

PAEDIATRIC NEW HIV INFECTIONS IN ZAMBIA: A BOX-JENKINS ARIMA APPROACH

Dr. Smartson. P. Nyoni

ZICHIRE Project, University of Zimbabwe, Harare, Zimbabwe

Mr. Thabani Nyoni

Department of Economics, University of Zimbabwe, Harare, Zimbabwe

Abstract:

Using annual time series data on the number of children (ages 0 – 14) newly infected with HIV in Zambia from 1990 – 2018, the study predicts the annual number of children who will be newly infected with HIV over the period 2019 – 2030. The paper applies the Box-Jenkins ARIMA approach to modeling and forecasting. The diagnostic ADF tests show that, T, the series under consideration is an I (2) variable. Based on the AIC, the study presents the ARIMA (2, 2, 0) model as the parsimonious model. The diagnostic tests further indicate that the presented model is indeed stable and its residuals are not serially correlated and are also normally distributed. The results of the research indicate that the number of new HIV infections in children in Zambia is expected to go down significantly from as high as 5096 in 2019 to as low as 2185 new infections by 2030. While zero new pediatric HIV infections may not be realized anytime soon, it is important to note that if the government continues to scale up the PMTCT programme throughout the country, the burden of HIV can be minimized.

1.0 INTRODUCTION

Human Immunodeficiency Virus (HIV) is a chronic infection that leads to Acquired Immunodeficiency Syndrome (AIDS)(Lauritano et al., 2020). Globally, there are about 3.3 million children under the age of 15 years living with HIV. Of this number 88% live in Sub-Saharan Africa (Gyamfi et al., 2017). In fact, almost 3.4 million children and adolescents in Sub-Saharan Africa (SSA) are infected with the Human Immunodeficiency Virus (HIV), amounting to about 10% of all persons in the region living with HIV or AIDS (Avert, 2017). HIV/AIDS continues to be a major developmental challenge for Zambia, which still has one of the highest prevalence rates in the world (National AIDS Council, 2014). In Zambia, approximately 72000 (age 0-14 years) are infected with HIV, representing nearly 1% of the population within that age group (UNAIDS, 2017). Figure 1 below shows that the number of new HIV infections in children in Zambia. Between 1990 and 2002 new pediatric HIV infections were on the rise, from 9700 in 1990 to 18000 new infections in 1997-2002. In

around 2003, when the Prevention of Mother-To-Child Transmission of HIV (PMTCT) program was introduced; new infections dramatically fell until. The lowest number of new HIV infections in children which has so far been recorded in the country is 5400 new infections for the year 2018. The main goal of this study is to predict the number of children newly infected with HIV in Zambia over the period 2019 – 2030. This study will go a long way in determining the possibility of ending the HIV scourge in Zambia. After all, effective planning and delivering of pediatric HIV prevention and control programmes depend on understanding the trends of new infections as well as getting a picture of what the future will look like (through out-of-sample forecasts).

2.0 LITERATURE REVIEW

Studies on modeling and forecasting new HIV infections are scanty in literature. Here we review closely related studies. In an attempt to examine the awareness and knowledge of mother-to-child transmission of HIV/AIDS and the methods to prevent mother-to-child transmission of HIV, Adeleke et al. (2009) conducted a descriptive study at the pediatric HIV clinic of Aminu Kano Teaching Hospital. The research established that the level of knowledge and perceptions of mother-to-child transmission of HIV is still inadequate in the country. In an effort to investigate the determinants of Early Infant Diagnosis (EID) and early treatment initiation among HIV exposed children from informal settlements in Nairobi, Kenya, Makau et al. (2015), conducted a descriptive cross-sectional study, where HIV-infected mother-infant pairs attending healthcare facilities were recruited. The paper indicated that knowledge on PMTCT and EID was low. In a Zambian study, Kandala et al. (2011) analyzed the impact of geographical location on HIV prevalence based on a Bayesian Geo-additive Mixed Model. The study indicated that there was an increased HIV prevalence in Western Zambian province. No study has looked at forecasting new HIV infections and yet such information is important for future planning and effective delivery of HIV preventive and control measures. By filling this information gap, this study will add value to the existing literature.

3.0 METHODOLOGY

3.1 The Box – Jenkins (1970) Methodology

The first step towards model selection is to difference the series in order to achieve stationarity. Once this process is over, the researcher will then examine the correlogram in order to decide on the appropriate orders of the AR and MA components. It is important to highlight the fact that this procedure (of choosing the AR and MA components) is biased towards the use of personal judgement because there are no clear – cut rules on how to decide on the appropriate AR and MA components. Therefore, experience plays a pivotal role in this regard. The next step is the estimation of the tentative model, after which

diagnostic testing shall follow. Diagnostic checking is usually done by generating the set of residuals and testing whether they satisfy the characteristics of a white noise process. If not, there would be need for model re – specification and repetition of the same process; this time from the second stage. The process may go on and on until an appropriate model is identified (Nyoni, 2018c). This approach will be used to analyze, T_t , the series under consideration.

3.2 The Applied Box – Jenkins ARIMA Model Specification

If the sequence $\Delta^d T_t$ satisfies an ARMA (p, q) process; then the sequence of T_t also satisfies the ARIMA (p, d, q) process such that:

$$\Delta^d T_t = \sum_{i=1}^p \beta_i \Delta^d L^i T_t + \sum_{i=1}^q \alpha_i L^i \mu_t + \mu_t \dots \dots \dots [1]$$

where Δ is the difference operator, vector $\beta \in \mathbb{R}^p$ and $\alpha \in \mathbb{R}^q$.

3.3 Data Collection

This study is based on annual observations (that is, from 1990 – 2018) on the number of children newly infected with HIV (ages 0 – 14) [denoted as T] in Zambia. Out-of-sample forecasts will cover the period 2019 – 2030. All the data was collected from the World Bank online database.

3.4 Diagnostic Tests & Model Evaluation

3.4.1 Stationarity Tests: Graphical Analysis

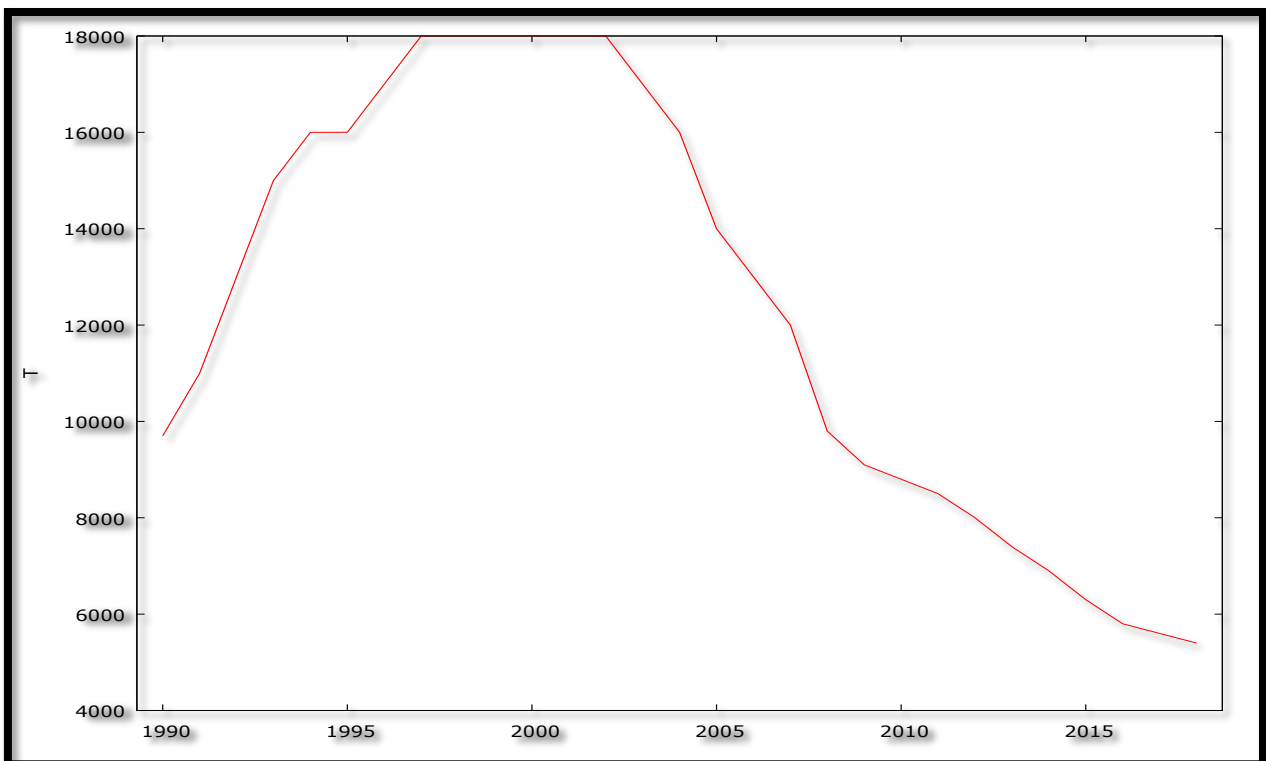


Figure 1

3.4.2 The Correlogram in Levels

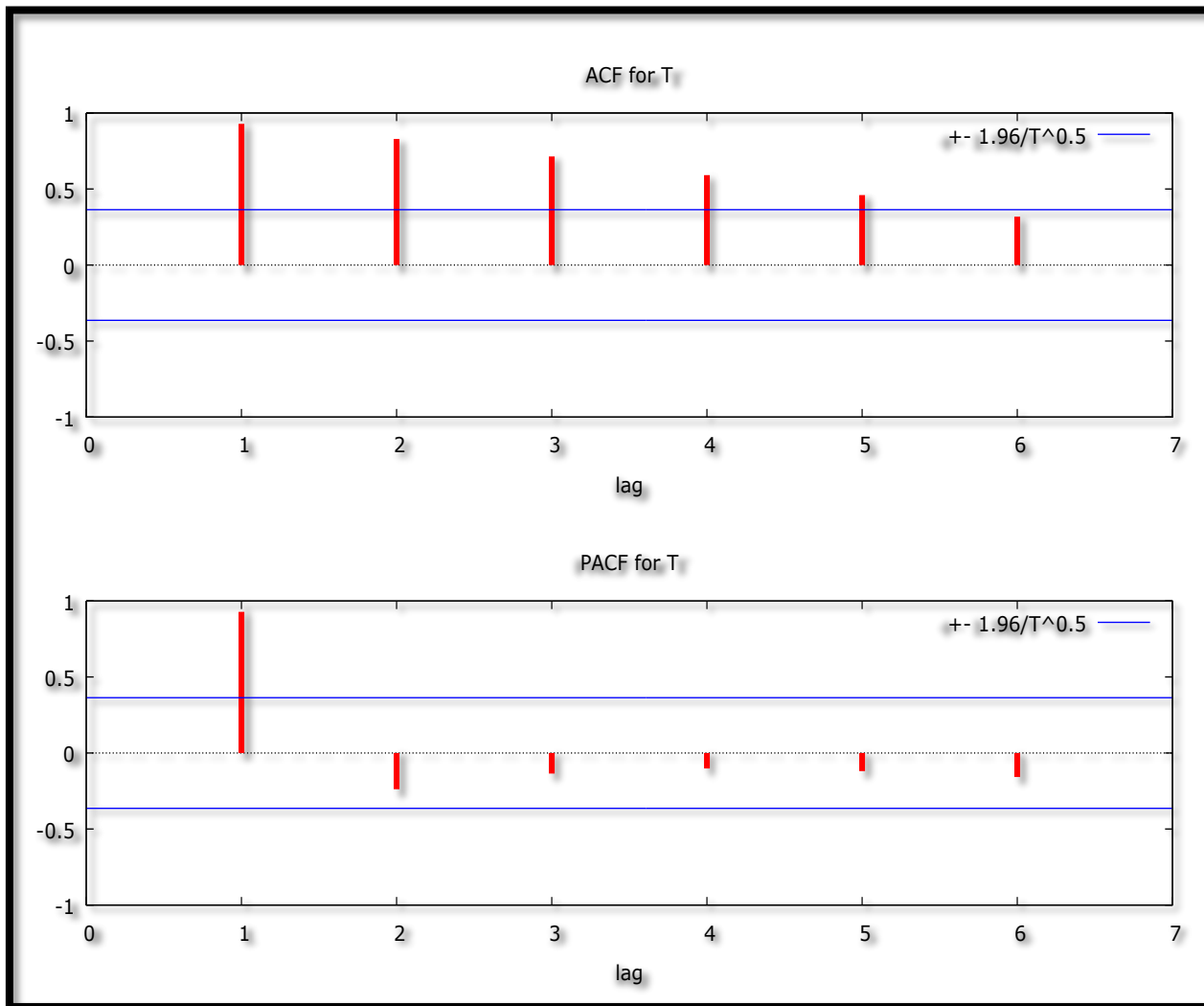


Figure 2: Correlogram in Levels

3.4.3 The ADF Test in Levels

Table 1: with intercept

Variable	ADF Statistic	Probability	Critical Values		Conclusion
T	-0.993058	0.7410	-3.699871	@ 1%	Non-stationary
			-2.976263	@ 5%	Non-stationary
			-2.627420	@ 10%	Non-stationary

Table 1 shows that T is not stationary in levels as indicated in figures 1 and 2.

3.4.4 The Correlogram (at First Differences)

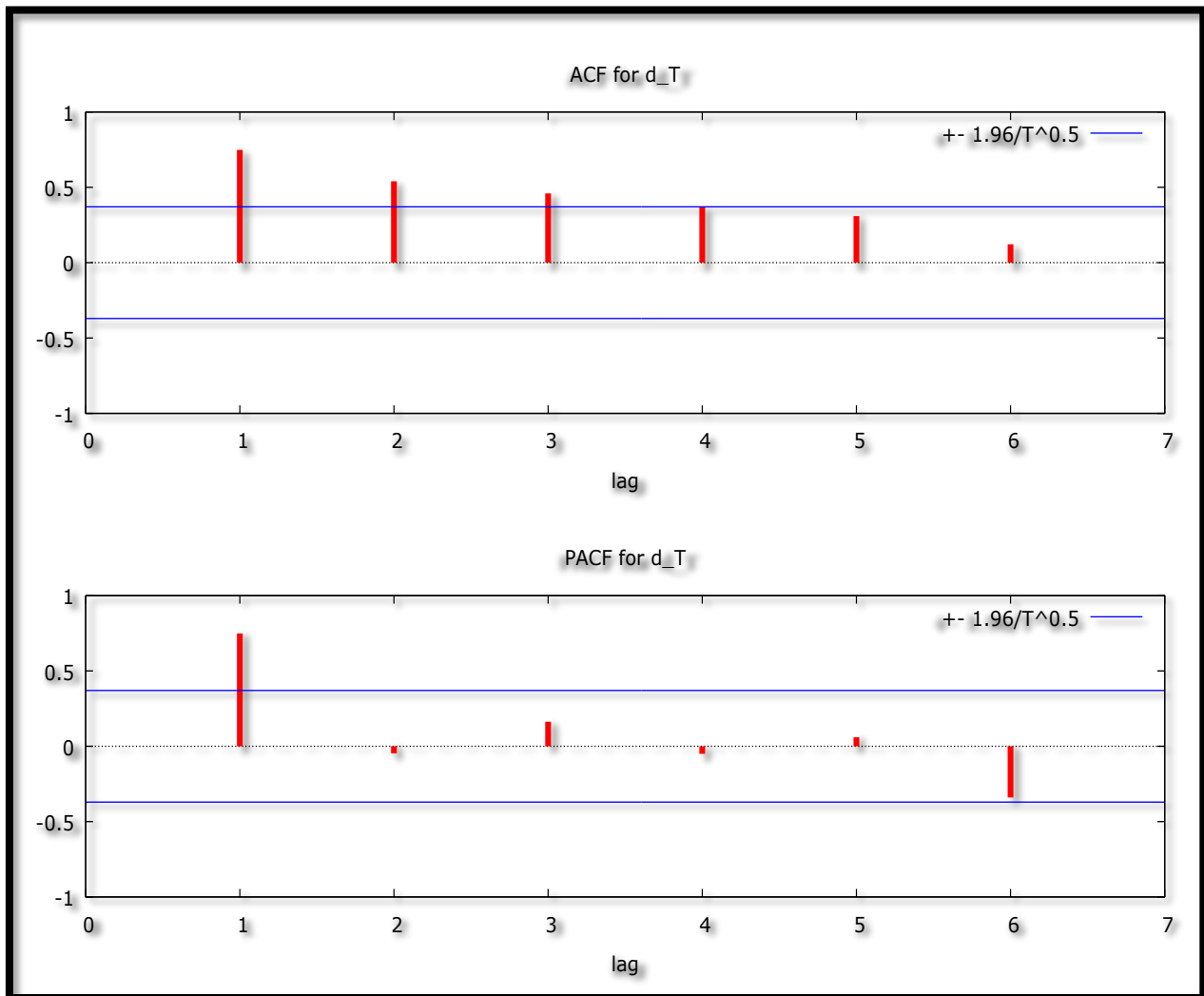


Figure 3: Correlogram (at First Differences)

3.4.5 The ADF Test (at First Differences)

Table 2: with intercept

Variable	ADF Statistic	Probability	Critical Values		Conclusion
ΔT	-2.098238	0.2468	-3.699871	@ 1%	Non-stationary
			-2.976263	@ 5%	Non-stationary
			-2.627420	@ 10%	Non-stationary

Figure 3 and table 2 indicate that T is also not an I (2) variable.

3.4.6 The Correlogram (at Second Differences)

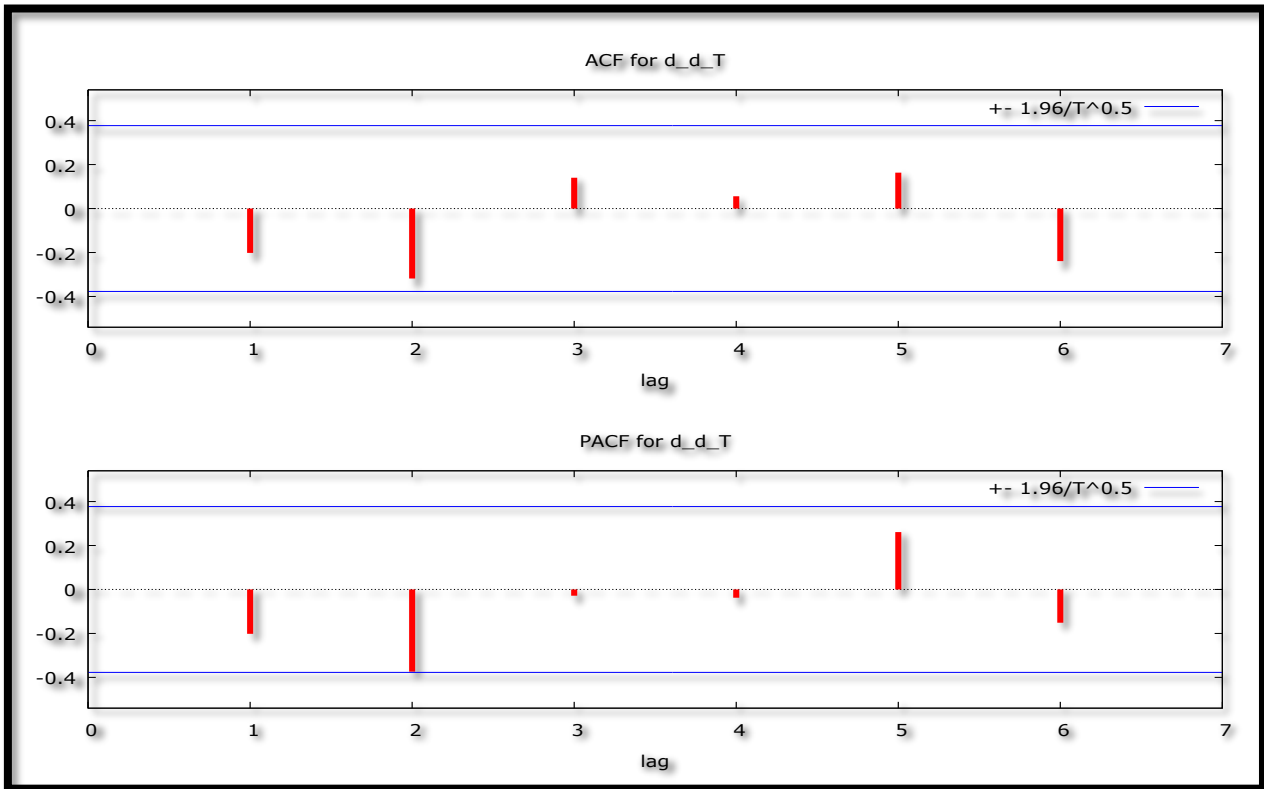


Figure 4: Correlogram (at Second Differences)

3.4.7 The ADF Test (at Second Differences)

Table 3: with intercept

Variable	ADF Statistic	Probability	Critical Values		Conclusion
$\Delta^2 T$	-6.180770	0.0000	-3.711457	@ 1%	Stationary
			-2.981038	@ 5%	Stationary
			-2.629906	@ 10%	Stationary

Figure 4 and table 3 indicate that T is an I (2) variable.

3.4.8 Evaluation of ARIMA models (with a constant)

Table 4: Evaluation of ARIMA Models (without a constant)

Model	AIC	U	ME	RMSE	MAPE
ARIMA (1, 2, 1)	430.1232	0.65002	-95.804	623.51	3.8084
ARIMA (1, 2, 0)	429.6280	0.67514	-66.137	641.1	3.8633
ARIMA (2, 2, 0)	428.0778	0.62754	-94.948	599.36	3.6804
ARIMA (3, 2, 0)	430.0739	0.62738	-93.478	599.32	3.6916
ARIMA (0, 2, 2)	429.3258	0.63645	-102.42	613.95	3.6917
ARIMA (0, 2, 1)	428.4306	0.6564	-89.804	627.1	3.9183
ARIMA (1, 2, 2)	429.2775	0.58995	-95.227	592.85	3.562
ARIMA (1, 2, 3)	430.3161	0.61537	-61.588	581.78	3.7639
ARIMA (2, 2, 1)	430.0744	0.62737	-93.668	599.33	3.6906

A model with a lower AIC value is better than the one with a higher AIC value (Nyoni, 2018b) Similarly, the U statistic can be used to find a better model in the sense that it must lie between 0 and 1, of which the closer it is to 0, the better the forecast method (Nyoni, 2018a). In this research paper, only the AIC is used to select the optimal model. Therefore, the ARIMA (2, 2, 0) model is was chosen.

3.5 Residual & Stability Tests

3.5.1 Correlogram of the Residuals of the ARIMA (2, 2, 0) Model

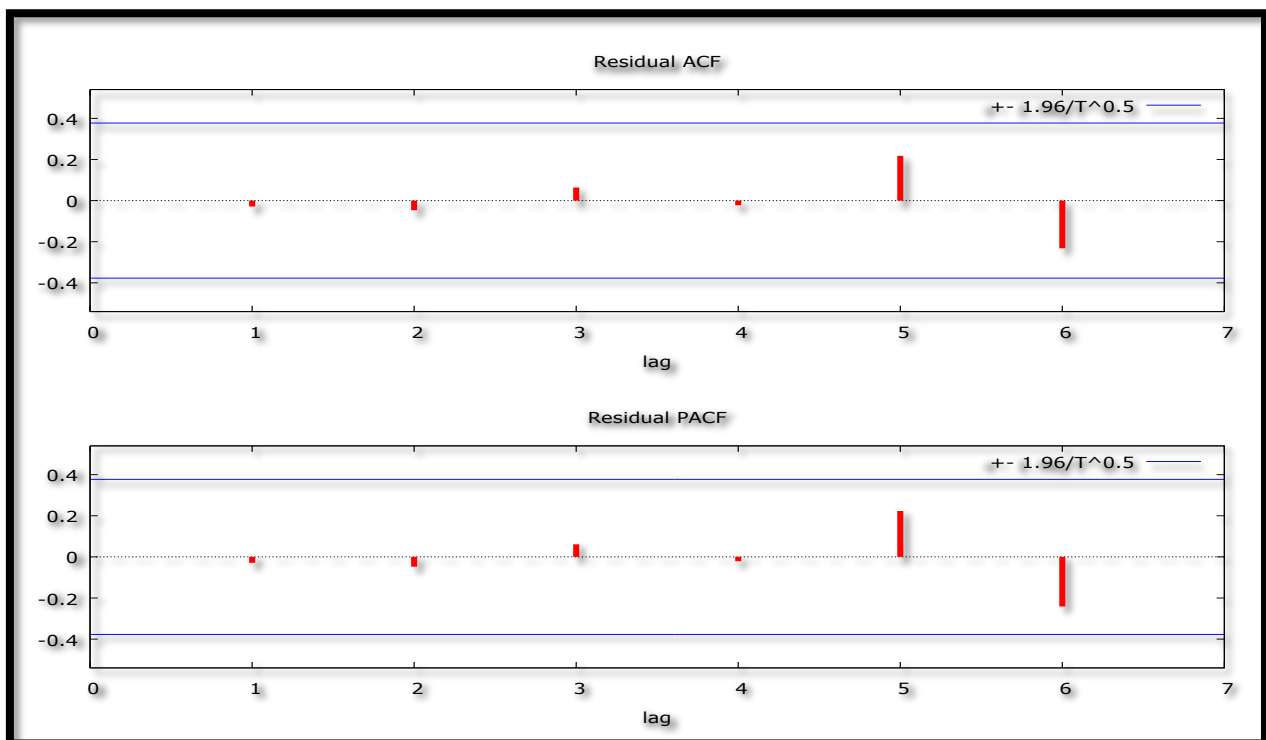


Figure 5: Correlogram of the Residuals

Figure 5 shows that the estimated model is adequate since ACF and PACF lags are quite short and within the bands.

3.5.2 Stability Test of the ARIMA (2, 2, 0) Model

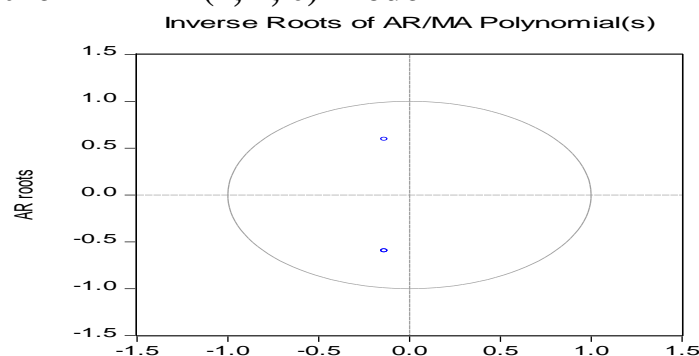


Figure 6: Inverse Roots

Owing to the fact that all the AR roots lie inside the unit circle, it implies that the estimated ARIMA process is (covariance) stationary; thus confirming that the ARIMA (2, 2, 0) model is really stable and suitable for forecasting annual number of new HIV infections in Zambia.

3.5.3 Normality Test of the Residuals of the ARIMA (2, 2, 0) Model

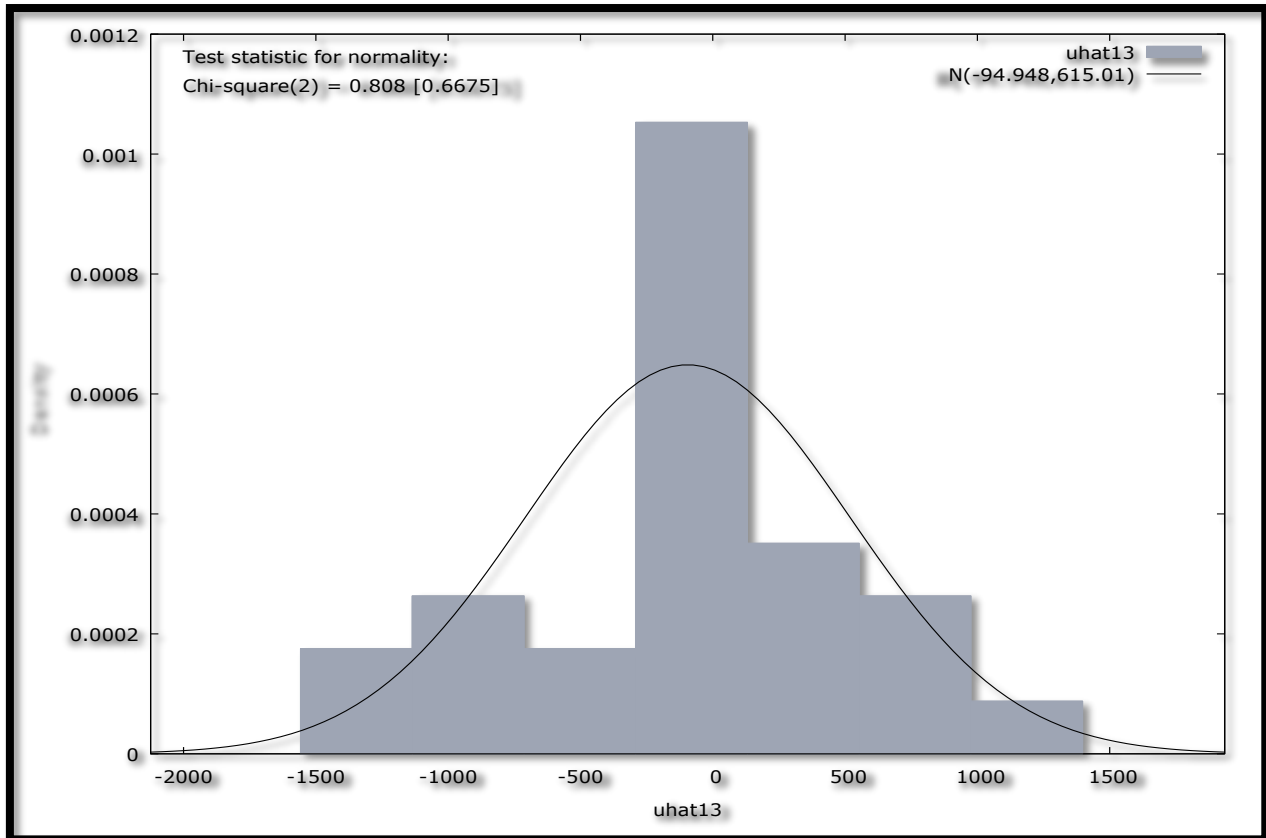


Figure 7: Normality Test

Given that the probability value of the chi-square statistic is insignificant, we reject the null hypothesis and conclude that the residuals of the ARIMA (2, 2, 0) model are normally distributed.

4.0 FINDINGS OF THE STUDY

4.1 Descriptive Statistics

Table 5: Descriptive Statistics

Description	Statistic
Mean	12390
Median	13000
Minimum	5400
Maximum	18000

Over the study period, the annual average number of new HIV infections in children in Zambia is 12390. The minimum number of new HIV infections over the study period was 5400 and has been recorded in 2018 while the maximum is 18000 and was observed from 1997 – 2002.

4.2 Results Presentation

Table 6: Main Results

ARIMA (2, 2, 0) Model:				
The chosen best model, the ARIMA (2, 2, 0) model can be expressed as follows: $\Delta^2 T_t = -0.261565\Delta^2 T_{t-1} - 0.346724\Delta^2 T_{t-2} \dots \dots \dots [2]$				
Variable	Coefficient	Standard Error	z	p-value
β_1	-0.261565	0.181197	-1.444	0.1489
β_2	-0.346724	0.180084	-1.925	0.0542*

Table 6 shows the main results of the ARIMA (2, 2, 0) model.

Forecast Graph

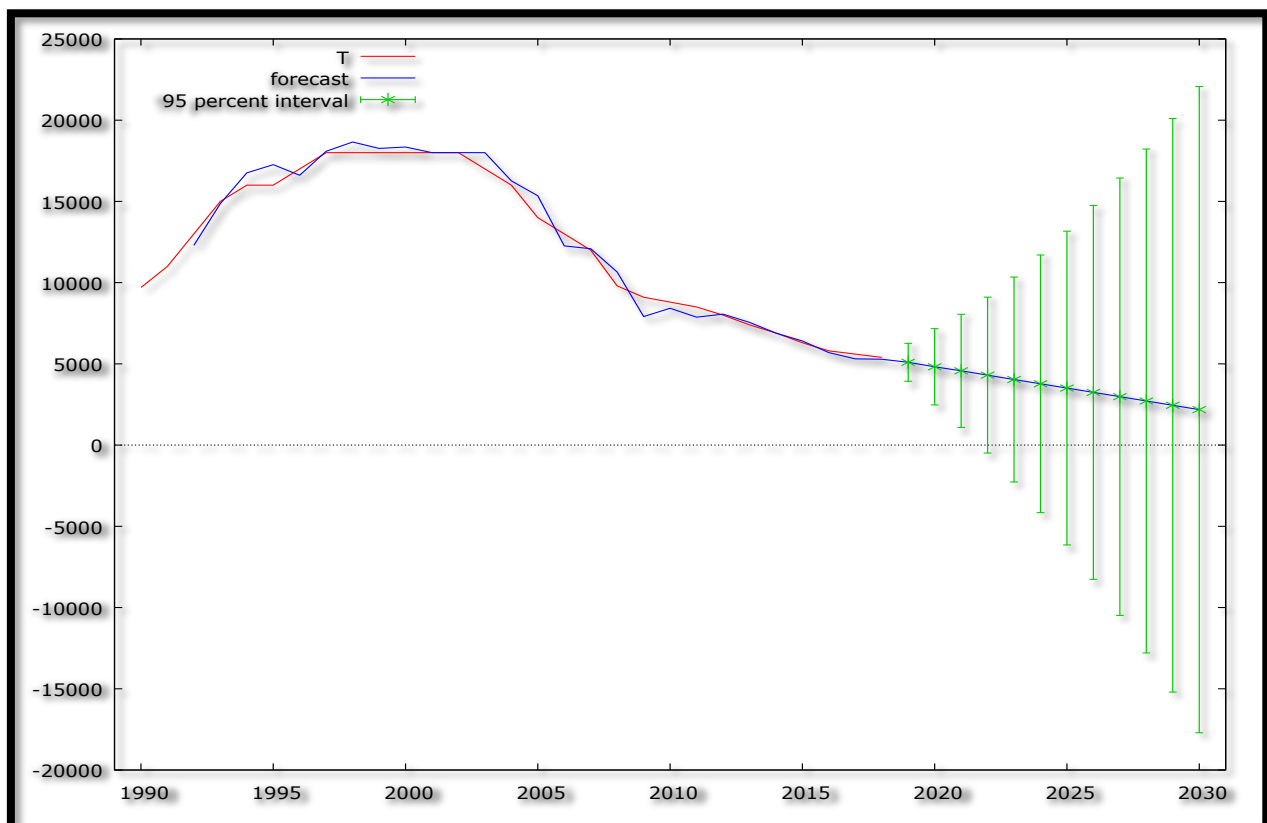


Figure 8: Forecast Graph – In & Out-of-Sample Forecasts

Figure 8 shows the in-and-out-of-sample forecasts of the series, T. The out-of-sample forecasts cover the period 2019 – 2030.

Predicted T– Out-of-Sample Forecasts Only

Table 7: Predicted T

Year	Predicted T	Standard Error	95% Confidence Interval
2019	5095.98	596.966	(3925.95, 6266.02)
2020	4819.17	1197.23	(2472.64, 7165.71)
2021	4571.31	1776.50	(1089.44, 8053.18)
2022	4306.45	2448.33	(-492.186, 9105.08)
2023	4035.99	3218.48	(-2272.12, 10344.1)
2024	3772.89	4045.63	(-4156.40, 11702.2)
2025	3509.81	4927.64	(-6148.18, 13167.8)
2026	3244.17	5870.06	(-8260.93, 14749.3)
2027	2979.19	6866.71	(-10479.3, 16437.7)
2028	2714.93	7912.64	(-12793.6, 18223.4)
2029	2450.25	9006.93	(-15203.0, 20103.5)
2030	2185.43	10147.9	(-17704.0, 22074.9)

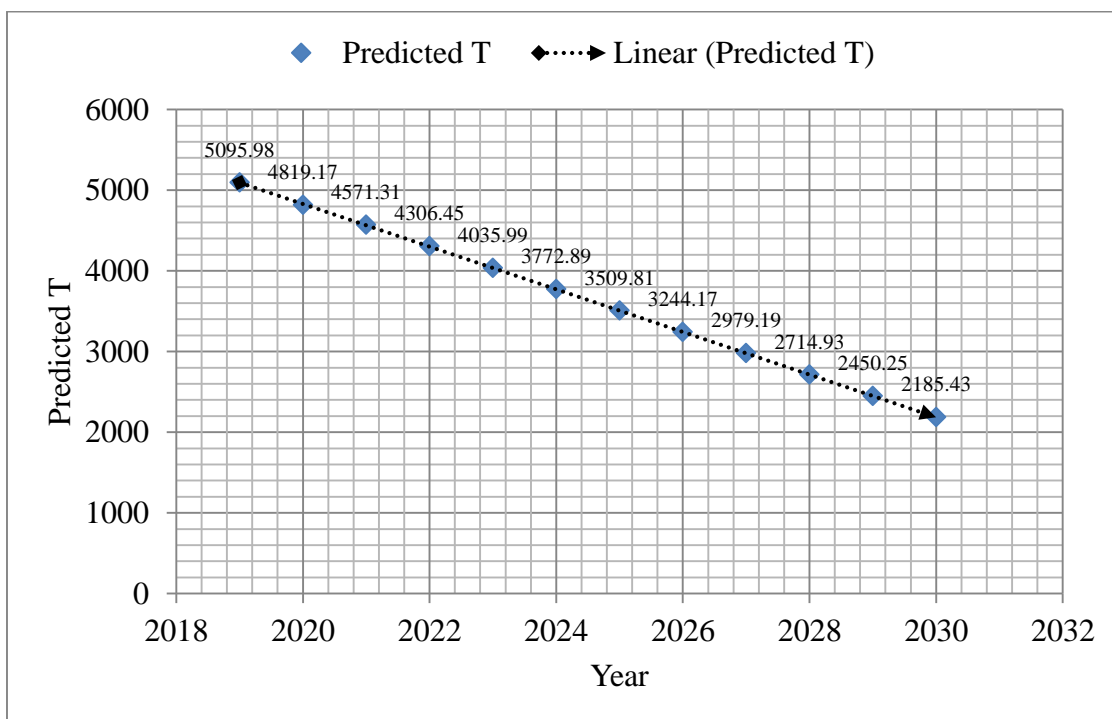


Figure 9: Graphical Analysis of Out-of-Sample Forecasts

Table 7 and figure 9 show the out-of-sample forecasts only. The number of new HIV infections in children in Zambia is projected to decline significantly from 5096 in 2019 to about 2185 new infections by 2030.

5.0 CONCLUSION

The study indicates that the ARIMA (2, 2, 0) model is not only stable but also the most suitable model to forecast the annual number of new HIV infections in children in Zambia

over the period 2019 – 2030. The model forecasts a commendable decrease in the annual number of new pediatric HIV infections in the country. The country is actually in the right direction as far as pediatric HIV prevention and control is concerned. However, we encourage the government of Zambia to continue scaling up the PMTCT programme as it plays a pivotal role in the reduction of vertical transmission of HIV.

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