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TEMPORAL MODELLING OF DENGUE CASES IN CÔTE D'IVOIRE FROM 2017 TO 2023: APPLICATION OF THE ARMA MODELS

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Abstract

Background and objectives. Dengue fever is a persistent public health problem in Côte d'Ivoire, with a recent upsurge in cases leading to instability in the health system. The aim of this study was to train the ARMA and SARMA models to analyze time series on the weekly prevalence of confirmed and suspected dengue cases in Côte d'Ivoire and to use these models to forecast dengue prevalence for the next 52 weeks.

Methods. This secondary study, based on weekly data on confirmed and suspected cases from 2017 to 2023, uses the ARMA (autoregressive moving average) and SARMA (seasonal autoregressive moving average) models to forecast dengue prevalence in Côte d'Ivoire. The data comes from the Institut National de l'Hygiène Publique.

Results. The $\mathrm{ARMA}(1, 0, 4)$ and $\mathrm{SARMA}(1, 0, 0)(1, 0, 0)_{(52)}$ models were identified as the best performing models, with respective MAE and RMSE of (MAE): 4.41 and 8.68 for the ARMA model and (MAE): 4, 3 and RMSE: 8.66 for the $\mathrm{SARMA}(1, 0, 0)(1, 0, 0)_{(52)}$ model.

Conclusion. These models provide valuable information for healthcare planning and resource allocation, even though external factors and complex interactions need to be taken into account.

1. Introduction

Dengue fever is a viral disease transmitted by mosquitoes of the genus Aedes, mainly Aedes aegypti and Aedes albopictus. It occurs in most tropical regions of the world [1]. The disease takes two main clinical forms, including a severe form that can lead to plasma leakage and potentially fatal haemorrhaging.

The alarming figures for dengue illustrate the scale of its impact worldwide. Around two-fifths of the world's population, or almost 2.5 billion people, are at risk of infection. Its prevalence has increased considerably in recent decades. Every year, between 50 and 500 million people contract the disease, resulting in between 10,000 and 20,000 deaths [2, 3].

Since the beginning of 2023, eighteen African Union (AU) countries have reported a total of 21,999 confirmed cases of dengue fever and 187,786 suspected cases, including 808 deaths, giving a case-fatality rate of 0.3% [4].

Côte d'Ivoire is not immune to this trend. The country has experienced recurrent dengue epidemics since 1990s, with an intensification in recent decades. In 2023, there were 3,895 cases and 27 deaths. In 2023, the health authorities declared a new epidemic, with at least 92 confirmed cases, mainly in the communes of Cocody and Bingerville, and two deaths recorded. This was the sixth epidemic recorded in the country since 2009 [5].

Dengue fever is a major strain on healthcare systems, not least because there is no specific treatment. Severe forms of the disease can rapidly develop and compromise vital prognosis. Against this backdrop, early warning of epidemics would make it possible to improve the effectiveness of control campaigns and better target preventive measures. Early intervention

could slow or halt the spread of the disease, while reducing the impact on health infrastructures.

To support these efforts, numerous mathematical models have been developed, in particular using the Box-Jenkins method. A systematic review by Leung et al. [6] classified existing forecasting models. It reveals that modelling techniques are broadly divided into two categories: statistical models (60.6%) and those based on machine learning (39.4%). Statistical models include linear regression models (18.3%) and time series/autoregressive models (26.7%) [6].

Among these time series models, ARIMA (autoregressive integrated moving average) is one of the most commonly used methods for time series analysis in epidemiology. Authors such as Siregar et al. [7, 8] have used this approach to predict the incidence of dengue fever in India. Ho and Ting [9] have also published a study on time series modelling of dengue cases in Malaysia.

In Côte d'Ivoire, very few dengue modelling initiatives have been documented to date. Yet these tools could prove essential for anticipating epidemic outbreaks. The general aim of this work is to model dengue epidemics in Côte d'Ivoire in order to predict their occurrence, using appropriate statistical methods such as ARMA models.

2. Methodology

This is an analytical retrospective that was carried out on a historical cohort from 2017 to 2023 for data on dengue fever in Côte d'Ivoire. The data are derived from health surveillance data on diseases with epidemic potential for dengue over the last 7 years. These data are reported in the weekly epidemiological bulletin: the "vigil".

Statistical analysis

Suspected and confirmed cases were described using position (mean, median) and dispersion (standard deviation, minimum, maximum)

parameters. The temporal evolution of cases was illustrated by curves describing the weekly trends in suspected and confirmed cases over the study period. For modelling purposes, the dataset was divided into two subsets. The training set included observations from the first week of morbidity in 2017 to the last week in 2022. The test set included all weeks in 2023. Autoregressive integrated moving average (ARIMA) models, first described by Box and Jenkins [10], were used to analyze the time series in order to develop a forecasting model. The ARMA(p, q) model combines autoregressive (AR) and moving average (MA) components:

$$X_t = \phi_1 X_{t-1} + \cdots + \phi_p X_{t-p} + \varepsilon_t + \theta_1 \varepsilon_{t-1} + \cdots + \theta_q \varepsilon_{t-q},$$

where

X_t is the number of cases of dengue fever t,

$\phi_1, \ldots, \phi_p$ are the autoregressive coefficients,

$\theta_1, \ldots, \theta_q$ are the moving average coefficients,

ε_t is white noise with zero mean and constant variance,

p is the order of the AR process,

q is the order of the MA process.

The SARIMA$(p, d, q)(P, D, Q)_{(s)}$ model first described by Wang et al. [11] is written in the following form:

$$\Phi_P(B^s)\phi_p(B)(1-B)^d(1-B^s)^D X_t = \Theta_Q(B^s)\theta_q(B)\varepsilon_t,$$

where

(p, d, q) are the parameters of the ARIMA model,

(P, D, Q) are the seasonal parameters,

s is the seasonal periodicity,

B is the delay operator.

Before modelling, the stationarity of the series was checked using the KPSS (Kwiatkowski-Phillips-Schmidt-Shin) and ADF (Augmented Dickey-Fuller) tests. The order of the autoregression (AR) and moving average (MA) was determined using the autocorrelation function (ACF) and partial autocorrelation function (PACF).

Several parameter combinations were tested, and the best model was selected according to three performance criteria: the Bayesian information criterion (BIC), the mean absolute percentage error (MAPE) and the stationary R^2. An internal validation of the selected model was carried out using the Ljung-Box test, in order to assess the presence of residual autocorrelation. A graph comparing the observed and adjusted values was also produced. Finally, an external validation was carried out using data for the year 2023, and the model's performance measures were calculated. These are the RMSE and the MAE.

3. Results

The years 2019 and 2023 recorded the highest number of suspected cases, with weekly peaks of 303 and 483 cases, respectively (Table 1). These two years probably correspond to major epidemic episodes. The high standard deviation of the years 2019 and 2023 reflects a strong weekly variation in the number of cases, reflecting periods of intense peaks followed by troughs. The years 2018 and 2020 saw very low activity, with weekly averages close to zero and very low maxima.

Table 1. Descriptive analysis of suspected and confirmed dengue cases from 2017 to 2023

Years	Cases	Average	Median	Standard deviation	Minimum	Maximum
2017	Suspected cases	16	1	26.9	0	101
	Confirmed cases	1	0	1.81	0	10
2018	Suspected cases	1	0	0.85	0	3
	Confirmed cases	0	0	0	0	0
2019	Suspected cases	46	13	66.15	0	303
	Confirmed cases	2	0	2.54	0	10

2020	Suspected cases	2	1	1.78	0	7
	Confirmed cases	0	0	0	0	0
2021	Suspected cases	3	1	2.32	0	10
	Confirmed cases	1	0	0.38	0	2
2022	Suspected cases	10	5	1.6	0	57
	Confirmed cases	2	0	4.64	0	20
2023	Suspected cases	73	19	122.3	0	483
	Confirmed cases	5	1	7.85	0	34

The graph shows the weekly trend in suspected cases (red curve) and confirmed cases (blue curve) from 2017 to 2023 (Figure 1). There are significantly more suspected cases than confirmed cases throughout the period. There are several marked epidemic peaks in the series of suspected cases. Confirmed cases generally follow the same trend as suspected cases, but with much smaller amplitudes. Certain peaks appear to occur at similar times, suggesting a possible seasonality in the appearance of cases, which is precisely what the SARMA model is designed to capture.

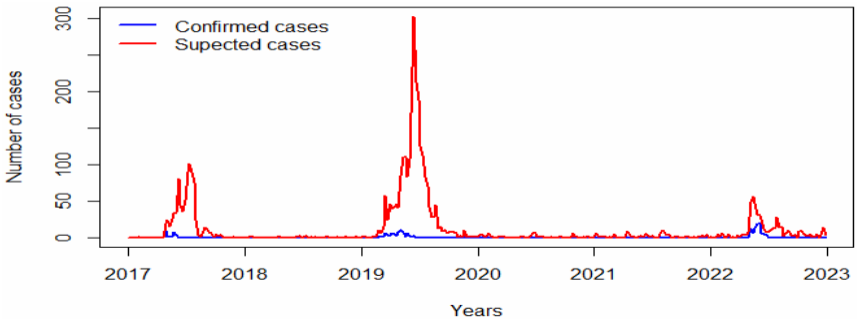

Figure 1. Weekly trends in suspected cases (red curve) and confirmed cases (blue curve) from 2017 to 2023.

Analysis of the ACF and PACF graphs reveals an exponential decay in the ACF, with a very high first lag followed by a regular decay, suggesting the presence of an MA component. PACF, on the other hand, shows a major peak at lag 1, followed by negligible or insignificant values at the other lags, indicating an AR(1) component (Figure 2). The augmented Dickey-Fuller and KPSS stationarity tests showed that the series is stationary with respective *p*-values of 0.01 and 0.1. Thus, taking into account the result of

the stationarity test and the ACF and PACF plots, the series appears to be well modelled by an ARMA $(1, 0, 1)$ or possibly an ARMA $(0, 0, 1)$.

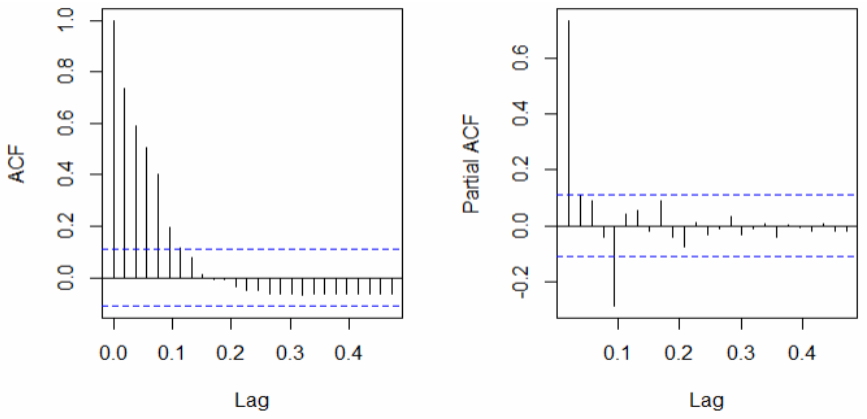

Figure 2. ACF and PACF of confirmed dengue cases from 2017 to 2023.

Among the statistical models tested, two models proved interesting for predicting the incidence of dengue. These were the SARMA $(1, 1, 0)(0, 0, 1)_{(52)}$ model, with lower RMSE and MAE of 4.36 and 8.66, respectively, and the ARMA $(1, 0, 4)$ model, with lower AIC and BIC of 1183.32 and 1209.6, respectively (Table 2). Based on the simplicity of the model (low AIC/BIC), the absence of autocorrelation of the residuals (Ljung-Box test), and a good stationary R^2, the ARMA $(1, 0, 4)$ model offers the best overall compromise (Table 2). This model explained 58.8% of the variance of the series (stationary *R*-squared). The parameters of the non-seasonal model were significant (P-value < 0.001) with a ϕ_1 of (ar1) is 0.4575 (sd = 0.1) and for the MA component $\theta_1 = 0.191$ (sd = 0.09), $\theta_2 = 0.2201$ (0.07), $\theta_3 = 0.2382$ (sd = 0.06) and $\theta_4 = 0.37$ (sd = 0.06). For the SARIMA model, the autoregressive coefficient was estimated at 0.7320 (sd = 0.03), and the seasonal lag-1 coefficient $\beta = 0.0248$ (sd = 0.09).

The Ljung-Box test suggests that there is no significant autocorrelation between the residuals at different lag times and that the residuals are white

noise (Table 2). This was corroborated by the graphs of the residuals (Figure 3). The actual adjusted dengue cases are shown in Figure 4. Figure 3 clearly shows that the model fits with near-perfect accuracy.

Table 2. Comparison of the performance of the ARMA and SARMA models in predicting confirmed cases of dengue fever in Côte d'Ivoire (2017-2023)

Models	AIC	BIC	MAE	RMSE	Ljung-Box (p-value)	R^2 stationary
ARMA(1, 0, 1)	1208.622	1223.67	4.4	8.685	0.01	0.544
ARMA(5, 0, 0)	1185.427	1211.761	4.41	8.679	0.952	0.585
ARMA(1, 0, 4)	1183.325	1209.659	4.41	8.681	0.983	0.588
SARMA $(1, 0, 0)(1, 0, 0)_{[52]}$	1213.09	1228.146	4.3	8.668	0.145	0.538

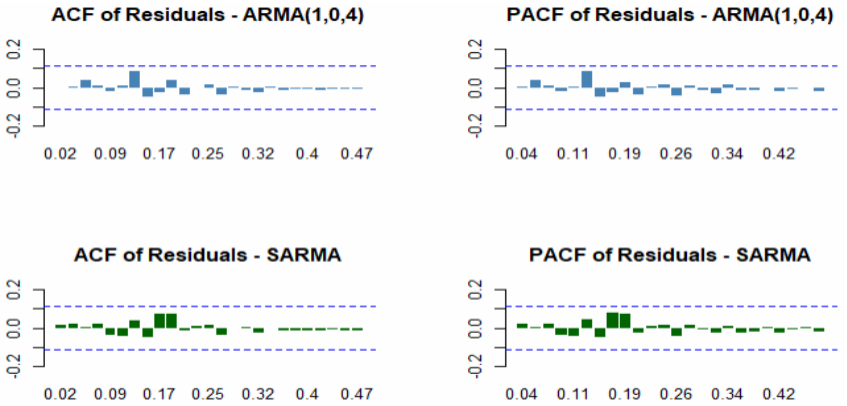

Figure 3. Diagnosis of ARMA and SARMA model residuals.

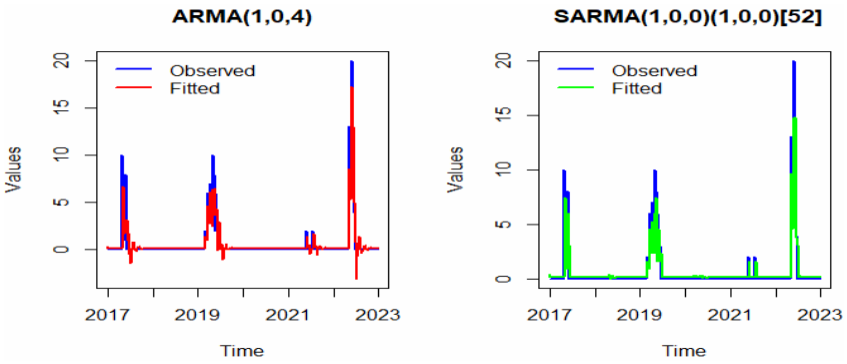

Figure 4. Comparison between actual values and fitted values of the ARMA model for confirmed cases of dengue fever in Côte d'Ivoire (2017-2023).

4. Discussion

The general objective of this work is to model dengue epidemics in Côte d'Ivoire in order to predict their occurrence using statistical time series methods, in particular the ARMA and SARMA models. The approach adopted aims to provide a decision-making tool for epidemiological surveillance.

Descriptive analysis of the data collected over the period 2017 to 2023 reveals that suspected cases of dengue far outnumber confirmed cases, and that this has been the case consistently from year to year. This finding most likely reflects an increased sensitivity of the surveillance system, or a tendency to widely report associated syndromes, without necessarily having systematic confirmation. Although there is a quantitative difference, it should be noted that confirmed cases appear to follow a similar pattern to suspected cases, albeit on a smaller scale. This suggests a structural correlation between the two series, and justifies the use of univariate ARIMA-type models to model the dynamics of confirmed cases based on their own behaviour, bearing in mind that suspected cases could play a complementary role in subsequent multivariate approaches.

The modelling results show that the $\mathrm{ARMA}(1, 0, 4)$ and $\mathrm{SARMA}(1, 0, 0)(1, 0, 0)_{(52)}$ models perform well. The $\mathrm{ARMA}(1, 0, 4)$ model, in particular, presents a good balance between accuracy (low MAE/RMSE), good fit (lowest AIC/BIC) and absence of autocorrelation of residuals. The SARMA model, on the other hand, captures prediction errors slightly better, but seems to perform less well according to the global adjustment criteria.

In a study carried out by Bhatnagar et al. [12] in Rajasthan, the $\mathrm{SARIMA}(0, 0, 1)(0, 1, 1)_{(12)}$ model was found to be the best predictor of dengue incidence. Also, in recent research conducted in Brazil, the $\mathrm{SARIMA}(2, 1, 3)(1, 1, 1)_{(12)}$ model was found to be the best fit for dengue incidence data [13]. However, in previous research by Hasan et al. [14] in

Bangladesh, two models were used to predict dengue incidence. These were the $\text{ARIMA}(1, 1, 1)$ and $\text{SARIMA}(1, 2, 2)(1, 1, 2)_{(12)}$ models. The accuracy of these fitted models was checked using the mean absolute error (MAE) and the root mean square error (RMSE). The results of the selection criteria for the $\text{ARIMA}(1, 1, 1)$ model were: MAE = 1,266.08 and root mean square error (RMSE): 5343.230. For the $\text{SARIMA}(1, 2, 2)(1, 1, 2)_{(12)}$, it was MAE: 1246.442, and RMSE: 5175.860. These performance criteria are much higher than the values found in our study, which were for the $\text{ARIMA}(1, 0, 4)$ model (MAE): 4.41, and RMSE: 8.68 and for the $\text{SARMA}(1, 0, 0)(1, 0, 0)$ model (MAE): 4.3, and RMSE: 8.66.

Although the ARIMA models have enabled satisfactory modelling of confirmed cases of dengue fever in Côte d'Ivoire from 2017 to 2023, their forecasts may nevertheless have limitations, particularly during epidemics. Dengue outbreaks can be strongly influenced by biological factors, such as the introduction of a new viral serotype into a population that has not yet developed specific immunity. In such cases, peak cases no longer follow the usual temporal dynamics, making predictions based on purely statistical models less reliable [13].

Furthermore, previous studies have shown that climatic factors - such as temperature, humidity and precipitation - have a significant influence on the dynamics of dengue transmission [15]. Incorporating these meteorological variables into more advanced models, such as ARIMAX or SARIMAX, would improve the accuracy of predictions and enable seasonal peaks to be anticipated more effectively. Such an approach could be considered in future work.

Despite these limitations, ARIMA modelling remains a relevant tool for interpreting surveillance data, detecting anomalies and guiding prevention and rapid response measures. It provides decision-makers with a useful forward-looking vision.

5. Conclusion

In conclusion, ARIMA modelling is a useful tool for epidemiological surveillance of dengue fever, making it possible to anticipate trends, identify anomalies and support public health decision-making. However, these forecasts are not prophecies, and the models have certain drawbacks. It is crucial to take into account the wider epidemiological context, external factors and any deviations from the fundamental assumptions.

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