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TOTAL NEW HIV INFECTIONS IN VIETNAM: A BOX-JENKINS ARIMA APPROACH

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Abstract:

Using annual time series data on the total number of new HIV infections in Vietnam from 1990 – 2018, the study makes predictions for the period 2019 – 2030. The paper applies the Box-Jenkins ARIMA methodology. The diagnostic ADF tests show that, C, the series under consideration is an I (2) variable. Based on the AIC, the study presents the ARIMA (1, 2, 0) model as the optimal model. The diagnostic tests further reveal that the presented model is very 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 Vietnam is projected to decrease significantly by 80.2% from the estimated 4743 new infections in 2019 to approximately 937 new infections by 2023. Approximately four years from now, Vietnam could materialize an AIDS-free society.

1.0INTRODUCTION

HIV remains the leading cause of heavy disease burden and death in Vietnam (NCADPP, 2014). The HIV epidemic remains concentrated among populations at higher risk (for example, female sex workers and injecting drugs users) since the first case was reported in 1990 in Vietnam (Zhang et al., 2013). HIV prevalence for the general population in the country is around 0.26% (Ministry of Health, 2013). New HIV infections in Vietnam continue to decline dramatically (NCADPP, 2014), and this is consistent with declining HIV prevalence among key populations at highest risk of transmission (Ministry of Health, 2014). The main goal of this study is to predict the number of new HIV infections in Vietnam over the period 2019 – 2030. This study attempts to assess the possibility of ending the HIV scourge in the country.

2.0 LITERATURE REVIEW

Literature on forecasting new HIV infections in Vietnam is highly scanty. Here we review closely related papers: Nyoni & Nyoni (2019) analyzed new HIV infections in the rural community of Silobela in Zimbabwe. The study showed that new HIV infections in the

community of Silobela will continue to decline over the period 2019 to 2021. Consistently, Nyoni & Nyoni (2020a) investigated the trends of new HIV infections in children aged between 0 and 14 years in Zimbabwe, based on annual time series data and employed the generalized ARIMA model. The study indicated that new pediatric HIV infections will continue to decline in the country over the period 2019 to 2023. Furthermore, Nyoni & Nyoni (2020b); applied the ANN model to forecast the number of new HIV infections in pregnant women at Gweru District Hospital (GDH). The employed ANN (12, 12, 1) model revealed that new HIV infections in pregnant women will most likely decline over the period January 2020 to December 2021. No similar study has been done in Vietnam. Hence, it is this information gap that we seek to fill. This study follows the methodological intuition already presented by Nyoni & Nyoni (2020a).

3.0 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, C, the series under consideration.

3.2 The Applied Box – Jenkins ARIMA Model Specification

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

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

where Δ is the difference operator, vector $\beta \epsilon \Re^p$ and $\alpha \epsilon \Re^q$.

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 C] in

Vietnam. 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
C	-2.525774	0.1212	-3.711457	@1%	Non-stationary
			-2.981038	@5%	Non-stationary
			-2.629906	@10%	Non-stationary

Table 1 shows that C 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
ΔC	-1.157126	0.6769	-3.711457	@1%	Non-stationary
			-2.981038	@5%	Non-stationary
			-2.629906	@10%	Non-stationary

Table 2 indicates that C 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
$\Delta^2 C$	-5.684805	0.0001	-3.711457	@1%	Stationary
			-2.981038	@5%	Stationary
			-2.629906	@10%	Stationary

Table 3 indicates that C 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)	448.5294	0.383	-85.878	876.64	5.1669
ARIMA (1, 2, 0)	**446.5609**	0.3828	-87.597	877.14	5.1245
ARIMA (0, 2, 1)	446.5991	0.38053	-87.784	877.76	5.1007
ARIMA (2, 2, 1)	450.4720	0.38158	-79.497	875.82	5.2448
ARIMA (1, 2, 2)	450.3892	0.38126	-74.559	874.72	5.3441
ARIMA (2, 2, 0)	448.4769	0.38156	-80.289	875.89	5.2417
ARIMA (0, 2, 2)	448.4037	0.38033	-73.841	874.91	5.3173

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 (1, 2, 0) model is finally presented.

3.5 Residual & Stability Tests

3.5.1 Correlogram of the Residuals of the ARIMA (1, 2, 0) Model

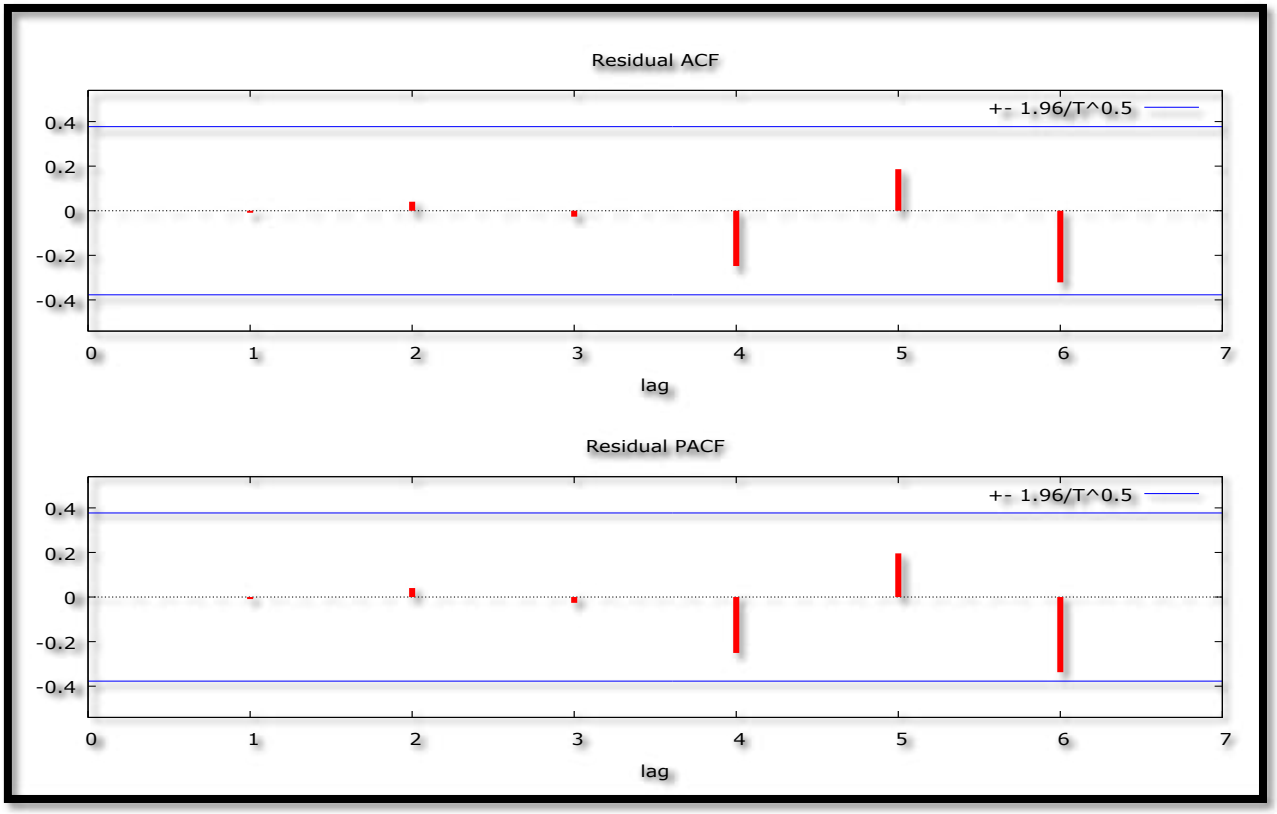

Figure 1: Correlogram of the Residuals

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

3.5.2 Stability Test of the ARIMA (1, 2, 0) Model

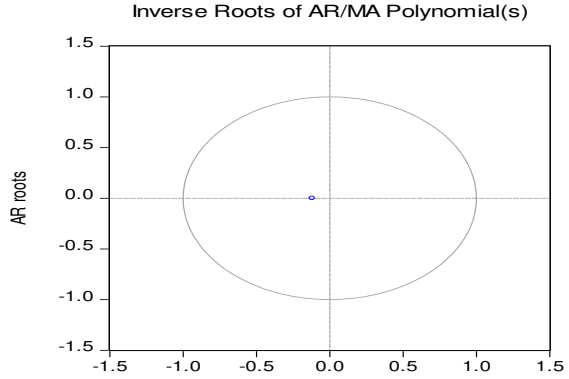

Figure 2: Inverse Roots

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Since the AR root lies inside the unit circle, it implies that the estimated ARIMA process is (covariance) stationary; thus confirming that the ARIMA (1, 2, 0) model is stable.

3.5.3 Normality Test of the Residuals of the ARIMA (1, 2, 0) Model

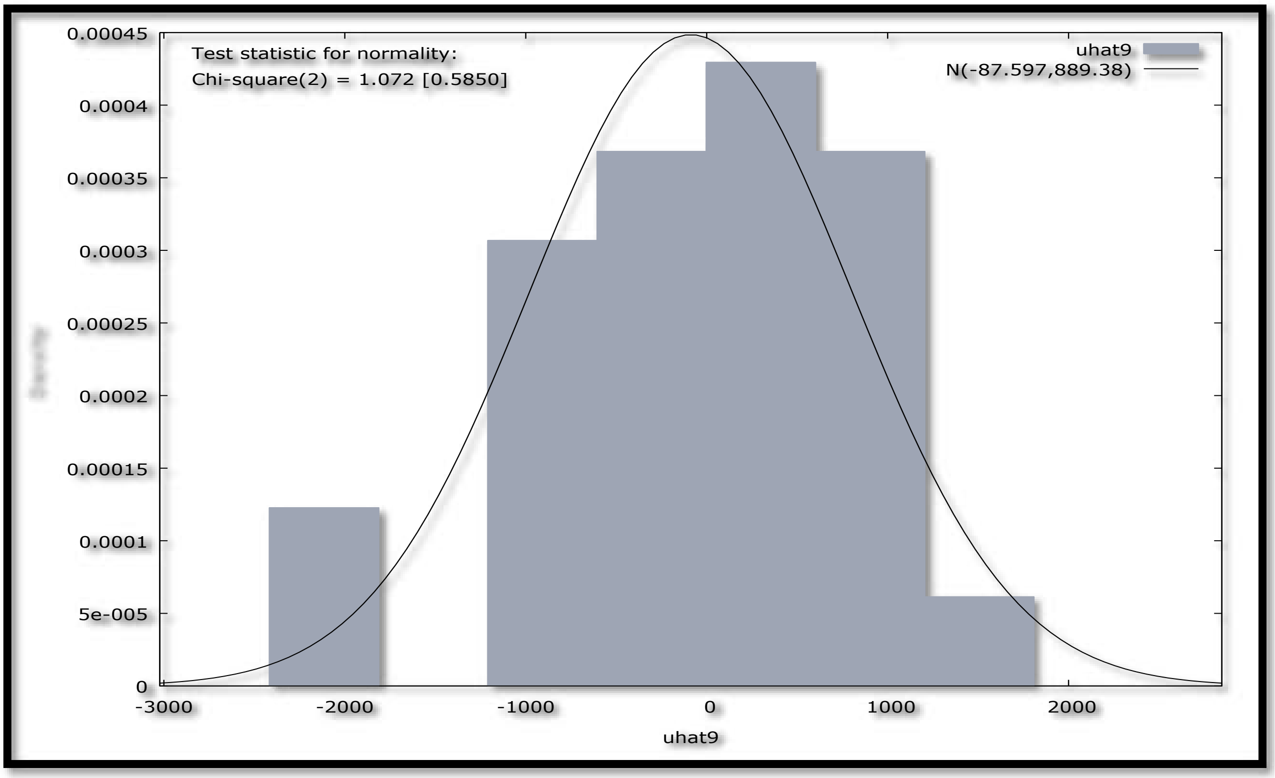

Figure 3: Normality Test

Since the probability value of the chi-square statistic is insignificant, we reject the null hypothesis and conclude that the residuals of the ARIMA (1, 2, 0) model are normally distributed.

4.0 FINDINGS OF THE STUDY

4.1 Results Presentation

Table 5: Main Results

ARIMA (1, 2, 0) Model:				
The chosen optimal model, the ARIMA (1, 2, 0) model can be expressed as follows: $\Delta^2 C_t = -0.114828\Delta^2 C_{t-1} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots [2]$				
Variable	Coefficient	Standard Error	z	p-value
β_1	-0.114828	0.192296	-0.5971	0.5504

Table 5 shows the main results of the ARIMA (1, 2, 0) model.

Forecast Graph

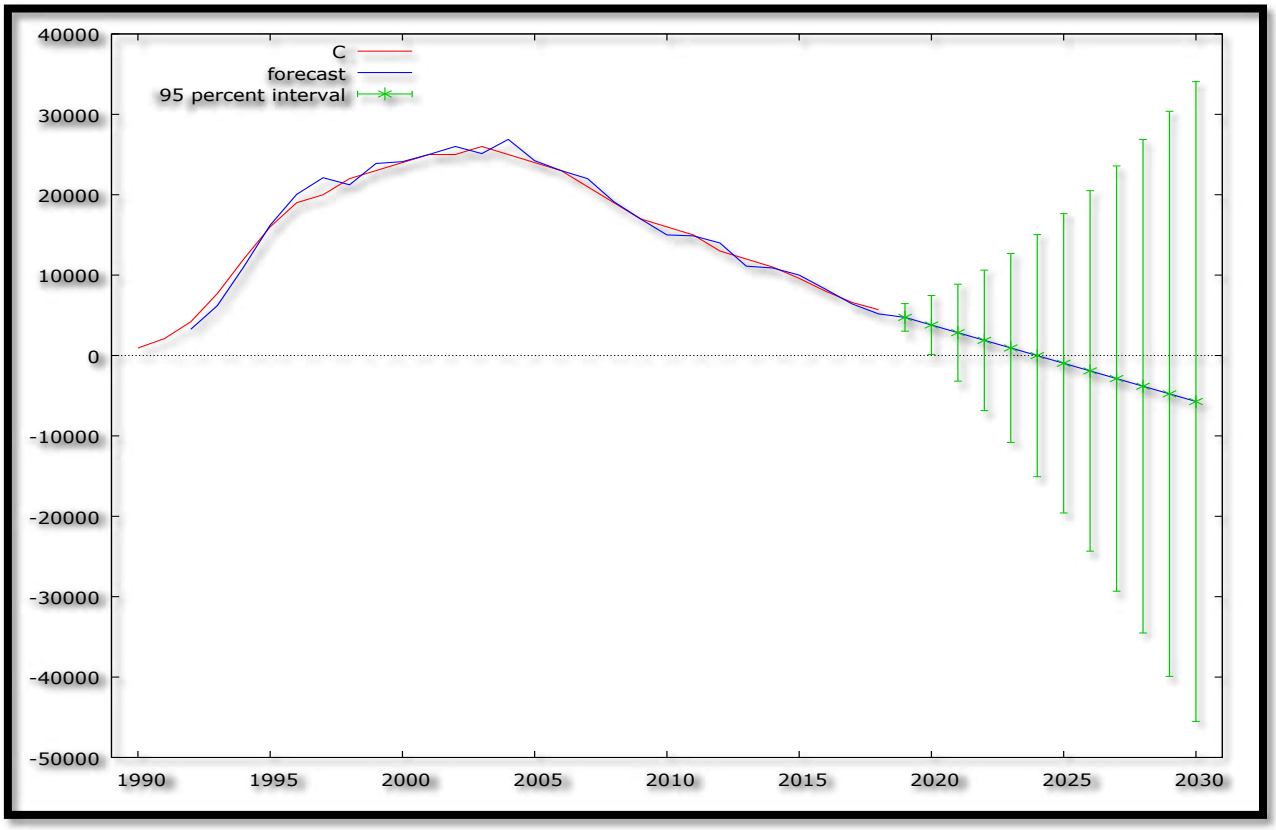

Figure 4: Forecast Graph – In & Out-of-Sample Forecasts

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

Predicted C– Out-of-Sample Forecasts Only

Table 6: Predicted C

Year	Predicted C	Standard Error	95% Confidence Interval
2019	4742.59	876.896	(3023.90, 6461.27)
2020	3791.76	1871.28	(124.125, 7459.40)
2021	2840.19	3075.63	(-3187.94, 8868.31)
2022	1888.69	4458.14	(-6849.10, 10626.5)
2023	937.194	5998.86	(-10820.4, 12694.8)
2024	-14.3067	7683.15	(-15073.0, 15044.4)
2025	-965.807	9499.79	(-19585.0, 17653.4)
2026	-1917.31	11439.8	(-24338.9, 20504.3)
2027	-2868.81	13495.8	(-29320.1, 23582.5)
2028	-3820.31	15661.7	(-34516.7, 26876.0)
2029	-4771.81	17932.1	(-39918.1, 30374.4)
2030	-5723.31	20302.4	(-45515.3, 34068.7)

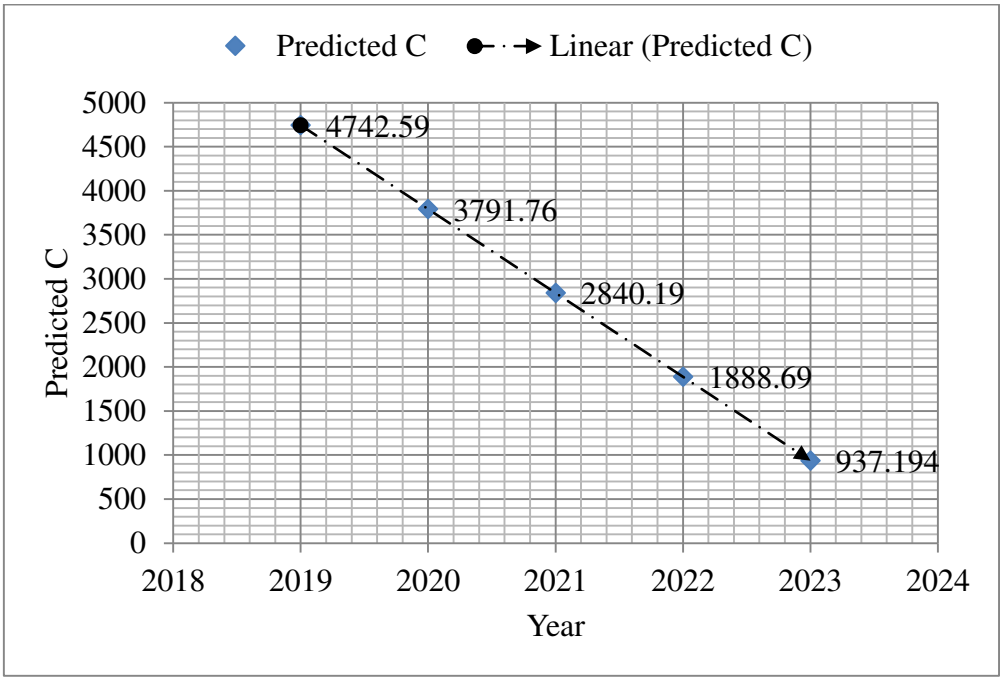

Figure 5: Graphical Analysis of Out-of-Sample Forecasts

Table 6 and figure 5 show the out-of-sample forecasts only. The total number of new HIV infections in Vietnam is projected to decrease significantly by 80.2% from the estimated 4743 new infections in 2019 to approximately 937 new infections by 2023. Approximately four years from now, Vietnam could materialize an AIDS-free society. The results of this study are in line with the scientific observation made by NCADPP (2014): that new HIV infections in Vietnam are significantly going down.

5.0 CONCLUSION

The study shows that the ARIMA (1, 2, 0) model is not only stable but also the most suitable model to forecast the total annual number of new HIV infections in Vietnam over the out-of-sample period. The model predicts a commendable decrease in the annual number of new HIV infections in the country over the out-of-sample period. Somewhere around 2024, Vietnam is likely to be having zero new HIV infections. This study essentially shows that the HIV/AIDS epidemic is under control in Vietnam. However, we still recommend that the government of Vietnam must continue strengthening its national AIDS response strategy, and that special emphasis be directed towards behavior change interventions such as increased condom use as well as reduction of sexual partners.

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