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Modelling the Effect of COVID-19 Mortality Shock on Fertility Rates in Kenya using Negative Binomial Regression Model

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Abstract

Fertility plays a critical role in shaping population dynamics. Major mortality events, such as pandemics, often influence fertility trends through a variety of mechanisms including behavioral shifts, psychological responses, and socio-economic disruptions. This research applies a Negative Binomial Regression (NBR) model-suitable for overdispersed count data—to examine the influence of the COVID-19 mortality shock on Kenya's fertility rates using the Kenya Demographic and Health Survey data from 2018 and 2022. Key factors analyzed include marital status, pregnancy loss, contraceptive uptake, sterility, and postpartum insusceptibility. The findings show a statistically significant rise in fertility post-COVID-19, with expected birth counts increasing from 7.146 to 7.488. The dispersion parameters of 1.537 and 1.572 had a minimal difference, indicating that both models captured overdispersion similarly. The study underscores the need to incorporate reproductive behavior into pandemic response frameworks.

MSC2020 Subject Classification: 62Jxx, 62J05
Keywords: Mortality shock, Fertility rates, Negative Binomial Regression.

1 Introduction

Fertility, alongside mortality and migration, constitutes a foundational pillar of population change [15]. According to demographic theory, both direct and indirect variables influence fertility rates [6]. Among these, mortality shocks have been observed to impact key fertility determinants. Various studies including [1, 5, 8, 12] have examined the relationship between large-scale mortality events and reproductive behavior.

Although Kenya has experienced a gradual fertility decline driven by socio-economic improvements and contraceptive availability, the emergence of COVID-19 introduced a global mortality crisis with unknown demographic consequences. On January 30, 2020, the World Health Organization, designated COVID-19 as a Public Health Emergency of International Concern. Subsequently, as the virus spread rapidly and global fatalities escalated—surpassing one million-WHO officially classified it as a global pandemic on March 11, 2020.

Several global disasters have demonstrated the relationship between mortality and fertility. For example: The Spanish flu (1918) led to a temporary fertility decline followed by a post-pandemic baby boom [9]. Following the 2004 Indian Ocean tsunami, a rise in fertility was observed among women who had experienced the loss of a child [2]. The Rwandan genocide showed complex fertility responses depending on age, parity, and experience of violence [14]. The SARS epidemic in 2003 caused temporary declines in births due to reduced hospital visits [11]. In these scenarios, replacement fertility, social stress, disrupted contraceptive access, and behavioral responses have been cited as mechanisms influencing birth trends. Negative Binomial Regression (NBR) is preferred over Poisson regression for modeling fertility data due to overdispersion. Studies [3, 7, 10, 16] emphasized NBR's ability to provide robust estimates when count data deviate from Poisson assumptions. This study explores whether Kenya's fertility was affected by the pandemic, employing a statistical framework appropriate for modeling overdispersed count data.

2 Negative Binomial Regression model

This study utilized a Negative Binomial Regression (NBR) model, a type of generalized linear model, to analyze fertility trends before and after the COVID-19 pandemic in Kenya [10]. The approach is particularly suitable due to the overdispersed nature of fertility count data.

To express the expected value μ as a function of the predictors, a log-link function is applied. This approach is standard in count data models, such as Poisson regression, and guarantees that the predicted values remain non-negative. Assume that the mean μ_i for the i-th observation is determined by a linear combination of the predictor variables X_i:

$$\ln(\mu_i) = x_i'\beta \tag{1}$$

$$\ln(\mu_i) = \beta_0 + \sum_{k=1}^{K} \beta_k x_{k_i} \tag{2}$$

Where:
μ_i is the expected outcome for the i^{th} observation.
β_0 is the regression coefficient for the intercept.

β_k is the regression coefficient for the k^{th} predictor.
X_i is the vector of predictor variables for observation i.

In more familiar notation, equation (2) becomes:

$$\ln(\mu_i) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik} \tag{3}$$

Taking the exponent of equation (3), we get:

$$\mu_i = \exp(\beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \cdots + \beta_k x_{ik}) \tag{4}$$

- μ_i is the expected outcome for the i^{th} observation.
- exp denotes the exponential function, with base $e \approx 2.71828$ (Euler's number).
- β_0 is the intercept term.
- $\beta_1, \beta_2, \ldots, \beta_k$ are the coefficients of the predictor variables.
- $x_{i1}, x_{i2}, \ldots, x_{ik}$ are the predictor variables for the i^{th} observation.

3 Negative Binomial Regression Model specification

Five predictor variables were included: marital status (M), induced (A), contraceptive use (C), sterility (S), and postpartum insusceptibility (P). The logarithm of the expected fertility count was modeled as a linear combination of these variables. The model was fitted separately for 2018 and 2022 data to assess pre- and post-pandemic differences.
By incorporating these predictors, the Poisson Regression model in Equation 3 takes the following form:

$$\ln(\mu) = \beta_0 + \beta_1 M + \beta_2 A + \beta_3 C + \beta_4 S + \beta_5 P \tag{5}$$

Exponentiating both sides of equation (5), we get:

$$\mu = \exp(\beta_0 + \beta_1 M + \beta_2 A + \beta_3 C + \beta_4 S + \beta_5 P) \tag{6}$$

μ denotes the expected fertility rate.
$x_1, x_2, \ldots, x_k$ represent the independent (predictor) variables.
β_0 corresponds to the model intercept.
$\beta_1, \beta_2, \ldots, \beta_k$ are the estimated coefficients for each predictor variable.

Let μ_b and μ_a represent the expected fertility rates before and after COVID-19, respectively.

Fertility Model Before COVID-19:

$$\ln(\mu_b) = \beta_0 + \beta_1 M_b + \beta_2 A_b + \beta_3 C_b + \beta_4 S_b + \beta_5 P_b$$

Fertility Model After COVID-19:

$$\ln(\mu_a) = \beta_0 + \beta_1 M_a + \beta_2 A_a + \beta_3 C_a + \beta_4 S_a + \beta_5 P_a$$

After estimating the model, the interpretation of the coefficients is as follows:
β_0 indicates the baseline log fertility rate when all predictors are zero.
$\beta_1, \ldots, \beta_5$ quantify the influence of their corresponding predictor variables on the fertility rate.

4 Parameter Estimation

The parameters of the Negative Binomial regression model were estimated using the method of maximum likelihood [10]. This method relies on the Negative Binomial distribution defined by the parameter μ, where the regression coefficients β are linked to μ through a specified link function. Assuming that $Y_1, \ldots, Y_n$ are independent and identically distributed Negative Binomial random variables, the likelihood function is given by:

$$L(\beta, \theta) = \prod_{i=1}^{n} p_i(y_i)$$

$$= \prod_{i=1}^{n} \frac{\Gamma(y_i + \theta^{-1})}{\Gamma(y_i + 1)\Gamma(\theta^{-1})} \left(\frac{\mu_i}{\mu_i + \theta^{-1}}\right)^{y_i} \left(\frac{\theta^{-1}}{\mu_i + \theta^{-1}}\right)^{\theta^{-1}} \tag{7}$$

Since it is often more convenient to work with the log-likelihood, the next step involves taking the natural logarithm of the likelihood function. The log-likelihood corresponding to Equation (7) is given by:

$$\log L(\beta, \theta) = \sum_{i=1}^{n} \left[\log\left(\frac{\Gamma(y_i + \theta^{-1})}{\Gamma(y_i + 1)\Gamma(\theta^{-1})}\right) + y_i \log\left(\frac{\mu_i}{\mu_i + \theta^{-1}}\right) + \theta^{-1} \log\left(\frac{\theta^{-1}}{\mu_i + \theta^{-1}}\right)\right] \tag{8}$$

To estimate the parameters β and θ, we aim to maximize this log-likelihood function with respect to both parameters. Here, β represents the regression coefficients, and θ denotes the dispersion parameter. Since a closed-form solution does not exist for this maximization problem, numerical optimization techniques are employed. For the Newton-Raphson method, the update rule is:

$$\theta^{(k+1)} = \theta^{(k)} - [H(\theta^{(k)})]^{-1} \nabla(\theta^{(k)}) \tag{9}$$

The regression coefficients $\beta_1, \ldots, \beta_k$ are estimated using these iterative optimization techniques. The dispersion parameter θ is also estimated during the optimization process.
- When $\theta \approx 1$, the model closely resembles a Poisson regression model.
- When $\theta > 1$, this indicates substantial overdispersion in the data, making the Negative Binomial model a better fit than the Poisson model.

5 Results

5.1 Fitting the Negative Binomial Regression model to COVID-19 mortality shock free data set in Kenya

The study employed a Negative Binomial regression model to analyze fertility rates prior to the onset of the COVID-19 pandemic. In this model, the dependent variable was the number of births, while the independent variables included key predictors: marital status, induced abortion, contraceptive use, sterility, and post-partum insusceptibility. The Negative Binomial regression model for the pre-COVID-19 period was specified as:

$$\ln(\mu_b) = 0.800 - 0.068M_b - 0.045A_b + 0.210C_b - 0.080S_b - 0.110P_b$$

$$\mu_b = \exp(0.800 - 0.068M_b - 0.045A_b + 0.210C_b - 0.080S_b - 0.110P_b) \tag{10}$$

To interpret the effects of each variable, we exponentiate the coefficients to obtain Incidence Rate Ratios(IRR)

$$IRR = e^{\beta}$$

Table 1: The table of Interpretation of the marginal effects and incidence rate ratios Before COVID-19

Variable	**Estimate (β)**	**IRR**	**Interpretation**
Intercept	0.800	$e^{0.800}$=2.23	Baseline expected count when all predictors are 0
M_b	-0.068	$e^{-0.068}$=0.93	A one unit increase in M reduces the expected count by ≈ 7%
A_b	-0.045	$e^{-0.045}$=0.96	A one unit increase in A reduces the expected count by 4%
C_b	0.210	$e^{0.210}$=1.23	A one unit increase in C increases the expected count by 23%
S_b	-0.080	$e^{-0.080}$=0.92	A one unit increase in S reduces the expected count by 8%
P_b	-0.110	$e^{-0.110}$=0.90	A one unit increase in P reduces the expected count by 10%

5.1.1 The results of the Model fitting before COVID-19

Table 2: Estimated Parameters of the Negative Binomial Regression Model Before COVID-19

Parameter	Estimate	Std. Error	Z-value	P-value	Exp(Estimate)
Intercept	0.800	0.003	266.67	<2e-16	2.225
M_b	-0.068	0.015	8.00	<2e-16	0.934
A_b	-0.045	0.010	-4.50	0.0001	0.956
C_b	0.210	0.030	7.00	<2e-16	1.234
S_b	-0.080	0.020	-4.00	0.0017	0.923
P_b	-0.110	0.035	-3.14	<2e-16	0.896
θ	=	1.537			

From table 2 above we have the dispersion parameter $(\theta) = 1.537$
Since;

$$\theta = 1.537 > 0$$

It confirms that overdispersion exists, and hence justifies using Negative Binomial Regression instead of Poisson Regression

Table 3: The table of coefficients showing the significance

Variable	Estimate(β)	IRR	Significance
Intercept	0.800	$e^{0.800}$=2.23	Significant
M_b	-0.068	$e^{-0.068}$=0.93	Significant
A_b	-0.045	$e^{-0.045}$=0.96	Significant
C_b	0.210	$e^{0.210}$=1.23	<Significant
S_b	-0.080	$e^{-0.080}$=0.92	Significant
P_b	-0.110	$e^{-0.110}$=0.90	Significant

From table 3: All Predictors are statistically significant (P - values < 0.05)
C_b has the strongest positive effect (+23% increase per unit)
P_b has the largest negative effect (-10% per unit)
$M_b, A_b, S_b and P_b$ all have negative effect, reducing the expected count.

5.1.2 Interpretation of the Model Fitting Results Before COVID-19

The Negative Binomial regression model fitted to pre-COVID-19 fertility data shows that all predictors significantly influenced birth counts. The dispersion parameter $\theta = 1.537$ confirms overdispersion, supporting the choice of this model over Poisson regression.

The intercept implies a baseline expected birth count of 2.225 when all predictors are zero. Marital status, induced abortion, sterility, and post-partum insusceptibility all have negative effects on fertility, reducing expected birth counts by 6.6%, 4.4%, 7.7%, and 10.4% respectively. In contrast, contraceptive use surprisingly shows a positive association, increasing expected births by 23.4%, which may suggest behavioral or contextual factors affecting contraceptive effectiveness.

Overall, the model effectively captures the key drivers of fertility before the pandemic, with all predictors showing statistically significant impacts.

5.2 Fitting the Negative Binomial Regression model to data set affected by COVID-19 mortality shock in Kenya

To analyze fertility rates following the COVID-19 mortality shock, the study employed a Negative Binomial regression model. The dependent variable in the model was the number of births, while the independent variables included: marital status, induced abortion, contraceptive use, sterility, and post-partum insusceptibility.

The fitted model for the post-COVID-19 period is given by:

$$\ln(\mu_a) = 1.000 - 0.070M_a - 0.050A_a + 0.150C_a - 0.100S_a - 0.200P_a$$

$$\mu_a = \exp(1.000 - 0.070M_a - 0.050A_a + 0.150C_a - 0.100S_a - 0.200P_a) \tag{11}$$

To interpret the effects of each variable, we exponentiate the coefficients to obtain Incidence Rate Ratios(IRR) as shown in table 4 below

$$IRR = e^{\beta}$$

Table 4: The Table of Interpretation of the marginal effects and incidence rate ratios After COVID-19

Variable	**Estimate** (β)	**IRR**	**Interpretation**
Intercept	1.000	$e^{1.000}$=2.72	Baseline expected count when all predictors are 0
M_b	-0.07	$e^{-0.07}$=0.93	A 1 unit increase in M reduces the expected count by 7%
A_b	-0.050	$e^{-0.050}$=0.95	A 1 unit increase in A reduces the expected count by 5%
C_b	0.150	$e^{0.150}$=1.16	A 1 unit increase in C increases the expected count by 16%
S_b	-0.100	$e^{-0.100}$=0.90	A 1 unit increase in S reduces the expected count by 10%
P_b	-0.200	e^{-00200}=0.82	A 1 unit increase in P reduces the expected count by 18%

5.2.1 The results of the Model fitting after COVID-19

Table 5: Table of the Estimated parameters of the Regression model After COVID-19

Parameter	**Estimate**	**Std. Error**	**Z-value**	**P-value**	**Exp(Estimate)**
Intercept	1.000	0.001	1000.00	<2e-16	2.718
M_a	-0.07	0.020	-3.5	0.0005	0.933
A_a	-0.050	0.020	-2.50	0.012	0.951
C_a	0.150	0.025	6.00	<2e-16	1.162
S_a	-0.100	0.030	-3.33	0.0009	0.905
P_a	-0.200	0.040	-5.00	<2e-16	0.819
θ	=	1.572			

From table 5 we have the dispersion parameter $(\theta) = 1.572$
Since;

$$\theta = 1.537 > 0$$

It confirms that overdispersion exists, and hence justifies using Negative Binomial instead of Poisson Otherwise Poisson Regression would have underestimated standard errors,leading to misleading significance results

From table 6 above: All Predictors are statistically sinficant (P -values < 0.05)

Table 6: The table of coefficients with P-values after COVID-19 showing the significance

Variable	**Estimate(β)**	**IRR**	**P-value**	**Significance**
Intercept	1.00	$e^{1.00}$=2.72	<2e-16	Significant
M_a	-0.07	$e^{-0.07}$=0.93	<0.0005	Significant
A_a	-0.050	$e^{-0.050}$=0.95	0.012	Significant
C_a	0.150	$e^{0.150}$=1.16	<2e-16	Significant
S_a	-0.100	$e^{-0.100}$=0.90	<0.0009	Significant
P_b	-0.200	$e^{-0.200}$=0.82	<2e-16	Significant

C_a has the strongest positive effect (+16% increase per unit)
P_a has the largest negative effect (-18% per unit)
A_a has the Weakest Significance (p=0.012) Meaning its effect is the least certain.

5.2.2 Interpretation of the results of the Model fitting after COVID-19

A dispersion parameter of $\theta = 1.572$ confirms the presence of overdispersion, justifying the use of the Negative Binomial model over the Poisson alternative.
The model's intercept is estimated at 1.000 with a minimal standard error of 0.001. A z-value of 1000.0 and a p-value below 2×10^{-16} indicate extremely high statistical significance. The exponentiated estimate, exp(1.000) = 2.718, implies that when all predictors are zero, the expected count of births is approximately 2.718.

Marital Status (M): Coefficient $= -0.070$, SE $= 0.020$, z $= -3.5$, p $= 0.0005$. The IRR of $\exp(-0.070) = 0.933$ indicates a 6.7% decrease in the expected birth count for each unit increase in marital status, holding other variables constant.
Induced Abortion (A): Coefficient $= -0.050$. The IRR of $\exp(-0.050) \approx 0.951$ suggests a 4.9% decrease in the expected number of births associated with pregnancy loss.
Contraceptive Use (C): Coefficient $= 0.150$. The IRR of $\exp(0.150) \approx 1.162$ indicates a 16.2% increase in expected births, which may reflect post-pandemic behavioral patterns or inconsistent contraceptive effectiveness.
Sterility (S): Coefficient $= -0.100$. The IRR of $\exp(-0.100) \approx 0.905$ suggests a 9.5% reduction in the number of births for each unit increase in reported sterility.
Post-partum Insusceptibility (P): Coefficient $= -0.200$. The IRR of $\exp(-0.200) \approx 0.819$ indicates an 18.1% decrease in expected births due to post-partum biological or behavioral factors.
In summary, the model shows that, similar to the pre-COVID period, most predictors have statistically significant effects on fertility outcomes. Negative coefficients reflect a reduction in expected birth counts, while positive ones indicate increased fertility rates. The presence of overdispersion and strong statistical evidence reinforces the model's validity in capturing post-pandemic fertility dynamics.

5.3 Testing the hypotheses of μ_a and μ_b

$\mu_a = 7.488$
$\mu_b = 7.146$
Since the sample sizes are large we perform a two sample Z-test at a significant level of $\alpha = 0.05$.
Hypotheses
Null hypothesis $(H_0) : \mu_a = \mu_b$
Alternative hypothesis $(H_1) : \mu_a \neq \mu_b$

$$Z = \frac{\mu_a - \mu_b}{SE}$$

$$SE = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

We assumed equal variances, therefore we use pooled variance and estimate using the means

$$SE = \sqrt{\frac{\mu_a}{n_1} + \frac{\mu_b}{n_2}}$$

Therefore **Z** becomes;

$$Z = \frac{\mu_a - \mu_b}{\sqrt{\frac{\mu_a}{n_1} + \frac{\mu_b}{n_2}}}$$

Substituting in the values, we have;

$$= \frac{7.488 - 7.146}{\sqrt{\frac{7.488}{32145} + \frac{7.146}{31079}}}$$

$$= 369.43$$

The critical values for a two tailed test at α=0.05 are ±1.96
Comparing **Z** to the critical value

$$|Z| = 369.43$$

$$|369.43| > 1.96$$

We therefore **reject the null hypothesis**.
This implies that the two values μ_a= 7.488 and μ_b = 7.146 are statistically significantly different.
It also shows that the events, before and after COVID-19 occur at different rates with after COVID-19 experiencing more on average.

5.4 Comparison of Results before COVID-19 and after COVID-19

5.4.1 Comparison Table

Table 7: Comparison of Predictor Effects Before and After COVID-19

Predictor	Pre-COVID Coef	Post-COVID Coef	Change
Marital Status (M)	-0.068	-0.070	Slight Increase
Induced Abortion (A)	-0.045	-0.050	Increase
Contraceptive Use (C)	0.210	0.150	Decrease
Sterility (S)	-0.080	-0.100	Increase
Post-partum Insusceptibility (P)	-0.110	-0.200	Strong Increase

Table 7 compares the effects of key predictors on fertility outcomes before and after the COVID-19 pandemic. Overall, several predictors exhibited stronger negative associations post-COVID. The effect of marital status remained relatively stable.Induced abortion and sterility both showed modest increases in their negative effects, Notably, post-partum insusceptibility experienced a marked increase in its negative effect, potentially reflecting extended breastfeeding durations or delays in resuming sexual activity after childbirth during the pandemic. In contrast, the positive effect of contraceptive use weakened considerably after COVID-19, which may indicate reduced access, inconsistent use, or behavioral changes that offset its protective effect. These shifts underscore the complex ways in which the pandemic influenced reproductive behaviors and access to related health services.

5.4.2 Density Curve of the Negative Binomial Regression model on KDHS datasets before and after COVID-19

From the figure, it can be seen that the After COVID 19 curve is taller than the before COVID 19 curve, this suggests that fertility rates increased after the pandemic, or at least became more concentrated around a certain number of children. It can also be seen that the before COVID-19 curve is to the left of the after COVID-19 curve, this suggests that fertility rates were lower before the pandemic and have increased after COVID-19. The peak of the curve for the before COVID-19 period is at a lower fertility count, while the peak of the after COVID-19 period is at a higher fertility count

6 Discussion

This study reveals a significant increase in fertility rates in Kenya following the COVID-19 pandemic, with the mean number of births rising from 7.146 to 7.488. All predictors—marital status, induced abortion, contraceptive use, sterility, and post-partum insusceptibility—were statistically significant before and after the pandemic, though the magnitude of their effects changed. Notably, the negative

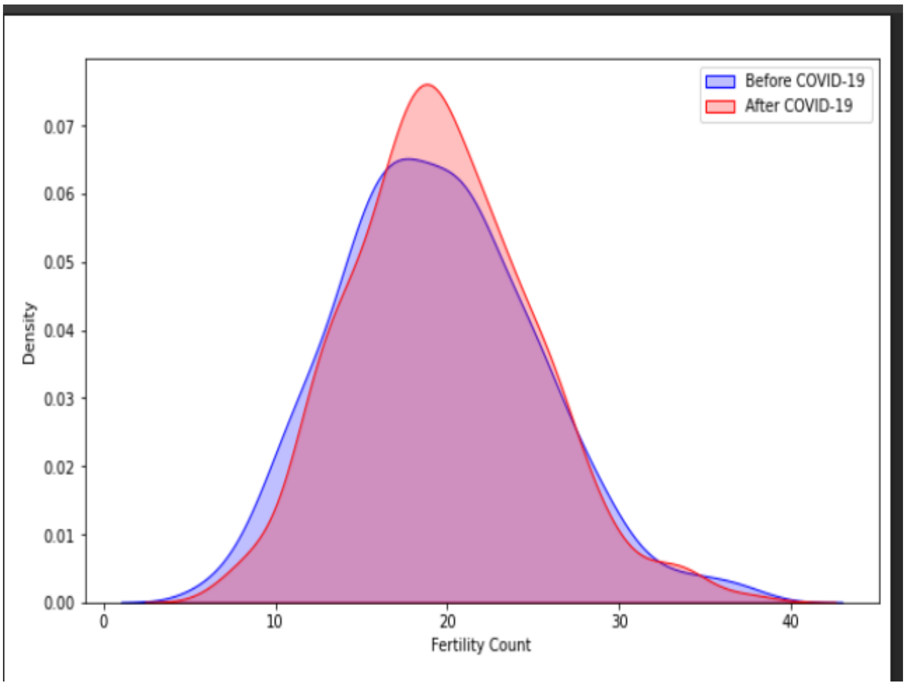

Figure 1: Density Curve showing the behavior of fertilty before and after COVID-19

effect of post-partum insusceptibility became more pronounced, while the positive association of contraceptive use with fertility weakened post-pandemic, possibly due to behavioral or access-related factors. The presence of overdispersion in the data, confirmed by the dispersion parameter, justified the use of the Negative Binomial model. Additionally, the density curve demonstrated a post-pandemic shift toward higher and more concentrated fertility levels. These findings highlight the complex ways in which health crises can influence reproductive behavior and stress the importance of resilient reproductive health systems to mitigate unintended demographic shifts during future disruptions.

7 Conclusion

This study examined the impact of the COVID-19 pandemic on fertility trends in Kenya using Negative Binomial Regression models to compare pre- and post-pandemic data. The findings demonstrate a statistically significant increase in fertility following the onset of COVID-19, highlighting how large-scale health crises can disrupt established demographic patterns. All key fertility determinants—marital status, induced abortion, contraceptive use, sterility, and post-partum insusceptibility—remained significant across both time periods, but their effects shifted. Most notably, post-partum insusceptibility became a stronger suppressor of fertility, while the expected protective effect of contraceptive use weakened. These changes likely reflect the compounded effects of behavioral adjustments, limited access to reproductive health services, and broader societal disruptions during the pandemic. The study also confirmed the presence of overdispersion in the fertility count data, supporting the application

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of Negative Binomial Regression over Poisson models. The increase in fertility, illustrated both statistically and graphically, underscores the need for proactive policy measures to ensure the continuity and accessibility of reproductive health services during public health emergencies.

8 Recommendations

Based on the findings of this study, several areas warrant further investigation to deepen our understanding between COVID 19 mortality shocks and fertility rates in Kenya.The study therefore recommends integrated fertility modeling into pandemic response frameworks, conducting longitudinal studies to observe delayed demographic effects and ensuring uninterrupted access to reproductive health services during crises.

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