Chapter 4

Quasi-Stationary Distribution of Recurrent Epidemic Model with Initial Preventive Measures

4.1 Introduction

In the previous chapter, the transient state distribution for the stochastic version of recurrent epidemic model with initial preventive measures has been derived. For the deterministic version of the same model, stability of the system has been discussed near the equilibrium points. Now in this chapter, we will make an attempt to derive quasi-stationary distribution and diffusion approximation of the same model.

The quasi-stationary distribution or conditional limiting distribution has proved to be a potential tool in describing the properties of Markov population processes such as recurrent epidemic model. Bartlett (See, [19, 105]) was the first to use the term
quasi-stationarity while discussing the recurrent epidemic model. Later Darroch and Seneta [106] gave a theoretical framework on quasi-stationary distributions for continuous time Markov Chain with finite state space. However, more precisely, the term Quasi-stationary was first used by Kryscio and Lefevre [107] in their study on stochastic logistic epidemic model described as SIS model. In this model, an individual who recovers from an infection and is assumed to be susceptible for reinfection. The same model has been analyzed further by Nasell [108] by extending the results of Kryscio and Lefevre [107] and studied the asymptotic behavior of the epidemic. Such approximations are conceptually useful in a search for qualitative features of the stochastic epidemic models. Further, approximations of the quasi-stationary distributions are also important, since explicit solutions for SIS model is not available.

The concept of approximating quasi-stationary distribution in Markov population processes using diffusion approximation about the deterministic path was first introduced by Barbour [109]. He proved that this approximation alone may not help, however, it answers to all possible questions related to the process. Many processes have different phases, for example near boundaries, where a different approximation is required; are better described by a succession of diffusion and special approximations alternatively. In different approaches of epidemic modelling, many authors have discussed the application of quasi-stationary distribution and diffusion approximations. For example, Nasell [25] derived an approximation for quasi-stationary distribution and an expected time to extinction for a stochastic model for recurrent epidemics. Ngwa [104] obtained the numerical solution for the diffusion approximation of the dynamics of epidemic malaria in a growing population. A bibliography of literature on quasi-stationary distribution may be obtained from the website www.maths.uq.edu.au/ pkp/papers/qsds/qsds.html
Pollett [110]. The theoretical work by Darroch and Seneta and applied work by Pielou [111], Nisbet-Gurney [112] and Renshaw [113] appears to be independent in their approach, unable to make any comparative study. However the work of Nasell is seen to be remarkable in this area of epidemic modelling. More discussion on recent theoretical work on quasi-stationary distribution in this context can be obtained from Kijima [114].

In fact, the epidemic model in this chapter is the modification of the recurrent epidemic model [25] by introducing preventive measures, hence we obtained different results following same method (See, Nasell [25]) of analysis.

The rest of the Chapter is organized as follows: Section 4.2 deals with the stochastic model formulation. In Section 4.3 we briefly outline the derivation of the Basic Reproduction Number, for the deterministic version of the model. Section 4.4 deals with the possible insights into the derivation of quasi-stationary distribution. In Section 4.5 we derive, the distribution of the time to extinction. The diffusion approximation for the process is presented in Section 4.6. Approximations for the quasi-stationary distribution and time to extinction are derived in Section 4.7 and concluded the Chapter with some concluding remarks in Section 4.8.

4.2 Model formulation

For convenience, we restate the stochastic model defined in Section 3.3, of Chapter 3. Let us consider three state variables, namely, the number of susceptible individuals $S(t)$, the number of infected individuals $I(t)$ and the immunized individuals $V(t)$ at time $t$. Let at the initial time $t_0$, the total number of individuals in the population is denoted by $N$, then the number of removals at time $t$, is denoted by $R(t) = N - S(t) - I(t) - V(t)$.  

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Table 4.1: Hypothesized transition rates for the stochastic model of the recurrent epidemic model with initial preventive measures.

<table>
<thead>
<tr>
<th>Events</th>
<th>Transition</th>
<th>Transition Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Recruitment of susceptible individual</td>
<td>$(s, i, v) \rightarrow (s + 1, i, v)$</td>
<td>$\mu$</td>
</tr>
<tr>
<td>Infection of susceptible individual</td>
<td>$(s, i, v) \rightarrow (s - 1, i + 1, v)$</td>
<td>$\beta s i$</td>
</tr>
<tr>
<td>Immunization of susceptible individual</td>
<td>$(s, i, v) \rightarrow (s + 1, i, v)$</td>
<td>$\alpha s$</td>
</tr>
<tr>
<td>Natural death of a susceptible individual</td>
<td>$(s, i, v) \rightarrow (s - 1, i, v)$</td>
<td>$\lambda s$</td>
</tr>
<tr>
<td>Recovery of an infected individual</td>
<td>$(s, i, v) \rightarrow (s, i - 1, v)$</td>
<td>$\gamma i$</td>
</tr>
<tr>
<td>Natural death of an infected individual</td>
<td>$(s, i, v) \rightarrow (s, i - 1, v)$</td>
<td>$\lambda i$</td>
</tr>
<tr>
<td>Natural death of an immunized individual</td>
<td>$(s, i, v) \rightarrow (s, i, v - 1)$</td>
<td>$\lambda v$</td>
</tr>
</tbody>
</table>

Define,

$$P_{s, i, v} (t) = \begin{cases} \Pr \{ S (t) = s, I (t) = i, V (t) = v \}, & \text{for } (s, i, v) \in D; \\ 0, & \text{for } (s, i, v) \notin D. \end{cases} \quad (4.1)$$

be the joint distribution of $S (t)$, $I (t)$ and $V (t)$ at time $t$, where

$$D = \{(s, i, v) \in \mathbb{R}_+^3 : 0 \leq s \leq \infty, 0 \leq i \geq \infty, 0 \leq v \leq \infty \} \quad (4.2)$$

be the state space.

We make use of Markov property, which states that the probability distribution at some future date given the present state is independent of the past. The resulting multivariate stochastic process, with discrete state space and continuous parametric space, accounting in five events: birth of a susceptible by an indigenous susceptible or an immigrant susceptible or infective and recovery of an infective. When these are examined closely, we obtain several elementary events whose combined effects constitute the overall dynamics of the system, are summarized in Table 4.1.
Let parameters $\mu, \beta, \gamma$ and $\lambda$ respectively denote, the rate of recruitment of susceptible, the contact rate, the immunization (vaccination) rate, the recovery rate and the natural death rate per individual (who can be susceptible, infected or immunized individual). All parameters are assumed to be strictly positive.

Then the Kolmogorov forward differential difference equations, accounting the change in the state of the process in an infinitesimal length of time interval is given by

$$p_{s,i,v}(t) = \mu p_{s-1,i,v}(t) + \lambda (s + 1) p_{s+1,i,v}(t) + \beta (s + 1) (i - 1) p_{s+1,i-1,v}(t)$$
$$+ \alpha (s + 1) p_{s+1,i,v-1}(t) + (\gamma + \lambda) (i + 1) p_{s,i+1,v}(t) + \lambda (v + 1) p_{s,i,v+1}(t)$$
$$- \{\mu + \lambda s + \beta s i + \alpha s + (\gamma + \lambda) i + \lambda v\} p_{s,i,v}(t), \text{ for } (s,i,v) \in D \tag{4.3}$$

All the states $(s,0,v) \in D$ communicate with each other, but not with any state $(s,i,v) \in D$ for $i \geq 1$. Thus the states $(s,0,v)$ are absorbing states and all other states $(s,i,v), i \geq 1$, are transient. Since, we are interested in studying the behaviour of the epidemic within the set of transient states using quasi-stationary distribution, and without loss of generality we shall consider the transient state space $\mathcal{Q}$ defined by,

$$\mathcal{Q} = \{(s,i,v) : 0 \leq s \leq \infty, 1 \leq i \leq \infty, 0 \leq v \leq \infty\} \tag{4.4}$$

Further, the derivation of quasi-stationary distribution needs re-parametrization, obtained from the deterministic approximation of the above stochastic model, discussed in the next section.
4.3 The deterministic model and re-parameterization

The deterministic approximation of the above stochastic model can be expressed by the following system of equations (for more details See, Section 3.3 of Chapter 3):

\[
S'(t) = \mu - \beta S(t)I(t) - (\alpha + \lambda)S(t) \\
I'(t) = \beta S(t)I(t) - (\gamma + \lambda)I(t) \\
V'(t) = \alpha S(t) - \lambda V(t)
\]

(4.5)

The threshold parameter also known as Basic Reproduction Number (BRN), \( R_\alpha \), is given by,

\[
R_\alpha = \frac{\mu \beta}{(\alpha + \lambda)(\gamma + \lambda)}
\]

This value is smaller than the corresponding value derived by Nasell [25] for a recurrent epidemic model without immunization, hence the rate of spread of epidemic is rather slow in the present case.

The above system of differential equations in 4.5 has two equilibrium points. The first one is called infection free equilibrium point given by \( (\frac{\mu}{\alpha+\lambda}, 0, 0) \) and the second one is endemic equilibrium point, given by \( \left( \frac{\mu}{R_\alpha(\alpha+\lambda)} \left( \frac{(\alpha+\lambda)(R_\alpha-1)}{\beta}, \frac{\mu}{\lambda(\alpha+\lambda)R_\alpha} \right) \right) \), where \( R_\alpha > 1 \).

We have proved in Subsection 3.3.1 of the Chapter 3, that bifurcation occurs at \( R_\alpha = 1 \) and we express this by saying that the deterministic model has a threshold value at \( R_\alpha = 1 \). We will show in the Section 4.7, that the threshold values of \( R_\alpha \) for the stochastic model will be substantially larger than 1, and hence the threshold parameter for the deterministic model is a poor approximation of the stochastic threshold.
4.4 The quasi-stationary distribution

Since we are interested in studying the behaviour of the epidemic model in the transition states belonging to the state space \( \mathcal{S} \), let

\[
p_I(t) = \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p_{s,i,v}(t) = \Pr \{ I(t) = i \} \tag{4.6}
\]

be the marginal distribution of the number of infected individuals at time \( t \). Put \( I = 0 \) and summing the forward differential difference equation 4.3 for all values of \( s \) and \( v \), we have

\[
\sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p'_{s,0,v}(t) = \mu \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p_{s-1,0,v}(t) + \lambda \sum_{s=0}^{\infty} (s + 1) \sum_{u=0}^{\infty} p_{s+1,0,v}(t)
+ \beta \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} (s + 1)(0 - 1)p_{s+1,-1,v}(t) + \alpha \sum_{s=0}^{\infty} (s + 1) \sum_{u=0}^{\infty} p_{s+1,0,-1}(t)
+ (\gamma + \lambda) \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p_{s,1,v}(t) + \lambda \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} (u + 1)p_{s,0,u+1}(t) - \mu \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p_{s,0,u}(t)
- \lambda \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p_{s,0,u}(t) - \alpha \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p_{s,0,u}(t) - \lambda \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} v p_{s,0,u}(t)
\]

Further simplification gives,

\[
\sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p'_{s,0,v}(t) = (\gamma + \lambda) \sum_{s=0}^{\infty} \sum_{u=0}^{\infty} p_{s,1,v}(t)
\]

Using equation 4.6, the above equation can be written as

\[
p'_{0,0}(t) = (\gamma + \lambda) p_{1,0}(t) \tag{4.7}
\]

To derive quasi-stationary distribution, denote the state probabilities on the transient state \( \mathcal{S} \) as \( q_{s,i,v}(t) \) and are given by

\[
q_{s,i,v} = \Pr \{ S(t) = s, I(t) = i, V(t) = v \mid I(t) \neq 0 \}
= \frac{\Pr \{ S(t) = s, I(t) = i, V(t) = v \}}{\Pr \{ I(t) \neq 0 \}}
= \frac{p_{s,i,v}(t)}{1 - p_a} \quad \text{for} \quad (s, i, v) \in \mathcal{S} \tag{4.8}
\]
Let \( q_{i.}(t) = \sum_{s=0}^{\infty} \sum_{v=0}^{\infty} q_{s,i,v}(t) \) be the marginal distribution for the number of infected individuals at time \( t \) on the transient state space \( \mathcal{S} \). Differentiating equation 4.8. with respect to \( t \), we have,

\[
q'_{s,i,v}(t) = \frac{P'_{s,i,v}(t)}{1 - P_{0}(t)} + (\gamma + \lambda) q_{1.}(t) \frac{P_{s,i,v}(t)}{1 - P_{0}(t)}
\]

(4.9)

Now dividing equation 4.3 by \( \{1 - P_{0}(t)\} \) we get

\[
\frac{P'_{s,i,v}(t)}{1 - P_{0}(t)} = \mu q_{s-1,i,v}(t) + \lambda (s + 1) q_{s+1,i,v}(t) + \beta (s + 1) (i - 1) q_{s+1,i-1,v}(t) + \alpha (s + 1) q_{s+1,i,v-1}(t) + (\gamma + \lambda) (i + 1) q_{s,i+1,v}(t) + \lambda (v + 1) q_{s,i,v+1}(t) - \{\mu + \beta s i + (\lambda + \alpha) s + (\gamma + \lambda) i + \lambda v\} q_{s,i,v}(t)
\]

(4.10)

Thus equation 4.9 and 4.10 together gives forward differential difference equation for
the conditional state probabilities \( q_{s,i,v} (t) \) and is given by

\[
q'_{s,i,v} (t) = \mu q_{s-1,i,v} (t) \\
+ \lambda (s + 1) q_{s+1,i,v} (t) \\
+ \beta (s + 1) (i - 1) q_{s-1,i-1,v} (t) \\
+ \alpha (s + 1) q_{s+1,i,v-1} (t) \\
+ (\gamma + \lambda) (i + 1) q_{s,i-1,v} (t) \\
+ \lambda (v + 1) q_{s,i,v+1} (t) \\
+ (\gamma + \lambda) q_{1} (t) q_{s,i,v} (t) \\
\]

\[- \{ \mu + \beta s + (\alpha + \lambda) s + (\gamma - \lambda) i + \lambda v \} q_{s-1,v} (t), \]

for \((s, i, v) \in \mathcal{S}\) (4.11)

Thus, the quasi-stationary distribution \( q_{s,i,v} (t) \) is the stationary (trivial) solution of the Kolmogorov forward differential difference equation 4.11. But the stationary solution of the system 4.11 is mathematically intractable and our interest is to derive the marginal distribution \( q_{i,v} (t) \) of the number of infected individuals using recursion relationship obtained below. Equating \( q'_{s,i,v} (t) = 0 \) in equation 4.11, we have

\[
\mu q_{s-1,i,v} (t) + \lambda (s + 1) q_{s+1,i,v} (t) + \beta (s + 1) (i - 1) q_{s-1,i-1,v} (t) \\
+ \alpha (s + 1) q_{s+1,i,v-1} (t) + (\gamma + \lambda) (i + 1) q_{s,i-1,v} (t) - \lambda (v + 1) q_{s,i,v+1} \\
- \{ \mu + \lambda s + \beta s + (\gamma + \lambda) i + \lambda v \} q_{s,i,v} (t) + (\gamma + \lambda) q_{1} (t) q_{s,i,v} (t) = 0
\]

Taking for all values of \( s \) and \( v \), we get,

\[
\beta (i - 1) \sum_{s=0}^{\infty} s q_{s,i} (t) - (\gamma + \lambda) i q_{i,v} (t) + (\gamma + \lambda) (i + 1) q_{1,v+1} (t) \\
- \beta i \sum_{s=0}^{\infty} s q_{s,i} (t) - (\gamma + \gamma) i q_{i,v} (t) + (\gamma + \lambda) q_{1} (i + 1) q_{1} (i + 1) q_{i,v} (i + 1) = 0 (4.12)
\]
Let
\[ e_s(i) = \sum_{s=0}^{\infty} s q_{s,i}(t) / q_{i,i} \]
be the conditional expectation of \( S \), given \( I = i \), obtained from quasi-stationary distribution. Substituting the above conditional expectation in equation 4.12, we have
\[
\begin{align*}
\beta (i - 1) e_s(i - 1) q_{(i-1),i} (t) + (\gamma + \lambda) (i + 1) q_{(i+1),i} (t) &- \beta i e_s(i) q_{i,i} (t) \\
- (\gamma + \lambda) i q_{i,i} (t) + (\gamma + \lambda) q_{i,i} (t) q_{i,i} (t) &= 0
\end{align*}
\] (4.13)

Now multiplying equation 4.13 by \( \frac{\beta}{(\gamma + \lambda) (\alpha + \lambda)} \) (i.e. \( R_\alpha / \beta \)) and putting \( \xi = \frac{\mu}{(\alpha + \lambda)} \), we get,
\[
R_0 (i - 1) e_s(i - 1) q_{(i-1),i} (t) - \xi i q_{i,i} (t) - R_0 i e_s(i) q_{i,i} (t) \xi (i + 1) q_{(i+1),i} (t) + \xi q_{i,i} (t) q_{i,i} (t) = 0
\] (4.14)

Again let,
\[
f(i) = \xi i q_{i,i} (t) - R_0 (i - 1) q_{(i-1),i} (t) e_s(i - 1), \quad \text{for } i = 1, 2, \ldots
\] (4.15)
and substituting this in equation 4.14, we find that
\[
f(i + 1) = f(i) - \xi q_{i,i} (t) q_{i,i} (t) , \quad \text{for } i = 1, 2, \ldots
\] (4.16)

To solve the above recursion relationship, put \( i = 1 \) in the equation 4.15 we have,
\[
f(1) = \xi q_{1,1} (t)
\]
for \( i = 2 \), the equation 4.16 becomes,
\[
f(2) = f(1) \xi q_{2,1} (t) q_{1,1} (t)
\]
for \( i = 3 \), the equation 4.16 becomes,
\[
f(3) = f(2) \xi q_{3,1} (t) q_{2,1} (t)
\]
Using the above result for \( f(2) \), we have

\[
f(3) = \left\{ 1 - \sum_{k=1}^{2} q_k(t) \right\} \xi q_1(t)
\]

Continuing this procedure for \( i = 1, 2, \ldots \) we can show that

\[
f(i + 1) = \left\{ 1 - \sum_{k=1}^{i} q_k(t) \right\} \xi q_1(t), \quad \text{for } i = 1, 2, \ldots \quad (4.17)
\]

To establish the recursion relationship for the marginal distribution \( q_i(t) \) for infected individuals substitute the above result 4.17 in equation 4.14. We have

\[
- \left\{ 1 - \sum_{k=1}^{i-1} q_k(t) \right\} \xi q_1(t) + \{ \xi (i + 1) q_{i+1}(t) - R_0 i q_i(t) \} e_s(i) + \xi q_1(t) q_i(t) q_s(t) = 0
\]

Further simplification gives,

\[
q_{i+1}(t) = \frac{R_0}{\xi} \frac{i}{i+1} q_i(t) e_s(i) + \left\{ 1 - \sum_{k=1}^{i} q_k(t) \right\} \frac{i}{i+1} q_1(t) \quad (4.18)
\]

The above result cannot be used to solve the marginal distribution of infected individuals in quasi-stationary, because the conditional expectation \( e_{n(i)} \) is unknown. However, this result may be useful for the future discussion of the present problem.

### 4.5 The distribution of the time to extinction

In the epidemiological context, the threshold parameter is of great interest because of its epidemiological interpretation and for deterministic models, this has been derived through graphical method or by stability analysis at the equilibrium point. For the stochastic epidemic models, threshold parameter can be defined using the random variable—the time to extinction of the epidemic (See, [115]).

To obtain the distribution of the time to extinction, denote the time to extinction by \( T \). It is easy to obtain the distribution of time to extinction when the initial
distribution is equal to the quasi-stationary distribution. However, there were two initial distributions, one is the quasi-stationary distribution and the other corresponds to infected individuals. Threshold for both of these cases occur at those values of $R_a$ for which the expected time to extinction equals to some fixed value (See, [115]). Further, the corresponding function of $N$ gives the persistence threshold when the initial distribution is quasi-stationary. Thus we compute below the persistent threshold using quasi-stationary distribution as initial distribution.

Again following Nasel [115], since the event, time to extinction- $T$ exceeds $t$ is equivalent to the number of infected individuals at time $t$ is positive. In other words,

$$Pr\{T \leq t\} = Pr\{i(t) = 0\} = p_0(t) \quad (4.19)$$

Thus, the marginal probability distribution $p_0(t)$-the distribution of zero-number of infected individuals at time $t$ is equivalent to the cumulative distribution function of time to extinction at time $t$. To be explicit, denote the time to extinction from quasi-stationary by $T_Q$. Now stationary values can be obtained by equating the equation 4.9 to zero, that is $q_{s,i,v}'(t) = 0$. This makes

$$\frac{p_{s,i,v}'(t)}{p_{s,i,v}(t)} = -(\gamma + \lambda) q_{s,i,v}(t), \text{ for } (s,i,v) \in \mathcal{S} \quad (4.20)$$

Integrating equation 4.20 with respect to $t$. taking the initial condition $p_{s,i,v}(0) = q_{s,i,v}$ for $(s,i,v) \in \mathcal{S}$ giving

$$p_{s,i,v}(t) = q_{s,i,v} \exp\{- (\gamma + \lambda) q_{s,i,v}(t) t\}, \text{ for } (s,i,v) \in \mathcal{S} \quad (4.21)$$

Summing for all values of $s$ and $v$ on both sides of equation 4.21, we get

$$p_{i}(t) = q_{i} \exp\{- (\gamma + \lambda) q_{i}(t) t\}, \text{ for } i = 1, 2, \cdots \quad (4.22)$$
Now substituting equation 4.22 for $p_{1}(t)$ in equation 4.7, we have

$$p'_{1}(t) = (\gamma + \lambda) q_{1} \exp \{ - (\gamma + \lambda) q_{1} (t) - t \}$$  \hspace{1cm} (4.23)$$

Thus the distribution of time to extinction $T_{q}$ is in quasi stationary has an exponential form and its expected value is

$$E\{T_{q}\} = \frac{1}{(\gamma + \lambda) q_{1}(t)}$$  \hspace{1cm} (4.24)$$

Comparing the $E\{T_{q}\}$ with that of Nasell [25], it is found that the expected time to extinction of an epidemic is less in the presence of immunization programmes.

### 4.6 Diffusion approximation

Here we derive a diffusion approximation for the Kolmogorov equation for the present epidemic model 4.3, given in Section 4.2 on page 75. Assuming $R_{0} > 1$ and following the method of diffusion approximation proposed by Kurtz [116], Barbour [109], Pollett [117] and Nasell [25] it can be shown below that the quasi stationary distribution follows trivariate normal distribution for $N$ sufficiently large.

Rescaling the state space by putting $x_{1}(t) = \frac{S(t)}{N}$, $x_{2}(t) = \frac{I(t)}{N}$, and $x_{3}(t) = \frac{V(t)}{N}$ and setting $\mu' = \frac{\mu}{N}$, $\beta' = 3N$, $\alpha' = \alpha$, $\gamma' = \gamma$ and $\lambda' = \lambda$ to obtain size-independent quantities, the system of differential equations in 4.5 can be written as:

$$x'_{1}(t) = \mu' - \beta' x_{1}(t) x_{2}(t) - (\lambda' + \alpha') x_{1}(t)$$
$$x'_{2}(t) = \beta' x_{1}(t) x_{2}(t) - (\lambda' + \alpha') x_{2}(t)$$
$$x'_{3}(t) = \alpha' x_{1}(t) - \lambda' x_{3}(t)$$
The equilibrium point of the above rescaled deterministic model corresponding to an endemic infection level $R_a > 1$ is obtained by setting the right hand side of above system of the equations to zero and solving for the state variables we get
\[
\mathbf{x} = (\mathbf{x}_1, \mathbf{x}_2, \mathbf{x}_3) = \left\{ \frac{\mu}{R_a} \left( \alpha' + \lambda \right) (R_a - 1), \frac{\alpha' \mu}{\beta} \right\} (4.25)
\]

Let the changes in the scaled state variables $x_1, x_2$ and $x_3$ during the time interval $(t, t + \delta t)$ are denoted by $\delta x_1, \delta x_2$ and $\delta x_3$, where $\delta x_i(t) = x_i(t + \delta t) - x_i(t), i = 1, 2, 3$.

From the hypothesis for the original process on the sequence of transitions, mean vector and covariance matrix for the changes in the scaled state variables during the time internal $(t, t + \delta t)$ are obtained as follows.

Assume that we are in the state $(S, I, V)$, then there are 6 possible transitions from this state, are described below:

1. $S$ increases by 1 at the rate $\mu$.
2. $S$ decreases by 1 and $I$ increases by 1 at the rate $\beta SI$
3. $S$ decreases by 1 at the rate $(\lambda + \alpha)S$
4. $I$ decreases by 1 at the rate $(\lambda + \gamma)I$
5. $V$ increases by 1 at the rate $\alpha S$
6. $V$ decreases by 1 at the rate $\lambda S$

Then the random variable $\delta x_1$ equals $\frac{1}{N}$ in case (1), $-\frac{1}{N}$ in cases (2) and (3), and zero in all other cases. Similarly $\delta x_2$ equals $\frac{1}{N}$ in case (2), $-\frac{1}{N}$ in case (4) and zero in all other cases. Where as $\delta x_3$ equals $\frac{1}{N}$ in case (5), $-\frac{1}{N}$ in case (6) and zero in all other
cases. Then

\[ E \{ \delta x_1 \} = (\mu' - \beta' x_1 x_2 - (\lambda' + \alpha') x_1) \delta t + o(\delta t), \]
\[ E \{ \delta x_2 \} = (\beta' x_1 x_2 - (\lambda' + \gamma') x_2) \delta t + o(\delta t) \]
and
\[ E \{ \delta x_3 \} = (\alpha' x_1 - \lambda' x_3) \delta t + o(\delta t) \]

Thus,

\[ E \{ \delta x \} = b(\mathbf{x}) \delta t + o(\delta t) \quad (4.26) \]

where,

\[ b(\mathbf{x}) = \begin{pmatrix} 
\mu' - \beta' x_1 x_2 - (\lambda' + \alpha') x_1 \\
\beta' x_1 x_2 - (\lambda' + \gamma') x_2 \\
\alpha' x_1 - \lambda' x_3 
\end{pmatrix} \]

The vector \( b(\mathbf{x}) \) measures the rate of growth of the expectation. The local drift matrix for the diffusion process is obtained by computing Jacobian matrix of the vector \( b(\mathbf{x}) \).

To derive variance and covariance matrix, let \( B(\mathbf{x}) \) be the Jacobin Matrix at the point \( \mathbf{x} \) obtained from the \( b(\mathbf{x}) \) as

\[ B(\mathbf{x}) = \frac{\partial b(\mathbf{x})}{\partial \mathbf{x}} = \begin{pmatrix}
-\beta' x_2 - (\lambda' + \alpha') & -\beta' x_1 & 0 \\
\beta' x_2 & \beta' x_1 - (\lambda' + \gamma') & 0 \\
\alpha' & 0 & -\lambda'
\end{pmatrix} \]

Approximating the matrix \( B(\mathbf{x}) \) at the deterministic equilibrium point \( \mathbf{x} = (\bar{x}_1, \bar{x}_2, \bar{x}_3) \) (given in equation 4.25), we have,

\[ B(\bar{x}) = \begin{pmatrix}
-(\alpha' + \lambda') R_\alpha & -(\gamma' + \lambda') & 0 \\
(\alpha' + \lambda')(R_\alpha - 1) & 0 & 0 \\
\alpha' & 0 & -\lambda'
\end{pmatrix} \quad (4.27) \]
The variance of $\delta x_1$ is given by

$$Var(\delta x_1) = E \{(\delta x_1)^2\} - [E \{\delta x_1\}]^2$$

The first of these terms is of the order of $\delta t$, while the second term is of the order of $(\delta t)^2$ which is infinitesimally small, hence is considered as $o(\delta t)$. The square of a random variable that takes the value $\left(\frac{1}{N}\right)^2 = \frac{1}{N^2}$ in case (1), the value $\left(-\frac{1}{N}\right)^2 = \frac{1}{N^2}$ in case (2) and (3), and Zero in all other cases. Thus it takes the same value in all non-zero value cases. Its expected value equals this constant value multiplied by the sum of the probabilities of these non-zero value events. Thus

$$Var(\delta x_1) = \frac{1}{N} \{\mu' + \beta' x_2 + (\alpha' + \lambda') x_1\} \delta t + o(\delta t)$$

Variances of $\delta x_2$ and $\delta x_3$, and covariance $Cov(\delta x_1, \delta x_2)$, $Cov(\delta x_1, \delta x_3)$ and $Cov(\delta x_2, \delta x_3)$ are treated in a way that is very similar to the treatment of the variance of $\delta x_1$. Thus the covariance matrix is given by
We also approximate the matrix $S(x)$ by evaluating it at the deterministic equilibrium point $x = \bar{x}$ corresponding to the endemic infection level:

$$S(\bar{x}) = \begin{pmatrix}
2R_\alpha & -(R_\alpha - 1) & 0 \\
-(R_\alpha - 1) & 2(R_\alpha - 1) & 0 \\
0 & 0 & \frac{2\alpha'}{(\alpha' + \lambda')}
\end{pmatrix}$$  \hfill (4.29)

It follows from Theorem 3.2 of Pollett P. K. [118] and Ingemar Nasell [25] that the process $\sqrt{N} (x(t) - \bar{x})$ is approximated for large $N$ by a three-variate Ornstein-Uhlenbeck process with local drift matrix $B(\bar{x})$ and the local covariance matrix $S(\bar{x})$. It is known from Ingemar Nasell [25], that the stationary distribution of this Ornstein-Uhlenbeck process approximates the quasi-stationary distribution. It is approximately normal with mean zero and the local covariance matrix $\Sigma$, where $\Sigma$ is obtained from the matrices $B(\bar{x})$ and $S(\bar{x})$. By solving the matrix equation

$$B(\bar{x}) \Sigma + \Sigma B^T(\bar{x}) = -S(\bar{x})$$  \hfill (4.30)

where $B^T(\bar{x})$ is the transpose of the matrix $B(\bar{x})$. Since $\Sigma$ is a 3x3 matrix, there are actually 9 equations, we use the fact that $\Sigma$ is symmetric to reduce the number of equations to 6. This leads to solve the following 6 equations in 6 unknowns.

$$(\alpha' + \lambda') R_\alpha \Sigma_{11} + (\gamma' + \lambda') \Sigma_{12} = \mu'$$
\[(\alpha' + \lambda') R_\alpha \Sigma_{12} + (\gamma' + \lambda') \Sigma_{22} - (\alpha' + \lambda') (R_\alpha - 1) \Sigma_{11} = -\frac{\mu'(R_\alpha - 1)}{R_\alpha}\]

\[\{ (\alpha' + \lambda') R_\alpha + \lambda' \} \Sigma_{13} + (\gamma' + \lambda') \Sigma_{23} - \alpha' \Sigma_{11} = 0\]

\[(\alpha' + \lambda') (R_\alpha - 1) \Sigma_{12} = -\frac{\mu'(R_\alpha - 1)}{R_\alpha}\]

\[(\alpha' + \lambda') (R_\alpha - 1) \Sigma_{13} + \alpha' \Sigma_{13} + \alpha' \Sigma_{12} - \lambda' \Sigma_{23} = 0\]

\[\alpha' \Sigma_{13} - \lambda' \Sigma_{33} = \frac{-\alpha' \mu'}{R_\alpha (\alpha' + \lambda')}\]

The solution of the above system of equations gives \(\Sigma\) as given below.

\[
\Sigma = \begin{pmatrix}
\Sigma_{11} & \Sigma_{12} & \Sigma_{13} \\
\Sigma_{12} & \Sigma_{22} & \Sigma_{23} \\
\Sigma_{13} & \Sigma_{23} & \Sigma_{33}
\end{pmatrix}
\]

where,

\[\Sigma_{11} = \frac{\mu' \{(\alpha' + \lambda') R_\alpha + (\delta' + \lambda')\}}{R_\alpha^2 (\alpha' + \lambda')^2} \]

\[\Sigma_{12} = \frac{\mu'}{R_\alpha (\alpha' + \lambda')} \]

\[\Sigma_{13} = \frac{\mu' \{(\alpha' + \lambda') R_\alpha + (\delta' + \lambda') (R_\alpha - 1)\}}{R_\alpha^2 (\alpha' + \lambda')^2} \]

\[\Sigma_{22} = \frac{\mu' \{R_\alpha^2 (\alpha' + \lambda') + (\gamma' + \lambda') (R_\alpha - 1)\}}{R_\alpha (\alpha' + \lambda') (\gamma' + \lambda')} \]

\[\Sigma_{23} = \frac{\mu' \{(\alpha + \lambda') R_\alpha + \gamma' (\alpha' + \lambda') R_\alpha + \lambda' (\gamma' + \lambda')\}}{\lambda' R_\alpha (\alpha' + \lambda') (\gamma' + \lambda')} - \frac{\alpha' \mu'}{\lambda' R_\alpha (\alpha' + \lambda')} \]

\[\Sigma_{33} = \frac{\mu' \{(\alpha' + \lambda') R_\alpha + \gamma' (\alpha' + \lambda') R_\alpha + \lambda' (\gamma' + \lambda')\}}{\lambda' R_\alpha (\alpha' + \lambda')^2} \]

\[
\frac{\mu' \{(\alpha' + \lambda') R_\alpha + \gamma' (\alpha' + \lambda') R_\alpha + \lambda' (\gamma' + \lambda')\}}{\lambda' R_\alpha (\alpha' + \lambda') (\gamma' + \lambda')} + \frac{\alpha' \mu'}{\lambda' (\alpha' + \lambda') R_\alpha}
\]
4.7 Approximation for the time to extinction

It is known by the previous result that the marginal distributions of the number of susceptible, infected and immunized individuals in quasi-stationary are approximately normal with means $\mu_S, \mu_I$ and $\mu_V$ respectively and standard deviations $\sigma_S, \sigma_I$ and $\sigma_V$ respectively, where

$$
\mu_S = \frac{N\mu'}{R_0(\alpha' + \lambda')}
$$

$$
\sigma_S = \sqrt{N\Sigma_{11}}
$$

$$
\mu_I = \frac{N(\alpha' + \lambda')(R_0 - 1)}{\beta'}
$$

$$
\sigma_I = \sqrt{N\Sigma_{22}}
$$

$$
\mu_V = \frac{N\alpha'\mu'}{\lambda'(\alpha' + \lambda')R_0}
$$

$$
\sigma_V = \sqrt{N\Sigma_{33}}
$$

(4.31) to (4.33)

Ingemar Nasell [108] identifies three regions in parameter space with qualitatively different behaviours of the quasi-stationary distribution while studying the asymptotic analysis of the SIS model. He has shown that, in these three-parameter regions the deterministic threshold parameter $R_0$ is distinctly above the threshold value 1, in the first region, distinctly below the threshold value 1, in the third region and it lies in the transition region close to the deterministic threshold value 1 in the second region.

Further he has shown that the quasi-stationary distribution is approximated by normal distribution in the first region and by a geometric distribution in the third region, whereas the behaviour is more complicated in the transition region. While studying recurrent epidemic model Ingemar Nasell [25] limited his investigation to $R_0 > 1$, that is in the region where the persistence threshold always occurs. Again, in this parameter range
he has investigated two parameter regions corresponding to two qualitatively different
behaviours of quasi-stationary distribution, that is \( R_0 \) is distinctly large' and \( R_0 \) is
in the transition region'. Now following Nasell [25], we approximate quasi-stationary
distribution in the transient region by normal distribution. Here we claim that transition
region is larger to the extent of immunization effect.

We now modify the approximated normal distribution of the number of infected
individuals \( T \) in quasi-stationary, by truncation at 0.5 to achieve consistency with the
fact that \( I \) is positive. Thus we find that this distribution can be approximated by the
expression.

\[
q_{1.1} \approx \frac{1}{\sigma_I} \frac{\varphi\left\{(i - \mu_I)/\sigma_I\right\}}{\Phi\left\{(\mu_I - 0.5)/\sigma_I\right\}}.
\]

(4.34)

where \( \Phi \) and \( \varphi \) denote the normal cumulative distribution function and the normal
density function respectively.

Now we approximate the expected time to extinction from quasi-stationary de­
vided in equation 4.24, by substituting the approximation to \( q_{1.1} \), from expression 4.34
into the relationship that express \( E\{T_Q\} \) in terms of \( q_{1.1} \), we find that

\[
E\{T_Q\} \approx \frac{\sigma_I}{\gamma + \lambda} \frac{\Phi\left\{(\mu_I - 0.5)/\sigma_I\right\}}{\varphi\left\{(\mu_I - 1)/\sigma_I\right\}}
\]

(4.35)

Comparing the approximation of the \( E\{T_Q\} \) with that of Nasell [25], it is found that
the approximate expected time to extinction of an epidemic is less in the presence of
immunization programmes.
4.8 Conclusion

Intervention measures to prevent or reduce the transmission of infectious diseases are currently being used, with a degree of success, in some parts of the world. Some of these methods used include: immunization programs, avoiding all mediating agencies from contact to keep away from the attack of disease. For instance, immunization of children to protect them against diphtheria, whooping cough, polio, TB and measles. Prevention of malaria through the use of mosquito nets, these methods reduce the contact rate and hence exposure to infection. Thus it is important to incorporate these facts while modelling the transmission dynamics of infectious diseases. In this Chapter we have analyzed the stochastic recurrent epidemic model with initial preventive measures. Though our primary objective is to study time to extinction of the epidemic, which is purely stochastic phenomenon, we have presented results of the previous chapter for the deterministic version, that are useful in the reparameterization for studying the quasi stationary distribution. Nasell [25] has shown that the persistence threshold in order of magnitude is larger than the deterministic threshold. Our results are parallel to the results of the Nasell [25], however the presence of preventive measures increases the range of transition region. The theoretical framework that we have presented is based on the concept of quasi-stationarity and diffusion approximation.