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A seasonal autoregressive integrated moving average model to predict incidence of dengue cases in Kuantan, Malaysia

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ABSTRACT

A time series analysis model. Could provide useful information to facilitate the planning of public health interventions to minimize the frequency of dengue fever (DF) outbreaks. The objectives of this study were to analyze the trend of monthly DF cases from Kuantan, Malaysia during 2011-2019 to develop a seasonal autoregressive integrated moving average (SARIMA) model, test the accuracy of model parameters by forecasting monthly cases of DF in 2018 and comparing it with actual monthly cases of DF in 2018, and construct a SARIMA model, by adopting the Box-Jenkins method, to forecast the monthly DF cases in 2019. Monthly-confirmed DF cases from 2011 to 2018 fit the model while the prediction was validated using epidemiological data from January 2018 to December 2018. The study concluded that the SARIMA (0,1,0) $(3,0,2)_{12}$ model was the best-fit and could be used to extrapolate case numbers up to 12 months in advance. Our predicted number of monthly DF cases in 2019 was relatively close to the actual number of monthly DF cases and fell within the confidence interval. Therefore, the SARIMA model developed by this study is capable of accurately forecasting and predicting future DF cases. This can help improve existing intervention programs, which are an integral component of minimizing the burden of the disease in Kuantan.

Keywords: dengue fever; time series analysis; prediction; SARIMA

1. INTRODUCTION

Dengue fever (DF) is a burgeoning public health problem in Malaysia (Bujang et al., 2017). Therefore, formulating disease prevention, intervention, and control methodologies are vital to reduce the likelihood of new infection as well as the burden of the disease in the country. The proposed strategies would be more effective if they were supported by accurate statistical and scientific data. Time series analysis is one of the statistical techniques that is used to predict future occurrences of DF by assessing past trends, which is achieved by analyzing a continuous sequence of numerical data points. In an investment industry, for instance, time series is represented by the movement of specific data points, such as the price of a commodity; over a specified period with regularly reported data points. There is no time period to allow policy makers or analysts to obtain important and highly sought-after data. Often, time series analysis is related to trend analysis, cyclical fluctuation analysis and issues of seasonality. For example,

disease such as malaria or tuberculosis can be analyzed daily, weekly or by a monthly basis. Time series analysis will also show whether the disease is seasonal by evaluating if it goes through peaks and troughs at specific times of the year. The onset of DF in Malaysia backdated to 1901, following its transmission from Singapore to Penang (Skae, 1902). The first outbreak of epidemic proportions was reported in 1973 and resulted in a total of 969 confirmed cases and 54 mortality cases (Wallace et al., 1980); such situation continued to deteriorate with the rampant spread of the disease in urban populations. Subsequent outbreaks in the following years resulted in 1,487 cases and 54 deaths in 1973, 2,200 cases and 104 deaths in 1974, and 3,006 cases and 35 deaths in 1982 (Mudin, 2015). The number of confirmed DF cases has only continued to increase since 2000, with the highest number of cases recorded in 2015.

According to Ler et al. (2011), DF can be caused by any of the four genetically related but antigenically distinct dengue virus (DENV) serotypes, which are DENV-1, DENV-2, DENV-3, and DENV-4. Multiple serotypes circulate simultaneously in Malaysia with DENV-1, -2 and -3 identified in Negeri Sembilan (Ahmad et al., 2012), multiple entries of DENV-2 and -4 in Sarawak (Holmes et al., 2009) and cases in Kuala Lumpur and Selangor predominantly from DENV-4 (Chew et al., 2012). Although each DENV serotype has a distinct clinical and epidemiological profile, accurately identifying each serotype's clinical characteristics proves to be a challenge. Studies indicate that DENV-2 and -3 have more severe disease outcomes while DENV-4 is the mildest (Nisalak et al., 2016; Vaughn et al., 2000). All genders and ethnicities have been found to be equally vulnerable. Severe cases of dengue haemorrhagic fever (DHF) and dengue shock syndrome (DSS) affect paediatric patients between the ages of 2 years and 15 years throughout Southeast Asia. (Bhatia et al., 2013).

DF is an emerging threat in non-endemic countries. Despite warning, the number of tourists travelling into dengue-endemic areas has increased. Imported DF cases can further spread in non-endemic areas when competent vectors, such as *Aedes albopictus* and *Aedes aegypti* mosquitos, are present. Following disease importation in recent years, autochthonous DF outbreaks have been reported in several non-endemic countries such as France, Croatia, Portugal, and the United States (Gjenero-Margan et al., 2011).

In Malaysia, nearly all age groups are vulnerable to the disease. The most vulnerable age group between 15 years to 49 years old (Mudin, 2015). DF is considered a highly contagious health threat with a growing trend of infection in Malaysia. Between 2000 to 2010, the number of DF cases and DF-related deaths increased by an average of 14% and 8%, respectively, each year (Mia et al., 2013). Malaysia suffered a 151% increase in cases in 2014 compared to the year of 2013, as seen in Figure 1.

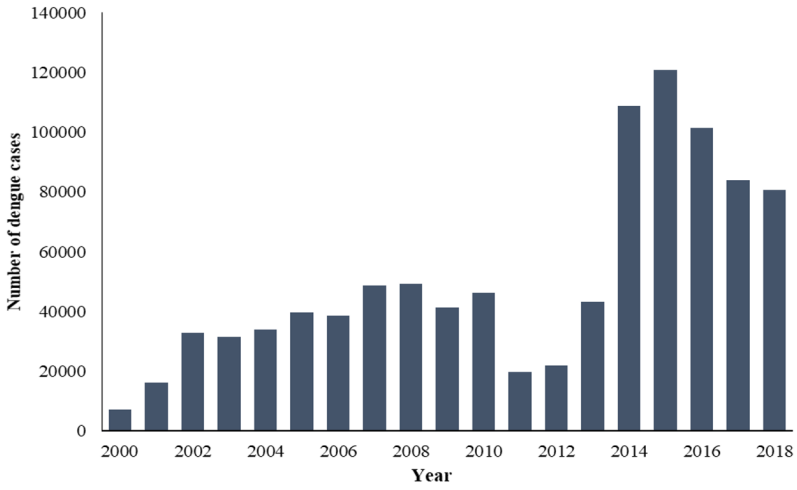

Figure 1. Dengue cases situation reported in Malaysia from 2000 to 2018

2. MATERIALS AND METHODS

This study used systematically sampled data of confirmed DF cases reported by the Vector-borne Disease Sector, Disease Control Division, Pahang State Health Department at the Ministry of Health, Malaysia's real-time national database of dengue cases that is eDengueV2 (http://edenguev2.moh.gov.my/index.php?r=site%2Flogin). The eDengue V2 contains individual DF patient's information as well. Complete data of each individual confirmed case from 2011 to 2018 were downloaded and placed in a specific folder in Microsoft Office format. Data saved was updated using Microsoft Excel and statistically analyzed using Statistical Package for Social Science Version 20 (SPSS Version 20.0). Box et al. (2015) and Boudrioua and Boudrioua, (2020) expressed the seasonal autoregressive integrated moving average (SARIMA) model as follows:

$$\Phi_p(B^s)\phi_p(B)\nabla_S^D\nabla^d\chi_t = \Theta_\varrho(B^s)\omega_t$$

where the seasonal difference component can be represented by: $\nabla_S^D = (1\text{-}B^s)^D$ $\Phi_p(B^s)$ and $\Theta_\varrho(B^s)$ are polynomial B represents respectively the seasonal autoregressive and moving average components, given as follow:

$$\Phi(B^s) = 1 - \Phi_1 B^s - \Phi_2 B^{2s} - \cdots - \Phi_p B^{ps}$$
$$\Theta(B^s) = 1 - \Theta_1 B^s - \Theta_2 B^{2s} - \cdots - \Theta_\varrho B^{\varrho s}$$

The model used autoregression terms (P, D, Q) extracted through autocorrelation and added to the seasonality element (p, d, q) to develop a model capable of predicting dengue. The null hypothesis of a SARIMA against stationary and alternatively was tested in the augmented Dickey-Fuller test (ADF). The $\Delta X_t = \beta_0+\alpha_t+\beta_1 X_{t-1}+\sum_{i=1}^{p} \gamma i\ \Delta X_{t-1}+\varepsilon_t$ regression formula (Cryer and Chan, 2008) can test both and, if necessary, fulfil the underlying assumption via differencing before forecasting using the Box-Jenkins method. Auto-correlation function (ACF) and partial auto-correlation function (PACF) plots were generated to measure the degree of correlation between observations in the time series. Both ACF and PACF were compared to determine their characteristic and theoretical behaviors. The model was estimated using mean squared error (MSE), mean absolute percentage error (MAPE), mean absolute error (MAE) and root-mean-square error (RMSE). The final model's goodness of fit was tested using Bayesian information criterion (BIC). To obtain a forecast with minimal errors, a SARIMA model must possess good features. The model should be parsimonious (smallest coefficients), stationary and have constant mean and variance values while its coefficient must be significant and have white noise as a residual. Lastly, the time series model should be distributed normally to appropriately fit the forecast with minimal error.

3. RESULTS

Figure 2 shows 8,005 confirmed DF cases between 2011 and 2018 in Kuantan. An increasing trend of DF cases, beginning in 2011 and finally showing a peak in 2015, was observed during such period. It increased by 216% in magnitude and frequency as indicated by the 541 cases and 1,711 cases in 2011 and 2015, respectively. The number of cases subsequently decreased to 1,684 in 2016, further decrease in DF cases was observed to be 963 in 2017, and 578 in 2018.

A pattern of short-term changes was observed in the data indicating the existence of seasonal fluctuations. The decomposition method estimated the trends while the moving average method calculated the seasonal fluctuations. This produced a single figure that showed the original series (observed), trend, seasonal effects, and random elements (Figure 3). The additive model seemed more appropriate than the multiplicative model because, over time, the frequency of the seasonal fluctuations and the pattern did not vary. Increased in variance of the random element meant that log transformation was more suitable for the sequence.

Natural logarithm and natural differentiation were carried out to stabilize the time series variance. Furthermore, stationarity testing of the time series was carried out using the ADF test and the Kwiatkowski–Phillips–Schmidt–Shin (KPSS) test for the monthly DF cases in Kuantan. Hypothesis were H_0: X_t is non-stationary and H_a: X_t is the stationary sequence tested using ADF. H_0: X_t hypotheses are levels or patterns of stationarity that have been tested for the H_a: X_t non-stationary series.

As shown in Table 1, the 0.513 *p*-value of the ADF test (p>0.05) indicated that the original time series was non-stationary. This non-stationarity was also supported by the 0.024 was *p*-value of the KPSS test (p<0.05). Therefore, differencing was used to convert the original time series to stationary. The first differencing of the original time series detrended and stabilized it. Table 1 also shows the ADF test's *p*-value of 0.01, indicating a rejection of the non-hypotheses and demonstrating the success of differencing the time series. The KPSS test's *p*-value of 0.1 (p>0.05) indicated that the non-hypotheses of stationarity in the time series was not rejected, thereby making the series stationary.

Table 1. Unit root test before differentiation and after first differentiation

Unit root test	t-statistic	*P*-value
Before differentiation		
ADF	-2.1536	0.513
KPSS	0.583	0.024
After first differentiation		
ADF	-4.6066	0.01
KPSS	0.0445	0.1

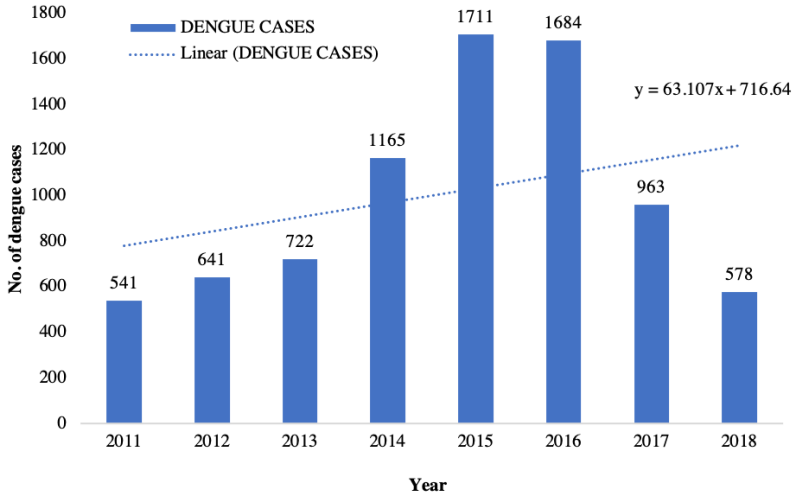

Figure 2. Time series plot of yearly dengue cases in Kuantan, from 2011 to 2018

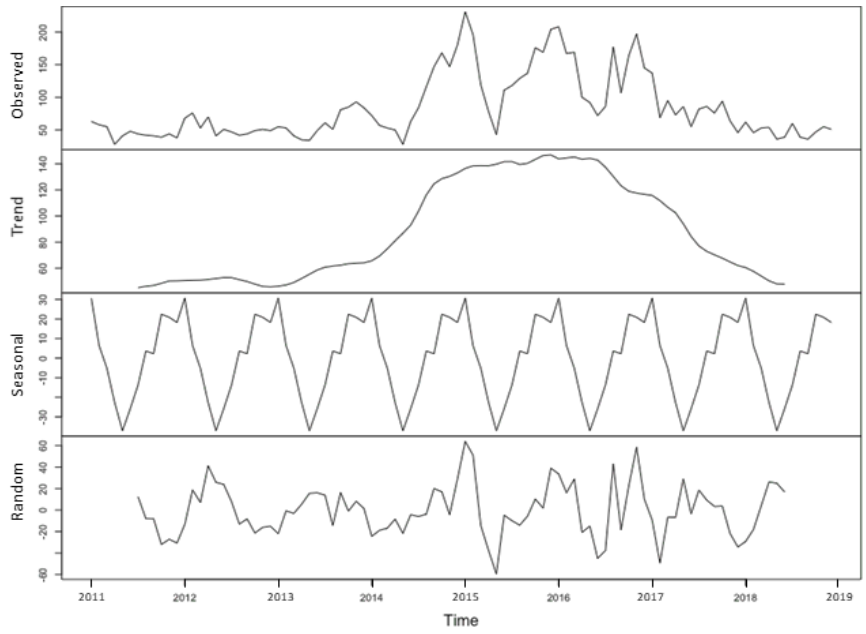

Figure 3. Decomposition of dengue fever cases in Kuantan during 2011-2019

The structure dependence of the coefficient rates was calculated by testing ACF and PACF analyses. The ACF and PACF plots in Figures 4B and 4C defined the dependence of the coefficient structure, suggesting that non-seasonal (p, d, q) and seasonal (P, D, Q) parameters were required in the model design. Major cuts were observed at lags 1 and 12 on the ACF and PACF plots after non-seasonal differentiation as shown in Figures 4E and 4F. ACF and PACF analyses suggested that the *p* and *q* values should be equal to 0 or 1.

Table 2 shows the BIC, RMSE, MAE and MAPE parameter values of the developed SARIMA models in relation to different *p*, *d*, and *q* parameters. From the models, the SARIMA (0,1,0) $(3,0,2)_{12}$ model had the lowest BIC, RMSE, MAPE and MAE parameter values, and the highest coefficient of determination (R^2) value which made it the most appropriate, compatible, and best-fit model for DF cases. The parameters were estimated using maximum likelihood estimation (MLE), the best and most appropriate method of estimation. A Ljung-Box test of the SARIMA (0,1,0) $(3,0,2)_{12}$ model had a *p*-value >0.05, which indicated that the model was appropriate.

Figure 5A shows the ACF plot and estimation of the residual SARIMA (0,1,0) $(3,0,2)_{12}$ model data. For all the time lags, the plot showed that the ACF parameters fell within the 95% confidence interval (CI) and the plot values were close to zero, indicating that the series is considered white noise. The normality plot, shown in Figure 5B, revealed that the residual data was distributed normally. The *p*-value = 0.844, shown in Table 3, indicated that the alternative hypothesis was rejected, and that the data was distributed normally.

The statistical data, shown in Table 3, were from Shapiro-Wilk and Kolmogorov-Smirnov tests. The Shapiro-Wilk test was used to observe datasets smaller than 2,000, otherwise, the Kolmogorov-Smirnov test was used. Since there were only 96 observable data records, the Shapiro-Wilk test would have been used. If the residuals were distributed normally, it would support the efficacy of this model.

After diagnostic testing of the time series, the model was tested using actual DF case values from January 2011 to December 2018, that was named as training dataset. The dataset was executed using SARIMA (0,1,0) $(3,0,2)_{12}$ model to forecast DF cases in 2018. The results were validated by comparing it to the actual DF case numbers in 2018 using metrics specifically BIC, R^2, RMSE, MAPE, and MAE in the developed predictive models, which allowed for an objective view of the strengths and weaknesses of each model. The validation results of the forecasts are shown in Figure 6.

The ideal model for DF prediction for the year 2018 in Kuantan was the SARIMA (0,1,0) $(3,0,2)_{12}$ model. Later, the model was used to forecast monthly DF cases for 2019 (Figure 7). The blue line shows the predicted DF case numbers from Jan 2011 to December 2018. The results showed that the SARIMA (0,1,0) $(3,0,2)_{12}$ model's forecast was reasonably accurate, with the predicted DF case pattern for 2019 being almost identical to the actual DF case pattern and fell within the 95%, CI confirming that the forecasted data was adequate and efficient.

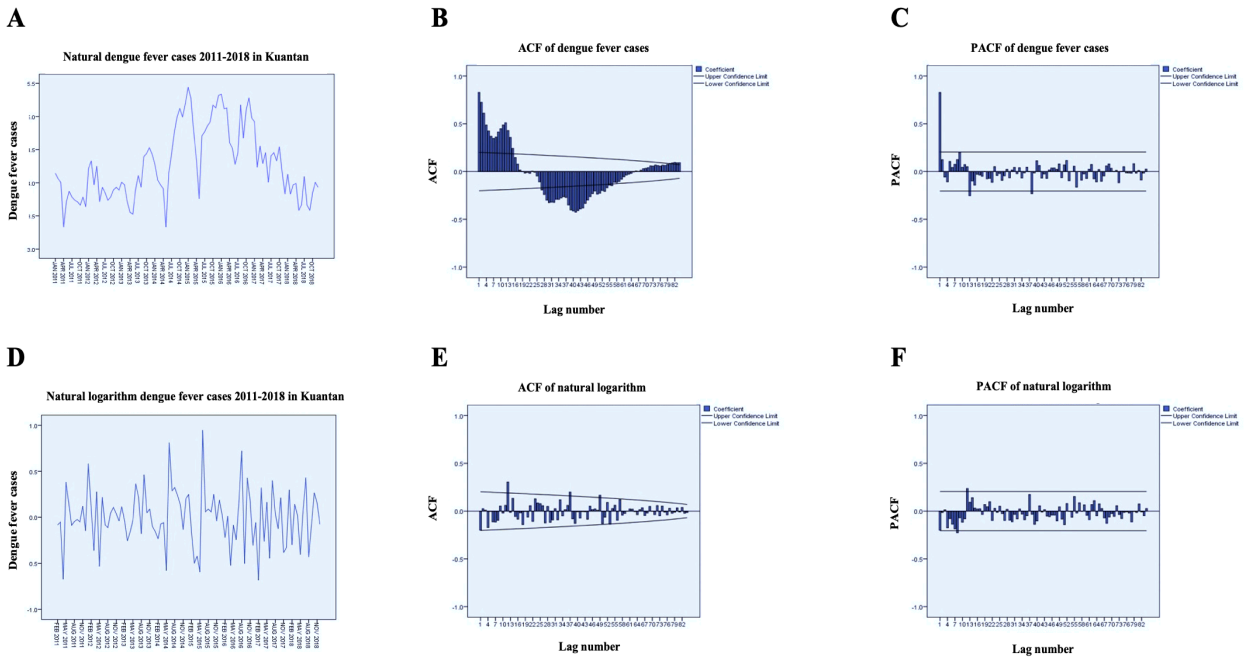

Figure 4. (A) Natural series of dengue fever cases, (B) ACF plot of natural series dengue fever cases, (C) PACF plot of natural series dengue fever, (D) natural logarithm with first differencing of dengue fever series, (E) ACF plot of natural logarithm with first differencing of dengue fever and (F) PACF of natural log with first differencing of dengue fever cases

Table 2. Tentative model of SARIMA for dengue fever cases in Kuantan

SARIMA models	BIC	R^2	RMSE	MAPE	MAE
$(0,1,1)(1,1,1)_{12}$	6.630	0.813	22.849	23.422	17.331
$(1,1,1)(0,0,2)_{12}$	6.621	0.797	23.161	20.032	15.59
$(1,1,1)(0,1,1)_{12}$	7.010	0.666	29.916	26.855	21.842
$(1,1,2)(1,1,1)_{12}$	7.181	0.675	30.084	25.470	21.166
$(2,1,1)(2,1,1)_{12}$	7.185	0.695	29.363	22.178	19.392
$(1,1,1)(0,0,1)_{12}$	6.558	0.798	22.991	20.028	15.588
$(1,1,1)(2,0,1)_{12}$	6.844	0.731	26.524	23.94	18.392
$(1,1,0,)(2,0,1)_{12}$	6.687	0.808	22.821	18.912	15.244
$(0,1,1)(2,0,1)_{12}$	6.685	0.808	22.801	18.9	15.241
$(0,1,0)(1,0,2)_{12}$	6.637	0.806	22.804	19.142	15.445
$(0,1,0)(2,0,1)_{12}$	6.609	0.811	22.483	19.012	15.204
$(0,1,0)(1,0,1)_{12}$	6.589	0.804	22.804	19.01	15.326
$(0,1,0)(2,0,3)_{12}$	6.736	0.81	22.837	19.131	15.363
$(0,1,0)(3,0,2)_{12}$	6.505*	0.849**	20.347*	17.806*	13.669*

Note: *Lowest value for each parameter estimation
**Highest value for each parameter estimation

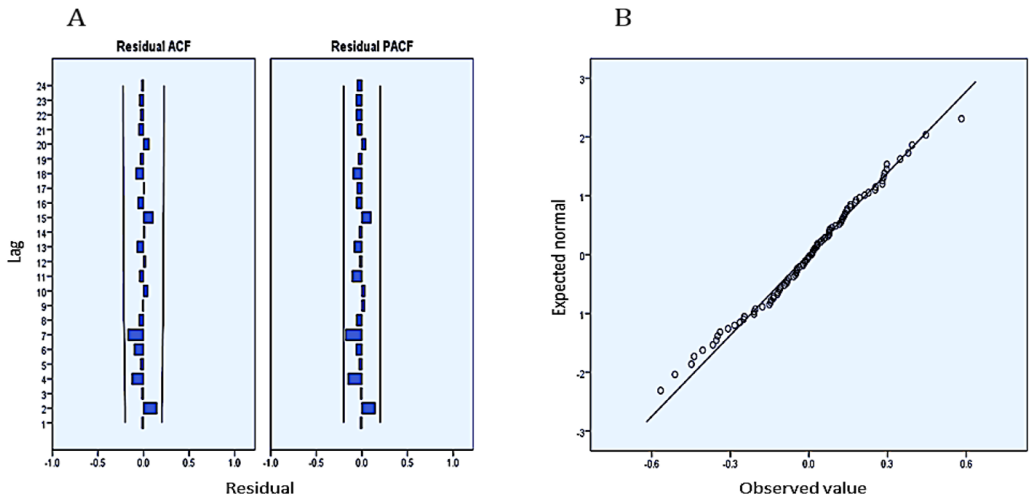

Figure 5. (A) Residual plots of SARIMA (0,1,0) $(3,0,0)_{12}$ and (B) normality plot of residuals SARIMA (0,1,0) $(3,0,2)_{12}$

Table 3. Shapiro-Wilk normality test SARIMA (0,1,0) $(3,0,2)_{12}$

Tests of normality	Kolmogorov-Smirnov[a]			Shapiro-Wilk		
	Statistic	df	Significance	Statistic	df	Significance
Noise residual from SARIMA (0,1,0) $(3,0,2)_{12}$ in 2011-2019	0.057	95	0.200*	0.992	95	0.844

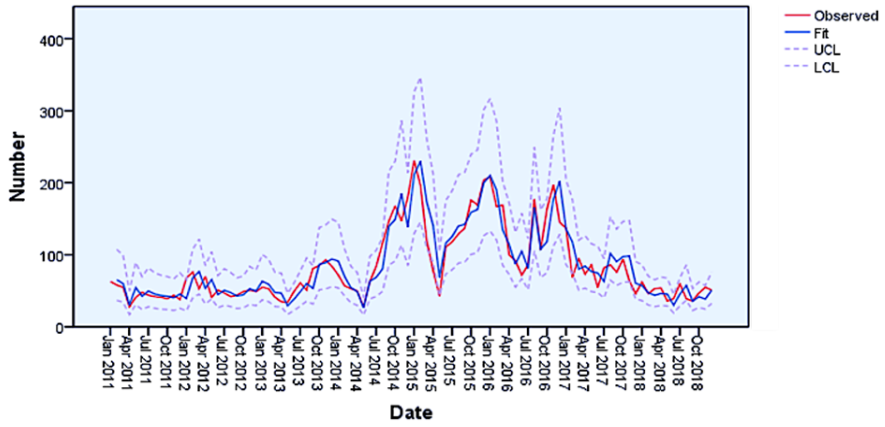

Figure 6. Validation of SARIMA (0,1,0) $(3,0,2)_{12}$ model with actual dengue fever cases from 2011 to 2018

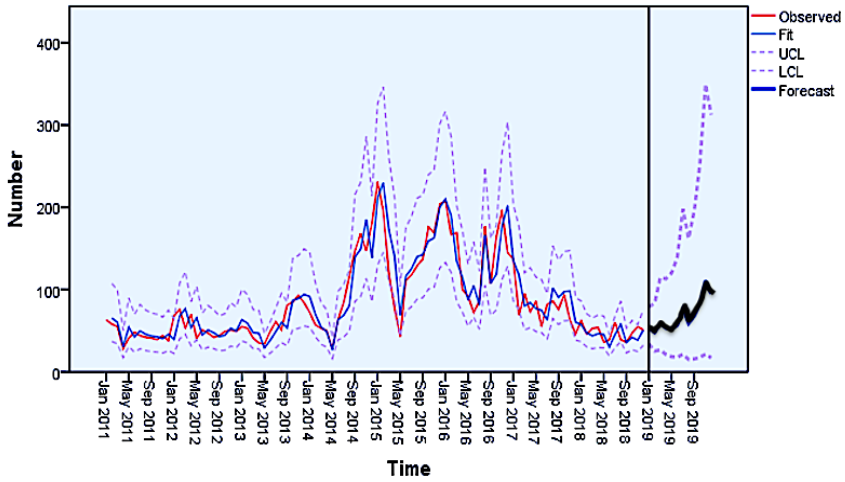

Figure 7. Plot of predicted dengue cases in 2019 using SARIMA (0,1,0) $(3,0,2)_{12}$ with 95% of confidence interval

4. DISCUSSION

To assess the risk of an outbreak, particularly DF, an early prediction tool is necessary. Instead of controlling the disease, early diagnosis will not only allow for early intervention but prevention as well. Therefore, an early warning system must be established to identify and quantify the threat of DF in the population. The existing system of DF outbreak prediction focuses solely on various entomological indices while ignoring epidemiological indices. The SARIMA model is a useful tool for tracking and interpreting data. It has great potential as a public health decision-making tool to improve contingency planning and mitigation initiatives (Dom et al., 2013). The SARIMA model developed in this study closely mimicked the pattern of DF cases in Kuantan. The model was tested by forecasting DF case numbers for 2019 through auto-regression and moving average parameters. Therefore, using multi-month trend extrapolation, this model can successfully forecast the number of DF cases.

This study focused on forecasting DF cases in Kuantan using a SARIMA model. It has been determined that, of all the models developed in this study, the SARIMA $(0,1,0)(3,0,2)_{12}$ model was the most appropriate and parsimonious model with the lowest BIC, RMSE, MAE and MAPE parameter values and the highest R^2 value. It was found to accurately predict the number of DF cases for which it was months ahead of time, indicating that the method could be used to predict DF case numbers for 2019 in Kuantan. The model forecasted a total of 814 DF cases in 2019 with the highest number of cases (14% or 111) occurring in November and the lowest number of cases (6% or 48) occurring in February (Table 4). A SARIMA model, utilizing the same BIC, RMSE, MAE and MAPE parameters, was used to predict DF case numbers in Selangor and found to closely reflect the actual number of DF cases (Thiruchelvam et al., 2018). Several other studies have reported similar findings using SARIMA models developed using secondary data and Akaike information criterion, RMSE, MAE, MAPE parameters (Phuthomdee et al., 2018; Dom et al., 2013). This model was able to consistently predict and tally with actual DF case numbers. Many studies could also consider and discuss climate change impacts, such as precipitation, temperature, and humidity, to increase forecast accuracy.

Table 4. Summary of the forecasted values with the lower and upper 95% confident interval

Model $(0,1,0)(3,0,2)_{12}$	Jan 2019	Feb 2019	Mar 2019	Apr 2019	May 2019	Jun 2019	Jul 2019	Aug 2019	Sep 2019	Oct 2019	Nov 2019	Dec 2019
Forecast	53	48	59	53	52	57	76	59	68	83	111	95
UCL	79	83	115	113	120	139	198	162	196	252	350	313
LCL	34	25	27	21	18	18	21	15	16	18	21	17

Note: UCL = upper control limit
LCL = lower control limit

5. CONCLUSION

In conclusion, the objective of this study was successfully achieved. Based on prediction model, Kuantan can expect a 41% (236) increase of dengue fever (DF) cases in 2019 from the 578 cases reported in 2018. This model is a good fit for these cases only because they are localized transmission (peri-domestic infection). DF transmission is very complex with the risk of transmission varying in different locations and from season-to-season. The disease cycle depends on seasonal conditions, immunity, and changes in hyper-endemic areas where various serology types are in circulation.

Due to the intrinsically complex nature of these processes, time series prediction is a challenge. Whether a sequence is stochastically or deterministically chaotic, or some mixture of both systems, is near impossible to tell. More importantly, it is unknown to what degree a non-linear deterministic system preserves its properties when distorted by white noise. White noise may influence a model in various ways even though the model's equations remain deterministic. Since there is no single accurate statistical measure of chaos, it is crucial to combine multiple tests, especially when working with small and white noise datasets such as in disease, economic and financial time series.

Ideally, this model can be used to track and predict the occurrence of DF in Kuantan. This is in line with the need to develop DF monitoring and prediction strategies to reduce not only local and national cases but regional cases as well. Therefore, the SARIMA model can accurately forecast DF cases, thereby enhancing the current intervention programme by allowing them to install vector control measures a few months ahead of DF seasons.

REFERENCES

Ahmad, N. M. G., Rozita, H., Mazrura, S., Zainudin, M. A., Hidayatulfathi, O., Faridah, M. Z., Ismail, N., and Choy, E. A. (2012). Dengue infections and circulating serotypes in Negeri Sembilan, Malaysia. *Malaysian Journal of Public Health Medicine*, 12(1), 21-30.

Bhatia, R., Dash, A. P., and Sunyoto, T. (2013). Changing epidemiology of dengue in South-East Asia. *WHO South-East Asia Journal of Public Health*, 2(1), 23-27.

Boudrioua, M. S., and Boudrioua, A. (2020). Modeling and forecasting the algerian stock exchange using the Box-Jenkins methodology. *Journal of Economics, Finance and Accounting Studies*, 1(1), 1-15.

Box, G. E., Jenkins, G. M., Reinsel, G. C., and Ljung, G. M. (2015). *Time Series Analysis: Forecasting and Control*, 5th, New Jersey: John Wiley & Sons, pp. 52.

Bujang, M. A., Mudin, R. M. B., Haniff, J., Ikhwan, T. M., Sidik, T. A. B., Nordin, N. A. M., Sulaiman, N., Md-Sani, S. S., Kadir, S. S. A., Mohammed, S., and Pin, G. P. (2017). Trend of dengue infection in Malaysia and the forecast up until year 2040. *International Medical Journal*, 24(6), 438-441.

Chew, M. H., Rahman, M. M., Jelip, J., Hassan, M. R., and Isahak, I. (2012). All serotypes of dengue viruses circulating in Kuala Lumpur, Malaysia. *Current Research Journal of Biological Sciences*, 4(2), 229-234.

Cryer, J. D., and Chan, K. S. (2008). *Time Series Analysis: with Applications in R*, 2nd, New York: Springer Science & Business Media, pp. 191.

Dom, N. C., Hassan, A. A., Abd Latif, Z., and Ismail, R. (2013). Generating temporal model using climate variables for the prediction of dengue cases in Subang Jaya, Malaysia. *Asian Pacific Journal of Tropical Disease*, 3(5), 352-361.

Gjenero-Margan, I., Aleraj, B., Krajcar, D., Lesnikar, V., Klobučar, A., Pem-Novosel, I., Kurečić-Filipović, S., Komparak, S., Martić, R., Đuričić, S., Betica-Radić, L., Okmadžić, J., Vilibić-Čavlek, T., Babić-Erceg, A., Turković, B., Avšić-Županc, T., Radić, I., Ljubić, M., Šarac, K., Benić, N., and Mlinarić-Galinović, G. (2011). Autochthonous dengue fever in Croatia, August-September 2010. *Eurosurveillance*, 16(9), 19805.

Holmes, E. C., Tio, P. H., Perera, D., Muhi, J., and Cardosa, J. (2009). Importation and co-circulation of multiple serotypes of dengue virus in Sarawak, Malaysia. *Virus Research*, 143(1), 1-5.

Mia, M. S., Begum, R. A., Er, A. C., Abidin, R. D. Z. R., and Pereira, J. J. (2013). Trends of dengue infections in Malaysia, 2000-2010. *Asian Pacific Journal of Tropical Medicine*, 6(6), 462-466.

Mudin, R. N. (2015). Dengue incidence and the prevention and control program in Malaysia. *IIUM Medical Journal Malaysia*, 14(1), 5-9.

Nisalak, A., Clapham, H. E., Kalayanarooj, S., Klungthong, C., Thaisomboonsuk, B., Fernandez, S., Reiser, J., Srikiatkhachorn, A., Macareo, L. R., Lessler, J. T., Cummings, D. A. T., and Yoon, I. K., (2016). Forty years of dengue surveillance at a tertiary pediatric hospital in Bangkok, Thailand, 1973-2012. *The American Journal of Tropical Medicine and Hygiene*, 94(6), 1342-1347.

Phuthomdee, S., Soontornpipit, P., Viwatwongkasem, C., and Sillabutra, J. (2018). Dengue forecasting model using SARIMA model to predict the incidence of dengue in Thailand. *Current Applied Science and Technology*, 18(2), 58-65.

Skae, F. M. T. (1902). Dengue fever in Penang. *British Medical Journal*, 2(2185), 1581-1582.

Ler, T. S., Ang, L. W., Yap, G. S. L., Ng, L. C., Tai, J. C., James, L., and Goh, K. T. (2011). Epidemiological characteristics of the 2005 and 2007 dengue epidemics in Singapore – similarities and distinctions. *Western Pacific Surveillance and Response Journal*, 2(2), 24-29.

Thiruchelvam, L., Dass, S. C., Zaki, R., Yahya, A., and Asirvadam, V. S. (2018). Correlation analysis of air pollutant index levels and dengue cases across five different zones in Selangor, Malaysia. *Geospatial Health*, 13(1), 613.

Vaughn, D. W., Green, S., Kalayanarooj, S., Innis, B. L., Nimmannitya, S., Suntayakorn, S., Endy, T. P., Raengsakulrach, B., Rothman, A. L., Ennis, F. A., and Nisalak, A. (2000). Dengue viremia titer, antibody response pattern, and virus serotype correlate with disease severity. *The Journal of Infectious Diseases*, 181(1), 2-9.

Wallace, H. G., Lim, T. W., Rudnick, A., Knudsen, A. B., Cheong, W. H., and Chew, V. (1980). Dengue hemorrhagic fever in Malaysia: the 1973 epidemic. *The Southeast Asian Journal of Tropical Medicine and Public Health*, 11(1), 1-13.