Supplementary material

Equations

$$\frac{dS_v}{dt} = \lambda_v(S_v + I_v) - \beta g(I_h)S_v - \gamma g(C_h)S_v - \lambda_v S_v$$
$$\frac{dI_v}{dt} = \beta g(I_h)S_v + \gamma g(C_h)S_v - \lambda_v I_v$$
$$\frac{dS_h}{dt} = \lambda_h(S_h + I_h + C_h) - \eta f(I_v)S_h - \lambda_h S_h$$
$$\frac{dI_h}{dt} = \eta f(I_v)S_h - \alpha I_h - \lambda_h I_h$$
$$\frac{dC_h}{dt} = \alpha I_h - \lambda_h C_h$$

The infection rate of the susceptible populations S_v and S_h by biting an infected host (I_h) and feeding on an infected vector (I_v) respectively, is described by a Functional Response Holling type II defined as:

$$g(I_h) = \frac{\epsilon I_h}{(\rho + I_h)}$$

$$g(C_h) = \frac{\epsilon C_h}{(\rho + C_h)}$$

$$f(I_v) = \frac{\phi I_v}{(\sigma + I_v)}$$

Variables

S_v: Susceptible vector population

I_v: Infected vector population

S_h: Susceptible host population

I_h: Infected host population

C_h: Chronically infected host population

Parameters

λ_v: Vector birth rate. $[\frac{1}{time}]$

λ_h: Host birth rate (community). $[\frac{1}{time}]$

β: Probability of infection from infected host population (I_h) to susceptible vector population (S_v).

γ: Probability of infection from chronically infected host population (C_h) to susceptible vector population (S_v).

α: Host movement rate from infected (I_h) to chronically host (C_h). $[\frac{1}{time}]$

η: Probability that intake infects the host.

ϵ^*: Maximum number of host bitten per week per vector. $[\frac{1}{time}]$

ρ^*: Proportion of hosts when vector bitting is $\phi/2$.

ϕ^*: Maximum number of vectors eaten per week per host. $[\frac{1}{time}]$

σ^*: Proportion of vectors when vector consumption is $\phi/2$.

*This parameters correspond to the Functional response type II.

Next-generation matrix

To determine the contribution of vectors and hosts (at each stage of infection) to the transmission of *T.cruzi*, we used the Next Generation Matrix method (NGM) [1, 2]. The NGM has the number of new infected individuals of a class by an infected individual of every other class. Thus for building the NGM, we only considered three of five compartments of our system belonging to infected stages (I_v, I_h and C_h). By finding the largest eigenvalue of NGM, we computed the basic reproduction number R_0 or the average number of infections produced by the contribution of the whole network.
For building the NGM, we only considered three of five compartments of our system belonging to infected stages (I_v, I_h and C_h).

$$NGM(G) = \begin{pmatrix} I_v \to I_v & I_h \to I_v & C_h \to I_v \\ I_v \to I_h & I_h \to I_h & C_h \to I_h \\ I_v \to C_h & I_h \to C_h & C_h \to C_h \end{pmatrix}$$

Disease Free Equilibrium

$$x_0 = \{S_v = \lambda_v/\lambda_v, I_v = 0, S_h = \lambda_h/\lambda_h, I_h = 0, C_h = 0\}$$

$$F = \begin{pmatrix} \frac{\beta\epsilon I_h}{(I_h+\rho)}S_v + \frac{\gamma\epsilon C_h}{(C_h+\rho)}S_v & \frac{\beta\epsilon\rho}{(I_h+\rho)^2}S_v + \frac{\gamma\epsilon C_h}{(C_h+\rho)}S_v & \frac{\beta\epsilon I_h}{(I_h+\rho)}S_v + \frac{\gamma\epsilon\rho}{(C_h+\rho)^2}S_v \\ \frac{\eta\phi\sigma S_h}{(I_v+\sigma)^2} & \frac{\eta\phi I_v}{I_v+\sigma}S_h & \frac{\eta\phi I_v}{I_v+\sigma}S_h \\ 0 & 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \lambda_v & \lambda_v I_v & \lambda_v I_v \\ (\alpha+\lambda_h)I_h & \alpha+\lambda_h & (\alpha+\lambda_h)I_h \\ \lambda_h C_h - \alpha I_h & \lambda_h C_h - \alpha & \lambda_h - \alpha I_h \end{pmatrix}$$

We evaluate at the Disease Free Equilibrium ($\lambda_v = \lambda_v$ and $\lambda_h = \lambda_v$)

$$F = \begin{pmatrix} 0 & \frac{\beta\epsilon}{\rho} & \frac{\gamma\epsilon}{\rho} \\ \frac{\eta\phi}{\sigma} & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} \lambda_v & 0 & 0 \\ 0 & \alpha+\lambda_h & 0 \\ 0 & -\alpha & \lambda_h \end{pmatrix}$$

Compute matrix G (NGM) which is the product FV^-1

$$NGM = \begin{pmatrix} 0 & \frac{\beta\epsilon}{\rho(\alpha+\lambda_h)} + \frac{\alpha\epsilon\gamma}{\lambda_h\rho(\alpha+\lambda_h)} & \frac{\epsilon\gamma}{\lambda_h\rho} \\ \frac{\phi\eta}{\sigma\lambda_v} & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

From this product, the greatest eigenvalue is the basic reproductive number.

$$R_0 = \sqrt[2]{\frac{\phi\epsilon\eta(\beta\lambda_h + \alpha\gamma)}{\sigma\rho\lambda_v\lambda_h(\alpha + \lambda_h)}}$$

This value represents the expected number of new cases caused by one primary case on a generation basis. R_0 considers the system as a whole, regardless of whether the cases are vectors or hosts [3]. Using Latin Hypercube Sampling we could perform a parameter sensitivity analysis on the global reproductive number R_0 for the system of equations including host vertical transmission.

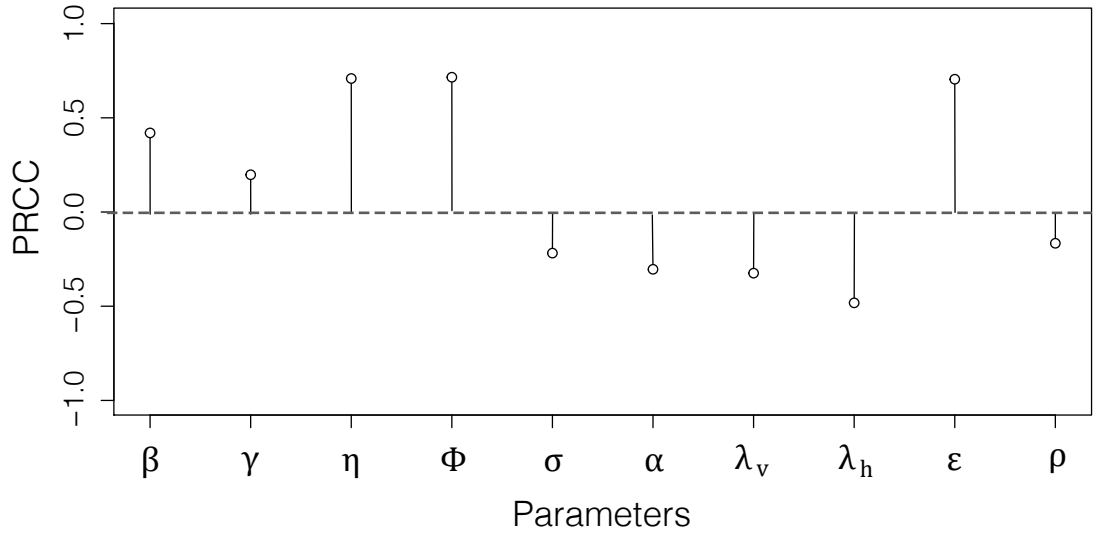

Figure 1: Latin Hypercube Sampling output for the global reproductive number R_0. PRCC: Partial Rank Correlation Coefficient.

Equations including host vertical transmission

$$\begin{aligned}
\frac{dS_v}{dt} &= \lambda_v(S_v + I_v) - \beta g(I_h)S_v - \gamma g(C_h)S_v - \lambda_v S_v \\
\frac{dI_v}{dt} &= \beta g(I_h)S_v + \gamma g(C_h)S_v - \lambda_v I_v \\
\frac{dS_h}{dt} &= \lambda_h(S_h) - \eta f(I_v)S_h - \lambda_h S_h \\
\frac{dI_h}{dt} &= \lambda_h(I_h + C_h) + \eta f(I_v)S_h - \alpha I_h - \lambda_h I_h \\
\frac{dC_h}{dt} &= \alpha I_h - \lambda_h C_h
\end{aligned}$$

Following the same procedure conducted for the first model, the next generation matrix is:

$$NGM = \begin{pmatrix} 0 & \frac{\alpha\epsilon\gamma+\beta\epsilon\lambda_h}{\alpha\lambda_h\rho+\lambda_h)^2\rho} & \frac{\epsilon\gamma}{\lambda_h\rho} \\ \frac{\phi\eta}{\sigma\lambda_v} & 1 & 1 \\ 0 & 0 & 0 \end{pmatrix}$$

And the basic reproductive number is:

$$R_0 = \frac{1}{2}\left(1 + \sqrt[2]{\frac{4\alpha\epsilon\eta\gamma\phi + 4\beta\epsilon\eta\lambda_h\phi + \alpha\lambda_h\lambda_v\rho\sigma + {\lambda_h}^2\lambda_v\rho\sigma}{\lambda_h\lambda_v\rho\sigma(\alpha+\lambda_h)}}\right)$$

Using Latin Hypercube Sampling we could perform a parameter sensitivity analysis on the global reproductive number R_0 for the system of equations including host vertical transmission.

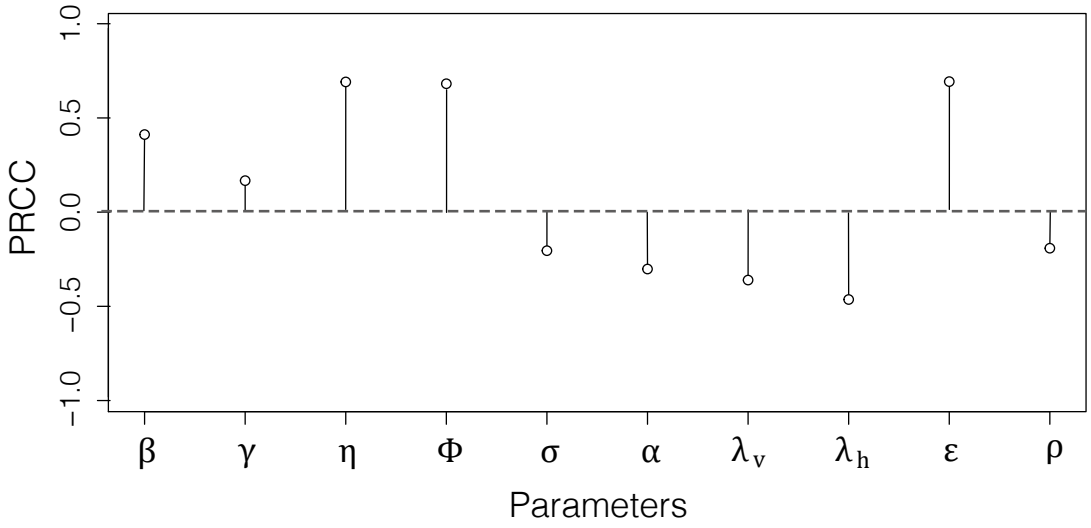

Figure 2: Latin Hypercube Sampling output for the global reproductive number R_0. PRCC: Partial Rank Correlation Coefficient.

Host species parameters

Table 1: Model parameters

Species	Litter size [4]	Litter per year [4]	λ_h*	α**	ϕ***	Diet
Bos taurus	1	1	0.009	0.25	0.1	Herbivore [5]
Sus scrofa	7	1.5	0.098	0.125	1	Omnivore [6]
Canis familiaris	6	2	0.109	0.083	2	Omnivore [5]
Mustela sp.	6.2	1	0.057	0.125	1	Carnivore [7]
Potos flavus	1	1	0.009	0.025	0.1	Frugivore [8]
Didelphis marsupialis	6	2	0.102	0.083	2	Omnivore [9]
Marmosa sp.	10	1.5	0.122	0.083	2	Insectivore [5]
Metachirus nudicaudatus	5	2	0.096	0.083	2	Omnivore [10]
Philander opossum	5	3	0.104	0.083	2	Omnivore [11]
Allouata palliata	1	0.6	0.005	0.25	0.1	Folivore [12]
Cebus sp.	1	0.7	0.006	0.25	0.5	Omnivore (fruits) [13]
Coendu bicolor	1	1	0.009	0.25	0.1	Frugivore [14]
Heteromyidae sp	4	1.44	0.041	0.125	1	Omnivore (granivore) [5]
Mus musculus	7	5.4	0.353	0.083	2	Omnivore [5]
Sciurus sp.	2	2	0.034	0.125	0.1	Frugivore [13]
Choloepus hoffmani	1	0.7	0.006	0.25	0.1	Folivore [15]
Cyclopes didactylus	1	1	0.010	0.25	0.1	Mainly ants [16]
Tamandua mexicana	1	1	0.010	0.25	0.1	Mainly ants [13]

*units: $\frac{individuals}{female.week}$. It Assumes a female-male ratio equals to 1:1. **units: $\frac{1}{week}$. ***units: $\frac{bugs}{host.week}$

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