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STOCHASTIC MODELING APPROACH OF INFECTIOUS DISEASE WITH SIR EPIDEMIOLOGICAL COMPARTMENT MODEL

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Abstract: The aim of this paper is to present a review on the stochastic version of the deterministic SIR (Susceptible – Infectious - Recovery) epidemiological compartment model through the branching process approximation. The stochastic process (branching process) approximation was developed using the Continuous Time Markov Chains where the time variable is continuous and the state variable is discrete. The state random variables are the compartments: S(t), I(t) and R(t). In this review two ways of estimating the state transition probability has been provided and some stochastic thresholds of the branching process (basic reproduction number, Malthusian parameter and the average number of infections produced by an infectious individual in a single generation) have also been deduced. Finally, the probability of major and minor outbreak of the branching process (epidemic process) has been presented. The theoretical methods have also been validated with some examples of numerical simulations.

Keywords: continuous time Markov chains; branching process; maximum likelihood estimation; SIR model.

2010 AMS Subject Classification: 60J25, 93A30.

1. INTRODUCTION

Models employed to study the transmission of communicable diseases are termed dynamic epidemiological models since they study the performance of infectious disease over time. The

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huge spread of communicable diseases in living organisms has increased the need for mathematical epidemiology research in the world by building models to help foretell the spread of communicable disease for development of strategies to help prevent their occurrence. These models can be either deterministic or stochastic depending on the assumptions made during the development of the model.

Using deterministic models in studying the epidemiology of communicable disease has a very long history. These models have been utilized enormously in studying communicable diseases like: influenza, chicken pox, measles and many more in various contexts [1]. The accuracy of these models developed determines the variability and reliability of the remedies suggested to curb the disease [2]. Stochastic model on the other hand is a model that estimates the likelihood distributions of possible outcomes by permitting random variation in one or more input over time. This model relies on variation in risk exposure, other diseases as well as the disease itself. The model is often employed when random change remains significant [3, 4].

In deterministic modeling it is presumed that every individual contacts every other individual at the same rate which maybe false for an infectious disease because the time for exposure maybe different. It is against this backdrop that the deployment of stochastic model is particularly relevant. It is revealed that the deterministic mathematical model has certain challenges or drawbacks for which the stochastic model seeks to address but in all stochastic models average outcome of the deterministic mathematical model [5, 6].

In this study, the focus is on the development of stochastic version of the SIR compartment model with demographic characteristics using branching process approximation for an epidemic through markovian property and the development of some thresholds such as the Malthusian parameter (intrinsic growth rate of the branching process), the average number of infection produce by an infectious individual in a single generation and basic reproduction number. Also two methods for determining the state transition probabilities will be deduced. The branching process conjecture will also be used to deduce the likelihood of epidemic disappearance even at the beginning of the study.

2. Deterministic SIR Epidemic Model

In this section we introduce the deterministic mathematical model formation of the SIR models with demographic characteristics as an extension of the model in [7] and a reduced form of the model in [8, 9]. The assumption of constant population size is made (demography: birth rate (λ) equal to death rate (μ)). The model is formulated by dividing the host population into three classes: Susceptible (S), Infectious (I) and Recovery (R). Mathematically: N = S+I+R. Figure 1 presents the flow chart diagram of the SIR compartment model.

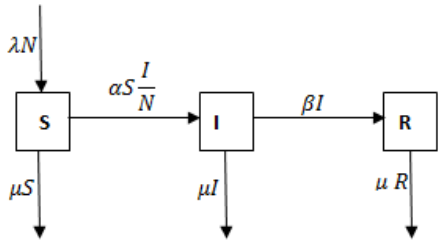

FIGURE 1. Flow chart of the SIR model

Where λ = birth rate, μ = death rate, α = infection rate, and β = recovery rate of the infectious individual. The above stated assumptions together with Figure 1 lead to the following system of ordinary differential equations to indicate the rate of change from one class to the other.

$$\begin{aligned} \frac{dS}{dt} &= \lambda N - \mu S - \alpha S \frac{1}{N} \\ \frac{dI}{dt} &= \alpha S \frac{1}{N} - (\beta + \mu) I \\ \frac{dR}{dt} &= \beta I - \mu R \end{aligned} \tag{1}$$

From equation 1 the basic reproduction number is mostly deduced using the next generation matrix. The original nonlinear system of ODEs including these compartments can be written as spectral radius of HK^{-1} where H = matrix of infection rates and K^{-1} = the inverse of matrix of transition rates as presented in [8-13]. According to Mettle and his group, Affi, Odo and Heesterbek and many more mathematical epidemiological studies: when the basic reproduction

number $R_0 > 1$ then the endemic equilibrium point is stable which means the infection will persist in the population but when $R_0 \leq 1$, the disease free equilibrium point will be stable which means the infection will die out in the long run [3-17]. These theorems have been proven deterministically in the respective studies above.

3. STOCHASTIC SIR EPIDEMIC MODEL

This section is where the focus of the paper is presented; that is deriving the stochastic version of the deterministic SIR compartment epidemic model with demographic characteristics. The stochastic version of the model presented in equation (1) is derived using Continuous Time Markov Chains. This model takes into account the random effect of birth and death processes. In this Continuous Time Markov Chain the time variable is continuous $s \in [0,t)$ but the state variable is discrete. The discrete random variables S(t), I(t) and R(t) represent Susceptible, Infectious and Recovered individuals respectively. $S(t), I(t), R(t) \in 0,1,2,\cdots,k$ where k is the maximum population size. Initially when $t = 0$ the host population is made up of n susceptible individuals and infection is introduced by infecting one individual, the infected individual stay in the infectious class for an exponential time with rate β unless he or she dies out. But after this period the individuals from the infectious class recovers to attain permanent immunity to remain in the recovery/remove class unless he or she dies. During the infectious period the infective has infectious contact randomly in time according to homogeneous Poisson process with rate α, each time with a uniformly selected random individual. The contacted individual if susceptible moves to the infectious class else the contact has no influence. For the CTMC stochastic model the transition from one state to a new state occurs at any time and the transition probabilities and population component are presented in Table 1.

3.1. Alternative Method for State Transition Probabilities Estimation.

Suppose the discrete states: Susceptible (State 0), Infected (State 1) and Removed/Recovery (State 2). Let$(X_i, i = 0,1,2)$ represent the number of individuals at any state from the underlying epidemics at any time t. Clearly, X_i is a stochastic process with states 0, 1 and 2. Thus, the First-Order Time Markov dependency can statistically be modeled as;

Table 1: State transitions and rates of the CTMC SIR model

Event	Population Component at t	Population Component at △t+t	Transition probabilities
Birth	(S,I,R)	$(S+1,I,R)$	$\lambda\triangle$t
Susceptible death	(S,I,R)	$(S-1,I,R)$	$\mu S\triangle$t
Susceptible Infection	(S,I,R)	$(S-1,I+1,R)$	$\alpha S\frac{I}{N}\triangle$t
Death of infectious	(S,I,R)	$(S,I-1,R)$	$\mu I\triangle$t
Recovery	(S,I,R)	$(S,I-1,R+1)$	$\beta I\triangle$t
Death of recovered	(S,I,R)	$(S,I,R-1)$	$\mu R\triangle$t

$$P(X_n = i_n | X_{n-1} = i_{n-1}, ..., X_1 = i_1, X_0 = i_0)$$

$$P(X_n = i_n | X_{n-1} = i_{n-1}) \tag{2}$$

Then, the transition probability P_{ij} for $i, j = 0, 1, 2$ is denoted in matrix form as;

$$P = \begin{bmatrix} P_{00} & P_{01} & P_{02} \\ P_{10} & P_{11} & P_{12} \\ 0 & 0 & 1 \end{bmatrix}$$

Where, $\sum_{i=0}^{2} P_{ij} = 1, i = 0, 1, 2$

The susceptible state (S): is made up of individuals who are prone but not yet victims of the epidemic. The infectious state (I): is made up of infected individuals and carriers of the infection. The remove/recovered state (R): is made up of individuals who either died from the disease or found to be immune after recovery in the course of the study period. Also the components of the transition probability matrix represent the following: P_{00}: Probability of remaining in a susceptible state, P_{01}: transition Probability from susceptible state to infectious state, P_{02}: transition probability from susceptible to a removed state, P_{10}: transition probability from infectious state to susceptible state, P_{11}: Probability of remaining in an infectious state, P_{12}: transition probability from an infectious state to a removed state and P_{22}: Probability of remaining in a removed state. $P_{01}$is mostly referred to in literature as discrete time force of infection. P_{02} and P_{12} signify mortality for uninfected and infected individuals, respectively, while P_{10} is the recovery or defection probability (Cohen, 1973). The removed state is an

absorbing state since the probability of becoming susceptible or infected is zero. Below are the assumptions made for the alternative method for State transition probabilities estimation:

- The current state of an individual is dependent only on the state of the individuals at the previous time step.
- No individual at the removed state can be susceptible or infected.
- Transitioning probabilities are independent of time and remain constant over time or the study period.
- Successive transitions or relapse, confirmed co-infections of the diseases or other medical complications were not taken into consideration.
- The removed state comprised of subjects who either died of the infection or found to be immune after recovery.
- The only assumption required regarding losses and withdrawals is that they have the same future experience as those remaining under observation.

3.1.1. *Estimating the Transition Probabilities.* With this alternative method of transition probability estimation, the maximum likelihood estimation (MLE) approach is employed to estimate the transition probabilities. Table 2 shows the number of individuals during the study period at any state (S, I, R) for the infection.

Table 2: Number of individuals at any state

Class	Susceptible	Infected	Recovery/Remove
Susceptible individuals	X_{00}	X_{01}	X_{02}
Infected individuals	X_{10}	X_{11}	X_{12}

X_{00}: Number of susceptible individuals who remained susceptible at the end of study period, X_{01}: Number of susceptible individuals who became infected at the end of study period, X_{02}: Number of susceptible individuals who either died or remained immune after recovery at the end of the study period, X_{10}: Number of infected individuals who recovered at the end of the study period, X_{11}: Number of infected individuals who remained infected at the end of the study period and X_{12}: Number of infected individuals who remained immune after recovery at the end of the study period.

3.1.2. *Distribution of Transitions.* The number of individuals in each transition state follows a binomial distribution. This is because, there are fixed number of subjects in each state at the end of the study period; where the disease outcome of an individual is independent of the other within each state. Also, each person is subjected to two mutually exclusive outcomes (either to remain or leave that state); with a constant probability P_{ij}. Thus, the transition events are independent of one another (as defined by the Markov principle). The likelihood of the transition probability P_{ij} follows a binomial distribution as in equation (3):

$$L(P_{ij} \setminus N, x) = \binom{N_{ij}}{x_{ij}} P_{ij}^{x_{ij}} (1 - P_{ij})^{N_{ij} - x_{ij}} \tag{3}$$

Where N_{ij} is the number of observed transition that starts from state i to j and

$$\sum_j P_{ij} = 1$$

3.1.3. *Maximum Likelihood estimation.* The maximum likelihood estimation (MLE) is a method which estimates the parameters of a statistical model given the observations, by finding the parameter values that maximize the likelihood function of making the observations given the parameters. Anderson and Goodman proved that the estimator obtained from equation (3) is a maximum-likelihood estimator of the transition probabilities [19]. Other researchers proposed that the MLE in a way assumes a uniform prior distribution of the underlying parameters. Thus, ML estimator is known to coincide with the most probable Bayesian estimator given a uniform prior distribution on the parameters. The maximum likelihood estimate of the transition probability is given as;

$$\hat{P}_{ij} = \frac{x_{ij}}{\sum x_{ij}} \tag{4}$$

for $i = 0, 1$ and $j = 0, 1, 2$; with standard errors from the sampling distribution of the ML estimate given as:

$$SE(\hat{P}_{ij}) = \sqrt{\frac{\hat{P}_{ij}(1 - \hat{P}_{ij})}{N_i}} \tag{5}$$

3.2. Branching Process Approximation of the SIR Model. We employed the single-type Galton-Watson branching process in the approximation. The single – type was used because the individuals are of the same kind. This type of branching process is a Continuous Time Markov Chain process as described in section 3. It is a Markov chain because of the fact that it makes use of the Markov property where the population size at generation n+1 depends on only the population size at generation n.

At the initial stage of the epidemic the infection rate is small. The infectious class at any time I(t) is fed with a rate $\frac{\alpha I(t)S(t)}{N(t)}$ and is being reduced by the rate $(\beta+\mu)I(t)$. At the initial stage the host population $N(t)$ is almost the same as the susceptible population $S(t)$, implying that the ratio of the two is approximately one $(\frac{S(t)}{N(t)} \simeq 1)$. Hence the infectious class turns to be increased by the rate $\alpha I(t)$ instead of $\frac{\alpha I(t)S(t)}{N(t)}$. We let $I_n(t)$ be the number of infected individual at time t. From the above relation $I_n(t)$ can be approximated by the branching process according to theorem 1.

Theorem 1: if $I_n(t)$ is epidemic process and $I_\infty(t)$ be the branching process then $I_n(t)$ converges weakly to $I_\infty(t)$ that is $I_n \Rightarrow I_\infty, n \to \infty$ on any finite interval $[0,t_1]$.

For proof of Theorem 1 see ([11], page 54). This approximation is possible due to the fact that when I hits zero it stays in the state zero. This means I has reached the absorbing state and the disease transmission stops, that is $I(t) \to 0$ as $t \to \infty$ [20]. The approximation of the stochastic SIR process is near the disease – free equilibrium where there is no disease in the system. This is so because when the initial infectious are few the branching process will either grow exponentially or hit zero. The branching process is a birth and death process for the infectious I where αI is the infection rate (birth) and βI is the recovery rate (death).The approximation was possible based on the following assumption:

- The susceptible population is sufficiently large
- Every infectious individual has the same chance of recovery and same chance of transferring an infection
- Every infectious individual lives independent from other infectious individuals

3.2.1. *Computation of the stochastic Thresholds of the SIR model.* In this subsection we deduced the thresholds R_0 (basic reproduction number), ρ(Malthusian parameter) and $f^{|}(1)$ (the average number of infections produced by an infectious individual in a single generation) for the branching process I_∞. These thresholds are used in making decisive decision so far as the spread of an epidemic is concern.

Malthusian parameter: is the intrinsic exponential growth rate of the epidemic branching process (I_∞). We denote it by ρ hence:

$$\int_0^\infty e^{-\rho t} g(t)dt = 1 \tag{6}$$

Where $g(t)$ is the average rate at which an individual gives birth (infectious contact) at time t [21]. In the SIR model, the contact rate during the infectious period is α. Hence it follows that:

$$g(t) = \alpha e^{-\mu t} \int_0^t e^{-\beta(t-s)} ds \Rightarrow g(t) = \alpha e^{-(\mu+\beta)t} \int_0^t e^{\beta s} ds$$

Integrating $g(t)$ with respect to s and applying the limit gives

$$g(t) = \begin{cases} \frac{\alpha}{\beta}(e^{-\mu t} - e^{-(\beta+\mu)t}), if \alpha \neq \beta \\ e^{-\mu t} - e^{-(\beta+\mu)t}, if \alpha = \beta \end{cases}$$

Substituting $g(t)$ obtained above into (6) and solving for the value of ρ gives:

$$\rho = \begin{cases} \alpha - (\mu+\beta), \quad if \quad \alpha \neq \beta \\ \alpha - \mu, \quad if \quad \alpha = \beta \end{cases}$$

By considering a situation where $\alpha \neq \beta$, we have $\rho = \alpha - (\mu + \beta)$

Basic reproduction number(R_0): is the mean number of secondary infections produced by one infective individual in a completely susceptible population at the disease – free equilibrium point [3-10]. This is the most important threshold used to predict the spread of an epidemic and the other two thresholds as supporting thresholds. At this subsection we deduced the basic reproduction using the branching process approximation. We denote X to be the number of infectious contact that an individual has during the infection period. Hence,

$$P(X=0)=\frac{\beta+\mu}{\alpha+\beta+\mu} \tag{7}$$

Which follows a zero - modified geometric distribution and for all positive integer r we have:

$$P(X=r)=(\frac{r}{\alpha+\beta+\mu})^r\frac{\beta+\mu}{\alpha+\beta+\mu} \tag{8}$$

If the number of infectious contact before a secondary infection is produced follows a geometric distribution then it has a parameter $A=\frac{\beta+\mu}{\alpha+\beta+\mu}$ [21, 23]. Then the expectation of X having a zero modified geometric distribution is:

$$E(X)=\frac{1-A}{A}=\left\{\frac{1-\frac{\beta+\mu}{\alpha+\beta+\mu}}{\frac{\beta+\mu}{\alpha+\beta+\mu}}\right\}$$

$$E(X)=\left\{\frac{\frac{\alpha+\beta+\mu-(\beta+\mu)}{\alpha+\beta+\mu}}{\frac{\beta+\mu}{\alpha+\beta+\mu}}\right\}$$

$$\Rightarrow E(X)=\frac{\alpha}{\alpha+\beta+\mu}\frac{\alpha+\beta+\mu}{\beta+\mu}$$

Hence:

$$R_0=E(X)=\frac{\alpha}{(\beta+\mu)} \tag{9}$$

The average number of infections produced by an infectious individual in a single generation $[f^{|}(1)]$***:***

We assumed geometric offspring probability generating function [22].

$$f(z)=\sum_{r=0}^{\infty}P(X=r)z^r, z\in[0,1] \tag{10}$$

Where $P(X=r)$ is the probability that an individual will infect r new individuals of the same type. Expanding equation (10) results in:

$$f(z)=\frac{\beta+\mu}{\alpha+\beta+\mu}+\frac{\alpha}{\alpha+\beta+\mu}z^2, z\in[0,1] \tag{11}$$

Differentiating the offspring probability generating function in equation (11) and evaluating the derivative obtained at 1(one) gives$[f^{|}(1)] = \dfrac{2\alpha}{\alpha+\beta+\mu}$

3.2.2. *Relationship between these Thresholds.* We consider the instances where the intrinsic growth rate of the epidemic is greater than zero and the average number of offspring produced by an infectious individual in a single generation greater than one. That is:

$$\rho > 0 \Rightarrow \alpha - (\mu+\beta) > 0$$

then

$$\alpha > \mu+\beta$$

Dividing both sides of the inequality above by $\mu+\beta$

$$\Rightarrow \frac{\alpha}{\mu+\beta} > \frac{\mu+\beta}{\mu+\beta} \Rightarrow R_0 > 1$$

Also if

$$[f^{|}(1)] = \frac{2\alpha}{\alpha+\beta+\mu} > 1 \Rightarrow 2\alpha > \alpha+\beta+\mu$$
$$2\alpha - \alpha > \beta+\mu \Rightarrow \alpha > \mu+\beta$$

Dividing both sides of the inequality above by $\mu+\beta$

$$\Rightarrow \frac{\alpha}{\mu+\beta} > \frac{\mu+\beta}{\mu+\beta} \Rightarrow R_0 > 1$$

Hence $\rho > 0$ only if $R_0 > 1$ and $f^{|}(1) > 1$ only when $R_0 > 1$.

3.2.3. *Probability of Epidemic Extinction.* In this section we derive the probability of extinction using the branching process approximation. The probabilities of extinction of the epidemic when started with one infectious individual will be derived. We will also derive the probability of extinction of the epidemic when it starts with n infectious individuals. To derive this we assumed geometric offspring probability generating function in equation (10) [3, 22]. From equation (11), $\dfrac{\mu+\beta}{\mu+\alpha+\beta}$ term is the chance that an individual recovers or die and $\dfrac{\alpha}{\mu+\alpha+\beta}$ which is the coefficient of the second term in (11) represent the probability that an infectious individual infects another individual. The index of z represents the number of infectious individual generated from one infectious individual. z^0 means the individual recovers or die out hence no new infectious are generated and z^2 also means the infection is transferred to another

individual and hence there are now two individuals infectious. This offspring probability generating function is different from the discrete-time branching process where the parent will die and the child represents the parent in the next generation. The difference is due to the fact that the time interval is small and also the continuous - time process upon which this stochastic process is built, the infectious individual that infect another individual is still counted as infectious hence the number of infectious individual are two. To derive the probability for extinction we solved for the roots of the relation $f(z) = z \in [0,1]$ where $f(z)$ is given in equation (10) and its expansion in equation (11), hence:

$$\frac{\beta+\mu}{\alpha+\beta+\mu} + \frac{\alpha}{\alpha+\beta+\mu}z^2 = z$$

$$\frac{\alpha}{\alpha+\beta+\mu}z^2 - z + \frac{\beta+\mu}{\alpha+\beta+\mu} = 0 \tag{12}$$

Simplifying by multiplying equation (12) by $\alpha+\beta+\mu$ gives:

$$\alpha z^2 - (\alpha+\beta+\mu)z + (\beta+\mu) = 0 \tag{13}$$

Factorizing the quadratic equation (13) for the values of z gives the probabilities of minor outbreak whose stability is condition on the value of R_0.

$$(\alpha z^2 - \alpha z) - \{(\beta+\mu)z + (\beta+\mu)\} = 0$$

$$\{\alpha z - (\beta+\mu)\}\{z-1\} = 0 \Rightarrow z = \frac{\beta+\mu}{\alpha} = \frac{1}{R_0} \quad and \quad z = 1$$

This yields the two points:

$$p(minor \quad outbreak) = P_0 = \begin{cases} 1 & if \quad R_0 \leq 1 \\ \frac{1}{R_0} & if \quad R_0 > 1 \end{cases}$$

$$p(major \quad outbreak) = 1 - P_0 = \begin{cases} 0 & if \quad R_0 \leq 1 \\ 1 - \frac{1}{R_0} & if \quad R_0 > 1 \end{cases}$$

We also present the probability of both major and minor outbreak when the system starts with q infectious individual.

$$p(minor \quad outbreak) = P_0 = \begin{cases} 1 & if \quad R_0 \leq 1 \\ (\frac{1}{R_0})^q & if \quad R_0 > 1 \end{cases}$$

$$p(major \quad outbreak) = 1 - P_0 = \begin{cases} 0 & if \quad R_0 \leq 1 \\ 1 - (\frac{1}{R_0})^q & if \quad R_0 > 1 \end{cases}$$

4. Numerical Simulations

In this section we present some numerical simulations to validate the theoretical results presented above. We give some examples of stochastic simulations of epidemics starting with three infectious individuals and 500 susceptible individuals. We employed EpiModel package in R statistical software with 1000 simulations over 50 time point to study the dynamics of some scenarios. We also present the compartment size plot of the simulations at the end of the study period. The simulations are presented in two scenarios with the following parameters:

Scenario 1: $\lambda = \beta = 0.007$, $\alpha = 0.2$, $\beta = 0.005$, then $R_0 = 16.667$, $\rho = 0.188$, $f^{|}(1) = 1.887$, probability of minor outbreak $(P) = 0.0002$ and major outbreak $(1-P) = 0.9998$. Fig 2 and Fig 3 display the infection dynamics and compartment size plot at the end of the study respectively.

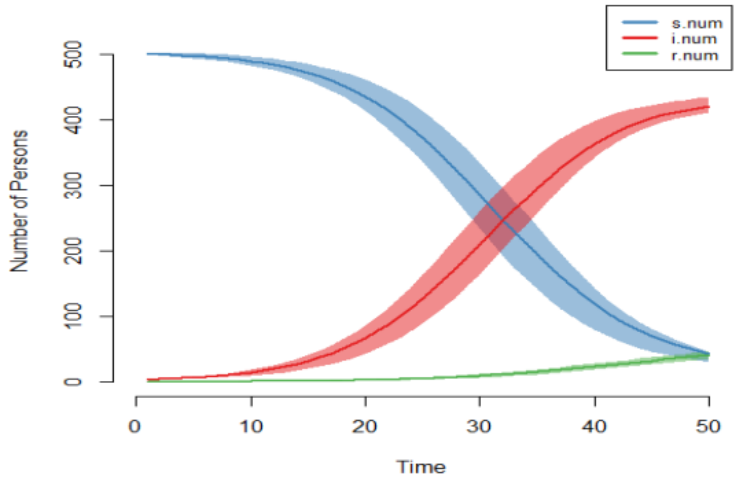

FIGURE 2

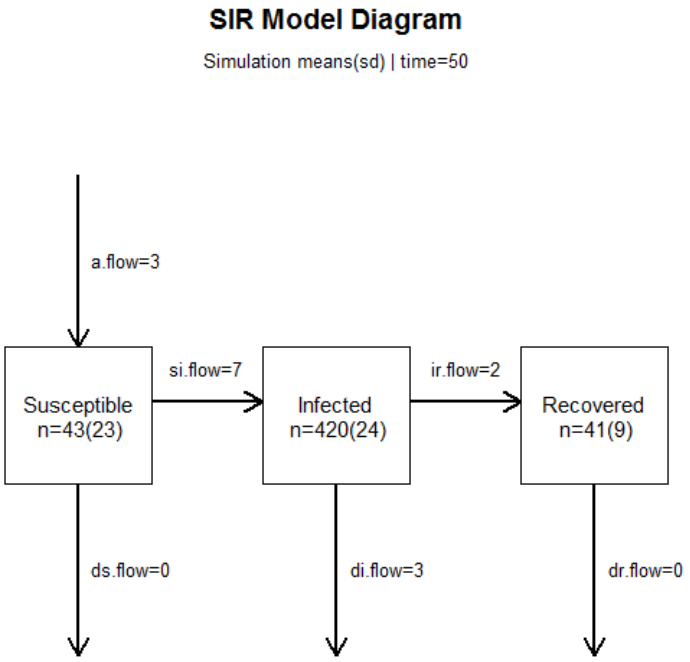

FIGURE 3

Scenario 2: $\lambda = \beta = 0.007$, $\alpha = 0.2$, $\beta = 0.5$, then $R_0 = 0.394$, $\rho = -0.307$, $f^{|}(1) = 0.566$, probability of minor outbreak $(P) = 1.000$ and major outbreak $(1-P) = 0.000$. Fig 4 and Fig 5 display the infection dynamics and compartment size plot at the end of the study respectively.

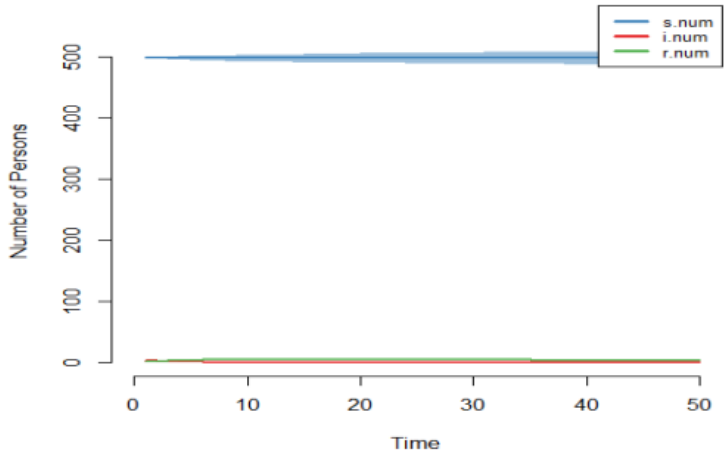

FIGURE 4

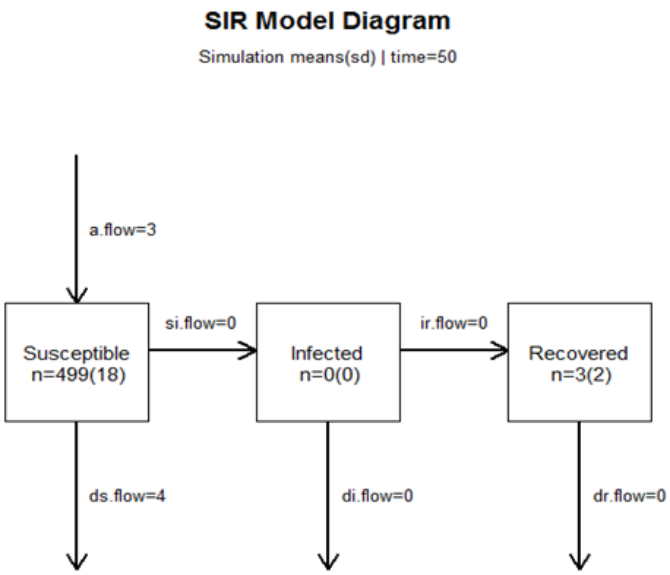

FIGURE 5

The two scenarios of numerical simulations presented above to validate the theoretical results depict two possible equilibrium points of the SIR model (endemic and disease free). Thus for the first scenario the basic reproduction number was greater than one ($R_O > 1$) hence endemic equilibrium point is stable. This was confirmed by the other derived thresholds: $\rho = 0.188 > 0$, $f^{|}(1) = 1.887 > 1$ and a probability of a major outbreak $(P) = 0.9998$. This outcome is consistent with that of Obuasi Municipal when tuberculosis was modeled in Ashanti region of Ghana [3]. In scenario two the basic reproduction number was in contrast to that of the first scenario that is $R_O < 1$ as a result disease free equilibrium point is stable(meaning the infection will not persist in the population but die out) and was confirmed by the other stochastic thresholds. This was also in line with a study by Affi [9]. Also from Fig3 we present Table 3 to reflect Table 2 so as to validate the alternative theory deduced for the transition probabilities. This was done for only scenario one.

Table 3: Number of individuals at any state of scenario one at the end of the study period

Class	Total	Susceptible State	Infected State	Recovery/Remove
Susceptible individuals	503	43	420	40
Infected individual	420	19	326	75

From the maximum likelihood method derived in equation (4) the transition probabilities for scenario one are presented below. Table 4 displays the transition probabilities estimates and their corresponding standard error.

Table 4: ML-estimates of transition probabilities for scenario one

Parameters	Estimate	S.E
P_{00}	0.09	0.0413
P_{01}	0.83	0.0183
P_{02}	0.08	0.0429
P_{10}	0.04	0.0450
P_{11}	0.78	0.0229
P_{12}	0.18	0.0444

Hence, it can be concluded from the above estimates that the transition probability matrices for scenario one is presented as;

$$P_{scenario1} = \begin{array}{c} \\ 0 \\ 1 \\ 2 \end{array} \begin{array}{c} \begin{array}{ccc} 0 & 1 & 2 \end{array} \\ \begin{pmatrix} 0.09 & 0.83 & 0.08 \\ 0.04 & 0.78 & 0.18 \\ 0 & 0 & 1 \end{pmatrix} \end{array}$$

5. CONCLUSION

We have shown that the stochastic SIR model equivalent of the deterministic SIR is developed using the Continuous Time Markov Chains. Two ways of estimating the state transition probability have been deduced. Unlike the deterministic model where the next generation matrix is very popular in deriving the basic reproduction number, this paper revealed that basic reproduction number also can be deduced together with some stochastic thresholds such as the Malthusian parameter, the average number of infections produced by an infectious individual in a single generation, the probability of major outbreak and minor outbreak (extinction probability) through the branching process approximation. Finally all the theoretical results obtained have been validated through numerical simulations.

CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

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