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Full Length Research

Statistical simulations of infectious diseases in Southwestern Nigeria (A case study of Ekiti and Oyo State)

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ABSTRACT: This study adopts Markov chain to simulate some infectious diseases in two States (Ekiti and Oyo) of southwestern Nigeria, to describe the situations where the outcome of infectious diseases depends only on the outcome of the previous cases of the diseases. The next state of the process depends only on the present state, not on the preceding states. The main objective of this research is to model infectious diseases in Nigeria using Markov chain approach, determine the transition pattern and the fundamental matrix of the diseases, test for Markovian property of the data and how stationary the process is over time and predict the future prevalence of infectious diseases in the states. Transition probability matrix of how patients move from one state (exposed, infected, immune, recovered and dead) of the diseases to another state revealed that the inhabitants of the two States were highly exposed to infectious diseases. The estimated probabilities, p, of being infected with infectious diseases were higher ($0 \leq p \leq 1$) in Ekiti State than Oyo State ($0 \leq p \leq 1$). This indicates that higher proportions of people in Ekiti State were more infected with infectious diseases than those people living in Oyo State. The future transient state and the probability of reaching the absorption state indicate that about 98% of the populations will be exposed to infectious diseases in the future and about 50% of the dwellers will be immunized and as many that are infected will be recovered if necessary precautions are taken. The study advocates for renewed efforts in the area of prevention, environmental sanitation, vaccination and control of infectious diseases instead of spending billions of naira on curtailing the spread of diseases and medical tourism.

Keywords: Absorption, infectious diseases, Markov chain, transition matrix.

INTRODUCTION

The term infectious disease does not refer to a homogeneous set of illnesses but rather to a broad group of widely varying conditions. The relative and absolute importance of particular infectious or groups of infectious diseases varies dramatically across regions. In high-income countries, deaths from infectious diseases are overwhelming due to respiratory infections and HIV/AIDS. In sub-Saharan Africa, respiratory infections, diarrhea diseases, HIV/AIDs, tuberculosis and malaria account for roughly similar proportions of total infectious diseases deaths (UNICEF, 2004). The rates of specific infectious diseases are generally much higher in poor countries, regardless of the relative importance of these diseases. In both relative and absolute terms, infectious diseases are a considerably higher burden in low-income than high-income countries. An analysis of the global burden of diseases study data concludes that the poorest 20% of the world's population experiences a far higher burden of infectious disease compared to the remaining 80% of the world's population. (Saker et al., 2004). Consequently, in regions where a high proportion of the population is made up of young people (such as Africa, Latin America, and many other developing countries), infectious diseases usually extract a relatively high toll on the population (UNICEF, 2004).

The major area of concern for infectious diseases in Nigeria is the prevention of the diseases, inadequate health facilities, accessible road infrastructures and high cost of accessing health care. These constitute the main problem why prevention is a bit difficult. Again, curtailing

the diseases on time even when they occur is another serious area of concern, because most often it takes time to detect and report cases of outbreak of infectious diseases and lastly, predicting the future occurrence of infectious diseases is the most difficult aspect of it because of inadequate keeping of record/data. This is the gap which this study intends to fill by applying Markov chain to available data in Ekiti and Oyo States respectively. Many works have been reviewed on infectious diseases globally, out of which are Adigun et al. (2019) worked on the application of Markov chain in modeling infectious diseases in Nigeria. They examined certain factors that led to the spread of infectious diseases. From their research, transition probability of how patients move from one state of the diseases to another state were estimated after the data had satisfied Markov property as well as stationary process. It was concluded that the past history of infectious diseases will definitely affect the future only through the present state of the diseases.

Alyssa (2011) proposed a newer method involving Bayesian inference and then Markov Chain Monte Carlo to estimate the parameters involved in analyzing infectious diseases. He built a model that specifies the mechanism of the spread of the disease using certain variables which include latent periods, variable infectivity rates or natural immunity, immunity upon recovery, time of infection and more. He formulated the problem using Bayesian inference and used Markov Chain Monte Carlo techniques to estimate the solution because of its flexibility and allowing for missing data. He also discovered that one could use this method to determine the unknown infection times instead of the times at which symptoms appeared.

Again, Ross and Taimre (2006) analyzed hospital infections data, using Markov Models. They presented a general approach to estimating parameters of continuous-time Markov Chains from discrete sampled data. Their methodology was combined with a new stochastic model for transmission of hospital-acquired infections one which accounts for dynamic bed occupancy providing a method for estimating the parameters of such system. Their study provides a new method for incorporating partial observability and comparing the results from this method to the commonly used existing approach. They provided a model and accompanying methodology for addressing an important problem often encountered when analyzing hospital infection data, namely dynamic bed occupancy. They also investigated when it is necessary to incorporate dynamic bed occupancy in estimation procedures and they provide clear methodology for how this may be practiced effectively. Their results are anticipated to have wide application in studying nosocomial infections, and for assessing the efficacy of possible management strategies designed to decrease the prevalence of such infections. In their research it was found out that large amount of variation exists in their estimations and hidden Markov model approach needs to be carefully reviewed for further research.

Arnoldo and Bernd (2015) applied Markov chain for modeling how the system moves from one state to another in time. Transitions between states are random and governed by a conditional probability distribution which assigns a probability to move into a new state, given the current state of the system. This dependence represents the memory of the system. It was discovered that staying in the diseased state 1 over many days could increase the probability of transition to death which makes it possible to model a system with longer memory and one can formulate such a model as Markov chain over a more complex state space which includes the length of stay in the current state. The transitions probabilities, from susceptible to immune, susceptible to dead (R) and the loop susceptible to susceptible, must sum to one and can depend on characteristics of the individuals modeled, like age, gender, life style, etc. All individuals start in susceptible, and move at each time unit (say a day). Given observations of the sequence of visited states (called trajectory) for a sample of individuals, with their personal characteristics, one can estimate the transition probabilities, by logistic regression, for example. The model assumes that the transition probability at time t from one state A to state B only depends on the state A and not on the trajectory that leads to A. They concluded that the analysis of the stationary behavior of a (uniformizable) continuous time Markov chain reduces to that of a discrete time Markov chain.

Infectious diseases are still major causes of morbidity and mortality worldwide, particularly in developing and developed countries. Approximately 26 percent of global deaths and 26 percent of global burden of diseases were attributed to infectious diseases (Kramer and Khan, 2010). The vast human resources often lost to these diseases, which are the number of productive and active lives that died from these diseases constitutes a serious concern to government at different levels, international and local health organizations. One in two deaths that are mostly preventable occurs in developing countries (Folch et al., 2003; Kim-Farley., 2004). The data for this research work is secondary in nature sourced from Ekiti State University Teaching Hospital Ado-Ekiti for a period of eleven years from 2008 to 2019 and Oyo State Ministry of Health data bank for three years 2011, 2013 and 2014. This study will test the Markovian property of the data in order to know if the conditional probability of the future state of infectious diseases depend on the current state and not on the preceding state and the transition probability of how patients move from one state of the diseases to another will be developed. This work will also estimate the number of people that will be infected and finally predict the future survival rate in the states respectively.

Ethical approval

Ethical approval was obtained from Ethical Committee, Ekiti State University Teaching Hospital (ESKUTH) Ado –

Ekiti, Nigeria. All information obtained was strictly confidential with written permission obtained from the ethical committee of the hospital. The information about participant's identity was not included with other data and only the researcher had access to this information. No reference to the participant's identity was made at any stage during data collection.

METHODOLOGY

Study areas and source of data

Oyo State is located in the South-west geopolitical zone of Nigeria with a geographical Coordination of 8°00′N and 4°00′E. It is one of the three states carved out of the former western state of Nigeria in 1976. Oyo state consists of 33 local governments and 29 local council development area. The state covers a total of 28454 square kilometers of land mass. The topography of the state is of gentle rolling low land in the south, rising to a plateau of about 40 m. The current metro area population of Oyo State in 2020 is 428,000, a 3.13% increase from 2019. (https://oyostate.gov.ng/).

On the other hand, Ekiti State is located in the South-west geopolitical zone of Nigeria with a geographical Coordination of 7°40′N and 5°15′E It was carved out of the former Ondo State of Nigeria in 1996 by the Military regime, it has a population of about 2 million with 16 local government council. Ekiti cover an area of 8,55km^2, and it is generally an upland zone with elevations being generally above 450 m throughout the state. (https://ekitistate.gov.ng/).

The data for this research were sourced from Ekiti State University Teaching Hospital Ado-Ekiti and Oyo State Ministry of Health data bank.

Markov chain

In probability theory and statistics, the term Markov property refers to the memory less property of a stochastic process. A stochastic process has the Markov property if the conditional probability distribution of future states of the process (conditional on both past and present states) depends only upon the present state, not on the sequence of events that preceded it. A process with this property is called a Markov process. Examples are Random walk, Brownian (waver process), Poison process to mention a few. A discrete –time stochastic process satisfying the Markov property is known as a Markov chain (Ogunsakin et al., 2014).

A Markov chain is a discrete-time stochastic process $(X_n, n \geq 0)$ such that each random variable X_n takes values in a discrete set $S(S = \mathbb{N}, typically)$ and $P\left(X_{n+1=j} \middle| X_{n=i}, X_{n-1=i-1}, \dots, X_{0=io}\right) = P(X_{n+1=j} | X_{n=i}) \forall n \geq 0, j, i, i_{n-1}, \dots, i_0 \boldsymbol{\epsilon S})$. That is, as time goes by, the process loses the memory of the past.

Moreover if $P\left(X_{n+1=j} \middle| X_{n=i}\right) = p_{ij}$ is independent of n, then X is said to be a time homogeneous Markov chain. $p_{ij}$is called the One-Step transition probability from state i to state j, while $P = \left[p_{ij}\right]_{i,j \epsilon S}$ is called the One-Step Transition Probability Matrix or Transition Matrix. The transition probabilities in a homogeneous Markov chain obey the Chapman Kolmogorov equation.

$$P_{ij}^{(n+m)} = \sum_{k=S} P_{ik}^{(n)} P_{kj}^{(m)}, \quad i,j \in S, \ n,m \geq 0$$

And

$$P_{ij}^{(0)} = \delta_{ij} = \left\{p_{0,}^{1,} \quad \begin{matrix} if\ i=j \\ otherwise \end{matrix}\right\}$$

In terms of the transition matrix$P$, the equation reads

$$(P_{ij}^{n+m}) = \sum_{k=S} (P_{ik}^{n})\,(P_{kj}^{m}), \qquad i,j \in S, \qquad n,m \geq 0$$

$P_{ij}^{0} = I$, the identity matrix

Model formulation

The possible states are Exposed (E), Infected (I), Immune (A), Recovered (R) and Dead (D).

Exposed (E): Persons that can be infected.
Infected (I): Transmittable stage of the infection.
Immune (A): Those who have Immunity.
Recovered(R): Persons who will recover from the disease.
Dead (D): Persons who will die of the disease.

The possible transition from one state to another are as follow; from E to I or R, E to R, or D from E to I or R, E to A or R, or D from I to A or R, or D From A to A or R, or D, R to D, D to D only, and lot more.

Hypothesis for testing Markovian property and stationary process of the data is stated below

H_o: The conditional probability of the future state of infectious diseases does not depend on the current state of the diseases.
H_1: The conditional probability of the future state of infectious diseases depend on the current state of the diseases.
H_1: The process is not stationary over time
H_0: The process is stationary over time

Tests for Markovian property

A discrete time and discrete state space stochastic process is Markovian if and only if the conditional

probabilities $P(X_{n+1}|X_0,\dots,X_n)=\frac{P(X_0,\dots,X_n,\ X_{n+1})}{P(X_0,\dots,X_n)}$ do not depend on $(X_0,\dots,X_n)$ in full, but only on the most recent state X_n:

$$P(X_{n+1}|X_0,\dots,X_n)=P(X_{n+1}|X_n)$$

The Markov property validates the model and since the future state of infectious diseases depends on the present case of infectious diseases it validates the data and the model.

The likelihood of going to any next state at time *n* + 1 depends only on the state we find ourselves in at time *n*. The system is said to have *no memory*. Also, the Markovian property can be tested for using Likelihood Ratio Criterion (Anderson and Goodman, 1957), the criterion is given by:

$H_0: P_{ij} = P_1$ vs

$H_1: P_{ij} \neq P_{0,}\ i = 1,2,3,\dots\dots m+1; j = 1,2,3,\dots\dots,m+1.$

$$\mathrm{P} = \pi\left(\frac{P}{P}\right)^{n}$$

$$= \frac{n_i}{n..}$$

$$P = \frac{n_i}{\sum n}$$

$$= \frac{n_{ij}}{n}$$

$$= \frac{n_{ij}}{n}$$

n_{ij} Denotes the number of observed transitions from ith state to the jth state.

Tests for stationarity

Definition: A (discrete-time) stochastic process $\{X_n: n \geq 0\}$ is stationary if for any time points $(i_{1,}\dots,i_{n,})$ and any $m \geq 0$, the joint distribution of $(X_{i\ 1,\dots,}X_{i\ n})$ is the same as the joint distribution of $(X_{i\ 1+m,\dots\dots}X_{i\ n+m})$. So "stationary" refers to "stationary in time". In particular, for a stationary process, the distribution of $X_n$is the same for all n. As we have in Table 4 (Bessent and Bessent, 1980).

Probability transition matrix

The maximum likelihood approach for estimating the transition matrix (Tables 1 and 2) involves likelihood function which can be maximized by taking its derivatives. Let us consider a patient in state $i = 1,2,3,\dots,k$. Let:

$P_1 = p_{ij}$ The transition probability of being exposed

$P_2 = p_{i,i+1}$ The transition probability of being infected
$P_3 = p_{i,k+1}$ The transition probability of being immune
$P_4 = p_{i,y+1}$ The transition probability of being recovered
$P_5 = p_{i,w+1}$ The transition probability of being dead

Considering these indicators functions which describe the measure of states of patients,

$$y_1 = \begin{cases} 1, if\ the\ patient\ is\ in\ exposed\ state\ i \\ 0, \qquad\qquad elsewhere \end{cases}$$

$$y_2 = \begin{cases} 1, if\ the\ patient\ is\ in\ infected\ state\ i+1 \\ 0, \qquad\qquad elsewhere \end{cases}$$

$$y_3 = \begin{cases} 1, if\ the\ patient\ is\ in\ immune\ \ state\ i+2 \\ 0, \qquad\qquad elsewhere \end{cases}$$

$$y_4 = \begin{cases} 1, if\ the\ patient\ is\ in\ recovered\ state\ i+3 \\ 0, \qquad\qquad elsewhere \end{cases}$$

$$y_5 = \begin{cases} 1, if\ the\ patient\ is\ in\ Dead \\ 0, \qquad\qquad elsewhere \end{cases}$$

Then $y_1+y_2+y_3+y_4+y_5 = 1$

$$P_r\left(y_1, y_{2,} y_{3,} y_{4,} y_5\right) = \begin{cases} {p_1}^{y_1}{p_2}^{y_2}{p_3}^{y_3}{p_4}^{y_4}\left(1-p_1-p_2-p_3-p_4\right)^{1-y_1-y_2-y_3-y_4} \\ 0, \qquad\qquad elsewhere \end{cases}$$

For any patient in state $i, i = 1,2,3\dots\dots k$, from a sample size $ni = n_{i1} + n_{i2} + n_{i3} + n_{i4} + n_{i5}$ have the likelihood function as

$$P_r\left(y_1, y_{2,} y_{3,} y_{4,} y_5\right) = \begin{cases} {p_1}^{n_{i1}}{p_2}^{n_{i2}}{p_3}^{n_{i3}}{p_4}^{n_{i4}}\left(1-p_1-p_2-p_3-p_4\right)^{n_{i1}n_{i2}n_{i3}n_{i4}} \\ 0, \qquad\qquad elsewhere \end{cases}$$

Taking the logarithm and differentiating with respect to P_1, P_2, P_3, P_4,

$$lnP_r = n_{i1}lnp_1 + n_{i2}lnp_2 + n_{i3}lnp_3 + n_{i4}lnp_4 + (n_i - n_{i1} - n_{i2} - n_{i3} - n_{i4})\ln(1 - p_1 - p_2 - p_3 - p_4)$$

P_r at maximum

$$\frac{dlnP_r}{dP_1} = n_{i1}\frac{1}{p_1} + (n_i - n_{i1} - n_{i2} - n_{i3} - n_{i4})\left(\frac{1}{1-p_1-p_2-p_3-p_4}\right) = 0$$

$n_{i1}(1-p_1-p_2-p_3-p_4) - p_1(n_i - n_{i1} - n_{i2} - n_{i3} - n_{i4}) = 0$

Table 1. Transition pattern of diseases in Ekiti State.

Transition pattern	Exposed	Immune	Infected	Recovered	Dead
Diarrhoea					
Exposed	0.3557	0.3222	0.0000	0.0022	3e-04
Immune	0.0000	0.5000	0.0000	0.4994	6e-04
Infected	0.0000	0.0000	1.0000	0.0000	0e+04
Recovered	0.0000	0.0000	0.0000	1.0000	0e+04
Dead	0.0000	0.0000	0.0000	0.0000	1.0000
Hepatitis					
Exposed	0.9934	0.0033	0.0000	0.0032	0.0001
Immune	0.0000	0.5000	0.0000	0.4825	0.0175
Infected	0.0000	0.0000	1.0000	0.0000	0.0000
Recovered	0.0000	0.0000	0.0000	1.0000	0.0000
Dead	0.0000	0.0000	0.0000	0.0000	1.0000
Tuberculosis					
Exposed	0.9934	0.0022	0.0000	0.0089	0.0022
Immune	0.0000	0.4000	0.0000	0.4000	0.2000
Infected	0.0000	0.0000	1.0000	0.0000	0.0000
Recovered	0.0000	0.0000	0.0000	1.0000	0.0000
Dead	0.0000	0.0000	0.0000	0.0000	1.0000

Table 2. The transition pattern of the diseases in Oyo State.

Transition pattern	Exposed	Immune	Infected	Recovered	Dead
Diarrhoea					
Exposed	0.3557	0.3222	0.0000	0.0022	3e-04
Immune	0.0000	0.5000	0.0000	0.4994	6e-04
Infected	0.0000	0.0000	1.0000	0.0000	0e+04
Recovered	0.0000	0.0000	0.0000	1.0000	0e+04
Dead	0.0000	0.0000	0.0000	0.0000	1.0000
Hepatitis					
Exposed	0.9934	0.0033	0.0000	0.0032	0.0001
Immune	0.0000	0.5000	0.0000	0.4825	0.0175
Infected	0.0000	0.0000	1.0000	0.0000	0.0000
Recovered	0.0000	0.0000	0.0000	1.0000	0.0000
Dead	0.0000	0.0000	0.0000	0.0000	1.0000
Tuberculosis					
Exposed	0.9934	0.0022	0.0000	0.0089	0.0022
Immune	0.0000	0.4000	0.0000	0.4000	0.2000
Infected	0.0000	0.0000	1.0000	0.0000	0.0000
Recovered	0.0000	0.0000	0.0000	1.0000	0.0000
Dead	0.0000	0.0000	0.0000	0.0000	1.0000

$$p_1(-n_{i1} - n_i + n_{i1} + n_{i2} + n_{i3} + n_{i4}) - n_{1i}p_2 - n_{1i}p - n_{1i}p_4 = 0$$

$$p_1(-n_i + n_{i2} + n_{i3} + n_{i4}) - p_2 n_{i1} - p_3 n_{i1} - p_4 n_{i1} = 0$$

Differentiate with respect to P_2

$$\frac{dlnP_r}{dP_2} = n_{i1}\frac{1}{p_2} + (n_i - n_{i1} - n_{i2} - n_{i3} - n_{i4})\left(\frac{1}{1 - p_1 - p_2 - p_3 - p_4}\right) = 0$$

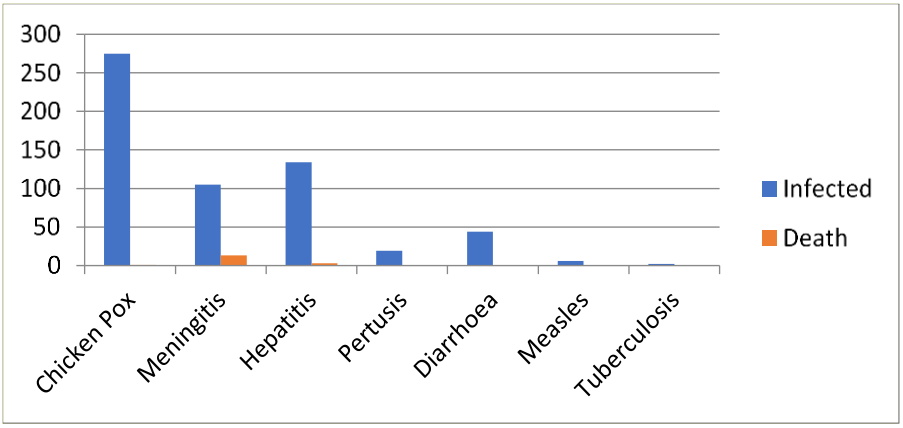

Figure 1. Summary statistics of number of infected and death cases of infectious diseases between 2008 t0 2019 in Ekiti State.

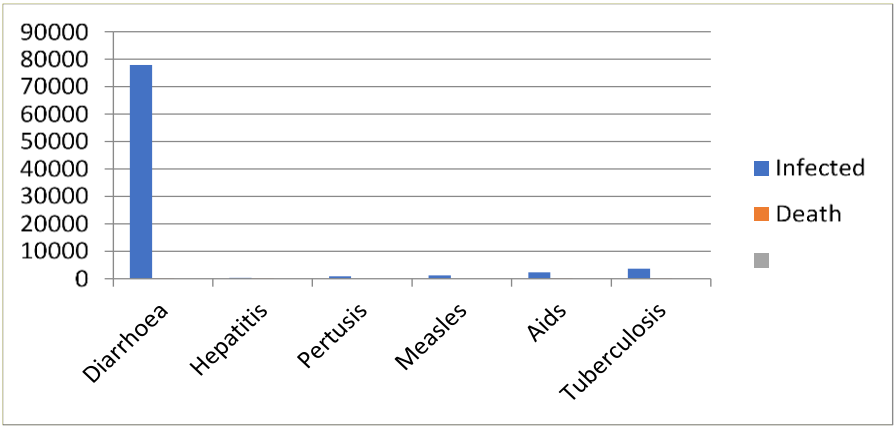

Figure 2. Summary statistics of number of infected and death cases of infectious diseases for 2011, 2012 and 2013 in Oyo State.

$n_{i1}(1-p_1-p_2-p_3-p_4)-p_2(n_i-n_{i1}-n_{i2}-n_{i3}-n_{i4})=0$

$p_2(-n_{i1}-n_i+n_{i1}+n_{i2}+n_{i3}+n_{i4})-n_{1i}p_1-n_{1i}p_3-n_{1i}p_4=0$

$p_2(-n_i+n_{i2}+n_{i3}+n_{i4})-p_1n_{i1}-p_3n_{i1}-p_4n_{i1}=0$

Multiply (1) by n_i-n_{i1} and take their differences we have

$P_1=\frac{n_{i1}}{n_i}$

$P_5=\frac{n_{i5}}{n_i}$

Hence,

$p_{i1}=\frac{n_{i1}}{n_i},\ p_{ij.1}=\frac{n_{i2}}{n_i},\ p_{ik.1}=\frac{n_{i3}}{n_i},p_{im.1}=\frac{n_{i4}}{n_i},\ p_{in.1}=\frac{n_{i5}}{n_i}$

Fundamental matrix

This gives the expected number of visits to each state before absorption occurs (Table 3) and is defined as $F=(I_n-\mathrm{Q})^{-1}$. I_n is the $n\ x\ n$ identity matrix corresponding in size to matrix Q, so that the difference I_n – Q exists. Consider a Markov chain currently in state j. The expected number of times that the chain visits state j at this step 1 for i to 0 for all other states. The expected number of times the chain visits state j at the next step is given by the element in row i, column j of the transition matrix Q. R studio is used to carry out the results.

RESULTS AND DISCUSSION

Descriptive statistic for all the infectious disease and transition matrices

Figures 1 and 2 depict the summary statistics of the

Table 3. The fundamental matrix of the diseases in Ekiti State.

State	Disease	Level	Exposed	Immune
Ekiti	Diarrhoea	Exposed	80	1.008
		Immune	0.0000	2.00000
	Hepatitis	Exposed	26.88172	1.0000
		Immune	0.0000	2.0000
	Tuberculosis	Exposed	151.5152	0.555556
		Immune	0.00000	1.6666667
Oyo	Diarrhoea	Exposed	1.552072	1.000155
		Immune	0.000000	2.00000
	Hepatitis	Exposed	151.5152	1.0000
		Immune	0.000000	2.00000
	Tuberculosis	Exposed	151.5152	0.55556
		Immune	0.00000	1.666667

Table 4. Markov property and Stationarity

State	Diseases	Markov property		Stationarity	
		Chi-Square	Tabulated	Chi-Square	Tabulated
Ekiti	Diarrhoea	40.4	9.488	4.137931	168.3
	Hepatitis	40.4	9.488	4.137931	168.3
	Tuberculosis	40.4	9.488	4.137931	168.3
Oyo	Hepatitis	40.4	9.488	4.137931	168.3
	Tuberculosis	40.4	9.488	4.137931	168.3
	Diarrhea	40.4	9.488	4.137931	168.3

infected and death cases of selected infectious diseases in Ekiti and Oyo State during the study period respectively. Results indicate that 275 people were infected with chicken pox with only one death, 105 people were infected with meningitis with 13 death, 134 were infected with Hepatitis with only one death, 19 with Pertussis, 44 people with Diarrhea, 6 people with Measles and 2 people with Tuberculosis and no death cases in Ekiti State (Figure 1). The breakdown of what happen in Oyo state where larger people were infected with Diarrhea and small proportion to other diseases (Figure 2).

Transition probabilities reveal the probability of moving from one state of infectious diseases to another state (EIARD). The probabilities of being exposed to all the diseases is about 100 percent in both States, which indicate that virtually all the people in the state are exposed to infectious disease, except in the case of diarrhea in Oyo state with lesser percentage of exposure, fewer percentages of the people are immune and as many that are infected eventually recovered of the diseases.

The fundamental matrices indicate the expected number each patient visit each state of the diseases before absorption/death occur.

Test for Markovian property and stationarity

The Markovian property and stationarity of the data sequence was tested using the chi-square as the test statistic. Since the chi-square calculated is greater than the observed table values in all cases (Table 4), the hypothesis H_o is therefore rejected. Hence, it be concluded that the process is not of zero order which implies that the current state determines the future state. Also, since the chi-squared value obtained (4.138) in testing for stationarity in all cases is less than the chi-squared tabulated value of 168.3, and the p-value is (1) at 5% significance level, the hypothesis that the sequence is stationary is therefore accepted.

Predicting the future occurrence of infectious diseases

Given an initial vector which contains the current state of patients for certain diseases over a specific year, the future state of infectious diseases can be predicted by using the formula below as shown in Table 5.

Table 5. Future transient state of infectious diseases.

Diseases	Level	Exposed/ Immune	Exposed	Immune
Diarrhea (Ekiti)	Q	Exposed	0.9875	0.0063
		Immune	0.00000	0.5000
	Q^2	Exposed	0.975153	3.969e – 07
		Immune	0.00000	2.500e – 01
	Q^3	Exposed	0.9629668	2.50047e - 07
		Immune	0.00000000	1.2500e - 01
	Q^4	Exposed	0.9509297	1.575296e - 09
		Immune	0.00000000	6.250000e - 02
	Q^5	Exposed	0.9390431	9.924365e – 12
		Immune	0.0000000	3.125000e - 02
Tuberculosis (Ekiti)	Q	Exposed	0.9934	0.0022
		Immune	0.00000	0.4000
	Q^2	Exposed	0.9868436	4.88e – 06
		Immune	0.0000000	1.84e – 01
	Q^3	Exposed	0.9803304	1.0648e - 11
		Immune	0.0000000	6.4000e- 02
	Q^4	Exposed	0.9738602	2.34256e – 14
		Immune	0.0000000	2.56000e – 02
	Q^5	Exposed	0.9674327	5.153632e – 14
		Immune	0.0000000	1.0240000e - 02
Diarrhea (Oyo)	Q	Exposed	0.3557	0.3222
		Immune	0.0000	0.5000
	Q^2	Exposed	0.1265225	0.1038128
		Immune	0.000000000	0.2500000
	Q^3	Exposed	0.04500405	0.033485
		Immune	0.0000000	0.1250000
	Q^4	Exposed	0.01600794	0.1077711
		Immune	0.0000000	0.06250000
	Q^5	Exposed	0.005694020	0.003472383
		Immune	0.00000000	0.031250000
Tuberculosis (Oyo)	Q	Exposed	0.9745	0.0089
		Immune	0.0000	0.5000
	Q^2	Exposed	0.9496503	7.921e – 05
		Immune	0.000000	2.500e – 01
	Q^3	Exposed	0.9254342	7.04969e – 07
		Immune	0.0000000	1.25000e – 01
	Q^4	Exposed	0.9018356	6.274224e – 09
		Immune	0.000000	6.250000e – 02
	Q^5	Exposed	0.8788388	5.584059e – 11
		Immune	0.00000000	3.125000e - 02

$P^n = P^0 P^{*(n)}$

Probability of absorption

In an absorbing Markov chain, the probability that the process will be absorbed is 1 (i.e.$Q^n \to 0\ as\ n \to \infty$) as shown in Table 6. The results of the future transient's state (Table 5) revealed that almost 98 percent, 99 percent, 87 percent and 97 percent will be exposed to these diseases across the states which implies that the probability that people living in Ekiti and Oyo state will be exposed to all

Table 6. Probability of absorption of infectious diseases.

Parameters	Probability of absorption		
	Infected	Recovered	Dead
Ekiti State			
Diarrhea			
Exposed	0	0.9805088	0.0194912
Immune	0	0.9772000	0.0228000
Tuberculosis			
Exposed	0	0.55555556	0.44444444
Immune	0	0.6666666667	0.333333333
Oyo State			
Diarrhea			
Exposed	0	0.9989343	0.001065715
Immune	0	0.9988000	0.001200000
Tuberculosis			
Exposed	0	0.6976204	0.3023796
Immune	0	0.9988000	0.0012000

these diseases are almost certain, this is similar to the work of Saker et al. (2004) who worked on the global burden of diseases, and conclude that the poorest 20% of the world's population experiences a far higher burden of infectious disease compared to the remaining 80% of the world's population. The only exception to this is the case of Diarrhea in Oyo state which has a very small percentage of exposure in the future, which is in line with the work of UNICEF (2004) who discovered a decline in major infectious diseases like malaria and AIDS as a result of an adoption of effective prevention strategies and treatment or, like in the case of hepatitis B and hepatitis C, as a consequence of worldwide vaccination programs. The probability that the population considered will be immune to these diseases in the future is zero which implies that people in those states may not be immunized against the diseases. In a related development, sub-Saharan Africa respiratory infections, diarrhea, HIV/AIDs, tuberculosis and malaria account for roughly similar and high proportions of total infectious diseases deaths due to low rate of immunization (UNICEF, 2004). The probability of absorption (Table 6) for the future state of all the diseases indicates that almost 100 percent of population will recover from all the diseases except in the case of tuberculosis and Hepatitis with lesser percent of recovery.

Conclusion

This study verified the Markovian property of the data of infectious diseases in the Ekiti and Oyo States in Nigeria with five possible states (exposed, infected, immune, recovered and dead). The probability transition matrix of moving from one state to another state revealed that 99% of Ekiti dwellers were exposed to diarrhea and tuberculosis while 97% of the people in Oyo state were exposed to tuberculosis and 35% were exposed to diarrhea. However, lesser percentage of the population (50%) had immunity against the diseases and as many people that are infected recovered (98%). This study shows that high percentage (97%) of the people in the study area will be exposed in the future if proper care is not taken by the state governments. This revealed that the future state of infectious diseases depends on the present state of the diseases. Also, the study recommends that public health education, adequate portable water supply, sanitation facilities, personal hygiene, regular immunization and affordable health service could help in curtailing the spread of infectious diseases.

CONFLICT OF INTEREST

The authors declare that they have no competing interests.

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