

Multivariate time series analysis: A Statistical application on Mortality and Patient Admissions count data for Kabwe

Research Article

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Abstract: In this study, multivariate time series method was used to model, forecast and analyse the relationship between monthly mortality and patient admissions time series count data and also to investigate the correlation between the female and male mortality and admissions data due to Malaria, Tuberculosis, cryptococcal meningitis and cardiac disease in medical wards at Kabwe Central Hospital using data collected from 2013 to 2022.

The relationship between mortality and patient admission for Kabwe Central Hospitals has been explored and examined. Mortality and patients admission data are cointegrated with rank $r = 1$. The best model selected using least information criteria was VEC(3) model with a speed of adjustment of 31.5%. Granger causality test results showed a unidirectional causality i.e. admissions granger cause mortality.

The study also revealed a positive correlation of 0.8956, 0.7884 and 0.927365 between the female and male mortality due to Malaria, Tuberculosis, cryptococcal meningitis respectively. The results further showed a moderate and strong positive correlation of 0.6783 and 0.92825 between female mortality and admissions due tuberculosis and cryptococcal meningitis respectively, and a correlation of 0.899137 between male mortality and admissions due cryptococcal meningitis. These results will help to find ways to improve health care outcome for the patients admitted to the hospital.

MSC: 62M10 • 62P10 • 62P25 • 62F03

Keywords: Cointegration • Granger causality • Correlation • Mortality and patient admissions • Malaria • Tuberculosis and the cryptococcal Meningitis

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1. Introduction

Since the development of multivariate time series by Tio and Box (1980), Multivariate time series has been utilised in different fields like engineering, physical science, economics, medicine and public health science. In health research the technique can be useful in the analysis of hospital data, where many variables may be interrelated and affect one another. Mortality and patient admissions are two such variables that might be closely related. Therefore, it is important to investigate their causal relationship.

Studying mortality and patient admissions plays an essential role in understanding the details about the two variables and be able to devise preventive measures which might improve patient care outcome. These two variables are therefore considered an integral part of planning public health intervention of diseases [1]. A study conducted in

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Kenya at a public hospital revealed that about 22% of the patient admitted during week days died [2]. Therefore it is important to understand that there are numerous factors that are contributing to patient admissions and mortality across the globe. In recent years there have been some changes in causes of mortality across the globe. For example the COVID 19 pandemic was the main cause of mortality and admissions in health facilities in many parts of the world. A study on transmission dynamics of Hepatitis B infection showed that increase in reproduction number due to changes in probability for individual with chronic disease depended on transmission. While a similar study on Zika virus suggested that basic reproduction number of about 7.03 suggested that the disease was persistent when ever there was an outbreak [3] [4]. This also provide insight on understanding admissions and mortality.

However, over the years Malaria, tuberculosis, cryptococcal meningitis still remained the main reason for mortality in sub-saharan Africa. A study conducted in Kenya on malaria showed that it was the major cause of death, and that mortality rates were highest in children under five. [5]. In another study conducted in Pretoria, South Africa, People with HIV/AIDS continue to frequently contract the opportunistic infection cryptococcal meningitis, which resulted in admissions and a high mortality rate among those hospitalized [6]. The situation is not different in Zambia, at Kabwe Central hospital the annual mortality data shows that malaria, meningitis, tuberculosis and cardiac diseases are among the the top contributor of mortality at the hospital. Mortality and patient admissions may be attributed as factors in health care system, it becomes essential to understand the relationship between the two variables hence we employ a multivariate time series method.

Multivariate time series models describes relationships between a vector or variables, $Y_{1t}, Y_{2t}, \dots, Y_{kt}$ of k -time series. The main idea of analyzing a multivariate process is to gain insight into the relationship overtime between the variables and improve accuracy of prediction for an individual time series by utilizing the additional information, hence increases the explanatory power of the model. The most commonly used methods for the multivariate time series is the vector auto-regressive models (VAR), Vector error correction models (VECM), vector autoregressive moving average (VARMA) and Multivariate Generalized Auto regressive Conditional Heteroskedasticity model (M-GARCH). In a VAR model, each variable is a linear function of the past values of itself and past value of all other variables, this allows for analysis of relationship among variables. [7].

The main objective of this study was to employ a multivariate time series method to forecast and understand the relationship between mortality and patient admissions count data for medical wards at Kabwe Central Hospital and investigate the correlation between the female and male mortality and admission due to malaria, tuberculosis, cryptococcal meningitis and cardiac diseases from 2013 to 2022. The relationship between mortality and patient admission has been explored and examined and the detailed results have been discussed in the results section.

It is envisaged that this study will add to the already existing knowledge and provide valuable insight into understanding long run relationship between mortality and patient admission counts at the hospital as such will be regarded as an integral part of planning health system like capacity building, infrastructure and equipment development to improve patient out.

2. Literature Review

In modeling and forecasting multivariate time series data, much studies has already been done in the development of ways or methods of analysing such data. The modeling methods includes the vector auto-regressive, vector auto regressive moving average, vector error correction methods [8]. In order to improve accuracy of the results, a systematic technique or methodology in the analysis of multivariate time series data with an assumption of stationarity as an important factor and estimation of the model using maximum likelihood is very important [9]. In time series, the concept of stationarity is important in that it enables useful modeling of time series data. The process is said to be stationary if it is invariant with respect to shift in time which simply means the properties (mean and variance) of the time series do not change or do not depend on the time at which the series is observed. [10]

Multivariate time series models often provide superior forecasts to those from univariate time series model and elaborate theory based simultaneous equation models [11] as such it has been applied in many areas, a study conducted in Indonesia on export of oil and coal, suggest a VARMA (1,2) as best it fit model. [12]. In most studies as the case was in the investigations of relationship between the demand for essential medical supplies in the emergency unit of the hospital and admission of the inpatients, multivariate time series approach was used to study the relationship between variables and a Vector autoregressive model performed better compared to univariate time series methods. In another study a vector error correction model was used to forecast COVID 19 in hospital local incidences for 7days [13], [14]. In a global time series study for monthly prices of silver and Gold from 2016 to 2019, and stocks forecast in six Nigerian banks, the VARMA(1,2) and VAR(1) was used as a forecasting models respectively [15], [16]. The multivariate analysis was used to structure the relationship between important variables on the macro level in a banking sector [17].

The concept of cointegration and Granger causality have been applied in many studies in multivariate time series analysis. The granger causality results on six major economic indicators in a study in Nigeria revealed a unidirectional and bidirectional between economic indicators [18], [19]. Further, the investigation on granger causality between industrial out put and consumer price index in Sweden, revealed that consumer price index granger cause industrial

output [20]. The results of the Johansen-fisher cointegration test for COVID-19 data on infection and deaths in United state,India, Canada and Ukraine indicated that there was only one cointegration equation.The granger causality test and vector error correction model showed that long-term and short-term relationship existed between study variables. [21]. A study conducted in 2021 by L. Loves showed co-integration on the variables and employed a vector Error correction model.The best model for the study was found to be VECM(4) with rank=2 [22].

The vector error correction model enables one to describe the relationship between non stationary time series variables [23]. A Vector error correction model was also used to demonstrate that the (variables) mortality rate and cause of death had a common stochastic trend. The results of the study confirmed long- run relationship between five main causes of death [24]. A study on macro economic variables in Romania, revealed existence of cointegration and a VECM was used to fit the data. It was found that the economic crisis caused significant influence on FDI [25]. Further, a bivariate time series study on patients admitted in hospital due to COVID-19 and those take to intensive care due COVID-19 using data from Italian region, Switzerland and Spain used a VECM to forecast and also showed that patients admission Granger cause those in ICU due to COVID-19. [26]

3. Methodology and Materials

In this section, we consider a multivariate process $Y_t : t \in Z$ Where Y_t is an $N \times N$ vector $Y_t = (Y_{1t}, Y_{2t}, \dots, Y_{nt})$. The process is made up of N univariate processes $Y_{it} : i = 1, 2, 3, \dots, N$, each of which may be studied separately. But we may be able to understand better the behaviour of any of the compound of univariate process and make more accurate predictions of its future values if these are studied together, instead of merely considering it in isolation. A multivariate time series consist of more than one time dependent variable, and each depends not only on its past values but also some dependency on past values for other variables. Thus, in a multivariate approach we shall be interested in the interrelationship among variable especially expressed in terms of their cross-variation and cross -correlation. The most commonly used statistical methods for modeling multivariate time series is the vector auto-regression, Vector error correction, Vector autoregression moving average and Multivariate Generalized Autoregressive Conditional Heteroskedasticity usually denoted as VAR, VECM, VARMA and M-GARCH respectively.To analyse the data in this study, the R 3.5.1 statistical software will used.

3.1. Stationary multivariate time series

Stationarity of the time series is one of the most important factors to be investigated before analysing multivariate time series data. The mostly commonly used unit root test is the Augmented Dick-fuller test (ADF), Phillip-Perron (PP) unit root test and Kwiatkowski, Phillip Schmidt and Shin (KPSS). In this study, the Agumented Dickey- Fuller test will be used to check for stationarity since it also performs better with sample size greater than 100 samples [27]. The Dickey- Fuller test is defined as shown below.

$$\Delta Y_t = \alpha + \phi Y_{t-1} + \sum_{i=1}^p \phi_i \Delta Y_{t-p} + \epsilon_t \tag{1}$$

Where ΔY_t is the difference and ϵ_t is white noise The test statistic is given by.

$$ADF = \Gamma = \frac{\phi}{se(\phi)} \tag{2}$$

H_0 : Unit roots present (non stationary time series).

H_a : Unit roots not present (stationary time series).

The decision rule is that if the ADF test statistics is less than critical value or the p-value is less that the significant level, we reject the null hypothesis.

3.2. Vector Auto-regression model

In the VAR model, each variable is modelled as a linear combination of past values of itself and the past values of other variable in the system of equation

Let's say we need to predict the values of the time series Y_1 and Y_2 at time t . To compute Y_{1t} , VAR will use the past values of both Y_{1t} as well as Y_{2t} . Similarly to compute Y_{2t} , the past values of both Y_{1t} and Y_{2t} Will be used.

Given below is the system of an equation for a VAR(2) Model with two variable.

$$Y_{1t} = \phi_{01} + \phi_{11,1} Y_{1t-1} + \phi_{12,1} Y_{2t-1} + \phi_{11,2} Y_{1t-2} + \phi_{12,2} Y_{2t-2} + \epsilon_{1t} \tag{3}$$

$$Y_{2t} = \phi_{02} + \phi_{21,1} Y_{1t-1} + \phi_{22,1} Y_{2t-1} + \phi_{21,2} Y_{1t-2} + \phi_{22,2} Y_{2t-2} + \epsilon_{2t} \tag{4}$$

The system of the equation for the VAR model can be written in matrix form as below.

$$\begin{bmatrix} Y_{1t} \\ Y_{2t} \end{bmatrix} = \begin{bmatrix} \phi_{01} \\ \phi_{02} \end{bmatrix} + \begin{bmatrix} \phi_{11,1} & \phi_{12,1} \\ \phi_{21,1} & \phi_{22,1} \end{bmatrix} \begin{bmatrix} Y_{1t-1} \\ Y_{2t-1} \end{bmatrix} + \begin{bmatrix} \phi_{11,2} & \phi_{12,2} \\ \phi_{21,2} & \phi_{22,2} \end{bmatrix} \begin{bmatrix} Y_{1t-2} \\ Y_{2t-2} \end{bmatrix} + \begin{bmatrix} \epsilon_{1t} \\ \epsilon_{2t} \end{bmatrix} \tag{5}$$

The reduced form of the VAR equation is as given below;

$$Y_t = \phi_0 + \phi_1 Y_{t-1} + \phi_2 Y_{t-2} + \epsilon_t \quad (6)$$

which is a matrix equation containing cross-dependencies between the series.

3.3. Cointegration

In a multivariate time series (VAR) modelling, the prerequisite is that the analysed time series data are stationary at level. However, variables have a long-run equilibrium relationships which makes them stationary without taking a differencing [28], hence the concept of cointegration. Variables are said to be cointegrated if they have common stochastic trends.

Let $y_t = (Y_{1t}, Y_{2t}, \dots, Y_{kt})'$ denote a $k \times 1$ vector of $I(1)$ time series. Y_t is cointegrated if there exist an $k \times 1$ vector $\beta' = [\beta_1 \ \beta_2 \dots \beta_k]$.

In order to check for cointegration, Johansen cointegration technique is applied using the maximum eigen value and trace statistic test. The null hypothesis is no cointegration. If both eigen value and trace statistic are greater than critical values then there is cointegration. If cointegration is present at $I(1)$, then VAR form of a model is not the most convenient, instead we suggest the VEC(p) model [29]. The requirement of estimating VECM is that there is co-integration relationship in it.

3.4. Vector Error Correction model

If the time series is first differenced from the original data, there is always a possibility of loss of long-run information about relationship among integrated series. So the solution is to test for cointegration and if the series are co-integrated at $I(1)$, we then use Vector Error Correction models (VECM).

The Vector Error correction model is designed to be used in non-stationary time series data, but has co-integration relationship between variables [30].

The model is defined as given below:

$$\Delta Y_t = \phi_i + \Pi Y_{t-1} + \sum_{i=1}^{p-1} \Gamma_i \Delta Y_{t-i} + \epsilon_t. \quad (7)$$

Model stability

The VAR process is stationary if the Eigen values i.e. $\det[\lambda I - \phi] = 0$ are less than one in absolute value $|\phi| < 1$.

3.5. Model Selection (Optimal lag selection.)

Alkaike information criteria (AIC), Hannan-Quinn information criteria (HQC), Schwarz- Bayesian information criteria (SBC) and Alkaike final prediction error criteria (FPE) was used to determine optima; lag. According to Alkaike (1973), the model with the lowest expected information loss is selected as the best fit for data.

$$AIC = 2K - 2 \ln(L) \quad (8)$$

Where L is the maximum of the likelihood and K is the number of parameters estimated. Another alternative model selection criteria is the Bayesian information criteria and Hannan-Quinn information criterion as defined below.

$$BIC = -2 \ln(L) + \ln(N) \quad (9)$$

Where N is the number of observations that enter into the likelihood calculation.

$$HQIC = \frac{L}{N} + \frac{2K \ln(\ln(N))}{N} \quad (10)$$

N = Number of data observations

K = Number of estimated parameters.

L = The log likelihood function $(-\frac{N}{2} + \ln(2\pi) + \ln(\frac{1}{N} \sum_{i=1}^N (Y_i - \hat{Y})^2))$

3.6. Diagnostic check (Goodness of fit test)

The purpose of the diagnostic check or the goodness of fit test is that we want to check the 95% confidence level for the model. Such a model use standard errors of the parameters, to checks if the residual in the model agrees with the assumption. To quickly diagnose if the time series is white noise, we may visualized using plots.

- Serial correlation Plot should have the auto-correlation values which falls between the 95% boundary (confidence interval)

- Box-plot of residuals help to check how well the data set are normally distributed. Visual interpretation of the noise is subjective but still provide a quick identity of any violation of the assumption of white noise.

For more objective evaluation of a model ,we use the following statistical test:

- Jarque-Bera (JB),skweness and kurtosis
- Breusch-Godfrey LM test

3.6.1. Test for Normality

The Jarque-Bera test is a goodness of fit statistical tool to test for normality and is used to determine whether residuals in the data set has skewness and Kurtosis that matches normally distributed residuals.

The test statistic is as defined below:

$$JB = \frac{n-k}{6} [S^2 + \frac{(K-3)^2}{4}] \tag{11}$$

Where n = Number of sample

$$S = \text{Expected skweness} = \frac{\frac{1}{n} \sum_{i=1}^n (X - \bar{X})^3}{(\frac{1}{n} \sum_{i=1}^n (X - \bar{X})^2)^{3/2}} \tag{12}$$

$$K = \text{Expected kurtosis} = \frac{\frac{1}{n} \sum_{i=1}^n (X - \bar{X})^4}{(\frac{1}{n} \sum_{i=1}^n (X - \bar{X})^2)^2} \tag{13}$$

Hypothesis test.

H_0 : The residual are normally distributed.

H_a :The residual are not normally distributed.

The JB test has chi-square χ^2 distribution with 2 degrees of freedom (Jarque and Berra, 1987).The test decision rule is that if the chi-square estimated value is greater than the critical value, we reject the null hypothesis and accept the alternative.

3.6.2. Breusch-Godfrey LM test

Breusch-Godfery LM test (Breusch,T.S and Godfrey,L.G(1981)) is a statistical test used to check for serial correlation of residuals in a model, and it's defined as below:

$$(N - q) * R^2 \sim \chi^2 \tag{14}$$

Where N - is the sample size, q is the number of lags in a model and R^2 is a statistical measure that determines the proportion of variance in the dependent variable that can be explained by variance in independent

Hypothesis test

H_0 : Serial correlation does not exist.

H_a :Serial correlation exist.

If the BG LM test statistic > critical value, or p-value less than significant level there is statistical evidence that the data is auto-correlated.

3.7. Granger causality

Granger causality is a method used to for check the short run and long-run relationship between variable in a vector time series [31].

$$Y_{1t} = \phi_{01} + \phi_{11,1} Y_{1t-1} + \phi_{12} Y_{1t-2} + \dots + \phi_{1p} Y_{1t-p} + \epsilon_{1t} \tag{15}$$

The model Y_{1t} is called a restricted model because it only uses its past values to forecast the future observations.

$$Y_{2t} = \phi_{02} + \phi_{21} Y_{1t-1} + \phi_{22} Y_{2t-1} + \phi_{21} Y_{1t-2} + \phi_{22} Y_{2t-2} + \epsilon_{2t} \tag{16}$$

The model Y_{2t} is called unrestricted model because it also include past values of the model Y_{1t} and itself .

$$\begin{bmatrix} Y_{1t} \\ Y_{2t} \end{bmatrix} = \begin{bmatrix} \phi_{01} \\ \phi_{02} \end{bmatrix} + \begin{bmatrix} \phi_{11,1} & \phi_{12,1} \\ \phi_{21,1} & \phi_{22,1} \end{bmatrix} \begin{bmatrix} Y_{1t-1} \\ Y_{2t-1} \end{bmatrix} + \dots + \begin{bmatrix} \phi_{11,p} & \phi_{12,p} \\ \phi_{21,p} & \phi_{22,p} \end{bmatrix} \begin{bmatrix} Y_{1t-p} \\ Y_{2t-p} \end{bmatrix} + \begin{bmatrix} \epsilon_{1t} \\ \epsilon_{2t} \end{bmatrix} \tag{17}$$

The granger causality test is based on the F -Test.

Calculate the F- Statistics

$$F = \frac{(RSS_1 - RSS_2)/P}{RSS_2/T - 2P - 1} \tag{18}$$

Where RSS_1 is a residual sum of squares for restricted model and RSS_2 is a residual sum of squares unrestricted model p and $T - 2p - 1$ are degrees of freedom respectively.

H_0 : is rejected if $F > F_{0.05,(p,T-2p-1)}$

3.8. Impulse response Function (IRF)

In order to determine on how the endogenous variables react to the impulse or shock of another variable in the long-run, we will use a method of impulse response function. A VAR model like an AR model can be written as an infinite VMA as defined below:

$$X_t = \mu + \mu_t + \Psi_1\mu_{t-1} + \Psi_2\mu_{t-2} + \dots \tag{19}$$

Thus, the matrix Ψ_s has interpretation.

$$\frac{\delta X_{t+s}}{\delta \mu_t} = \Psi_s \tag{20}$$

The Row i , column j elements of Ψ_s identifies the consequence of increasing one unit in the j innovation of variable at time $t + s$ for the value of the i variable at the time $t + s$ (X_{t+s}). making all other innovation constant. If the first μ_t element is changed by δ_1 , at the same time the second element is changed by δ_2and element n by δ_n then the resultant effects of the change on the vector value X_{t+s} is shown below:

$$\Delta X_{t+s} = \frac{\delta X_{t+s}}{\delta \mu_t} \delta_1 + \frac{\delta X_{t+s}}{\delta \mu_t} \delta_2 + \dots + \frac{\delta X_{t+s}}{\delta \mu_t} \delta_n = \Psi_s \delta \tag{21}$$

A Plot of row i and column j element Ψ_s is called impulse response function (IRF)

4. Results and Discussion

In this study, we applied a multivariate time series methods to analyse the monthly data for patient admissions and Mortality count collected from Kabwe Central Hospital medical wards action plan documents from 2013 to 2022 and discussed the relationship between the two variables. The R 3.5.1 statistical software was used to the analyse the data.

4.1. Stationarity Assumption

The time series data was plotted in the form of a time plot as shown in Figure 1. The visual analysis of the time plot for mortality and patient admission data showed fluctuations in the trend suggesting that the mean and the variance was not constant and hence we concluded that the series was not stationary.

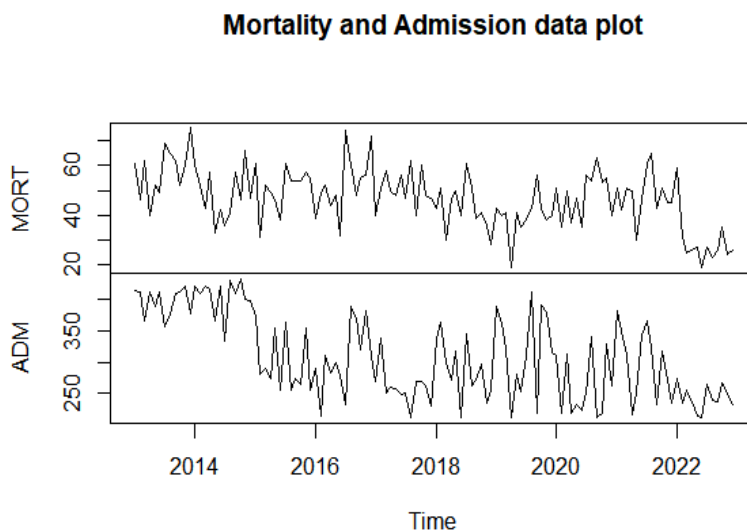


Fig. 1. The time plot for the original time series for mortality and admission

The visual analysis of the ACF plot in Figure 2 showed that the auto-correlations decreased or decays very slowly, this confirmed that the time series for both mortality and patient admission were non-stationary. So there was need to difference the data to make the time series data stationary.

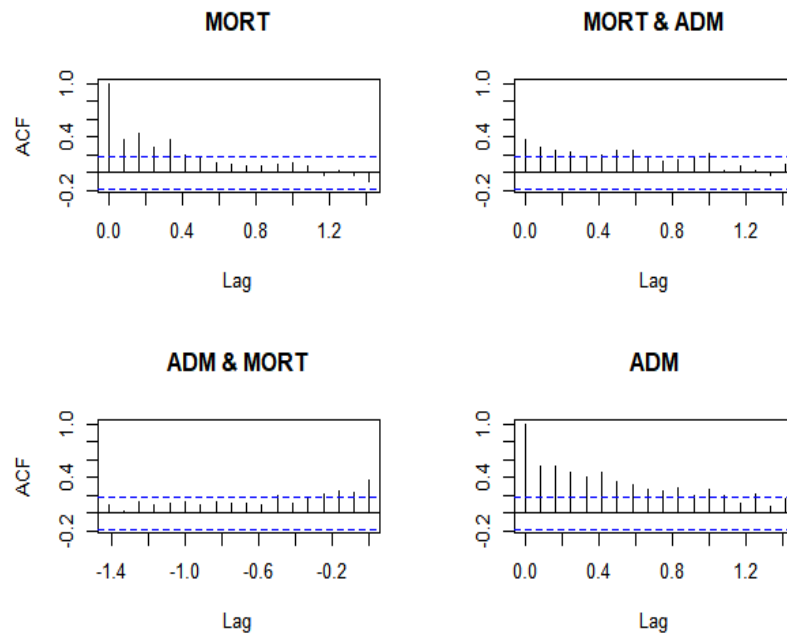


Fig. 2. Shows the auto correlation function plot for un-transformed admission data

Table 1. Augmented Dickey-fuller unit root test for undifferenced data

Variable	Lag	Test statistic	critical value at (5%)	p-value (5%).
Mortality	4	-2.664	-2.87	0.3015.
Patient admission	4	-2.6572	-2.87	0.3036.

In order to objectively determine if the variables were stationary or not, the statistical test for the presence of unit roots using the dickey-Fuller test (1976) was performed. The test results are shown in the Table 1 below. From Table 1, The test statistic F-value for Mortality data is -2.664 with the p-value 0.3015 and test statistic F-value for Patient admissions data is -2.6572 with p-value 0.3036. Since the P-values for both variables are greater than 0.05 significant level, we fail to reject the null hypothesis that there is a presence of unit roots. Therefore, we conclude that the data for both variables were not stationary at level. Therefore, a VAR model can't be applied.

The data was transformed by first difference and the results were plotted in the Time plot in Figure 3. The ADF statistical test results are also tabulated in Table 2:

The visual analysis of the time plot figure 3 of the differenced time series data showed no trend this suggested that the series had a constant mean and variance. This indicated a stationary time series.

The ACF plot, Figure 4 sharply decline or drop after the first lag suggesting that differencing had removed the trend component hence concluded that the data was stationary.

Table 2. Augmented Dickey-fuller test for diff=1 mortality and admission data

Variable	Lag	Test statistic	critical value at(5%)	p-value(5%).
Mortality	4	-6.1502	-2.87	0.01.
Patient admission	4	-7.1292	-2.87	0.01.

From Table 2, mortality and Patient admission ADF test statistic values are -6.1502 and -7.1292 with the P-values 0.01 respectively. Since the P-values for both variables was less than 0.05 significant level. We concluded that there were no unit roots therefore, the data was stationary at first difference.

4.2. Cointegration Test Results

In order to check for cointegration and establish Rank = r, we used Johansen's technique. If the variables are found to be cointegrated, then there exist a stable long-run linear relationship between the two variables. The cointegration

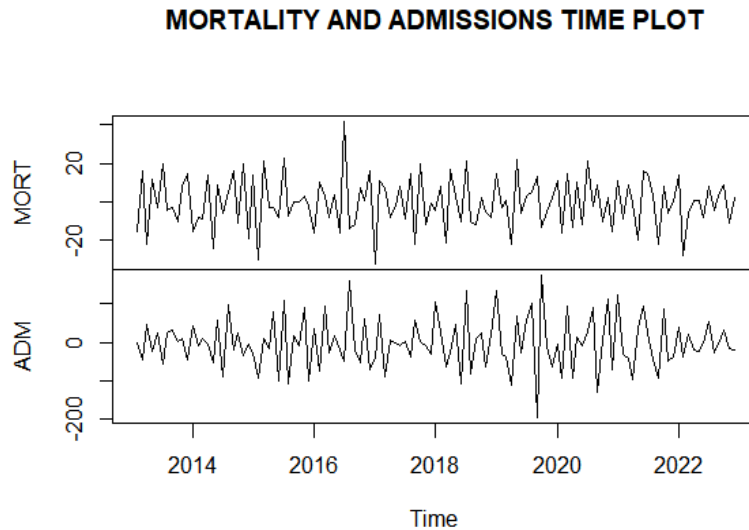


Fig. 3. Time plot for the differenced time series data for mortality and patient admissions

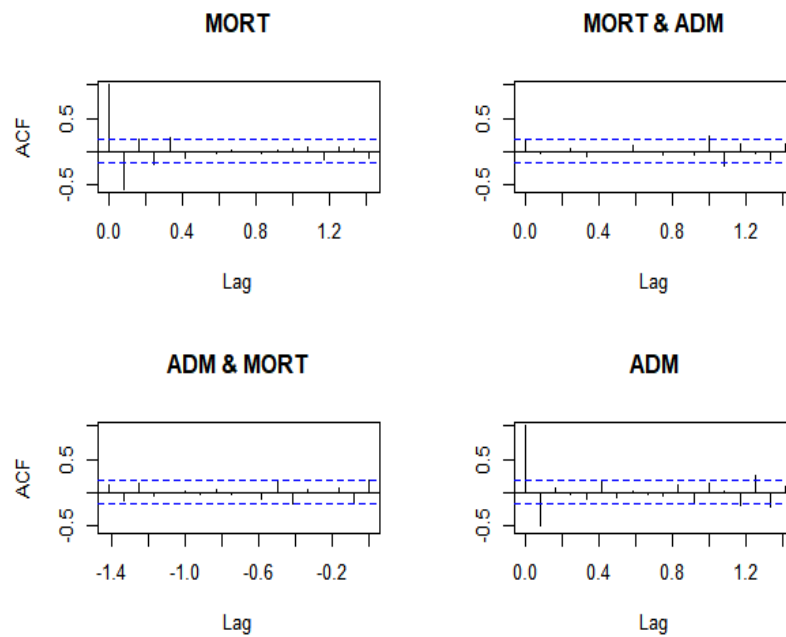


Fig. 4. The ACF plot for the differenced mortality and patient admissions time series

results are tabulated below:

Tables 3 shows the cointegration test using maximum eigen value and trace statistic. The hypothesis test $H_0 : r = 0$, (i.e. no cointegration), The results shows that the test statistic from both maximum eigen value and trace statistic were $14.906 > 14.90$ critical value and $22.19 > 17.95$ critical value at 0.05 significant level respectively. Therefore, we reject the null hypothesis and conclude that there is cointegration between the two variables with Rank $r = 1$. This suggest a linear relationship between mortality and patient admissions, so we applied the Vector Error Correction model (Johansen.S, (2014)).

Table 3. Cointegration test- maximum eigen value statistic test.

Rank	Test statistic	critical value(10%)	critical value (5%)	critical value (1%)
r<=1	7.38	6.50	8.18	11.65
r=0	14.906	12.91	14.90	19.19
Trace statistic test.				
Rank	Test statistic	critical value (10%)	critical value (5%)	critical value (1%)
r<=1	7.38	6.50	8.18	11.65
r=0	22.19	15.66	17.95	23.52

4.3. Model Selection (Optimal lag selection test results)

In order to determine the optimal lag order for our model, we used the least information criteria : Akaike information criteria (AIC), Hannan-Quinn information criteria (HQC), Schwarz- Bayesian information criteria (SBC) and Akaike final prediction error criteria. (FPE).According to Akaike (1973), the model with the lowest expected information loss is selected as the best fit for the data.

Table 4. Criteria for selection of model for all endogeneous variables

Lag	AIC	HQC	SBC	Final Prediction Error (FPE)
VAR 1	12.89680	12.95524	13.04081	399042
VAR 2	12.77690	12.91327	13.11292	354054
VAR 3	12.73410*	12.83151*	12.97412*	339154*
VAR 4	12.78986	12.96520	13.22157	358798
VAR 5	12.79628	13.010058	13.32432	361307
VAR 6	12.81632	13.06958	13.44036	368911

Table 4 : shows the results of the optimal lag selection test. In this study, the model with the lowest information loss is at lag 3.

4.4. Vector Error Correction Model-Parameter Estimation

From the analysis in Table 3, 4 the multivariate time series has cointegration test at lag 3 with Rank r=1. The coefficients results are shown in Table 5 below.

Table 5. Estimate results of the VEC model with 2 lagged differences

	MORT.d	ADM.d
Π		
Constant	-0.314580	1.035088
MORT.d1	0.785456	-6.478363
ADM.d1	-0.785166	-0.004572
MORT.dl2	0.028937	-0.666602
ADM.dl2	-0.416447	0.566185
	0.036419	-0.332801
The long-run parameter Beta estimate (β)		
	Π	
MORT.l3	1.0000000	
ADM.l3	-0.1399994	

In this study, we employed the vector error correction model, and the estimate results are shown in Table 5. The monthly mortality (X) in the medical wards is our dependent variables while the patient admissions (Y) in the medical wards is the independent variable. The coefficient for the *ect1* is negative indicating that the two variables has a long-term relationship

The co-integrating vector (*ect_{t-1}*) shown below represent the long -run relationship between mortality(X) and patient admission(Y)

$$ect_{t-1} = 1.0000000X_{t-1} - 0.1399994Y_{t-1} \tag{22}$$

In equation form, we represented a Vector error correction model for Mortality (X) and Patient admissions (Y) results as :-

$$\Delta X_t = 0.785456 - 0.317655(X_{t-1} - 0.1399994Y_{t-1}) - 0.785166\Delta X_{t-1} - 0.004572\Delta Y_{t-1} - 0.416447\Delta X_{t-2} + 0.566185\Delta Y_{t-2} + \epsilon_t \tag{23}$$

$$\Delta Y_t = -6.478363 + 1.035088(X_{t-1} - 0.1399994Y_{t-1}) + 0.666602\Delta Y_{t-1} + 0.028973\Delta X_{t-1} - 0.33280\Delta Y_{t-2} + 0.036419\Delta X_{t-2} + \epsilon_t \tag{24}$$

The reduced form of the equation is shown below.

$$\Delta \begin{bmatrix} X_t \\ Y_t \end{bmatrix} = \begin{bmatrix} 0.785456 \\ -6.478363 \end{bmatrix} + \begin{bmatrix} 0.317655 & 0.044472 \\ 1.035088 & -0.144912 \end{bmatrix} \begin{bmatrix} X_{t-1} \\ Y_{t-1} \end{bmatrix} + \begin{bmatrix} -0.785166 & -0.004572 \\ -0.02893 & 0.666602 \end{bmatrix} \Delta \begin{bmatrix} X_{t-1} \\ Y_{t-1} \end{bmatrix} + \begin{bmatrix} -0.416447 & 0.566185 \\ 0.036419 & 0.332801 \end{bmatrix} \Delta \begin{bmatrix} X_{t-2} \\ Y_{t-2} \end{bmatrix} + \begin{bmatrix} \epsilon_{1t} \\ \epsilon_{2t} \end{bmatrix} \tag{25}$$

4.5. Test for the fitness of multivariate model.

In order to test for the fitness of the model, the assumption is that residuals in the fitted model should not be auto-correlation and that the residuals should be normally distributed. The following tests were performed.

Normality and serial correlation test for residuals.

To test for normality and serial correlation of the residual for the model, the Jarque-Bera (JB), Breusch-Godfrey LM test, serial correlation plot and box-plot were used. The results are shown in the residual plots in Figure 5, 6 and Table 6 below:

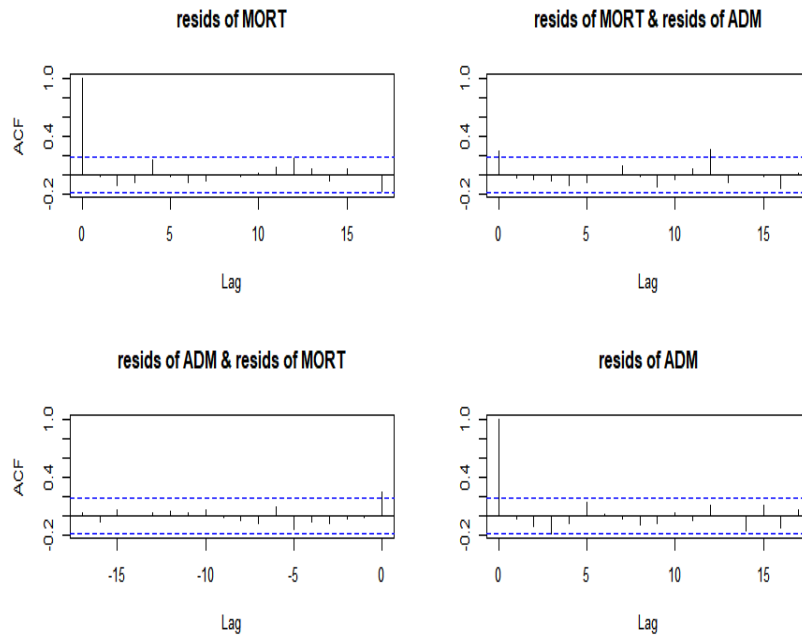


Fig. 5. The ACF of residuals for the fitted model. MORT=Mortality, ADM=Admissions

From Figure 5, the model was checked for the assumption of independence of residuals using the ACF plot. The plots showed that the auto correlation function of residuals were within the 95% confidence level, hence we concluded that there was no serial correlation between the residuals. Therefore, the assumption of independence of residual were satisfied. .

The Figure 6 is the Box plot of residuals for the fitted model, the plot shows that the residual are close to zero relative to the scale an assumption that residual were normally distributed i.e the model fitted the data well.

From Table 6, the statistical test results for normality of residual for the fitted model are shown, the Jarqua-Bera test, i.e Skweness, Kurtosis test statistic was 0.73872, 0.40323 and 0.32969 less than the Chi-square critical values of 5.991, 5.991 and 5.991, respectively at 5% significant level with P-values of 0.9465, 0.8174 and 0.8456 respectively.

H_0 : is that the residuals are normally distributed.

H_a : the residual are not normally distributed.

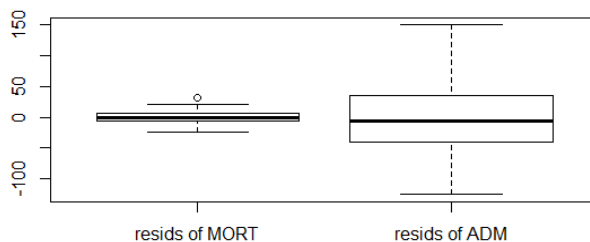


Fig. 6. The boxplot for fitted model. MORT=Mortality, ADM=Admissions

Table 6. Test results for Normality, serial correlation and ARCH-effects of residuals

Test	Test statistic(χ^2 -value)	degree of freedom	χ^2 - critical value at 5%	P-value
Jarque-Bera	0.73872	2	5.991	0.9465
Skweness	0.40323	2	5.991	0.8174
Kurtosis	0.33549	2	5.991	0.8456
Breusch-Godfrey	23.6	20	31.41	0.2715
ARCH effects	19.66	18	40.11	0.3522

Since the *P*-value is greater than the 0.05 significant level, we conclude that the residual are normally distributed. We also conducted a Breusch-Godfrey LM test to check for serial correlation of the residual in the model. The above results show that the test statistic was estimated to be 23.6 which was less than 31.41 critical value at 5% significant level with a *P*-value of 0.2715. We fail to reject the null hypothesis of no serial correlation and conclude that the model had no autocorrelation of residuals at all lags. The model was also tested for ARCH effects i.e to check whether the residual were homoscedastic or heteroscedastic. The null hypothesis is that there is no ARCH effects. From test results, we concluded that the model had no ARCH effects.

Stability test results. Test for stability was conducted to check whether the model was stable. The results showed that the (eigen values) $|\lambda I - \phi| = 0$ were all less one that zero in absolute values, with values 0.40272 and 0.22910 an indication that the model was stable

4.6. Test results for causality

To assess whether there was a causal relationship between the variables and also to determine the direction of causality, we used granger-causality test and the results are presented in the table below :

Table 7. Characteristics of the granger causality test between variables

Null hypothesis	F-statistic value	F-critical value	P-value (5%)
MORT(X) Does not granger cause ADM(Y)	0.078778	3.841	0.7792
ADM(Y) Does not granger cause MORT(X)	5.4963	3.841	0.0199

From Table 7 results, MORT(X) F-statistic value is 0.078778 less than the F-critical value 3.841 with the *P*-value of 0.7792 greater than 0.05 significant level. We fail to reject the null hypothesis and conclude that Mortality does not cause Patient admission. ADM(Y) F-statistic value is 5.4963 greater than the F-critical value 3.841 with the *P*-value of 0.0199 less than 0.05 significant level. We reject the null hypothesis and conclude that patient admission granger cause mortality. Therefore it is clear from the results that mortality data was not only influenced by past information from itself but also by information from patient admission data. We also concluded that there was unidirectional causality between the study variables

4.7. Impulse response function

Impulse response function shows how one variable reacts to a shock by another variable over the period of time. It tells the effects of one standard deviation shock to one of the innovations. It predicts the reaction of one variable

after the shock.

The Figure 7 below shows the impulse response for mortality and patient admission when there is a shock in patient admission and mortality, respectively

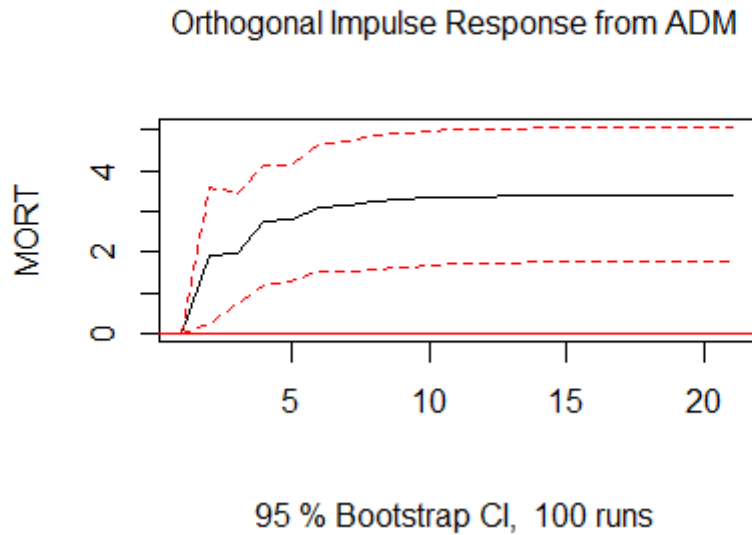


Fig. 7. Plot on how mortality respond to impulse or shock from admission data

A one standard deviation shock in the patient admission series caused a sharp positive response (increase) in mortality up to period 2, thereafter there was a constant movement before a slight increase again from period 3 up to 4 and then it reached a steady state after period 5.

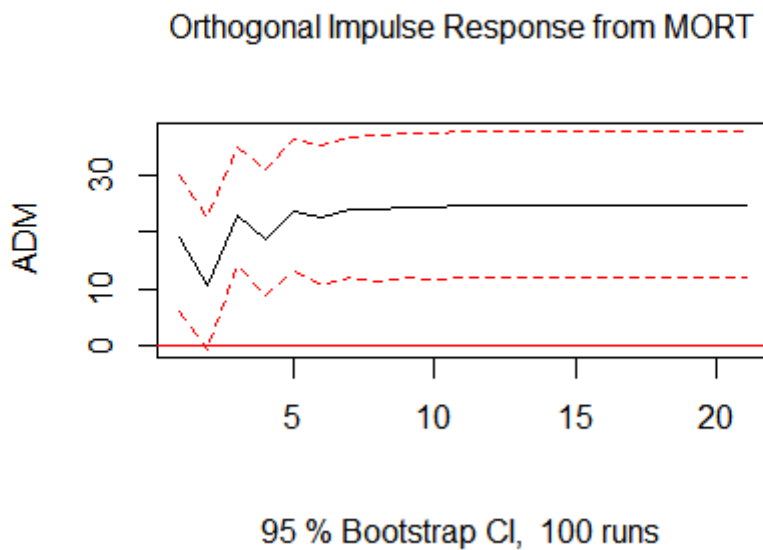


Fig. 8. Plot on how admissions respond to the impulse or shock from mortality.

4.8. Forecasting

The selection of a proper model is very important as it reflects the underlying structure of the time series and in turn used for forecasting future values. The VEC(3) model was selected and tested for fitness, results showed that the model passed statistical normality, stability and serial correlation test. The model was then used to forecast the Mortality and Patient admission future values for next 60 months. The forecast results for next twenty periods are shown in the Table 8 below.

Table 8. Forecasting for the next 20 periods of mortality and patient admission

variable	obs	fcst	lower	upper	95% Conf Interval
MORT	[1,]	29.38324	9.3017283	49.46476	20.08152
	[2,]	29.55609	8.6344313	50.47775	20.92166
	[3,]	30.55469	7.6808739	53.42851	22.87382
	[4,]	30.99688	6.8184337	55.17532	24.17845
	[5,]	31.26121	5.9552542	56.56716	25.30595
	[6,]	31.41146	5.0533282	57.76960	26.35814
	[7,]	31.46141	4.1178244	58.80500	27.34359
	[8,]	31.43567	3.1630960	59.70825	28.27258
	[9,]	31.36462	2.1977555	60.53149	29.16687
	[10,]	31.25592	1.227548	61.28430	30.02837
	[11,]	31.12122	0.2591131	61.98333	30.86211
	[12,]	30.96839	-0.7037976	62.64059	31.67219
	[13,]	30.80195	-1.6585804	63.26249	32.46053
	[14,]	30.62598	-2.6032994	63.85526	33.22928
	[15,]	30.44314	-3.5369184	64.42320	33.98006
	[16,]	30.25532	-4.4588465	64.96950	34.71417
	[17,]	30.06396	-5.3688334	65.49676	35.43280
	[18,]	29.87005	-6.2668916	66.00699	36.13694
	[19,]	29.67429	-7.1531873	66.50178	36.82748
	[20,]	29.47722	-8.0279929	66.98244	37.50522
ADM	[1,]	234.4780	128.4428075	340.5131	106.0352
	[2,]	221.9234	110.1573460	333.6894	111.7660
	[3,]	218.0089	95.0956295	340.9221	122.9133
	[4,]	214.8470	80.1489408	349.5451	134.6981
	[5,]	210.7763	67.8020609	353.7506	142.9743
	[6,]	208.3477	56.4935278	360.2018	151.8542
	[7,]	205.9426	45.8654600	366.0198	160.0772
	[8,]	203.7747	35.9920755	371.5574	167.7826
	[9,]	201.8919	26.6276472	377.1561	175.2642
	[10,]	200.0977	17.6854710	382.5099	182.4122
	[11,]	198.4116	9.1143268	387.7088	189.2972
	[12,]	196.8020	0.8482649	392.7557	195.9537
	[13,]	195.2383	-7.1528643	397.6294	202.3911
	[14,]	193.7132	-14.9207624	402.3472	208.6340
	[15,]	192.2145	-22.4833656	406.9125	214.6979
	[16,]	190.7344	-29.8619588	411.3307	220.5963
	[17,]	189.2681	-37.0742880	415.6104	226.3424
	[18,]	187.8115	-44.1353667	419.7583	231.9468
	[19,]	186.3619	-51.0577027	423.7815	237.4196
	[20,]	184.9174	-57.8520349	427.6868	242.7694

The forecasting charts for admissions (ADM) and mortality (MORT) are show in the diagrams below: Figure 9 and 10

4.9. Correlation analysis matrix

The correlation coefficient is a quantitative assessment that measure the strength of the relationship between two variables. A correlation between two variables indicate that there is a linear relationship between variables. In this study, we also determined the correlation coefficients between mortality among the female (F), males(M) and admission (Adm) due to various diseases in the medical wards. The matrices below shows, the correlation coefficients for the top four(4) diseases contributing to mortality from 2013 to 2022. These are malaria, cardiac diseases, Meningitis and tuberculosis.

Fanchart for variable ADM

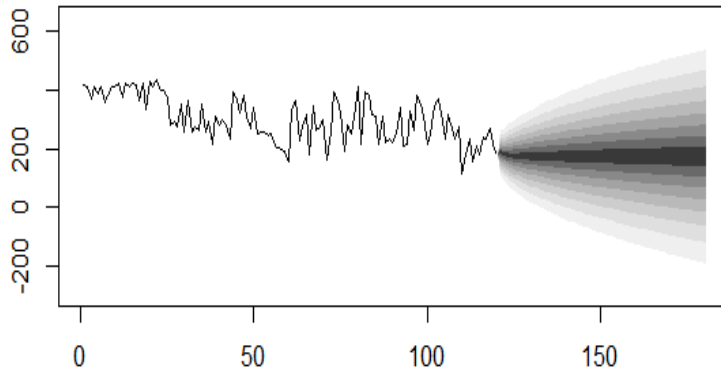


Fig. 9. Plot for admission forecasting chart

Fanchart for variable MORT

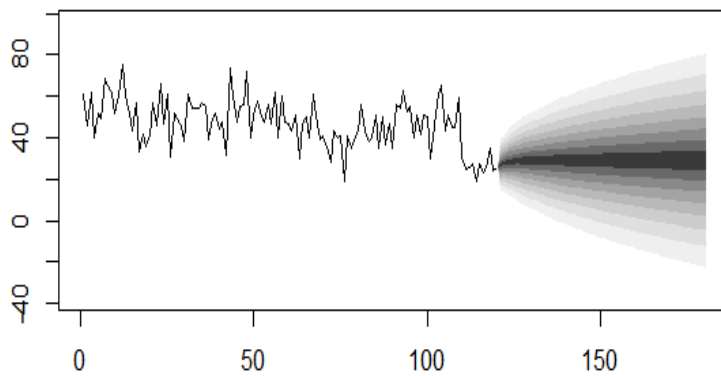


Fig. 10. Plot for the mortality forecasting chart

$$\text{Malaria} = \begin{bmatrix} & F & M & Adm \\ F & 1.000 & 0.8956 & 0.1528 \\ M & 0.8956 & 1.000 & 0.2706 \\ Adm & 0.1528 & 0.2706 & 1.000 \end{bmatrix}$$

$$\text{Cardiac} = \begin{bmatrix} & F & M & Adm \\ F & 1.000 & 0.2705 & 0.5098 \\ M & 0.2705 & 1.000 & 0.0122 \\ Adm & 0.5098 & 0.0122 & 1.000 \end{bmatrix}$$

$$\text{Meningitis} = \begin{bmatrix} & F & M & Adm \\ F & 1.000 & 0.9283 & 0.92736 \\ M & 0.9283 & 1.000 & 0.8992 \\ Adm & 0.92736 & 0.8992 & 1.000 \end{bmatrix}$$

$$\text{Tuberculosis} = \begin{bmatrix} & F & M & Adm \\ F & 1.000 & 0.7884 & 0.6783 \\ M & 0.7884 & 1.000 & 0.5431 \\ Adm & 0.6783 & 0.5431 & 1.000 \end{bmatrix}$$

4.9.1. Hypothesis test results for correlation analysis

In order to determine if there was correlation between Mortality among Females, Males and Admissions in the medical wards, we conducted a hypothesis testing. The null hypothesis test is that the correlation coefficient zero, meaning there is no correlation among the two variables and the alternative hypothesis is that there is a correlation between the variables. The test results is tabulated in the tables below.

Table 9. Pearson correlation test for mortality and admissions due to malaria among females and Male

corr. test:Female and males				
t-statistic	t-critical value	P-value	95% Confidence.Interval	corr. estimate
5.3278	1.895	0.00109	0.57140475-0.9780224	0.8956458
corr. test:Female and admission				
t-statistic	t-critical value	P-value	95%confidence Interval	corr. estimate
0.40911	1.895	0.6947	-0.5690604-0.7416659	0.1528134

Table 9 , is the correlation test results between female and male mortality due to malaria. The t-statistic value was 5.327 with a P-value of 0.00109 at 0.05 significant level. The correlation estimate was 0.895645. We conclude that there was a strong positive correlation between female and male mortality due to malaria. The test also revealed that the test statistic for the correlation between female mortality and admission due malaria was 0.40911 with P-value 0.6947 at 0.05 significant level. We conclude that there was no correlation between female mortality and admissions due malaria.

Table 10. Pearson correlation test for mortality and admissions due to Tuberculosis among female and males

corr. test : Female and adm				
t-statistic	t-critical value	P-value	95% Confidence.Interval	corr. estimate
2.4421	1.895	0.04462	-0.02572762 - 0.92549516	0.6782604
corr. test:Female and Males				
t-statistic	t-critical value	P-value	95%confidence Interval	corr. estimate
3.3908	1.895	0.01159	0.2608580 - 0.9533517	0.7883967
corr. test:Males and adm				
t-statistic	t-critical value	P-value	95%confidence Interval	corr. estimate
1.7112	1.895	0.1308	-0.1893287 - 0.8872099	0.5430782

Table 10, the t-statistic value for the correlation between female mortality and admission due tuberculosis was 2.4421 with P-value of 0.04462 at 0.05 significant level. We conclude that there was moderate correlation between female mortality and admissions due to tuberculosis with an estimate value of 0.67826. The correlation between female and male mortality test statistic was 3.3908 with P-value of 0.01159 and correlation estimate of 0.7884. We conclude that there was a strong positive correlation between female and male mortality due tuberculosis. The correlation test results between male mortality and admission due to tuberculosis was 1.7112 with P-value of 0.1308 with correlation estimate value of 0.5431. We concluded that there was no correlation between male mortality and admissions due to tuberculosis.

Table 11 The correlation test statistic value for female mortality and admission was 6.603 with P-value of 0.0003035 and a correlation estimate of 0.92855. We conclude that there was a very strong positive correlation between female

Table 11. Pearson correlation test for mortality and admissions due to Meningitis among female and males

corr. test : Female and admission				
t-statistic	t-critical	P-value	95% Confidence.Interval	corr. estimate
6.603	1.895	0.0.0003035	0.6886992 - 0.9850926	0.9282554
corr. test: Female and Males				
t-statistic	t-critical	P-value	95%confidence Interval	corr. estimate
6.5576	1.895	0.0003166	0.6853225 - 0.9849021	0.9273654
corr. test: Males and admissions				
t-statistic	t-critical	P-value	95%confidence Interval	corr. estimate
5.4354	1.895	0.000971	0.5833638 - 0.9787886	0.8991375

mortality and admissions due to meningitis. Further, the test statistic for the correlation between female and male mortality due to meningitis was 6.5576 with P-value of 0.0003166. We concluded that there was also a very strong positive correlation between female and male mortality. The analysis also showed that the correlation test statistic between male mortality and admissions was 5.4354 with P-value of 0.000971 at 0.05 significant level respectively. We concluded that there was a strong positive correlation between male mortality and admissions due to meningitis.

4.10. Conclusion and Recommendations

Mortality and admission at Kabwe Central hospital are cointegrated with a rank $r = 1$. The selected model was VEC(3) model with a speed of adjustment of 31.5%. Granger causality test showed a unidirectional effect namely, patient admission Granger cause mortality.

The investigation on linear relationship concluded that there was strong positive correlation of 0.8956, 0.7884 and 0.927365 between males and females dying of Malaria, Tuberculosis and Meningitis respectively. A very strong positive correlation was also observed between female mortality and admissions of 0.6783 and 0.92825 due tuberculosis and meningitis respectively, the correlation between male mortality and admissions due meningitis was 0.899137. These findings suggests that in order to improve patient care outcome, the Hospital need to closely monitor patient inflow as the correlation means high admissions is associated with high mortality

A similar study on patients admission to medical wards due COVID 19 and patients in intensive care unit due to COVID 19 with data collected from Italian regions, Switzerland and Spain used a VEC model to forecast the two variables. The result showed that patients admission counts in the wards due to COVID 19 was useful in predicting those taken to ICU due to COVID 19.

However, it is recommended that future study should include data from all regional hospitals in the country and more related factors in the time series analysis of mortality and patient admissions for optimal prediction. It is also recommended that future research should find out why there is a high positive correlation between mortality and admission for both males and females due to cryptococcal meningitis at the Hospital.

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