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Comparison of Several Parameter Estimation Methods in Overcoming Multicollinearity in the Model Poisson Inverse Gaussian (Case Study:HIV)

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Abstract: Human Immunodeficiency Virus (HIV) cases remain a public health problem that continues to increase in West Java Province [1]. Data on the number of HIV cases are classified as count data and generally exhibit overdispersion and multicollinearity among predictor variables, making the ordinary Poisson regression model less appropriate for analysis [2]. Therefore, this study aims to compare the performance of several parameter estimation methods in the Poisson Inverse Gaussian (PIG) regression model, namely the Maximum Likelihood Estimator (MLE), Poisson Inverse Gaussian Ridge Estimator (P-IGRE), Poisson Inverse Gaussian Liu Estimator (P-IGLE), Poisson Inverse Gaussian Liu-Type Estimator (P-IGLTE), and Poisson Inverse Gaussian New Improved Liu-Type Estimator (P-IGNLTE) in handling multicollinearity problems [3][4]. The data used in this study consist of HIV case data from 27 regencies/cities in West Java Province in 2023 obtained from Badan Pusat Statistik Provinsi Jawa Barat [5]. The independent variables include the percentage of the poor population, the number of condom users, the number of health workers, the number of health facilities, the number of injectable contraceptive users, population size, and population density. The best model was selected based on the smallest Mean Square Error (MSE) value. The results indicate that the Poisson Inverse Gaussian New Improved Liu-Type Estimator (P-IGNLTE) with the shrinkage function $f_5(k)$ is the best estimator because it produces the smallest MSE value of 0.2653, indicating that the estimator provides more stable and efficient parameter estimates in the presence of multicollinearity.

Keywords: *Poisson Inverse Gaussian; Multicollinearity; PIGML; PIGRE; PIGLE; PIGLTE; PIGNLTE; Mean Square Error.*

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I. INTRODUCTION

Human Immunodeficiency Virus (HIV) remains one of the major public health problems worldwide, including in Indonesia. HIV attacks the human immune system, particularly CD4 cells, causing a gradual decline in immune function and increasing susceptibility to opportunistic infections [1]. In West Java Province, the number of HIV cases has continued to increase over time. Based on data published by Badan Pusat Statistik Provinsi Jawa Barat, HIV cases increased from 8,812 cases in 2022 to 9,710 cases in 2023 [5]. This condition indicates that HIV prevention and control efforts still face various challenges related to socioeconomic conditions, population density, and access to health services.

The number of HIV cases is classified as count data, which are discrete and non-negative in nature. One of the statistical approaches commonly used for analyzing count data is Poisson regression. However, the Poisson regression model assumes equidispersion, meaning that the mean and variance of the response variable are equal. In practice, health-related count data often exhibit variance greater than the mean, a condition known as overdispersion. Overdispersion causes the Poisson regression model to become less efficient and may produce unstable parameter estimates. Cameron and Trivedi explained that violations of the equidispersion assumption frequently occur in empirical count data and recommended the use of alternative count regression models capable of accommodating overdispersion [2]. One of the regression models that can effectively handle overdispersion is the Poisson Inverse Gaussian (PIG) regression model.

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Besides overdispersion, multicollinearity among explanatory variables is another major issue in regression analysis. Multicollinearity occurs when strong linear relationships exist among independent variables, causing the variance of parameter estimates to increase and resulting in unstable estimators. This issue becomes more problematic in Poisson Inverse Gaussian regression because the Maximum Likelihood Estimator (MLE) is highly sensitive to correlations among predictors. To address this problem, several shrinkage estimators have been developed, including the Poisson Inverse Gaussian Ridge Estimator (P-IGRE), Poisson Inverse Gaussian Liu Estimator (P-IGLE), and Poisson Inverse Gaussian Liu-Type Estimator (P-IGLTE), which aim to improve estimation stability under multicollinearity conditions [4].

Recent developments introduced the Poisson Inverse Gaussian New Improved Liu-Type Estimator (P-IGNLTE), which extends the Liu-type estimator by incorporating a more flexible shrinkage parameter. This estimator was developed to produce more stable and efficient parameter estimates in the presence of severe multicollinearity and overdispersion. Previous studies reported that the P-IGNLTE estimator generated smaller Mean Square Error (MSE) values than conventional estimators, indicating superior estimation performance and improved model accuracy [3].

Therefore, this study aims to compare the performance of the Maximum Likelihood Estimator (MLE), Poisson Inverse Gaussian Ridge Estimator (P-IGRE), Poisson Inverse Gaussian Liu Estimator (P-IGLE), Poisson Inverse Gaussian Liu-Type Estimator (P-IGLTE), and Poisson Inverse Gaussian New Improved Liu-Type Estimator (P-IGNLTE) in handling multicollinearity in the Poisson Inverse Gaussian regression model. In addition, this study applies these estimators to identify factors influencing HIV cases in West Java Province. The best estimator is determined based on the smallest Mean Square Error (MSE) value. The results of this study are expected to provide a more stable and efficient estimation approach for count data characterized by overdispersion and multicollinearity.

II. LITERATURE VIEW

Poisson regression is a regression model used to model count data with a response variable in the form of a non-negative integer. According to McCullagh and Nelder [6], Poisson regression belongs to the Generalized Linear Model (GLM) family with a logarithmic link function. The Poisson regression model is expressed as:

$$Y_i \sim Poisson(\mu_i)$$

With the probability function:

$$P(Y;y) = \frac{\mu^y e^{-\mu}}{y!}, y = 0,1,2,\ldots, dan\ \mu > 0$$

The mean and variance of the Poisson distribution are:

$$E(Y) = Var(Y) = \mu$$

To address overdispersion, Poisson Inverse Gaussian (PIG) regression is used. Herindrawati et al. stated that Poisson Inverse Gaussian regression is more flexible than Poisson regression because it can better accommodate overdispersion in count data [4]. Parameter estimation in Poisson Inverse Gaussian regression is generally performed using the Maximum Likelihood Estimator (MLE) method. According to Ronald Fisher, the Maximum Likelihood method is used to obtain parameter estimates that maximize the likelihood function of the observed data. The Maximum Likelihood estimator in Poisson Inverse Gaussian regression is expressed as:

$$\mu_i = e^{x_i^T \beta}$$

Parameter estimation in Poisson Inverse Gaussian regression generally uses the Maximum Likelihood Estimator (MLE) method. According to Fisher, the Maximum Likelihood method is used to obtain a parameter estimator that maximizes the likelihood function of the observed data. The Maximum Likelihood Estimator in Poisson Inverse Gaussian regression is expressed as:

$$\hat{\beta}_{ML} = \left(\boldsymbol{X^T \hat{G} X}\right)^{-1} \boldsymbol{X^T \hat{G}}_{\hat{z}}$$

Where $\boldsymbol{\hat{G}} = diag(\mu_i + \phi\mu_i^3)$ and $\hat{z}_i = log(\mu) + \frac{y_i - \mu_i}{\mu_i + \frac{\mu^3}{\phi}}$ Parameter estimation is performed using the Iteratively Weighted Least Squares (IWLS) method. The bias of the estimator $\hat{\beta}_{ML}$ is zero, and its variance-covariance matrix is given by oleh $Var - Cov(\hat{\beta}_{ML}) = \hat{\phi}\left(\boldsymbol{X^T \hat{G} X}\right)$. The Mean Square Error (MSE) value of the Maximum Likelihood estimator is:

$$MSE\left(\hat{\beta}_{ML}\right) = \sum_{j=1}^{p} \frac{\hat{\phi}}{gj}$$

The Maximum Likelihood estimator is unbiased and efficient when the assumptions of the regression model are satisfied. However, this estimator is highly sensitive to multicollinearity among independent variables. Multicollinearity is a condition in regression analysis where strong linear relationships occur among explanatory variables, causing parameter estimates to become unstable and less reliable [7]. Therefore, multicollinearity testing is conducted to determine whether linear relationships exist among the independent variables in the regression model. The variance inflation factor (VIF) can be calculated as follows:

$$VIF_j = \frac{1}{1 - R_j^2}$$

To overcome the problem of multicollinearity, shrinkage estimators are commonly applied in regression analysis. One of the estimators used is the Poisson Inverse Gaussian Ridge Estimator (P-IGRE). According to Arthur E. Hoerl and Robert W. Kennard, the Ridge estimator is obtained by adding a bias parameter $k$to the diagonal elements of the matrix in order to reduce the variance of the estimator and produce more stable parameter estimates compared to the classical estimator [8].

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Furthermore, Batool et al. stated that the Ridge estimator is capable of handling multicollinearity because it produces smaller estimator variances than the Maximum Likelihood estimator, resulting in more efficient parameter estimation under multicollinearity conditions [9]. The form of the P-IGRE estimator is expressed as:

$$\hat{\beta}_k = \left(\boldsymbol{X^t\widehat{G}X} + k\boldsymbol{I}_P\right)^{-\mathbf{1}}\boldsymbol{X^t\widehat{G}X\widehat{\beta}_{ML}}$$

With Mean Square Error (MSE) value:

$$MSE(\hat{\beta}_k) = \hat{\phi}\sum_{j=1}^{p}\frac{g_j}{\left(g_j + k_r\right)^2} + \sum_{j=1}^{p}\frac{k_r^2\hat{\alpha}_j^2}{\left(g_j + k_r\right)^2}$$

The next development is the Poisson Inverse Gaussian Liu Estimator (P-IGLE). According to Kejian Liu, the Liu estimator introduces a shrinkage parameter $d$to control the trade-off between bias and variance in the estimator, thereby producing more stable parameter estimates under multicollinearity conditions [10]. The form of the P-IGLE estimator is expressed as:

$$\hat{\beta}_d = \left(\boldsymbol{X^T\widehat{G}X} + \boldsymbol{I_P}\right)^{-\mathbf{1}}\left(\boldsymbol{X^T\widehat{G}X} + d\boldsymbol{I_P}\right)\hat{\beta}_{ML}$$

With Mean Square Error (MSE) value:

$$MSE(\hat{\beta}_d) = \hat{\phi}\sum_{j=1}^{p}\frac{\left(g_j + d\right)^2}{g_j\left(g_j + 1\right)^2} + \sum_{j=1}^{p}\frac{(d-1)^2\hat{\alpha}_j^2}{\left(g_j + 1\right)^2}$$

Furthermore, the Poisson Inverse Gaussian Liu-type Estimator (P-IGLTE) is a development of the Ridge estimator and the Liu estimator by incorporating two bias parameters, namely the ridge parameter k and the Liu parameter d. Akram et al. explained that the Liu-type estimator provides greater flexibility in controlling the balance between bias and variance compared to previous estimators, resulting in more stable and efficient parameter estimates under multicollinearity conditions [11]. The form of the P-IGLTE estimator is:

$$\hat{\beta}_{kd} = \left(\boldsymbol{X^T\widehat{G}X} + k\boldsymbol{I_P}\right)^{-\mathbf{1}}\left(\boldsymbol{X^T\widehat{G}X} + kd\boldsymbol{I_P}\right)\hat{\beta}_{ML}$$

With Mean Square Error (MSE) value:

$$SE(\hat{\beta}_{kd}) = \hat{\phi}\sum_{j=1}^{p}\frac{\left(g_j + kd\right)^2}{g_j\left(g_j + k\right)^2} + \sum_{j=1}^{p}\frac{k^2(d-1)^2\hat{\alpha}_j^2}{\left(g_j + k\right)^2}$$

The latest development is the Poisson Inverse Gaussian New Improved Liu-type Estimator (P-IGNLTE) introduced by Alghamdi et al. This estimator is an extension of the Liu-type estimator by incorporating a more flexible biasing function $f(k)$ to obtain more stable and efficient parameter estimates under severe multicollinearity conditions [4]. The form of the P-IGNLTE estimator is expressed as:

$$\hat{\beta}_{f(k)} = \left(\mathbf{X}^T\widehat{\mathbf{G}}\mathbf{X} + k^*\mathbf{I}_{\boldsymbol{p}}\right)^{-\mathbf{1}}\left(\mathbf{X}^T\widehat{\mathbf{G}}\mathbf{X} + f(k)\mathbf{I}_{\boldsymbol{p}}\right)\hat{\beta}^*$$

With Mean Square Error (MSE) value:

$$MSE(\hat{\beta}_{f(k)}) = \hat{\phi}\sum_{j=1}^{p}\frac{(g_j + f(k))^2}{g_j(g_j + k^*)^2} + \sum_{j=1}^{p}\frac{(f(k) - k^*)^2\alpha_j^2}{(g_j + k^*)^2}$$

According to Alghamdi et al., the Poisson Inverse Gaussian New Improved Liu-Type Estimator (P-IGNLTE) produces smaller Mean Square Error (MSE) values compared to the Maximum Likelihood (MLE), Poisson Inverse Gaussian Ridge Estimator (P-IGRE), Poisson Inverse Gaussian Liu Estimator (P-IGLE), and Poisson Inverse Gaussian Liu-Type Estimator (P-IGLTE), indicating that the estimator provides more accurate, stable, and efficient parameter estimates in overcoming multicollinearity problems in Poisson Inverse Gaussian regression models [4].

III. METHODOLOGY

The data used in this study are secondary data obtained from official publications of the Badan Pusat Statistik West Java Province (https://jabar.bps.go.id/id). The data cover 27 regencies/cities in West Java Province in 2023 and consist of the following variables: number of HIV/AIDS cases (Y), percentage of poor population (X_1), number of condom family planning users (X_2), number of health workers (X_3), number of health facilities (X_4), population density (X_5), Human Development Index (X_6), and average years of schooling (X_7). These variables were selected because they are socio-demographic and health-related factors that potentially influence the number of HIV/AIDS cases. With the following steps:

- Descriptive statistical analysis
- Poisson distribution test using the Kolmogorov-Smirnov test.
- Overdispersion test to determine if there is overdispersion in the data.
- Multicollinearity test using the Variance Inflation Factor (VIF).
- Modeling using PIGML, PIGRE, PIGLE, PIGlTE and PIGNLTE.
- Selection of the best model based on the smallest Mean Squared Error (MSE) value.
- Parameter test on the best model: Simultaneous test (Likelihood Ratio Test), Partial test (Wald Test).

IV. RESULTS AND DISCUSSION

To evaluate and compare the performance of the Poisson Inverse Gaussian Maximum Likelihood Estimator (P-IGML), Poisson Inverse Gaussian Ridge Estimator (P-IGRE), Poisson Inverse Gaussian Liu Estimator (P-IGLE), Poisson Inverse Gaussian Liu-type Estimator (P-IGLTE), and Poisson Inverse Gaussian New Improved Liu-type Estimator (P-IGNLTE) in overcoming overdispersion and multicollinearity in Poisson Inverse Gaussian regression models, a descriptive statistical

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analysis of HIV/AIDS case data at the regency/city level in West Java Province was first carried out. This analysis was conducted to provide a general overview of the characteristics of the data used in the study. The results of the descriptive statistical analysis are presented in Table 1.

Table 1 Descriptive Analysis

Variable	Min	Max	Mean	Median	SD
Y	54	1,059	359.63	259	270.84
X_1	2.38	12.13	8.18	8.46	2.68
X_2	848	25,398	6,933.19	3,250	7,069.15
X_3	1,162	12,793	4,449.11	3,294	2,695.59
X_4	212	5,273	2,028.81	1,751	1,327.62
X_5	11,228	401,338	127,893.44	101,579	92,636.26
X_6	207.51	5,627.02	1,846.68	1,859.64	1,216.14
X_7	8.79	15,047	3,814.92	1,320	4,664.73

Based on Table 1, the variable number of HIV/AIDS cases (Y) shows a very wide distribution, with a minimum value of 54.00 and a maximum value of 1,059.00, indicating that the number of HIV/AIDS cases varies considerably across regencies/cities in West Java Province. The mean value of 359.63 is higher than the median value of 259.00, indicating that the data distribution is positively skewed or skewed to the right. This condition shows that most regions have relatively low to moderate numbers of HIV/AIDS cases, while several regions have considerably higher numbers of cases, causing the average value to increase. In addition, the relatively large standard deviation indicates substantial variation in HIV/AIDS cases among regions. Before performing the Poisson Inverse Gaussian regression modeling, a Poisson distribution test was conducted using the Kolmogorov–Smirnov test to evaluate the suitability of the response variable distribution. The results of the Kolmogorov–Smirnov test are presented in Table 2.

Table 2 Kolmogorov-Smirnov Test

Kolmogorov-Smirnov	
D	0.13335
P-value	0.6741

Based on Table 2, the obtained p-value was greater than the 5% significance level, indicating that the null hypothesis was not rejected. Therefore, it can be concluded that the HIV/AIDS case data follow a Poisson distribution. This result implies that the data satisfy the initial assumption required for further Poisson Inverse Gaussian regression modeling. Prior to selecting the appropriate regression model, an overdispersion test was conducted to determine whether the variance exceeded the mean value. The results of the overdispersion test are presented in Table 3.

Table 3 Overdispersion Test

Test Statistic	Value	P-value
Z	5.1316	0.00000014
Dispersion	44.9031	-

At a significance level of 5%, the test results showed that the p-value was less than 0.05. Therefore, the H_0 is rejected, and it can be concluded that over dispersion is occurring in the data. To examine the existence of strong linear relationships among the independent variables, multicollinearity testing was performed using the Variance Inflation Factor (VIF). The test results are presented in table 4.

Table 4 Multicollinearity Test

Independent Variable	Nilai VIF
X_1	2.79
X_2	6.01
X_3	8.90
X_4	12.13
X_5	7.33
X_6	21.90
X_7	3.63

Based on Table 4, several independent variables have relatively high VIF values. In particular, the variables number of health facilities ($\boldsymbol{X_4}$) and population size ($\boldsymbol{X_6}$) show $\boldsymbol{VIF \geq 10}$, indicating the presence of serious multicollinearity in the model. This condition causes the parameter estimates to become unstable and less reliable. Therefore, shrinkage estimators were applied to overcome the multicollinearity problem.

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To address multicollinearity, several shrinkage estimators were applied, namely Poisson Inverse Gaussian Ridge Estimator (P-IGRE), Poisson Inverse Gaussian Liu Estimator (P-IGLE), Poisson Inverse Gaussian Liu-type Estimator (P-IGLTE), and Poisson Inverse Gaussian New Improved Liu-type Estimator (P-IGNLTE). The estimation results are presented in Table 5.

Table 5 Parameter Estimates and MSE of PIGML, PIGRE, PIGLE, PIGLTE, and PIGNLTE

Estimator	**Parameter**	$\boldsymbol{\beta_0}$	$\boldsymbol{\beta_1}$	$\boldsymbol{\beta_2}$	$\boldsymbol{\beta_3}$	$\boldsymbol{\beta_4}$	$\boldsymbol{\beta_5}$	$\boldsymbol{\beta_6}$	$\boldsymbol{\beta_7}$	**MSE**
ML	-	5.6671	0.2324	0.0884	0.4043	-0.193	-0.395	0.7899	0.2738	0.2813
PIGRE	k_1	5.6658	0.2318	0.0884	0.4044	-0.192	-0.394	0.7884	0.2741	0.2699
PIGRE	k_2	5.6474	0.2251	0.0892	0.4053	-0.171	-0.387	0.7679	0.2772	0.2763
PIGLE	d_2	5.6671	0.2323	0.0884	0.4043	-0.193	-0.395	0.7899	0.2738	0.2812
PIGLE	d_2	5.6669	0.2322	0.0885	0.4044	-0.193	-0.394	0.7897	0.2739	0.2882
PIGLTE	k, d	5.6620	0.2309	0.0887	0.4045	-0.188	-0.393	0.7859	0.2746	0.2706
PIGNLTE	$f_1(k)$	5.6559	0.2299	0.0893	0.4048	-0.186	-0.392	0.7835	0.2753	0.2812
PIGNLTE	$f_2(k)$	5.6645	0.2317	0.0886	0.4044	-0.191	-0.394	0.7884	0.2742	0.2709
PIGNLTE	$f_3(k)$	5.4277	0.1809	0.1063	0.4158	-0.046	-0.335	0.6530	0.3056	0.2677
PIGNLTE	$f_4(k)$	5.3393	0.1619	0.1129	0.4200	0.008	-0.313	0.6025	0.3173	0.2662
PIGNLTE	$f_5(k)$	5.3281	0.1594	0.1137	0.4205	0.014	-0.311	0.5960	0.3188	0.2653

Based on the results of the Poisson Inverse Gaussian regression analysis, several estimators were obtained, namely Maximum Likelihood (ML), Poisson Inverse Gaussian Ridge Estimator (PIGRE), Poisson Inverse Gaussian Liu Estimator (PIGLE), Poisson Inverse Gaussian Liu-Type Estimator (PIGLTE), and Poisson Inverse Gaussian New Liu-Type Estimator (PIGNLTE). The best estimator was determined based on the smallest Mean Square Error (MSE) value. Among all estimators, the PIGNLTE model with the $f_5(k)$ function produced the lowest MSE value, namely 0.2653. This value was smaller than the MSE values generated by the other estimators, including the Maximum Likelihood estimator with an MSE of 0.2813. These findings indicate that the PIGNLTE $f_5(k)$ estimator provides more accurate and stable parameter estimates in overcoming multicollinearity problems in the data. The regression model formed by the PIGNLTE $f_5(k)$ estimator is expressed as follows:

$$log(\mu) = 5{,}3281 + 0{,}1594X_1 + 0{,}1137X_2 + 0{,}4205X_3$$
$$+0{,}0149X_4 - 0{,}3110X_5 + 0{,}5960X_6 + 0{,}3188X_7$$

Based on the Poisson Inverse Gaussian regression model obtained, it can be concluded that the independent variables have different effects on the number of HIV/AIDS cases, where variables X_1, X_2, X_3, X_4, X_6, and X_7 have positive effects that increase the average number of HIV/AIDS cases, while variable X_5 has a negative effect that decreases the average number of HIV/AIDS cases; moreover, variable X_6 shows the largest positive influence in the model, indicating that this variable contributes the most to the increase in HIV/AIDS cases in West Java Province. simultaneous parameter testing was conducted using the Likelihood Ratio test to determine whether the independent variables jointly affect the number of HIV/AIDS cases. The results of the simultaneous test are presented in Table 6.

Table 6 Simultaneous Significance Test

Statistik Uji	Nilai
Likelihood Rasio Value (G)	42,99555
Degrees of Freedom (df)	7
p-value	0,000000334

Based on Table 6, the obtained p-value was less than 0.05, indicating that the null hypothesis was rejected. Therefore, it can be concluded that the independent variables simultaneously have a significant effect on the number of HIV/AIDS cases in West Java Province.

Furthermore, partial parameter testing was conducted using the Wald test to determine the individual effect of each independent variable on the number of HIV/AIDS cases. The results of the partial significance test are presented in Table 7.

Table 7 Partial Parameter Test

Parameter	**Estimase**	**Z**	**p-value**	**Decision**
Intercept	5.3280	63.7584	0.0000	Significant
X_1	0.1594	1.5331	0.1252	Not Significant
X_2	0.1138	0.9223	0.3563	Not Significant
X_3	0.4206	3.3022	0.0009	Significant
X_4	0.0150	0.1141	0.9091	Not Significant
X_5	-0.3111	-2.4778	0.0132	Significant
X_6	0.5961	4.5738	0.000005	Significant
X_7	0.3188	2.8126	0.0049	Significant

At a significance level of $\alpha = 0.05$ the Wald test results indicate that variables X_3, X_5, X_6, and X_7 significantly affect the number of HIV/AIDS cases because their p-values are smaller than 0.05. Variable X_3 has a Z-value of 3.3022 with a p-value of 0.0009, indicating that this variable has a significant positive effect on the number of HIV/AIDS cases. Variable X_5 has a Z-value of -2.4778 with a p-value of 0.0132, indicating a significant negative effect on the number of HIV/AIDS cases. Furthermore, variable X6 has the largest Z-value, namely 4.5738 with a p-value of 0.000005, indicating that this variable has the most significant positive influence in the model. Variable X_7 also significantly affects the number of HIV/AIDS cases with a Z-value of 2.8126 and a p-value of 0.0049. Therefore, the null hypothesis for these variables is rejected because they significantly contribute to explaining the variation in HIV/AIDS cases in West Java Province.

V. CONCLUSION

Based on the analysis conducted using the Poisson Inverse Gaussian regression model, the Poisson Inverse Gaussian New Liu-Type Estimator (PIGNLTE) was identified as the best estimator for handling multicollinearity. This result can be observed from the smallest Mean Square Error (MSE) value obtained among all estimators. The minimum MSE value was produced by the PIGNLTE estimator with the $f_5(k)$ parameter, namely 0.2653, indicating that this estimator provides more accurate and stable parameter estimates in modelling the number of HIV/AIDS cases in West Java Province.

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