



# A Novel Application of Transition Probabilities in Analyzing the Spread of Infectious Diseases

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## ABSTRACT

Most mathematical models of diseases are hinged on a basic premise that the population of interest can be partitioned into a set of distinct groups based on their level of encounter with the disease. Classical mathematical models have been severally employed to study the dynamics of infectious diseases over a population, and have also served to evaluate prospects of identifiable intervention strategies to control and limit the devastating effect of the disease. The simplest of these models classify members of the population into one of susceptible, infectious and recovered compartments, commonly referred to as the SIR model. The classical modelling process is often tedious and tasking with recourse to differential equations and computer simulation techniques. This paper presents a novel approach that employs the theory of transition probabilities to evaluate the strength of control strategies. Methodology was to re-design the epidemiological system as a transition probability matrix, using the compartments as states and transforming the transition rates of the population between compartments into probability values. The initial probabilities and limiting distribution of the resulting transition matrix were then employed to identify the priority rating of each compartment at any stage, in terms of attention that should be given to each epidemic state as part of an intervention strategy. The study provides a general form of the re-designed transition matrix for the SIR, SIS, and SEIR models of infectious disease spread, with the appropriate rates of transition from one compartment to another. An illustrative demonstration is provided in retrospect with the parameters of COVID-19 spread in Nigeria using the SIR model. This approach reduces the mathematical complexities of solving resulting differential equations and the associated simulation processes while retaining the ability to guide the course of intervention.

**Keywords:** Infectious diseases, states of the system, transition probabilities, limiting distributions.

## 1 INTRODUCTION

The modeling of infectious diseases is a tool which has been used to study the mechanisms by which diseases spread, so as to predict the future course of an outbreak, as well as to evaluate strategies put in place for its control [1]. Models are used to study the spread, design intervention, control and prevent further outbreaks and limit the devastating effect on a population [2]. Most mathematical models of diseases are hinged on a basic premise, that the population of interest can be partitioned into a set of distinct groups based on their level of experiences with respect to an infection [3]. The simplest of these models classify individuals into one of susceptible (S), infectious (I), and recovered (R), often referred to as the SIR model [4,5]. It assumes that individuals are born into the susceptible class, consisting of subjects who have never come into contact with the disease, but are capable of catching the disease, which brings them into the infectious class. Infectious individuals have the likelihood of transmitting the disease to susceptible. They also remain in the infectious class for some variable period of time

(called the infectious period), before perhaps, moving into the recovered class. Individuals in the recovered class are eventually assumed to be immune against the infection for life or enjoy temporal immunity for a while.

John Graunt was the first recorded scientist who tried to quantify the causes of death, in his work titled “Natural and Political Observations made upon the Bills of Mortality” of 1662 [1,4]. His analysis presented a weekly listing of numbers and causes of death and was considered to be the beginning of formal studies on the theory of competing risk. Daniel Bernoulli is also credited with the earliest account of mathematical modeling of spread of disease in a work carried out in 1766 which presented a mathematical model to support the practice of inoculating against smallpox [6]. The acclaimed work of McKendrick and Kermack reported in [4] is generally accepted as a milestone in the use of a simple deterministic (compartmental) model. The model was considered significant because it predicted the behaviour of outbreaks in a fashion quite similar to that observed in many subsequent records of epidemics [7]. Some recent works on modeling the spread of infectious diseases include [2,5,8,9]. It is on record that [8] incorporated what was called ‘the power law with respect to space and time’ to improve on model fit and prediction, [5] expressed the need to distinguish between the population and the contact networks of both immunizing infections and infections that do not confer immunity upon the recovered, while [9] proposed the ‘greenwood model’ of using the Markov chain to explain the SIR model.

### 1.1 Between Deterministic and Stochastic Models

In the deterministic model, any subject in the population is uniquely identified with a compartment representing a particular stage of epidemic. The size of a compartment is seen as a function of time, and the epidemic process is such that the changes in population structure of a compartment can be estimated using only historical data [7]. Deterministic models are particularly useful when dealing with cases of large populations.

A stochastic model is used to estimate likely probability distributions of potential outcomes that allows for random variations in some inputs over time [3,10]. Such models will depend on the chance variations due to risk of exposure and disease dynamics and are assumed appropriate when the fluctuations are of interest as in small populations.

The SIR class of models is an example of the deterministic, compartment model. It was initially proposed by Kermack and McKendrick over a fixed population with only three compartments [1], viz:

- a) Susceptible  $S(t)$ , the subset of the population not yet infected with the disease at time  $t$ .
- b) Infectious  $I(t)$ , which denotes the subset that have been infected, and are capable of transmitting the disease to those in the susceptible category.
- c) Recovered  $R(t)$ , which connotes those subjects that were infected, but have recovered from the disease. By assumption, those in this category cannot be infected again, and are not capable of passing the infection to another subject.

The flow of this model is assumed to be

$$S \rightarrow I \rightarrow R,$$

and with a fixed population size,  $N$ , satisfying

$$N(t) = S(t) + I(t) + R(t),$$

Kermack and McKendrick was reported by [4], under some assumptions, to have derived the following differential equations:

$$\frac{dS}{dt} = -\beta SI,$$

$$\frac{dI}{dt} = \beta SI - \gamma I,$$

and  $\frac{dR}{dt} = \gamma I$

where  $\beta$  is the infection rate of the disease on the susceptible, and  $\gamma$  represents the mean recovery rate of infected persons. Under the assumptions made, an individual in the population must be considered as having an equal probability as every other individual of contracting the disease. In its simplest form, the SIR model ignores the factors of birth and death. It is assumed that the rate of infection and recovery is much faster than the time scale of

births and deaths and therefore, these factors are ignored in this model [11]. However, the SIR model with births and deaths is a modification that allows for births and deaths of individuals in the population.

Another modification is the SIS model which is adapted from the SIR model by assuming that infected subjects recover with no immunity to the disease. That is, they are immediately susceptible once they have recovered. This eliminates the Recovered as a distinct class, resulting in the removal of the equation representing the recovered sub-population from the SIR model, and merging the population of those removed from the infected with the susceptible population.

Furthermore, the SIRS model is another modification of the SIR model that allows members of the recovered class to rejoin the susceptible class after some time, resulting in the flow:

$$S \rightarrow I \rightarrow R \rightarrow S.$$

Literature is full of Models with More Compartments. When an Exposed Latent period  $E(t)$  of an infection is put into reckoning, we encounter another class of models with four or more compartments [4,12]. The exposed latent period of an infection is a phase during which infected subjects are not regarded as infectious. Common models in this class include the SEIS, SEIR, and SEIRS models [3,10].

The SEIS model assumes that an infection does not leave a long lasting immunity. It therefore takes into reckoning the exposed latent period of infection, a phase during which the individual is said to be infected but not infectious. This leads to an additional compartment,  $E(t)$  in the SIS model and the flow becomes

$$S \rightarrow E \rightarrow I \rightarrow S$$

Individuals that have once recovered return to being susceptible again, moving back into the  $S(t)$  compartment.

The SEIR model is similarly obtained when  $E(t)$  is introduced into the SIR model, with the population defined as

$$N(t) = S(t) + E(t) + I(t) + R(t)$$

These models may further be adjusted to reflect the case where it is assumed that an individual is born with a passive immunity inherited from the mother. To express this mathematically, an additional compartment,  $M(t)$ , is added to the appropriate model to obtain the MSIR model or the MSEIR model or the MSEIRS model with their resulting flow and differential equations.

## 1.2 Covid-19 Studies

Since the outbreak of the dreaded COVID-19 in China, the global community has been on edge pacing the floor. A lot of attempts were made to predict the spread across the world to aid its mitigation. For instance, while comparing the spread pattern of COVID-19 in Italy and India, [13] observed that up to middle of April 2020 the spread was exponential, but eventually turned logarithmic by July 2020. On the other hand, in India the spread was highly nonlinear, but became nearly exponential over time. This implies that the spread around the world does not follow a single trend, and as such cannot be modelled using a single mathematical model. Thus, the virus posed a lot of unprecedented challenges especially in the under-developed and developing world with relatively under-developed socio-economic settings. In line with this, some researchers [14] studied the spread in Egypt, Algeria, Nigeria, Senegal, and Kenya. Reference [15] incorporated the relationship between socioeconomic factor and the distribution of COVID-19 into their study. The observations from [14,15] were insightful in the study of the spread. An SIR model was employed by [16] to study and predict the spread of covid-19 and the effects of mitigation efforts in India, and it was observed with early data that the spread curve was rapidly changing due to lockdown, isolation, and testing. However, it was predicted that the pandemic may last in India till the end of 2020, with the peak expected by early August 2020, and with up to 90% reduction by the end of September 2020. Another effort towards using SIR models [17] employed the logistic growth model to predict the maximum number of COVID-19 active cases and the virus peak-time, and adapted a Time Interrupted Regression model to analyse the impact of intervention measures. The study suggested that there was no significant evidence of any positive impact of lockdown in India on the reduction of new cases.

Since the first case was reported on 25th February 2020, there was an astronomical increase in the number of new cases in Brazil that made it a COVID-19 hotspot in South America. Contextualized epidemiological, clinical, and

demographic findings on COVID-19 cases for the first three months of the pandemic in Brazil was reported by [15] which identified a positive relationship between COVID-19 diagnosis and higher per-capita income. Still on Brazil, a Susceptible – Infectious – Quarantined - Recovered (SIQR) model was applied to analyse data obtained from Brazilian Department of Health [18]. The study estimated the basic reproduction number to be  $R_0 = 5.25$ , that the ratio of unidentified infectious persons to confirmed cases was 10 to 1 and also observed that the epidemic was doubling every 2.72days.

Africa's COVID-19 burden as at 7th August 2020 stood at about 1,000,054 with 21,724 deaths, with South Africa accounting for more than 53% of the cases in the continent [19]. It was then the fifth most affected country in the world and hence, the nature of the spread in this nation became of special interest to researchers. To study the spread of the disease in Africa with rapid infection growth rate and relatively under-developed socio-economic situation, [14] used the Maximum-Hasting parameter estimation method and an improved Susceptible-Exposed-Infectious-Recovered (SEIR) model to simulate and forecast the spread in South Africa, Algeria, Senegal, Kenya, Egypt and Nigeria. It was projected that the epidemic could be brought under control by the end of April 2020 if strict measures were adopted, and that while a moderate measure was not be good enough, a weak measure will extend the control to much later, and that by then, the number of infected persons would have multiplied. However, [20] observed that with limitations on the health facilities in South Africa, the use of Remdesivir vaccine could only prevent deaths by reducing the number of days a person may spend in ICU. Reference [21] investigated the place of social distancing and community lockdown as mitigation strategies for covid-19 in Nigeria and used simulations to establish necessary levels of both strategies to curtail the spread of the disease. In addition, the study observed that if there were no such interventions, the peak could be attained much faster. Hence lockdown delays the attainment of peak and provides policy makers ample planning time to effectively control the spread.

To study the dynamics of COVID-19 in Ghana, a mathematical model to consider the impact of testing and quarantining of immigrants, contact tracing and isolation as measures in the mitigation of the spread of the pandemic was developed by [22]. The simulation results agree with existing data, indicating that early quarantine measure and high quarantine rate are especially important in the control of the disease. The employment of geospatial technologies in Ghanaian COVID-19 fight was also considered by [23], who observed that the trend of the pandemic in Ghana is in tandem with population concentration, and with higher figures in the south of the country. The study further noted that incessant mobility patterns aided the spread of the disease to the middle parts and then the northern parts of the country.

The Auto – Regressive Integrated Moving Average (ARIMA) model was used by [24] to predict the outbreak of covid-19 in Morocco, and to provide information and better understanding of the epidemiology of the disease. A mathematical model was developed and analyzed by [25] to examine the impact of an imperfect vaccine on the transmission dynamics of COVID-19 disease, and to explore a relationship between vaccination rate and transmission dynamics of the disease. Findings showed that corona virus burden in terms of the cumulative number of deaths, decreased with an increasing vaccine rate. Vector Autoregressive Approach was used by [26] to model and forecast Covid-19 cases and deaths in Nigeria, and tried to show that there was limited autocorrelation and total absence of heteroscedasticity in the data. Reference [27] used the Pearson's correlation coefficient to establish a strong positive relationship between the number of deaths and detected cases of COVID-19, and obtained an estimate of the case-fatality rate that can be used to forecast deaths resulting from COVID-19.

Sequential analysis approach was used by [28] to obtain and compare some epidemiological metrics of five African countries, as well as developed measures of risk of wrong reporting. Reference [29] used human - human – surface-human model to identify the trend, compare transmission rates and predict future patterns of Covid-19 between regions of Nigeria, and adopted a subinterval method for gathering statistical data to do a state space analysis of the transition probabilities of the susceptible-infective class of Covid-19 in Nigeria. From the foregoing, it is obvious that a lot of studies have been carried out using the traditional, compartmental modelling techniques. However, this study leveraged on the randomness and intuitive transition probabilities associated with compartments to support the ordering of control steps in addressing the scourge of an infectious disease.

**2 MATERIALS AND METHODS**

This work adopted the simple notion of transition probabilities to establish the pattern of spread of a disease and to identify appropriate compartments for priority of intervention strategies. Hypothetical data were first used for illustrations. The covid 19 data used for application were obtained as secondary data from [19]. Excel Spreadsheet and MATLAB software were used for matrix computations data analysis.

**2.1 A Probabilistic Design for Deterministic, Compartmental Models**

Markov-Chain models are mathematical models used in analyzing a system which are prone to changes over a period of time, transiting among a finite number of possible states [9,30]. Such a model is designed to quantitatively describe the flow from one state to another in terms of transition probabilities associated with various states. In the same light, [31] transformed a stock market data into a 5-state Markov Chain process and adopted the stochastic features of Markov Chains models to compute limiting distributions which were utilized to compare some existing markets.

If compartments in the deterministic model are regarded as the states of the system, then, each model earlier described can be represented in terms of a transition probability matrix  $P = \{p_{ij}\}$ , where  $p_{ij}$  is interpreted to mean a probability of transition from compartment  $i$  to compartment  $j$  in one step [32,33]. Clearly,

$$p_{ij} \geq 0 \forall i, j \text{ and } \sum_j p_{ij} = 1 \quad (1)$$

The probabilities  $p_{ij}$  could be obtained through a historical analysis of the system. The initial probability vector is denoted as  $P(t_0) = (p_1, p_2, \dots, p_n) = \alpha^{(0)}$ , and it is related to the initial proportion of each compartment at time  $t_0$ . The entries of the transition probability matrix are estimated from the available parameters that define the dynamics of the disease.

Under the SIR model, there are three transitional states of the system (compartments), namely, the susceptible (state 1), the infectious (state 2), and the recovered (state 3).

Let  $p_{ij}$  be the probability of transition from state  $i$  to state  $j$  (in one step); where  $i, j = 1, 2, 3$ . The appropriate transition matrix for this model is

$$P = \begin{pmatrix} p_{11} & p_{12} & p_{13} \\ p_{21} & p_{22} & p_{23} \\ p_{31} & p_{32} & p_{33} \end{pmatrix} = \begin{bmatrix} 1 - \beta^* & \beta^* & 0 \\ 0 & 1 - \gamma^* & \gamma^* \\ 0 & 0 & 1 \end{bmatrix} \quad (2)$$

where  $\beta^*$  is the probability of transition from susceptible to the infectious class and  $\gamma^*$  the probability of transition from the infected compartment to the recovered.

And for the SIS model, the transition matrix is of order 2, since there are two distinct states: susceptible (state 1), the infectious (state 2). This matrix is expressed as

$$P = \begin{pmatrix} p_{11} & p_{12} \\ p_{21} & p_{22} \end{pmatrix} = \begin{bmatrix} 1 - \gamma^* & \gamma^* \\ \frac{s}{N} & \frac{N-s}{N} \end{bmatrix}, \quad (3)$$

where S and N represent the size of the susceptible compartment and the total population, respectively.

The SEIR model has four states, which are susceptible (state 1), exposed (state 2), the infectious (state 3), and the recovered (state 4). Its transition matrix is given by

$$P = \begin{bmatrix} p_{11} & p_{12} & p_{13} & p_{14} \\ p_{21} & p_{22} & p_{23} & p_{24} \\ p_{31} & p_{32} & p_{33} & p_{34} \\ p_{41} & p_{42} & p_{43} & p_{44} \end{bmatrix} \quad (4)$$

These transition probabilities are to be estimated from the parameters of spread of the disease. For each of these transition matrices, the limiting distribution is an indicator of how the infection will eventually stabilize over the population when there are no conscious intervention measures to check the dynamics of the disease. This limiting distribution is the theoretical stable distribution, denoted by  $\lim_{n \rightarrow \infty} P^n$  (5)

For a model consisting of n compartments, the stable probability of the model will be obtained from the limiting distribution in (5) as

$$P(t) = (\pi_1, \pi_2, \dots, \pi_n). \quad (6)$$

This stable probability will be of immense benefit in determining the process and priority point of intervention. If the largest stable probability is  $\pi_k$ , for some k, then the compartment corresponding to state k is to take priority of attention in the intervention schedules, the other states follow in decreasing order of their stable probabilities.

### 3 RESULTS

Suppose there was an outbreak of a certain infectious disease in a college community of 500 persons. At the time of first documentation, 20 persons had already recovered from the disease, while 80 still have the infection and are capable of transmitting it. It was estimated that the rate of spread was 40 new cases per week while recovery was at 20 persons per week.

It is our objective to present this scenario as a SIR or SIS model via the transition probability approach, and to advise an effective strategy for checking the spread of the disease.

#### 3.1 The SIR model approach

Under SIR model approach, we hold the assumption that the population is fixed, and that the recovered class R(t) is conferred with permanent immunity. The population equation is

$$N(t) = S(t) + I(t) + R(t),$$

with the compartment vector as  $N = (400, 80, 20)$ .

The initial probability vector is  $\alpha^{(0)} = (0.8, 0.16, 0.04)$ .

The Transition Probability matrix is

$$P = \begin{bmatrix} p_{11} & p_{12} & p_{13} \\ p_{21} & p_{22} & p_{23} \\ p_{31} & p_{32} & p_{33} \end{bmatrix}$$

$$= \begin{bmatrix} 0.9 & 0.1 & 0 \\ 0 & 0.75 & 0.25 \\ 0 & 0 & 1 \end{bmatrix} \quad (7)$$

The stationary distribution of this matrix is

$$\lim_{n \rightarrow \infty} P^n = \begin{bmatrix} 0 & 0 & 1 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{bmatrix} \quad (8)$$

This is so because the state  $R(t)$  is an absorbing state. This will become the dominant state in the long run. The best strategy towards combating the spread of the disease is the one which gives priority to this state. That strategy is to bring as many as possible to the state  $R(t)$  in the shortest possible time. Immunization will bring a weak form of the disease on recipients and then accelerated recovery, which leads to permanent immunity.

Also observe that the distribution of the disease at period  $k$  is given by

$$a^{(k)} = a^{(0)} P^k, \quad (9)$$

where  $a^{(0)}$  is the initial probability vector of the epidemic. For instance

$$\begin{aligned} a^{(4)} &= a^{(0)} P^4 \\ &= (0.5249, 0.2318, 0.2433), \end{aligned} \quad (10)$$

which shows that at the 4<sup>th</sup> week of infection, 52.5%, 23.2% and 24.3% of the population will be in the compartments  $S(t)$ ,  $I(t)$ , and  $R(t)$  respectively.

### 3.2 The SIS model approach

Under SIS, the population is also assumed to be fixed, but no immunity is conferred on the recovered class against being infected again. Hence recovered individuals become susceptible again almost immediately. Therefore, the population equation is

$$N(t) = S(t) + I(t),$$

The component vector is  $N = (420, 80)$

and the initial probability vector is

$$a^{(0)} = (0.84, 0.16).$$

The Transition Probability matrix is

$$\begin{aligned} P &= \begin{Bmatrix} p_{11} & p_{12} \\ p_{21} & p_{22} \end{Bmatrix} = \begin{bmatrix} \frac{19}{21} & \frac{2}{21} \\ \frac{1}{4} & \frac{3}{4} \end{bmatrix} \\ &= \begin{bmatrix} 0.9048 & 0.0952 \\ 0.25 & 0.75 \end{bmatrix} \end{aligned} \quad (11)$$

The stationary distribution of this matrix is

$$\lim_{n \rightarrow \infty} P^n = \begin{bmatrix} 0.7241 & 0.2759 \\ 0.7241 & 0.2759 \end{bmatrix} \quad (12)$$

Similarly, the epidemic distribution in the 4<sup>th</sup> week is

$$a^{(4)} = a^{(0)} P^4 = (0.7456, 0.2544). \quad (13)$$

The interpretation of this is that after four periods of the outbreak, 74.6% of the population will be susceptible, while 25.4% will be infected. In the long run, the stationary distribution of the epidemic will be 72.4% and 27.6% for the susceptible and the infected classes, respectively. Under this distribution the best intervention strategy is that which targets the susceptible class. That strategy will be preventive measures such as improved personal hygiene, use of face shields or masks, imposition of regulated lockdown in suspected endemic areas, isolation or quarantine of the infected individuals until they are recovered, to cut down on community transmission.

### 3.3 Application to Spread of COVID-19 in Nigeria

In this section, we shall apply the transition probability model to the spread of COVID-19 in Nigeria. The data in Table 1 was obtained from the website of [19]. It is a monthly summary of data obtained on the incidence of COVID-19 pandemic in Nigeria from April to August, 2020.

**Table 1.** Monthly summary of incidence of COVID-19 in Nigeria

Period	No of Tests	Confirmed Cases	Active Cases	Recovered Cases	Deaths
1 (April)	7153	493	317	159	17
2 (May)	138462	25694	15358	9746	590
3 (June)	279675	43151	22707	19565	879
4 (July)	317496	46577	12446	33186	945
5 (Aug)	338084	47290	12725	33609	956

Source [19]

An SIR model compartmentalization of data in Table 1 gives Table 2. The entries for April were ignored because of initial constraints experienced by NCDC in the testing ability of their laboratories.

**Table 2.** An SIR model compartmentalization of the spread of COVID-19 in Nigeria

Time	Susceptible	Infected	Recovered	Total
1 (May)	112768	15948	9746	138462
2 (June)	236524	23586	19565	279675
3 (July)	270919	13391	33186	317496
4 (Aug)	290794	13681	33609	338084
<b>Average</b>	<b>227751.25</b>	<b>16651.5</b>	<b>24026.5</b>	<b>268429.25</b>

**Table 3.** Compartmental Proportions for the Spread of COVID-19 in Nigeria

Time	Susceptible	Infected	Recovered	Total
1 (May)	0.8144	0.1152	0.0704	1.0000
2 (June)	0.8457	0.0843	0.0700	1.0000
3 (July)	0.8533	0.0422	0.1045	1.0000
4 (Aug)	0.8601	0.0405	0.0994	1.0000
<b>Average</b>	<b>0.8485</b>	<b>0.0620</b>	<b>0.0895</b>	<b>1.0000</b>

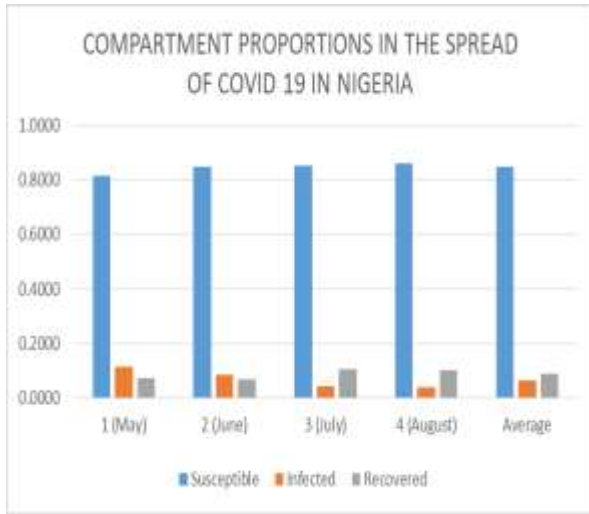


Figure 1. Compartmental proportions of COVID-19 in Nigeria

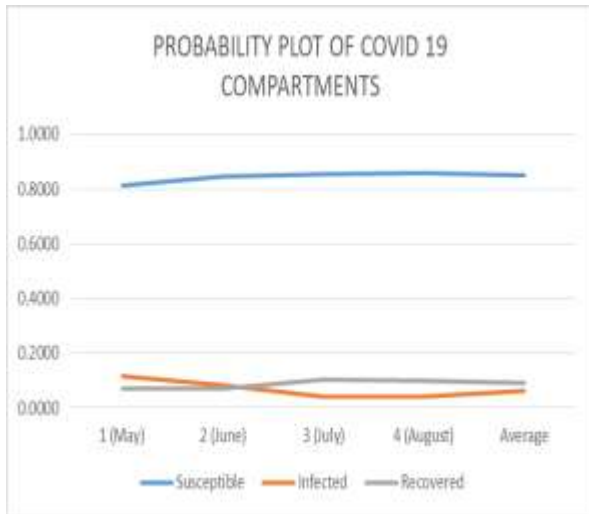


Figure 2. Probability plot of compartments

### 3.31 The Transition Matrix

Table 1 shows the raw data as extracted from the source. Table 2 is a rearrangement of Table 1 to pattern it after the SIR design, while Table 3 is a conversion of Table 2 into an intuitive probability model. Figure 1 is an illustrative graph of the relative proportion of each SIR compartment over the range of data, while Figure 2 is a probability plot of each compartment to ascertain its relative stability over the range of study.

From Table 2, the following can be deduced:

- i) For the first period, infection rate was **19.2%** of tested cases, while recovery rate was **54.6%** of confirmed infections.

- ii) For the second period, infection rate was 12.4% of tested cases, while recovery rate was 38.0% of confirmed infections.
- iii) For the third period, infection rate was 9.1% of tested cases, while recovery rate was 56.2% of confirmed infections.
- iv) For the fourth period, infection rate was 3.5% of tested cases, while recovery rate was 59.3% of confirmed infections.

Over the entire period, average infection rate was 8.3% of tested cases, while average recovery rate was 52.1% of confirmed infections. In terms of probability measures, estimates of the initial probability vector  $\alpha^{(0)}$  and the transition probability matrix  $P$  were obtained as follows:

$$\alpha^{(0)} = (0.848, 0.062, 0.090) \quad (14)$$

and

$$P = \begin{bmatrix} 0.821 & 0.179 & 0 \\ 0 & 0.409 & 0.591 \\ 0 & 0 & 1 \end{bmatrix} \quad (15)$$

The matrix (15) is valid only if a recovery from the infection confers permanent immunity. Otherwise, when no permanent immunity is guaranteed for the recovered, we have that

$$\alpha^{(0)} = (0.848, 0.062, 0.090)$$

and

$$P = \begin{bmatrix} 0.821 & 0.179 & 0 \\ 0 & 0.409 & 0.591 \\ 0.090 & 0.095 & 0.815 \end{bmatrix} \quad (16)$$

For (15) the limiting distribution of  $P$  is

$$\lim_{n \rightarrow \infty} P^n = \begin{bmatrix} 0 & 0 & 1 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{bmatrix} \quad (17)$$

In the case of (16), the limiting distribution is

$$\lim_{n \rightarrow \infty} P^n = \begin{bmatrix} 0.277 & 0.172 & 0.551 \\ 0.277 & 0.172 & 0.551 \\ 0.277 & 0.172 & 0.551 \end{bmatrix} \quad (18)$$

#### 4 DISCUSSION

The implication of (17) is that when a recovery from an infection confers permanent immunity against that infection, then in the long run, a drift towards the recovered class is imminent. The recovered compartment becomes an absorbing state in the long run. Hence, the best strategies to address the outbreak of such an infection are measures that will bring members of the community to the recovered state in the shortest possible time. This, of course, is the focus and essence of mass production and administration of effective vaccines.

The limiting distribution (18) is a case where it was assumed that it is possible for recovered individuals to be re-infected with the same disease because of limited immunity. In the limiting distribution of the COVID 19 data, the long run projection shows that about 28% of the community will be susceptible, 17% will be in active infection stage, while 55% will belong to the recovered class. The best strategy, therefore, to combat the spread of this epidemic is to give top priority to actions that will bring as many susceptible individuals as possible to the recovered class without going through active infection stage. The next priority will be to adopt measures that will protect the susceptible population from getting infected, while less priority is accorded to treatment of infected individuals.

The dynamical behaviour of an infectious disease in the long run, can be related to the limiting distribution of the transition matrix appropriate to the dynamic parameters of a disease under an assumed model. The n-step transition matrix, when computed for any n, is a predictor of the likely spread of the disease after n cycles of time. Also, the limiting distribution obtained from the transition probability matrix becomes relevant in that its knowledge will help to guide intervention measures intended to inhibit the level of devastation. The transition matrix approach has the advantage of less computational complexity, transforming what would have been some systems of differential equations to some less rigorous algebra of matrices and probability theory. The approach is also embedded with the ability to identify the compartment of priority (from the limiting distribution) in the design of control measures. The major challenge, however, is the ability to correctly transform the dynamic parameters of a disease into probability values appropriate for a transition matrix. Mathematical codes are readily available for the computation of the limiting distributions of a transition probability matrix. A vital implication of this is that it may not be necessary to instantly enforce a hundred percent attention on the population (such as total vaccination of the population) to inhibit its spread. An attention to any person in the identified compartment of priority through preventive or curative means will always imply a reasonable reduction in the risk of infection for other members of the population.

### **CONCLUSION**

Infectious disease models are tools which have been used to study the mechanisms by which diseases spread, so as to predict the future course of an outbreak, as well as to evaluate strategies put in place for its control. Models are used to study the spread, design intervention, control and prevent further outbreaks and limit the devastating effect on a population. This study has presented a novel modeling approach that eliminates the mathematical complexities associated with differential equations and other analytic concepts of classical models. The epidemiological system was re-designed as a stochastic model with transition probabilities, using the compartments as states, and transforming the transition rates between compartments into probability values. The limiting distribution of the resulting probability matrix was then analyzed and adapted as a tool to aid the assignment of intervention priorities to compartments.

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The author declares that there is no conflict of interest whatsoever.

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