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Bivariate Inverse Gaussian Regression on Stunting and Malnutrition in Children

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Abstract

Background: *Research on Bivariate Inverse Gaussian Regression (BIGR) as a multivariate model is currently limited to theoretical applications. Furthermore, no studies have addressed BIGR parameter estimation using optimization methods like Broyden-Fletcher-Goldfarb-Shanno (BFGS). Meanwhile, a robust analysis is needed to identify the driving factors of child stunting and malnutrition in Central Java, given their fluctuating rates. Since stunting and malnutrition are inherently correlated, BIGR provides an appropriate joint modeling for this context.*
Objective: *The purpose of this study is to identify the contributing variables to stunting and malnutrition in children with BIGR.*
Methods: *The analysis transitions from a univariate Inverse Gaussian Regression (IGR) to a BIGR framework to effectively capture the inherent dependency between the two nutritional deficiencies. Parameter estimation was performed via Maximum Likelihood Estimation (MLE), where the non-linear log-likelihood functions were numerically optimized using the BFGS.*
Results: *Based on the BIGR model, the correlation coefficient between stunting and malnutrition in children was 0.48, reflecting a relatively strong correlation between the two conditions. Additionally, BIGR outperformed the independent IGR model due to its smaller AIC. The model further revealed that the number of infants with early initiation of breastfeeding is the primary driving factor for both stunting and malnutrition.*
Conclusion: *BIGR modeling results show that the factors causing stunting and child malnutrition in Central Java are the number of infants with early initiation of breastfeeding.*

Keywords : *BIGR, BFGS, Stunting, Malnutrition in Children.*

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Abstrak

Latar Belakang: Penelitian Regresi Bivariat Invers Gaussian (BIGR) sebagai model multivariat saat ini masih terbatas pada teori. Selain itu, belum ada penelitian yang membahas estimasi parameter BIGR menggunakan metode optimasi seperti Broyden-Fletcher-Goldfarb-Shanno (BFGS). Di lain pihak, analisis yang kuat sangat diperlukan untuk mengidentifikasi faktor penyebab stunting dan malnutrisi pada anak di Jawa Tengah, mengingat angkanya berfluktuasi. Karena stunting dan malnutrisi secara inheren saling berkorelasi, BIGR menyediakan pemodelan bersama yang tepat untuk konteks ini.
Tujuan: Tujuan penelitian ini adalah mengidentifikasi variabel yang berpengaruh terhadap *stunting* dan malnutrisi pada anak dengan BIGR.
Metode: Analisis transisi dari Regresi Univariat Invers Gaussian (IGR) ke BIGR digunakan untuk menangkap ketergantungan antara kedua masalah kekurangan gizi tersebut secara efektif. Estimasi parameter dilakukan dengan *Maximum Likelihood Estimation* (MLE), di mana fungsi log-likelihood non-linear dioptimalkan secara numerik menggunakan BFGS.
Hasil: Berdasarkan model BIGR, koefisien korelasi antara persentase *stunting* dan malnutrisi pada anak sebesar 0,48, yang mencerminkan korelasi yang relatif kuat antara kedua kondisi tersebut. Selain itu, BIGR berkinerja lebih baik daripada GR karena memiliki nilai AIC yang lebih kecil. Model tersebut lebih lanjut menyatakan bahwa jumlah bayi yang mendapatkan inisiasi menyusu dini merupakan faktor pendorong bagi *stunting* maupun malnutrisi.
Kesimpulan: Hasil pemodelan BIGR menunjukkan bahwa faktor penyebab *stunting* dan malnutrisi pada anak di Jawa Tengah adalah jumlah bayi yang mendapat inisiasi menyusu dini.

Kata kunci: BIGR, BFGS, Stunting, Malnutrisi pada Anak.

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INTRODUCTION

Multivariate statistics is very important in analyzing social research that requires many variables (Finch, 2016). Multivariate analysis offers a deeper and more comprehensive approach than univariate analysis because it can examine the complex interrelationships and dependencies among numerous variables simultaneously, rather than analyzing them in isolation. In a regression framework, when multiple response variables exhibit structural dependencies, evaluating them jointly significantly enhances the statistical power and prevents the loss of crucial covariance information that univariate models inherently ignore (Roustaei, 2024)

According to the Report on The Acceleration of Stunting Reduction Implementation in Central Java, the percentage of stunting in Central Java will decrease 0.1% in 2022. However, in 2023 it increased 1%, and in 2024 it fell again by 0.1% (Wati & Musnadi, 2022). This fluctuating condition makes it necessary to know the factors that impact stunting and malnutrition in children.

Stunting and malnutrition in children are two health conditions caused by poor and unbalanced nutritional intake according to a child's age and growth that impact a child's overall growth and health (Bahar et al., 2024). A long-term loss of nutritional intake, usually brought on by eating food that is not in line with nutritional demands, can result in stunting, a chronic nutritional issue (Kementerian Kesehatan, 2018). The disease known as stunting occurs when a toddler suffers from growth abnormalities and falls short of the average height for their age due to prolonged malnutrition (Khoiriyah & Ismarwati, 2023). Human development can take place inside an already-existing fetus and only manifests when the toddler is two years old. While malnutrition in children is a condition where the child's weight according to length or height is lower than the normal range for children of his age (Tim Medis Siloam Hospitals, 2024).

Stunting and malnutrition are two conditions of nutritional deficiency with the same cause. One of the causes of stunting is bad nutrition for the mother and child (Suyantri et al., 2024). Apart from children, mothers play an important role in supporting children's health. From the womb until the child experiences growth in the world, the nutrition given by the mother really supports the child's health, including the occurrence of stunting and malnutrition (Jusni et al., 2024). Besides the mother, the condition of the baby also influences the occurrence of stunting. The result of research from Qusrinie et al. (2024) stated that the baby's birth weight and exclusive breastfeeding contributed to the condition of stunting. Likewise, malnutrition is caused by factors such as inadequate nutritional intake and infectious diseases such as diarrhea (Sari et al., 2023). Therefore, a model is needed that can analyze both cases together.

Modeling stunting and malnutrition data jointly presents unique statistical challenges. These epidemiological indicators seldom follow a normal distribution (Nisa & Maulina, 2024); rather, they are an exponential family with data in the form of positive continuous, such as inverse Gaussian (Morita et al., 2021). The plot tilts to the right since the data is consistently positive (Hu et al., 2025). Both stunting and malnutrition percentage data can be disseminated IG since they have a plot that is skewed to the right. The Bivariate Inverse Gaussian (BIG) model is employed to capture the dependency between stunting and malnutrition in the analysis.

The BIG distribution extends IG to accommodate two interdependent response variables (Hu et al., 2025). The BIG was theoretically introduced in early statistical literature, followed by recent advancements that explain the parameter estimation for BIG distribution and its computational

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frameworks (Morita et al., 2021; Chen et al., 2022). Feng et al. studied the form of the bivariate inverse Gaussian probability density function and produced two forms. The first form was obtained from the joint distribution of the first passage time of a Wiener process, and the second form from the marginal function combined with the correlation coefficient (Feng et al., 2025).

In previous research, there was no application of data. Hanagal & Pandey (2020) still use the univariate inverse Gaussian to model survival data. Furthermore, existing studies on IG models rely heavily on standard, restrictive estimation techniques. Goward et al. (2025) estimate parameters of IG with Bayesian. There is a glaring research gap regarding the performance of advanced numerical optimization techniques like Broyden-Fletcher-Goldfarb-Shanno (BFGS). Moreover, there has been no research on the use of BIG with BFGS. Consequently, this research will be novel because it will examine BIG both in inference statistics with BFGS and application to data.

The application of BIG will be more useful if the regression is modelled. One useful parameter estimation method is Maximum Likelihood Estimation (MLE). MLE often produces a non-closed form, which requires further numerical calculations. A numerical method is needed that can solve non-linear MLE results, such as BFGS. Nisa & Miasary (2024) applied Broyden-Fletcher-Goldfarb-Shanno (BFGS) to continue the parameter estimation process on univariate RIG. Furthermore, Auliarahmi et al. (2025) also used BFGS to estimate parameters in bivariate Poisson generalized inverse Gaussian regression because it is efficient and does not require second derivatives. Moreover, this paper will apply bivariate inverse Gaussian regression (BIGR) with BFGS on stunting and malnutrition data in Central Java.

METHOD

This research was designed quantitatively, starting with inverse Gaussian regression modeling and continuing with bivariate inverse Gaussian regression modeling.

Research Design

BIGR is a development of IGR. To ensure BIGR is appropriately applied to stunting and malnutrition in children, it is necessary to match the inverse Gaussian distribution and the bivariate inverse Gaussian distribution. A family of two-parameter exponentials with non-negative continuous random variables is the Inverse Gaussian (IG) distribution, sometimes referred to as the Wald distribution. Schrowdinger and Smoluchowski initially investigated the Inverse Gaussian distribution in connection with Brownian motion (Chhikara & Folks, 2024). Assume that if a continuous random variable Y fulfills the probability density function, it has an inverse Gaussian distribution with μ location and λ scale parameters.

$$f(y;\mu;\lambda) = \begin{cases} \left(\dfrac{\lambda}{2\pi y^3}\right)^{1/2} exp\left(-\dfrac{\lambda(y-\mu)^2}{2\mu^2 y}\right), & y>0,\mu>0 \\ 0 & , \quad y \text{ others} \end{cases} \tag{1}$$

Data with an inverse Gaussian distribution is never negative, so that the distribution curve is positively skewed (Hu et al., 2025). Usually applied in the field of survival, such as patient resistance to disease, and machine resistance. The bivariate inverse Gaussian is a multivariate form of the IG distribution. An IG distribution with two positive continuous variables is called a bivariate inverse Gaussian. Suppose y_1 and y_2 follow an Inverse Gaussian distribution with location parameters μ and scale parameters λ so that the probability density function is as follows (Chen et al., 2022):

$$f(y_1,y_2)=f(y_1)f(y_2)\left[1+\rho(y_1-\mu_1)(y_2-\mu_2)h(y_1)h(y_2)\right] \quad (2)$$

with ρ is the correlation coefficient between the response variables, μ_1 location parameters for y_1, μ_2 location parameters for y_2, λ_1 shape parameter for y_1, λ_2 shape parameter for y_2 and h function is the modification of the dependency between the response variables. Furthermore, the bivariate inverse Gaussian probability density function is

$$f(y_1,y_2)=\frac{1}{2\pi}\left(\frac{\lambda_1\lambda_2}{y_1^3y_2^3}\right)^{\frac{1}{2}}\exp\left[-\left(\frac{\lambda_1(y_1-\mu_1)^2}{2\mu_1^2y_1}+\frac{\lambda_2(y_2-\mu_2)^2}{2\mu_2^2y_2}\right)\right]$$
$$\left[1+\rho(y_1-\mu_1)(y_2-\mu_2)\exp\left[-\frac{\lambda_1(y_1-\mu_1)^2}{2\mu_1^2y_1}+\frac{\lambda_2(y_2-\mu_2)^2}{2\mu_2^2y_2}\right]\right] \quad (3)$$

with $y_l>0,\mu_l>0,\lambda_l>0,\ \ l=1,2$

Inverse Gaussian regression is a generalized linear model (GLM) from the exponential family. GLM is formed from three components, namely random variables y follows exponential family distribution, linear predictors, and a link function that connects random variables and linear predictors (Surjanovic et al., 2024;, Jo et al., 2021). One of the link functions that is often used by the exponential distribution is the natural logarithm link function (Jahan et al., 2016). Suppose x predictor variable, β is the regression parameter, and k is the number of parameters, so probability density function for IGR (Nisa & Maulina, 2024) is

$$f(y_i)=\left(\frac{\lambda}{2\pi y_i^3}\right)^{1/2}\exp\left(\frac{-\lambda\left(y_i-\exp\left(\mathbf{x}_i^T\boldsymbol{\beta}\right)\right)^2}{2\left(\exp\left(\mathbf{x}_i^T\boldsymbol{\beta}\right)\right)^2y_i}\right) \quad (4)$$

If one response variable is added, it will become BIGR with the following link function, like Equation (5).

$$\begin{aligned}\mu_i&=\exp(\beta_0+\beta_1x_{i1}+\beta_2x_{i2}+\ldots+\beta_kx_{ik})\\&=\exp\left(\mathbf{x}_i^T\boldsymbol{\beta}\right)\end{aligned} \quad (5)$$

with $i=1,2,\ldots,n$.

Therefore, Equation (3) can be written completely as follows.

$$f(y_1,y_2)=\frac{1}{2\pi}\left(\frac{\lambda_1\lambda_2}{y_1^3y_2^3}\right)^{\frac{1}{2}}\exp\left[-\left(\frac{\lambda_1\left(y_1-\exp\left(x_i^T\boldsymbol{\beta}\right)_1\right)^2}{2\exp\left(x_i^T\boldsymbol{\beta}\right)_1^2y_1}+\frac{\lambda_2\left(y_2-\exp\left(x_i^T\boldsymbol{\beta}\right)_2\right)^2}{2\exp\left(x_i^T\boldsymbol{\beta}\right)_2^2y_2}\right)\right]$$
$$\left[\begin{array}{l}1+\rho\left(y_1-\exp\left(x_i^T\boldsymbol{\beta}\right)_1\right)\left(y_2-\exp\left(x_i^T\boldsymbol{\beta}\right)_2\right)\\ \exp\left[-\left(\frac{\lambda_1\left(y_1-\exp\left(x_i^T\boldsymbol{\beta}\right)_1\right)^2}{2\exp\left(x_i^T\boldsymbol{\beta}\right)_1^2y_1}+\frac{\lambda_2\left(y_2-\exp\left(x_i^T\boldsymbol{\beta}\right)_2\right)^2}{2\exp\left(x_i^T\boldsymbol{\beta}\right)_2^2y_2}\right)\right]\end{array}\right] \quad (6)$$

The BIGR parameter estimation process uses Maximum Likelihood Estimation (MLE). This strategy is based on the MLE method, which yields unbiased parameters (Awasthi et al., 2022). It begins by determining the likelihood function, then resolving the natural logarithm of the likelihood function from Equation (6) as follows.

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$$\ln L(y_1,y_2)=\ln\left[\prod_{i=1}^{n}\left[\frac{1}{2\pi}\left(\frac{\lambda_1\lambda_2}{y_1^3y_2^3}\right)^{\frac{1}{2}}\exp\left[-\left(\frac{\lambda_1\left(y_1-\exp\left(x_i^T\boldsymbol{\beta}\right)_1\right)^2}{2\exp\left(x_i^T\boldsymbol{\beta}\right)_1^2 y_1}+\frac{\lambda_2\left(y_2-\exp\left(x_i^T\boldsymbol{\beta}\right)_2\right)^2}{2\exp\left(x_i^T\boldsymbol{\beta}\right)_2^2 y_2}\right)\right]\left[1+\rho\left(y_1-\exp\left(x_i^T\boldsymbol{\beta}\right)_1\right)\left(y_2-\exp\left(x_i^T\boldsymbol{\beta}\right)_2\right)\exp\left[-\left(\frac{\lambda_1\left(y_1-\exp\left(x_i^T\boldsymbol{\beta}\right)_1\right)^2}{2\exp\left(x_i^T\boldsymbol{\beta}\right)_1^2 y_1}+\frac{\lambda_2\left(y_2-\exp\left(x_i^T\boldsymbol{\beta}\right)_2\right)^2}{2\exp\left(x_i^T\boldsymbol{\beta}\right)_2^2 y_2}\right)\right]\right]\right]\right] \tag{7}$$

The next step is to solve the first derivative of each parameter. If the results are not close, a numerical analysis such as the Broyden-Fletcher-Goldfarb-Shanno (BFGS) method is used. The BFGS, as a quasi-Newton method, offers high computational convergence and stability without requiring the explicit calculation of the second-order derivative (Hessian) matrix, which is notoriously intractable in bivariate non-normal frameworks (Mishra et al., 2020). The BFGS algorithm can be outlined as follows (Yuan et al., 2025):

1. Begin with a specified starting point $\boldsymbol{\gamma}_0$, an inverse Hessian matrix $\mathbf{H}(\boldsymbol{\gamma}_0)$, a convergence tolerance ε greater than 0, and m to 0 when $\boldsymbol{\gamma}_0$ is $\boldsymbol{\gamma}=\begin{bmatrix}\beta_0\\ \beta_1\\ \beta_2\\ \beta_3\\ \beta_4\\ \lambda\end{bmatrix}$ on iteration $m=0$.
2. Determine
$$\mathbf{g}(\boldsymbol{\gamma}_m)=\begin{bmatrix}\dfrac{\partial \ln L(\boldsymbol{\beta},\lambda|y_1,y_2,\ldots,y_n)}{\partial\boldsymbol{\beta}^T}\\ \dfrac{\partial \ln L(\boldsymbol{\beta},\lambda|y_1,y_2,\ldots,y_n)}{\partial\lambda}\end{bmatrix}.$$
If $\|\mathbf{g}(\boldsymbol{\gamma}_m)\|<\varepsilon$ the iteration stops and vice versa $\|\mathbf{g}(\boldsymbol{\gamma}_m)\|>\varepsilon$ to the next step.
3. Compute $\mathbf{p}_m=-\mathbf{H}^{-1}(\boldsymbol{\gamma}_m)\,\mathbf{g}(\boldsymbol{\gamma}_m)$ with $\mathbf{p}_m$ a *search direction vector* in *m iteration*,
$$\mathbf{H}(\boldsymbol{\gamma}_m)=\begin{bmatrix}\dfrac{\partial^2 \ln L(\boldsymbol{\beta},\lambda|y_1,y_2,\ldots,y_n)}{\partial\boldsymbol{\beta}^T\partial\boldsymbol{\beta}} & \dfrac{\partial^2 \ln L(\boldsymbol{\beta},\lambda|y_1,y_2,\ldots,y_n)}{\partial\boldsymbol{\beta}^T\partial\lambda}\\ \dfrac{\partial^2 \ln L(\boldsymbol{\beta},\lambda|y_1,y_2,\ldots,y_n)}{\partial\lambda\partial\boldsymbol{\beta}^T} & \dfrac{\partial^2 \ln L(\boldsymbol{\beta},\lambda|y_1,y_2,\ldots,y_n)}{\partial\lambda^2}\end{bmatrix}$$
4. Compute $\alpha_m=-\dfrac{\mathbf{g}^T(\boldsymbol{\gamma}_m)\,\mathbf{p}_m}{\mathbf{p}_m^T\mathbf{p}_m}$ with the objective of satisfying the Wolfe conditions:
Sufficient decrease condition:
$$\ln L(\boldsymbol{\gamma}_m+\alpha_m\mathbf{p}_m)<\ln L(\boldsymbol{\gamma}_m)+c_1\,\alpha_m\,\mathbf{g}^T(\boldsymbol{\gamma}_m)\,\mathbf{p}_m$$
Curvature condition:
$$\mathbf{g}(\boldsymbol{\gamma}_m+\alpha_m\mathbf{p}_m)^T\,\mathbf{p}_m\ge c_2\,\mathbf{g}^T(\boldsymbol{\gamma}_m)\,\mathbf{p}_m.$$
5. Determine $\boldsymbol{\gamma}_{m+1}=\boldsymbol{\gamma}_m+\alpha_m\mathbf{p}_m$, $\mathbf{s}_m=\boldsymbol{\gamma}_{m+1}-\boldsymbol{\gamma}_m$, and $\mathbf{d}_m=\mathbf{g}(\boldsymbol{\gamma}_{m+1})-\mathbf{g}(\boldsymbol{\gamma}_m)$
6. Compute
$$\mathbf{H}(\boldsymbol{\gamma}_{m+1})=\left(\mathbf{I}-\frac{\mathbf{s}_m\mathbf{d}_m^T}{\mathbf{d}_m^T\mathbf{s}_m}\right)\mathbf{H}(\boldsymbol{\gamma}_{m+1})\left(\mathbf{I}-\frac{\mathbf{d}_m\mathbf{s}_m^T}{\mathbf{d}_m^T\mathbf{s}_m}\right)+\frac{\mathbf{s}_m\mathbf{s}_m^T}{\mathbf{d}_m^T\mathbf{s}_m}$$
7. Return to step 2 with $m=m+1$

Population and Sample

Secondary data from the Central Java Statistics Agency (BPS) and the public health office were used in this study, specifically data on stunting and malnutrition among children from 35 districts/cities in Central Java in 2024.

Sampling Techniques

Because all districts/cities in Central Java were used as samples in this study and there was homogeneity, the sampling technique used was saturated sampling (Bouncken et al., 2026; Hennink & Kaiser, 2022).

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Research Subjects

The variables used consist of three response variables and five predictor variables, detailed in Table 1.

Table 1. Response and Predictor Variables

Variable	Annotation
Y_1	Percentage of stunting cases
Y_2	Percentage of malnutrition cases in children
X_1	Number of infants with early initiation of breastfeeding
X_2	Number of infants with exclusive breastfeeding
X_3	Low birth weight cases
X_4	Number of toddlers with diarrheal infections
X_5	Number of pregnant women consuming iron supplements

The percentage of stunting and malnutrition as response variables in BIGR, because the data is continuously positive, and the plot is skewed to the right. The determination of predictor variables in this study is based on the findings of previous studies, which state that there is a correlation between response and predictor factors listed in Table 1.

Data Analysis Techniques

This research has the following stages:

1. Univariate goodness of fit test
   To ensure that the data used has a bivariate inverse Gaussian distribution, a Kolmogorov-Smirnov (KS) distribution goodness-of-fit test is performed. The KS test is a more powerful test than the Chi-Square test and is appropriate for use when the population has a specific distribution (Ahadi & Zain, 2023). $F(y)$ is the empirical distribution function and $F_0\ (y)$ is the theoretical distribution function. In this study, the inverse Gaussian distribution function, then the hypothesis tested is as follows:

   $H_0: F(y) = F_0(y)$ (the data follows an inverse Gaussian distribution)
   $H_1: F(y) \neq F_0(y)$ (the data does not follow an inverse Gaussian distribution)

   The Kolmogorov-Smirnov test statistic is based on the largest vertical distance between $S(y)$ the probability distribution function based on the sample data and $F_0(y)$ the theoretical distribution function.

   $$D = \sup[F_0(y) - S(y)]$$

   H_0 is rejected if $D > D_{(\alpha,n)}$ with α is significant level.

2. Bivariate goodness of fit test
   Goodness of fit test in multivariate (also bivariate) also uses KS because it remains powerful (Jo et al., 2021) although it is a bit difficult when there is more than one variable. The KS test on multivariate is developed by transforming the multivariate distribution to an univariate distribution (Cui et al., 2025). The following is a hypothesis in the bivariate inverse Gaussian:

   $H_0: F(y_1, y_2) = F_0(y_1, y_2)$ (the data follows the bivariate inverse Gaussian distribution)
   $H_1: F(y_1, y_2) \neq F_0(y_1, y_2)$ (the data does not follow the bivariate inverse Gaussian distribution).

   Cui et al. (2025) recommend transforming multivariate random variables into a uniform distribution. Suppose $u_1 = F(y_1)$ and $u_2 = F(y_2)$. $G_n(u_1, u_2)$ are the empirical distribution function of the uniform 0-1 transformed sample $F(y_1, y_2)$, and $S(u_1, u_2)$ is the probability distribution function based on the sample data, so that the test statistic is

   $$D_n = \sup[G_n(u_1, u_2) - S(u_1, u_2)]$$

   With α is significant level. H_0 is rejected if $D_n > D_{(\alpha,n)}$ (Difinubun et al., 2023)

3. Detecting multicollinearity
   In a linear model or General Linear Model, such as BIGR, there is a condition where

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there is a relationship between predictor variables that can have a negative impact on research results, which is called multicollinearity (Dalal, 2023). Detecting multicollinearity through the Variance Inflation Factor (VIF). If VIF < 10, multicollinearity does not occur (Shrestha, 2020). VIF value is obtained from the calculation of the coefficient of determination R^2 as follows

$$VIF = \frac{1}{1-R^2}$$

4. Checking for correlation between response variables
   In addition to checking the correlation between predictor variables, it is also necessary to test the correlation between response variables. Unlike checking for multicollinearity, here a correlation is expected between response variables. The null hypothesis is $\rho = 0$. It means there is no correlation between responses, while the alternative hypothesis states there is a correlation between responses. The correlation test used is the Spearman correlation, which is a nonparametric correlation (Hawkins, 2019). Where n is the number of ordered pairs and d denotes the difference between the two levels, the Spearman correlation coefficient formula is as follows (Al-Hameed, 2022):

$$\rho_s = 1 - \frac{6\sum d^2}{n(n^2-1)}$$

5. IGR parameter estimation
   This parameter estimation uses MLE followed by BFGS if not closed form.
6. IGR parameter testing
   IGR parameter testing was carried out simultaneously with the Maximum Likelihood Ratio Test (MLRT) (Nurhikmah & Supandi, 2025) and partially with the Z test. MLRT simultaneous parameter testing with the following hypothesis

   $H_0: \beta_1 = \beta_2 = ... = \beta_k = 0$ (all parameters are significant simultaneously)

   H_1 : At least one $\beta_j \neq 0$, $j = 1, 2, ..., k$ (at least one parameter is not significant simultaneously)

   Suppose statistics test G^2, likelihood function under population H₁ $L(\widehat{\omega})$, and likelihood function under population H₀ $L(\widehat{\Omega})$.

$$G^2 = -2ln\Lambda = -2\ln\left(\frac{L(\widehat{\omega})}{L(\widehat{\Omega})}\right)$$

   The likelihood ratio is approximated by a chi-square distribution so that the null hypothesis is rejected when $G^2 > \chi^2_{k,\alpha}$.

   Partial parameter hypothesis testing using the Z test with a standard normal distribution approach (Nisa & Maslihah, 2024). If the null hypothesis is that the parameter is not partially significant, then the alternative hypothesis is that the parameter is partially significant.

$$Z = \frac{\beta}{SE(\beta)}$$

   with *SE* is standard error.
7. Determining the best IGR model with AIC
   Determining the best model from several models obtained using Akaike's Information Criterion (AIC). The smallest AIC value indicates the best model (Nisa & Muanalifah, 2021; Putri et al., 2021). One advantage of utilizing AIC is that it already includes a big number of predictor variables, which is highly helpful in choosing the best regression model (Nisa & Maulina, 2024). However, for small samples, $k > \frac{n}{k}$ with n sample size and k number of parameters to prevent overfitting, AIC is developed into the corrected AIC (AIC_c). The corrected AIC with the following formula (Portet, 2020)

$$AIC_c = AIC + \frac{2k(k+1)}{n-k-1}$$

   with $AIC = -2\ln L(.) + 2k$

   $L(.)$: likelihood function

k : number of parameters

8. BIGR parameter estimation
9. BIGR parameter testing
10. Determining the best BIGR model with AIC

RESULTS AND DISCUSSION

The first step in the analysis is to test the suitability of the univariate data distribution. Here is the hypothesis.

H_0: Data on the number of stunting or malnutrition cases in children follow an inverse Gaussian distribution.

H_1: Data on the number of stunting or malnutrition cases in children does not follow an inverse Gaussian distribution

Using KS, the test statistic values for variables Y_1 and Y_2 are written in Table 2.

Table 2. Kolmogorov Smirnov test statistic

Response variable	D	$D_{(0.05,35)}$
Y_1	0.030274	0.2299
Y_2	0.014378	0.2299

Table 2 informs that for both Y_1 and Y_2, $D > D_{(0.05,35)}$ (0.030274 < 0.2299 for Y_1 and 0.014378 < 0.2299 for Y_2). It concludes that H_0 failed to be rejected. In other words, the data for the number of stunting (Y_1) and number of malnutrition in children (Y_2) are distributed inverse Gaussian.

When univariate data has an inverse Gaussian distribution, it is not necessarily also distributed bivariately inverse Gaussian, so its suitability needs to be tested. The bivariate data fit test also uses KS, but KS has been developed for multivariate cases. The null hypothesis is that the data on stunting and malnutrition in children have an inverse Gaussian bivariate distribution, and the alternative hypothesis is vice versa. From the calculation of the D value obtained, it is 0.0096427. This value is smaller than $D_{(0.05,35)}$, so that H_0 fails to be rejected. This means that the bivariate data of stunting and malnutrition simultaneously follows a bivariate inverse Gaussian (BIG) distribution.

To model BIG, first ensure that the predictor variables are independent. There is no multicollinearity. Below are the VIF values for each predictor variable.

Table 3. VIF for each predictor variable

Predictor variable	VIF
X_1	1.189
X_2	1.147
X_3	1.293
X_4	1.521
X_5	1.262

Based on Table 3, the VIF value for each variable is less than 10, which indicates that there is no multicollinearity. The variables of the number of babies with early initiation of breastfeeding, the number of babies with exclusive breastfeeding, the birth weight of babies, diarrheal disease in toddlers, and the number of pregnant women consuming blood supplement tablets are independent.

As previously explained, BIGR is formed from the marginal IGR, also known as Univariate IGR probability density function, and a dependency function between the response variable. Furthermore, it will be analyzed comprehensively, starting with univariate IGR. Stunting and malnutrition data in children will each be modeled with IGR and analyzed visually as follows.

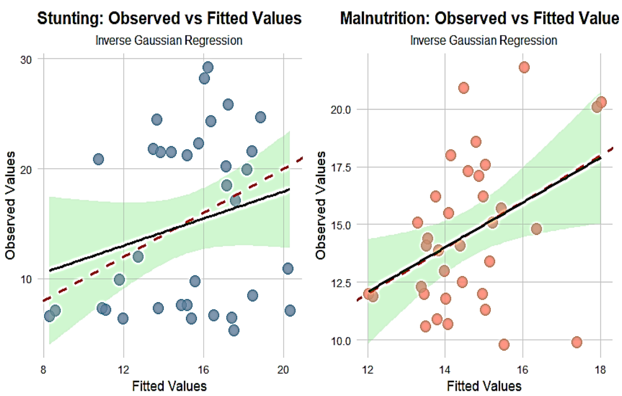

Figure 1. Observed vs Fitted Values Plot

Figure 1 shows that the Stunting plot shows that the observation points are spread quite far from the regression line, resulting in a fairly high dispersion pattern. This means that the fit of the stunting data to IGR is less than optimal. This is in contrast to the

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malnutrition data, where the observation points follow the regression line more closely than the Stunting plot. Therefore, the malnutrition data is more in line with IGR.

In addition to visuals, the data will be analyzed using hypothesis testing. First, an IGR model will be created for each response.

Table 4. Inverse Gaussian Regression Modeling

Response	Parameter	Estimate	Z-value	p-value
Y_1	β_0	16.521	1.082	0.279
	β_1	-0.119	-2.118	0.034
	β_2	0.235	0.981	0.327
	β_3	0.356	0.190	0.849
	β_4	-0.275	-1.980	0.421
	β_5	-0.108	-0.815	0.068
	λ	47.591	199.09	0.000
Y_2	β_0	-13.979	-0.945	0.345
	β_1	-0.215	-2.372	0.043
	β_2	-0.021	-0.673	0.501
	β_3	-0.199	-0.380	0.704
	β_4	0.007	0.340	0.734
	β_5	-0.322	2.181	0.029
	λ	64.482	1524.754	0.000

Based on Table 4, the IGR model estimation for the stunting rate (Y_1) can be formed as follows:

$$\hat{\mu}_i = \exp\begin{pmatrix} 16.521 - 0.119X_1 + 0.235X_2 \\ +0.356X_3 - 0.275X_4 - 0.108X_5 \end{pmatrix},\ i = 1,2,\ldots,35$$

The IGR model with the child malnutrition rate as the response variable (Y_2) is written below:

$$\hat{\mu}_i = \exp\begin{pmatrix} -13.979 - 0.215X_1 - 0.021X_2 \\ -0.199X_3 + 0.007X_4 + 0.322X_5 \end{pmatrix},\ i = 1,2,\ldots,35$$

Furthermore, the parameters of the IGR model for both Y_1 and Y_2 will be tested simultaneously with the following hypothesis.

$H_0 : \beta_1 = \beta_2 = \ldots = \beta_k = 0$ (all parameters are significant simultaneously)

H_1 : At least one $\beta_j \neq 0$, $j = 1,2,\ldots,k$ (at least one parameter is not significant simultaneously)

The simultaneous parameter testing results for Y_1 is 46.063. G_1^2 is greater than χ_5^2 (46.063 > 11.071), so reject H_0, and all parameters are significant in the model. Similarly, for Y_2, the value of $G_2^2 > \chi_5^2$ (58.142 > 11.071) indicates that all parameters are also significant in the IGR model.

The next step is to test the parameters partially with the Z test. Here is the hypothesis:

$H_0 : \beta_j = 0$ (the parameter is not partially significant)

$H_1 : \beta_j \neq 0$ (the parameter is partially significant)

Table 4 shows that the parameters β and λ are significant in the IGR model for Y_1 because Z > $Z_{0.025;4}$ or p-value < α. For the IGR model for Y_2 according to Table 4, the significant parameters are β_1, β_5 and λ. Because there are several parameters that are not significant, re-regression modeling was carried out using only significant predictor variables.

Table 5. Inverse Gaussian Regression Remodeling

Response	Parameter	Estimate	Z-value	p-value
y_1	β_0	8.137	0.093	0.136
	β_1	-0.089	1.314	0.007
	λ	33.949	85.091	0.000
y_2	β_0	-7.979	-1.037	0.175
	β_1	-0.029	1.714	0.016
	β_5	-0.051	1.081	0.043
	λ	34.482	86.464	0.000

Table 5 shows that all parameters are significant. Moreover, analysis of the marginal IGR model indicates that the number of infants with early initiation of breastfeeding impacts stunting. Another factor influencing child malnutrition rates is the number of pregnant women consuming blood supplement tablets.

Table 6. AIC_c for IGR

	AIC_c	
	IGR	IGR Remodeling
Y_1	242,18	226,97
Y_2	200,93	193,69

Table 6 shows that AIC_c for both the IGR

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remodeling of stunting and malnutrition response variables in children is smaller than the IGR. This indicates that the IGR remodeling (reduced model) for each response variable is the best model.

To show that the two response variables can be modeled in bivariate form, it is necessary to test the relationship between the two. The following hypotheses are given:

$H_0: \rho = 0$ (there is no correlation between stunting and malnutrition in children)
$H_1: \rho \neq 0$ (there is correlation between stunting and malnutrition in children)

At α = 5%, the p-value obtained was 0.004. Because the p-value < α, H_0 was rejected. It means there is a correlation between stunting and malnutrition in children. Likewise, the correlation coefficient is 0.48, which indicates that there is a fairly strong relationship between stunting and malnutrition in children.

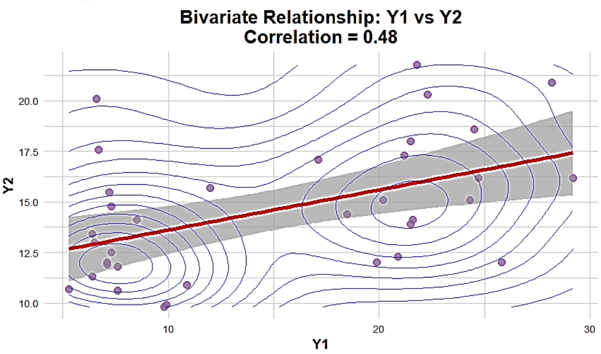

Figure 2. Bivariate Relationship Plot

The relationship between stunting and malnutrition in children is also shown in Figure 2, with a correlation of 0.48, which indicates that there is a fairly strong relationship between stunting and malnutrition in children. The next step can be modeled in BIGR.

The following parameter estimator values for BIGR were obtained.

Table 7. Bivariate Inverse Gaussian Regression Modeling

	Estimate	Z-value	p-value
β_{10}	0.552	0.89	0.371
β_{11}	-0.199	2.53	0.011
β_{12}	2.139	0.03	0.977
β_{13}	1.104	0.44	0.663
β_{14}	0.108	-1.43	0.152
β_{15}	-0.042	-0.06	0.953
β_{20}	-11.671	-0.74	0.459
β_{21}	-0.071	1.87	0.038
β_{22}	-0.008	-0.27	0.789
β_{23}	0.069	-0.13	0.899
β_{24}	0.005	-0.02	0.982
β_{25}	-0.282	1.83	0.067
λ_1	2.929	11.78	0.000
λ_2	4.884	17.81	0.000
ρ	1.193	5.90	0.000

The parameter estimates in Table 7 include all twelve β , two λ, and a ρ dependency parameter. A positive sign on the estimates indicates a positive effect. For example, β_{13} has a value of 1.104. It means the babies with low birth weight are 1.104 times more likely to experience stunting. A negative sign indicates a negative effect, such as β_{25}, which has a value of -0.282, indicating that the more pregnant women consume iron tablets, the lower the rate of malnutrition in children by 0.282 times.

Parameter test with five parameters β, the following hypothesis is determined:
$H_0 : \beta_{11} = \beta_{12} = ... = \beta_{15} = \beta_{21} = ... = \beta_{25} = 0$ (all parameters are significant simultaneously)

H_1 : At least one $\beta_{ij} \neq 0$, $j = 1, 2, ..., 5,\ i = 1, 2$ (at least one parameter is not significant simultaneously)

The G^2 value as the MLTR test statistic is 111.729. From the calculation of G^2, a value greater than χ^2_5 (111.729 > 11.071), so H_0 is rejected, which means that all parameters are simultaneously significant. In addition, to determine which parameters have an influence on the model, partial estimator testing is carried out using the Z test. The following is a partial β testing hypothesis.

$H_0 : \beta_{ij} = 0$ (the parameter is not partially significant)
$H_1 : \beta_{ij} \neq 0$, $j = 1,2,3,4,5,\ i = 1,2$ (the parameter is partially significant)

Meanwhile, for the λ and ρ (dependecy parameter) parameter as follows

$H_0 : \lambda_i = 0$ $\quad$ $H_0 : \rho = 0$
$H_1 : \lambda_i = 0$, $i = 1,2$ $\quad$ $H_1 : \rho \neq 0$

If $Z_{0.025;4}$ value is 1.645 then based on Table 7, Z value > $Z_{0.025;4}$ for all parameters. Only β_{11} and β_{21} are significant in the model with the stunting and child malnutrition response variable. However, the parameters λ_1, λ_2, and ρ (dependency parameter) are all significant. Furthermore, re-regression is necessary, including only the significant parameters. The following are the results of the estimation and retest of the parameters.

Table 8. Bivariate Inverse Gaussian Regression Remodeling

	Estimate	Z-value	p-value
β_{10}	1.634	0.030	0.976
β_{11}	-0.206	2.810	0.005
β_{20}	6.894	0.522	0.602
β_{21}	-0.009	0.325	0.013
λ_1	2.891	11.570	0.000
λ_2	4.912	18.176	0.000
ρ	1.140	5.632	0.000

Table 8 shows that the direction of the correlation between the predictor variables and the response is the same as the estimate shown in Table 7. In addition, the parameter test was repeated simultaneously. MLRT re-test statistic 128.011. Because χ^2 is 5.991, the null hypothesis is rejected, and all parameters are significant in the second-stage BIGR model.

The partial test results were the same as those obtained in the first-stage partial test: β_1 was significant for stunting and child malnutrition. This is shown in Table 7. The results of this hypothesis test align with previous research that found that the number of infants with early initiation of breastfeeding has an effect on stunting (Susianto et al., 2022; Punuh et al., 2021). Likewise, according to research findings by Simanjuntak et al. (2018), early initiation of breastfeeding can improve nutrition in babies or children.

To ensure that the repeated BIGR is better than the previous BIGR, it can be determined from the AIC_c value.

Table 9. AIC_c on Bivariate Inverse Gaussian Regression

BIGR	BIGR remodeling
449.28	436.12

Based on Table 9, it can be concluded that the BIGR with repeated one predictor variable is better than the previous BIGR (with 5 predictor variables) because it has the smallest AIC_c score.

The BIGR model outperformed the independent IGR model due to its smaller AIC_c value, thereby serving as the best-fitting model to capture the relationship between child stunting and malnutrition. Finally, BIGR with the number of infants with early initiation of breastfeeding as the predictor variable is the best model. The alignment of the number of infants with early initiation of breastfeeding as a primary determinant in this model is strongly supported by epidemiological studies, which demonstrate that introducing breastfeeding within the first hour of birth significantly lowers the risk of concurrent growth failure, effectively addressing both acute wasting and chronic stunting trajectories (Neves et al., 2021; Fentahun et al., 2016).

CONCLUSION

Conclusion

The bivariate inverse Gaussian regression (BIGR) can effectively model the prevalence of stunting and malnutrition in children. Using BFGS as a numerical iteration in parameter estimation, BIGR parameters can be generated without constraints. The BIGR model reveals the number of infants with

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early initiation of breastfeeding.

Suggestions

Given that child health indicators often exhibit strong geographical clustering, future studies should incorporate spatial effects into the current model. Expanding the Bivariate Inverse Gaussian Regression into a spatial bivariate regression model, like Geographically Weighted Bivariate Inverse Gaussian Regression, will capture spatial autocorrelation among neighboring regions in Central Java, leading to more precise parameter estimations and helping policymakers identify specific critical clusters that require immediate intervention. In addition, by identifying the factors causing stunting and malnutrition in children, the Central Java government can create policies related to mentoring pregnant and breastfeeding mothers regarding the importance of breastfeeding babies from an early age in order to reduce the number of stunting and malnutrition in children in Central Java.

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