispersion components. A general and tractable expression for the derivative of the log-likelihood function with respect to λ is derived, enabling efficient numerical optimization.

Maximum Likelihood Estimation (MLE) is employed due to its optimal statistical properties, including consistency, asymptotic normality, and efficiency under regularity conditions, making it highly suitable for

complex statistical models [18]. This study employs the Maximum Likelihood Estimation (MLE) approach to estimate the parameters of the proposed model. MLE seeks to identify parameter values that maximize the likelihood function, thereby representing the highest probability of observing the given sample data under the specified model. Due to the complexity of the likelihood function in the PGIG framework, the resulting score equations often lack closed-form solutions, necessitating the use of iterative numerical optimization techniques for parameter estimation. Parameter estimation involves the Berndt-Hall-Hall-Hausman (BHHH) algorithm [19], selected for its computational efficiency and numerical stability in complex likelihood optimization scenarios. The iterative BHHH algorithm updates parameter estimates based on the gradient of the likelihood function, significantly improving convergence properties compared to alternative optimization algorithms such as Newton-Raphson or Fisher Scoring, which may require intensive computation of Hessian matrices and often experience convergence issues [20].

In the present study, maternal data from East Java Province are used as the model for PGIG Regression (PGIGR). Maternal deaths constitute critical public health concerns, influenced by multifaceted factors such as antenatal care access, nutritional status, healthcare facility availability, and sanitation practices [21], [22]. Despite ongoing public health efforts, substantial disparities and high variability persist across different regions within East Java, necessitating a robust statistical approach capable of accurately modeling dispersion in mortality count data [23], [24]. The PGIGR model accommodates these complexities effectively, providing nuanced insights into the determinants of mortality while accurately accounting for dispersion. Empirical application of the PGIGR model leverages advanced numerical strategies to overcome computational challenges associated with special functions (e.g., modified Bessel functions), ensuring stable and reliable parameter estimation. The explicit mean parameterization allows for greater interpretability and facilitates integration with covariate structures relevant to public health policy. The objectives of this study are (1) to propose and formulate the PGIGR model with explicit mean structure; (2) to implement an efficient BHHH-based estimation strategy for parameter inference; and (3) to demonstrate the empirical applicability of the model using real world data on maternal mortality. The expected benefit is to improve the reliability of statistical inference and policy interpretation in modeling dispersed count data in health applications.

2. RESEARCH METHODS

2.1 Poisson Generalized Inverse Gaussian (PGIG) Distribution

The Poisson distribution is one of the distributions used for count data. It is an approximation of the Binomial distribution for large population sizes. There are characteristics of experiments that follow the Poisson distribution, namely the probability of an event in an experiment being very small for a large population, the experiments are observed over a certain interval, whether it's a specific time period or a specific area, and the experiments are repetitions of events that follow a Binomial distribution [20].

Poisson distribution as the random variable Y has parameter λ and exposure variable q if and only if it has a probability mass function [20]:

$$P(Y=y)=\frac{e^{-\lambda(q)}\lambda(q)^{y}}{y!}, y=0,1,2,\ldots\ldots;\lambda(q)>0. \quad (1)$$

The assumption underlying of the Poisson distribustion is that the variance and mean of the $P(Y=y)$ is $E(Y)=Var(Y)=\lambda(q)$, as dictated by the characteristics of a Poisson distribution. The parameter λ in Eq. (1) represents average number of events of an event per unit exposure (q). Exposure (q) is a value of the population of the response variable measured. Exposure can also be defined as the number of individuals at risk of a response variable being measured [25]. This assumption of Poisson is often rare in many practical applications. This is because real-world data rarely exhibit such characteristics. An error term ε is added to λ,

$$e^{\left(X^{T}\beta+\varepsilon\right)}=\lambda e^{\varepsilon}=\lambda\nu. \quad (2)$$

Thus, the term $\nu\lambda$represents the expected value of the response variable. Considering the exposure term in Eq. (2), the response variable follows a mixed Poisson distribution, written as $Y\sim$ Mixed Poisson$(\lambda(q)\nu)$ [25]. The characteristics of a mixed Poisson model depend on the probability distribution assumed for the latent mixing variable V. In this study, $V$is assumed to follow a generalized inverse Gaussian (GIG)

distribution. Consequently, the resulting model corresponds to a Poisson–GIG mixture whose probability mass function is given in [26].

In probability theory, the distribution $g(v;\tau,\xi,\gamma)$is a continuous three-parameter distribution with probability density function defined in [14] as follows:

$$g(v;\tau,\xi,\gamma)=\frac{\xi^{-\gamma}}{2K_{\gamma}\left(\sqrt{\tau^2+\xi^2}-\xi\right)}v^{\gamma-1}\exp\left(-\left(\frac{\sqrt{\tau^2+\xi^2}-\xi}{2}\right)\left(\frac{v}{\xi}+\frac{\xi}{v}\right)\right),v>0, \tag{3}$$

where$-\infty<\gamma<\infty,\tau>0,\xi>0$, and $K_{\gamma}\left(\sqrt{\tau^2+\xi^2}-\xi\right)$ in Eq. (3) is the modified Bessel function of the second kind of order γ dan $\omega\in\mathbb{R}$ [27]. Hence, the joint probability distribution for the PGIGR [28] formulation is written as follows:

$$P(Y=y|\lambda(q),\tau,\xi,\gamma)=\frac{\xi^{-\gamma}\left(\lambda(q)\right)^{y}}{K_{\gamma}(\varpi)y!}\left(\frac{\varpi\xi^2}{2\xi\lambda(q)+\varpi}\right)^{\frac{y+\gamma}{2}}K_{y+\gamma}\left(\sqrt{(2\varpi\xi\lambda(q)+\varpi^2)}\right) \tag{4}$$

where $-\infty<\gamma<\infty;\tau>0;\xi>0;\lambda(q)>0;\varpi=\sqrt{\tau^2+\xi^2}-\xi$ mean and variance of PGIG made up

$$E(Y)=\left(\lambda(q)\right)\xi\frac{K_{\gamma+1}(\varpi)}{K_{\gamma}(\varpi)}, \tag{5}$$

and

$$Var(Y)=\left(\lambda(q)\right)^2\xi^2\frac{K_{\gamma+2}(\varpi)}{K_{\gamma}(\varpi)}+\left(\lambda(q)\right)\xi\frac{K_{\gamma+1}(\varpi)}{K_{\gamma}(\varpi)}-\left(\left(\lambda(q)\right)\xi\frac{K_{\gamma+1}(\varpi)}{K_{\gamma}(\varpi)}\right)^2, \tag{6}$$

with

$$VMR=\frac{Var(Y)}{E(Y)}=1+\left(\lambda(q)\right)\xi\frac{\frac{K_{\gamma+2}(\varpi)}{K_{\gamma}(\varpi)}-\left(\frac{K_{\gamma+1}(\varpi)}{K_{\gamma}(\varpi)}\right)^2}{\frac{K_{\gamma+1}(\varpi)}{K_{\gamma}(\varpi)}},$$

this yields the following dispersion implication: $VMR=1+\lambda(q)\ \frac{Var\ (V)}{E(V)}$.

Eq. (5) shows that the PGIG model is not in an explicit form for regression [29]. The mean of the GIG distribution in [30] is equal to one, indicating that the parameters of the GIG distribution are constants. Consequently, the mean of the PGIG distribution is also constant. Another approach, CCBP, as presented in [17], considers two parameters in the mixed Poisson model to be constants, specifically $\gamma=-{}^1/_2$ and $\xi=1$. Consequently, this method has certain limitations, such as the restriction that the response variable cannot equal zero. In this study, we adopt and combine these models but simplify the approach by fixing only one parameter, namely the shape parameter $\gamma=-{}^1/_2$ to facilitate modeling in regression analysis.

The PGIG Regression, if response variable Y_i~PGIG$(\lambda(q_i))$ from the distribution in Eq. (4), where $i=1,2,\ldots,n$ the PGIGR model can be stated as follows:

$$P(Y_i=y_i|\lambda(q_i),\tau,\xi,\gamma)=\frac{\left(\lambda(q_i)\right)^{y_i}}{K_{\gamma}(\varpi)y_i!}\left(\frac{\varpi}{2\lambda(q_i)+(\varpi)}\right)^{\frac{2y_i-1}{4}}K_{y_i+\gamma}\left(\sqrt{(\varpi)^2+2\lambda(q_i)\varpi}\right), \tag{7}$$

where $\tau>0,\xi>0,\sqrt{\tau^2+\xi^2}\neq\xi,\lambda(q_i)>0$, so

$$\lambda(q_i)=\frac{q_i\exp\left(x_i^T\beta\right)}{\xi}, \tag{8}$$

Let q_i denote the exposure term, representing the observational weight for unit i. The regression specification in Eq. (8) is built using the predictor vector $\mathbf{x}_i=(1,x_{i1},x_{i2},\ldots,x_{ip})^{\top}$for $i=1,2,\ldots,n$, which has dimension $(p+1)$. The predictor coefficient vector is $\boldsymbol{\beta}=(\beta_0,\beta_1,\beta_2,\ldots,\beta_p)^{\top}$, a $(p+1)\times1$ parameter vector linked to the response.

2.2 MLE for PGIGR Parameters

We use the MLE framework to obtain parameter estimates by maximizing the likelihood of the observed data. Since the underlying probability model is known and the sample units are treated as independent, the likelihood can be formulated directly. Let $\theta_{PGIGR} = [\beta^T \tau\ \xi]^T$ denote the set of unknown parameters. The $\ln L(\theta_{\text{PGIGR}})$ following state

$$\ln L(\theta_{\text{PGIGR}}) = \ln\left(\prod_{i=1}^{n} P(y_i|\beta,\tau,\xi)\right) \tag{9}$$

$$= \sum_{i=1}^{n} \ln P(y_i|\beta,\tau,\xi).$$

Differentiating $\ln L(\theta_{\text{PGIGR}})$ can be written below:

$$\frac{\partial \ln L(\theta_{\text{PGIGR}})}{\partial \theta_{\text{PGIGR}}} = \frac{\partial \ln(\prod_{i=1}^{n} P(y_i|\beta,\tau,\xi))}{\partial \theta_{\text{PGIGR}}} \tag{10}$$

$$= \sum\nolimits_{i=1}^{n} \frac{\partial \ln P(y_i|\beta,\tau,\xi)}{\partial \theta_{\text{PGIGR}}}$$

The first differentiated of θ_{PGIGR} in Eq. (10) as follows:

$$\ln L(\theta_{\text{PGIGR}}) = \sum\nolimits_{i=1}^{n} \left(\ln\left(\frac{\sqrt{\xi}}{K_\gamma(\varpi)}\right) + \ln(A_i B_i C_i)\right) \tag{11}$$

with $A_i = \frac{\left(q_i \exp(x_i^T\beta)\right)^{y_i}}{\xi^{y_i} y_i!}$; $B_i = \left(\frac{\varpi\xi^2}{2q_i \exp(x_i^T\beta)+\varpi}\right)^{\frac{2y_i-1}{4}}$; $C_i = K_{y_i+\gamma}\left(\sqrt{\varpi^2 + 2\varpi q_i \exp(x_i^T\beta)}\right)$.

Then the Eq. (11) derives to the parameter θ_{PGIGR} ,with the following equation is simplified:

$$\frac{\partial \ln L(\theta_{\text{PGIGR}})}{\partial \beta} = \sum\nolimits_{i=1}^{n} \frac{\partial}{\partial \beta}\left(\ln\left(\frac{\sqrt{\xi}}{K_\gamma(\varpi)}\right) + \ln(A_i B_i C_i)\right)$$

$$= \sum_{i=1}^{n} \left(y_i x_i^T + \left(\frac{2y_i-1}{4}\right) \frac{2q_i e^{x_i^T\beta}}{\left(2q_i e^{x_i^T\beta} + \left(\sqrt{\tau^2+\xi^2}-\xi\right)\right)} x_i^T \right. \tag{12}$$

$$\left. - \frac{q_i e^{x_i^T\beta}\left(\sqrt{\tau^2+\xi^2}-\xi\right)\left(K_{y_i-\frac{3}{2}}(z) + K_{y_i+\frac{1}{2}}(z)\right)}{2zK_{y_i-\frac{1}{2}}(z)} x_i^T \right)$$

The first derives of τ as the scale parameter can be formulated by:

$$\frac{\partial \ln L(\theta_{\text{PGIGR}})}{\partial \tau} = \sum\nolimits_{i=1}^{n} \frac{\partial}{\partial \tau}\left(\ln\left(\frac{\sqrt{\xi}}{K_\gamma(\varpi)}\right) + \ln(A_i B_i C_i)\right) \tag{13}$$

$$= \sum_{i=1}^{n} \left(\frac{\partial}{\partial \tau}\left(\left(\frac{2y_i-1}{4}\right)\left(\ln\left(\sqrt{\tau^2+\xi^2}-\xi\right) + \ln\xi^2 - \ln\left(2q_i e^{x_i^T\beta} + \left(\sqrt{\tau^2+\xi^2}-\xi\right)\right)\right)\right) - \right.$$

$$\left. \frac{\partial}{\partial \tau}\left(\ln\left(K_{-\frac{1}{2}}\left(\sqrt{\tau^2+\xi^2}-\xi\right)\right)\right) + \frac{\partial}{\partial \tau}\left(\ln\left(K_{y-\frac{1}{2}}\left(\sqrt{\left(2q_i e^{x_i^T\beta} + \left(\sqrt{\tau^2+\xi^2}-\xi\right)\right)\left(\sqrt{\tau^2+\xi^2}-\xi\right)}\right)\right)\right)\right)$$

The first derives of ξ as the dispersion parameter can be formulated by:

$$\begin{aligned}\frac{\partial \ln L(\boldsymbol{\theta}_{\text{PGIGR}})}{\partial \xi} &= \sum_{i=1}^{n} \frac{\partial}{\partial \xi}\left(\ln\left(\frac{\sqrt{\xi}}{K_{\gamma}(\varpi)}\right)+\ln\left(A_i B_i C_i\right)\right) \\ &= \sum_{i=1}^{n}\left(\left(-\frac{\partial\left(y_i \ln \xi\right)}{\partial \xi}+\frac{\partial}{\partial \xi}\left(\left(\frac{2y_i-1}{4}\right)\left(\ln\left(\sqrt{\tau^2+\xi^2}-\xi\right)+\ln \xi^2-\ln\left(2q_i e^{\mathbf{x}_i^{\mathrm{T}}\boldsymbol{\beta}}+\left(\sqrt{\tau^2+\xi^2}-\xi\right)\right)\right)\right)\right. \\ &+\frac{\partial}{\partial \xi}\left(\frac{1}{2}\ln(\xi)\right)-\frac{\partial}{\partial \xi}\left(\ln\left(K_{-\frac{1}{2}}\left(\sqrt{\tau^2+\xi^2}-\xi\right)\right)\right) \\ &\left.+\frac{\partial}{\partial \xi}\left(\ln\left(K_{y-\frac{1}{2}}\left(\sqrt{\left(2q_i e^{\mathbf{x}_i^{\mathrm{T}}\boldsymbol{\beta}}+\left(\sqrt{\tau^2+\xi^2}-\xi\right)\right)\left(\sqrt{\tau^2+\xi^2}-\xi\right)}\right)\right)\right)\right)\end{aligned} \tag{3}$$

Eqs. (12), (13), and (14) Setting the score equations to zero leads to implicit expressions that cannot be solved analytically. For this reason, we employ an iterative optimization scheme. We choose the BHHH method because it constructs an approximation to the Hessian matrix from the gradients, eliminating the requirement for second-order derivatives of the PGIGR parameters. Starting from initial parameter guesses, the algorithm updates the estimates iteratively to reach the maximum of the lnlikelihood, as described made up:

1. Establish the initial value for the parameter $\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(0)}=\left[\hat{\boldsymbol{\beta}}^{T(0)} \quad \hat{\tau}^{(0)} \quad \hat{\xi}^{(0)}\right]$. The initial value of parameter $\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(0)}$ is obtained while using the univariate Poisson Regression [30]. The initial value for dipersion parameter serves as a statistical measure that quantifies the relative spread of data by incorporating the variance and mean. The parameter τ it is defined as the difference between the variance and the mean, divided by the square of the mean [17]. This formulation enables dispersion to capture the balance between the data's variability and its central tendency, making it particularly useful for understanding proportional fluctuations in datasets where the mean holds significant relevance. Furthermore, the parameter ξ, defined as the square root of the variance, corresponds to the standard deviation of the distribution. Expressing dispersion through this parameter allows the variability to be measured in the same scale as the observed data, thereby providing a more interpretable measure of the average deviation from the mean.

2. Execute $\mathbf{g}(\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)})$ as the gradient vector which is the structure made up:
$$\mathbf{g}^{T}(\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)})=\left[\frac{\partial \sum_{i=1}^{n} \ln P(\boldsymbol{\theta}_{i,\text{PGIGR}})}{\partial \boldsymbol{\beta}} \quad \frac{\partial \sum_{i=1}^{n} \ln P(\boldsymbol{\theta}_{i,\text{PGIGR}})}{\partial \tau} \quad \frac{\partial \sum_{i=1}^{n} \ln P(\boldsymbol{\theta}_{i,\text{PGIGR}})}{\partial \xi}\right]_{\theta=\hat{\theta}_{(m)}}$$

3. Determine the Hessian matrix $\mathbf{H}(\hat{\boldsymbol{\theta}}^{(m)})$, whose elements consist of
$$\mathbf{H}(\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)})=-\sum_{i=1}^{n}\mathbf{g}_i(\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)})\mathbf{g}_i(\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)})^{T}, \mathbf{g}_i\left(\boldsymbol{\theta}_{\text{PGIGR}}\right)=\frac{\partial}{\partial \boldsymbol{\theta}_{\text{PGIGR}}}\left(\ln\left(\frac{\sqrt{\xi}}{K_{\gamma}(\varpi)}\right)+\ln\left(A_i B_i C_i\right)\right);$$
$$A_i=\frac{\left(q_i \exp\left(\mathbf{x}_i^{T}\boldsymbol{\beta}\right)\right)^{y_i}}{\xi^{y_i} y_i!}; B_i=\left(\frac{\varpi\xi^2}{2q_i \exp\left(\mathbf{x}_i^{T}\boldsymbol{\beta}\right)+\varpi}\right)^{\frac{2y_i-1}{4}}; C_i=K_{y_i+\gamma}\left(\sqrt{\varpi^2+2\varpi q_i \exp\left(\mathbf{x}_i^{T}\boldsymbol{\beta}\right)}\right).$$

4. The iterative process begins with $m=0$. The parameter vector is updated according to $\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m+1)}=\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)}-\mathbf{H}^{-1}\left(\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)}\right)\mathbf{g}(\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)})$ where $\hat{\boldsymbol{\theta}}_{\text{PGIGR}}{}^{(m)}$ denotes the parameter estimate at the m-th iteration. The updating procedure is repeated by increasing the iteration index $m=m+1$. Convergence is achieved when the difference between two successive estimates satisfies

The hypothesis testing of the PGIGR model was undertaken by the Maximum Likelihood Ratio Test (MLRT) method both simultaneously and partially. Simultaneous hypothesis testing is performed in order to determine the significance of the regression parameters in the model simultaneously with hypothesis:

$H_0: \beta_1=\beta_2=\ldots=\beta_p=0$

H_1: at least one $\beta_k \neq 0$,with $k=1,2,\ldots,p$.

Let Ω denote the parameter space of the PGIGR model in the population, defined as $\boldsymbol{\Omega}_{\text{PGIGR}} = \{\boldsymbol{\beta}, \tau, \xi\}$. Under the null hypothesis, the parameter vector is restricted to a subset $\omega \subset \Omega$, expressed as $\omega_{\text{PGIGR}} = \{\beta_{0\omega}, \tau_\omega, \xi_\omega\}$, which represents the parameter values specified by the null hypothesis. The likelihood function and its natural logarithm for the parameter set under the population are denoted respectively by the equations $L(\omega_{\text{PGIGR}})$. Subsequently, the logarithmic likelihood function $L(\omega_{\text{PGIGR}})$ is differentiated with respect to each parameter and equated to zero. The result of the first derivative for each parameter under H_0 is not in closed form, thus necessitating numerical iteration. The estimators for the parameters under H_0, is $\hat{\theta}_{\omega\text{PGIGR}}$ further, the odds ratio is determined as follows:

$$\Lambda_{\text{PGIGR}} = \frac{L(\widehat{\omega}_{\text{PGIGR}})}{L(\hat{\Omega}_{\text{PGIGR}})} < \Lambda_0, \text{ for } 0 < \Lambda_0 < 1.$$

This equation is equivalent to:

$$G^2_{\text{PGIGR}} = -{\Lambda_{\text{PGIGR}}}^2 = 2\left(\ell(\hat{\Omega}_{\text{PGIGR}}) - \ell(\widehat{\omega}_{\text{PGIGR}})\right), \tag{15}$$

Then, from Eq. (15) we construct the likelihood function and the log-likelihood function for a set of parameters under the null hypothesis. Find $L(\hat{\Omega}_{\text{PGIGR}}) = \max_{\Omega_{\text{PGIGR}}} L(\Omega_{\text{PGIGR}})$ and $L(\widehat{\omega}_{\text{PGIGR}}) = \max_{\omega_{\text{PGIGR}}} L(\omega_{\text{PGIGR}})$ using the MLE method to obtain the parameter estimator values under the population, namely β, τ, ξ and parameter estimator values under H_0 are $\beta_{0\omega}, \tau_\omega, \xi_\omega$.

The likelihood-ratio statistic G^2_{PGIGR} converges in distribution to a chi-square random variable with $p$degrees of freedom, i.e., $G^2_{\text{PGIGR}} \xrightarrow{d} \chi^2_p$. We reject H_0if the computed value exceeds the chi-square critical value at level α, namely if $G^2_{\text{PGIGR}} > \chi^2_{p,\alpha}$, with $p = n(\Omega) - n(\omega)$. When the joint test is significant, subsequent partial tests are conducted to determine which covariates contribute significantly. The partial hypotheses are stated as follows:

$H_0 : \beta_k = 0$

$H_1 : \beta_k \neq 0$,with k = 1, 2,.,p.

The test statistic used is:

$$Z_{PGIGR;k} = \frac{\hat{\beta}_k}{SE(\hat{\beta}_k)} \underset{n\to\infty}{\sim} N(0,1). \tag{16}$$

The standard error of the estimator $\hat{\beta}_k$ is obtained as $SE(\hat{\beta}_k) = \sqrt{\widehat{Var}(\hat{\beta}_k)}$. The variance–covariance matrix of the parameter estimates is derived from Eq. (6). Specifically, the variance of $\hat{\beta}_k$ corresponds to the k-th diagonal element of this matrix. Asymptotically, the covariance matrix can be approximated by the inverse of the Hessian matrix of the log-likelihood function, namely $\widehat{Cov}(\hat{\theta}_{\text{PGIGR}}) = -\hat{E}\left(H^{-1}(\hat{\theta}_{\text{PGIGR}})\right) \underset{n\to\infty}{\approx} -H^{-1}(\hat{\theta}_{\text{PGIGR}})$. The rejection region for $H_0$is determined by Eq. (16), where the test statistic satisfies $|Z_{\text{PGIGR;k}}| > Z_{\alpha/2}$with α representing the chosen significance level.

2.3 Testing the PGIG Distribution

The distribution test is conducted to determine whether the response data follows the PGIG distribution. This test evaluates the degree of discrepancy between the empirical and theoretical distribution functions. Suppose Y is a random variable. Let $F(y)$ denote the empirical distribution function based on a sample of Y, and let $F_0(y)$ represents the theoretical PGIG distribution function. The hypotheses to be tested are formulated as follows [31]:

H_0: $F(y) = F_0(y)$ (The empirical data follows the PGIG distribution).

H_1: $F(y) \neq F_0(y)$ (The empirical data does not follow the PGIG distribution).

3. RESULTS AND DISCUSSION

The following section presents the results of the study through the real-world application of the PGIGR model. The application of the PGIGR model to actual maternal mortality data from East Java is discussed, including the dataset's characteristics, descriptive statistics of the variables, goodness-of-fit tests, and parameter estimation. The findings are organized to address the research objectives systematically and to provide insights into the key determinants influencing maternal mortality.

The proposed model is implemented to analyze maternal mortality counts. The data were obtained from the East Java Health Profile 2023, which includes observations from 38 cities and regencies in East Java, Indonesia. In this study, the response variable is the number of maternal deaths. Maternal death is defined as the death of a woman while pregnant or within 42 days following the termination of pregnancy, irrespective of the duration or location of the pregnancy, due to causes related to or aggravated by the pregnancy or its management, excluding accidental or incidental causes.

The six predictor variables made up Percentage of iron supplementation/blood supplement tablets in Maternal (X_1), this variable represents the proportion of pregnant women who have consumed the recommended iron or multivitamin tablets during their pregnancy to prevent anemia and ensure maternal and fetal health, Percentage of Malnutrition Pregnant Women (X_2), the definition of this variables indicates the proportion of pregnant women who are classified as malnourished based on specific nutritional indicators. Percentage of Contraceptive users (X_3): the proportion of individuals, typically women of reproductive age, who actively participate in family planning programs, including the use of contraceptive methods to regulate births and manage reproductive health. Percentage of Antenatal care visits (X_4) is about the proportion of pregnant women who complete the recommended number of antenatal care visits during their pregnancy, as per national or international health guidelines. Percentage of Healthcare Professionals (X_5) reflects the proportion of healthcare professionals available in the population of pregnant women. It serves as an indicator of healthcare access and service availability. The percentage of proper sanitation (X_6) represents the proportion of households or individuals in a population with access to proper sanitation facilities, such as clean, functional toilets, which are critical for preventing disease and promoting overall public health [21]. The exposure variable, maternal count, is essential for comparing cities or municipalities.

Table 1. The Summary of Response Variables

Variable	Mean	Variance	Coefficient of Variation	Min	Max
Maternal Mortality (Y)	12.97	101.92	77	0	50

According to Table 1, the mean of the response variable descriptions is 12.97, and the coefficient of variation (CoV) is 77, a useful metric for this purpose, as illustrated in Figure 1, which illustrates the distribution of maternal mortality.

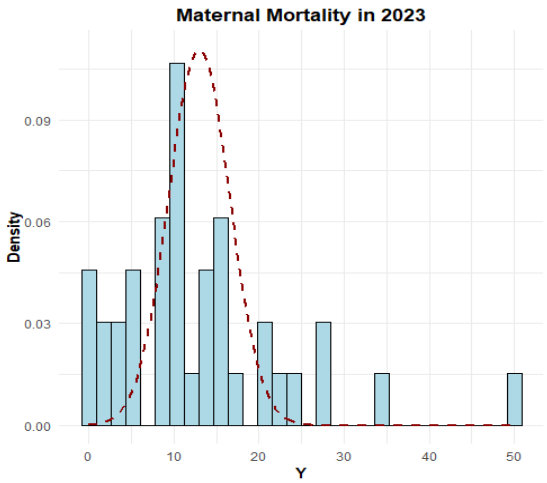

Figure 1. Histogram Response Variables

***Data source**: East Java Health Profile 2023; analysis performed using R version 4.3.3*

Table 2 presents the characteristics of each predictor presumed to influence neonatal and maternal mortality. The attributes of each predictor are detailed through the mean and standard deviation. As vital health indicators, achieving the specified targets for these predictors is crucial to improving overall health quality in Indonesia.

Table 2. Summary Statistics (Mean and Standard Deviation) for Predictor Variables Across Cities/Municipalities in East Java

Variable	X_1	X_2	X_3	X_4	X_5	X_6
Mean (SD)	81.66 (14.57)	45.08 (15.79)	59.88 (16.37)	78.04 (10.95)	19.53 (53.22)	92.35 (7.88)

***Data source**: East Java Health Profile 2023; analysis performed using R version 4.3.3*

Based on the Cramér-von Mises Test [28] in Figure 2 test results, the hypothesis that the empirical data follows the PGIG distribution cannot be rejected. The computed W^2 statistic, which represents the maximum difference between the empirical CDF and the theoretical CDF of the PGIG distribution, was calculated to be 0.086. The critical D value at a 5% significance level ($\alpha = 0.05$) was found to be 0.1902. Since the D value is smaller than the critical D value, we fail to reject the null hypothesis (H_0), which suggests that the empirical data follows the PGIG distribution. This indicates that the PGIG distribution is a suitable model for the data under analysis at a 95% confidence level.

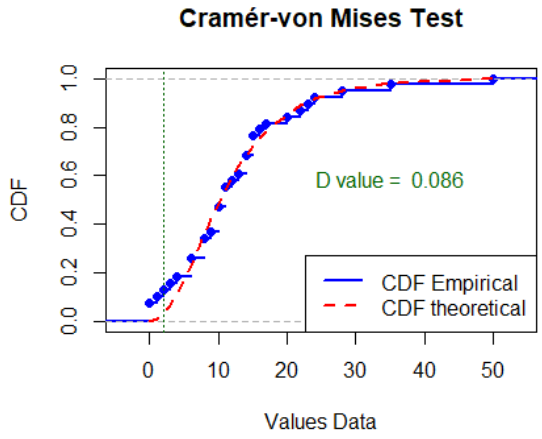

Figure 2. PGIG Distribution Test

***Data source**: East Java Health Profile 2023; analysis performed using R version 4.3.3*

Table 3 provides the initial parameter values used in estimating the PGIGR model, where $\boldsymbol{\beta}$ is the coefficient from the Poisson Regression Model, and τ and ξ are the dispersion parameters used in numerical iteration.

Table 3. Initial Value of PGIGR Parameter Model

Parameter	Initial Value
β_0	-6.950453181
β_1	-0.011879532
β_2	0.025191120
β_3	0.005677316
β_4	-0.023889631
β_5	0.062519436
β_6	0.009536554
τ	11.003026355
ξ	1.000000000

The PGIGR model was applied to determine which explanatory variables significantly influence the response variable. The estimated parameters for the model, involving one response variable and six explanatory variables, are presented in Table 4. The statistical significance of each predictor is evaluated using the corresponding p-values associated with the parameter estimates.

We fitted the PGIGR model to evaluate the effects of six predictors on the response variable. The estimated parameters are reported in Table 4, and statistical significance for each covariate is assessed using the corresponding p-values. Model adequacy is further examined via a likelihood-ratio test derived from the

MLRT framework. The obtained statistic is 1351.03, which exceeds the χ^2 critical value of 12.59 for 6 degrees of freedom at $\alpha = 0.05$. Therefore, the null hypothesis is rejected, indicating that the six predictors jointly have a significant association with the response.

The parameter estimation results of the PGIGR model indicate that several factors significantly influence MMR. The negative coefficient for the intercept serves as the baseline, while the variables that follow demonstrate notable relationships with maternal mortality. A 1% increase in zinc tablet consumption for pregnant women is associated with a decrease in maternal mortality, highlighting the importance of nutrition.

A higher proportion of malnourished pregnant women is linked to an increase in maternal mortality, highlighting the pivotal role of adequate maternal nutrition. Both contraceptive users' participation and the availability of healthcare professionals exhibit negative associations with maternal mortality, reinforcing the importance of accessible health services and effective contraceptive users' interventions. Notably, the positive effect observed for antenatal care visits suggests that a greater number of completed visits may correspond with slightly higher maternal mortality, indicating the need for further examination into the quality and outcomes of antenatal care.

Table 4. Parameter Estimation of PGIGR model

Parameter	Estimate	SE	Z	p-Value
β_0	-6.8202	0.0006	-11366.9933	0.0000
β_1	-0.0133	0.0009	-14.7306	0.0000
β_2	0.0262	0.0012	21.8639	0.0000
β_3	0.0065	0.0007	9.3279	0.0000
β_4	-0.0251	0.0010	-25.1453	0.0000
β_5	0.0627	0.0007	89.6554	0.0000
β_6	0.0115	0.0034	3.3995	0.0007
τ	1.9225	0.0001	19225.1510	0.0000
ξ	0.7336	0.0212	34.5970	0.0000

Moreover, a greater percentage of proper sanitation is significantly associated with reduced maternal mortality, underlining the role of improved sanitation in safeguarding maternal health. The dispersion parameters, τ and ξ, characterize the model's shape and sensitivity, lending additional support to the significance of the included predictors. Collectively, these results demonstrate the necessity of a comprehensive, multidimensional strategy to address and reduce maternal mortality effectively. Moreover, the finding that a higher percentage of proper sanitation is significantly associated with reduced maternal mortality is consistent with numerous studies highlighting the critical role of sanitation in maternal health. Improved sanitation reduces exposure to infectious diseases and prevents complications during pregnancy and childbirth, which are major contributors to maternal mortality. This aligns with research by [32] and [33], which emphasize sanitation as a key determinant of maternal outcomes.

The model's dispersion parameters, which define its shape and sensitivity, further reinforce the robustness of the analysis. Similar modeling approaches in previous studies have demonstrated that accounting for dispersion improves the accuracy of predictions of maternal health outcomes [34]. Such parameters help capture variability and highlight important predictors that might otherwise be overlooked.

Together, these results underscore the importance of adopting a comprehensive, multi-dimensional approach that includes sanitation improvements alongside other healthcare interventions. This approach echoes global health frameworks that advocate integrated strategies to reduce maternal mortality by combining environmental, social, and medical factors.

4. CONCLUSION

Overall, the PGIGR model is an evolution of the Sichel regression model. In this research context, the PGIGR model accounts for dispersion by incorporating exposure variables that reflect each unit's quality. The model provides consistently reliable results using MLE and the BHHH optimization algorithm.

Author Contributions

Yusrianti Hanike: Conceptualization, Methodology, Software, Visualization, Writing – Original Draft. Purhadi: Conceptualization, Methodology, Validation, Supervision, Writing – Review and Editing. Achmad Choiruddin: Conceptualization, Methodology, Validation, Supervision, Writing – Review and Editing. All authors discussed the results and contributed to the final manuscript.

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Declarations

The authors declare that no conflicts of interest related to this study.

Declaration of Generative AI and AI-assisted Technologies

AI-assisted technology (ChatGPT) was used to support sentence restructuring and clarity improvements. The authors confirm that the underlying ideas, arguments, data analyses, and conclusions are original and were not generated by AI. All AI-assisted edits were critically reviewed and validated by the authors.

Declaration of Generative AI and AI-assisted technologies

Generative AI tools (e.g., ChatGPT) were used solely for language refinement (grammar, spelling, and clarity). The scientific content, analysis, interpretation, and conclusions were developed entirely by the authors. The authors reviewed and approved all final text.

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