Total new HIV infections in Togo: a box-jenkins arima approach

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ABSTRACT
Using annual time series data on the total number of new HIV infections in Togo from 1990 – 2018, the study makes predictions for the period 2019 – 2030. The research applies the Box-Jenkins ARIMA methodology. The diagnostic ADF tests show that, J, the series under consideration is an I (2) variable. Based on the AIC, the study presents the ARIMA (0, 2, 2) model as the optimal 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 study indicate that the total number of new HIV infections in Togo is projected to decline sharply by 53.5% from the estimated 4791 new infections in 2019 to approximately 2229 new infections by 2030.

1. INTRODUCTION

The Acquired Immunodeficiency Syndrome (AIDS) is a disease caused by the Human Immunodeficiency Virus (HIV) which is currently a global pandemic (UNAIDS, 2008). HIV infection continues to be a public health problem in Sub-Saharan Africa, where at least 25.6 million people already live with HIV, although there has been a reduction in new infections of HIV of about 41% between 2000 and 2015 (Yaya *et al*., 2018). The decline in the incidence of HIV infection is the effect of multiple interventions implemented to prevent HIV transmission among heterosexual and especially from mother-to-child HIV transmission (UNAIDS, 2016). HIV prevalence is Togo is now around 3.2% (UNAIDS, 2008). The main goal of this study is to predict the number of new HIV infections in Togo over the period 2019 – 2030. This piece of work will go a long way in assessing the possibility of ending the HIV scourge in the country.

2. LITERATURE REVIEW

Landoh *et al*. (2014) conducted a systematic review and concluded that HIV incidence in Togo remains high, especially in key risk populations. Consistently, Djibril *et al*. (2015) described both the epidemiology and prognosis of people living with HIV (PLHIV) in intensive care. The study basically found out that the proportion of patients with HIV infection is high in medical intensive care units in Togo. In a Zimbabwean study, Nyoni & Nyoni (2019) assessed new HIV infections in the rural community of Silobela. The research showed that new HIV infections in the community of Silobela will continue to decline over the period 2019 to 2021. No similar study has been in Togo, this study is the first its kind in the country.

3. METHODODOLOGY

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, J, the series under consideration.

3.2 The Applied Box – Jenkins ARIMA Model Specification

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

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

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 total number of new HIV infections, that is, adults (ages 15+) and children (ages 0 – 14) [denoted as J] in Togo. 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 The ADF Test in Levels

Table 1: with intercept

Variable	ADF Statistic	Probability	Critical Values		Conclusion
J	-0.393841	0.8972	-3.689194	@1%	Non-stationary
			-2.971853	@5%	Non-stationary
			-2.625121	@10%	Non-stationary

Table 1 shows that J is not stationary in levels.

3.4.2 The ADF Test (at First Differences)

Table 2: with intercept

Variable	ADF Statistic	Probability	Critical Values		Conclusion
ΔJ	-2.529962	0.1198	-3.699871	@1%	Non-stationary
			-2.976263	@5%	Non-stationary
			-2.627420	@10%	Non-stationary

Table 2 indicates that J is not an I (1) variable.

3.4.3 The ADF Test (at Second Differences)

Table 3: with intercept

Variable	ADF Statistic	Probability	Critical Values		Conclusion
$\Delta^2 J$	-3.838493	0.0077	-3.724070	@1%	Stationary
			-2.986225	@5%	Stationary
			-2.632604	@10%	Stationary

Table 3 indicates that J is an I (2) variable.

3.4.4 Evaluation of ARIMA models (without a constant)

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

Model	AIC	U	ME	RMSE	MAPE
ARIMA (1, 2, 1)	410.5753	0.62615	-89.298	432.16	3.4392
ARIMA (1, 2, 0)	408.8656	0.61955	-95.228	434.55	3.3771
ARIMA (0, 2, 1)	411.1869	0.64265	-94.645	454.82	3.3495
ARIMA (2, 2, 0)	410.3296	0.63147	-82.379	430.13	3.4741
ARIMA (0, 2, 2)	408.5350	0.61547	-69.79	416.48	3.3989

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 (0, 2, 2) model is finally chosen.

3.5 Residual & Stability Tests

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

Figure 1: Correlogram of the Residuals

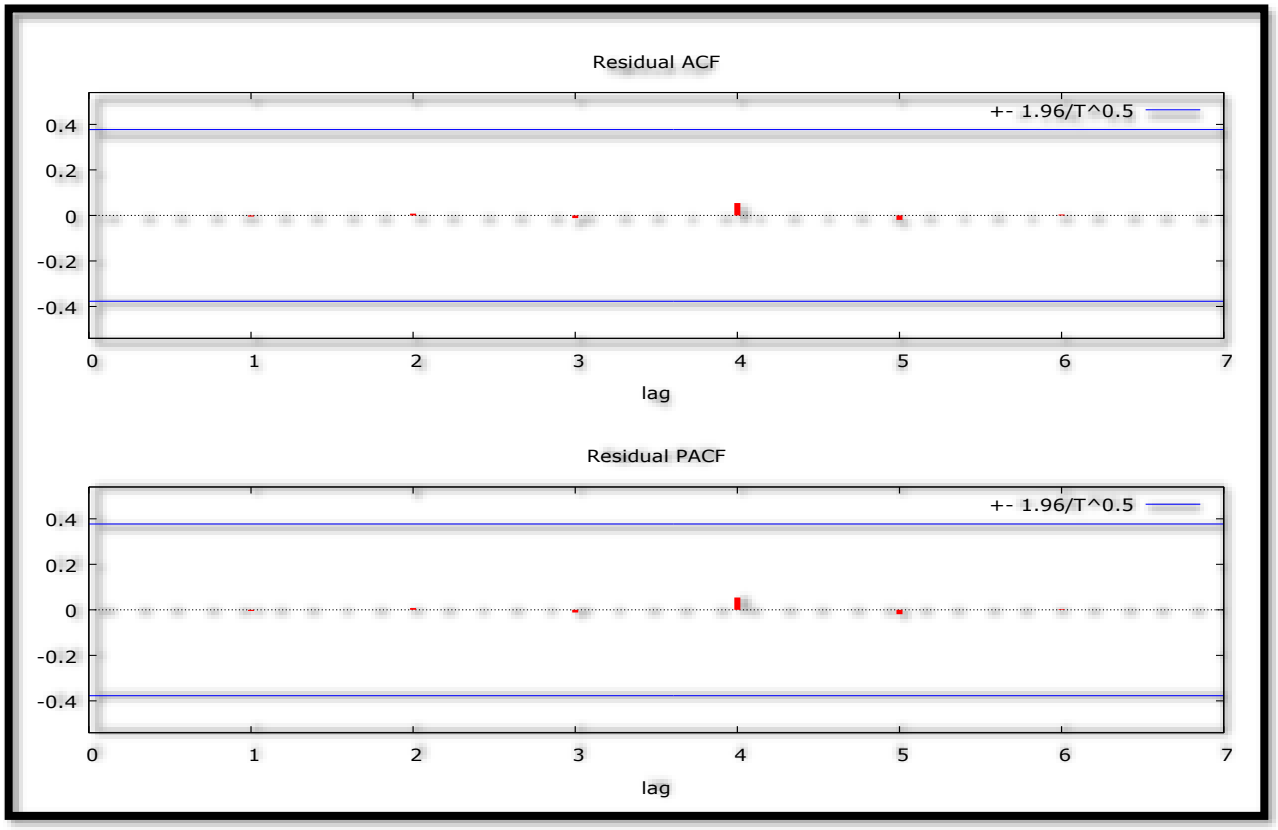
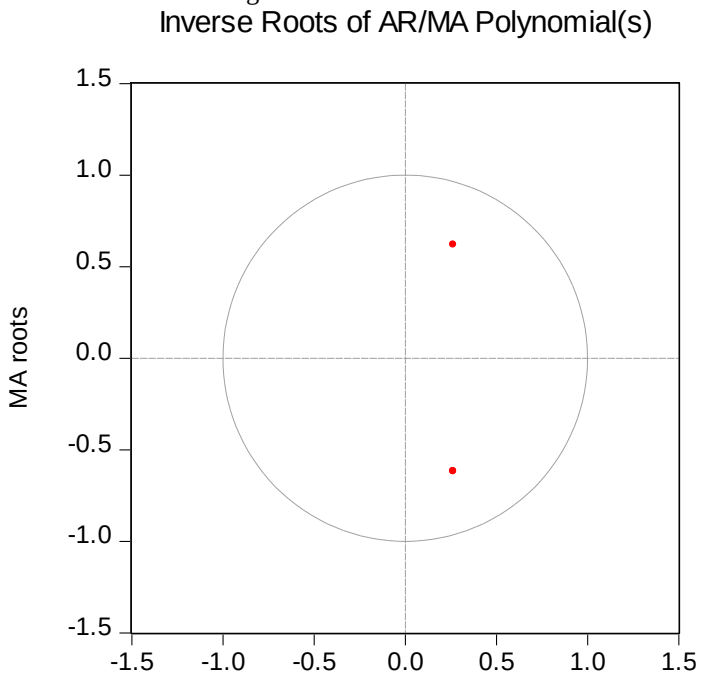


Figure 1 indicates that the estimated parsimonious model is adequate because ACF and PACF lags are quite short and within the bands.

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

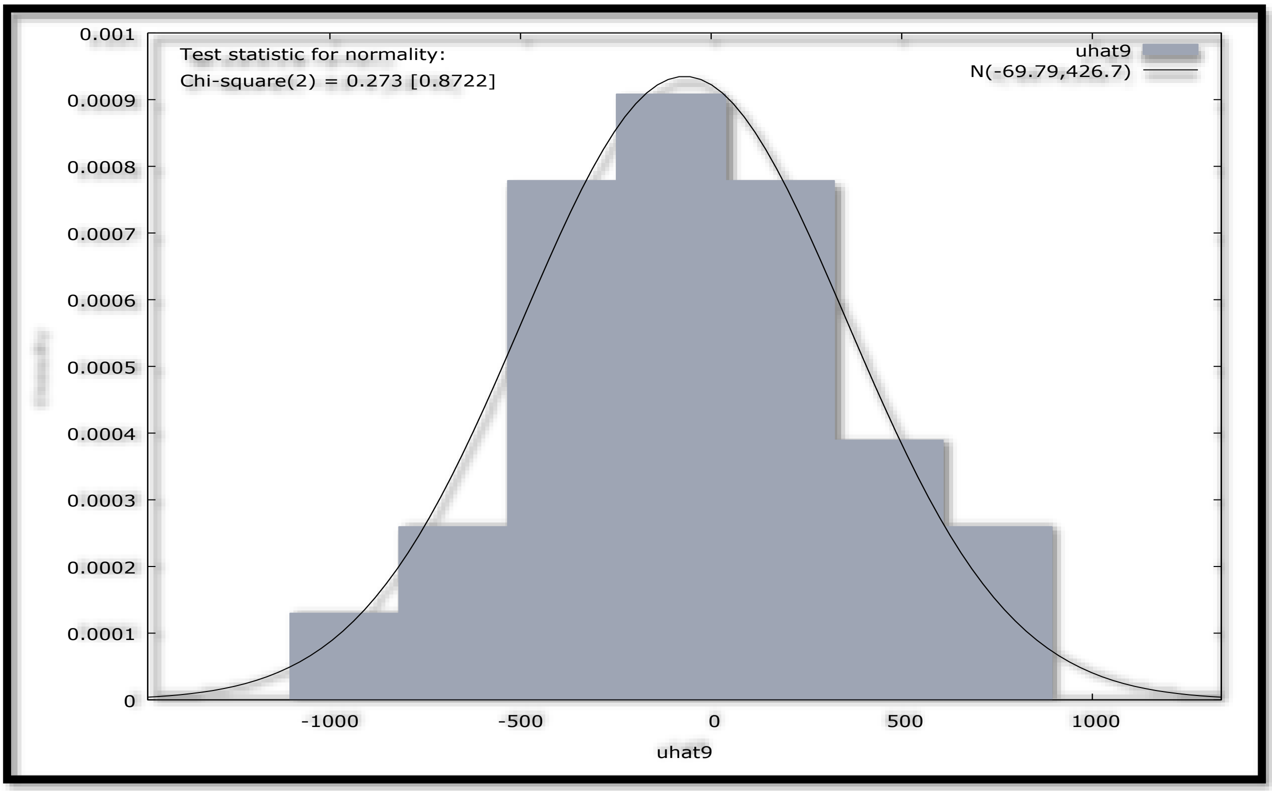
Figure 2: Inverse Roots



Since all the MA roots lie inside the unit circle, it implies that the estimated ARIMA process is (covariance) stationary; thus confirming that the ARIMA (0, 2, 2) model is stable.

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

Figure 3: Normality Test



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

4.0 FINDINGS OF THE STUDY

4.1 Results Presentation[1]

Table 5: Main Results

ARIMA (0, 2, 2) Model:

The chosen optimal model, the ARIMA (0, 2, 2) model can be expressed as follows:

$$\Delta^2 J_t = -0.487163\mu_{t-1} + 0.412547\mu_{t-2} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots [2]$$

Variable	Coefficient	Standard Error	z	p-value
α_1	-0.487163	0.175660	-2.773	0.0055***
α_2	0.412547	0.182468	2.261	0.0238**

Table 9 shows the main results of the ARIMA (0, 2, 2) model.

Forecast Graph

Figure 4: Forecast Graph – In & Out-of-Sample Forecasts

[1] *The *, ** and *** imply statistical significance at 10%, 5% and 1% levels of significance; respectively.*

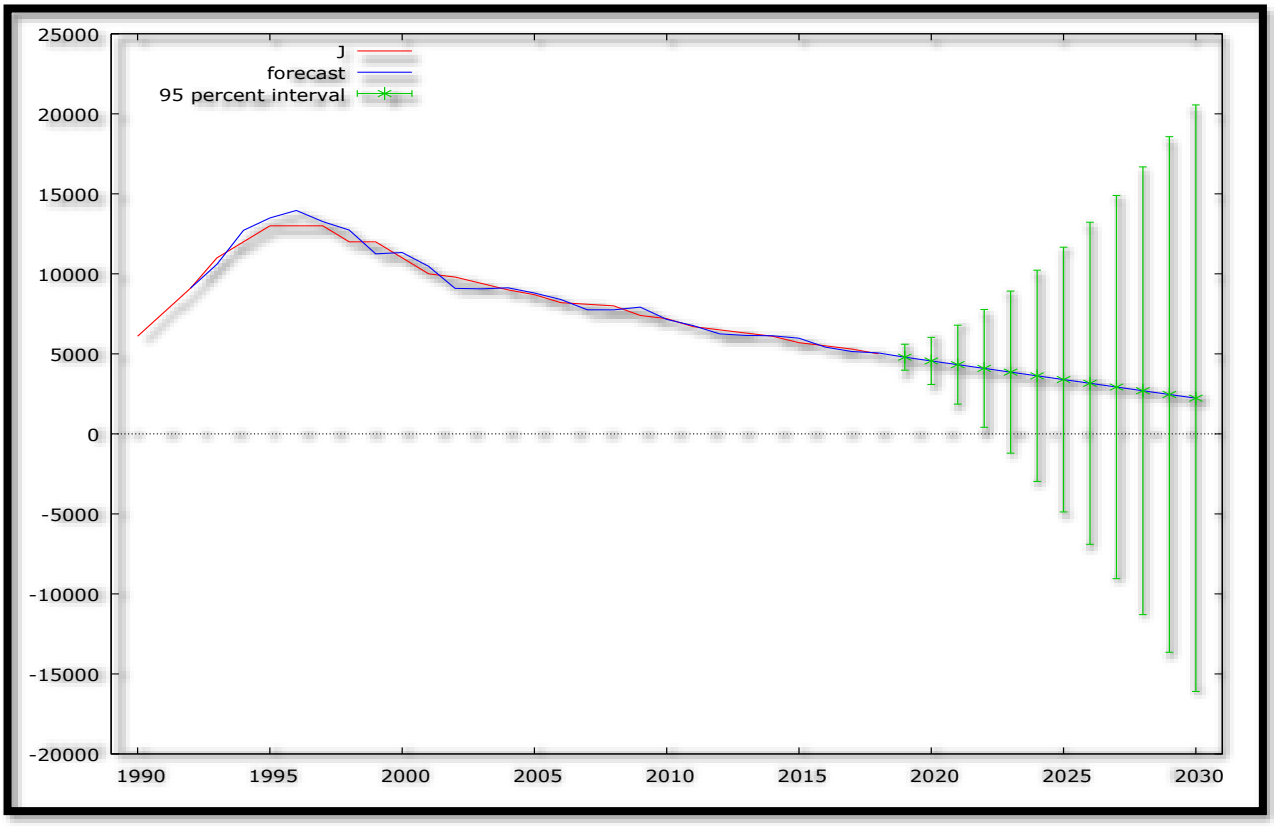


Figure 4 shows the in-and-out-of-sample forecasts of the J series. The out-of-sample forecasts cover the period 2019 – 2030.

Predicted J– Out-of-Sample Forecasts Only

Table 6: Predicted J

Year	Predicted J	Standard Error	95% Confidence Interval
2019	4791.08	414.121	(3979.41, 5602.74)
2020	4558.17	750.996	(3086.25, 6030.10)
2021	4325.27	1258.38	(1858.89, 6791.65)
2022	4092.37	1877.18	(413.166, 7771.57)
2023	3859.47	2584.29	(-1205.64, 8924.58)
2024	3626.57	3367.71	(-2974.02, 10227.2)
2025	3393.66	4219.75	(-4876.89, 11664.2)
2026	3160.76	5134.85	(-6903.36, 13224.9)
2027	2927.86	6108.72	(-9045.01, 14900.7)
2028	2694.96	7137.88	(-11295.0, 16684.9)
2029	2462.06	8219.42	(-13647.7, 18571.8)
2030	2229.15	9350.87	(-16098.2, 20556.5)

Figure 5: Graphical Analysis of Out-of-Sample Forecasts

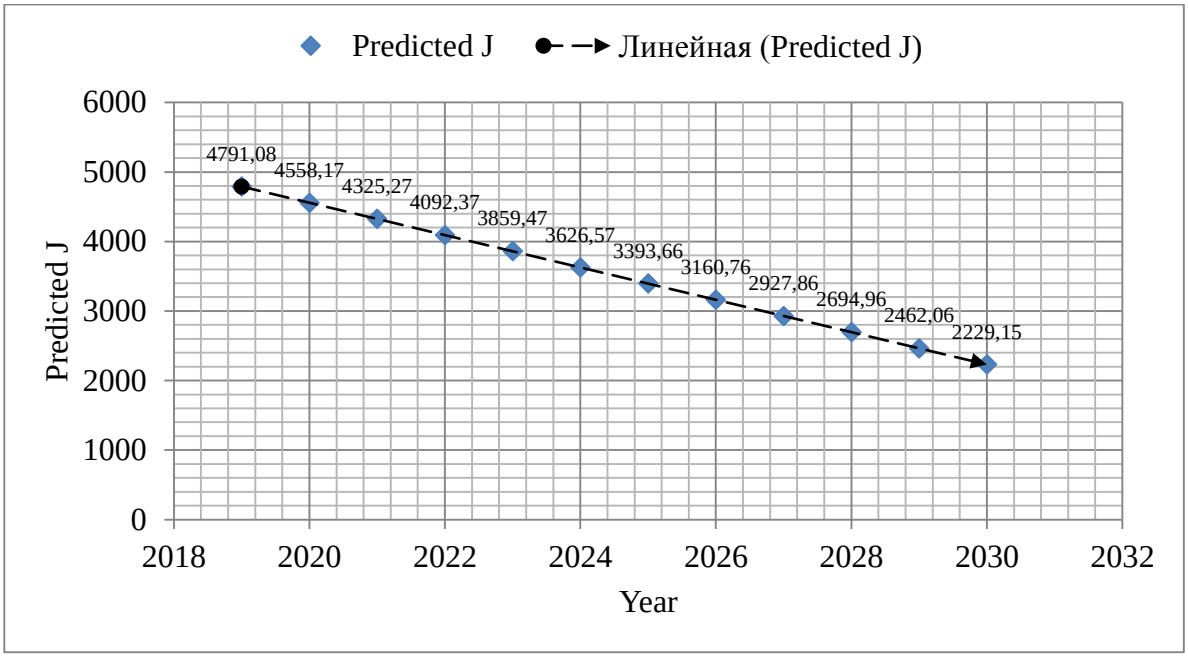


Table 6 and figure 5 show the out-of-sample forecasts only. The total number of new HIV infections in Togo is projected to decline sharply by 53.5% from the estimated 4791 new infections in 2019 to approximately 2229 new infections by 2030.

5.0 CONCLUSION

The study shows that the ARIMA (0, 2, 2) model is not only stable but also the most suitable model to forecast the total annual number of new HIV infections in Togo over the period 2019 – 2030. The model predicts a commendable decrease in the annual number of new HIV infections in Togo and this is quite encouraging for the country. The paper recommends that the government of Togo should continue scaling up HIV prevention and treatment access throughout the country. Special emphasis must be directed towards behavior change interventions such as increased condom use as well as reduction of sexual partners. Togo is a low circumcision country; therefore, it would be beneficial for the government to up scale voluntary medical male circumcision as an additional HIV prevention strategy.

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