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Predicting the neonatal, infant and under-five mortality outcomes in the Philippines using Count TS GLM and GLARMA

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ABSTRACT

Mortality statistics are often considered indicators of overall population health, highlighting the need for accurate forecasting to support public health planning and policy development. While various statistical models have been applied to mortality forecasting globally, research on the use of count time series modeling for mortality trends in the Philippines remains limited. Addressing this gap, this study provides the first systematic comparison of Count Time Series Generalized Linear Models (TS GLM) and Generalized Linear Autoregressive Moving Average (GLARMA) models for forecasting Philippine neonatal, infant, and under-five mortality. The predictive performance of these models was evaluated for the period 2023–2027. Prior to model implementation, stationarity was assessed using the KPSS test, after which predictive models were developed and compared, with the best-performing specifications selected based on the Akaike Information Criterion (AIC) and Mean Absolute Error (MAE). Results show that TS GLM consistently outperforms GLARMA in predictive accuracy, with the negative binomial distribution yielding the best results. The optimal TS GLM models for neonatal (1,2), infant (1,2), and under-five mortality (1,5) surpass their GLARMA counterparts. Projected trends indicate rising absolute numbers of deaths across all subgroups. These findings provide valuable guidance for government agencies, health institutions, and insurance providers in monitoring child mortality, anticipating healthcare demand, improving actuarial projections, and informing targeted strategies, while also serving as a reference for future research on mortality forecasting using count time-series models.

Keywords: Child mortality, forecasting, GLARMA, TS GLM

INTRODUCTION

Child mortality, commonly measured through neonatal (death within the first month of life), infant (death before one year), and under-five mortality, remains a central indicator of population health and health system performance. In 2020, approximately five million children under five died worldwide, many from preventable causes such as infectious diseases, birth complications, and malnutrition. Although global under-five deaths declined substantially from 12.8 million in 1990 to five million in 2020, progress remains uneven. Under Sustainable Development Goal (SDG) 3.2, countries aim to end preventable deaths of newborns and children under five by 2030 through specific mortality reduction targets. Projections, however, suggest that millions of child deaths may still occur before 2030 if current trajectories persist. In the Philippines, continued monitoring and forward-looking planning are necessary to sustain gains and fully achieve these targets.

Reliable forecasting of child mortality trends is therefore essential for tracking progress, guiding resource allocation, and strengthening public health planning. Time series methods are widely used for mortality forecasting, yet many studies rely on rate-based or traditional models that may not fully account for the discrete, non-negative, and potentially overdispersed nature of mortality counts. Count time series approaches, which directly model death counts while incorporating temporal dependence, offer a theoretically appropriate alternative. Among these, Count Time Series following Generalized Linear Models (TS GLM) and Generalized Linear Autoregressive Moving Average (GLARMA) models have been applied to count data in various fields. However, empirical comparisons of these two frameworks in the context of child mortality forecasting remain limited, particularly in the Philippines.

This study addresses this gap by systematically comparing TS GLM and GLARMA models in forecasting neonatal, infant, and under-five mortality in the Philippines. Using annual data from 1993 to 2022 obtained from the United Nations Inter-agency Group for Child Mortality Estimation (UN IGME), the analysis evaluates the predictive performance of both modeling approaches and generates forecasts for 2023–2027. The primary objective is to determine which framework provides superior predictive accuracy for mortality counts and to examine projected trends across the three child mortality subgroups. The study focuses exclusively on methodological comparison and forecasting performance; it does not investigate causal determinants of mortality outcomes.

By providing the first systematic, comparative applications of TS GLM and GLARMA to Philippine child mortality data, this research contributes to the methodological literature on count time-series modeling in demographic forecasting. The findings offer evidence-based guidance for government agencies in monitoring mortality trends, for health institutions in anticipating service needs, and for insurance providers in refining actuarial projections. More broadly, the study establishes a foundation for future research applying count time series methods to mortality and other public health indicators in similar settings.

LITERATURE REVIEW

Child mortality remains a critical global health indicator, shaped by socioeconomic, environmental, biological, and healthcare factors (EPA, 2023; Maródi, 2006). Neonatal (less than one month), infant (less than one year), and under-five mortality rates are particularly important, with neonates accounting for nearly 45% of under-five deaths worldwide (WHO, 2018; USC, 2023). Despite being largely

preventable through adequate nutrition, immunization, and healthcare, infections, malnutrition, and complications from preterm births remain leading contributors to these deaths (Huber, 2016; Bhutta, 2013; WHO, 2022). Global initiatives, including MDG 4 and SDG 3.2, have significantly reduced child mortality; however, disparities persist. Low-income regions such as Sub-Saharan Africa and Southern Asia contribute to over 80% of under-five deaths, highlighting persistent inequities (HNN, 2023; UN IGME, 2024). In the Philippines, around 60,000 children die annually before age five, underscoring the need for targeted policy interventions (Peña, 2023).

Forecasting child mortality is essential for public health planning, resource allocation, and monitoring progress toward SDG 3.2 targets (Sharro, 2022; UN IGME, 2023). Traditional models, such as ARIMA and state-space models, have been widely applied to project mortality trends (Nasir, 2020; Nyomi & Nyomi, 2023). While informative, these approaches assume continuous data with Gaussian errors, limiting their suitability for discrete, overdispersed mortality counts. To address these limitations, advanced count time series models, specifically Count Time Series based on Generalized Linear Models (TS GLM) and Generalized Linear Autoregressive Moving Average (GLARMA), have been developed. TS GLM models, implemented via the R package *tscount*, enable estimation of Poisson and negative binomial models through maximum likelihood, accommodating overdispersed count data while allowing model fitting, testing, and prediction (Liboschik, 2017; Rohaeti, 2021). GLARMA models provide flexible autoregressive and moving average structures that account for serial dependence in discrete count data. By incorporating past observations and innovations into the model, GLARMA extends generalized linear models to handle temporal correlation while maintaining appropriate distributions such as Poisson or negative binomial (Dunsmuir & Scott, 2015; Petukhova, 2018). This makes GLARMA well suited for modeling overdispersed and autocorrelated child mortality counts.

Synthesis

Despite global progress in reducing child mortality, including through MDG 4 and SDG 3.2 initiatives, preventable deaths remain a major concern, particularly in low- and middle-income countries (UN IGME, 2024; Peña, 2023). Accurate forecasting models are critical for guiding policy, resource allocation, and targeted interventions. While conventional approaches such as ARIMA and state-space models have provided valuable trend projections (Nasir, 2020; Nyomi & Nyomi, 2023), they often rely on continuous or rate-based data and assume Gaussian errors, limiting their applicability to discrete mortality counts and overdispersed outcomes.

Recent advances in count time series modeling, specifically TS GLM and GLARMA, allow for the direct analysis of discrete mortality data with temporal dependence (Liboschik, 2017; Dunsmuir & Scott, 2015). TS GLM has been shown to handle overdispersion effectively through Poisson and negative binomial formulations, while GLARMA offers flexible autoregressive and moving average structures (Rohaeti, 2021; Petukhova, 2018). However, few studies have applied these models comparatively to child mortality data, particularly in the Philippine context, leaving a gap in understanding which approach provides the most accurate and reliable forecasts for neonatal, infant, and under-five mortality.

This study addresses this gap by systematically evaluating and comparing TS GLM and GLARMA models for Philippine child mortality outcomes, focusing on predictive accuracy and model suitability. By doing so, it provides methodological insights into the strengths and limitations of count-based time series approaches, offering guidance to researchers, policymakers, and health practitioners to improve mortality forecasting and inform targeted interventions to reduce preventable child deaths.

METHODOLOGY

Data Source

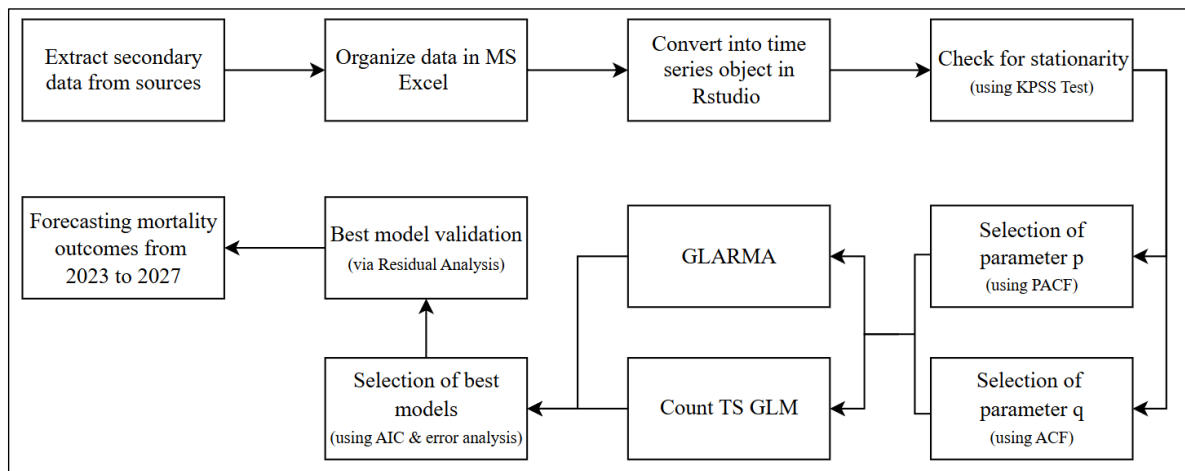
The data used in this study were obtained from the United Nations Inter-agency Group for Child Mortality Estimation (UN IGME), focusing on neonatal, infant, and under-five mortality in the Philippines. The data were organized into three subgroups and prepared for time series analysis in RStudio.

The identification of the model parameters was carried out using the autocorrelation function (ACF) and partial autocorrelation function (PACF), which provide information on the correlation between the current and past observations and hence help identify the autoregressive (p) and moving average (q) parameters. The parameters were assessed using both single-point and cumulative lag definitions. In a single-point lag definition (for example, $p = [3]$), only one lag is considered in the model, implying that the current observation depends only on that specific past observation. On the other hand, in the cumulative lag definition (for example, $p = [1, 2, 3]$), multiple consecutive lags are considered simultaneously, implying that the model can capture the joint effect of several past time periods. By considering both definitions, a more flexible analysis of the dependence structure of the mortality outcomes was possible.

For both the Count TS GLM and GLARMA models, candidate models were compared based on AIC and forecasting accuracy, and the best models were used to forecast mortality outcomes over the next 5 years for each subgroup. The whole methodology is illustrated in Figure 1.

Figure 1

Flowchart of the proposed methodology



Data Gathering

This research uses secondary data from recognized global sources, including the World Bank, which compiles data from the United Nations Inter-Agency Group for Child Mortality Estimation (UN IGME). The dataset acquired consists of count data on neonatal, infant, and under-five mortality in the Philippines from 1993 to 2022. The primary variables of interest in this study are mortality counts. This data source aligns with the research aim of predicting mortality outcomes over a specified period. In

addition, the use of credible sources, such as the World Bank, supports the reliability of the research findings.

Statistical Instruments

The study uses statistical techniques to evaluate data, build models, and assess their performance. These diagnostics are essential for accurate predictions. RStudio 4.1.2 handles computations and analysis, while Spyder 5.1.5 is used for graphing. Mortality predictions for under-five, infant, and neonatal groups are made using these methods.

The Kwiatkowski–Phillips–Schmidt–Shin (KPSS) test was employed in this study to determine if the mortality time series data conformed to the assumption of stationarity necessary for time series modelling. The test was conducted in RStudio using the *kpss.test* function from the *aTSA* package.

The p-value determined the test results: if it was greater than 0.05, the null hypothesis of stationarity was not rejected, and the data were considered stationary and ready for modelling. However, if the p-value was less than 0.05, the data were considered non-stationary and required further processing before modelling.

The KPSS statistic is calculated by Equation 1.

$$KPSS = n^{-2} \sum_{t=1}^n \frac{S_t^2}{\sigma^2} ; \quad S_t = \sum_{i=1}^t e_i \quad (1)$$

where n is the total number of observations, 30, e_i are the residuals from the regression of mortality outcomes on an intercept and time trend, $\hat{\sigma}^2$ is the long-run variance of the residuals estimate, which is calculated by the total number of observations multiplied by the sample mean variance, and S_t is the partial sum of the residuals.

Count Time Series following Generalized Linear Model (TS GLM)

Count Time Series following Generalized Linear Models (TS GLM) analyses count data over time, such as mortality counts, using the *tsglm* function in the *tscount* package (Liboschik, 2017). This method selects a suitable count distribution, Poisson or Negative Binomial, and uses the log link function, based on Rohaeti (2021). The general model is given by Equation 2.

$$g(\lambda_t) = \beta_0 + \sum_{k=1}^p \beta_k \tilde{g}(Y_{t-i_k}) + \sum_{\ell=1}^q \alpha_\ell g(\lambda_{t-j_\ell}) + \eta^T X_t, \quad (2)$$

where Y_{t-i_k} is based on the previously observed values of the mortality outcomes at time t minus i_k from the parameter p , and λ_{t-j_ℓ} is based on the conditional mean of the dataset which was fitted to a generalized linear model at time t minus j_ℓ from parameter q . $g(\cdot)$ is the link function that corresponds with the suitable type of distribution of the data set with $\tilde{g}(\cdot)$ as its inverse. β_0 , β_k and α_ℓ are the coefficients with $\eta^T X_t$ denoted as being the time-varying covariate vector. The general form has been further simplified to Equation 3, as in Rohaeti (2021), given the dataset's lack of covariate variables.

$$g(\lambda_t) = \beta_0 + \sum_{k=1}^p \beta_k \tilde{g}(Y_{t-i_k}) + \sum_{\ell=1}^q \alpha_\ell g(\lambda_{t-j_\ell}), \quad (3)$$

To account for the single-point method, the equation can be simplified further into Equation 4 by removing the summations from both terms so that the lag used will only contain that lagged value:

$$g(\lambda_t) = \beta_0 + \beta_p \tilde{g}(Y_{t-i_p}) + \alpha_q g(\lambda_{t-j_q}) \quad (4)$$

Parameters are estimated using the BFGS optimization algorithm. This approach models count data with autocorrelation, allowing accurate mortality predictions.

Generalized Linear Autoregressive Moving Average (GLARMA)

Generalized Linear Autoregressive Moving Average (GLARMA) models analyze count time series data using an autoregressive structure, in which current values depend on past observations and residuals. It combines generalized linear models (GL) and autoregressive moving average (ARMA) models, suitable for Poisson and Negative Binomial distributions, matching the data characteristics. The *glarma* package in R implements this via the *glarma* function given in Equation 5.

$$\log(\mu_t) = W_t = X_t^T \beta + k_t + Z_t, \quad (5)$$

where μ_t is the mean mortality outcome at time t , $X_t^T \beta$ is a series of terms that specify the linear predictors and intercept of the mortality outcomes. k_t is the offset, a fixed value added or subtracted from the predicted mortality outcomes. Z_t is the moving average process, which uses past error outcomes to predict future mortality outcomes. The k_t term can be removed since no offset will be applied to the model, and the $X_t^T \beta$ term can be modified into the intercept term because the dataset has no predictors, leading to Equation 6.

$$\log(\mu_t) = W_t = \text{intercept} + Z_t, \quad (6)$$

The formula of the moving average process is described by Equation 7.

$$Z_t = \sum_{i=1}^p \phi(Z_{t-i} + e_{t-i}) + \sum_{i=1}^q \theta_i(e_{t-i}) \quad (7)$$

where Z_{t-i} is the previously computed process at time $t - i$, and e_{t-i} are the previously observed residuals at time $t - i$. The equation can be further simplified to account for single-point variation by removing the summations from both terms, so that the lag term contains only that lagged value, as given by Equation 8.

$$Z_t = \phi_p(Z_{t-p} + e_{t-p}) + \theta_q(e_{t-q}) \quad (8)$$

Parameters ϕ and θ are estimated by Fisher scoring via the glarma function, using Pearson residuals to ensure stable estimation (Dunsmuir, 2015).

Model Selection

The study utilizes various model selection methods to properly identify the most appropriate model for the selected form of mortality. The Akaike Information Criterion (AIC) is a statistical technique for comparing models by balancing goodness of fit and model complexity. The AIC considers the number of parameters to avoid overfitting. In this research, AIC was used to determine which model best fit the chosen form of mortality, and the model with the lower AIC value was selected. The AIC function is available in RStudio's "stats" package.

The Mean Absolute Error (MAE) was employed in this research to assess and compare the predictive ability of the TSGLM and GLARMA models. The average absolute difference between the observed and predicted mortality values was calculated for each model, and the models' forecasting accuracy was determined based on this. The model with the smaller MAE value was chosen as the better-performing model. The MAE function is available in RStudio's *Metrics* package.

RESULTS AND DISCUSSION

The descriptive statistics of the three collected datasets were analyzed for patterns, trends, and insights that could help establish relationships and significant differences in the data. As shown in Table 1, the variances across all subgroups exceed their respective means. This indicates overdispersion in the count data, suggesting that the negative binomial distribution could be a better fit and yield more accurate predictions than models that assume equal mean and variance.

Table 1

KPSS Test Results

KPSS Test		
<i>Dataset</i>	<i>stat</i>	<i>p-value</i>
Neonatal	0.305	0.1*
Infant	0.635	0.1*
Under-Five	0.722	0.1*

Test of Stationarity

Table 2 summarizes the results of the KPSS test for stationarity, which is necessary for the assumptions of the Count TS GLM and GLARMA models. The null hypothesis of the KPSS test is that the data are stationary. Since the p-values across all datasets are greater than 0.05, the null hypothesis was rejected, indicating that the datasets are stationary.

Table 2

KPSS Test Results

KPSS Test		
<i>Dataset</i>	<i>stat</i>	<i>p-value</i>
Neonatal	0.305	0.1*
Infant	0.635	0.1*
Under-Five	0.722	0.1*

*Note: p-value = 0.1 means p-value ≥ 0.10

Partial Autocorrelation Function (PACF) and Autocorrelation Function (ACF) Plots

The Autocorrelation Function (ACF) and Partial Autocorrelation Function (PACF) plots (see Figures 2 through 4) are used to identify the appropriate autoregressive (p) and moving average (q) orders for the models. Across the Neonatal, Infant, and Under-Five Mortality data, the PACF plots consistently show a significant spike only at lag 1, indicating a direct influence primarily from the immediate past observation. In contrast, the ACF plots exhibit multiple significant lags, mostly ranging from lag 0 to 6, suggesting both direct and indirect correlations over several previous time points. Higher lag values, such as those beyond 6, tend to be less meaningful and could add unnecessary complexity to the models without improving accuracy.

Based on these patterns, initial p and q values ranging from 1 to 6 are chosen for model testing across all subgroups. This range balances capturing significant temporal dependencies with model simplicity, with further adjustments guided by model selection criteria such as the Akaike Information Criterion (AIC).

Figure 2

PACF and ACF plots for Neonatal Mortality

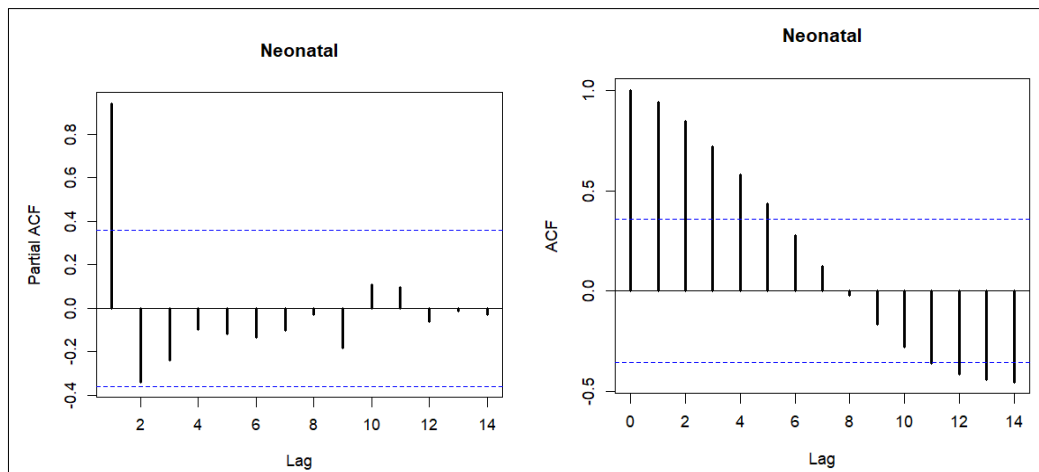


Figure 3

PACF and ACF plots for Infant Mortality

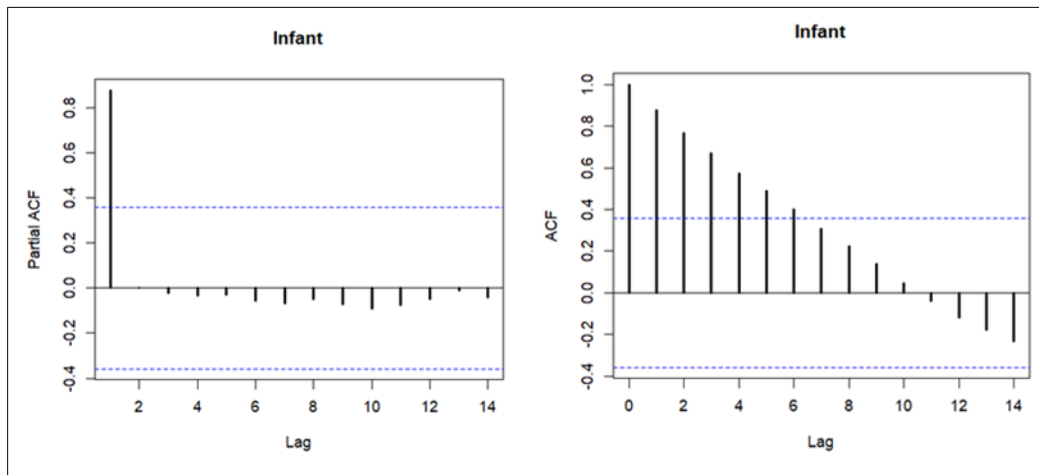
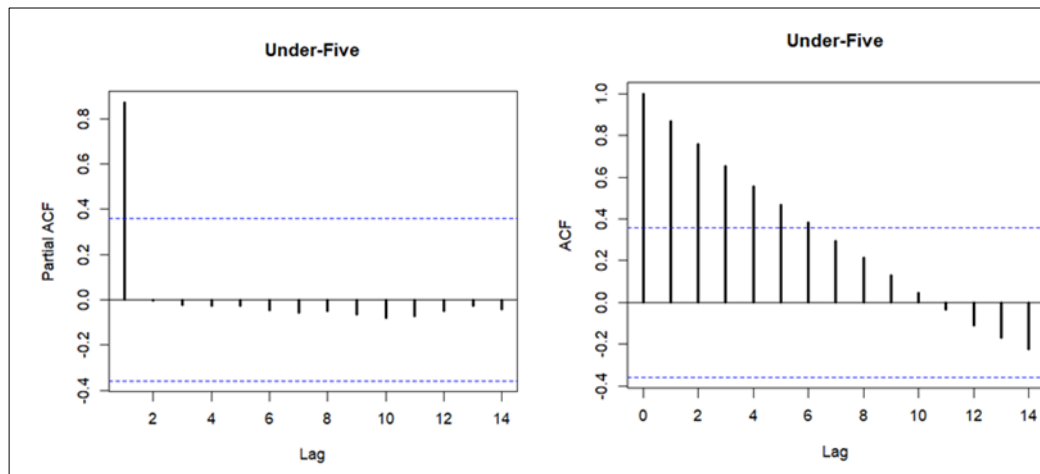


Figure 4

PACF and ACF plots for Under-Five Mortality



Model Metric Test Results

Model performance was compared across different P and Q values using Negative Binomial and Poisson distributions for neonatal, infant, and under-five mortality data. The best models were selected based on AIC, with MAE used to assess forecast accuracy. Results include Single-Point and Cumulative lag variations. Tables show the top models and their performance.

Count TS GLM

Table 3 shows the optimal Count TS GLM model for every distribution and variation over all datasets. The best P, Q values for every dataset are as follows: Neonatal Mortality (P = 1, Q = 2) with AIC 469.04, Infant Mortality (P = 1, Q = 2) with AIC 504.82, and Under-Five Mortality (P = 1, Q = 5) with AIC 543.45. The outputs also indicate that, although the AIC values for both probability distributions are quite close, the Negative Binomial models consistently have lower AIC values than the Poisson models and are therefore the best choice. This may indicate that the variance of each dataset exceeds its

mean, a characteristic of a negative binomial distribution. Also, of the two model variations, Single-Point was superior only for Infant Mortality, whereas the Cumulative method performed better for the other two datasets.

Table 3

Best Count TS GLM Across Datasets

				Metrics	
Variation	P, Q	Distribution	AIC	MAE	
Neonatal Mortality					
Single-Point	1, 5	Negative Binomial	474.75	404.14	
Single-Point	1, 5	Poisson	658.98	404.14	
Cumulative	1, 2	Negative Binomial	469.04	410.48	
Cumulative	1, 2	Poisson	590.90	410.48	
Infant Mortality					
Single-Point	1, 2	Negative Binomial	504.82	849.78	
Single-Point	1, 2	Poisson	880.06	849.78	
Cumulative	1, 3	Negative Binomial	515.89	884.91	
Cumulative	1, 3	Poisson	987.13	884.91	
Under-Five Mortality					
Single-Point	1, 5	Negative Binomial	568.13	2305.83	
Single-Point	1, 5	Poisson	3613.64	2305.83	
Cumulative	1, 5	Negative Binomial	543.45	1108.41	
Cumulative	5, 6	Poisson	1327.85	1239.78	

GLARMA

Table 4 summarizes the best GLARMA models for each distribution and approach across all datasets. The optimal P and Q values are: Neonatal Mortality ($p = 5$, $q = 6$) with an AIC of 1584.17, Infant Mortality ($p = 3$, $q = 4$) with an AIC of 636.03, and Under-Five Mortality ($p = 4$, $q = 2$) with an AIC of 615.92. The Poisson distribution provides the best fit for Neonatal Mortality, while the Negative Binomial distribution is preferred for Infant and Under-Five Mortality. For all datasets, the single-point variation was selected, as the cumulative approach consistently produced errors and failed to deliver comparable results.

Additionally, convergence issues were observed when p equaled q , particularly with the cumulative approach. These convergence failures across all parameter combinations suggest that the cumulative variation may not be suitable for modeling these child mortality subgroups using GLARMA.

Table 4

Best GLARMA Models Across Datasets

				Metrics	
Variation	P, Q	Distribution	AIC	MAE	
Neonatal Mortality					
Single-Point	2, 6	Negative Binomial	3863.21	11259.65	
Single-Point	5, 6	Poisson	1584.17	872.23	
Cumulative	-	Negative Binomial	-	-	
Cumulative	-	Poisson	-	-	
Infant Mortality					
Single-Point	3, 4	Negative Binomial	636.03	5227.56	
Single-Point	2, 1	Poisson	5579.36	2549.19	
Cumulative	-	Negative Binomial	-	-	
Cumulative	-	Poisson	-	-	
Under-Five Mortality					
Single-Point	4, 2	Negative Binomial	615.92	5449.79	
Single-Point	2, 1	Poisson	11033.86	4190.89	
Cumulative	-	Negative Binomial	-	-	
Cumulative	-	Poisson	-	-	

*Note: “-” indicates that there was no result for that type of model

Accuracy of Best Models

The fitted values from the best-performing GLARMA and TS GLM models were extracted for each dataset to compare their predictive performance directly. Figures 5 through 7 present the fitted values of both models against the actual mortality counts for neonatal, infant, and under-five categories. Across all three datasets, the TS GLM model consistently aligns more closely with the observed values, indicating superior predictive accuracy compared to the GLARMA model. In contrast, the GLARMA model exhibits noticeable deviations from the actual trends, particularly in the infant dataset, where a cyclical pattern is apparent.

The comparison of Mean Absolute Error (MAE) values, presented in Table 5, further supports these graphical findings. For all mortality subgroups, the TS GLM model records lower MAE values than the GLARMA model, confirming its stronger overall forecasting performance.

Figure 5

Actual vs TS GLM vs GLARMA for Neonatal Mortality

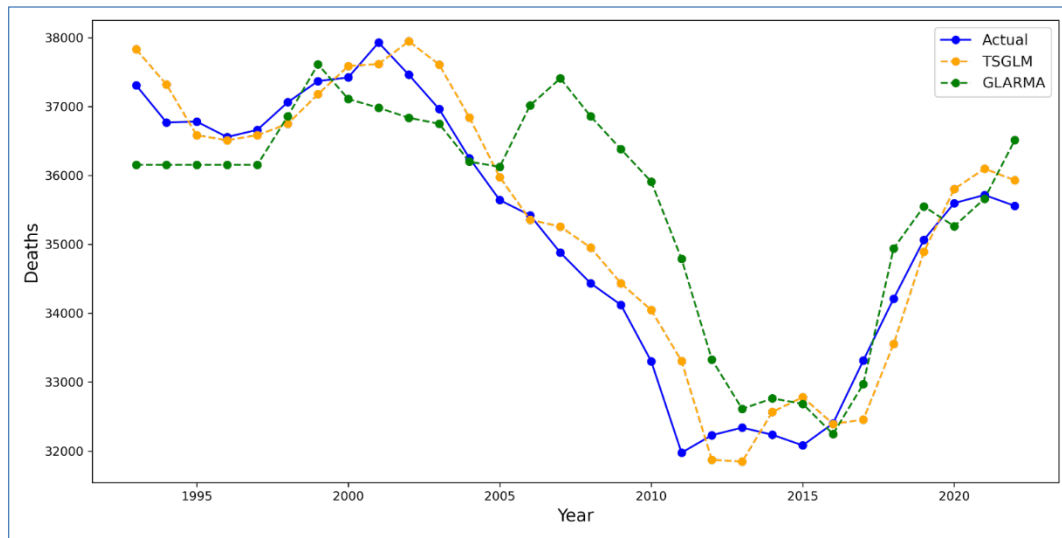


Figure 6

Actual vs TS GLM vs GLARMA for Infant Mortality

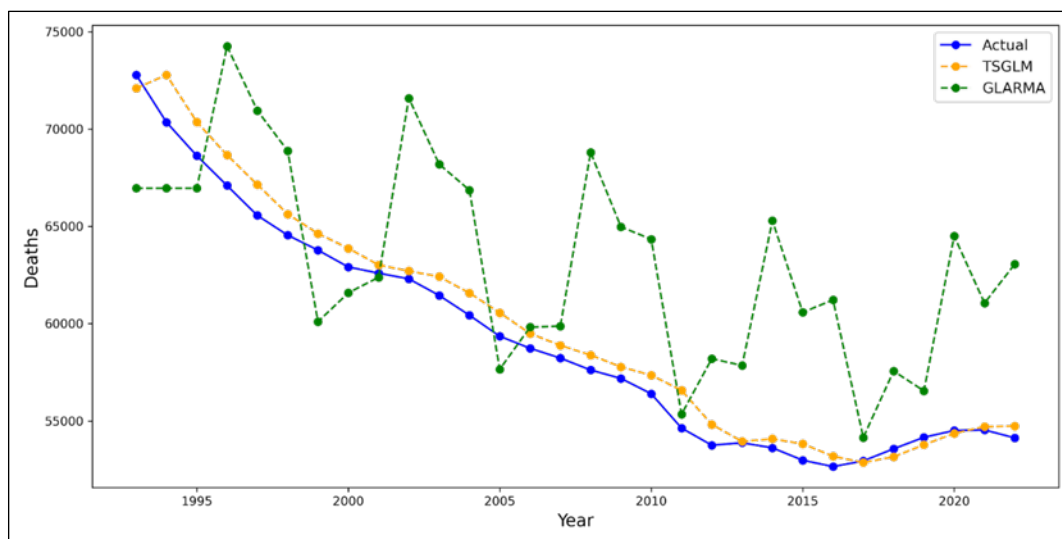


Figure 7

Actual vs TS GLM vs GLARMA for Under-Five Mortality

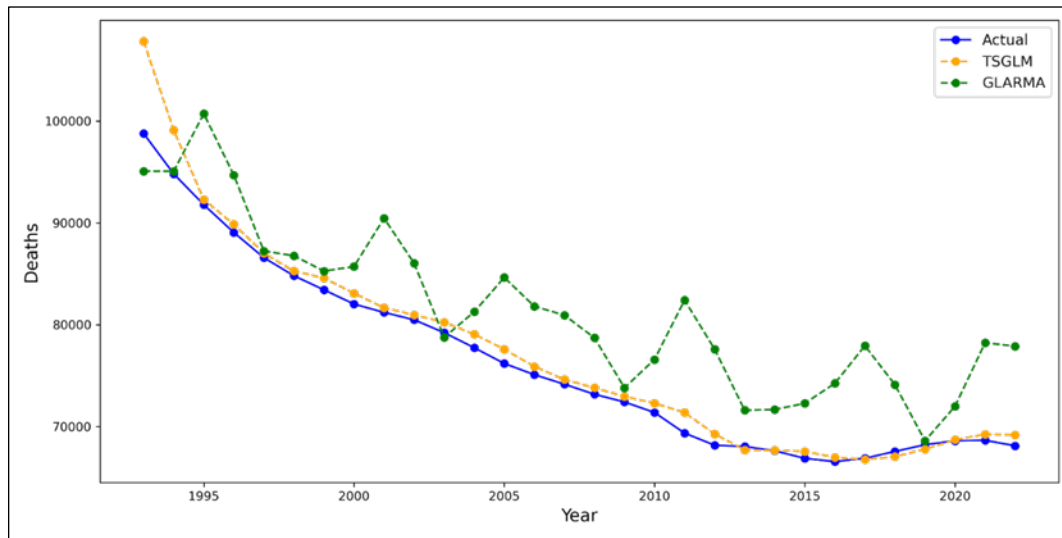


Table 5

MAE of Best Models for Neonatal Mortality

Model	Neonatal	Infant	Under-Five
TS GLM	410.48	849.78	1108.41
GLARMA	872.23	2549.19	4190.88

Model Parameters

The parameter estimation process for the best model is then conducted for the three age groups, to construct a model to predict future mortality outcomes. Once the optimal P and Q values were identified and compared with the best models from the other methods, the forecasting process began.

Modeling begins with estimating the model parameters, as shown in Tables 6 through 8. The negative binomial distribution approach of Count TS GLM can also estimate the magnitude of the dispersion parameter, σ^2 , which measures the variability of the count data beyond what a Poisson distribution would assume. The model was displayed similarly to the studies by Atmanegara (2019) and Liboschik (2017), who both used the log link function in a linear combination. They also display the mortality outcome for each subgroup using a TS GLM approach with a negative binomial distribution given by $Y_t | \lambda_t \sim \text{NegBin}(\lambda_t, \sigma^2)$.

Equations 9 through 11 show that the conditional mean of the outcome in year t is affected by the outcomes of the previous n years, where Y_{t-1} represents the outcome from the previous year and λ_{t-1} , λ_{t-2} , ..., λ_{t-n} represent the conditional means from the prior n years.

Table 6

Best Model Parameter Estimates for Neonatal Mortality

Parameters	Estimate	Std. Error	CI (lower)	CI (upper)
Intercept	0.469265	0.364	-0.24513	1.184
β_1	0.981310	0.146	0.69427	1.268
α_1	0.415391	0.209	0.00586	0.825
α_2	-0.441219	0.126	-0.6888	-0.194
σ^2	0.000209			

$$\log(\lambda_t) = 0.469265 + 0.981310Y_{t-1} + 0.415391\lambda_{t-1} - 0.441219\lambda_{t-2} \quad (9)$$

Table 7

Best Model Parameter Estimates for Infant Mortality

Parameters	Estimate	Std. Error	CI (lower)	CI (upper)
Intercept	0.142679	0.390	-0.622	0.907
β_1	0.990501	0.185	0.629	1.352
α_2	-0.003257	0.170	-0.336	0.329
σ^2	0.000269			

$$\log(\lambda_t) = 0.142679 + 0.990501Y_{t-1} - 0.003257\lambda_{t-2} \quad (10)$$

Table 8

Best Model Parameter Estimates for Under-Five Mortality

Parameters	Estimate	Std. Error	CI (lower)	CI (upper)
Intercept	0.088102	0.186	-0.277	0.454
β_1	0.962571	0.439	0.101	1.824
α_1	0.376683	0.693	-0.982	1.735
α_2	-0.372608	0.717	-1.778	1.033
α_3	0.233334	0.825	-1.383	1.850
α_4	-0.305782	0.600	-1.482	0.870
α_5	0.098200	0.243	-0.377	0.574
σ^2	0.000527			

$$\log(\lambda_t) = 0.088102 + 0.962571Y_{t-1} + 0.376683\lambda_{t-1} - 0.372608\lambda_{t-2} + 0.233334\lambda_{t-3} - 0.305782\lambda_{t-4} + 0.098200\lambda_{t-5} \quad (11)$$

Forecasting Results and Model Projections

The mortality projection results for the neonatal, infant, and under-five categories are presented using the best models. Figures 8 through 10 show the actual and forecasted values for the period 2023-2027. For all three categories, the forecasted values align with the actual values up to 2022, indicating that the models capture the trend accurately. However, from 2023 onwards, the forecast values show a steady increase in mortality rates across categories over a period of five years. The detailed numerical projections are presented in Table 9.

Figure 8

Actual vs. Predicted Neonatal Mortality

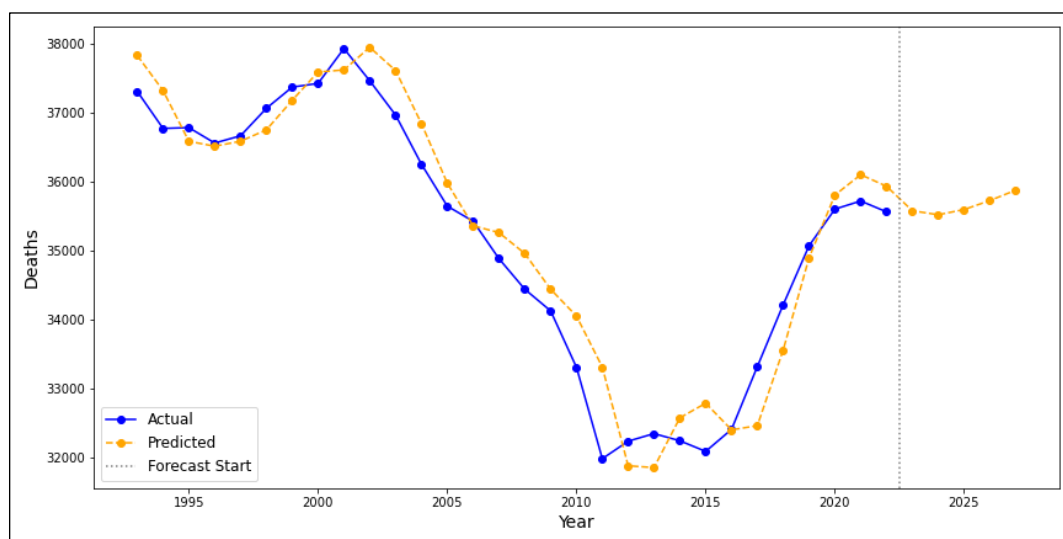


Figure 9

Actual vs. Predicted Infant Mortality

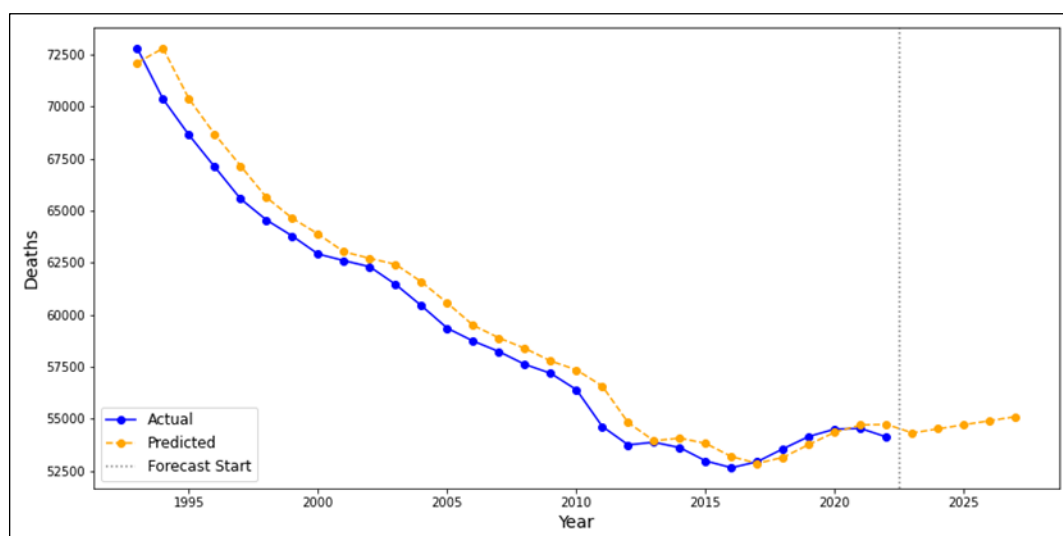


Figure 10

Actual vs. Predicted Under-Five Mortality

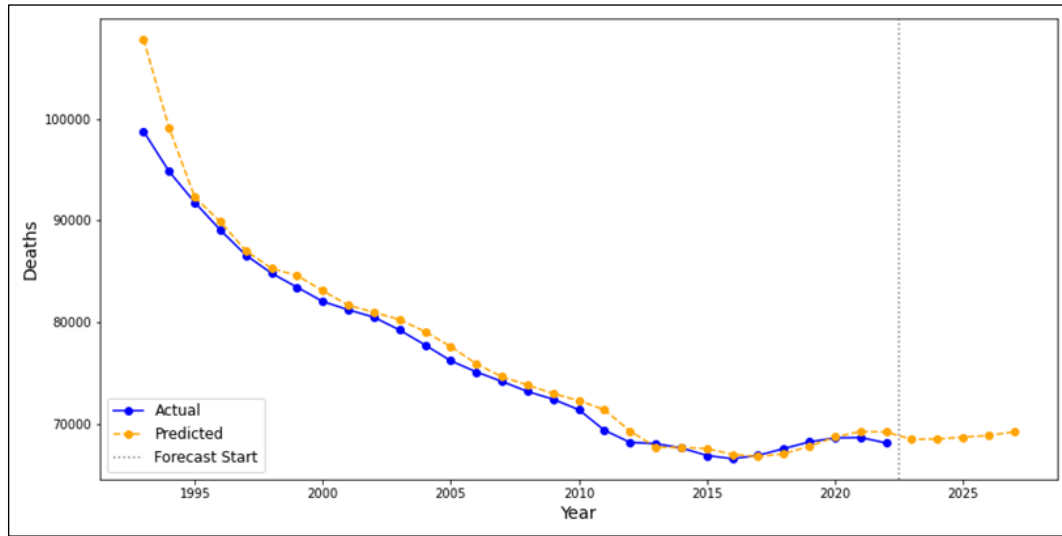


Table 9

Child Mortality Outcomes Forecasts

Year	Neonatal	Infant	Under-Five
2023	35574.80	54325.38	68474.61
2024	35517.23	54521.49	68485.82
2025	35592.66	54717.78	68684.02
2026	35723.81	54912.25	68845.80
2027	35874.19	54325.38	69206.19

Discussion

This study contributes to the existing literature by addressing gaps in research on time series modeling of child mortality using Count Time Series Generalized Linear Models (TS GLM) and Generalized Linear Autoregressive Moving Average (GLARMA) models. In particular, there are very few studies that directly compare TS GLM and GLARMA in terms of model performance, and none in particular in the context of forecasting child mortality. While both methods have been applied in various fields, their comparative effectiveness in this specific domain remains largely unexamined. As a result, there are very few prior findings against which the results can be directly compared, making it difficult to assess how well each method performs relative to established benchmarks. However, the study provides initial insights into their effectiveness in capturing child mortality trends, as well as a preview of each model's strengths and limitations. The results indicate that TS GLM generally outperforms GLARMA in terms of model accuracy. This suggests that TS GLM may be more effective for modeling child mortality trends, particularly for this specific univariate count-based time series with values within this range. This may also be because the GLARMA models showed cyclical patterns in their projected mortality results that did not fit the data trend. On the other hand, TS GLM had more stable and consistent results, making it more appropriate for this data. This is supported by the fact that, across all subgroups, the best-performing models (those that most accurately captured the actual values) were TS GLM models, as determined by AIC and MAE metrics.

Another essential part of the analysis is the comparison between cumulative and single-point variations in the TS GLM and GLARMA models. There is very limited research explicitly stating the use of cumulative versus single-point variations in forecasting within TS GLM and GLARMA models. For this reason, there are no well-established guidelines on when one might be more suitable than the other, so direct comparisons are often difficult. Combining both methods could give a wider picture of their efficiency, but more research is required to investigate their use in other settings. For TS GLM, the cumulative variation yielded better results for two subgroups, neonatal and under-five mortality, whereas for single-point, this was only 1 subgroup. Conversely, the single-point variation proved more efficient for all GLARMA subgroups, since the cumulative variation did not yield usable results for this model. These distinctions reflect the different ways each model represents mortality trends.

In addition, GLARMA has significant limitations when choosing model parameters. Both the moving average and the autoregressive terms may have simultaneous effects that interfere, and identifying their individual effects would be difficult. This may render the optimization procedure vulnerable to experiencing non-uniqueness or a lack of convergence to a solution. This problem is even more evident when $p = q$, in which no definite solution can be derived. These problems may lead to inconsistent estimates or computational errors in the model, further complicating its application to forecasting. Such shortcomings may account for the failure of the cumulative method to yield meaningful results for GLARMA, since the model's structural constraints may render it incapable of handling aggregated data. These results concur with and are validated by the research of Camara (2024) and Dunsmuir (2015), who recorded identical convergence problems when setting p and q values in GLARMA models. However, they made no mention of their findings on using the cumulative approach. Their study confirms the established limitations of GLARMA for time series prediction, especially where parameter identifiability and model stability are involved.

Further, our results demonstrate that the Negative Binomial (NB) distribution is preferred over the Poisson distribution in most models. This stems mainly from overdispersion in the data set, which causes the variance to be considerably larger than the mean, consistent with the descriptive statistics of the datasets. The use of the NB distribution is consistent with earlier studies, which reveal that overdispersion frequently occurs with real-world count data sets and tends to make the Poisson assumption inappropriate. Most notably, this result mirrors that of Rohaeti (2021), where their Count TS GLM model similarly preferred the NB over the Poisson due to overdispersion, as indicated by their estimated overdispersion parameter.

Despite external projections, such as the PSA SDG Watch Report, estimating a reduction in the mortality rate as part of global child health initiatives, the results of this study indicate that the absolute number of deaths could still be on the rise even when the mortality rate is falling. This is because the mortality rate is estimated as a ratio of deaths to live births, while the models in this study project the absolute number of deaths. If the number of live births is rising at a rate that is faster than the rate at which the mortality rate is falling, then the absolute number of deaths could still be on the rise.

A similar contrast appears in projections of neonatal mortality from other studies. By 2030, the rates were projected to decline to 8 (Nyomi, 2023) and 6.5 according to the 2023 PSA SDG Watch Report, highlighting a variation in anticipated progress depending on the source. While both references show a falling trend, the contrast between them points to the importance of examining the factors behind these differences further. Variations in data sources, methods, or assumptions regarding healthcare progress and demographic trends may be the cause of these inconsistencies. Also, although the above projections are specifically for neonatal mortality, similar inconsistencies may occur in infant and under-five

mortality rates as well, underscoring the importance of cross-checking multiple sources to understand future child mortality trends better.

SUMMARY AND RECOMMENDATIONS

Summary

This study compared the performance of Count Time Series Generalized Linear Models (TS GLM) and Generalized Linear Autoregressive Moving Average (GLARMA) models in forecasting neonatal, infant, and under-five mortality outcomes. The findings suggest that TS GLM, especially using the negative binomial distribution, outperformed GLARMA in terms of model fit and forecasting stability.

TS GLM handled overdispersion in the mortality outcomes more effectively and performed better in cumulative and single-point models than GLARMA, which faced issues with parameter estimation and convergence, especially when autoregressive and moving average parameters were estimated simultaneously. This made GLARMA less applicable in this particular data context.

The forecast from 2023 to 2027 using the best-performing TS GLM models indicates expected increments in mortality counts for the subgroups, which reiterates the need for specific public health interventions. The differences in expected values for the subgroups reiterate the importance of monitoring and planning at the subgroup level. The results suggest the applicability of TS GLM as a more stable and reliable approach for modeling and forecasting count mortality data in this scenario.

Recommendations

The results show an increase in projected child mortality, highlighting the importance of enhanced policy and programmatic responses. It is important to continue investing in health system strengthening, enhanced maternal and child health service delivery, increased nutrition programs for at-risk groups, and continued vaccination and health education campaigns. Monitoring of data should inform policy implementation to ensure that interventions are assessed and adjusted based on results.

The study concludes that the Time Series Generalized Linear Model (TS GLM) outperforms the Generalized Linear Autoregressive Moving Average (GLARMA) model in predicting child mortality outcomes. Therefore, the TS GLM model is recommended as a better approach for count-based time series forecasting in the healthcare domain. To increase generalizability, future studies are recommended to test the performance of the models on various datasets and populations.

Future work should also further compare TS GLM with more advanced forecasting models, such as machine learning models, on a comparable basis. It is also important to have a good validation strategy, such as using the 80-20 split for training and testing. Since this study has used mortality estimates from the United Nations Inter-Agency Group for Child Mortality Estimation (UN IGME), future studies should also use other data sources, such as the Philippine Statistics Authority (PSA) and the Department of Health (DOH) of the Philippines, to compare the estimates with the international estimates. Future research may explore alternative model specifications to address issues related to parameter identifiability and convergence. Expanding the dataset's time horizon and incorporating additional subgroup analyses, such as regional differences, maternal health indicators, demographic factors, and socioeconomic variables, may also improve model performance and provide deeper insight into the underlying drivers of child mortality trends.

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CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

DECLARATION OF GENERATIVE AI USE

No AI was used in the writing, preparation, or any other aspect of this manuscript.

DATA AVAILABILITY

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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