A Metapopulation Model of Chagas Disease in Colombia with Human Mobility

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1 Introduction

Chagas disease, also known as American trypanosomiasis, is a zoonose and a tropical parasitic infection that originated in the Americas and is caused by the flagellate protozoan *Trypanosoma cruzi* [11]. Discovered in 1909, Chagas disease was progressively shown to be widespread throughout Latin America, affecting millions of rural regions with a high impact on morbidity and mortality. In the last few years, the disease has become an emerging import and has spread to countries in North America, Asia, and Europe due to the migration from Latin Americas [10]. There are approximately 8 to 10 million people in Latin America, who suffer from Chagas disease and another 28 million who are at risk of contracting it [18].

The most domestic specie is *Triatoma infestans* and it is the principal vector of the Southern cone. In northern South America geographical insect distribution changes, the *Rhodnius prolixus*, a blood-sucking triatomine with domiciliary anthropophilic habits, is the main vector of Chagas disease. The current paradigm of *Trypanosoma cruzi* (*T. cruzi*) transmission in Colombia includes a sylvatic and domiciliary cycle co-existing with domestic and sylvatic populations of reservoirs. The eco-epidemiological factors shape the transmission dynamics of *T. cruzi*, creating diverse scenarios of disease transmission [22]. Infection cycle occurs when an infected triatomine insect vector (or "kissing" bug) takes a blood meal and releases trypomastigotes in its feces near the site of the bite wound. Trypomastigotes enter the host through the wound or through intact mucosal membranes, such as the conjunctiva.

In Colombia, the prevalence of Chagas disease has been estimated as 1,300,000 habitants infected and 3,500,000 habitants at risk of infection depending on the geographical distribution of the vector [13], hence, establishing endemic areas throughout the country. The principal endemic areas are: Caribbean coastal region, Orinoquia region, and Andes mountain region. The risk of infection varies in each endemic area in the country (Figure 1). There are several reasons for this change. The principal reason is the difference among the environmental characteristics in each region that affect the life cycle of the vector. Furthermore, allowing for the creation of variable interactions between vector and host in these specific areas increasing or decreasing the risk of infection. There has been a reasonable number of cases confirmed in Bogotá where there are no parasites. This is an alarming finding. We would like to mathematically ascertain if human mobility is contributing to the dispersal and incidence of Chagas disease.
Currently, Chagas disease treatment is most effective in the acute phase. However, treatment does not always produce complete parasite eradication during both the indeterminate and chronic phases. Although more effective trypanocidal drugs are needed, treatment with benznidazole (or nifurtimox) is reasonably safe and effective, and is now recommended for a widened range of patients. Improved models for risk stratification are available, and certain guided treatments could halt or reverse disease progression [21]. In economic terms, the cost-benefit relationship between intervention (insecticide spraying, serology in blood banks) and the reduction of Chagas disease (in terms of medical and social care and improved productivity) is highly positive [10].

The mathematical model is a tool used to estimate local and global basic reproductive numbers as well as an estimate $q$ for the proportion of reported cases. We compare reported incidence with computed model-adjusted incidence rates. This process allows us to quantify the levels of underreporting via modeling framework through the perspective of human mobility. Early detection of Chagas disease can cease the progression of infection. Immediately after infection an individual enters the acute phase. This phase lasts for the first few weeks or months of infection. It usually occurs unnoticed because it is symptom free or exhibits only mild symptoms and signs that are not unique to Chagas disease. Some symptoms include fever, fatigue, body aches, headache, rash, loss of appetite, diarrhea, and vomiting, [20]. Once a individual misses the optimal window time for treatment, they enter the chronic phase of infection where they remain for a life time. Symptoms in the chronic phase are typically silent for the life time. The side effects of being chronically infected include cardiac or intestinal complications. Both complications lead to non-repairable damage.

There are many studies exploring the dynamics of transmission using deterministic mathematical models. One study examines the transmission of the disease in a population of houses. This study is expanded by another by incorporating controlled spraying. They find it is nearly impossible to control the vector population as most vector-borne models conclude. Their suggestion includes annual spraying of homes giving priority to homes made of the material that is highly likely to serve as a habitat for the vector.

2 Methods

Mathematical Model We employ a metapopulation model with separate human and vector populations in each patch. This tool allows us to
• study within and across patch transmission dynamics,
• assess potential heterogeneity contributions on epidemics, and
• synchrony between populations (leader-follower regions), [23].

The model is inspired by the two-patch model incorporating resident time by Lee & Castillo-Chavez, [17]. In the analysis of Lee & Castillo-Chavez, they focused on the influence of human mobility between two patches on the temporal sequence of disease spread between patches, thus, showing the influence of movement and the basic reproduction number $R_0$ on the relative timing of epidemic peaks.

For our model, each patch is derived on the basis of ecological and epidemiological reasoning. Furthermore, each patch has a principle vector with an unique transmission rate. We will define a deterministic model for the disease in each patch.

![Model patches illustration](image)

Figure 2: Patches with heterogeneous environments that could affect the transmission Chagas disease.

![Principle vectors for each region in Colombia](image)

Figure 3: Principle vectors for each region in Colombia REFERENCE?

The rate of change for susceptible, acutely infectious, chronically infectious, and treated humans are considered. Also, the susceptible and infectious vectors' rate of change are included. This is the first time, to our knowledge, the infectious class for humans have been subdivided while modeling Chagas disease. Pathologically, the infection stage is divided into three phases: acute, latent, and chronic. We consider the acute and latent phase as one state because the latent stage is completely asymptomatic and coined as indeterminate. After several months, years or decades, about 30% of infected humans enter into a chronic stage consisting of severe cardiomyopathy and/or gastrointestinal dysfunctions [9]. During the acute phase, there is evidence of high levels of parasitemia followed...
by a significant decrease during the chronic stage. Experimental rat data suggests that after the initial spike in parasitemia, the host does not experience the same spiked level of parasitemia again and a remarkable lesser amount of blood circulating parasites were recorded during this period of observation. Hence, hinting at some sort of immunity where the host immune system is able to control the parasite proliferation through mediating mechanisms as the humoral response [3]. The parasitemia levels alter the effective transmission from an infectious human to susceptible vector. We explore this phenomena closely.

<table>
<thead>
<tr>
<th>State Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_h$</td>
<td>Population of susceptible humans</td>
</tr>
<tr>
<td>$I_h$</td>
<td>Population of acutely infected humans</td>
</tr>
<tr>
<td>$C_h$</td>
<td>Population of chronically infected humans</td>
</tr>
<tr>
<td>$T_h$</td>
<td>Population of humans in treatment</td>
</tr>
<tr>
<td>$S_v$</td>
<td>Population of susceptible vectors</td>
</tr>
<tr>
<td>$I_v$</td>
<td>Population of infected vectors</td>
</tr>
</tbody>
</table>

Table 1: Subpopulations of the model and descriptions

$h$ denotes the human populations and $v$ are the vectors. The human population is increased by a natural birth rate. The infection occurs at a rate $\beta_h$ when a susceptible human is bitten by an infectious vector. The human then becomes acutely infectious. During this time, two situations can occur. First, the acutely, infectious individual can become treated if the disease in recognized in time. Treatment yields a temporary immunity to reinfection before returning to the susceptible class. Secondly, the infection could go unnoticed and consequently, the individual will progress to the chronic phase. During this period, disease induced mortality can occur. There is no effective treatment and thus the individual will remain in the chronic phase for the remainder of the time. Natural death can occur in all populations. The vector class is also increased and decreased by a natural birth/death rate, $\mu_v$.

A novel component of this model is the additive effective transmission rates, $\beta_a$ and $\beta_c$. Literature suggest that $\beta_a >> \beta_c$ as a result of fluctuations in the levels of parasitemia, [3]. In other words, a susceptible vector can become infectious as a result of an effective interaction with with an acutely infectious or chronically infectious human.

A multi-patch Chagas disease transmission model is introduced to explore the role of human mobility, environmental heterogeneity, and early disease detection on the transmission dynamics of Chagas. The model follows the assumptions of the highly studied single patch model. Furthermore, the equations for each patch follow these assumptions specified for a single patch model with the subpopulations in terms of the home(local) patch. Additional assumptions include:

- Humans move between patches and vectors do not move between patches.
- Transmission rates are particular to principle vector.
- The vector population is constant.
- Disease status only changes within patch and not during movement between patches.

The patches are coupled via the resident time matrix. The resident time matrix, $P$, represents the proportion of time that a person residing in their home patch budgets and spends visiting another patch. The matrix takes the form of an $n \times n$ matrix where $\sum_{j=1}^{n} (P)_{n \times n} = 1$.

The flow diagram demonstrates the schematics of Chagas disease transmission. Then, we derived equations based on the rate of change for each compartment in Figure 4.
Figure 4: Schematics of Chagas disease transmission.

The multi-patch model dynamics are captured by the following patch-specific system of nonlinear ordinary differential equations:

**Humans**

\[ S'_{hi} = \mu_h N_{hi} - S_{hi} \sum_{j=1}^{n} \beta_{hj} p_{ij} I_{vj} + \eta T_{hi} - \mu_h S_{hi} \]  

(1)

\[ I'_{hi} = S_{hi} \sum_{j=1}^{n} \beta_{hj} p_{ij} I_{vj} - q \gamma I_{hi} - (1 - q) \gamma I_{hi} - \mu_h I_{hi} \]  

(2)

\[ C'_{hi} = q \gamma I_{hi} - (\mu_h + \delta_c) C_{hi} \]  

(3)

\[ T'_{hi} = (1 - q) \gamma I_{hi} - \mu_h T_{hi} - \eta T_{hi} \]  

(4)

**Vectors**

\[ S'_{vi} = \mu_v N_{vi} - S_{vi} \left( \beta_a \sum_{j=1}^{n} p_{ji} I_{hj} + \beta_c \sum_{j=1}^{n} p_{ji} C_{hj} \right) - \mu_v S_{vi} \]  

(5)

\[ I'_{vi} = S_{vi} \left( \beta_a \sum_{j=1}^{n} p_{ji} I_{hj} + \beta_c \sum_{j=1}^{n} p_{ji} C_{hj} \right) - \mu_v I_{vi} \]  

(6)

for \( i = 1, 2 \). Chagas disease has a very long infectious period that ranges from 10 to 30 years in the chronic stage. As a result, we believe it is inappropriate to assume a constant human population. On the other hand, assuming a constant vector population seems reasonable. The model should consist of both natural and disease induced mortality.

**Human Mobility** We are assuming that human travel contributes to the spread of the disease, as the vectors only travel a very limited distance. The idea of modeling human movement using the resident time matrix approach is inspired by the work of Lee & Castillo-Chavez [17]. We assume that individuals do not move permanently from their patch of residence to another patch, but may visit other patches. The rate at which individuals become infected then depends upon the fraction of their time that they spend in each patch together with the transmission rates in those patches. This approach is the Lagrangian in that it labels and, in some sense, tracks individual humans or vectors [7].
3 Quantities of Interest

4 Disease Free Equilibrium and Basic Reproduction Number

4.1 Single Patch Analysis

We first analyze the system in the absence of movement in order to understand the baseline dynamics of the system. For simplicity, we take the disease induced mortality rate, \( \delta \), to be zero. This is a reasonable assumption since the units for the analysis are per week and death is nearly negligible.

The system of nonlinear ordinary differential equations are:

**Humans**

\[
S_h' = \mu_h N_h - \beta S_h I_v + \eta T_h - \mu_h S_h \\
I_h' = \beta S_h I_v - \gamma I_h - \mu_h I_h \\
C_h' = (1 - q) \gamma I_h - (\delta_c + \mu_h) C_h \\
T_h' = q \gamma I_h - \eta T_h - \mu T_h
\]

**Vectors**

\[
S_v' = \mu_v N_v - S_v (\beta_a I_h + \beta_c C_h) - \mu_v S_v \\
I_v' = S_v (\beta_a I_h + \beta_c C_h) - \mu_v I_v
\]

where, \( N_h = S_h + I_h + C_h + T_h \) and \( N_v = S_v + I_v \).

**Disease Free Equilibrium** Solving the system for the equilibrium points yield the findings below. Setting the system equal to zero and solving for the state variables gives the following cases. The first case we consider is coined as the infection free state. This is the case where all the infectious classes are zero and further implying all of the population is susceptible. The Disease Free Equilibrium (DFE) is given by:

\[
(S_{h0}, I_{h0}, C_{h0}, T_{h0}, S_{v0}, I_{v0}) = (N_h, 0, 0, N_v, 0, 0).
\]

**Local Basic Reproduction Number** As it is commonly used in epidemiological models, the calculation of the basic reproduction number, \( R_0 \), gives insight to the dynamics of the disease. In general, the basic reproduction number, \( R_0 \), represents the number of secondary infections generated by an infected individual when introduced to a completely susceptible group. In reference to this model, it represents the expected number of secondary infections in fully susceptible humans resulting from one newly introduced infected vector. When \( R_0 < 1 \), an epidemic of Chagas disease will not occur. When \( R_0 = 1 \), one vector from the infected class infects one human from the susceptible class of humans. When \( R_0 > 1 \) every vector of the infected class will infect at least one human of the susceptible class of humans. \( R_0 \) will help in determining the equilibrium of the system and will be used in the stability analysis for the system.

To compute the basic reproduction number, \( R_0 \), we use the Next Generation Operator Method \([16]\). Let \( \mathcal{F} \) represent the rate of new infections caused by transition from the susceptible or the treated group to the infected classes. \( \mathcal{V} \) will symbolize the rate of transfer into or out of the infected and treatment classes by other means. Following this method,

\[
\mathcal{F} = \begin{bmatrix}
\beta_h S_h I_v \\
0 \\
S_v (\beta_a I_h + \beta_c C_h)
\end{bmatrix}
\quad\text{and}\quad
\mathcal{V} = \begin{bmatrix}
\gamma q I_h + \mu_h I_h \\
-(1 - q) \gamma I_h + (\delta + \mu_h) C_h \\
\mu_v I_v
\end{bmatrix}
\]

Next, take the Jacobian and evaluate at the \textit{DFE} (recall we are taking \( \delta = 0 \), resulting in:

\[
F = \begin{bmatrix}
0 & 0 & \beta_h N_h \\
0 & 0 & 0 \\
N_v \beta_a & N_v \beta_c & 0
\end{bmatrix}
\quad\text{and}\quad
V = \begin{bmatrix}
\gamma q + \mu_h & 0 & 0 \\
-(1 - q) \gamma & \mu_h & 0 \\
0 & 0 & \mu_v
\end{bmatrix}
\]
Calculate the product $F V^{-1}$:

$$
\begin{bmatrix}
\frac{N_v \beta_c \mu_h \mu_0}{\mu v^2 + \gamma \mu v} + \frac{N v \beta c (q \gamma v - \gamma v)}{\mu v^2 + \gamma \mu v} \\
0 & 0 & \frac{N 1 \beta (\mu^2 + \gamma \mu)}{\mu v^2 + \gamma \mu v}
\end{bmatrix}
$$

From this product, we coin the greatest eigenvalue as the basic reproductive number. This dimensionless parameter was computed with the presence of a control. The control in this case is the treatment where temporary immunity is granted. Therefore, we define the parameter as the control reproduction number. The control reproductive number is the average number of secondary cases generated by primary cases under specified controls. Again in our situation, it is when $q \in (0, 1)$ and is given by:

$$R_c(q) = \sqrt{\frac{N_h N_v ((1-q) \beta_c \gamma + \beta_a \mu_h)}{\mu h v (\gamma + \mu_h)}} \quad (14)$$

When modeling endemic regions, it is essential to compute the control reproduction number to characterize the reforms of having controls. $R_0$ is computed in the absence of control measures when no one in the population is immune to the disease. More specifically, we compute $R_0$ when $q = 0$.

$$R_0 = R_c(0) = \sqrt{\frac{N_h N_v (\beta_c \gamma + \beta_a \mu_h)}{\mu h v (\gamma + \mu_h)}} \quad (15)$$

Notice the relationship between $R_c(q)$ and $R_c(0) = R_0$.

**Endemic Equilibrium** The second case that evolves from solving for the equilibrium points of the system is known as the Endemic Equilibrium. For this, we do not assume the disease induced mortality to be zero, $\delta = 0$. We have the following point:

$$S_h^* = \frac{(\gamma + \mu_h) (\beta_a \gamma \mu_h^2 N_h (q - 1) - (\delta + \mu_h) (\beta_a \mu_h^2 N_h + \mu_v (\mu_h (\gamma + \mu_h) + \eta^2 - \eta \eta) \right)}{(\beta_a (\delta + \mu_h) - \beta_c (q - 1) \gamma)(-\mu^2 (\gamma + \mu_h) + N_v \beta (q \gamma \eta + \eta^2 - \mu (\gamma + \mu_h)))},$$

$$I_h^* = \frac{\mu^2 (\delta - \mu) (\mu_v (\gamma + \mu) + \beta \beta_a N_h N_v) + \beta \beta_c \gamma N_h N_v (q - 1)}{(\beta a (\delta + \mu_h) - \beta_c (q - 1) \gamma)(-\mu^2 (\gamma + \mu_h) + N_v \beta (q \gamma \eta + \eta^2 - \mu (\gamma + \mu_h)))},$$

$$C_h^* = \frac{\gamma \mu^2 (q - 1)((\delta + \mu) (\mu_v (\gamma + \mu) - \beta a N_h N_v) + \beta \beta_c \gamma N_h N_v (q - 1))}{(\delta + \mu) (\beta a (\delta + \mu) + \beta c (\gamma - \gamma \eta)) (\mu^2 (\gamma + \mu) + N_v \beta (q \gamma \eta + \eta^2 - \mu (\gamma + \mu))},$$

$$T_h^* = \frac{\mu (q \gamma \eta - \eta)((\delta + \mu) (\mu_v (\gamma + \mu) - \beta a N_h N_v) + \beta \beta_c \gamma N_h N_v (q - 1))}{(\beta a (\delta + \mu_h) - \beta_c (q - 1) \gamma)(-\mu^2 (\gamma + \mu_h) + N_v \beta (q \gamma \eta + \eta^2 - \mu (\gamma + \mu))},$$

$$S_v^* = \frac{\mu_v (\delta + \mu) (\mu^2 (\gamma + \mu) + N_v \beta (q \gamma \eta - \eta (\mu (\gamma + \mu)))}{\beta (\beta c \gamma \mu^2 N pop (q - 1) - (\delta + \mu) (\beta a \mu^2 N h + \mu_v (\mu (\gamma + \mu) + \eta^2 - \eta \eta))}, \quad \text{and}$$

$$I_v^* = \frac{\mu^2 ((\delta + \mu) (\mu_v (\gamma + \mu) - \beta a N_h N_v) + \beta \beta_c \gamma N_h N_v (q - 1))}{\beta (\beta c \gamma \mu^2 N_h (q - 1) - (\delta + \mu) (\beta a \mu^2 N_h + \mu_v (\mu (\gamma + \mu) + \eta^2 - \eta \eta))}$$

### 4.2 2 Patch Analysis

We extend the system to include two patches. This transmission model explores human mobility between the patches and environmental heterogeneity. Human mobility is modeled via Resident-Time Matrix. This matrix
couples the system and allows us to explore its role on the transmission dynamics on human incidences. We consider three distinct coupling scenarios and analyze them numerically. The entries of the matrix are proportion of time that a person residing in Patch $i$ budgets and spends in Patch $j$. Because we are assuming that only humans move between patches, the matrix holds for $I_{hi}$ and $C_{hi}$. The matrix is of the following form:

$$P = \begin{bmatrix} P_{11} & P_{12} \\ P_{21} & P_{22} \end{bmatrix}$$ (16)

The system of nonlinear differential equations becomes:

**Humans**

$$S_{hi}' = \mu_h N_{hi} - S_{hi} \sum_{j=1}^{n} \beta_{hj} p_{ij} I_{vj} + \eta T_{hi} - \mu_h S_{hi}$$ (17)

$$I_{hi}' = S_{hi} \sum_{j=1}^{n} \beta_{hj} p_{ij} I_{vj} - q_i \gamma I_{hi} - (1 - q_i) \gamma I_{hi} - \mu_h I_{hi}$$ (18)

$$C_{hi}' = q_i \gamma I_{hi} - (\mu_h + \delta_c) C_{hi}$$ (19)

$$T_{hi}' = (1 - q_i) \gamma I_{hi} - \mu_h T_{hi} - \eta T_{hi}$$ (20)

**Vectors**

$$S_{vi}' = \mu_v N_{vi} - S_{vi} \left( \beta_a \sum_{j=1}^{n} p_{ji} I_{hj} + \beta_c \sum_{j=1}^{n} p_{ji} C_{hj} \right) - \mu_v S_{vi}$$ (21)

$$I_{vi}' = S_{vi} \left( \beta_a \sum_{j=1}^{n} p_{ji} I_{hj} + \beta_c \sum_{j=1}^{n} p_{ji} C_{hj} \right) - \mu_v I_{vi}$$ (22)

for $i = 1, 2$.

**Disease Free Equilibrium** The disease free equilibrium is extended to consider both patches. As before, this is the state where there is no infection present in the population of patches. The $DFE$ is given by:

$$(\tilde{S}_{h1}, \tilde{I}_{h1}, \tilde{C}_{h1}, \tilde{T}_{h1}, \tilde{S}_{v1}, \tilde{I}_{v1}, \tilde{C}_{v1}, \tilde{T}_{v1}, \tilde{S}_{v2}, \tilde{I}_{v2}) = (N_{h1}, 0, 0, N_{v1}, 0, N_{h2}, 0, 0, 0, N_{v2})$$ (23)

where $N_{hi} = S_{hi}$ and $N_{vi} = S_{vi}$ for $i = 1, 2$.

**Global Basic Reproduction Number** We compute the basic reproduction number across both patches coupled via resident time matrix. This process is similar to that for the single patch. The $R_0$ across both patches is referred to as global basic reproductive number while the $R_0$ of the single patch is referred to as the local basic reproductive number. Computations are completed using the Next Generation Operator Method. First, divide the classes into infected, $X$, and not infected, $Y$.

$$X = \begin{bmatrix} I_{h1} \\ C_{h1} \\ I_{v1} \\ I_{h2} \\ C_{h2} \\ I_{v2} \end{bmatrix}$$ and  $$Y = \begin{bmatrix} S_{h1} \\ T_{h1} \\ S_{v1} \\ S_{h2} \\ T_{h2} \\ S_{v2} \end{bmatrix}$$

Next we subdivide Matrix $X$. Newly infected rates are in $\mathcal{F}$ and the negation of the rates from the infected class by other means are in $\mathcal{V}$. 
Next evaluate the Jacobian of the system at the DFE. We then have the following:

\[
F = \begin{bmatrix}
S_{h1}(\beta_1 P_{11} I_{v1} + \beta_2 P_{12} I_{v2}) & 0 \\
S_{v1}(P_{11}(\beta_c C_{h1} + \beta_a I_{h1}) + P_{21}(\beta_c C_{h2} + \beta_a I_{h2})) & 0 \\
S_{v2}(P_{12}(\beta_c C_{h1} + \beta_a I_{h1}) + P_{22}(\beta_c C_{h2} + \beta_a I_{h2})) & 0
\end{bmatrix}
\]

and

\[
V = \begin{bmatrix}
(\mu_h + \gamma) I_{h1} \\
-(1 - q_1) \gamma I_{h1} + (\mu_h + \delta) C_{h1} \\
(\mu_h + \gamma) I_{h2} \\
-(1 - q_2) \gamma I_{h2} + (\mu_h + \delta) C_{h2} \\
\mu_a I_{v2}
\end{bmatrix}
\]

Calculate the product \( FV^{-1} \) and determine the eigenvalues. The greatest eigenvalue is the \( \tilde{R}_0 \) of the two patch system.

\[
\tilde{R}_0 = \sqrt{\frac{B + \sqrt{A}}{2\mu_h \mu_v (\gamma + \mu_h)}}, \quad (24)
\]

where,

\[
A = 4P_{11}(P_{21} - P_{22})(P_{12} P_{21} - P_{11} P_{22})S_{h1}S_{h2}S_{v1}S_{v2} \beta_1 \beta_2 ((1 - q_1) \beta_c \gamma + \beta_a \mu)((1 - q_2) \beta_c \gamma + \beta_a \mu)
+ ((P_{11}^2 S_{h1} S_{v1} \beta_1 + P_{11} P_{12} S_{h1} S_{v2} \beta_2)((1 - q_1) \beta_c \gamma + \beta_a \mu) + S_{h2}(P_{21}^2 S_{v1} \beta_1 + P_{22}^2 S_{v2} \beta_2)((1 - q_2) \beta_c \gamma + \beta_a \mu))^2
\]

\[
B = P_{11} S_{h1}(P_{11} S_{v1} \beta_1 + P_{12} S_{v2} \beta_2)((1 - q_1) \beta_c \gamma + \beta_a \mu) + S_{h2}(P_{21}^2 S_{v1} \beta_1 + P_{22}^2 S_{v2} \beta_2)((1 - q_2) \beta_c \gamma + \beta_a \mu)
\]

### 4.2.1 2 Patches: Isolated

Now let’s consider the case where the patches are isolated. In other words, this is the case where everyone is in their resident matrix. The system remains coupled via resident-time matrix. The matrix takes the following form:

\[
P_1 = \begin{bmatrix}
P_{11} & P_{12} \\
P_{21} & P_{22}
\end{bmatrix} = \begin{bmatrix}
1 & 0 \\
0 & 1
\end{bmatrix}, \quad (25)
\]

**Basic Reproduction Number** Equation 11 gives the DFE used to perform the Next Generation Operator Method. The methods remain the same; however, the \( F \) matrix is evaluated not only at the DFE but at the
'identity', \(P_1\), as well.

\[
F_{(p_{11}=1,p_{12}=0,p_{21}=0,p_{22}=1)} = \begin{bmatrix}
0 & 0 & S_{h1} \beta_1 P_{11} & 0 & 0 & S_{h1} \beta_2 P_{11} \\
0 & 0 & 0 & 0 & 0 & 0 \\
S_{v1} P_{11} \beta_a & S_{v1} P_{11} \beta_c & 0 & S_{v1} P_{21} \beta_a & S_{v1} P_{21} \beta_c & 0 \\
0 & 0 & 0 & S_{h2} \beta_2 P_{21} & 0 & 0 \ \\
S_{v2} P_{12} \beta_a & S_{v2} P_{12} \beta_c & 0 & S_{v2} P_{22} \beta_a & S_{v2} P_{22} \beta_c & 0
\end{bmatrix}
\]

\[
V = \begin{bmatrix}
(\mu_h + \gamma) & 0 & 0 & 0 & 0 & 0 \\
-(1-q_1)\gamma & \mu_h & 0 & 0 & 0 & 0 \\
0 & 0 & \mu_v & 0 & 0 & 0 \\
0 & 0 & 0 & (\gamma + \mu_h) & 0 & 0 \\
0 & 0 & 0 & -(1-q_1)\gamma & \mu_h & 0 \\
0 & 0 & 0 & 0 & 0 & \mu_v
\end{bmatrix}
\]

After solving the product \(FV^{-1}\) and the eigenvalues. We find that the basic reproductive number for the two patch, isolated case is below:

\[
\bar{R}_0 = \max \left\{ \frac{\beta_2 S_{h2} S_{v2}(\beta_a \mu_h + \beta_c \gamma (1 - q_2))}{\mu_h \mu_v (\gamma + \mu_h)}, \frac{\beta_1 S_{h1} S_{v1}(\beta_a \mu_h + \beta_c \gamma (1 - q_1))}{\mu_h \mu_v (\gamma + \mu_h)} \right\}
\]

(26)

5 Results

Figure 5: One way: Time interval \((0,300)\) of prevalence of Chagas cases among infected humans and vectors in two patches with \(R_c(q) > 1\).
Figure 6: Symmetric: Time interval (0,300) of prevalence of Chagas cases among infected humans and vectors in two patches with $\tilde{R}_c(q) > 1$.

Figure 7: Asymmetric: Time interval (0,300) of prevalence of Chagas cases among infected humans and vectors in two patches with $\tilde{R}_c(q) < 1$. 
Figure 8: The global basic reproduction number, $\tilde{R}_c(q)$, is plotted as a function of the local $R_{0i}$ under different resident-time scenarios.

Figure 9: The global basic reproductive number $\tilde{R}_c(q)$ is displayed as a function of the $P_{11}$ under three different values of $P_{22}$. The local reproduction number is fixed as $R_{0i} = 1.8$ for the left and $R_{0i} = 2.0$ on the right.

Sensitivity Analysis

Discussion Some challenges remain: Chagas disease is becoming an emerging health problem in non-endemic
areas because of growing population movements; early detection and treatment of asymptomatic individuals are underused; and the potential benefits of novel therapies (e.g., implantable cardioverter defibrillators) need assessment in prospective randomized trials [21].
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References


