

## STATISTICAL MODEL FOR THE OCCURRENCE OF TYPHOID FEVER IN TAKUM, TARABA STATE, NIGERIA: AN ARIMA MODEL APPROACH

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### Article Info:

Submitted: Aug 1, 2024	Revised: Aug 18, 2024	Accepted: Aug 21, 2024	Published: Aug 24, 2024
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### Abstract

This study analyzes Typhoid Fever incidence at General Hospital Takum from 2012 to 2021 using ARIMA model. The initial data was non-stationary, necessitating differencing to achieve stationarity. The ARIMA (4,1,1) model, selected based on AIC, AICC, and BIC criteria, showed parameters within stationarity and invertibility constraints. Diagnostic tests validated the model's robustness, with Box-Ljung (Chi-Square = 6.7435,  $p = 0.7598$ ), Shapiro-Wilk ( $W = 0.9754$ ,  $p = 0.1213$ ), and ARCH-LM (Chi-Square = 5.8762,  $p = 0.8176$ ) results supporting its adequacy. Forecasts for the next 24 months indicate a significant upward trend in Typhoid Fever cases. The study recommends among others a regular update to the model with new data to ensure accuracy, consideration of additional variables that may influence Typhoid Fever trends, and implementation of targeted public health interventions based on forecasted trends to mitigate the rising incidence.

**Keywords :** Typhoid; Diagnostic; ARIMA; Stationarity; Box-Ljung; Forecasting

## INTRODUCTION

Typhoid fever is a potentially life-threatening infectious disease caused by the bacterium *Salmonella enterica* serotype Typhi. It is a global health concern, particularly in regions with inadequate sanitation and limited access to clean water. The disease is primarily transmitted through the ingestion of contaminated food and water, making it a significant public health challenge in developing countries (Crump JA et al., 2018).

Typhoid fever has a long history, with documented outbreaks dating back centuries. The recognition of its distinct clinical features and the understanding of its transmission evolved over time. Advances in microbiology in the late 19th and early 20th centuries led to the identification of *Salmonella* Typhi as the causative agent, further shaping our understanding of the disease (Kaluse et al 2021). Despite these advancements, the global burden of typhoid fever remains substantial, with an estimated 11-21 million cases and over 128,000 deaths annually (WHO, 2018).

The prevalence of typhoid fever is disproportionately higher in low and middle-income countries, where poor sanitation, overcrowded living conditions, and limited healthcare resources create a perfect storm for the disease's persistence (Vale 2022). Typhoid fever manifests with a range of symptoms, including prolonged fever, abdominal pain, headache, and gastrointestinal disturbances, making early diagnosis and appropriate treatment with antibiotics crucial for preventing severe outcomes (Maganga 2019). The disease's progression through various stages, with potential complications such as intestinal perforation and septicemia, underscores the need for prompt and effective intervention.

Diagnostic methods for typhoid fever have evolved from clinical observation to modern laboratory techniques. Blood cultures, serological tests, and molecular methods play essential roles in confirming the presence of *Salmonella* Typhi. However, challenges in diagnosis remain, including the need for specialized facilities and the potential for false negatives during the early stages of infection (Neupane et al., 2021). Another critical issue is the emergence of antibiotic-resistant strains of *Salmonella* Typhi, which poses a significant threat to effective treatment. Strains resistant to commonly used antibiotics, such as chloramphenicol, ampicillin, and trimethoprim-sulfamethoxazole, have been identified in various regions. This underscores the importance of continuous surveillance and judicious use of antibiotics to combat resistance (Birhanie et al., 2021).

Typhoid fever continues to be a significant global health challenge, disproportionately affecting vulnerable populations in resource-limited settings. Comprehensive strategies, including vaccination, improved sanitation, and antibiotic stewardship, are essential for mitigating the impact of the disease. Continued research and international collaboration are crucial for advancing our understanding and addressing the evolving challenges associated with typhoid fever (Uneke, 2020).

In Nigeria, there is a pressing need to analyze and understand the time series data on the rates of typhoid fever. The co-occurrence of this disease poses a significant public health challenge. Despite various interventions and healthcare initiatives, the burden of typhoid fever continues to affect the population, significantly contributing to morbidity and mortality, especially among vulnerable groups (Olowolafe et al., 2024). This study aims to examine the historical data and trends of this disease (with a specific focus on General Hospital Takum, 2012-2021), examining its trends over time. Understanding the temporal patterns, seasonality, and potential influencing factors of typhoid fever can provide essential insights for healthcare providers and policymakers. The study's aim was achieved through the following specific objectives: To fit an appropriate ARIMA model to capture the pattern or behavior of typhoid fever in Takum, and to make predictions of typhoid fever trends in Takum.

## **Literature Review**

### **Typhoid Fever**

Typhoid fever is an infection caused by the gram-negative bacterium *Salmonella enterica* serovar Typhi, which continues to pose a significant global health burden, particularly in low- and middle-income countries (Kim et al., 2022). The disease is typically contracted through the ingestion of contaminated food or water, with risk factors including overcrowded conditions, unsanitary environments, and inadequate personal hygiene facilities (Maganga 2019). Typhoid fever is a major cause of morbidity and mortality, with an estimated 21.7 million cases and 217,000 deaths annually (Masuet-Aumatell, & Atouguia 2021).

The clinical presentation of typhoid fever varies from mild to severe, with symptoms such as fever, malaise, abdominal pain, and dry cough (Sinha et al., 1999). Diagnosing the disease is particularly challenging in settings with limited diagnostic facilities and often relies on clinical history and serological tests like the Widal test, which can yield

false positives (Olopoenia & King, 2000). Blood culture remains the most definitive method for confirming enteric fever, but it is only positive in about 40-60% of cases (Mukhopadhyay, 2019). Treatment usually involves antibiotics, with azithromycin and cefixime showing high clinical cure rates (Bhan et al., 2005).

Despite advancements in diagnostics and treatment, typhoid fever continues to be a significant public health challenge, especially in sub-Saharan Africa, where data on microbial culture and antimicrobial susceptibility is scarce (Kim et al., 2022). The Typhoid Fever Surveillance Africa program was launched to estimate the incidence of typhoid and invasive non-typhoid *Salmonella*, as well as to assess antimicrobial susceptibility (Masuet-Aumatell, & Atouguia, 2021). In Nigeria, the prevalence of typhoid fever is high, with rates ranging from 42% to 81.5% in different regions (Kim et al., 2019; Akinyemi et al., 2010; Kwala & Asika, 2020). Improved diagnostic methods and enhanced surveillance are crucial for reducing the burden of typhoid fever and developing effective public health strategies.

### **Empirical Review**

Kaigama and Madaki (2023) investigated the spatial distribution of typhoid fever in Maiduguri, Nigeria. The study aimed to address the challenges of effectively treating and preventing typhoid fever in the city. Utilizing Geographic Information System (GIS) tools, the researchers mapped reported cases and conducted spatial autocorrelation and hotspot analyses. The results identified clusters of high case incidence, revealing spatially correlated areas where intervention could be targeted. This research underscores the utility of spatial modeling for improving public health strategies in Maiduguri.

Aishatu and Umar (2023) performed a time series analysis of typhoid fever treatment in Maiduguri using the ARIMA model. Their analysis revealed a decreasing trend in typhoid cases in recent years and identified high-risk areas based on spatial modeling. The study highlighted the importance of linking environmental factors, such as water sources and sanitation, to disease occurrence and recommended targeted interventions in high-risk areas.

Oyenuga et al. (2023) explored the statistical patterns of typhoid fever incidence in Ijebu-Igbo, Ogun State. The research employed various modeling techniques, including linear, quadratic, and exponential models, and used data transformation methods guided by Bartlett's transformation table. The analysis revealed varying rates of typhoid fever across different quarters and provided forecasts for future occurrences. The study's methodology

enhances the accuracy of disease trend analysis and offers valuable insights for resource allocation and preventive measures.

Kaigama and Madaki (2023) also utilized the ARIMA model to perform a time series analysis on typhoid fever treatment in Maiduguri. The study identified trends and seasonal patterns in the data, revealing a recent decrease in typhoid fever cases. The ARIMA (1, 0, 0) model was found to be the best fit, and forecasts suggested a potential decrease in future cases. The study highlights the importance of using ARIMA modeling for predicting disease trends and recommends improvements in sanitation and hygiene to manage typhoid fever more effectively.

Obulezi et al. (2023) examined the prevalence of malaria and typhoid fever in Enugu using binary logistic regression and traditional time series analysis. The study analyzed data from 249 patients, revealing significant correlations between malaria and typhoid fever. The results, presented through odds ratios and chi-square statistics, emphasize the need for accurate diagnosis and management of these co-occurring illnesses. The study's findings underscore the importance of effective diagnostic practices and targeted treatment strategies.

Ogolo and Nkpordee (2022) examined typhoid fever trends in selected teaching hospitals in Awka, Anambra State. The study utilized secondary data from records of monthly typhoid fever cases spanning twelve years (2000-2021) and applied linear, quadratic, exponential, and s-curve trend models. Model accuracy was assessed using MAPE, MAD, and MSD. The quadratic model was identified as the best fit for forecasting typhoid fever cases for the year 2022, which indicated an expected increase in cases. The study recommended enhancing clean water access, sanitation infrastructure, and health education to manage typhoid fever effectively.

Atikilt et al. (2021) conducted a descriptive cross-sectional study on typhoid fever incidence in Jimma Zone, Oromia Region, Ethiopia, using five years of surveillance data (2015-2019). The study evaluated the distribution of typhoid fever cases by time, location, and demographic categories. The results showed an increase in incidence from 2015 to 2019, with a total of 36,641 cases. The study provided insights into temporal and spatial disease patterns, highlighting the rising incidence over the years.

Ogunlade et al. (2021) developed and analyzed deterministic and stochastic models to understand the spread of typhoid fever within a community. The deterministic model,

analyzed for its invariance and meaningfulness, yielded a control basic reproduction threshold ( $R_{typ}$ ) of approximately 0.744, indicating that current control measures are effective. The stochastic model, simulated using MATLAB, provided insights into the variability of typhoid fever spread and the impact of parameters on disease dynamics. The study's findings support the effectiveness of vaccination, screening, and treatment in controlling typhoid fever.

Oladipupo and Matthew (2020) investigated the transmission dynamics of typhoid fever in Ibadan, Nigeria, using the Susceptible-Infected-Carrier-Recovered (SIICR) model. Secondary data from 2010 to 2017 were analyzed to simulate the effects of treatment, isolation, and vaccination on typhoid fever transmission. The study revealed significant seasonal variations in typhoid cases and a decreasing trend due to improved health facilities. The simulations suggested that vaccination and isolation could significantly reduce the disease burden, potentially leading to disease-free periods during epidemics.

Sekubia and Mensah (2019) analyzed typhoid fever trends in Cape Coast Metropolis from 2011 to 2015 using secondary data from the District Health Information Management System (DHIMS). Descriptive statistics were employed to assess the data, revealing a mean age of 20-34 years for typhoid cases and a standard deviation of 4.15. The study indicated a wide spread in case incidences across age groups, suggesting a need for targeted interventions based on demographic patterns.

Kumar et al. (2019) compared and evaluated time series models of typhoid fever cases in Chandigarh, India, using data from 2014 to 2017. The analysis emphasized the need for improved sanitation to address current disease trends. The study's findings support the implementation of stricter sanitation measures to control the spread of typhoid fever.

Akinyemi et al. (2018) explored the trends of typhoid fever in Nigeria between 1993 and 2015 through a retrospective cohort study at hospitals in Lagos, Kano, and Abuja. The research found a declining trend in positive cases of Salmonella Typhi in Abuja but an upward trend in drug resistance in Lagos. The study emphasizes the need for continuous monitoring of drug resistance and effective treatment strategies.

Abdulkarim and Mohammed (2018) examined the spatial and temporal trends of typhoid fever in Kano metropolis from 2010 to 2014 using hospital records and ArcGIS. The study found an upward trend in prevalence with age but a downward trend over the

study period. The research recommended regular vaccination, improved eating and drinking habits, and enhanced hygienic practices to manage typhoid fever effectively.

## METHODS

### Method of Data Collection

Data for this research were collected from General Hospital Takum, covering the years 2012 to 2021. The data set includes patient records detailing the incidence of typhoid, providing a comprehensive basis for time series analysis.

### Exploratory Data Analysis (EDA)

Exploratory data analysis (EDA) involves summarizing the main characteristics of the data, often using visual methods (Tukey, 1977). In time series analysis, EDA begins with a time plot, which graphs the dependent variable against time. Additional visual methods such as decomposed series plots and seasonal plots are also employed (Hyndman & Athanasopoulos, 2018). To further understand and visualize some hidden characteristics of the series, it was decomposed into its several components using the additive method:

$$Z_t = T_t + S_t + C_t + I_t \quad (1)$$

where:  $Z_t$  is the time series,  $T_t$  is the trend component,  $S_t$  is the seasonal component,  $C_t$  is the cyclical component,  $I_t$  is the irregular component.

### Model Identification Process

The model identification process begins with examining the autocorrelation function (ACF) and partial autocorrelation function (PACF) plots. These plots help in determining the initial values for the ARIMA (p,d,q) model parameters (Box & Jenkins, 1970). To ensure the time series is stationary, we perform unit root tests such as the Augmented Dickey-Fuller (ADF) test and the Kwiatkowski-Phillips-Schmidt-Shin (KPSS) test. The ADF test checks for the presence of a unit root:

$$\Delta Z_t = \alpha + \beta t + \gamma Z_{t-1} + \delta \sum_{i=1}^p \Delta Z_{t-i} + \vartheta_t \quad (2)$$

where:  $\Delta Z_t$  is the differenced series,  $\alpha$  is a constant,  $\beta$  is the coefficient on a time trend,  $\gamma$  is the coefficient on the lagged level of the series,  $\vartheta_t$  is the error term (Dickey & Fuller, 1979).

The KPSS test checks for stationarity:

$$Z_t = \mu + \beta t + \dot{\varphi}_t \tag{3}$$

where  $\dot{\varphi}_t$  is a stationary process (Kwiatkowski et al., 1992).

If the series is non-stationary, differencing is applied:

$$\Delta^d Z_t = Z_t - Z_{t-d} \tag{4}$$

### Estimation of Model Parameters

Once the appropriate ARIMA ( $p, d, q$ ) model is identified, parameters are estimated using methods like maximum likelihood estimation. Model selection criteria such as the Akaike Information Criterion (AIC), corrected AIC (AICC), and Bayesian Information Criterion (BIC) are used:

$$AIC = -2\ln(L) + 2k \tag{5}$$

$$AICC = AIC + \frac{2k(k+1)}{n-k-1} \tag{6}$$

$$BIC = -2\ln(L) + k\ln(n) \tag{7}$$

where  $L$  is the likelihood of the model,  $k$  is the number of parameters, and  $n$  is the number of observations (Anderson, 2002).

### Diagnostic Checking for the Fitted Model

Diagnostic checks ensure the model's adequacy. The Box-Ljung test for serial correlation is given by:

$$Q = n(n+2) \sum_{k=1}^m \frac{\hat{\rho}_k^2}{n-k} \tag{8}$$

where  $n$  is the number of observations,  $\hat{\rho}_k$  is the sample autocorrelation at lag  $k$ , and  $m$  is the number of lags (Box & Pierce, 1970).

The Shapiro-Wilk test for normality of residuals uses:

$$W = \frac{\left( \sum_{i=1}^n a_i x_{(i)} \right)^2}{\sum_{i=1}^n (x_i - \bar{x})^2} \tag{9}$$



where  $x_i$  are ordered sample values and  $a_i$  are constants (Shapiro & Wilk, 1965).

The ARCH-LM test for heteroscedasticity involves regressing the squared residuals on lagged squared residuals and checking the significance of the regression (Engle, 1982).

**Model Forecast**

The fitted model is used to forecast the future occurrence of malaria and typhoid fever. The forecast estimation function for  $b$  periods ahead is:

$$\hat{Z}_{t+h|t} = \mu + \sum_{i=1}^p \phi_i Z_{t+h-i} + \sum_{j=1}^q \theta_j \hat{\epsilon}_{t+h-j} \tag{10}$$

where  $\mu$  is the mean,  $\phi_i$  and  $\theta_j$  are model parameters, and  $\hat{\epsilon}_i$  is the error term (Hyndman & Athanasopoulos, 2018).

**RESULTS AND DISCUSSION**

**Descriptive Statistics**

Table 1 shows that the average number of typhoid cases is 7.302, with a standard deviation of 2.153, indicating moderate variability. The cases range from 1 to 13. The skewness of -0.29 suggests a slight left skew, and the kurtosis of 0.99 indicates a nearly normal distribution. This suggests a fairly consistent pattern in the number of typhoid cases over the observed period.

Table 1: Descriptive Statistics

Variable	N	Mean	StDev	Variance	Min	Max	Skewness	kurtosis
Typhoid	96	7.302	2.153	4.634	1.000	13.000	-0.29	0.99

**Graphical Presentation of the Data**

The time series plot in Figure 1 illustrates the incidence of typhoid fever over the study period. This plot shows the number of typhoid fever cases on the Y-axis against equally spaced time intervals (Year) on the X-axis. It is used to evaluate the patterns and trends in the typhoid fever series.

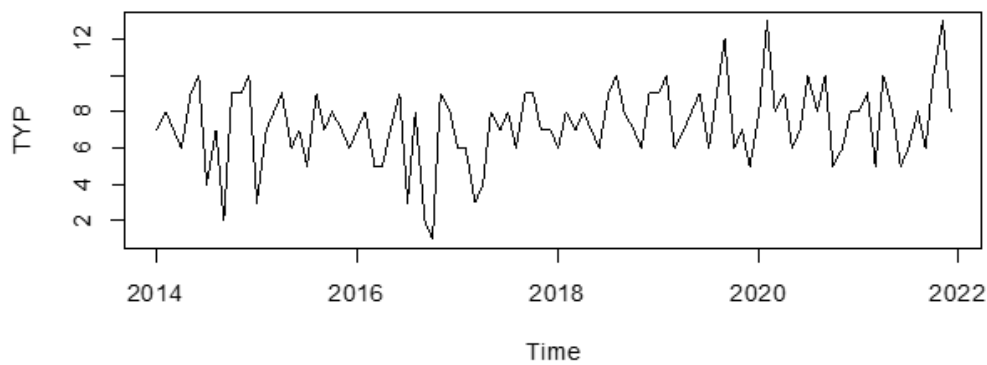


Figure 1: Time series plot for Typhoid-fever

The plot above clearly indicates an upward trend in the typhoid fever series from 2012 to 2021. The possible influences in the series are examined using the Autocorrelation Function (ACF) and Partial Autocorrelation Function (PACF) plots.

### Model Identification Process

The model identification process is crucial for fitting an Autoregressive Integrated Moving Average (ARIMA) model to the typhoid fever series. Before selecting a suitable model, the series must exhibit stationarity. Stationarity is checked using the sample ACF and PACF plots, the Kwiatkowski-Phillips-Schmidt-Shin (KPSS) test, and the Augmented Dickey-Fuller (ADF) test. A stationary series will have an ACF that rapidly decays to near zero, while a non-stationary series will show lag spikes that slowly decay. The PACF of a stationary series will display only a few significant lag spikes. Figure 2 shows the ACF and PACF plots of the data series. A critical look at these plots reveals that the data series is non-stationary.

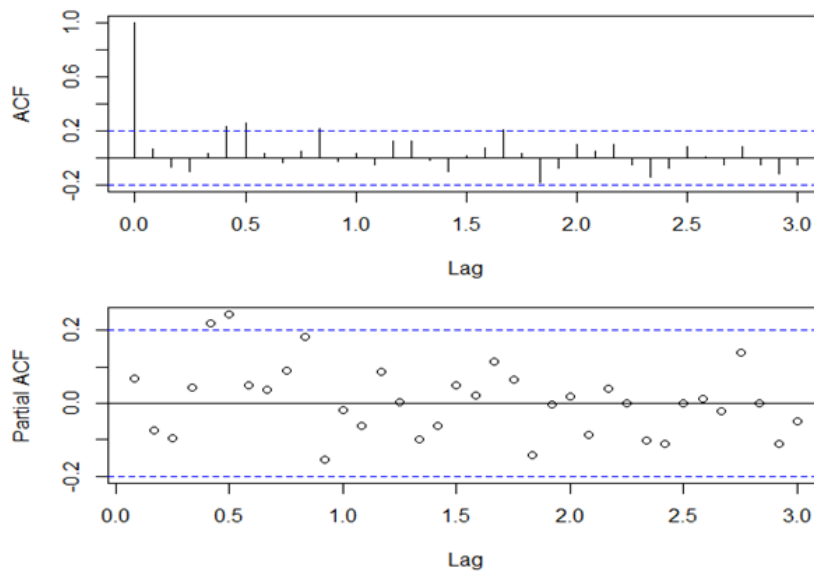


Figure 2: ACF and PACF plot for Typhoid

### Unit Root Test for Typhoid Fever Series

Table 2 presents the results of the Kwiatkowski-Phillips-Schmidt-Shin (KPSS) test for the null hypothesis of trend stationarity ( $H_0 : \rho < 0$ ) against the alternative of a unit root ( $H_1 : \rho = 0$ ). It also includes the results of the Augmented Dickey-Fuller (ADF) test for the null hypothesis of a unit root ( $H_0 : \rho = 0$ ) against the alternative of stationarity ( $H_1 : \rho < 0$ ). The KPSS test rejects the null hypothesis of trend stationarity with a test statistic of 0.38498 ( $P < 0.05$ ). Conversely, the ADF test fails to reject the null hypothesis of a unit root, with a test statistic of -1.9719 ( $P > 0.05$ ) at the 5% significance level. These results indicate that the typhoid fever series is non-stationary and requires differencing or transformation to achieve stationarity.

Table 2: Summary of test statistic

Test Type	Test Statistics	Lag Order	p-value
KPSS	0.68608	3	0.01481
ADF	-3.9542	4	0.01463

### Differenced Typhoid

The Typhoid Fever series was identified as non-stationary based on preliminary tests conducted on the original data. To achieve stationarity, the series was differenced once with respect to trend. Figure 3 displays the graphical plot of the first-order differenced Typhoid Fever series, which illustrates the series after this transformation.

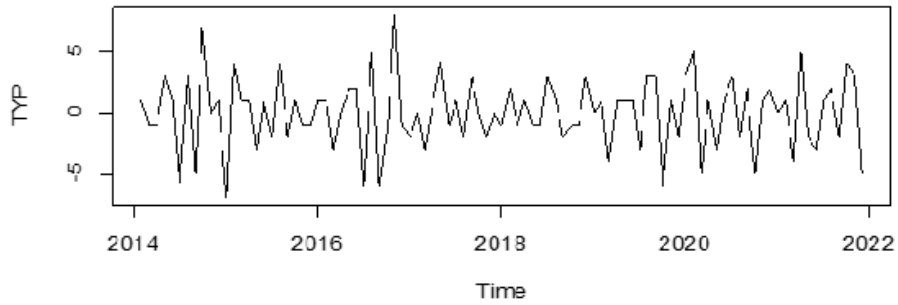


Figure 3: First-Order Differenced Typhoid Fever Series

The differenced series depicted in figure 4. 3with the superimposed line as the mean shows that the mean, variance and auto-covariance are constant over time, expressing series stationarity. The ACF and PACF plots, the KPSS and ADF unit root tests are performed to augment the graphical presentation of the differenced series. The correlogram plots in Figure 4 shows only a few significance lag spikes which depicts a stationary series.

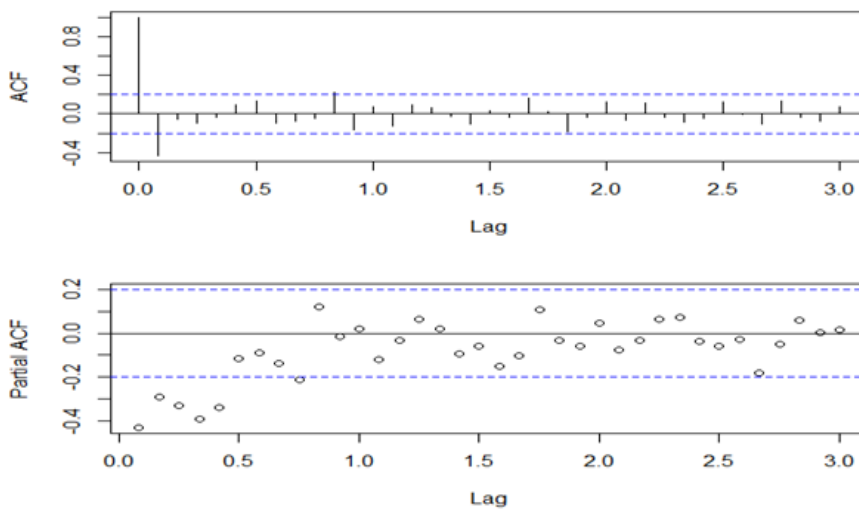


Figure 4: First-Order Differenced Typhoid Fever Series ACF and PACF Plots

The unit root test results for the first-order differenced Typhoid Fever series are presented in Table 3. The trend KPSS test yielded a statistic of 0.081248, with a p-value greater than 0.05, indicating that the null hypothesis of trend stationarity is not rejected. Conversely, the ADF test produced a statistic of -4.3794, with a p-value less than 0.05, leading to the rejection of the null hypothesis of a unit root. These results confirm that the first-order differenced Typhoid Fever series is stationary and suitable for modeling using the Box-Jenkins (ARIMA) methodology.

Table 3: Unit Root Test and Stationarity Test for the Differenced Series

Test Type	Test Statistics	Lag Order	p-value
KPSS	0.02129	3	0.1
ADF	-9.9097	4	0.01

### Estimation Of Model Parameters

The differenced Typhoid Fever series plot after the series is proven to be stationary is used to identify the appropriate model for this study. Based on the selection criteria, the ARIMA(4,1,1) model was identified as the best fit, representing an integration of order 1 (I(1)) and a moving average component of order 1 (MA(1)). Table 4 presents the model selection statistics, including the Akaike Information Criterion (AIC), the corrected Akaike Information Criterion (AICC), and the Bayesian Information Criterion (BIC). The ARIMA(4,1,1) model is preferred as its penalty statistics are lower compared to alternative models, with (\*\*\*) denoting it as the best fit according to these criteria.

Table 4: Comparison of ARIMA (p, d, q) Models fitted to Typhoid-fever

TENTATIVE MODEL SELECTION CRITERIA				
MODELS	AIC	AICc	BIC	LOGLIKELIHOOD
ARIMA(4,1,0)	429.53	430.2	442.3	-209.76
ARIMA(4,1,1)***	417.22	418.17	432.54	-202.61
ARIMA(5,1,1)	418.48	419.77	436.36	-202.24
ARIMA(4,1,2)	418.75	420.04	436.63	-202.37
ARIMA(5,1,2)	417.98	419.65	438.41	-200.99

### Model Parameter Estimates

From Table 5, the estimates for both the AR(4) and MA(1) components of the ARIMA(4,1,1) model are statistically significant, with t-values exceeding two, indicating their importance in the model. The estimated coefficients fall within the required bounds for stationarity and invertibility, as they lie between -1 and 1. Therefore, the chosen model, based on the principle of parsimony, is:

$$\hat{y}_t = \varepsilon_t + 0.2785y_{t-1} + 0.351y_{t-2} + 0.3789y_{t-3} + 0.2578y_{t-4} + 0.2785\varepsilon_{t-1} \quad (11)$$

This model effectively captures the dynamics of the Typhoid Fever series while adhering to the criteria for model stability and simplicity.

Table 5: Parameter for ARIMA(4,1,1)

Coefficient	Estimate	Std.Error	t-statistic	p-value
AR(1)	0.2785	0.351	2.066024	0.0388
AR(2)	0.351	0.119	2.94958	0.0031
AR(3)	0.3789	0.1158	3.272021	0.0001
AR(4)	0.2578	0.1189	2.168209	0.0301
MA(1)	0.7160	0.1113	6.433064	0.0001

### Diagnostic Checking for the Fitted Model

The model parameters have been estimated using maximum likelihood estimation technique and also found to be significant. This assessment involves several diagnostic checks. Correlogram plots of the residuals are examined to identify any remaining autocorrelation, while the Box-Ljung test is used to ensure the residuals are white noise and do not exhibit serial correlation. The Shapiro-Wilk test is conducted to verify that the residuals are normally distributed, and the ARCH-LM test is employed to detect any heteroscedasticity by analyzing the presence of volatility clustering in the squared residuals. The results of these diagnostic checks, presented in Figure 5, help ensure that the model is well-suited for accurate predictions.

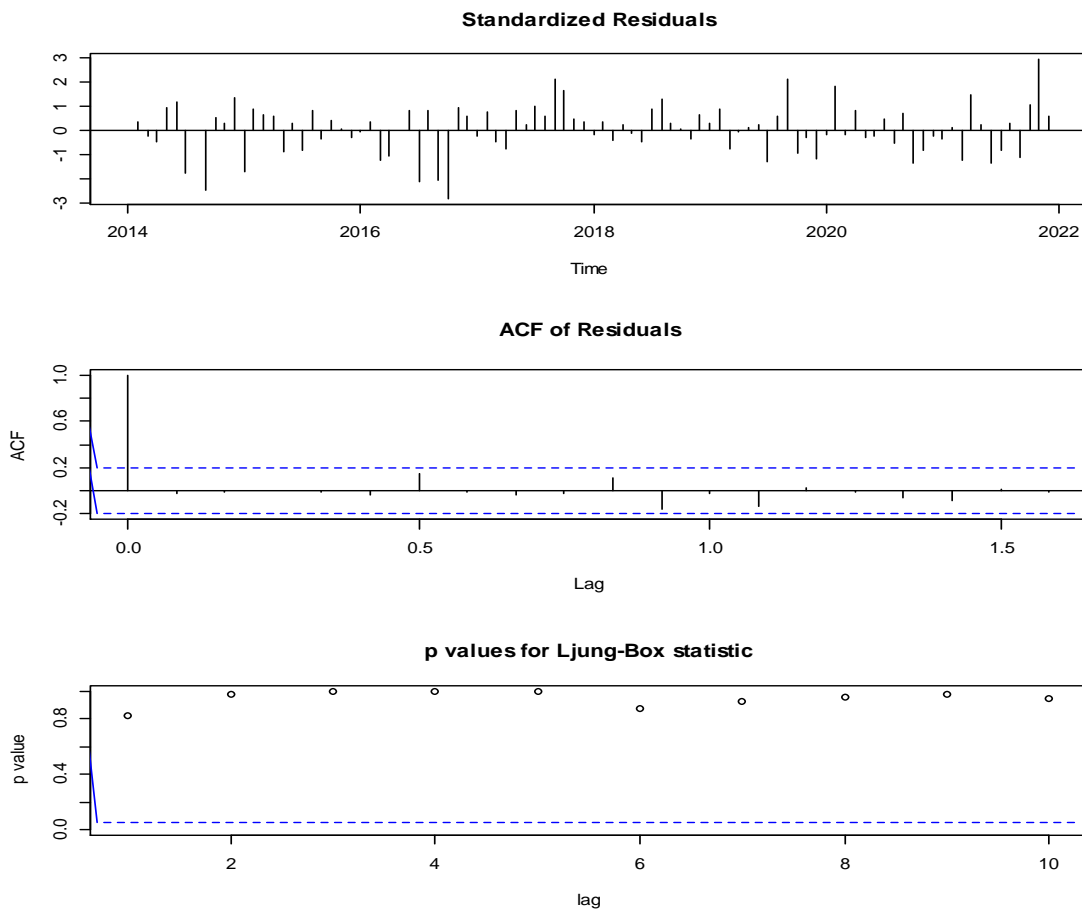


Figure 5: Series Standardized residuals, ACF and p-values

Table 6 presents the results of several diagnostic tests used to evaluate the adequacy of the fitted model. The Box-Ljung test, with a chi-square statistic of 8.7155 and a p-value of 0.8919, indicates that there is no significant autocorrelation in the residuals, suggesting that the residuals are independently distributed. The ARCH-LM test, with a chi-square statistic of 6.34325 and a p-value of 0.7632, shows that there is no significant heteroscedasticity in the residuals, meaning the variance of the residuals is constant over time. Lastly, the Shapiro-Wilk test, with a W statistic of 0.98393 and a p-value of 0.2909, indicates that the residuals are normally distributed. These results collectively suggest that the model is well-fitted, with residuals exhibiting properties consistent with the assumptions of the time series analysis.

Table 6: Box-Ljung test for uncorrelated residuals

Box-Ljung and ARCH-LM test Statistics			
Test Type	Chi-Square	DF	p-value
Ljung-Box	8.7155	15	0.8919
ARCH-LM	6.34325	13	0.7632
Shapiro-Wilk Test Statistics			
Test Type	W		p-value
Shapiro-Wilk	0.98393		0.2909

**Model Forecast**

Forecasting is a primary goal of model building. In this study, the forecast estimation for  $h$  periods ahead is given by:

$$\hat{y}_{T+h/T} = \theta_1 \hat{\varepsilon}_{T+h-1/T} \tag{12}$$

where  $\hat{y}_{T+h/T}$  represents the forecasted value and  $\hat{\varepsilon}_{T+h-1/T}$  is the forecast error from the previous period. The forecast error  $\hat{\varepsilon}_i(h)$  is calculated as:

$$\hat{\varepsilon}_i = y_{T+h/T} - \hat{y}_{T+h/T}$$

(13)with  $y_{T+h}$  being the actual Typhoid Fever value at  $(T + h)$ . Given that the model has passed all diagnostic tests, it is employed to forecast future Typhoid Fever cases. The forecast values for the twenty-four months spanning 2012 to 2021 are detailed in Table 7, and the forecast plot is illustrated in Figure 6.

Table 7: Forecast Values

	Point Forecast	LOWER 95% C.I	UPPER 95% C.I
Mar 2022	8.129930	4.168911	12.09095
Apr 2022	9.536755	5.563838	13.50967
May 2022	8.954493	4.971999	12.93699
Jun 2022	7.989262	3.815114	12.16341
Jul 2022	7.501637	3.239122	11.76415
Aug 2022	7.834237	3.551326	12.11715
Sep 2022	8.428615	4.142792	12.71444
Oct 2022	8.579916	4.284810	12.87502
Nov 2022	8.328807	3.990962	12.66665
Dec 2022	8.034674	3.642838	12.42651



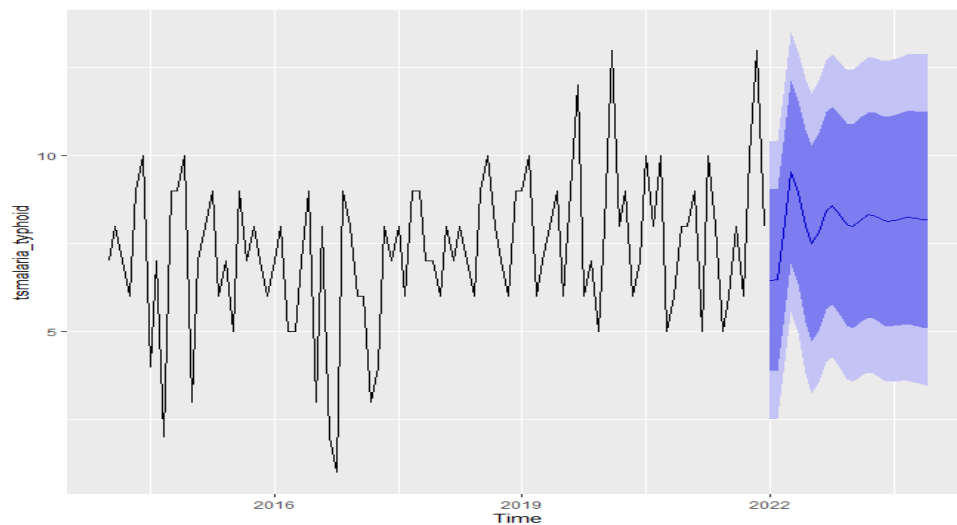


Figure 6: Plot of forecast values

## CONCLUSION

This study successfully applied time series analysis to forecast Typhoid Fever cases at General Hospital Takum from 2012 to 2021. By employing an ARIMA(4,1,1) model, the analysis addressed the non-stationarity of the data and ensured the robustness of the model through rigorous diagnostic testing. The model's effectiveness was demonstrated through its significant parameter estimates and favorable diagnostic results, including tests for serial correlation, normality, and heteroscedasticity.

The ARIMA(4,1,1) model was selected based on evaluation criteria including AIC, AICC, and BIC, which indicated it was the best fit. The model's parameters were estimated using maximum likelihood, and all coefficients were statistically significant and within the acceptable bounds for stationarity and invertibility.

Comprehensive diagnostic checks confirmed the model's robustness. The Box-Ljung test for serial correlation, Shapiro-Wilk test for normality, and ARCH-LM test for heteroscedasticity all supported the adequacy of the ARIMA(4,1,1) model. The model was then used to forecast Typhoid Fever cases for the next twenty-four months. These forecasts, presented in the study's tables and figures, demonstrate the model's effectiveness in predicting future trends in Typhoid Fever cases, underscoring its reliability for public health planning and response.

## Recommendations

Based on the results obtained, the following recommendations are made:

- i. Typhoid Fever cases in the future, aiding public health authorities in resource allocation and intervention planning.
- ii. Continuous monitoring of Typhoid Fever cases is essential to update and refine the forecasting model, considering the evolving nature of the disease and its potential impact on public health.
- iii. Further research could focus on exploring additional factors that may influence Typhoid Fever dynamics, such as environmental conditions, sanitation practices, and vaccination coverage, to enhance the predictive capabilities of the model and improve public health outcomes.

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