Dynamics of Triatomine Infestation in a Population of Houses

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Abstract

Trypanosoma cruzi, is the causal agent and parasite of Chagas disease, a neglected tropical disease transmitted mainly by blood-sucking triatomine insects in Latin America. Because of the unavailability of a cure for Chagas disease, disease control relies on the control of the vector population. In this work, we developed deterministic and stochastic mathematical models for the dynamics of bug infestation in a community of houses. We used a Levins metapopulation approach in which houses are considered to be patches that can be in one of three states: empty, infested, or treated. First, we considered spatially implicit models for homogeneous and heterogenous populations. We studied the effect of differences in housing quality in infestation dynamics and the effect of heterogeneity in the distribution of the houses. Then, we developed more realistic spatially explicit, agent-based, metapopulation models. The models were used to assess the effect of different control strategies on house infestation. The results show that spraying only bad houses is more beneficial than spraying the whole community while using the same treatment rate.

1 Introduction

More than 1 billion people all over the world are infected with neglected tropical diseases, such as Chagas disease in Latin America [12]. Chagas disease, also known as American trypanosomiasis, is caused by infection from the protozoan parasite Trypanosoma cruzi (T. cruzi) and is a major vector-borne disease [1, 4, 21, 22]. The organism T. cruzi and the infection in humans were first described in 1909 by the Brazilian physician Carlos R. J. Chagas [5]. T. cruzi is found in mammals and in a variety of bugs including blood-sucking triatomine insects or "kissing bugs". In most countries in the southern cone of South America, triatoma infestans (T. infestans) are by far the main vector of *T. cruzi* [18]. An important charachteristic of T. infestans is that this species has evolved into a primarily

domestic vector preferring to live in and around homes [22]. T. infestans are nocturnal predators that feed on mammals while they sleep, generally on their faces, thus the name kissing bugs [12]. They hide during the day and come out during the night to bite and feed on unsuspecting hosts [18].

The initial phase of Chagas disease is known as the acute phase, and lasts for roughly two months post-infection with little or no symptoms [14,18,19]. Blood tests are important for lowering the probability of infection through blood transfusions, which are a common method of disease transmission in places where the test cannot be afforded [20]. In the subsequent chronic phase, T. cruzi parasites primarily sequester in cardiac and digestive tissues, potentially causing gradual but severe damage to organs [19]. It is also the main cause of cardiopathy in the world [24]. Most cases of Chagas are caused by triatomines when they gorge on a host and instantaneously defecate near the bite. The feces contains the T. cruzi parasite, and when the host scratches the lesion, the contaminated feces enters the lesion and results in transmission of the disease [14]. This phase last 6 to 8 weeks [18] and the infected individuals appear healthy. During this period, the parasite can be detected only by serological or parasitological tests [18]. Several years after infection, untreated patients may start developing lesions on certain organs, mainly the heart and the digestive system.

Currently there are no vaccines available and there is no cure for Chagas disease. Therefore, control measures are focused on controlling vector populations. This may be achieved by different means like periodic insecticide spraying or improving the quality of houses. Mud and thatched houses can gather a tremendous amount of T. infestans over a long period of time [9, 11, 18]. Hay roofs and cracked walls provide an excellent environment for T. infestans populations [16]. Improved houses, with plastered walls and ceilings, provide significantly poorer conditions for the persistance of the T. infestans population. In this work, these two types of houses will be called "bad houses" and "good houses", respectively. In ecological terms, the bad houses act as *sources* because the environment is suitable for vector reproduction, while good houses act as *sinks* because a vector population cannot be sustained here. In this work we will study a source-sink metapopulation dynamic.

In this work we developed and studied several mathematical models on the dynamics of populations of houses. In the models, houses may be in one of three states: empty, infested, or treated. First, we considered a simple homogeneous case where the houses in a single community are all of the same quality and are randomly mixed. Next, we considered houses of two types of quality; bad and good. In the first scenario bad and good houses are distributed randomly in a single community. Then, we considered a segregated community where all of the bad houses are separated from the good houses. In all cases, we developed continuous-time Markov-chain models. Finally, we developed spatially-explicit, stochastic individual based models for the three different cases. Realizations of this model were compared with the solutions of the population level models.

2   Population Level Models

In this section we study house infestation dynamics following an implicit-space Levins metapopulation approach [13]. Each house in the community is considered as a patch which may be in only one of three states: empty, infested or treated [7]. In this simple framework, within house triatomine population dynamics is ignored. We assume that an infested house has some potential to spread the infestation to other houses in the community. We also consider that a house's bug population has some probability per unit of time of becoming extinct, and that houses may be treated (with insecticide, for example). Insecticide is assumed to provide protection against re-infestation for some period of time. We also explored the effect of house heterogeneity on population dynamics. First we considered the case in which the improved houses are randomly distributed. Then we considered the case in which improved houses are all in the same sector, or "neighborhood" of the community.

2.1   Basic Model for a Homogeneous Population

In this first scenario, there is a single community composed of houses of the same quality. The rate of house infestation depends on the number of infested houses as well as the proportion of empty houses in the village. More specifically we assume that infested houses spread the infestation at the rate c. Under the homogeneous mixing assumption only the fraction E/N of the houses is susceptible to infestation. Infested houses become extinct at the rate ϵ. Infested houses are treated at the rate τ and the protection conferred is lost at the rate α. In Figure 1 we show a transfer diagram of our compartmental model.
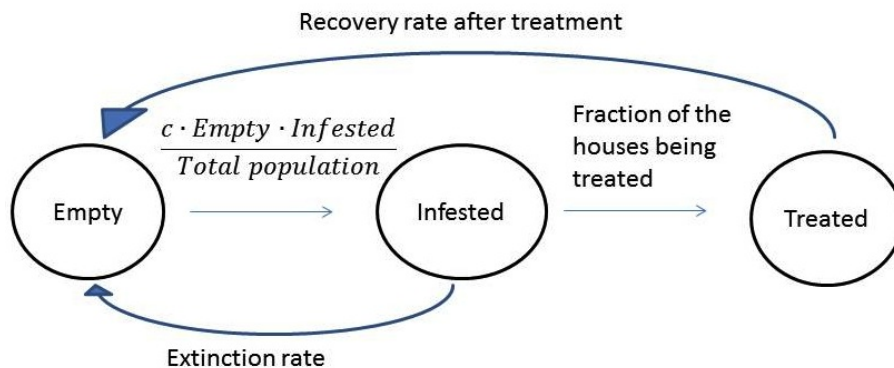

Figure 1: Compartment Model of a Community of Empty(E), Infested(I), and Treated Houses(T)

If E, I and T represent the number of empty, infested and treated houses respectively, then our first model becomes:

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Model 1

$$\frac{dE}{dt} = -\frac{cEI}{N} + \epsilon I + \alpha T \tag{1}$$

$$\frac{dI}{dt} = \frac{cEI}{N} - (\epsilon + \tau)I \tag{2}$$

$$\frac{dT}{dt} = \tau I - \alpha T \tag{3}$$

2.2 House Heterogeneity

In this section we consider two scenarios. In the first scenario, there is a community of good and bad houses which are randomly distributed. In the second scenario the community is composed of good and bad houses separated into two neighborhoods, one containing only good houses and the other containing only bad houses. Mud and thatch roof houses are considered "bad" houses as they may sustain high levels of triatomine infestation [9, 10]. Improved houses do not provide well enough conditions for the bug population to survive and are therefore labeled as "good" houses. We consider that bad houses act as sources, while good houses act as sinks. The reproductive number R_0 will be greater than one for a population of bad houses and less than one for a population of good houses. Because the bug population is substantially higher in bad houses it assumed that $c_b > c_g$ and that $\epsilon_b < \epsilon_g$.

2.2.1 Bad and Good Houses Randomly Distributed

When houses are randomly distributed, each house has the same probability to contact bad or good houses. A straightforward modification of Model 1 leads to:
  Model 2

$$\frac{dE_g}{dt} = -\frac{c_g E_g I_g}{N} - \frac{c_b E_g I_b}{N} + \epsilon_g I_g + \alpha_g T_g \tag{4}$$

$$\frac{dI_g}{dt} = \frac{c_g E_g I_g}{N} + \frac{c_b E_g I_b}{N} - (\epsilon_g + \tau_g)I_g \tag{5}$$

$$\frac{dT_g}{dt} = \tau_g I_g - \alpha_g T_g \tag{6}$$

$$\frac{dE_b}{dt} = -\frac{c_b E_b I_b}{N} - \frac{c_g E_b I_g}{N} + \epsilon_b I_b + \alpha_b T_b \tag{7}$$

$$\frac{dI_b}{dt} = \frac{c_b E_b I_b}{N} + \frac{c_g E_b I_g}{N} - (\epsilon_b + \tau_b)I_b \tag{8}$$

$$\frac{dT_b}{dt} = \tau_b I_b - \alpha_b T_b \tag{9}$$

where the variables denote the total number of houses in the corresponding state and the subindices g and b are used to label good and bad houses respectively. The total number

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of good and bad houses is given by $N_g = E_g+I_g+T_g$ and $N_b = E_b+I_b+T_b$, while the total number of houses is $N = N_b+N_g$. Again, we assume both N_g and N_b are constant and the parameter values used in the simulation are shown in table 1.

The first and second terms in equations (4) and (5) model infestation from bad and good infested houses. Infested good houses become extinct at the rate ϵ_g. Infested good houses are treated at the rate τ_g and the protection conferred is lost at the rate α_g. A similar description follows for bad houses.

2.2.2 Two Patch Model

In this case a further level of heterogeneity is incorporated because we assume that bad and good houses are in different locations of the community. We assume that infested houses are more likely to spread infestation within their own neighborhood. From the potential infestations that a bad house may produce, we assume that only a fraction p takes place among good houses. In general the situation is not symmetrical, we consider that good houses may infest at most a fraction q of bad houses. With this assumption we arrive to the following model:

Model 3

$$\frac{dE_g}{dt} = -\frac{c_b q E_g I_b}{N_g} - \frac{c_g(1-p)E_g I_g}{N_g} + \epsilon_g I_g + \alpha_g T_g \tag{10}$$

$$\frac{dI_g}{dt} = \frac{c_b q E_g I_b}{N_g} + \frac{c_g(1-p)E_g I_g}{N_g} - (\epsilon_g + \tau_g)I_g \tag{11}$$

$$\frac{dT_g}{dt} = \tau_g I_g - \alpha_g T_g \tag{12}$$

$$\frac{dE_b}{dt} = -\frac{c_b(1-q)E_b I_b}{N_b} - \frac{c_g p E_b I_g}{N_b} + \epsilon_b I_b + \alpha_b T_b \tag{13}$$

$$\frac{dI_b}{dt} = \frac{c_b(1-q)E_b I_b}{N_b} + \frac{c_g p E_b I_g}{N_b} - (\epsilon_b + \tau_b)I_b \tag{14}$$

$$\frac{dT_b}{dt} = \tau_b I_b - \alpha_b T_b \tag{15}$$

where $p \in [0, \frac{N_b}{N}]$ and $q \in [0, \frac{N_g}{N}]$; A significant feature of Model 3 is that it reduces to Model 2 for $p = \frac{N_b}{N}$ and $q = \frac{N_g}{N}$.

Table 1: Parameters for Model 1,2, & 3

Parameter	Definition	Value
c	Rate of Colonization	$0.8\ year^-1$
τ	Rate of Treatment	$0.2\ year^-1$
α	Removal Rate from Treatment	$3\ year^-1$
ϵ	Extinction Rate	$0.5\ year^-1$
c_g	Colonization Rate from a Good House	$0.2\ year^-1$
ϵ_g	Extinction Rate of the Vectors in a Good House	$0.4\ year^-1$
α_g	Rate it Takes to Become Empty after Being Treated for Good Houses	$3\ year^-1$
τ_g	Treatment Rate of the Good Houses	$[0,.05]\ year^-1$
c_b	Colonization Rate from a Bad House	$0.5\ year^-1$
ϵ_b	Extinction Rate of the Vectors in a Bad House	$0.2\ year^-1$
α_b	Rate it Takes to Become Empty after Being Treated for Bad Houses	$3\ year^-1$
τ_b	Treatment Rate of the Bad Houses	$[0,.1]\ year^-1$
q	Probability of Infestation from Bad to Good Community	.1
p	Probability of Infestation From Good to Bad Community	.1
β	Rate of Infestation Per Contact	$.137\ year^-1$
β_b	Rate of Infestation Per Contact of a Bad House	$.04\ year^-1$
β_g	Rate of Infestation Per Contact of a Good House	$.075\ year^-1$
R_{0g}	Basic Reproductive Number of Good Houses With no Treatment	.5
R_{0b}	Basic Reproductive Number of Bad Houses With no Treatment	2.5

2.3 Continuous-Time Markov Chain Models

As we are dealing with relatively small populations, stochastic effects are expected to be relevant. We developed Continuous Time Markov Chain models for each of the three scenarios described previously (Model 1, 2, and 3). Processes are defined on a continuous time scale, $t \in [0,\infty)$, but the states $E(t)$, $I(t)$, and $T(t)$ are discrete random variables, $E(t), I(t), T(t) \in 0, 1, 2, ..., N$. The $Prob(I(t_n + 1)|I(t_0), I(t_1), ..., I(t_n)) = Prob(I(t_{n+1})|I(t_n))$ for any sequence of real numbers satisfying $0 < t_0 < t_1 < ... < t_n < t_{n+1}$. The transition probability at time t_{n+1} only depends on the most recent time t_n. The transition probabilities are defined for a small time interval dt. For the simple case of an homogenous population without treatment the model is defined by:

$$P(I(t+\delta t)=j|I(t)=i) = \begin{cases} \frac{cEI}{N}\delta t & j=i+1 \\ \epsilon I \delta t & j=i-1 \\ 1-(\frac{cEI}{N}+\epsilon I)\delta t & j=i \\ 0 & j\neq i, i-1, i+1 \end{cases} \qquad (16)$$

$$P(E(t+\delta t)=j|E(t)=i) = \begin{cases} \frac{cEI}{N}\delta t & j=i-1 \\ \epsilon I \delta t & j=i+1 \\ 1-(\frac{cEI}{N}+\epsilon I)\delta t & j=i \\ 0 & j\neq i, i-1, i+1 \end{cases} \qquad (17)$$

Where parameters c, τ and ϵ have the same meaning as in model 1. In this model E and I are discrete variables taking only positive integer values or zero. The time interval between consecutive events is a continuous random variable exponentially distributed with mean $\frac{1}{(\frac{cEI}{N}+\epsilon I)}$. The rates of infestation $\frac{cEI}{N}$, and extinction ϵI, are known as the *transition rates* and give the probability per unit of time of occurrence of each one of the different events: infestation and extinction. Stochastic versions of models 2 and 3, including treatment, were developed in a similar way.

The numerical simulations for these systems were performed using the Gillespie method [8]. This is a generic algorithm that can be applied to any Markov Chain system. The first step is to initialize the number of E, I, and T houses in the system. The time interval between consecutive events is computed as $\delta t = \frac{log(\frac{1}{r})}{TR}$ where $r \in (0,1)$ is a random number uniformly distributed in $(0,1)$ and $TR = \frac{cEI}{N} + \epsilon I$ is the total transition rate. Then events are selected at some probability that is proportional to their transition rates. The variables are updated according to the event selected. For example in the case of infestation $E \to E - 1$, $I \to I + 1$. The process is iterated until desired.

3 Stability Analysis and Basic Reproduction Numbers

In this section we study the local stability of the equilibrium for each deterministic model. We also computed the basic reproductive numbers using the next generation operator method [2]. Details are provided in Appendix A.

3.1 Basic Model

Basic reproduction number computed for Model 1 is

$$R_0^{(1)} = \frac{c}{\epsilon + \tau} \qquad (18)$$

which has a straight forward interpretation as the number of secondary cases produced by one infested house in a population of empty houses. In this case houses are infested at rate c while $\frac{1}{\epsilon+\tau}$ is the mean infestation period.

Model 1 has two equilibrium points, the infestation free equilibrium $E_1 = (N, 0, 0)$, and the endemic equilibrium:

$$E_2 = (\frac{N(\epsilon+\tau)}{c}, \frac{\alpha N(c-\epsilon-\tau)}{c(\tau+\alpha)}, \frac{(N\tau)(c-\epsilon-\tau)}{c(\tau+\alpha)}) = (\frac{N}{R_0}, \frac{\alpha N}{\alpha+\tau}(R_0-1), \frac{\tau N}{\alpha+\tau}(R_0-1)).$$

This expression shows explicitly that endemic equilibrium exists only for $R_0 > 1$. The infestation free equilibrium is stable for $R_0 < 1$ and it is unstable for $R_0 > 1$ (see Appendix A for details).

3.2   Randomly Distributed Houses in the Same Community

For Model 2 the basic reproduction number can be expressed as the weighted average

$$R_0^{(2)} = \frac{N_b}{N} R_{0b} + \frac{N_g}{N} R_{0g} \tag{19}$$

where $R_{0b} = \frac{c_b}{\epsilon_b+\tau_b}$ and $R_{0g} = \frac{c_g}{\epsilon_g+\tau_g}$ are the basic reproductive numbers of Model 1 for the cases of only bad and only good houses. In our simulations we considered that in absence of treatment $R_{0g} = .5$ and $R_{0b} = 2.5$, and then $R_0^{(2)} = 1.5$. A low treatment rate of $\tau_b = .1$ (and $\tau_g = 0$) is then enough to put infestation under control as in this case $R_0^2 \approx 1$.
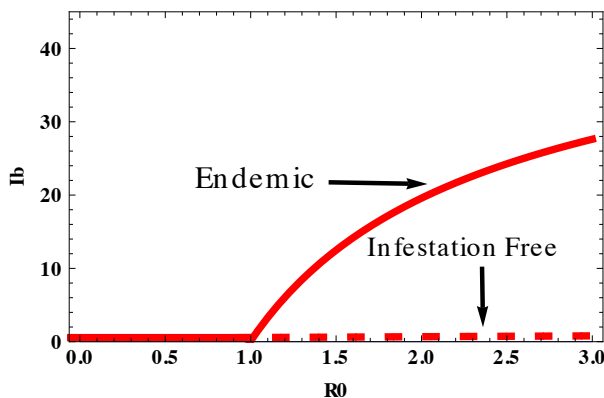

Figure 2: Bifurcation diagram of basic reproduction number vs. equilibrium value of I_b of model 2. When $R_0 = 1$, the endemic equilibrium becomes stable and the disease free equilibrium becomes unstable. This was done in a similar fashion for model 3 with the same qualitative behavior.

Figure 2 shows the bifurcation diagram for infested houses. This behavior is qualitatively the same for the two patch model but with different quantitative values.

3.3 Two Patch Model

When heterogeneity in house distribution is considered the basic reproduction number becomes

$$R_0^{(3)} = \frac{R_{0g}(1-p) + R_{0b}(1-q) + \sqrt{(R_{0g}(1-q) + R_{0b}(1-q))^2 - 4R_{0g}R_{0b}(1-p-q)}}{2}.$$

(20)

When $p = \frac{N_b}{N}$ and $q = \frac{N_g}{N}$, $R_0^{(3)}$ coincides with the expression for $R_0^{(2)}$ as expected. For $p = q = 0.1$ and $\tau_b = 0.1$, we obtain $R_0 = 1.51$. In the previous section, we observed that the infestation was under control ($R_0^2 \approx 1$) with $\tau_b = .1$. However, when there are separate patches infestation is well above the threshold. A higher constant rate of spraying of $\tau_b = 0.25$ is needed in order to obtain $R_0^{(3)} \approx 1$. This is a more than double of the per infested hose rate needed to control infestation in a randomly mixed community.

4 The Effect of Different Treatment Regimes: An assessment by Numerical Simulations

We explored the effect of different control strategies for the different scenarios under study using models 2 & 3. In all cases, we considered a village of 1024 houses[1]. Because of the small population size of the village, stochastic factors are expected to play a significant role on the dynamics [6, 15].

4.1 Randomly Distributed Houses in the Same Community

Without treatment, house infestation reaches its equilibrium values monotonically. Figure 3A displays typical solutions. As expected, the deterministic solution presents an initial phase of exponential growth which is not apparent in some stochastic simulations (which show an almost linear growth). The effect of treatment at a constant rate is shown in Figure 3B where the initial conditions correspond to the equilibrium values of the model without treatment.

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[1]Later we will consider spatial arrangements of $L \times L$ houses. A population of 1024 houses corresponds to the case $L = 32$
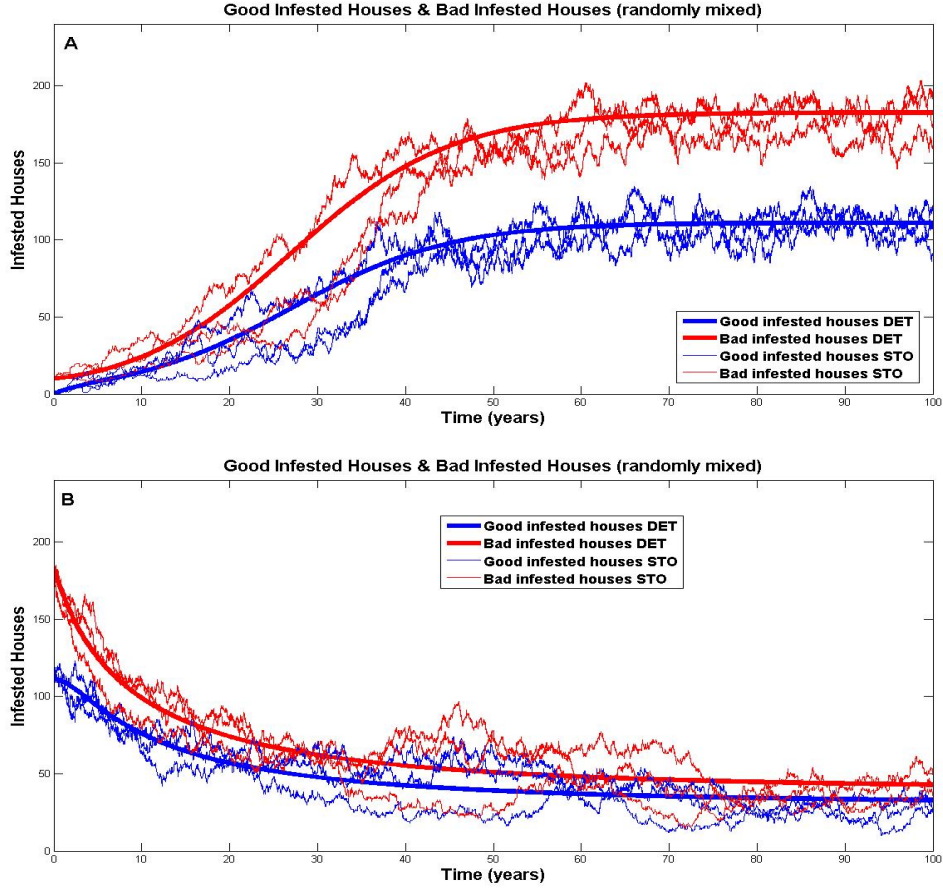
Figure 3: Figure A: Infested houses with a treatment of $\tau_b = 0$ and an initial value of 111 houses. Figure B: Infested houses with a treatment of $\tau_b = .1$ and an intial value of 183 houses

In Figure 3, we compare the solutions obtained with $\tau_b = 0$ and $\tau_b = .1$.

4.2 Two Patch Model

Again, we look at solutions of infested houses with the same initial conditions. The focus is now on a community with bad and good houses grouped separately.
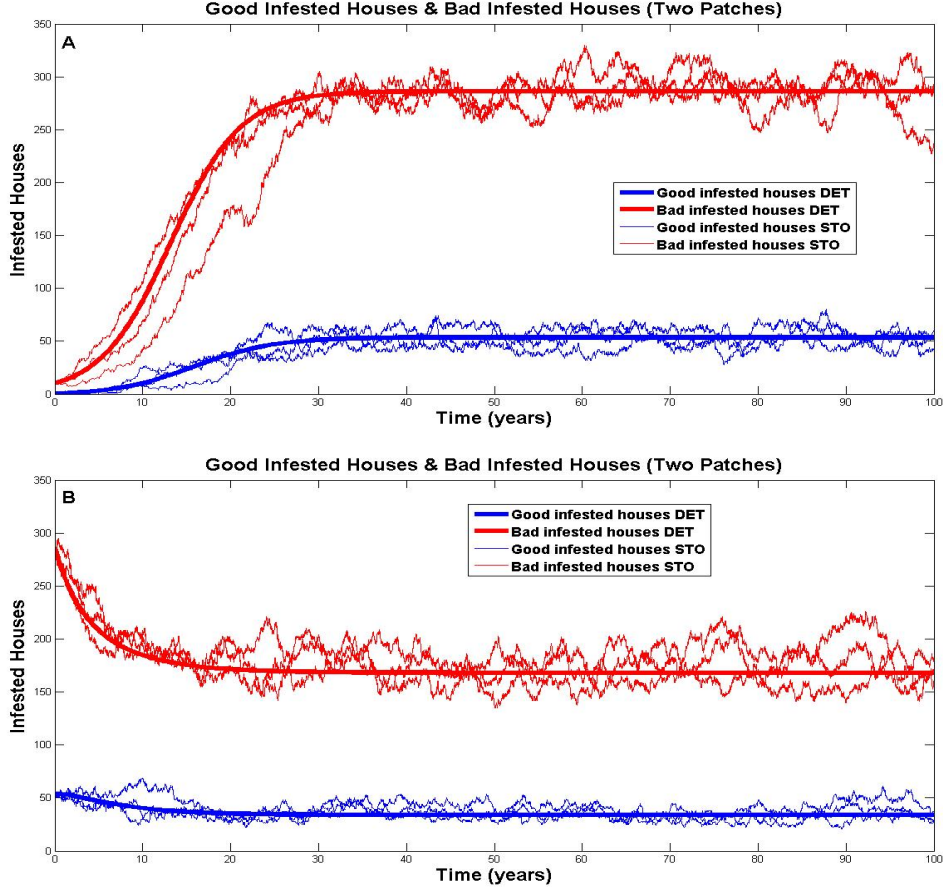
Figure 4: Figure A: Infested houses with a treatment of $\tau_b = 0$ and an initial value of 54 houses. Figure B: Infested houses with a treatment of $\tau_b = .1$ and an intial value of 286 houses

As in the previous case we first consider the dynamics in absence of treatment. The infested population rises exponentially after the introduction of infestation in the population then it reaches the equilibrium monotonically (see Figure 4A). Using these equilibrium values as initial conditions we studied the effect of treating only bad houses at a constant rate. In Figure 4B we show the results obtained for $\tau_b = 0.1$ ($\tau_g = 0$). Treatment is significantly less effective in this case than for the community with randomly mixed houses.

4.3 Insecticide Spray use: bad houses vs whole community

One question that may be asked is focusing on the bad houses in case of spray or the whole community including the good houses while keeping the percentage of pesticide used the same. An analysis is done on both the bad and good randomly distributed houses and the two patch model. We first spray only the bad houses, then the whole community with the

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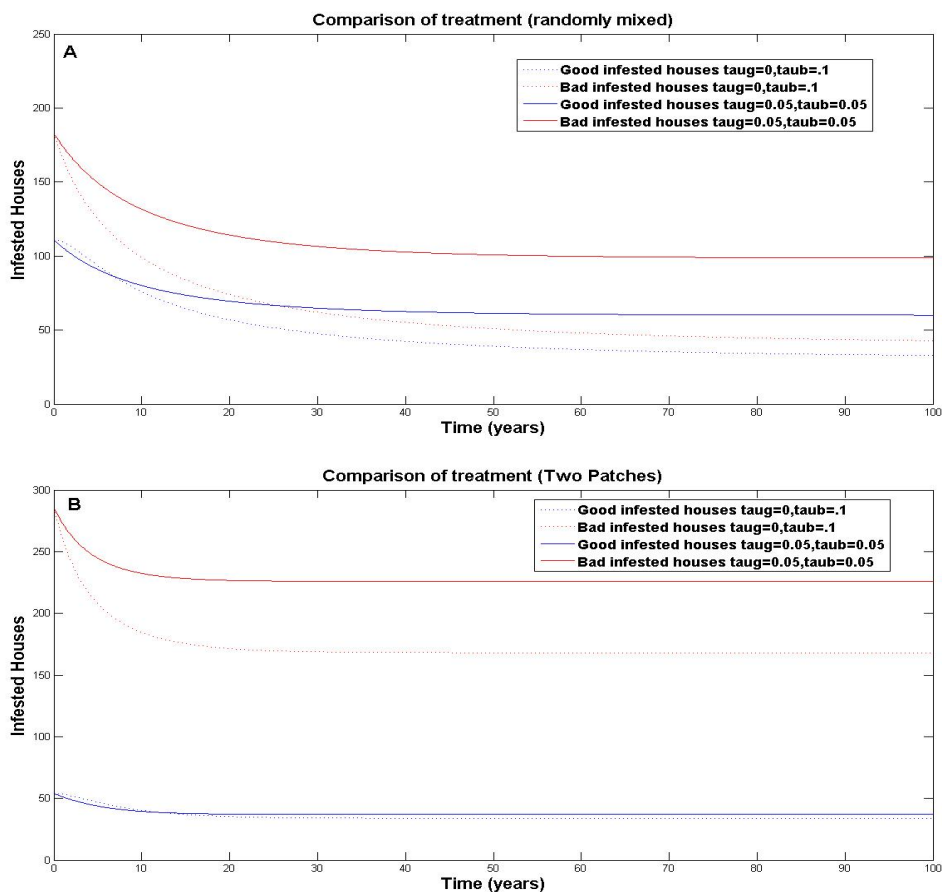same amount of pesticide to see which way is more efficient.

Figure 5: A. Equally spray with $\tau_b = .05$ and $\tau_g = .05$ vs. spray of only bad houses with $\tau_b = .05$ in randomly mixed community B. Equally spray with $\tau_b = .05$ and $\tau_g = .05$ vs. spray of only bad houses with $\tau_b = .05$ in two pacthes

Using the equilibrium values obtained without treatment we compared the effect of treating only bad houses or both types of houses. In the first case we used a constant rate $\tau_b = 0.1$ (and $\tau_g = 0$) while in the second we used $\tau_b = 0.5$ and $\tau_b = 0.05$. Simulations displayed in Figure 5 A and Figure 5 B show that concentrating the treatment on only the bad houses is more efficient. Should be noticed that because $I_g < I_b$ for all time we are not simulating the use of the same amount of insecticide in both cases.

5 Spatially Explicit Models

In this section we explore the consequences of space on the dynamics of infestation. In all cases we consider a square arrangement of $L \times L$ houses, in which all the houses are equally spaced apart from each other. In a period δt an infested house may become empty with probability $p_e = 1 - e^{-\epsilon \delta t}$. In a similar fashion we assume that an empty house in contact with one infested house may become infested with probability $p_I = 1 - e^{-\beta_i \delta t}$ where β_i is the rate of infestation per contact. Probability of infestation of an empty house in contact with n infested houses is given then by $1 - (1 - p_I)^n$. Treated houses may become susceptible to re-infestation with probability $p_e = 1 - e^{-\tau_i \delta t}$.

5.1 Spatial Spread Dynamics in a Homogeneous Population

In the following we will consider a square arrangement of $L \times L$ houses. Except in the borders, each house is surrounded by eight closest neighbors. We will assume that infestation may take place only from those neighbors. Figure 6 illustrates the smaller scale of a community of only infested and empty houses.
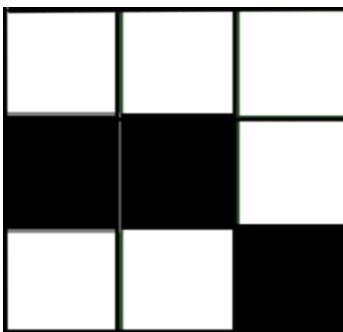

Figure 6: White squares are infested and black squares are empty. The center square can be infested by the top three, directly right, directly down and bottom left squares.

While the parameters ϵ, τ and α have the same meaning and values than those used in the population level models, the probability of infestation per house and per unit of time, β, is different (but related) to the infestation rate c.
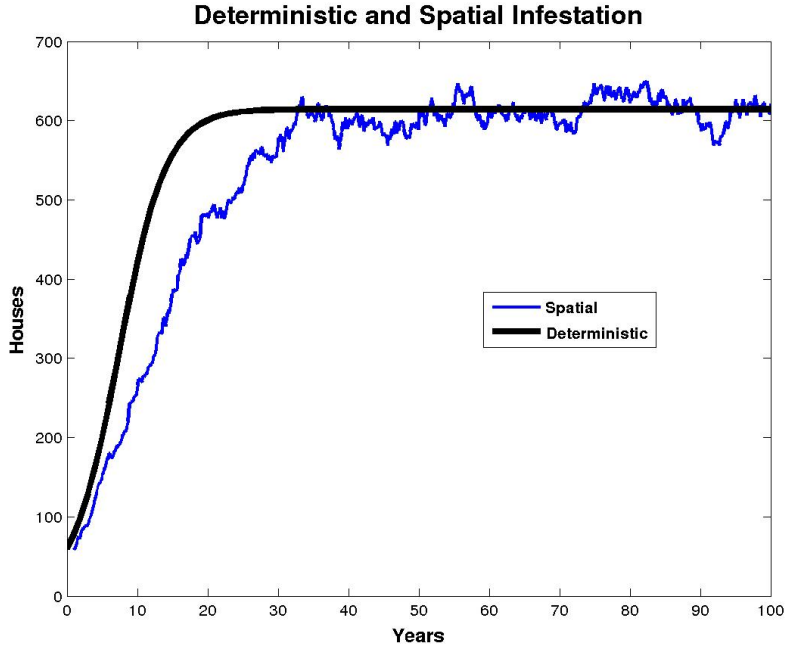
Figure 7: The case of only bad houses the infestation is increasing exponentially for the deterministic and linearly for the spatial model

The value of β was chosen by fitting the deterministic solutions of Model 1 (for good and bad houses). In figure 7 we show the solution of model 1 together with a realization of the stochastic spatial model. Since the spatial model allows only for infestation between neighboring houses, the number of infested houses does not show the initial phase of exponential growth characteristic of homogeneous mixing models (like Model 1).

5.2 House Heterogeneity and Infestation Dynamics in Spatially Explicit Models

We are modeling the same situation as in Models 2 and 3, but considering now the spatial distribution of houses.

5.2.1 Randomly Distribution of Different Quality Houses

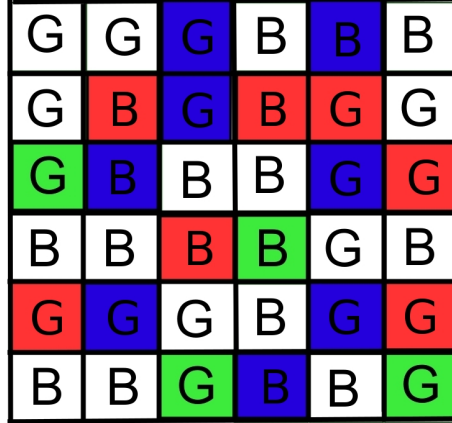Here it is assumed that N_g good houses are located at random throughout a village with a total of N houses.

Figure 8: The blue squares denote empty good quality houses. The red squares denote empty bad quality houses. White denotes infested houses and green denotes treated houses and "G" denotes good quality and "B" denotes bad quality houses.

The probability of house infestation is computed taking into account that neighboring infested houses may be 'good' or 'bad'. If n_g and n_b are the number of good and bad infested houses in contact with an empty house then the probability of infestation in a time interval δt is given by $1 - (1 - e^{-\beta_b \delta t})^{n_b}(1 - e^{-\beta_g \delta t})^{n_g}$ where β_b and β_g were estimated in the same fashion described in Section 5.1. A good treated house can go into an empty state with probability $1 - e^{-\alpha dt}$ and a bad treated house with probability $1 - e^{-\tau_b dt}$.

5.2.2 Two Patch Model

It is a plausible assumption that all houses good and bad are mixed in the same village. But it is also possible that for example, the people that are more wealthy have better houses and are separated from the rest of the bad houses.
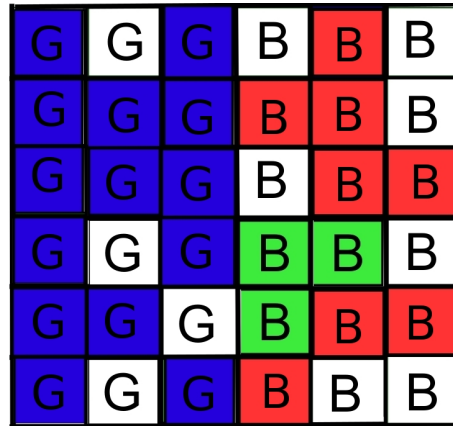
Figure 9: The blue squares denote empty good quality houses. The red squares denote empty bad quality houses. White denotes infested houses and green denotes treated houses and "G" denotes good quality and "B" denotes bad quality houses.

In the two patch model bad and god houses are in contact with each other only in the boundary between the two neighborhoods. In this case good houses are less likely to be infested from bad houses compared with the case of randomly mixed houses.

On the other hand, when houses are randomly mixed bad houses are less likely to infest other bad houses.

5.3   Treatment in a Spatial Context

Now we will assess the effect of treatment using the spatial models. First we simulated the spread of infestation without treatment for the randomly mixed and two-patch cases.
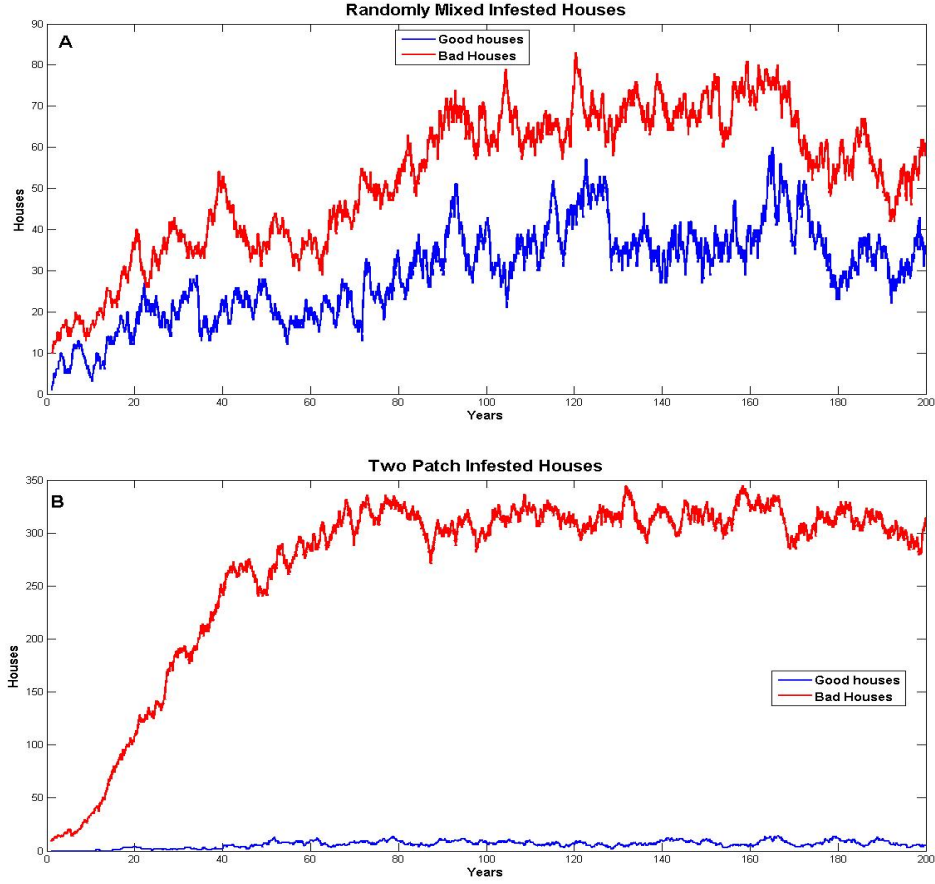
Figure 10: A. Randomly mixed spatial Infested Houses when $\tau_b = 0$ B. Two patches spatial Infested Houses when $\tau_b = 0$

In all cases we ran 100 simulations with the same initial conditions for a population of $32 \times 32 = 1024$ houses. We calculated the averages and standard deviations for the final value of infested good and bad houses (after transients). The parameter values are listed in Table 1.

For the case of randomly distributed houses, average infestation of bad houses is about 75 with a standard deviation of 43.2 while good houses infestation is about 42 with a standard deviation of 25. When the village is divided into two patches, mean infestation of bad and good houses are 311 and 7 with standard deviations of 16.4 and 2.6 respectively.
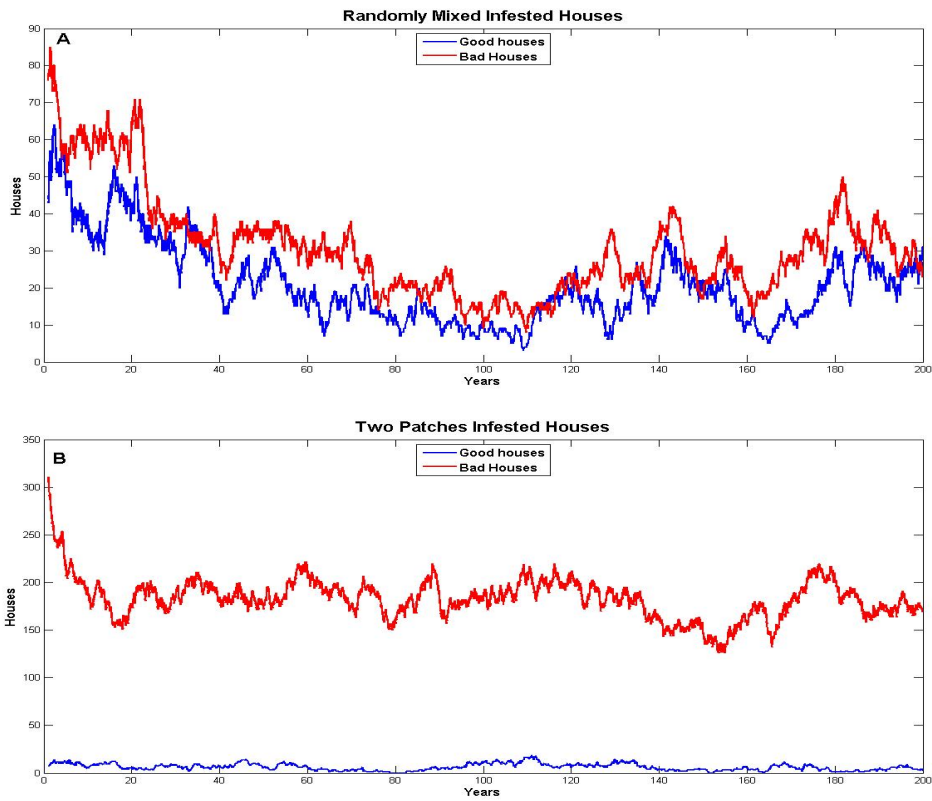
Figure 11: A. Randomly mixed spatial Infested Houses when $\tau_b = .1$ B. Two patches spatial Infested Houses when $\tau_b = .1$

Using the average infestation levels as initial conditions we explored the effect of a constant rate of treatment of bad houses ($\tau_b = .1$). From Figure 11 we see that extinction of infested populations is common for the randomly mixed case but not for the two patch model case. We estimated the probability of extinction for both models from 100 simulations. For the two-patch model infested populations never became extinct while for randomly distributed houses extinction was observed in 89 out of 100 simulations.

6 Discussion and conclusion

The transmission dynamics of Chagas is complex and varies on geographic location and economic factors [22]. In this work we used a simple metapopulation approach to understand the dynamics of house infestation in different settings. Stochastic continuous time Markov chain simulations were used to add realism to the deterministic models. Given that there are a relatively small number of houses, demographic stochasticity can be an

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important factor influencing extinction probabilities, even in a constant environment [17]. However seasonality is an important driver of population dynamics [3] and we expect that stochasticity will play an even more significant role in models including seasonality. Comparison of the results obtained with the spatially-explicit, agent-based models with those obtained with simple population levels models show that these last ones provide a good first approximation. Main differences are observed in the transient dynamics were spatial spread leads to an almost linear growth of the infested population while population-level, homogenous-mixing models exhibit a characteristic initial phase of exponential growth.

It is well known that house improvement greatly decrease levels of infestation. In this work we explored the consequences of improving a fraction of the houses of a given community. Two cases were considered: improved houses distributed randomly in the community or all of them in the same sector. The results obtained from both spatial and non spatial models show that house infestation is more controllable in a randomly mixed community. The models also predicted that spraying only the bad houses is more efficient than treating just part of the total houses at random or spraying the whole community. This result is consequence of the assumed reduced infestation potential of good houses respect to bad houses, and is apparent from the respective expressions of the basic reproduction numbers.

We take into account different quality type of houses and developed a flexible framework which include spatial distribution of houses in an explicit way. The infestation spread model may be improved by including distance-dependent probabilities of bug dispersal. Actual house distributions, for specific villages, may be straightforwardly incorporated. In this case houses are allocated in some cells in the grid leaving the rest as 'empty space' with null probability of colonization.

7   Future Work

In this section, we briefly describe some new ideas for future work. For more realistic case, it would be beneficial to collect real biological data for better parameter estimation. A further level of realism can be achieved by considering different level of infestation. One question that can be derive from this is to see the effect of infestation in the community when very low percentage of pesticide are applied to low infested houses. Because of their short life span of the T. infestans [18], one may also incorporate the life cycle of the vector in the model and look at the period of time that the pesticide take affect on the vector population and when it mostly affect the vectors and decrease infestation in the community. Finally we may include seasonality since the vector population growth takes place almost exclusively during spring and summer.

Acknowledgments

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Appendix A

Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission P. van den Driessche, James Watmough, Mathematical Biosciences 180 (2002) 2948.

Following van den Driessche and Watmough [23] we computed the matrices F and V to compute basic reproductive number for the different models. For the basic Model 1 we obtain

$$F = \begin{pmatrix} c \\ 0 \end{pmatrix} \tag{21}$$

$$V = \begin{pmatrix} \epsilon + \tau \\ 0 \end{pmatrix} \tag{22}$$

For the Randomly Mixed Model (Model 2) F and V matrices are given by

$$F = \begin{pmatrix} \frac{N_g c_g}{N} & \frac{N_g c_b}{N} \\ \frac{N_b c_g}{N} & \frac{N_b c_b}{N} \end{pmatrix} \tag{23}$$

$$V = \begin{pmatrix} \epsilon_g + \tau_g & 0 \\ 0 & \epsilon_b + \tau_b \end{pmatrix} \tag{24}$$

Finally for the Two-Patch Model

$$F = \begin{pmatrix} \frac{c_g N_g * (1-p)}{N} & \frac{c_b N_g q}{N} \\ \frac{c_g p N_b}{N} & \frac{c_b N_b (1-q)}{N} \end{pmatrix} \tag{25}$$

$$V = \begin{pmatrix} \epsilon_g + \tau_g & 0 \\ 0 & \epsilon_b + \tau_b \end{pmatrix} \tag{26}$$

Appendix B

Model 3**

Considering a similar but different assumptions of Model 3 where there are two types of houses in two different patches: one composed entirely by bad houses and the other composed entirely by good houses. The system if presented in the following form.

$$\frac{dE_g}{dt} = -\frac{c_g E_g I_g}{N_g} - \frac{c_b E_g I_b Q}{N_g} + \epsilon_g I_g + \alpha_g T_g \tag{27}$$

$$\frac{dI_g}{dt} = \frac{c_g E_g I_g}{N_g} + \frac{c_b E_g I_b Q}{N_g} - (\epsilon_g + \tau_g)I_g \tag{28}$$

$$\frac{dT_g}{dt} = \tau_g I_g - \alpha_g T_g \tag{29}$$

$$\frac{dE_b}{dt} = -\frac{c_b E_b I_b}{N_b} + \epsilon_b I_b + \alpha_b T_b \tag{30}$$

$$\frac{dI_b}{dt} = \frac{c_b E_b I_b}{N_b} - (\epsilon_b + \tau_b)I_b \tag{31}$$

$$\frac{dT_b}{dt} = \tau_b I_b - \alpha_b T_b \tag{32}$$

where $Q = e^{-d/d_0}$ is a function of the distance d between the two patches. As the distance between the patches increase Q tends to zero, thus for large distances infestation between patches is not possible. Q is a coupling parameter which model the fact that good houses are spatially separated from bad houses. Also it is assumed that the vectors are only going in the direction of the bad neighborhood to the good neighborhood. Thus the term $\frac{c_g E_b I_g}{N_g}$ from equation (9) and (10) that describes the vectors going from good houses to bad houses in Model 2 is not present in this model.

Model 4** : Low and High infestation in two separate community

It is known that in an infested community, all the houses will not have the same level of infestation. Thus it is appropriate to consider different level of infestation. Two levels of infestation assumed in this section in the bad neighborhood, the low infestation and bad infestation. The infestation in the good neighborhood are grouped into one (low infestation) since the houses are well constructed and it is more difficult for the T. infestans

to infest at higher levels. the mathematical model for this situation is presented below.

$$\frac{dE_b}{dt} = -\frac{c_b E_b (qL_b + H_b)}{N_b} + \delta_b T_b + \epsilon_b^L L_b + \epsilon_b^H H_b \tag{33}$$

$$\frac{dL_b}{dt} = \frac{c_b E_b q L_b}{N_b} - \gamma_b L_b - \alpha_2 L_b - \epsilon_b^L L_b \tag{34}$$

$$\frac{dH_b}{dt} = \gamma_b L_b - \alpha_1 H_b - \epsilon_b^H H_b + \frac{c_b E_b H_b}{N_b} \tag{35}$$

$$\frac{dT_b}{dt} = \alpha_1 H_b + \alpha_2 L_b - \delta_b T_b \tag{36}$$

$$\frac{dE_g}{dt} = -\frac{c_g E_g Q (qL_b + H_b)}{N_g} - \frac{c_g E_g L_g}{N_g} + \delta_g T_g + \epsilon_g^L L_g \tag{37}$$

$$\frac{dL_g}{dt} = \frac{c_g E_g Q (qL_b + H_b)}{N_g} + \frac{c_g E_g L_g}{N_g} - \alpha_3 L_g - \epsilon_g^L L_g \tag{38}$$

$$\frac{dT_g}{dt} = \alpha_3 L_g - \delta_g T_g \tag{39}$$

where
E_b, E_g, T_b, T_g have the same explanation as in model 3 and
L_b = Low infestation for bad houses
H_b = High infestation for bad houses
L_g = Low infestation for good houses

For this model $R_0 = max\{\frac{c_b}{\alpha_1 + \epsilon_b^h}, \frac{c_g}{\epsilon_g^L + \alpha_3}, \frac{c_b}{\epsilon_b^L + \alpha_2 + \gamma_b})$ and again if treatment is ignored then $R_0 = \frac{c_b}{\alpha_1 + \epsilon_b^h}$. Since bad houses with high infestation are the ones who sustain the most vectors it makes sense that the R_0 for this model depends on the individual R_0 for the high infested bad houses. The resources for spraying could be optimized if we spray only the houses that are highly infested and then the low infested bad houses from what the R_0 says.