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

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Abstract

Using annual time series data on the total number of new HIV infections in Malaysia from 1990 – 2018, the study makes predictions for the period 2019 – 2030. The research applies the Box-Jenkins ARIMA methodology. The diagnostic ADF tests indicate that, G, the series under consideration is an I (1) variable. Based on the AIC, the study presents the ARIMA (2, 1, 0) model as the parsimonious model. The residual correlogram further reveals that the presented model is quite stable and its residuals are not serially correlated. The results of the study indicate that the total number of new HIV infections in Malaysia is likely to continue on a gradual downwards trajectory over the period 2019 – 2030. By 2030, new HIV infections in Malaysia would have declined by approximately 6.2%.

1.0INTRODUCTION

HIV/AIDS has been a growing public health problem in Malaysia for over three decades (Sern et al., 2016). In fact, Malaysia is home to one of the fastest growing HIV epidemics in the East Asia and Pacific regions. Malaysia's first HIV case was reported in Kuala Lumpur in December 1986. By the end of 2015, a total of 105988 HIV cases have been recorded. The number of new HIV infections by 2015 was 3196 compared to 3517 new cases in 2014 (Kaur, 2015). Most HIV infections in Malaysia are from heterosexual transmission. The high risk populations for HIV transmission in the country are injecting drug users, sex workers, men who have sex with men, women, transgender people and migrant workers (Choy, 2014). The main goal of this study is to predict the number of new HIV infections in Malaysia over the period 2019 – 2030. This paper will go a long way in analyzing the possibility of ending the HIV scourge in the country.

2.0 LITERATURE REVIEW

Sern et al (2016) carried out an exploratory investigation of health communication and public awareness of HIV/AIDS, based on a cross-sectional survey of 384 respondents in Klang Valley, Malaysia. The results of the study showed that interpersonal channels are important HIV/AIDS informational sources, and that newspapers are a major mass communication or media source for HIV/AIDS information. In another Malaysian study,

Rutledge et al. (2018) examined correlates of recent HIV testing among transgender women in Greater Kuala Lumpur. The study employed both the bivariate logistic and penalized multivariate logistic regression. The research showed that HIV testing is the first step in linking individuals to prevention and treatment interventions. In an Asian review article, Hussain et al. (2018) uncovered the causes and consequences of HIV/AIDS in Pakistan and also examined the role of the Pakistani government in controlling the menace. The paper argued that Pakistan exhibits a low level of education regarding the topic of Sexually Transmitted Diseases (STDs) and HIV/AIDS. No similar study has been conducted in Malaysia. Hence, the need to fill-up this information hiatus.

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, G, the series under consideration.

3.2 The Applied Box – Jenkins ARIMA Model Specification

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

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

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

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 G] in Malaysia. 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
G	-1.450249	0.5392	-3.769597	@1%	Non-stationary
			-3.004861	@5%	Non-stationary
			-2.642242	@10%	Non-stationary

Table 1 shows that G 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
ΔG	-5.932498	0.0001	-3.724070	@1%	Stationary
			-2.986225	@5%	Stationary
			-2.632604	@10%	Stationary

Table 2 indicates that G is an I (1) variable.

3.4.3 Evaluation of ARIMA models (without a constant)

Table 3: Evaluation of ARIMA Models (without a constant)

Model	AIC	U	ME	RMSE	MAPE
ARIMA (1, 1, 1)	426.5082	1.0764	42.377	629.01	5.0782
ARIMA (2, 1, 0)	**415.4460**	0.98001	72.832	603.49	5.0235
ARIMA (0, 1, 1)	429.2812	0.85271	31.821	584.6	4.8988
ARIMA (1, 1, 0)	435.7704	1.0699	11.423	669.45	4.7908
ARIMA (3, 1, 0)	417.4130	0.97623	72.922	604.23	4.9838

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, 1, 0) model is finally chosen.

3.5 Residual & Stability Tests

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

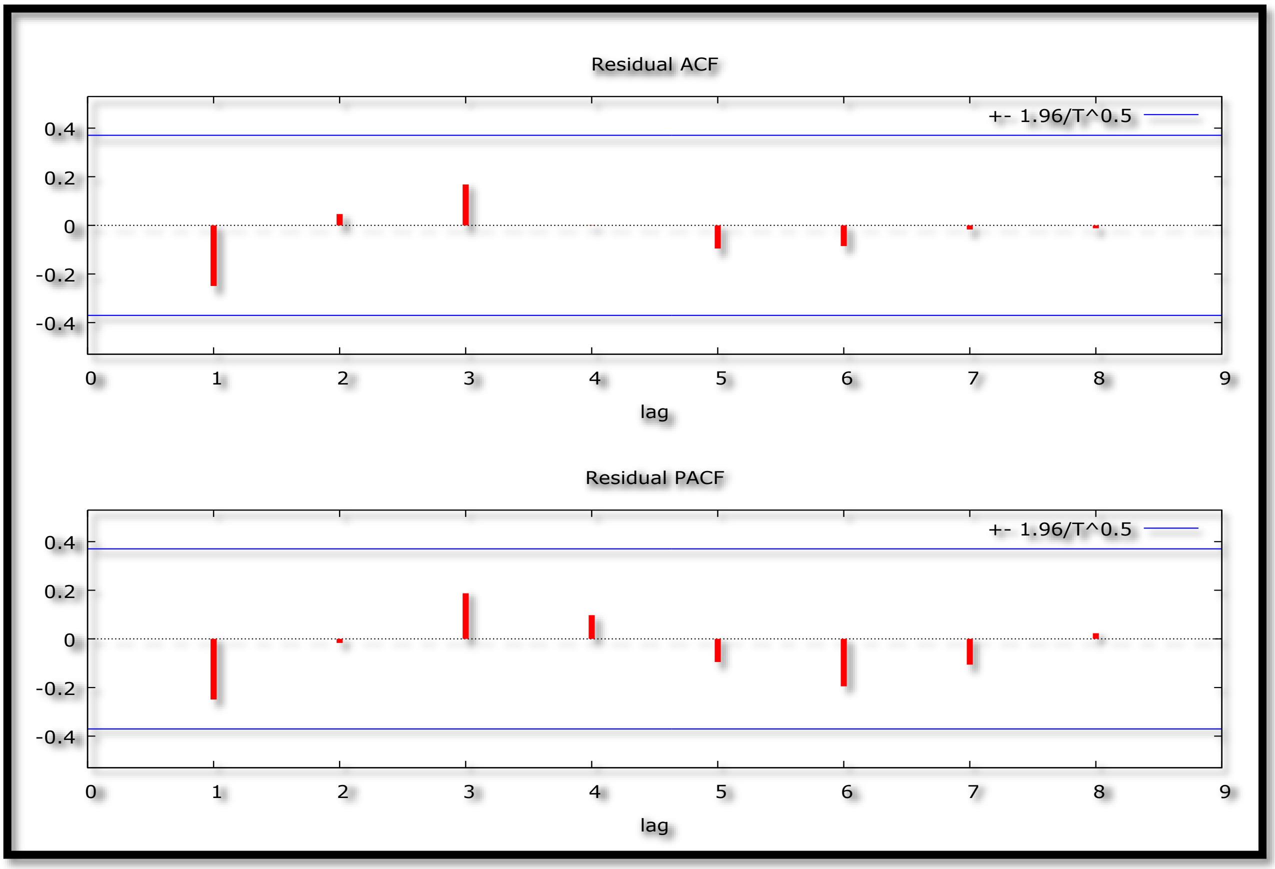

Figure 1: Correlogram of the Residuals

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

4.0 FINDINGS OF THE STUDY

4.1 Results Presentation

Table 4: Main Results

ARIMA (2, 1, 0) Model:				
The chosen optimal model, the ARIMA (2, 1, 0) model can be expressed as follows: $\Delta G_t = 1.22366\Delta G_{t-1} - 0.915041\Delta G_{t-2} \ldots \ldots \ldots \ldots \ldots [2]$				
Variable	Coefficient	Standard Error	z	p-value
β_1	1.22366	0.170445	7.179	0.0000***
β_2	-0.915041	0.120837	-7.573	0.0000***

Table 9 shows the main results of the ARIMA (2, 1, 0) model.

Forecast Graph

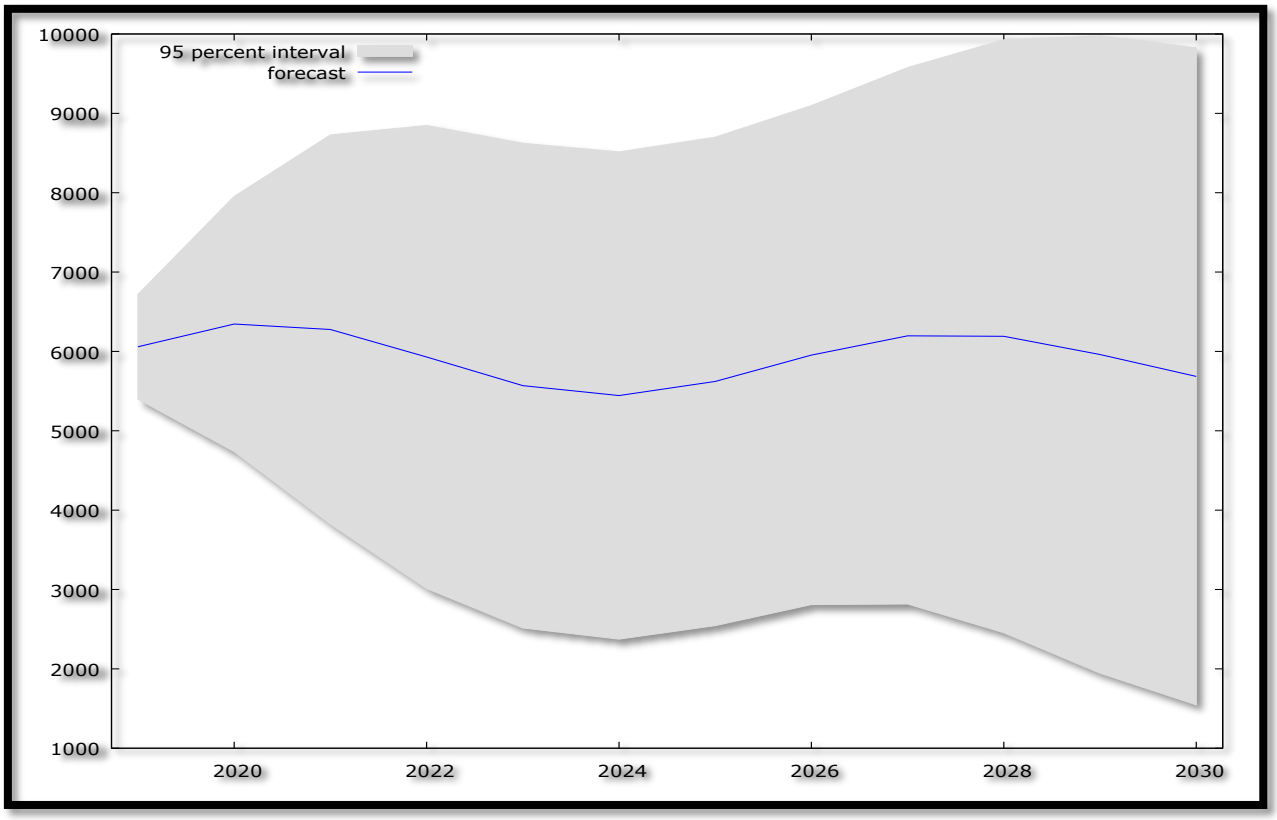

Figure 2: Forecast Graph – In & Out-of-Sample Forecasts

Figure 2 shows the in-and-out-of-sample forecasts of the G series. The out-of-sample forecasts cover the period 2019 – 2030.

Predicted G– Out-of-Sample Forecasts Only

Table 5: Predicted G

Year	Predicted G	Standard Error	95% Confidence Interval
2019	6058.60	336.425	(5399.22, 6717.98)
2020	6345.26	820.259	(4737.58, 7952.94)
2021	6276.39	1250.58	(3825.30, 8727.48)
2022	5929.82	1488.36	(3012.69, 8846.94)
2023	5568.74	1557.86	(2515.39, 8622.10)
2024	5444.05	1566.16	(2374.43, 8513.67)
2025	5621.86	1570.19	(2544.34, 8699.38)
2026	5953.54	1603.81	(2810.13, 9096.94)
2027	6196.70	1724.30	(2817.13, 9576.26)
2028	6190.74	1906.10	(2454.84, 9926.63)
2029	5960.95	2048.75	(1945.48, 9976.42)
2030	5685.22	2111.78	(1546.20, 9824.23)

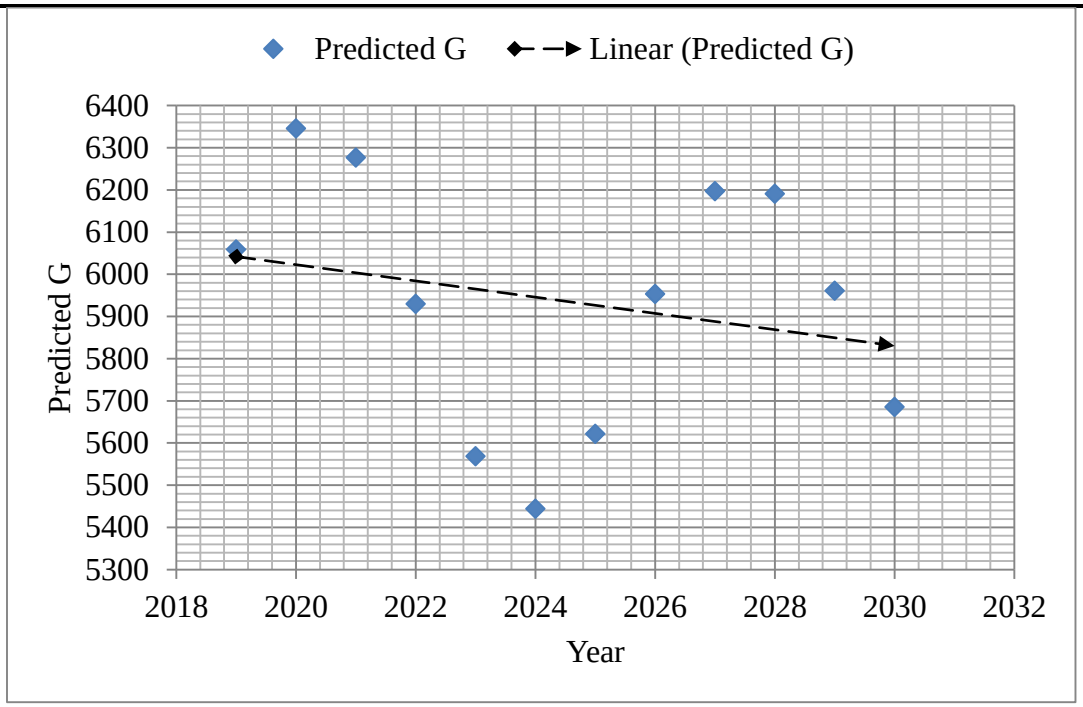

Figure 3: Graphical Analysis of Out-of-Sample Forecasts

Table 5 and figure 3 show the out-of-sample forecasts only. The total number of new HIV infections in Malaysia is projected to decrease gradually from the estimated 6059 new infections in 2019 to almost 5685 new infections by 2030.

5.0 CONCLUSION

The study shows that the ARIMA (2, 1, 0) model is not only stable but also the most suitable model to predict the total annual number of new HIV infections in Malaysia over the period 2019 – 2030. The model predicts a commendable decrease in the annual number of new infections in the country. This shows that the HIV/AIDS epidemic is under control in Malaysia. However, we still recommend that the government of Malaysia should continue strengthening its national AIDS response strategy. Special emphasis ought to be directed towards behavior change interventions such as increased condom use as well as reduction of sexual partners.

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