Research Article

Stochastic analysis of a closed SIS malaria model

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Abstract

A pseudo-equilibrium approximation model for the dynamics and transmission of malaria in human populations is studied. A stochastic version of this model is then formulated and analyzed based on the fact that the disease is endemic and therefore has a basic reproduction number greater than unity. Using a comprehensive theory on asymptotic approximation techniques in recurrent epidemics, approximations for the quasi-stationary distribution and the time to extinction are derived. We find that whenever the reproduction number is greater than unity, the time to extinction of the disease is exponentially distributed with positive exponent and therefore becomes very large within very large human population sizes. We then interpret the fact that it has been difficult to eradicate malaria with the exponentially large time to extinction of the number of infected individuals in the population of humans.

Key Words: Pseudo-equilibrium approximation, Stationary distribution, quasi-stationary distribution.

Résumé

On a étudié un modèle de rapprochement de pseudo-équilibre de la dynamique et de la transmission du paludisme dans les populations humaines. En utilisant une théorie complète sur les techniques d'approximation asymptotique en épidémies récurrentes, des approximations pour la distribution quasi stationnaire et le temps d'extinction sont dérivées. Nous trouvons que chaque fois que le nombre de reproduction est supérieur à un, le temps d'extinction de la maladie est distribué exponentiellement avec l'exposant positif et par conséquent devient très grand pour les tailles de grande population humaine. Ensuite, nous interprétons le fait qu'il a été difficile à éradiquer le paludisme vu le grand temps exponentiellement a l'extinction du nombre de personnes infectées dans la population humaine.

Mots Cle: rapprochement de Pseudo-équilibre, distribution stationnaire, distribution quasi- stationnaire.

1 Introduction

Deterministic mathematical models for the population dynamics of living organisms are well established in the literature[14, 7, 29, 32]. However, it is well known that only when numbers in a population become large, can the dynamics of the population be well approximated by a deterministic differential equation model [9]. In this case, it can be shown that the densities predicted by the deterministic equations will coincide with the mean values from a stochastic analysis [26]. Since populations of living organisms come in discrete units, stochastic models, which are models based on discrete events and probabilistic arguments, are actually the natural models for studying the occurrence of population of living organisms. Now, in studying the dynamics and transmission of human malaria, a parasitic vector-borne disease which is endemic in many parts of the world, most models [3, 2, 28, 35, 22, 23] have so far been based on the pioneering and Nobel Prize winning deterministic ordinary differential equation model first proposed by Sir Ronald Ross [33]. The important and striking result from Ross' model and from all other Ross-type models, is that there exist a deterministic threshold parameter with the property that if this parameter exceeds unity, there is a non-zero globally and asymptotically stable deterministic steady state solution which is always reached so long as we start of the process with at least one infective and the disease will always establish itself in the population, and when the threshold parameter is less than unity, the disease dies out from the community [26, 33]. Deterministic Ross-type models for malaria transmission have therefore served their purpose in informing us on the dynamics of malaria transmission. However, the deterministic model's prediction of a stable endemic equilibrium *whenever* we start off the process with even one infected individual (vector or human) so long as the threshold parameter is greater than unity is not realistic. The first event that could occur, in the sequence of possible events, could be the death of this infective in which case the infection will not spread into the populations irrespective of whether or not the threshold condition is satisfied. A far more likely occurrence is that the *probability that the disease establishes itself in the population* will change. It is in this regard that we deem it necessary to re-examine a simplified version of the deterministic differential equation model for malaria dynamics, earlier derived and studied by Ngwa and Shu [25, 26], within the context of a stochastic analysis.

Malaria in humans is caused by one of the four major protozoan species of genus *Plasmodium*, namely; *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium malariae* and *Plasmodium ovale*. Some authorities have indicated an emerging fifth species, *Plasmodium knowlesi*, which has been implicated in human malaria transmission mostly in South East Asia [4, 6, 30]. Our focus is on malaria caused by *Plasmodium falciparum* which is potentially life-threatening. Which ever species is involved, the parasites are transmitted from human to human by the female Anopheles mosquito when it bites a human being in order to harvest blood that she needs for the maturation of her eggs. It has been estimated that there are about 380 known species of Anopheles mosquitoes, but only about 60 of these have been identified as being capable of transmitting human malaria, [25]. This relatively small fraction of *Anopheles sp.* mosquitoes that prefer human blood therefore have a *human bitting habit* and it is this habit that helps drive the passage of the parasite from human to human. It is clear here that for the malaria infection to move from one person to another, the two humans must be visited by the same mosquito over a reasonable period of time.

When a Plasmodium infected mosquito bites a susceptible human host, it injects the sporozoite forms of the parasite from its salivary glands into the victim's blood stream. Within hours, the sporozoites invade the human's liver cells where they asexually divide and eventually thousands of merozoites forms of the parasite are released into the human's blood stream. The merozoites quickly invade the human's red blood cells and begin a second round of proliferation within the

cell. The infected red blood cells eventually rupture (owing to an increase in the number of parasites in them) and die, releasing more parasites and also toxins into the blood stream. When a susceptible mosquito takes a blood meal from an infected person, it can become infected with the malaria parasite. These parasites go through several stages of growth in the mosquito and the cycle begins again when this infected mosquito bites a susceptible human. The fact that the malaria parasite has divided its life cycle so that part of it is the mosquito while the other part is in the human, points to the inherent difficulties in eradicating the infection in human populations, especially in situations where humans are allowed to interact with mosquitoes. The resilience of the infection in the population can sometimes be attributed to the fact that the reservoir of infection is large. Thus questions such as, "when does an infection disappear in a population?" take on a real mathematical meaning when posed in an endemic setting.

In endemic areas of Africa, it has been estimated that an individual receives about 40 to 120 infectious bites per year compared with 2 per year in India [25]. The incubation period of the parasite depends on extrinsic factors such as temperature, as well as intrinsic factors such as the species of mosquito. For example, the incubation period for *Plasmodium falciparum* is 12 days in humans within a temperature range of 25^o-27^o and 10 days in the mosquito. A malaria attack is characterized by sweating, fever, chills, myalgia (muscle ache), headache, nausea, vomiting, dizziness, shivering, pains in the joints and a rise in temperature. The total load of human misery and suffering from malaria presents a formidable challenge to public health authorities. Mathematical modelling of malaria is important since it attempts to provide information about its transmission rates and spread and can assist in health decision making processes.

Mathematical modelling has flourished since the days of Ross, [33], who was the first to model the dynamics of malaria transmission [1]. Lotka [10], extended the analysis of Ross's model, while Macdonald, [11], modified and extended Ross's work by introducing the theory of superinfection (that is, a human host acquiring additional infection before recovery). Using data from the Garki project, [13], many studies have been carried out on the epidemiology of malaria and one of the most outstanding is the mathematical model proposed by Dietz et al [5], which Nedelman [21], analysed in detail. Ngwa and Shu, [25], modelled endemic malaria with variable human and mosquito populations, a factor which had been hitherto omitted in most models. Ngwa et. al. [24], modelled the dynamics of an age-structured endemic malaria transmission with varying populations. Most of the earlier works on the Mathematical modelling of disease transmission are essentially deterministic in character. In other words, they do not take into consideration the probabilistic aspects of the processes studied. However, Nåsell [18], derived an approximation for the expected time to extinction in a stochastic model for recurrent epidemics. He also derived approximations of the quasi-stationary distribution of the stochastic logistic epidemic in the transition regions near the deterministic threshold [17] by extending the earlier work of Kryscio and Lefe̋vre [8]. More recent models for malaria transmission have combined the life style and feeding habits of the mosquito [27, 28] into more realistic and complicated systems of differential equations [22, 23, 35], while others have examined co-infection of malaria with other diseases such as HIV and cholera [31, 34]. However, the crucial problem of the time to extinction, that is how long will it take, under given control measures, for the infection to be eradicated within the human population remains an unanswered and open problem. In this paper, we use the comprehensive theory on asymptotic approximation techniques in recurrent epidemics developed by Nåsell Ingemar [15, 16, 17, 18, 19, 20] to study the concept of quasi-stationarity and the time to extinction for malaria based on a simplified version of the malaria model for endemic malaria derived and studied by Ngwa and Shu [25].

In attempting to handle this problem, we must note that a major difference between determinis-

tic and stochastic models lies in the state space, which is continuous or discrete in the deterministic setting and purely discrete for the stochastic models. In this regard, the stochastic models are more realistic than the deterministic ones since counts of individuals are always discrete. The important results of the deterministic models are qualitative in nature as opposed to quantitative results of the stochastic models. Stochastic models are more difficult to handle mathematically than deterministic models. The difficulty is enhanced when either the associated deterministic model is nonlinear or the associated stochastic model has an absorbing state. In models with an absorbing state, the stochastic stationary distribution is degenerate and uninformative, and if the process has been going on for a long time and absorption has not yet occurred (as is the case with endemic malaria), we must address the the concept of quasi-stationarity. To do this, we shall construct a stochastic version of the deterministic model for the dynamics of endemic malaria with variable human and mosquito populations proposed by Ngwa and Shu, [25]. It is not possible to find an explicit expression for the quasi-stationary distribution or for the time to extinction of a stochastic model whose deterministic counterpart is non-linear. As a result, progress in the analysis of such a model rests on finding a good approximation to the quasi-stationary distribution and the time to extinction. Our motivation lies in the quest to understand why malaria is endemic in nature and also to address the interesting mathematical aspects arising from the modelling exercise.

The rest of the paper is organised as follows: in Section two, we re-examine the deterministic model whose general form was analysed by Ngwa and Shu, [25]. The system of equations in this model is reduced to a single equation by rescalling using the pseudo-steady state hypothesis from Michaelis-Menten theory [12], and consider a closed population containing N human individuals while the mosquito population size is held constant. In section three, we consider the stochastic counterpart of the reduced model, wherein, we assume large constant total human population made up of only two classes of persons, the infectives and the susceptibles. The Kolmogorov forward differential equations are then derived and their stationary distribution examined. In section four the quasi-stationary distribution and the time to extinction are then approximated via a rigorous analysis using a comprehensive theory on asymptotic approximation techniques in recurrent epidemics as in Nåsell Ingemar ([16, 18, 20]) . The paper concludes with a discussion in Section five.

2 The SIS malaria model

A version of the mathematical model for malaria transmission proposed by Ngwa and Shu [25], assumes that the human and vector populations are divided into classes or states representing disease status. Thus at any time $t \geq 0$, there are S_h, susceptible humans, E_h incubating humans, I_h infectious humans, R_h partially immune humans, S_v susceptible vectors, E_v incubating vectors and I_v infectious vectors. The model assumes per capita birth rates, $\lambda_h > 0$ and $\lambda_v > 0$, and per capita death rates f_h and f_v, for the human and mosquito populations respectively. All new-borns are assumed susceptible in both populations. When all the variables are put together, there are seven nonlinear autonomous ordinary differential equations for the seven state variables S_h, E_h, I_h, R_h, S_v, E_v, I_v, together with the over 14 parameters that measure the different rates. In the general system, the populations is growing needing that the total populations be determined by differential equations in their own right. The system is almost too large to be useful in the face of mathematical analysis.

In this paper, it is assumed that once an individual human is exposed to the infection, the

individual becomes infectious right away and that the total human population is a constant. In the vector population however, it is assumed that after exposure, there is an incubation period of approximate length $1/\nu_v$ before the vector becomes infectious. Therefore exposed vectors become infectious at rate $\nu_v > 0$. The vector's period of infectiousness is the remaining length of time of life after the onset of infectiousness. Thus, the class of disease being considered here is one whose incubation period in humans is short when compared with other aspects of the disease transmission; aspects such as the duration of infectiousness. The transmission process and dynamics is assumed to be driven by the human biting habit of the transmission agent, namely, the *Anopheles sp.* mosquito.

The following simple disease transmission model, whose general version was studied by Ngwa and Shu [25] is considered.

$$\left\{\begin{array}{lcl} \frac{dS_h}{dt} &=& \lambda_h N_h + r_h I_h - f_h(N_h)S_h - \big(\frac{C_{vh}a_v I_v}{N_h}\big)S_h, \frac{dI_h}{dt} = \big(\frac{C_{vh}a_v I_v}{N_h}\big)S_h - \big(r_h + f_h(N_h)\big)I_h, \\ \frac{dS_v}{dt} &=& \lambda_v N_v - f_v(N_v)S_v - \big(\frac{C_{hv}a_v I_h}{N_h}\big)S_v, \ \frac{dE_v}{dt} = \big(\frac{C_{hv}a_v I_h}{N_h}\big)S_v - \big(\nu_v + f_v(N_v)\big)E_v, \\ \frac{dI_v}{dt} &=& \nu_v E_v - f_v(N_v)I_v, \end{array}\right. \tag{1}$$

together with the appropriate initial data at time t = 0. Here $N_h = S_h + I_h$, while $N_v = S_v + E_v + I_v$ are the respective total human and vector populations. For these to be constant, it is sufficient that $\lambda_h = f_h(N_h)$ and $\lambda_v = f_v(N_v)$ which is equivalent to considering constant human and mosquito populations with sizes $N_h = f_h^{-1}(\lambda_h)$ and $N_v = f_v^{-1}(\lambda_v)$ which will always exist whenever f_h and f_v are continuously differentiable monotone decreasing functions of their arguments.

To analyse the model, it is assumed that the human and vector populations have linear death rates μ_h and μ_v and then introduce the following dimensionless parameters:

$$\tau = \mu_h t, \ \lambda = \frac{\lambda_h}{\mu_h}, \ r = \frac{r_h}{\mu_h}, \ \xi = \frac{C_{vh}a_v}{\mu_h}N_v, \ \varepsilon = \frac{\mu_h}{\mu_v}, \ a = \frac{\lambda_v}{\mu_v}, \ b = \frac{C_{hv}a_v}{\mu_v}, \ e = \frac{\nu_v}{\mu_v}. \tag{2}$$

In the present scaling, $\frac{1}{\mu_h}$ and $\frac{1}{\mu_v}$ are respectively the approximate life spans of the vector and human populations. If it is assumed that the *life span of the vector is short compared with that of the human*, then

$$0 < \frac{\mu_h}{\mu_v} = \varepsilon \ll 1. \tag{3}$$

Thus the parameter groupings in (2) are strictly different from those used in Ngwa and Shu [25] in that they explicitly highlight the presence of the small parameter, ε, in the system and also consider the vector and human populations as constants. Using (2) in (1) gives

$$\left\{\begin{array}{lcl} \frac{dS_h}{d\tau} &=& \lambda(N_h - S_h) + rI_h - \xi(\frac{I_v}{N_v})(\frac{S_h}{N_h}), \ \frac{dI_h}{d\tau} = \xi(\frac{I_v}{N_v})(\frac{S_h}{N_h}) - (r+\lambda)I_h, \\ \varepsilon\frac{dS_v}{d\tau} &=& a(N_v - S_v) - \big(\frac{bI_h}{N_h}\big)S_v, \ \varepsilon\frac{dE_v}{d\tau} = \big(\frac{bI_h}{N_h}\big)S_v - \big(e+a\big)E_v, \ \varepsilon\frac{dI_v}{d\tau} = eE_v - aI_v, \end{array}\right. \tag{4}$$

together with the appropriate initial conditions at time $\tau = 0$. From (4), it is seen that in each of the last three equations a small parameter is multiplying the derivative. So system (4) is therefore a *singular perturbation problem*. By applying the pseudo-steady state hypothesis [12], one can, to a first approximation, set $\varepsilon = 0$ to obtain from the last three equations the following relations:

$$S_v = \frac{aN_vN_h}{aN_h + bI_h}, \ E_v = (\frac{a}{a+e})(\frac{bI_h}{aN_h + bI_h})N_v, \ I_v = (\frac{e}{a+e})(\frac{bI_h}{aN_h + bI_h})N_v. \tag{5}$$

Substituting for I_v from (5) in the first equation of (4) with $\varepsilon = 0$, we obtain the following pseudo-equilibrium approximation for the system (1).

$$\left.\begin{array}{rcl} \frac{dS_h}{d\tau} & = & (\lambda + r)I_h - (\frac{\xi eb}{a(a+e)})(\frac{I_h S_h}{N_h(N_h + \frac{b}{a}I_h)}), \\ \frac{dI_h}{d\tau} & = & (\frac{\xi eb}{a(a+e)})(\frac{I_h S_h}{N_h(N_h + \frac{b}{a}I_h)}) - (r + \lambda)I_h. \end{array}\right\} \tag{6}$$

Since $S_h + I_h = N_h$ a constant, one of the equations in (6) is redundant since $S_h = N_h - I_h$. In this case, one simply drops the subscript h and write

$$I = I_h,\ N = N_h,\ \delta = \frac{b}{a},\ D = \frac{\xi eb}{a(a+e)},\ \mu = r + \lambda, \tag{7}$$

to have the single nonlinear equation,

$$\frac{dI}{d\tau} = \frac{D(N-I)I}{N(N+\delta I)} - \mu I. \tag{8}$$

This equation thus represents the pseudo-equilibrium approximation model for the original model and clearly shows the dependence of the system on the total population N. It also captures essential parameters such as D which is dependent on the human biting habit of the mosquitoes as well as on the total mosquito population N_v. An increase in D can therefore be regarded as an increase in N_v. The parameter δ measures the infectiousness of the vector in relation to the vector population linear growth rate.

Equation (8) has an exact integral which may be written in the form

$$\left\{\begin{array}{lll} \frac{(\delta+R_0)\log(I(\tau))-(\delta+1)R_0\log(N(R_0-1)-I(\tau)(\delta+R_0))}{\mu(R_0-1)(\delta+R_0)} = \tau + \text{ a constant} & \text{if} & R_0 = \frac{D}{\mu N} > 1, \\ \frac{N-\delta I(\tau)\log(I(\tau))}{\delta\mu I(\tau)+\mu I(\tau)} = \tau + \text{ a constant} & \text{if} & R_0 = \frac{D}{\mu N} = 1, \end{array}\right. \tag{9}$$

where the constant of integration can be determined by specifying the initial number of infective humans I at time $\tau = 0$. Observe however that this complete integral is too complicated to be of use in any analysis, and we cannot even begin to make sense of it when $R_0 < 1$. To gather relevant information however, we observe that equation (8) has two steady state solutions. That is solutions for which $\frac{dI}{d\tau} = 0$, namely;

$$I^* = I_1^* = 0,\ \text{and}\ I^* = I_2^* = \frac{(R_0(N)-1)N}{R_0+\delta}\ \text{where}\ R_0(N) = \frac{D}{\mu N}. \tag{10}$$

R_0 is the unique threshold parameter for the model. Clearly, when $R_0 \leq 1$, the only steady state is the trivial solution, I_1^*, which will be globally and asymptotically stable, while if $R_0 > 1$, the trivial solution, though it exists is linearly unstable while the nontrivial steady state solution, here given as I_2^*, is globally and asymptotically stable. Also, for a given D and μ, there is a critical population size $N_c = D/\mu$ above which the equation has only the trivial solution $I_1^* = 0$. In the context of the original system, this requirement will mean that in cases when N is very large, the simplified model will be useful when D is much larger than N. That is $D \to \infty$ for fixed parameters. In situations where malaria abounds, this requirement is often met since D increases linearly with increasing mosquito population.

Observe that equation (8) if $K = I_2^*$ can be rearranged as follows:

$$\frac{dI}{d\tau} = \frac{D(N-I)I}{N(N+\delta I)} - \mu I = D_0\left(1 - \frac{I}{K}\right)I \equiv f(I),\ D_0(N,I,R_0) = \left(\frac{\mu N}{N+\delta I}\right)(R_0 - 1), \tag{11}$$

The form (11) shows the constant solutions $I_1^* = 0$ and $I_2^* = K$ at a glance. Since the stability of the steady states is governed by the sign of $f'(I^*)$, it is easy to verify that

$$f'(I^* = 0) = \mu(R_0 - 1) \text{ and } f'(I^* = K) = -(\frac{\mu N}{N + K\delta})(R_0 - 1) \tag{12}$$

so that the steady state $I^* = 0$ is globally and asymptotically stable when $R_0 \leq 1$ and locally unstable if $R_0 > 1$, and the steady state $I^* = I_2^* = K$, which exists only when $R_0 > 1$, is globally and asymptotically stable when it does exist. Thus the representation (11) shows that for any given positive non-zero initial number of infected individuals, say $I(0) = I_0 > 0$, we have two solution regimes as $\tau \to \infty$ as follows:

$$(i) \lim_{\tau\to\infty} I(\tau) = 0 \text{ if } R_0 \leq 1, \quad (ii) \lim_{\tau\to\infty} I(\tau) = I_\infty = I_2^* = K \text{ if } R_0 > 1. \tag{13}$$

Clearly from the formulation, $I(t) = 0\, \forall t > 0$ whenever $I(0) = 0$. Figure 1 (a) and (b) respectively show the long term numerical solution of the equation (8) for the two regimes where $R_0 < 1$ and $R_0 > 1$ respectively. An examination of the behaviour of the steady state I_2^* as a function of R_0, See Figure 1(c), shows that the final finite amplitude steady state solution varies with R_0 only in a narrow band of reproduction numbers. So that a control measure that will reduce R_0 say from 500 to 50 will lead only to a small reduction in the number of infectives in the population. As we had reported before, [25], this behaviour has far reaching consequences on the control of malaria as control measures applied when the reproduction number is far above its critical value, and the number of infectives in the population is large will lead to very small effects in prevalence.

The limiting behaviour given by (13) is all the information that the deterministic model can offer for the reduced model. The interesting question is whether the stochastic analogue of the model can give more information than this. Given the pointers from this deterministic analysis, it is therefore reasonable to study the behaviour of the stochastic analogue of model (11) in the different regions of parameter space where the size of R_0 is compared with 1. We use the rearranged equation (11) to identify model (8) with the logistic type growth model with a density dependent growth rate D_0 and carrying capacity K. See, for example, Nåsel [20]. The total population N is seen here as a parameter in the model and also determines an upper bound for the variable I which in this case models the number of infected humans in the population.

3 Stochastic considerations

The deterministic model predicts a stable endemic equilibrium whenever we start off the process with at least one infected individual so long as the threshold parameter $R_0 > 1$. This prediction is not realistic since the first event, in the sequence of possible events, could be the death of this infective. In this case, the infection will certainly not spread into the population irrespective of whether or not $R_0 > 1$. To investigate this fully, we now study the stochastic analogue of the deterministic model by requiring that such a stochastic model examines the probability of the disease establishing itself in the population and its derivation built on the reduced deterministic model. The stochastic model should account for the basic events of recruitment (infection) and removal (recovery) of individuals in the appropriate state. In conformity with the fact that populations occur in discrete integer units, define a stochastic variable that is restricted to take non-negative integers. In the case here, use a single integer, state variable; namely, the number of infected humans in the population at time τ, $I(\tau)$. The variable, I, then takes values from the set $\{0, 1, 2, \cdots, N\}$ where N is the total human population. Referring to the simplified model (8), the

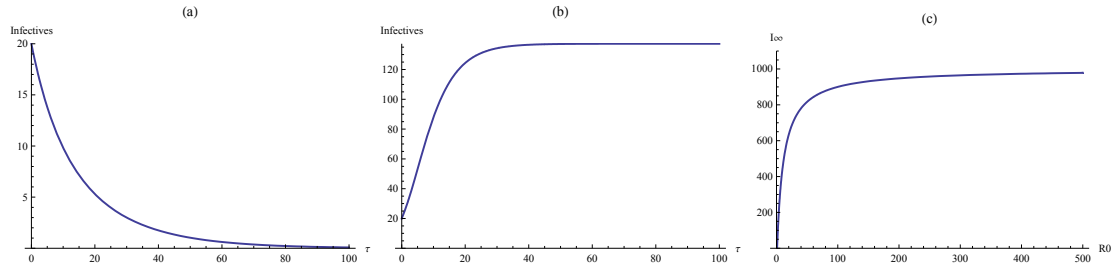

Figure 1: Long term behaviour of the solution of (8) for different values of the parameter R_0. (a) $R_0 = 0.75$ and so the solution converges to the trivial solution, $I = 0$, as $\tau \to \infty$. (b) $R_0 = 2.75$ and so we have an endemic equilibrium solution so that $I_\infty = I_2^*$ defined by (10). (c) The behaviour of the final solution $I_\infty = \lim_{\tau\to\infty} I(\tau)$ as a function of the basic reproduction number R_0. As $R_0 \to \infty$ the number of infectives rise very fast and soon saturates towards the final size of the total population, and the variation of the density of infectives with R_0 is large only in a narrow band of basic reproduction numbers. The parameters, as in [25], are $\mu = 0.2018$, $\delta = 9.998$, $N = 1000$, $D = 201.84R_0$.

	Basic Event	Transition	Transition rate in time $\triangle\tau$
1	Recruitment of a susceptible	$I \to I+1$	$\frac{DI(N-I)\triangle\tau}{N(N+\delta I)}$
2	Removal of an infective	$I \to I-1$	$\mu I \triangle\tau$

Table 1: Hypothesized transition rates for the elementary events which constitute the stochastic version of the deterministic model (8).

transition rates of the various events which constitute the dynamics of the system are displayed in Table 1.

Once the stochastic frame work is established, instead of writing down a set of equations whose solutions will give the number of individuals of a given state in the population at the given time τ, we attempt to calculate *the probability that there shall be a certain number of infected individuals in the population at a given time* τ and define

$$P_i(\tau) = \Pr\{I(\tau) = i\},\ i \in \{0, 1, 2, \cdots, N\}. \tag{14}$$

That is, $P_i(\tau)$ is the probability that there are i infectives in the population at time τ. The objective, then, would be to attempt to calculate the values of $P_i(\tau)$ for each $i \in \{0, 1, 2, \cdots, N\}$. One set of equations that model the rate of change of the probability defined by (14) is the set of *Kolmogorov differential equations*. To formulate the Kolmogorov equations, a time interval $(\tau, \tau + \Delta\tau)$ where $\Delta\tau$ is positive and very small compared with τ is considered. It is then assumed that the time interval between any two events in the system under consideration (in this case the events of recovery and infection) is long enough* so that only one of these events can occur at a time. One form of the Kolmogorov equations; the *Forward Kolmogorov differential equations* [32, 29], model the rate of change of probability defined by (14). In Table 1, $I \to I + 1$, for example indicates the change in the number of infectives from I to $I + 1$. N represents the total human population. The transition rate measures the rate of change of the corresponding transition

*Equivalently it is assumed that the time interval under consideration is so short that only one event can occur within it.

probabilities. Since the process hypothesized in Table 1 is a Markov process, the transition between states in the system is restricted only to the nearest neighbouring states. For example, given a state variable in state i, a transition can only occur from i to $i-1$ or to $i+1$. For the present, lets denote the transition rate per unit time from state i to state $i+1$ by λ_i and the rate of transition per unit time from state i to $i-1$ by μ_i. Then from Table 1,

$$\lambda_i = \frac{D(N-i)i}{N(N+\delta i)},\ \mu_i = \mu i,\ i = 0, \cdots, N. \tag{15}$$

Observe that $\mu_0 = \lambda_N = 0$. This is consistent with the assumption that the state space is limited to $\{0, 1, \cdots, N\}$, and also with the facts that when there are no infected persons in the population their removal rate is obviously zero and when $I = N$ (the entire population is infected) there are no susceptible individuals left to get exposed to the infection. Again observe that $\lambda_0 = 0$ is consistent with the assumption that when there are no infected individuals in the population, further infections cannot occur and the infection has been *eradicated* or has gone *extinct*. The state $I = 0$ is an *absorbing* state.

Starting from the definition of $P_i(\tau)$ together with the rates λ_i and μ_i whose specific forms are given by (15) and employing standard techniques [32], we derive the Kolomogorov forward differential equations for P_i, namely;

$$\frac{dP_i(\tau)}{d\tau} = \lambda_{i-1}P_{i-1}(\tau) - (\lambda_i + \mu_i)P_i(\tau) + \mu_{i+1}P_{i+1}(\tau),\quad P_i(0) = \begin{cases} 1, & i = i_0 \\ 0, & i \neq i_0, \end{cases} \tag{16}$$

where $i = 0, 1, \cdots, N$ and $P_i(\tau) = 0$ for $i < 0$ and $i > N$, and i_0 is the initial number of infectives. The $N + 1$ equations listed in (16) together with the $N + 1$ initial conditions constitute the stochastic analogue of the reduced deterministic model (8). The total human population size, N, appears as a parameter in the system of equations (16) with initial conditions shown. This is an advantage which the stochastic formulation has over its deterministic counterpart. We now examine the existence of stationary distributions for our problem.

3.1 Stationary Distributions

In this subsection, we establish that for any given initial probability distribution, the system of probability equations (16) satisfying the indicated initial condtions does not have a limiting equilibrium probability distribution of population sizes in which $i \neq 0$.

Theorem 3.1 (Absence of non-trivial equilibrium distributions.) *Let $P_i(\tau)$, for each $i \in \{0, 1, 2 \cdots, N\}$ be the probability whose distribution at time $\tau > 0$ satisfies the system* (16) *together with the indicated initial conditions. Then there does not exist a limiting equilibrium or stationary distribution for which $P_i \neq 0$ is constant $\forall\, i \in \{0, 1, \cdots, N\}$. That is*

$$\frac{dP_i}{d\tau} = 0 \Leftrightarrow P_i = \begin{cases} 1, & i = 0, \\ 0, & \textit{otherwise.} \end{cases} \tag{17}$$

Proof: If $P_i = 0$ or $P_i = 1$, $\forall\tau$, then obviously $\frac{dP_i}{d\tau} = 0$. Now let P_i^* be the equilibrium or stationary distribution of P_i. Then P_i^*, $i = 0, 1, 2, \cdots, N$ satisfies

$$\lambda_{i-1}P_{i-1}^* - (\lambda_i + \mu_i)P_i^* + \mu_{i+1}P_{i+1}^* = 0,\ i = 0, 1, 2, \cdots, N;\quad P_{-1}^* = P_{N+1}^* = 0, \tag{18}$$

where λ_i and μ_i are given by (15). Thus, there are, from (18), $N+1$ equations for the unknowns $P_0^*, P_1^*, \cdots, P_N^*$, which can be solved in turn. For $i=0$, we have the equation $\lambda_{-1}P_{-1}^* - (\lambda_0 + \mu_0)P_0^* + \mu_1 P_1^* = 0$. From the definition of the parameters, $P_{-1}^* = 0, \lambda_0 = \mu_0 = 0$ and so we have the single term $\mu_1 P_1^* = 0 \Rightarrow P_1^* = 0$. For $i=1$, we have the equation $\lambda_0 P_0^* - (\lambda_1 + \mu_1)P_1^* + \mu_2 P_2^* = 0$. But From the definition of the parameters $\lambda_0 = 0$, and we have already found $P_1^* = 0$ and so we are left with the equation $\mu_2 P_2^* = 0 \Rightarrow P_2^* = 0$. As we continue for subsequent i, we find that each $P_i^* = 0$ for $i = 1, 2, \cdots, N$ since $\lambda_0 = \mu_0 = \lambda_N = 0$ from (15). We then note that since P_i^*, $i = 0, 1, 2, \cdots, N$ are probabilities, $\sum_{i=0}^{N} P_i^* = 1 \Rightarrow P_0^* = 1$. □

Theorem 3.1 shows that the process $\{I(\tau)\}$ has the stationary distribution $(1, 0, 0, \cdots, 0)$ and no other. Thus the system (16) for any initial data does not have a limiting equilibrium or stationary probability distribution of population sizes in which the number of infective individuals, $I \neq 0$. Therefore, in this case, the *stationary solution is degenerate and non-informative*. The state $i = 0$ is, therefore, an absorbing state, since when the system enters this state it cannot come out again. In fact a disease dynamic with an absorbing state is desirable, especially if the absorbing state corresponds to the disease free state. We have here an eradication criterion in which we seek to find conditions such that the system gets absorbed and the infection eliminated. What is sure is that most diseases, for which the dynamics has an absorbing states, do not enter absorption in finite time. However, if it is known that the process whose probability distribution is given by the system (16) under the transition rates shown in Table 1, has been going on for a long time, and if absorption has not yet occurred, then the state of the system can be well approximated by a *quasi-stationary distribution* [20]. Unfortunately, the quasi stationary distribution is not easy to compute and we next seek ways of approximating it.

3.2 Two auxiliary processes

Even though the system that we have developed has a degenerate stationary distribution, we still seek to make approximations to what we shall refer to as a *quasi- stationary distribution* in the rest of this paper. To do this we start by studying two auxiliary process, originally discussed by Kryscio and Lefẽvre [8] and then in detail by Nåsell [16, 17, 20], that may initially serve as approximations to the stationary distribution. Both of the approximating processes are infection-recovery processes whose transition rates are *very close* to those given in (15), but with the advantage that the approximating processes now have non-degenerate stationary distributions that can be found explicitly. The state space of each of the approximating processes is $\{1, 2, \cdots, N\}$, and differs from the state space of the original process, $\{I(\tau), \tau \geq 0\}$ only by the fact that it does not include the state 0. If we denote the two auxiliary processes by $\{I^{(0)}(\tau), \tau \geq 0\}$ and $\{I^{(1)}(\tau), \tau \geq 0\}$, we proceed to define them as follows: For the process $\{I^{(0)}(\tau), \tau \geq 0\}$, denote its recovery and infection rates by $\mu_i^{(0)}$ and $\lambda_i^{(0)}$ respectively and demand that its recovery rate $\mu_1^{(0)}$ from the state 1 to the state $\{0\}$ is equal to 0, while all other transition rates are equal to the corresponding rates for the original process. It might be instructive to described this process as the original process with the origin removed. The process $\{I^{(1)}(\tau), \tau \geq 0\}$ should have recovery and infection rates denoted by $\mu_i^{(1)}$ and $\lambda_i^{(1)}$ respectively. It is derived from the original process by allowing for one permanently infected individual, so that each recovery rate $\mu_i^{(1)}$ is replaced by $\mu_i^{(1)} = \mu_{i-1}$ while each of the infection rates, $\lambda_i^{(1)}$, equals the corresponding infection rates of the original process. Let the state probabilities for the process $\{I^{(0)}(\tau), \tau \geq 0\}$ be denoted by $\mathbf{P}^{(0)}(\tau) = (P_1^{(0)}(\tau), P_2^{(0)}(\tau), \cdots, P_N^{(0)}(\tau))$, while those for the process $\{I^{(1)}(\tau), \tau \geq 0\}$ are denoted

by $\mathbf{P}^{(1)}(\tau) = (P_1^{(1)}(\tau), P_2^{(1)}(\tau), \cdots, P_N^{(1)}(\tau))$, then expressions for the stationary distribution for the two auxiliary processes can be found as it is now demonstrated.

Theorem 3.2 (The auxiliary process $\{I^{(1)}\}$.) *Let λ_i and μ_i be defined as in (15), then the stationary distribution, $P_i^{(1)}$, of the process $\{I^{(1)}(\tau)\}$ is given by the relation*

$$P_i^{(1)} = \rho_i P_1^{(1)},\ \rho_i = \begin{cases} \frac{\lambda_1\lambda_2\lambda_3\cdots\lambda_{i-1}}{\mu_1\mu_2\mu_3\cdots\mu_{i-1}}, i = 2, 3, \cdots, N, \\ 1, i = 1. \end{cases} \qquad P_1^{(1)} = \frac{1}{\sum_{i=1}^{N}\rho_i} \tag{19}$$

Proof: The Kolmogorov forward differential equations for the process $\{I^{(1)}(\tau)\}$ are given by the relation

$$\frac{dP_i^{(1)}(\tau)}{d\tau} = \lambda_{i-1}^{(1)}P_{i-1}^{(1)}(\tau) - (\lambda_i^{(1)} + \mu_i^{(1)})P_i^{(1)}(\tau) + \mu_{i+1}P_{i+1}^{(1)}(\tau), \tag{20}$$

where for $i = 1, 2, \cdots, N$, $\lambda_i^{(1)} = \lambda_i$, $\mu_i^{(1)} = \mu_{i-1}$ with λ_i and μ_i given by (15). As $\tau \to \infty$, $\boldsymbol{P}^{(1)}(\tau)$ takes on a positive constant value $\boldsymbol{P}^{(1)}$ (since a steady state exists for this process) and hence, from (20), one gets the relation $\lambda_{i-1}^{(1)}P_{i-1}^{(1)} - (\lambda_i^{(1)} + \mu_i^{(1)})P_i^{(1)} + \mu_{i+1}P_{i+1}^{(1)} = 0$, which in terms of the infection and recovery rates of the original process, is $\lambda_{i-1}P_{i-1}^{(1)} - (\lambda_i + \mu_{i-1})P_i^{(1)} + \mu_i P_{i+1}^{(1)} = 0$. Rearranging this, one gets the relation, $P_{i+1}^{(1)} = (\frac{\lambda_i}{\mu_i} + \frac{\mu_{i-1}}{\mu_i})P_i^{(1)} - \frac{\lambda_{i-1}}{\mu_i}P_{i-1}^{(1)},\ i = 1, 2, \cdots, N$, from which it follows that

$$P_2^{(1)} = \frac{\lambda_1}{\mu_1}P_1^{(1)},\ P_3^{(1)} = \frac{\lambda_1\lambda_2}{\mu_1\mu_2}P_1^{(1)},\ P_4^{(1)} = \frac{\lambda_1\lambda_2\lambda_3}{\mu_1\mu_2\mu_3}P_1^{(1)},\ P_5^{(1)} = \frac{\lambda_1\lambda_2\lambda_3\lambda_4}{\mu_1\mu_2\mu_3\mu_4}P_1^{(1)}, \cdots. \tag{21}$$

The general form is therefore, $P_i^{(1)} = \rho_i P_1^{(1)}, i = 1, 2, \cdots, N$. Since the $P_i^{(1)}$'s are probabilities, $\sum_{i=1}^{N} P_i^{(1)} = 1$. It then follows from (21) that

$$\rho_1 P_1^{(1)} + \rho_2 P_1^{(1)} + \cdots + \rho_N P_1^{(1)} = 1 \Rightarrow P_1^{(1)} = \frac{1}{\sum_{i=1}^{N}\rho_i}$$

which completes the proof of Theorem 3.2. □

In a similar way we establish an expression for the stationary distribution, $P_i^{(0)}$, of the process $\{I^{(0)}(\tau)\}$.

Theorem 3.3 (The auxiliary process $\{I^{(0)}\}$.) *Let ρ_i be defined as in (19) and*

$$\pi_i = \frac{\mu_1}{\mu_i}\rho_i,\ i = 1, 2, \cdots, N. \tag{22}$$

Then the stationary distribution, $P_i^{(0)}$, of the process $\{I^{(0)}(\tau)\}$ is given by the relation

$$P_i^{(0)} = \pi_i P_1^{(0)},\ i = 1, 2, \cdots, N, \quad \textit{with } P_1^{(0)} = \frac{1}{\sum_{i=1}^{N}\pi_i} \tag{23}$$

Proof: The Kolmogorov differential equations for the process $\{I^{(0)}(\tau)\}$ are given by

$$\frac{dP_i^{(0)}(\tau)}{d\tau} = \lambda_{i-1}^{(0)}P_{i-1}^{(0)}(\tau) - \left(\lambda_i^{(0)} + \mu_i^{(0)}\right)P_i^{(0)}(\tau) + \mu_{i+1}^{(0)}P_{i+1}^{(0)}(\tau), \tag{24}$$

where

$$\lambda_i^{(0)} = \frac{D(N-i)i}{N(N+\delta i)} = \lambda_i,\ \forall i \text{ and } \mu_i^{(0)} = \begin{cases} 0,\ i=1, \\ \mu i,\ i=2,3,\cdots,N. \end{cases} \tag{25}$$

As $\tau \to \infty$, one gets $\frac{dP_i^{(0)}(\tau)}{d\tau} = 0$, that is $\lambda_{i-1}P_{i-1}^{(0)} - (\lambda_i + \mu_i)\,P_i^{(0)} + \mu_{i+1}P_{i+1}^{(0)} = 0$, from which it follows that $P_{i+1}^{(0)} = \left(\frac{\lambda_i}{\mu_{i+1}} + \frac{\mu_i}{\mu_{i+1}}\right) P_i^{(0)} - \left(\frac{\lambda_{i-1}}{\mu_{i+1}}\right) P_{i-1}^{(0)}$. Thus

$$P_2^{(0)} = \frac{\mu_1}{\mu_2}\left(\frac{\lambda_1}{\mu_1}\right) P_1^{(0)},\ P_3^{(0)} = \frac{\mu_1}{\mu_3}\left(\frac{\lambda_1\lambda_2}{\mu_1\mu_2}\right) P_1^{(0)},\ P_4^{(0)} = \frac{\mu_1}{\mu_4}\left(\frac{\lambda_1\lambda_2\lambda_3}{\mu_1\mu_2\mu_3}\right) P_1^{(0)}, \cdots .$$

It therefore establishes the general form $P_i^{(0)} = \pi_i P_1^{(0)}, 1 = 1,2,\cdots,N$, which establishes the relation (23). Since the $P_i^{(0)}$'s are probabilities, it follows that $\pi_1 P_1^{(0)} + \pi_2 P_1^{(0)} + \cdots + \pi_N P_1^{(0)} = 1 \Rightarrow P_1^{(0)} = \frac{1}{\Sigma_{i=1}^N \pi_i}$ □

Having established that the process understudy does not have a stationary distribution because of the absorptive nature of the degenerate stationary state, we take on board the fact that the process can still run for a long time without absorption, and therefore must be in some from of equilibrium. *The equilibrium configuration conditioned on non absorption is what we have identified as the quasi-stationary* distribution. We formally identify the two processes: $\{I^{(0)}\}$ and $\{I^{(I)}\}$ as precursors to, and first approximation of, the stationary distribution of the process under study and then use them as a basis for studying the approximations of quasi stationary distribution and make use of the expressions for ρ_i and π_i arising from the definition of the two processes $\{I^{(0)}\}$ and $\{I^{(I)}\}$.

3.3 The quasi-stationary distribution

To define and study the quasi-stationary distribution, $\mathbf{q}$, of the process $\{I(\tau)\}$, the state space is partitioned into two subsets, one containing the absorbing state $\{0\}$ and the other equal to the set of transient states $\{1,2,\cdots,N\}$. Corresponding to this partition, the vector $\mathbf{P}(\tau)$ is written in the block form $\mathbf{P}(\tau) = (P_0(\tau), \mathbf{P}_Q(\tau))$ where $\mathbf{P}_Q(\tau) = (P_1(\tau), P_2(\tau), \cdots, P_N(\tau))$ is a row vector of state probabilities in the set of transient states. Let us denote the quasi-stationary state probabilities by $\tilde{q}_i(\tau)$. Then $\tilde{\mathbf{q}}(\tau) = (\tilde{q}_1(\tau),\ \tilde{q}_2(\tau), \cdots, \tilde{q}_N(\tau))$ is the row vector of conditional state probabilities. $\tilde{q}_i(\tau)$ is defined as

$$\tilde{q}_i(\tau) = \Pr\{I(\tau) = i | i > 0\} = \frac{\Pr\{I(\tau) = i,\ i > 0\}}{\Pr\{I(\tau) > 0\}} = \frac{P_i(\tau)}{1 - P_0(\tau)},\ i > 0. \tag{26}$$

Thus the vector of conditional state probabilities, $\tilde{\mathbf{q}}(\tau)$, can be determined from the vector $\mathbf{P}_Q(\tau)$ of state probabilities on the set of transient states via the relation

$$\tilde{\mathbf{q}}(\tau) = \frac{\mathbf{P}_Q(\tau)}{1 - P_0(\tau)}. \tag{27}$$

Differentiate the relation (27) with respect to τ, to obtain

$$\tilde{\mathbf{q}}'(\tau) = \frac{\mathbf{P}'_Q(\tau)(1 - P_0(\tau))}{(1 - P_0(\tau))^2} + \frac{P'_0(\tau)\mathbf{P}_Q(\tau)}{(1 - P_0(\tau))^2}. \tag{28}$$

Apply the relation $P_0'(\tau) = \mu_1 P_1(\tau)$ to have

$$\tilde{\mathbf{q}}'(\tau) = \frac{\mathbf{P}_Q'(\tau)}{1 - P_0(\tau)} + \frac{\mathbf{P}_Q(\tau)\mu_1 P_1(\tau)}{(1 - P_0(\tau))^2}. \tag{29}$$

Apply the relation (26) to obtain

$$\frac{d\tilde{\mathbf{q}}(\tau)}{d\tau} = \left(\frac{1}{1 - P_0(\tau)}\right)\left(\frac{d\mathbf{P}_Q(\tau)}{d\tau} + \mathbf{P}_Q(\tau)\mu_1\tilde{q}_1\right). \tag{30}$$

But $\mathbf{P}_Q(\tau) = (P_1(\tau), P_2(\tau), \cdots, P_N(\tau))$. Hence, $\mathbf{P}_Q'(\tau) = (P_1'(\tau), P_2'(\tau), \cdots, P_N'(\tau))$, and $P_i'(\tau)$ satisfies (16). Thus applying relation (27) and setting the time derivatives to zero, in view of obtaining the stationary solution, $\tilde{q} = \tilde{q}(\infty)$, the limiting value of the solution of the nonlinear differential equation (30) as $\tau \to \infty$, the quasi-stationary distribution is identified as the solution to the system of equations

$$\lambda_{i-1}\tilde{q}_{i-1} - (\lambda_i + \mu_i)\tilde{q}_i + \mu_{i+1}\tilde{q}_{i+1} = -\mu_1\tilde{q}_1\tilde{q}_i, i = 1, 2, \cdots, N, \quad \tilde{q}_i = 0 \text{ for } i < 1 \text{ and } i > N. \tag{31}$$

For notational convenience, simply write $\mathbf{q} = (q_1, q_2, \cdots, q_N)$ instead of $\tilde{\mathbf{q}} = (\tilde{q}_1, \tilde{q}_2, \cdots, \tilde{q}_N)$ for the row vector of quasi-stationary probabilities. Since the transition rates are non-linear, the system (31) has no explicit solution for the quasi-stationary probability distribution, since the solution depends on the unknown value of q_1. As a result, alternative means of obtaining the quasi-stationary distribution must be sought. The sought after *quasi-stationary distribution* $\boldsymbol{q}$ of the original process, that is the stationary solution conditioned on non-extinction, is the stationary solution of (30) which in expanded form satisfies (31).

We start by establishing the following expression for the quasi-stationary state probabilities, q_i.

Theorem 3.4 (The quasi-stationary probabilities) *Define π_i as in (22) and ρ_i as in (19), then the the state probabilities of the quasi-stationary distribution are given by the implicit relation*

$$q_i = \pi_i \sum_{j=1}^{i} \frac{\left(1 - \sum_{k=1}^{j-1} q_k\right)}{\rho_j} q_1, \ i = 1, 2, \cdots, N, \quad \textit{Where} \ \sum_{i=1}^{N} q_i = 1. \tag{32}$$

Proof: From equation (31), the probabilities q_i satisfy the following difference equation:

$$\mu_{i+1}q_{i+1} - (\lambda_i + \mu_i)q_i + \lambda_{i-1}q_{i-1} = -\mu_1 q_1 q_i, \ i = 1, 2, \cdots, N, \quad q_0 = 0 = q_{N+1} = q_{-1}. \tag{33}$$

Define

$$f_i = \mu_i q_i - \lambda_{i-1}q_{i-1}, \ i = 1, 2, \cdots, N. \tag{34}$$

Then

$$f_1 = \mu_1 q_1 \text{ since } \lambda_0 = 0 \text{ and } f_{i+1} = \mu_{i+1}q_{i+1} - \lambda_i q_i, i = 1, 2, \cdots, N-1 \tag{35}$$

From (33) with (34) and (35), it is easy to see the relation $f_{i+1} - f_i = -\mu_1 q_1 q_i \Rightarrow f_{i+1} = f_i - \mu_1 q_1 q_i, i = 1, 2, \cdots, N$. Hence, $f_2 = \mu_1 q_1[1 - q_1]$, $f_3 = \mu_1 q_1[1 - (q_1 + q_2)]$, $f_4 = \mu_1 q_1[1 - (q_1 + q_2 + q_3)]$, $\cdots$. These then give the general result

$$f_i = \mu_1 q_1 \left(1 - \sum_{k=1}^{i-1} q_k\right), \ i = 2, 3, \cdots, N. \tag{36}$$

Inserting (36) into (34) gives the relation $\mu_i q_i = \lambda_{i-1} q_{i-1} + \mu_1 q_1 \left(1 - \sum_{k=1}^{i-1} q_k\right)$, from which it follows that

$$q_i = \frac{\lambda_{i-1}}{\mu_i} q_{i-1} + \frac{\mu_1}{\mu_i} \left(1 - \sum_{k=1}^{i-1} q_k\right) q_1, \ \mu_i \neq 0, \forall i. \tag{37}$$

From (37),

$$\begin{aligned}
q_2 &= \frac{\lambda_1}{\mu_2} q_1 + \frac{\mu_1}{\mu_2} (1 - q_1) q_1, \\
q_3 &= \frac{\lambda_1 \lambda_2}{\mu_2 \mu_3} q_1 + \frac{\mu_1 \lambda_2}{\mu_2 \mu_3} (1 - q_1) q_1 + \frac{\mu_1}{\mu_3} (1 - (q_1 + q_2)) q_1, \\
q_4 &= \frac{\pi_4}{\rho_1} q_1 + \frac{\pi_4}{\rho_2} (1 - q_1) q_1 + \frac{\pi_4}{\rho_3} \left(1 - \sum_{k=1}^{2} q_k\right) q_1 + \frac{\pi_4}{\rho_4} \left(1 - \sum_{k=1}^{3} q_k\right) q_1, \\
q_5 &= \frac{\pi_5}{\rho_1} q_1 + \frac{\pi_5}{\rho_2} (1 - q_1) q_1 + \frac{\pi_5}{\rho_3} \left(1 - \sum_{k=1}^{2} q_k\right) q_1 + \frac{\pi_5}{\rho_4} \left(1 - \sum_{k=1}^{3} q_k\right) q_1, \\
&+ \frac{\pi_5}{\rho_5} \left(1 - \sum_{k=1}^{4} q_k\right) q_1, \cdots .
\end{aligned}$$

By calculating a few more terms, it is seen that the general form for q_i is given by (32). Since the q_i's are probabilities, it then follows that $\sum_{i=1}^{N} q_i = 1$. □

4 Approximating the quasi-stationary distribution and time to extinction

Approximations of quasi-stationary distributions are important since explicit solutions are not available. In fact, the expression (32) does not give the quasi-stationary distribution in explicit form since each term in the sum over j depends on the q_k values and each q_i, in turn, depends on the unknown probability q_1. However, it can be used to successively determine the values of q_2, q_3, and so on, if q_1 is known. Since q_1 can only be determined from the relation $\sum_{i=1}^{N} q_i = 1$ which requires knowledge of all the q_i, this method becomes impossible to apply. In any case, since the processes are recursive, we can employ iterative methods as, for example, described in Nisbert and Gurney [29], Nåsell [20]. In such iterative methods, q_1 is determined based on the recurrence relation (32) and the recognition method starts with an initial guess for q_1, determines $q_2, q_3, q_4, ..., q_N$, by repeated application of (32) and the requirement that $\sum_{i=1}^{N} q_i = 1$, computes the sum of the q_i and determines the result of the first iteration as the initial guess divided by this sum. The process is repeated until successive iterates are sufficiently close. Renshaw [32] describes a diffusion approximation as a alternative method for approximating the quasi-stationary distribution. The above mentioned methods for finding the quasi-stationary distribution do not take into consideration the threshold value, R_0, which we now consider. We shall then use our approximation for the quasi-stationary distribution to approximate the time to extinction.

4.1 Approximating the quasi-stationary distribution

We approach the approximation problem by using the results of the two approximating processes as defined and established in Theorems 3.2 and 3.3. Now, for linear transition rates such as $\lambda_i = i\lambda$ and $\mu_i = i\mu$, we obtain for ρ_i from (19) the relation $\rho_i = \left(\frac{\lambda}{\mu}\right)^{i-1}$, and expression given in terms of the ratio of the population infection rate to the population recovery rate. However, for processes in which one or both of the transition rates are non-linear, obtaining an explicit expression for ρ_i from (19) will become difficult. Now, in our case, not both of the expressions for the transition rates in (15) are linear in the variable i. λ_i, for example, is non-linear in i. An additional difficulty in our case comes from considering very large N. Inserting the transition rates for λ_i and μ_i from (15) into (19) and (22) for large N results in some non-explicit and complicated expressions for ρ_i and π_i. As a result, the method for deriving approximations of the quasi-stationary distribution and the time to extinction should start with deriving approximations of expressions for ρ_i and π_i. In fact, when we insert the expressions for the transition rates λ_i and μ_i given in (15), we arrive at expressions for ρ_i and π_i in terms of i and the three parameters N, R_0 and δ. To derive an asymptotic approximations for ρ_i, we need a precise definition of what we mean by an asymptotic expansion.

Definition 4.1 *Let $f : I \to \mathbb{R}$ be a real function that depends on a parameter ϵ so that its value at each $t \in I$ is $f(t;\epsilon)$, depending as well on the parameter ϵ. The sum $\sum_{k=0}^{\infty} a_k(t)\epsilon^k$ is an asymptotic expansion of $f(t;\epsilon)$ if and only if for all $n \geq 0$,*

$$\frac{f(t;\epsilon) - \sum_{k=0}^{n} a_k(t)\epsilon^k}{a_n(t)\epsilon^n} \quad \to \quad 0 \text{ as } \epsilon \to 0. \tag{38}$$

That is, the sum $\sum_{k=0}^{\infty} a_k(t)\epsilon^k$ is an asymptotic expansion of $f(t;\epsilon)$ if the remainder, $f(t;\epsilon) - \sum_{k=0}^{n} a_k(t)\epsilon^k$, is smaller than the last term in the expansion.

Remark 4.1 *Let $I \subseteq [0,\ \infty[$ be some domain. One way to recognize an asymptotic expansion is to assert that if the expansion is of the form $\sum_{k=0}^{\infty} a_k(t)\epsilon^k$, it is an asymptotic expansion (with respect to ϵ) of a function, for $t \in I$, then $\frac{a_{k+1}(t)\epsilon^{k+1}}{a_k(t)\epsilon^k} \to 0$ as $\epsilon \to 0$. That is, successive terms in the expansion are small compared with the previous terms.*

We start with an asymptotic approximation of ρ_i for large N.

Theorem 4.1 *Let ρ_i be defined as in (19). Let*

$$g(i) = \frac{\sqrt{1 + \frac{\delta i}{N}}}{R_0\sqrt{1 - \frac{i}{N}}}, \quad h(i) = i\log(R_0) - (N-i)\log(1 - \frac{i}{N}) - (\frac{N}{\delta} + i)\log(1 + \frac{\delta i}{N}). \tag{39}$$

Then

$$\rho_i \quad \approx \quad g(i)e^{h(i)},\ i = 1, 2, \cdots, N,\ N \text{ large}. \tag{40}$$

Proof: By inserting the expressions for the transition rates λ_i and μ_i given in (15) into the relation for ρ_i as given by (19), we obtain

$$\rho_i \;=\; \frac{(N-1)(N-2)(N-3)\cdots(N-(i-1))(i-1)!}{(\frac{N}{\delta}+1)(\frac{N}{\delta}+2)(\frac{N}{\delta}+3)\cdots(\frac{N}{\delta}+(i-1))(i-1)!}\left(\frac{R_0}{\delta}\right)^{i-1}. \tag{41}$$

The numerator of the right hand side of (41) can be expressed as $\frac{(N-1)!}{(N-i)!}$ and the denominator as $\frac{(\frac{N}{\delta}+(i-1))!}{(\frac{N}{\delta})!}$. Thus (41) becomes

$$\rho_i = \frac{(N-1)!(\frac{N}{\delta})(\frac{N}{\delta}-1)!}{(N-i)(N-i-1)!(\frac{N}{\delta}+(i-1))!}\left(\frac{R_0}{\delta}\right)^{i-1} = \frac{\Gamma(N)\Gamma(\frac{N}{\delta})N}{R_0(N-i)\Gamma(N-i)\Gamma(\frac{N}{\delta}+i)}\left(\frac{R_0}{\delta}\right)^{i}, \tag{42}$$

where the Gamma function, $\Gamma(x)$, defined by

$$\Gamma(x) \;=\; \int_0^\infty t^{x-1}e^{-t}dt,$$

has the property that $\Gamma(x+1) = x\Gamma(x)$ with $\Gamma(1) = 1$, so that when x is an integer, $\Gamma(x) = (x-1)!$. Nàsell [20] uses Stirling's formula, $x! \approx x^x e^{-x}\sqrt{2\pi x}$, to approximate the Gamma function as

$$\Gamma(x) \;\approx\; \left(\frac{x}{e}\right)^x\left(\frac{2\pi}{x}\right)^{\frac{1}{2}}. \tag{43}$$

Observe from the initial expression for ρ_i (42) that as N grows very large, $N-i$ grows very large as well as $\frac{N}{\delta}+i$ and $\frac{N}{\delta}$, for some fixed δ, since $\delta > 0$. Since the Stirling's formula is used to approximate $n!$ for n very large, we can, for large N, use the approximation (43) to approximate the Gamma function in (42) to obtain

$$\rho_i \;\approx\; \frac{1}{R_0}\frac{\sqrt{1+\frac{\delta i}{N}}\;R_0^i}{\sqrt{1-\frac{i}{N}}\left(1-\frac{i}{N}\right)^{N-i}\left(1+\frac{\delta i}{N}\right)^{\frac{N}{\delta}+i}} = g(i)e^{h(i)}. \tag{44}$$

□

Next, we shall use the approximation of ρ_i prescribed by Theorem 4.1, namely (44), to derive three other asymptotic approximations of ρ_i. The first is derived for i-values in the vicinity of the i-value, $i = K$, where $h(i)$ is maximum (since K is the deterministic endemic steady state), while the other two hold for smaller values of i. Precisely for $i = O(\sqrt{N})$ and $i = o(\sqrt{N})$ for N large. We verify that $i = K$ is the i-value for which $h(i)$ is maximum, i-real valued. By differentiating (39) with respect to i, we find that

$$h'(i) \;= \log R_0 + \log(1-\tfrac{i}{N}) - \log(1+\tfrac{\delta i}{N}) = \;\log\left(\frac{(1-\frac{i}{N})R_0}{1+\frac{\delta i}{N}}\right), \tag{45}$$

and then observe that $h'(i) = 0$ for $i = K$, the non-zero steady state for the deterministic model, where K is defined in (11). The second derivative gives $h''(K) < 0$, $K \neq N$, which shows that this point corresponds to the maximum for the function h.

Theorem 4.2 *Let* $\varphi(x) = \frac{1}{\sqrt{2\pi}} exp(-\frac{x^2}{2})$ *denote the standard normal density function. Let*

$$y_1(i) = \tfrac{i-K}{\sigma_1},\ K = \tfrac{N(R_0-1)}{R_0+\delta},\ \sigma_1 = \tfrac{\sqrt{NR_0(\delta+1)}}{R_0+\delta}, \beta_1 = \sqrt{2h(K)}, \tag{46}$$

and ρ_i *be defined as in (19). Then*

$$\rho_i \approx \frac{1}{\sqrt{R_0}} \frac{\varphi(y_1(i))}{\varphi(\beta_1)},\ y_1(i) = O(1),\ 1 \le i \le N,\ N \text{ large.} \tag{47}$$

Proof: For i-values in the vicinity of the i-values where $h(i)$ is maximum, we first approximate $g(i)$ and $h(i)$ using Taylor expansions about K and then we substitute these approximations in (40). We include only one term in the Taylor expansion of $g(i)$ and three terms in the Taylor expansion of $h(i)$ to best capture the result. The first three terms in the Taylor expansion of $h(i)$ about K are

$$h(i) \approx h(K) + h'(K)(i-K) + \frac{h''(K)}{2!}(i-K)^2. \tag{48}$$

where

$$\begin{aligned} h(K) &= K\log R_0 - (N-K)\log(1-\frac{K}{N}) - \left(\frac{N}{\delta}+K\right)\log(1+\frac{\delta K}{N}) \\ h'(K) &= 0, \text{ since } h(i) \text{ has a maximum at } K \\ h''(K) &= -\left\{\frac{1}{N-K} + \frac{\delta}{N+\delta K}\right\} = \frac{-N(1+\delta)}{(N-K)(N+\delta K)}. \end{aligned}$$

Define $\sigma_1^2 = -\frac{1}{h''(K)}$, β_1 and $y_1(i)$ as in (46). Then $\sigma_1^2 = \frac{(N-K)(N+\delta K)}{N(1+\delta)}$, $y_1^2(i) = \frac{N(1+\delta)}{(N-K)(N+\delta K)}(i-K)^2$. With these relations for σ_1^2, β_1 and $(y_1(i))^2$, $h(i)$ simplifies to

$$h(i) \approx \frac{1}{2}\beta_1^2 - \frac{1}{2}y_1^2(i). \tag{49}$$

The first (constant) term in the Taylor expansion of $g(i)$ about K gives

$$g(i) \approx \frac{1}{R_0}\sqrt{\frac{NR_0+\delta NR_0}{N\delta+N}} = \frac{1}{\sqrt{R_0}}. \tag{50}$$

These approximations of $h(i)$ and $g(i)$ are asymptotic since succeeding terms in each Taylor expansion are of decreasing order in N. Using the approximation (40) of ρ_i, we obtain
$\rho_i \approx g(i)e^{h(i)} \approx \frac{1}{\sqrt{R_0}} e^{\frac{\beta_1^2}{2} - \frac{y_1^2(i)}{2}} = \frac{1}{\sqrt{R_0}} \frac{\varphi(y_1(i))}{\varphi(\beta_1)}$. □

To approximate ρ_i for smaller values of i, we first approximate $g(i)$ and $h(i)$ by Taylor expansions about 0. We will include one term in the Taylor expansion of $g(i)$ and three terms in the Taylor expansion of $h(i)$. The following theorem establishes an approximation of ρ_i for smaller i-values and N large.

Theorem 4.3 *Define* $\varphi(x)$ *as in theorem (4.2),* ρ_i *as in (19), and*

$$\begin{cases} y_2(i) = \frac{i-\mu_2}{\sigma_2},\ \mu_2 = \frac{N}{1+\delta}\log(R_0),\ \sigma_2 = \sqrt{\frac{N}{1+\delta}},\ \beta_2 = \sqrt{\frac{N}{1+\delta}}\log(R_0), \\ y_2^2(i) = \left(\frac{1+\delta}{N}\right) i^2 - 2i\log(R_0) + \frac{N}{1+\delta}(\log(R_0))^2. \end{cases} \tag{51}$$

Then

$$\rho_i \approx \frac{1}{R_0}\frac{\varphi(y_2(i))}{\varphi(\beta_2)},\ i = O(\sqrt{N}),\ 1 \le i,\ N \text{ large} \tag{52}$$

$$\rho_i \approx R_0^{i-1},\ i = o(\sqrt{N}),\ 1 \le i,\ N \text{ large}. \tag{53}$$

Proof: The sum of the first three terms in the Taylor expansion of $h(i)$ about 0 gives the following result

$$h(i) \approx i\ \log(R_0) - \frac{1}{2}\frac{(1+\delta)}{N}i^2. \tag{54}$$

In terms of y_2 and β_2 defined in (51),

$$h(i) \approx \frac{1}{2}\beta_2^2 - \frac{1}{2}y_2^2,\ i = O(\sqrt{N}),\ N \text{ large}. \tag{55}$$

The constant term $h(0) = 0$ in this case. The constant term in the Taylor expansion of $g(i)$ about 0 gives

$$g(i) \approx \frac{1}{R_0},\ i = O(\sqrt{N}),\ N \text{ large}. \tag{56}$$

Both approximations are asymptotic since succeeding terms in each of the Taylor expansions are of decreasing order in N when $i = O(\sqrt{N})$. By inserting the approximations (55) and (56), of $h(i)$ and $g(i)$ respectively, into the asymptotic approximation (40) for ρ_i, we obtain $\rho_i \approx \frac{1}{R_0}e^{\frac{\beta_2^2}{2} - \frac{y_2^2(i)}{2}} = \frac{1}{R_0}\frac{\varphi(y_2(i))}{\varphi(\beta_2)}$, which gives the result (52). If we further impose a restriction that i is asymptotically smaller than $\sqrt{N}$, we obtain

$$h(i) \approx i\log(R_0),\ i = o(\sqrt{N}),\ 1 \le i,\ N \text{ large}. \tag{57}$$

From the relation $\frac{i}{N} < \frac{i}{\sqrt{N}}$, we deduce that for a given i, $\lim_{N\to\text{large}}\frac{i}{\sqrt{N}} = \lim_{N\to\text{large}}\frac{i}{N} = 0$. So, that Considering this argument in (39) will yield (57). Substituting $g(i) \approx \frac{1}{R_0}$ from (56) and $h(i) \approx i\log(R_0)$ from (57) in (40), for ρ_i, we obtain $\rho_i \approx \frac{1}{R_0}e^{i\log(R_0)} = R_0^{i-1}$. establishing the result (53). □

The following theorem establishes three asymptotic approximations of π_i.

Theorem 4.4 *Let $\varphi(x), y_1$ and β_1 be defined as in theorem 4.2, y_2, β_2 as in (51). Then*

$$\pi_i \approx \frac{1}{(R_0-1)\sqrt{R_0}}\left(\frac{R_0+\delta}{N}\right)\frac{\varphi(y_1(i))}{\varphi(\beta_1)}\ R_0 > 1,\ y_1(i) = O(1),\ N \text{ large}, \tag{58}$$

$$\pi_i \approx \frac{1}{iR_0}\frac{\varphi(y_2(i))}{\varphi(\beta_2)}, i = O(\sqrt{N}),\ N \text{ large}, \tag{59}$$

$$\pi_i \approx \frac{1}{i}R_0^{i-1}, i = o(\sqrt{N}),\ N \text{ large}. \tag{60}$$

Proof: From the relations $\pi_i = \frac{\mu_1}{\mu_i}\rho_i$ and $\rho_i \approx g(i)e^{h(i)}$ from (22) and (40) respectively, we find that π_i can be approximated as follows:

$$\pi_i \approx \frac{\mu}{\mu i}g(i)e^{h(i)} = g_0(i)e^{h(i)},\ \text{where } g_0(i) = \frac{1}{iR_0}\sqrt{\frac{N+\delta i}{N-i}},\ N \ne i, \tag{61}$$

and $h(i)$ is defined as in (39). The constant term in the Taylor expansion of $g_0(i)$ about $K = \frac{N(R_0-1)}{R_0+\delta}$ gives $g_0(i) \approx g_0(K) = \frac{1}{\sqrt{R_0}(R_0-1)}\left(\frac{R_0+\delta}{N}\right),\ R_0 > 1$. Inserting this approximation of $g_0(i)$ and the approximation $h(i) \approx \frac{1}{2}\beta_1^2 - \frac{1}{2}y_1^2(i)$ from (49) into the asymptotic approximation $\pi_i \approx g_0(i)e^{h(i)}$ from (61) gives
$\pi_i \approx \frac{1}{(R_0-1)\sqrt{R_0}}(\frac{R_0+\delta}{N})\frac{\varphi(y_1(i))}{\varphi(\beta_1)}$, which completes the proof of (58). From the definition of π_i in (22), we have that

$$\pi_i = \frac{1}{i}\rho_i,\ i = 1, 2, \cdots, N, \tag{62}$$

since $\mu_i = \mu i$. Substituting the approximation $\rho_i \approx \frac{1}{R_0}\frac{\varphi(y_2(i))}{\varphi(\beta_2)}$ for $i = O(\sqrt{N})$ and N large from Theorem 4.3 into the relation (62), we obtain $\pi_i \approx \frac{1}{iR_0}\frac{\varphi(y_2(i))}{\varphi(\beta_2)}$, which completes the proof of (59). Furthermore, substituting the approximation $\rho_i \approx R_0^{i-1}$ for $i = o(\sqrt{N})$ and N large from Theorem 4.3 in the relation (62) gives $\pi_i \approx \frac{1}{i}R_0^{i-1}$, which proves (60). □

The forgoing then allow us to write down the approximations for the stationary distribution $\mathbf{P}^{(1)}$ for $1 \le i \le N$. To do this it suffices to derive an approximation of $P_i^{(1)}$, the probability density function of the distribution $\mathbf{P}^{(1)}$. The derivations of the approximations of the stationary probabilities, $P_i^{(1)}$, which are based on the expression $P_i^{(1)} = \rho_i P_1^{(1)},\ i = 1, 2, \cdots, N$, from (19).

Theorem 4.5 *The stationary distribution $\boldsymbol{P}^{(1)}$ is approximated as*

$$P_i^{(1)} \ \approx\ \frac{1}{\sigma_1}\varphi(y_1(i)),\ R_0 > 1,\ R_0 \textit{ fixed},\ y_1(i) = O(1), \tag{63}$$

where σ_1 and $y_1(i)$ are defined as in Theorem 4.2.

Proof: Consider the relation $P_i^{(1)} = \rho_i P_1^{(1)}$. Since the approximation of ρ_i is known from the relation (40), it remains to find an approximation of $P_1^{(1)} = \frac{1}{\sum_{i=1}^N \rho_i}$. The approximation (47) of ρ_i, shows that ρ_i is proportional to the probability $\frac{1}{\sigma_1}\varphi(y_1(i))$ for a normally distributed random variable with mean K and standard deviation σ_1. This approximation is valid for $1 \le i \le N$, where the argument of the function φ is O(1). The sum of all these probabilities over i from 1 to N is asymptotically equal to 1, since this range of i-values cover the body of the distribution. We can thus approximate the sum $\sum_{i=1}^N \rho_i$ as follows:

$$\sum_{i=1}^{N}\rho_i \ \approx\ \frac{1}{\sqrt{R_0}}\frac{1}{\varphi(\beta_1)}\sum_{i=1}^{N}\varphi(y_1(i)) \ \approx\ \frac{\sigma_1}{\sqrt{R_0}\ \varphi(\beta_1)}, \tag{64}$$

since $\sum_{i=1}^N \frac{\varphi(y_1(i))}{\sigma_1} \approx 1$ as $1 \le i \le N$ covers the body of the distribution. It follows from (64) that

$$P_1^{(1)} \ \approx\ \frac{\sqrt{R_0}\varphi(\beta_1)}{\sigma_1} = \frac{R_0+\delta}{\sqrt{N(1+\delta)}}\varphi(\beta_1), R_0 > 1,\ R_0 \text{ fixed}, \tag{65}$$

where we have applied the definition of σ_1 from Theorem 4.2. From the result (65) and the approximation (47) of ρ_i, we obtain $P_i^{(1)} = \rho_i P_1^{(1)} \approx \frac{1}{\sqrt{R_0}}\frac{(R_0+\delta)}{\sqrt{N}\sqrt{(1+\delta)}}\varphi(y_1(i)) = \frac{\varphi(y_1(i))}{\sigma_1}$. □

Remark 4.2 *The result (63) shows that the distribution $\boldsymbol{P}^{(1)}$ is approximately normal for $1 \le i \le N$.*

Next we also derive three asymptotic approximations of the stationary distribution $\mathbf{P}^{(0)}$, one in the body of the distribution (for the range $1 \leq i \leq N$) and two in the left tail of the distribution, precisely for $i = O(\sqrt{N})$ and $i = o(\sqrt{N})$ for N large. These derivations are based on the relation $P_i^{(0)} = \pi_i P_1^{(0)}$ from (23). The approximations in the left tail of the distribution will be used to approximate the time to extinction.

Theorem 4.6 *Define φ, y_1 and β_1 as in theorem 4.2, $y_2(i)$, β_2 as in theorem 4.3. Then we have*

$$P_i^{(0)} \approx \frac{1}{\sigma_1}\varphi(y_1(i)), R_0 > 1, \ R_0 \text{ fixed}, \ y_1(i) = O(1), \ N \text{ large}. \tag{66}$$

$$P_i^{(0)} \approx \frac{(R_0-1)\sqrt{N}}{R_0\sqrt{\delta+1}}\frac{\varphi(\beta_1)}{\varphi(\beta_2)}\frac{\varphi(y_2(i))}{i}, \ R_0 > 1, R_0 \text{ fixed}, i = O(\sqrt{N}), \ N \text{ large}. \tag{67}$$

$$P_i^{(0)} \approx \frac{(R_0-1)\sqrt{N}}{\sqrt{\delta+1}}\varphi(\beta_1)\frac{R_0^{i-1}}{i}, \ R_0 > 1, R_0 \text{ fixed}, \ i = o(\sqrt{N}), \ N \text{ large}. \tag{68}$$

Proof: We use the approximation $\pi_i \approx \frac{1}{(R_0-1)\sqrt{R_0}}(\frac{R_0+\delta}{N})\frac{\varphi(y_1(i))}{\varphi(\beta_1)}$ from (58). As in the preceding section, we make use of the result $\sum_{i=1}^N \frac{\varphi(y_1(i))}{\sigma_1} \approx 1$ to evaluate the sum $\sum_{i=1}^N \pi_i$. From (58), we have

$$\sum_{i=1}^N \pi_i \approx \frac{1}{(R_0-1)\sqrt{R_0}}\left(\frac{R_0+\delta}{N}\right)\frac{1}{\varphi(\beta_1)}\sum_{i=1}^N \varphi(y_1(i)) \approx \frac{\sigma_1(R_0+\delta)}{\sqrt{R_0}(R_0-1)N\varphi(\beta_1)}.$$

From the relation $P_1^{(0)} = \frac{1}{\sum_{i=1}^N \pi_i}$, we obtain

$$P_1^{(0)} \approx \frac{(R_0-1)\sqrt{R_0}N\varphi(\beta_1)}{\sigma_1(R_0+\delta)}. \tag{69}$$

Making use of the approximation of π_i from (58) and $P_1^{(0)}$ from (69) we obtain from the relation $P_i^{(0)} = \pi_i P_1^{(0)}$ the approximation $P_i^{(0)} \approx \frac{1}{(R_0-1)\sqrt{R_0}}(\frac{R_0+\delta}{N})\frac{\varphi(y_1(i))}{\varphi(\beta_1)}\frac{(R_0-1)\sqrt{R_0}N\varphi(\beta_1)}{\sigma_1(R_0+\delta)} = \frac{\varphi(y_1(i))}{\sigma_1}$, establishing the proof of (66). This approximation is valid for $1 \leq i \leq N$. Using the approximation $\pi_i \approx \frac{1}{iR_0}\frac{\varphi(y_2(i))}{\varphi(\beta_2)}$ from (59) and the result (69) of $P_1^{(0)}$, we obtain $P_i^{(0)} \approx \frac{1}{iR_0}\frac{\varphi(y_2(i))}{\varphi(\beta_2)}\frac{(R_0-1)\sqrt{R_0}N\varphi(\beta_1)}{\sigma_1(R_0+\delta)} = \frac{(R_0-1)\sqrt{N}\varphi(\beta_1)\varphi(y_2(i))}{R_0\sqrt{\delta+1}\varphi(\beta_2)i}$, which completes the proof of (67). Using the approximation $\pi_i \approx \frac{1}{i}R_0^{i-1}$ from (60) and the approximation (69) of $P_1^{(0)}$, we are led to the result $P_i^{(0)} \approx \frac{(R_0-1)\sqrt{N}\varphi(\beta_1)R_0^{i-1}}{i\sqrt{\delta+1}}$, which completes the proof of (68). □

Now that we have approximations for the two approximating processes, we are in a position to write down approximations for the quasi-stationary distribution. To derive an approximation for the distribution $\mathbf{q}$, it suffices to derive approximations for the q_i's, the quasi-stationary probabilities whose values are based on the relation (32). To proceed, define

$$\alpha(j) = \frac{1 - \sum_{k=1}^{j-1} q_k}{\rho_j}. \tag{70}$$

The first step in approximating q_i is to find an approximation for the sum over j, or the sum of $\alpha(j)$ in (70), which is then followed by an approximation of the quasi stationary probability, q_1. The next theorem provides an approximation for the sum over j or $\alpha(j)$ (that is, the sum over j in (32)).

Theorem 4.7 *Let $\alpha(j)$ be defined as in (70) and R_0 the threshold value. Then*

$$\sum_{j=1}^{i}\alpha(j)\approx\frac{R_0}{R_0-1}\left(1-\left(\frac{1}{R_0}\right)^i\right), R_0>1, R_0 \text{ fixed}, i=o(\sqrt{N}), N \text{ large}. \tag{71}$$

Proof: We note that the numerator in each term in the sum in (32) is a decreasing function of j and the denominator an increasing function of j, since the quantity ρ_j is proportional to the probabilities $P_j^{(1)}$ which increase monotonically with j over the allowable range of j-values. Thus the terms in the sum over j decrease monotonically, in j, at least up to $j=[\![K]\!]$, where $[\![K]\!]$, denotes the largest integer less than or equal to K. The sum over j is dominated by the sum of the first several terms since the first term in the sum over j equals 1 while the term corresponding to $j=[\![K]\!]$ is very much smaller than 1. We consider j-values up to a value that grows very large as N becomes very large, but for which the growth is slower than $\sqrt{N}$. For such j-values, we make the assumptions $q_j=\ o(1)$ as N grows very large for $j=\ o(\sqrt{N})$. This implies that the numerator of each term is asymptotically equal to 1. From (53), we note that $\rho_j\approx R_0^{j-1}$ if $j=\ o(\sqrt{N})$, for N large. With these considerations, we have the approximation. $\sum_{j=1}^{i}\alpha(j)\approx\sum_{j=1}^{i}\frac{1}{\rho_j}\approx\sum_{j=1}^{i}\frac{1}{R_0^{j-1}}$ which gives (71) for a fixed $R_0>1$, and $i=o(\sqrt{N}), N$ large. □

The next step is to approximate q_1.

Theorem 4.8 *Define β_1 and φ as in theorem 4.2. Then the quasi-stationary probability, q_1, is approximated as*

$$q_1\approx\frac{(R_0-1)^2\sqrt{N}}{R_0\sqrt{\delta+1}}\varphi(\beta_1), R_0>1, R_0 \text{ fixed}, N \text{ large}. \tag{72}$$

Proof: As i becomes very large, we have from (71), $\frac{R_0}{R_0-1}\left(1-\frac{1}{R_0^i}\right)\approx\frac{R_0}{R_0-1}$, since $\left(1-\frac{1}{R_0^i}\right)\ \approx\ 1$. Assuming that the sum over j is approximated by this constant value for all large i-values, we obtain the approximation

$$q_i\ \approx\ \frac{R_0}{R_0-1}\pi_i q_1,\ R_0\ >\ 1,\ R_0 \text{ fixed},\ N \text{ large}. \tag{73}$$

This gives $\sum_{i=1}^{N}q_i\approx\frac{R_0}{R_0-1}\frac{1}{P_1^{(0)}}q_1$, where we have used the expression $\sum_{i=1}^{N}\pi_i=\frac{1}{P_1^{(0)}}$ from (23). Using the condition that $\sum_{i=1}^{N}q_i=1$, we obtain $q_1\approx\frac{(R_0-1)P_1^{(0)}}{R_0}\approx\frac{(R_0-1)^2\sqrt{N}\varphi(\beta_1)}{R_0\sqrt{\delta+1}}$, $R_0>1$, R_0 fixed, N large, where we have applied the approximation of $P_1^{(0)}$ from (69). □

It now remains to establish an explicit approximation for q_i from approximation (73).

Theorem 4.9 *Let y_1,φ and β_1 be defined as in theorem 4.2. Then*

$$q_i\ \approx\ \frac{\varphi(y_1(i))}{\sigma_1}, y_1(i)=O(1),\ N \text{ large}, R_0 \text{ fixed}, R_0\ >\ 1. \tag{74}$$

Proof: From (73), $q_i\approx\frac{\sqrt{R_0}(R_0+\delta)}{(R_0-1)^2N}\frac{\varphi(y_1(i))}{\varphi(\beta_1)}q_1=\frac{\varphi(y_1(i))}{\sigma_1}$, in which we have used the approximations (72) of q_1, and (58) of π_i. □

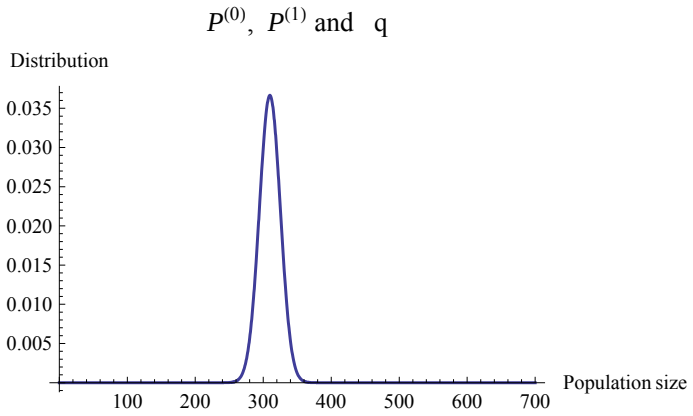

Figure 2: The distributions $\mathbf{P^{(0)}}$ and $\mathbf{P^{(1)}}$ are close to the quasi-stationary distribution, $\mathbf{q}$ when $R_0 > 1$. The two distributions are indistinguishable from $\mathbf{q}$. The parameters, as in [25], are $N = 1000, R_0 = 10.2,\ \delta = 19.5,\ K = 309.76,\ \sigma_1 = 15.396,\ D = 0.102$.

The approximation of q_i in (74) indicates that q_i has a normal distribution in the parameter region, where $R_0 > 1$. In summary, we note that the three distributions; $\mathbf{P}^{(1)}$, $\mathbf{P}^{(0)}$ and $\mathbf{q}$ are approximately normal for $1 \leq i \leq N$ with the mean equal to the non-zero steady state K and standard deviation σ_1, in the parameter region where $R_0 > 1$ is fixed, for N very large. Figure 1 shows a graphical representation of the distributions $\mathbf{P}^{(1)}$, $\mathbf{P}^{(0)}$, and $\mathbf{q}$ when $R_0 > 1$. The approximations $P^{(0)}$, $P^{(1)}$ are indistinguishable from computed q.

4.2 Approximating the time to extinction

The time to extinction, T, is a random variable which depends on the initial distribution. We denote this random variable by T_Q when the initial distribution $P(0)$ equals the quasi-stationary distribution, $\mathbf{q}$, and by T_i when $I(0) = i$, where $I(0)$ is the number of infectives at time 0. If the process has been going on for a long time and it is known that it has not been absorbed, then its distribution is well approximated by the quasi-stationary distribution. To obtain the expected time to extinction from quasi-stationarity, we need to know the probability of ultimate extinction. The following theorem states an approximation of the probability of ultimate extinction, $P_0(\tau)$.

Theorem 4.10 *The probability of ultimate extinction, $P_0(\tau)$, is approximated by*

$$P_0(\tau) \approx 1 - \exp(-\mu_1 q_1 \tau). \tag{75}$$

Proof: We recall that P_0 satisfies the initial value problem $P_0'(\tau) = \mu_1 P_1(\tau),\ P_0(0) = 0$ if absorption has not yet occurred. From (30) we note that at stationarity,

$$\mathbf{P}_Q'(\tau) = -\mu_1 q_1 \mathbf{P}_Q(\tau),\ \mathbf{P}_Q(0) = \mathbf{q}, \tag{76}$$

where $\mathbf{q}$ is the quasi-stationary probability. (76) has the solution $\mathbf{P}_Q(\tau) = \mathbf{q}\exp(-\mu_1 q_1 \tau)$. By the definition of $\tilde{q_i}$, the probability that $I(\tau) = 1$ given that extinction has not occurred, is $P_1(\tau) = \tilde{q_1}(\tau)(1-P_0(\tau)) \approx q_1(1-P_0(\tau)), \tau \to \infty$. Thus $P_0'(\tau) \approx \mu_1 q_1(1-P_0(\tau)) \Rightarrow log(1-P_0(\tau)) \approx -\mu_1 q_1 \tau$ $\Rightarrow P_0(\tau) \approx 1 - e^{-\mu_1 q_1 \tau}$. □

If absorption has occurred at time τ, then the waiting time to extinction, T_Q, is at most equal to τ and also, the state of the system is at zero, that is, $I(\tau) = 0$. Hence the event $\{T_Q \leq \tau\} \equiv \{I(\tau) = 0\}$. Applying (75), we obtain

$$Pr\{T_Q \leq \tau\} = Pr\{I(\tau) = 0\} \quad = \quad P_0(\tau) \approx 1 - \exp(-\mu_1 q_1 \tau).$$

Thus $P_0(\tau)$ is the probability of extinction up to and including the time τ. $\frac{dP_0(\tau)}{d\tau}$ is the probability density of extinction at time τ. This probability density can be used to obtain the expected time to extinction from quasi-stationarity for a population of initial size i which is stated in the next theorem.

Theorem 4.11 *The expected time to extinction from quasi-stationarity, ET_Q, has an exponential distribution with*

$$ET_Q \quad \approx \quad \frac{\sqrt{2\pi}\sqrt{\delta+1}\ R_0\ e^{\gamma_1 N}}{\mu_1(R_0-1)^2\sqrt{N}},\ R_0 > 1,\ R_0 \textit{ fixed},\ N \textit{ large}, \tag{77}$$

where

$$\gamma_1 \quad = \quad \frac{1}{R_0+\delta}\left\{(R_0-1)\log(R_0) - (\delta+1)\log\left(\frac{\delta+1}{R_0+\delta}\right) - R_0\left(\frac{\delta+1}{\delta}\right)\log(R_0)\left(\frac{\delta+1}{R_0+\delta}\right)\right\} = \frac{\beta_1^2}{2}$$

Proof: The mean or average time to extinction from quasi-stationarity for a population of initial size i is $ET_Q(i) = \int_0^\infty \tau\left[\frac{dP_0(\tau)}{d\tau}\right]d\tau$. Since $\lim_{\tau\to\infty}(1-\exp(-\mu_1 q_1\tau)) = 1$, we have that $P_0(\infty) = 1$. Thus from (75), $P_0(\infty) - P_0(\tau) = \exp(-\mu_1 q_1 \tau)$ from which it follows that $\frac{d}{d\tau}\left[P_0(\infty) - P_0(\tau)\right] = -\mu_1 q_1 \exp(-\mu_1 q_1\tau) \approx \frac{-dP_0(\tau)}{d\tau}$. Thus $ET_Q(i) = -\int_0^\infty \tau \frac{d}{d\tau}\left[P_0(\infty) - P_0(\tau)\right]d\tau = \int_0^\infty \left[1 - P_0(\tau)\right]d\tau$, provided that ultimate extinction is certain. Substituting the approximation of P_0, we obtain $ET_Q(i) = \int_0^\infty \exp(-\mu_1 q_1\tau)d\tau = \frac{1}{\mu_1 q_1}$. Since $ET_Q(i)$ is independent of i, we conclude that

$$ET_Q = ET_Q(i) = \frac{1}{\mu_1 q_1}. \tag{78}$$

Also, since the probability density of extinction, $\frac{dP_0(\tau)}{d\tau} = \mu_1 q_1 \exp(-\mu_1 q_1 \tau)$, we conclude that T_Q has an exponential distribution. From (72), $q_1 \approx \frac{(R_0-1)^2\sqrt{N}\varphi(\beta_1)}{R_0\sqrt{\delta+1}}$. Thus $ET_Q \approx \frac{R_0\sqrt{\delta+1}\sqrt{2\pi}e^{\frac{\beta_1^2}{2}N}}{\mu_1(R_0-1)^2\sqrt{N}} = \frac{R_0\sqrt{\delta+1}\sqrt{2\pi}e^{\gamma_1 N}}{\mu_1(R_0-1)^2\sqrt{N}}$

Nåsell [20] gives the expected time to extinction, ET_i, for the logistic growth model from a fixed initial state i as

$$ET_i = \frac{1}{\mu_1}\sum_{k=1}^{i}\frac{\sum_{j=k}^{N}\pi_j}{\rho_k} = \frac{1}{\mu_1 P_1^{(0)}}\sum_{k=1}^{i}\frac{\sum_{j=k}^{N}P_j^{(0)}}{\rho_k} \tag{79}$$

in terms of the probabilities $P_j^{(0)}$. Since the model studied in this work can be represented as a logistic model, it follows that we can apply this expression to our model. Note that the parameter sequences ρ_i and π_i both appear here. Since these parameter sequences are related to the distributions $\mathbf{P}^{(1)}$ and $\mathbf{P}^{(0)}$, we can interpret both numerator and denominator of each term in the sum with the aid of these distributions. By putting $i = 1$ in (79), we obtain

$$ET_1 \quad = \quad \frac{1}{\mu_1 P_1^{(0)}}\sum_{j=1}^{N}P_j^{(0)} = \frac{1}{\mu_1 P_1^{(0)}}, \tag{80}$$

for successive values of i we have

$$ET_2 = \frac{1}{\mu_1 P_1^{(0)}} \sum_{j=1}^{2} \frac{\left(1 - \sum_{k=1}^{j-1} P_k^{(0)}\right)}{\rho_j},\ ET_3 = \frac{1}{\mu_1 P_1^{(0)}} \sum_{j=1}^{3} \frac{\left(1 - \sum_{k=1}^{j-1} P_k^{(0)}\right)}{\rho_j}, \cdots .$$

Continuing with this substitution of values of i in equation (80), we obtain the general expression

$$ET_i \ = \ ET_1 \sum_{j=1}^{i} \frac{\left(1 - \sum_{k=1}^{j-1} P_k^{(0)}\right)}{\rho_j}. \tag{81}$$

Next we derive explicit approximations for the expected time to extinction from the state i.

Theorem 4.12 *The expected time to extinction from the state* 1 *is approximated as*

$$a)\ \ ET_1 \ \approx \ \frac{\sqrt{2\pi}\sqrt{1+\delta}\ e^{\gamma_1 N}}{\mu_1(R_0-1)\sqrt{N}},\ R_0 \ > 1\ ,\ R_0 \textit{ fixed},\ N \textit{ large}$$

The expected time to extinction from the state i is approximated as

$$b)\ ET_i \ \approx \ \frac{\sqrt{2\pi}\sqrt{1+\delta}\ R_0\ e^{\gamma_1 N}}{\mu_1(R_0-1)^2\sqrt{N}} \left(1 - \frac{1}{R_0^i}\right),\ R_0 > 1\ , R_0 \textit{ fixed},\ i = o(\sqrt{N}),\ N \textit{ large}.$$

Proof: Considering $P_i^{(0)} \approx \frac{(R_0-1)\sqrt{N}\varphi(\beta_1)}{\sqrt{\delta+1}} \frac{R_0^{i-1}}{i}$ from (68), for $i = 1$ we obtain $ET_1 \approx \frac{\sqrt{1+\delta}}{\mu_1(R_0-1)\sqrt{N}\varphi(\beta_1)} = \frac{\sqrt{2\pi}\sqrt{1+\delta}\ e^{\gamma_1 N}}{\mu_1(R_0-1)\sqrt{N}}$. The terms in the sum over j in equation (81) decrease monotonically at least up to $j = [\![K]\!]$, since the numerator in each term in the sum is a decreasing function of j and the denominator, an increasing function of j up to $j = [\![K]\!]$. We consider j-values up to a value that grows very large as N grows very large. For such j-values, we make the assumptions that $P_j^{(0)} = o(1)$ as N grows very large for $j = o(\sqrt{N})$. Thus the numerator of each term is asymptotically equal to 1. Since $\rho_j \approx R_0^{j-1}$ for $j = o(\sqrt{N})$ and N large,

$$ET_i \ \approx \ ET_1 \sum_{j=1}^{i} \frac{1}{R_0^{j-1}} \approx ET_1 \left(\frac{R_0}{R_0-1}\right)\left(1 - \frac{1}{R_0^i}\right) = \frac{\sqrt{2\pi}\sqrt{1+\delta}\ R_0\ e^{\gamma_1 N}}{\mu_1(R_0-1)^2\sqrt{N}} \left(1 - \frac{1}{R_0^i}\right).$$

□

Note that ET_i increases monotonically with i from the approximation of ET_1 towards the approximation of ET_Q. Note also that the Expected time to extinction increases exponentially with increasing N and becomes very large for very large values of N. In fact $ET_\star \to \infty$ as $N \to \infty$ so that for large values of N we can say that absorption will not occur readily. This is in conformity with the fact that the disease establishes itself in the population whenever $R_0 > 1$.

5 Discussion

We began by studying a simplified version the deterministic malaria model whose general version was originally derived and studied by Ngwa and Shu [25]. Borrowing a leaf from Michaelis-menten speaudo-steady state hypothesis we reduced the system to a single nonlinear ordinary differential equation under the assumption that the humans have a much longer life span than mosquitoes

and that disease induced death rate is negligible. We showed that the disease-free equilibrium always exists and is stable for $R_0 \leq 1$ and unstable otherwise, while the endemic equilibrium is globally and asymptotically stable for $R_0 > 1$.

We then incorporated stochasticity into the reduced model, and formulated the Kolmogorov forward differential equations for the stochastic model, which was then analysed for the existence and stability of the stationary distribution. The analysis revealed that the stochastic model does not have a non-zero steady state distribution of probabilities and that the stationary distribution is degenerate. This analysis led to the study of the quasi-stationary distribution of the stochastic model. Our results agreed with those obtained by Nåsell [15] who addressed the concepts studied in this paper but with the associated deterministic model being the the classical Ross malaria model. Modern deterministic differential equation models for malaria transmission employ more sophisticated techniques giving rise to equations that also account for the abundance of mosquitoes amidst disease dynamics [22, 23], and even with these more complicated models, vital information as time to extinction and other far reaching results derived in this paper are elusive. This is very understandable since stochastic models are really the natural models [19] and are the ones that are suitable for describing rate of change of populations of living organisms.

Using a comprehensive theory on asymptotic approximation techniques in recurrent epidemics developed by Nåsell Ingemar [15, 16, 17, 18, 19, 20], the quasi-stationary distribution was studied under the assumption that $R_0 > 1$. Owing to the absence of explicit solutions for the quasi-stationary distribution, two approximating distributions, $\mathbf{P}^{(0)}$ and $\mathbf{P}^{(1)}$, were discussed. These approximating processes were employed to get explicit approximations of the quasi-stationary distribution and of the expected time to extinction. We found that the quasi-stationary distribution is approximately normal and is approximated by the distributions $\mathbf{P}^{(0)}$ and $\mathbf{P}^{(1)}$ when $R_0 > 1$. We also found out that the expected time to extinction from quasi-stationarity is approximately exponential and that it can take infinite time for extinction to occur so long as $R_0 > 1$. This is in conformity with the results of the deterministic model which predict that the disease establishes itself in the population when $R_0 > 1$. The time to extinction, being infinite, is indicative of the fact that malaria eradication is not a simple issue when $R_0 > 1$. Thus, to fight against malaria, control measures which will help to bring down R_0 should be employed. With the resulting approximation for the quasi-stationary distribution, $\mathbf{q}$, we can approximate the probability of the disease in the population. The size of mosquito population appeared as a parameter in the model analysed in this paper so that an increase in R_0 was identified with an increase in mosquito populations and as such linking the present work to more recent models for mosquito abundance that have been developed and studied [28, 27]. These models, based on the fact that mosquitoes have a human biting habit, have confirmed the result that perhaps the most efficient mosquito control measure should be civic attitude by permanent human residents in a particular geographic locality in avoiding the creation of breeding sites for the *Anopheles sp.* mosquito. Since, unfortunately, community awareness develops slowly and fades away quickly, we have presented here another reminder that malaria is a real concern, and that the fight to eradicated the infection should be intensified in the face of the realization that the time to extinction is infinite when ever $R_0 > 1$.

When $R_0 \leq 1$, the story is different and we expect finite time to extinction. But this and some other aspects of the malaria problem, such as the issue of partial immunity, the length of the incubation period in humans, the analysis of the stochastic model when total human population is not constant and disease induced deaths are taken into account, numerical computations for approximating the three distributions studied here and other issues are subjects for future work.

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