

In endemic areas, *T. cruzi* infection is transmitted on three distinct spatial scales: regionally through human rural-to-urban migration and visitation between villages (1, 2); within a village when domestic triatomine bugs disperse among households or from surrounding sites or forests to houses, or when dogs, cats and humans visit among houses (3); and within each household, through intimate contact among humans, dogs, cats, and bugs (4). Transmission is most intense within the household. Hence, we developed a model of the seasonal transmission of *T. cruzi* in a single household and focussed on the means of intervention available to householders.

This Web supplement specifies the assumptions, variables, and formal structure of the model. It also lists the computing code used to generate and plot the numerical predictions of the model.

Biological setting of the model

The model aims to represent transmission of *T. cruzi* in the domestic or domiciliary area of a typical individual household in the Grand Chaco of northwestern Argentina. This area includes human sleeping quarters and the veranda covered by the same roof, as well as the occupants at night. It excludes the peridomestic area (corrals and buildings not connected to human sleeping quarters) because peridomestic *T. infestans* exhibit marginal rates of contact with domiciliary hosts and marginal *T. cruzi* infection rates (5, 6, 7). *T. infestans* does not have sylvatic foci in most of its present distribution.

The model treats an individual household as a closed system. The model neglects the introduction of *T. cruzi* into the household and its spread outward from the household. The model assumes that the spatial distribution of people, dogs, chickens and bugs within the household is unchanged from the situations in which the descriptive data were gathered. Changed spatial

arrangements could affect feeding contacts and transmission.

The model traces the household through two warm seasons within a single year, from the onset of spring to the end of summer, assuming that transmission is negligible during the cold seasons of fall and winter.

Counts of bugs refer exclusively to fourth- and fifth-instar nymphs and adult bugs. Late instars at the end of summer pass through the winter with greatly reduced activity; recommence feeding, molting, and egg-laying in spring; and die before summer. Most of the spring-born bugs disappear before the next spring. Hence, the model assumes that all bugs live for two seasons only, spring and the following summer, or summer and (after overwintering) the following spring.

Bugs acquire infection by feeding on infected humans and infected dogs (5, 6, 8). In the spring but not the summer, chickens belong to the pool of blood meal sources for the bugs, reducing the probability of a bug's acquiring infection in the spring and increasing the bug population size in the summer.

A feeding contact (or feeding) is defined as a full blood meal on a given individual host obtained by a bug on one feeding trip or bout, regardless of the total number of bites delivered on this host to secure the blood meal. "Full" is here used to match the experimental estimation of the probability of a bug becoming infected in a single blood meal (8). Full blood meals imply an increased chance of a bug defecating on the host's skin and of potential parasite transmission.

When the continuous variables used to measure the sizes of host or bug populations include fractions, the fractions may be interpreted as the average fraction of time individuals are present in the household (e.g., 0.5 dog means a dog inside the household half time). Cats are much less preferred by *T. infestans* than humans, dogs and chickens (5, 9) and are omitted from the model.

Assumptions of the model

The input and output variables of the model are listed, defined and illustrated in table 1. The user

of the model specifies the number of humans by age groups as well as numbers of chickens, infected dogs and uninfected dogs. These numbers are assumed fixed for any run of the model. Here the modeled household contains one human aged 0 to 4, one aged 5 to 9, one aged 10 to 14, one aged 25 to 29, and one aged 30 to 34 (three children, two parents). The base case assumes two chickens, two infected dogs, and no uninfected dogs. Other household compositions can be specified.

Chickens are assumed to nest or brood in bedroom areas in the spring but not the summer. The number is given by the variable C, for "chickens." Humans, dogs and bugs are assumed to live in bedroom areas in spring and summer. The user specifies how many of the household dogs are infected with *T. cruzi* as the input variable DI (for "dogs infected"). All dogs are assumed infected with *T. cruzi* in these calculations, as is nearly true in the highly infested houses (6), but the model can take account of any number of uninfected dogs as well (DU). The total number of dogs is D (for "dogs").

The number of bugs is treated as constant over time within each warm season (spring or summer) but differs between seasons. The suffixes g and r denote spring and summer, respectively. The size Bg of the spring bug population is a Monod function of the number of vertebrate hosts $V_r = H + R * D$ available the previous summer, where R is the user-specified relative feeding index of dogs and chickens as sources of feeding contacts compared to humans. With $R = 3$, one dog or chicken counts as three humans as far as the bugs are concerned, so a household with one person and one dog supports as many bugs as a household with four people only. The number Br of bugs in summer is a Monod function of the number of vertebrate hosts $V_g = H + R * (C + D)$ available in the previous spring.

The Monod function (see Bg, Br in table 1) is consistent with experimental evidence (10) and field studies in experimental huts (11) and rural houses (12). The Monod function has two user-specified coefficients, B_{limit} and V_{half}. The maximum number of bugs the physical

infrastructure of the house will support, B_{limit} , given an unlimited food supply, is higher if the mud walls of the house are cracked, providing places for bugs to hide and lay eggs, and is lower if the walls are smoothly plastered, if the roof of the house is built of materials resistant to bug infestation or if the roofs and walls are treated with non-professional aerosol insecticides or smokes. The value $B_{limit} = 500$ (late-instar and adult bugs) exceeds a census of 126 late instars of *T. infestans* in bedrooms of a house demolished in Córdoba, Argentina (13), as well as two of the three counts of 177, 682, and 137 late instars in three houses demolished in Goiás, Brazil (14), and is approximately consistent with an estimate of the bug carrying capacity of mud and thatch houses (15). The coefficient V_{half} (for "vertebrates halfway") is the number of vertebrate blood sources (in human equivalents) sufficient to support $B_{limit}/2$ bugs.

The user also specifies five parameters of transmission of infection.

1) The number of feeding contacts per bug per spring and summer combined is M , for "meals." With $M = 5$ feeding contacts per late instar and adult bug per spring and summer combined, most bugs are expected to feed on two or more vertebrate species (for example, humans and dogs). The fractions of feeding contacts from humans, dogs and chickens calculated in the model may correspond only approximately to the fractions of bugs whose guts have blood meals from each of the sources (5, 16), because a bug may feed multiple times on a given vertebrate host individual or species, and this repeat feeding is not detectable by routine immunological tests. For the same reason, neither the fraction of bugs fed nor the fraction of feeding contacts on a given species of vertebrate host can be interpreted as a surrogate for the number of host individuals of that species in a household.

2) The fraction α of a bug's M annual feeding contacts that a bug takes in the season in which it is in instar 4 or 5 or adult reflects the prolonged life cycle of bugs, as estimated in experimental huts under natural climatic conditions (11). The results of the model are insensitive to the value of α in the range from 0.5 to 1.0, so we took $\alpha = 0.75$. The model assumes that M

and α are independent of the number of vertebrate blood sources.

3) The bug-to-human transmission probability ($t_{B \rightarrow H}$) is the probability that, in one feeding contact by one infected bug on an initially uninfected human, the human acquires infection. In all simulations reported here, $t_{B \rightarrow H}$ is assigned the value $t_{B \rightarrow H} = 0.0008$. This value is based on numerical experimentation with possible alternatives. This value is close to the 0.0009 estimated from one field study (17) but is smaller than 0.01 assumed in a theoretical model (18).

4) The human-to-bug transmission probability $t_{H \rightarrow B}$ (here 0.03) is the probability that, in one feeding by an initially uninfected bug on a seropositive human, the bug acquires infection.

5) The dog-to-bug transmission probability $t_{D \rightarrow B}$ (here 0.49) is analogous to the human-to-bug transmission probability. The probabilities 0.03 and 0.49 of infecting an initially uninfected bug from a single full feeding on a *T. cruzi*-seropositive person or seropositive dog, respectively, were estimated experimentally by xenodiagnosis: laboratory-reared uninfected bugs were fed separately on seropositive people and seropositive dogs (8).

The user gives the model an arbitrary initial value of the household's prevalence among humans (p_H) at the onset of spring (p_{H0}). The model assumes that initially some humans or dogs are infected, i.e., $p_{H0} + DI > 0$. Under this assumption, the value assumed for p_{H0} has no effect on the computed equilibrium human prevalence.

Successive lines of code in "model 5" below compute as follows.

1. The total number D of dogs is $DI + DU$.
2. The total number H of humans is the sum of the number of humans of each age, that is, the sum of the input vector H_a , which in these calculations is always $[1, 1, 1, 0, 0, 1, 1]$.
3. The number V_g of spring vertebrates, in human equivalents, is $H + R \cdot (D + C)$, where C is the total number of chickens.
4. The number V_r of summer vertebrates, in human equivalents, is $H + R \cdot D$.
5. The number B_g of spring bugs is a Monod function of the number of previous summer

vertebrates, $B_{limit} * V_r / (V_{half} + V_r)$.

6. The number B_r of summer bugs is a Monod function of the number of previous spring vertebrates, $B_{limit} * V_g / (V_{half} + V_g)$.

7. The number of infected humans is $N_H = H * p_H0$.

8. The probability that, in one full feeding contact, an initially uninfected bug acquires *T. cruzi* infection is $T_g = (0.03 * N_H + 0.49 * R * DI) / V_g$ in the spring and $T_r = (0.03 * N_H + 0.49 * R * DI) / V_r$ in the summer. The latter denominator omits chickens because they are not available to bugs in the summer. The model assumes that each bug selects the host for its next feeding contact at random among the available vertebrate blood sources (after allowing for their different host preferences). Data which have been offered as relevant to this assumption have varying interpretations (19).

9. The prevalence rate p_{Bg} of *T. cruzi* infection in spring bugs is $1 - ((1 - T_g)^{M * \alpha}) * ((1 - T_r)^{M * (1 - \alpha)})$, assuming that the bug has $M * \alpha$ feeding contacts in spring and $M * (1 - \alpha)$ feeding contacts in the previous summer and that the transmission of infection is independent among feeding contacts. The prevalence rate p_{Br} of *T. cruzi* infection in summer bugs is computed in the identical way, with spring and summer exchanged.

10. The spring number of infected bugs N_{Bg} is the product $B_g * p_{Bg}$ of the number of spring bugs times the prevalence rate in spring bugs. The summer number of infected bugs N_{Br} is likewise $B_r * p_{Br}$.

11. The average number of feeding contacts per person per year (spring and summer combined) Bitespy is the sum of the average number of feeding contacts per person in spring plus the average number of feeding contacts per person in summer. Each season-specific average number of feeding contacts per person is the quotient of the number of feeding contacts from all bugs in that season divided by the number of all vertebrate hosts in that season. For example, the spring average number of feeding contacts per person is $(B_g * \alpha + B_r * (1 - \alpha)) / V_g$ because spring bugs

deliver $B_g \cdot \alpha$ feeding contacts to the household in spring, whereas summer bugs deliver $B_r \cdot (1 - \alpha)$ feeding contacts to the household in spring. These feeding contacts are uniformly distributed among the human-equivalent vertebrate hosts, and each human counts as one human-equivalent.

12. The average number of feeding contacts by *T. cruzi*-infected bugs per person per year Infbitespy is the sum of the average number of feeding contacts from infected bugs per person in spring plus the average number of feeding contacts from infected bugs per person in summer. The formulas are the same as for Bitespy except that the numbers of bugs, B_g and B_r , are replaced by the numbers of infected bugs, NB_g and NB_r respectively.

13. The average number C_a of feeding contacts with an infected bug a human of age a has experienced over his or her lifetime thus far is the product of the person's age times the average number of feeding contacts with infected bugs per person per year, $a \cdot \text{infbitespy}$. In these calculations, the input vector $a = [2.5, 7.5, 12.5, 17.5, 22.5, 27.5, 32.5]$.

14. The prevalence rate p_{Ha} in humans of age a is the complement of the probability that none of the feeding contacts with an infected bug has transmitted infection to the human, that is, $p_{Ha} = 1 - (1 - t_{B \rightarrow H})^{C_a}$.

15. The number N_{Ha} of infected humans of age a is $H_a \cdot p_{Ha}$, the product of the number of humans of age a times the prevalence rate in humans of age a .

16. The average (over all ages) of the prevalence rate of infection in humans is the sum of the number N_{Ha} of infected humans of all ages, divided by the total number of humans of all ages. This quantity is p_{H1} , the net result of the operation of the model through the spring and summer seasons starting from the initial prevalence rate p_{H0} at the onset of spring.

17. The fraction of feeding contacts with humans, dogs and chickens in spring and summer are calculated, using similar reasoning, in the concluding lines of model5.

Additional assumptions of the model are:

1) Transmission processes and probabilities are the same in spring and summer. The only

difference is that chickens are present in bedroom areas in spring and absent in summer.

2) *T. cruzi* infection does not affect significantly the vital parameters (feeding, growth, survival, and reproduction) of hosts and bugs.

3) Susceptibility to *T. cruzi* infection is independent of bug stage (for fourth- and fifth-instar nymphs and adult bugs), age and sex of mammal hosts, and ambient temperature.

4) The probability of bug infection after a single full blood meal on an infected host is independent of host age and ambient temperature.

5) Transmission mediated by *T. infestans* is the sole route of infection. Vertical transmission of *T. cruzi* from an infected human mother to her infant and transmission by transfusion are ignored.

6) The probability of transmission to an uninfected human per feeding contact is independent of (a) the intensity of bug infection [number of trypomastigote parasites (infectious forms of *T. cruzi*) per bug], (b) bug stage, (c) previous bloodmeal sources, (d) absolute or relative (per host) density of bugs, and (e) ambient temperature.

7) Host bloodmeal sources do not affect significantly the bugs' vital parameters, bloodmeal size, and acquisition or development of *T. cruzi* infection.

8) Individuals within each species of hosts, bug and parasite do not differ significantly in their course of infection.

9) The population dynamics of hosts, bugs and parasites are not significant for the equilibrium human prevalence of infection with *T. cruzi*, that is, it is sufficient to consider the effect of the steady-state population sizes on human prevalence.

Of these assumptions, 1, 2, and 7 have supporting evidence or are a reasonable approximation given current knowledge. Only partial evidence is available regarding assumption 6(d). A multiple linear regression (20) showed that, when *T. infestans* was interrupted while it was biting, the time to the first fecal drop was inversely and significantly related to blood intake

and was directly and significantly related to how long the bug was starved before feeding and how much the bug weighed at the start of feeding. Although previous experiments using restrained mice or unrestrained chickens held in small boxes showed that *T. infestans* blood intake was negatively density dependent, it does not necessarily follow that a feeding contact with a single bug at high bug population density has a lower risk of transmitting infection to an uninfected mammalian host than a feeding contact with a single bug at a low bug population density. The relation between bug population density and the probability of transmission by a single feeding contact with an infected bug remains to be assessed empirically. Mice have been infected with as few as 25 *T. cruzi* trypomastigotes inoculated intraperitoneally (21), whereas field-collected *T. infestans* had millions of infective trypomastigotes per milliliter of bug feces (22). Assumptions 3, 4, 5, and 8 are simplifications of convenience, against which there is some contradictory evidence. For example, contrary to assumption 4, children have many more trypomastigotes in their blood than older people with chronic infections and are therefore more infectious than adults (8). Dogs also may be slightly more infectious in the early than in the late chronic phase (8). Assumption 9 is appropriate for an equilibrium model applied to a chronic endemic disease transmitted by a K-strategist insect vector living close to equilibrium abundance (3, 10).

The prevalence rates neglect the latency between entry of *T. cruzi* into a susceptible host and that host's becoming infectious, because latent periods of bugs and hosts (1 to 3 weeks) are negligible compared to the remaining average lifetime of a dog, human or bug at the time when each acquires the infection.

Analysis of the model

The steady-state condition $pH_0 = pH_1$ means that the human prevalence rate at the end of summer equals the human prevalence rate at the onset of spring. This condition has exactly one mathematical solution, so the output of the model is uniquely defined, apart from limitations of numerical analysis in finding the mathematical solution. This steady-state solution pH is computed

approximately by numerical iteration (repeatedly replacing pH0 with pH1) by the Matlab function `iterate5` until the initial human prevalence rate pH0 at the onset of spring differs from the final human prevalence rate pH1 at the end of summer by no more than the user-specified criterion δ for convergence, here taken as 0.001; i.e., the iteration continues until $|\text{pH0}-\text{pH1}| < \delta = 0.001$.

The Matlab function `chidogtable5` (for "chicken-dog table") investigates how the assumed numbers of infected dogs and chickens affects the steady-state human prevalence of *T. cruzi* infection and other characteristics of the household system, such as bug population sizes by season. This function is the computational alternative to ethically impossible field experimentation. Fifteen numerical values [0, 0.1, 0.2, 0.3, 0.4, 0.6, 0.8, 1.0, 1.5, 2, 2.5, 3, 4, 5, and 6] were assigned in succession to the number of chickens C, and, for each value of C, the same 15 numerical values were assigned in succession to the number of infected dogs DI. Thus, model outputs were produced for $225 = 15 \times 15$ combinations of the numbers of chickens and infected dogs. These values for the input variables "chickens" and "dogs" were selected to display clearly how the model behaves in the region where output variables change rapidly, rather than to reflect the actual distribution of the numbers of chickens and infected dogs per household in the villages studied. All other parameters remained constant at the values shown in table 1.

Sensitivity analyses

The printed paper reports a sensitivity analysis with respect to the parameter values of Blimit, M, and R (see table 1 for definitions). In addition, four related models that differed in detailed structure were investigated numerically. These other models differed in the absence of seasonality, and (among the seasonal models) in the seasonality of keeping chickens indoors, in the dependence of the bug population size on the number of vertebrate hosts in the present versus prior season, and in other minor respects. Although the quantitative predictions of the models varied, the major conclusions for the control of *T. cruzi* transmission within households were remarkably robust.

If the model were simplified by replacing the age-structured human population with a single age group, the human prevalence rate could be significantly overestimated. Because the curve of the human prevalence rate as a function of age is concave in this model, using a single age group in which the age is the average age $A_{bar} = \sum(a \cdot H_a) / H$ will increase the predicted human prevalence rate as a mathematical consequence of Jensen's inequality. Numerical calculations not shown here indicate that ignoring age structure could introduce substantial bias.

Other related work

Two independent simulation models assessed the effects of chickens on the household transmission of *T. cruzi*. In the presence of humans and dogs infected with *T. cruzi*, maintaining 10 or 20 chickens in domiciliary areas depressed bug and human prevalence rates of infection substantially (23). The presence of a single brooding chicken in domiciliary areas in both spring and summer decreased the daily rate of potentially infective feeding contacts experienced by humans but did not significantly reduce the human incidence rate (24).

An existing model of zoonophylaxis in malaria (25) omits seasonality. A model for the insect-transmitted African horse sickness includes seasonality (26) but deals with only two susceptible host species that differ in infectivity and pathogen-induced mortality. In the red grouse-hare-louping ill virus system (27), the nonviremic hosts can amplify the tick (vector) population and cause the virus to persist or can cause the infection to die out. None of these models made any comparison with field data.

Computing software

All numerical calculations reported here were carried out on a Dell personal computer using MATLAB 5.2 (28). The three Matlab functions used to implement the model, namely, `chidogtable5`, `iterate5`, `model5`, are listed below. The user first defines numerical values for the variables `a`, `Ha`, `C`, `DI`, `DU`, `R`, `Blimit`, `Vhalf`, `M`, `t`, `pH0`, `alpha`, `delta`, `chickens`, `dogs`, which are defined in the internal comments of `chidogtable5`, then

commands:

```
out=chidogtable5(a,Ha,C,DI,DU,R,Blimit,Vhalf,M,t,pH0,alpha,
delta,chickens,dogs);
```

The function `chidogtable5` invokes the function `iterate5`, which in turn invokes `model5`. The function `iterate5` determines a steady-state human prevalence rate by iteration of `model5`. The function `chidogtable5` computes the steady-state human prevalence rates associated with different combinations of numbers of chickens and dogs, and plots the results.

Function model5

```
function
```

```
[pH1,NHa,Bg,Br,pBg,pBr,NBg,NBr,bitespy,infbitespy,humbloodg,dogb
loodg,chibloodg,humbloodr,dogbloodr,chibloodr]=model5(a,Ha,C,
,DI,DU,R,Blimit,Vhalf,M,t,pH0,alpha)
% [pH1,NHa,Bg,Br,pBg,pBr,NBg,NBr,bitespy,infbitespy,humbloodg,dogb
loodg,chibloodg,humbloodr,dogbloodr,chibloodr]=model5(a,Ha,C,D
I,DU,R,Blimit,Vhalf,M,t,pH0,alpha)
%Model of Chagas transmission in a household: 2 seasons (spring,
summer)
%Bug population size is set in previous season
%Bug prob. of acquiring infection and bug prevalence rate are set
in season of adulthood
%Suffix g = spring, r = summer
%a =vector of midpoints of age groups
%Ha=vector of number of people in each age group in household
%C =chickens
%DI=dogs infected
%DU=dogs uninfected
%R =relative attractiveness of dogs and chickens as blood meals
wrt humans
```

%Blimit=maximum number of bugs given unrestricted food
 %Vhalf=no.of vertebrate blood sources (in human equivalents)
 sufficient to support Blimit/2 bugs
 %M =meals per bug per summer
 %t =prob. that, in one bite by one infected bug on initially
 uninfected human, human acquires infection
 %pH0=initial prevalence rate of Chagas infection in humans
 %alpha = fraction of blood meals that adult bugs take during
 season of adulthood
 %27 December 1999; 9, 14, 25, 29 March 2000
 D=DI+DU; %dogs
 H=sum(Ha); %humans
 Vg=H+R*(D+C); %spring vertebrate blood sources, in human
 equivalents, chickens indoors
 Vr=H+R*D; %summer vertebrate blood sources, in human
 equivalents, chickens outdoors
 Bg=Blimit*Vr/(Vhalf+Vr); %spring IV-V-adult bugs in household set
 by summer vertebrates
 Br=Blimit*Vg/(Vhalf+Vg); %summer IV-V-adult bugs in household set
 by spring vertebrates
 NH=H*pH0; %initial prevalence in humans
 Tg=(0.03*NH+0.49*R*DI)/Vg; %spring prob. that an initially
 uninfected bug acquires infection in one blood meal
 Tr=(0.03*NH+0.49*R*DI)/Vr; %summer prob. that an initially
 uninfected bug acquires infection in one blood meal
 pBg=1-((1-Tg)^(M*alpha))*((1-Tr)^(M*(1-alpha))); %spring
 prevalence rate in spring-late-instar and adult bugs
 pBr=1-((1-Tr)^(M*alpha))*((1-Tg)^(M*(1-alpha))); %summer
 prevalence rate in summer-late-instar and adult bugs

```

NBg=Bg*pBg;           %spring number of infected spring-late-
    instar and adult bugs
NBr=Br*pBr;           %summer number of infected summer-late-
    instar and adult bugs
bitespy=(Bg*alpha+Br*(1-alpha))*M/Vg+(Bg*(1-
    alpha)+Br*alpha)*M/Vr;   %average number of bites per person
    per year
infbitespy=(NBg/Vg+NBr/Vr)*alpha*M + (NBg/Vr+NBr/Vg)*(1-alpha)*M;
%average number of bites by infected bugs per person per year
Ca=a*infbitespy;       %ave.no.times human aged a has been bitten
    by infected bug
pHa=1-(1-t).^Ca;       %prevalence rate in humans aged a
NHa=Ha.*pHa;          %prevalence in humans aged a
pH1=sum(NHa)/H;        %prevalence rate in humans
humbloodg=alpha*H/Vg+(1-alpha)*H/Vr; %human blood meals of
    spring-late-instar and adult bugs
dogbloodg=alpha*R*D/Vg+(1-alpha)*R*D/Vr; %dog blood meals
    of spring-late-instar and adult bugs
chibloodg=alpha*R*C/Vg; %chicken blood meals of spring-
    late-instar and adult bugs
humbloodr=alpha*H/Vr+(1-alpha)*H/Vg; %human blood meals of
    summer-late-instar and adult bugs
dogbloodr=alpha*R*D/Vr+(1-alpha)*R*D/Vg; %dog blood meals
    of summer-late-instar and adult bugs
chibloodr=(1-alpha)*R*C/Vg; %chicken blood meals of summer-
    late-instar and adult bugs
return

```

Function iterate5

```
function
    [pH1, PHa, Bg, Br, pBg, pBr, NBg, NBr, bitespy, infbitespy, humbloodg, do
    gbloodg, chibloodg, humbloodr, dogbloodr, chibloodr, aveage, aveinfage]
    =iterate5(a, Ha, C, DI, DU, R, Blimit, Vhalf, M, t, pH0, alpha, delta)
% [pH1, PHa, Bg, Br, pBg, pBr, NBg, NBr, bitespy, infbitespy, humbloodg, dogb
    loodg, chibloodg, humbloodr, dogbloodr, chibloodr]=iterate5(a, Ha, C
    , DI, DU, R, Blimit, Vhalf, M, t, pH0, alpha, delta)
%27 December 1999, rev. 2 Jan 2000, 9, 14, 25 March 2000
pH1=pH0;
pH2=model5(a, Ha, C, DI, DU, R, Blimit, Vhalf, M, t, pH0, alpha);
while abs(pH2-pH1)>delta
    pH1=pH2;
    pH2=model5(a, Ha, C, DI, DU, R, Blimit, Vhalf, M, t, pH1, alpha);
end
[pH1, PHa, Bg, Br, pBg, pBr, NBg, NBr, bitespy, infbitespy, humbloodg, dogbl
    oodg, chibloodg, humbloodr, dogbloodr, chibloodr]=model5(a, Ha, C, DI
    , DU, R, Blimit, Vhalf, M, t, pH0, alpha);
aveage=sum(a.*Ha)/sum(Ha);          %average age of humans
aveinfage=sum(a.*PHa)/sum(PHa);    %average age of infected humans
return
```

Function chidogtable5

```
function
    out=chidogtable5(a, Ha, C, DI, DU, R, Blimit, Vhalf, M, t, pH0, alpha, del
    ta, chickens, dogs)
%out=chidogtable5(a, Ha, C, DI, DU, R, Blimit, Vhalf, M, t, pH0, alpha, delta
    , chickens, dogs)
```

%Model of Chagas transmission in a household: 2 seasons (spring,
summer)

%Bug population size is set in previous season

%Suffix g = spring, r = summer

%a =vector of midpoints of age groups

%Ha=vector of number of people in each age group in household

%C =chickens

%DI=dogs infected

%DU=dogs uninfected

%R =relative attractiveness of dogs and chickens as feeding
contacts wrt humans

%Blimit=maximum number of bugs given unrestricted food

%Vhalf=no.of vertebrate blood sources (in human equivalents)
sufficient to support Blimit/2 bugs

%M =feeding contacts per bug per spring and summer combined

%t =prob. that, in one bite by one infected bug on initially
uninfected human, human acquires infection

%pH0=initial prevalence rate of Chagas infection in humans

%alpha = fraction of feeding contacts that late-instar and adult
bugs take during season when they become late-instar or adult

%delta=threshold for quasi-convergence of iteration: steady-state
iff $|pH2-pH1|<delta$

%chickens=vector of numbers of chickens to assume in household

%dogs=vector of numbers of dogs to assume in household

%out level 1 number of chickens in household

% level 2 number of dogs in household

% level 3 pH prevalence rate in humans

% level 4 Bg late-instar and adult bugs in household in spring

% level 5 Br late-instar and adult bugs in household in summer

```

% level 6 pBg prevalence rate in bugs in spring
% level 7 pBr prevalence rate in bugs in summer
% level 8 NBg number of infected bugs in spring
% level 9 NBr number of infected bugs in summer
% level 10 bitespy average number of bites per person per year
% level 11 infbitespy average number of bites by infected bugs
per person per year
% level 12 humbloodg fraction of feeding contacts on human blood
in spring
% level 13 dogbloodg fraction of feeding contacts on dog blood
in spring
% level 14 chibloodg fraction of feeding contacts on chicken
blood in spring
% level 15 aveage average age of humans
% level 16 aveinfage average age of infected humans
% level 17 humbloodr fraction of feeding contacts on human blood
in summer
% level 18 dogbloodr fraction of feeding contacts on dog blood
in summer
% level 19 chibloodr fraction of feeding contacts on chicken
blood in summer

%29 December 1999, rev. 2 January 2000, 25 March 2000, 7 May
2000; 23 May 2000; 6 May 2001

fnt=22;      %font size for lettering of figures
fntic=18;    %font size for labeling of tic marks
lc=length(chickens);
ld=length(dogs);
[chigrid,doggrid]=meshgrid(chickens,dogs); %grid for each
combination of chickens & dogs

```

```

out=cat(3,chigrd,doggrid); %first 2 layers of output
    array 'out'
out=cat(3,out,zeros(ld,lc,17)); %holder for remaining
    17 layers of 'out'
chibloodrmat=zeros(ld,lc);
for i=1:ld %for each combination of dogs(i) and chickens(j),
    get steady-state behavior
    for j=1:lc
        [pH1,PHa,Bg,Br,pBg,pBr,NBg,NBr,bitespy,infbitespy,humbloodg,dogbloodg,chibloodg,humbloodr,dogbloodr,chibloodr,aveage,aveinfage]=iterate5(a,Ha,chickens(j),dogs(i),DU,R,Blimit,Vhalf,M,t,pH0,alpha,delta);
        chibloodrmat(i,j)=chibloodr;
        temp=[pH1,Bg,Br,pBg,pBr,NBg,NBr,bitespy,infbitespy,humbloodg,dogbloodg,chibloodg,aveage,aveinfage,humbloodr,dogbloodr,chibloodr];
        for k=1:17
            out(i,j,k+2)=temp(k); %load output values into
        'out'
        end
    end
end
end

%Figure 1B, bloodmealssummerbugprevrte
figure(14)
h=plot3(out(:,:,14),out(:,:,13),out(:,:,7),'k.-');
grid
set(gca,'fontsize',fntic)
title('summer bug prevalence rate','FontSize',fnt)

```

```

xlabel('chicken feedings','FontSize',fnt),ylabel('dog
        feedings','FontSize',fnt),zlabel('bug prevalence
        rate','FontSize',fnt)
print -deps -tiff bloodmealssummerbugprevrate.eps

%Figure 1D, humchibloodmealsvsummerbugs
figure(16)
x=[out(:,:,5),out(:,:,5)];    % late-instar and adult bugs in
    household in SUMMER ONLY!!!!
y1=[out(:,:,12),out(:,:,17)]; %humbloodg and humbloodr
y2=[out(:,:,14),out(:,:,19)]; %chibloodg and chibloodr
h=plot(x(:),y1(:),'o',x(:),y2(:),'x');
set(gca,'fontsize',fntic)
title('spring & summer feeding contacts','FontSize',fnt)
xlabel('summer bugs in household','FontSize',fnt),ylabel('human
        (o), chicken (x) feeding contacts','FontSize',fnt)
%print
print -deps -tiff humchibloodmealsvsummerbugs.eps

```

```

%Figure 2A springbugsinhousehold
figure(1)
mesh(chigrid,doggrid,out(:,:,4))
colormap([0 0 0])
title('spring bugs in household','FontSize',fnt)
xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('spring bugs','FontSize',fnt)
set(gca,'fontsize',fntic)
%print
print -deps -tiff springbugsinhousehold.eps

```

```

%Figure 2B summerbugsinhousehold
figure(2)
mesh(chigrid,doggrid,out(:, :, 5))
colormap([0 0 0])
title('summer bugs in household','FontSize',fnt)
xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('summer bugs','FontSize',fnt)
set(gca,'fontsize',fntic)
%print
print -deps -tiff summerbugsinhousehold.eps

%Figure 2C humanbloodmeals
figure(3)
mesh(chigrid,doggrid,out(:, :, 12))
colormap([0 0 0])
title('spring feeding contacts with humans','FontSize',fnt)
xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('fraction of feeding contacts with
    humans','FontSize',fnt)
set(gca,'fontsize',fntic)
%print
print -deps -tiff humanbloodmeals.eps

%Figure 2D springdogbloodmeals
figure(4)
mesh(chigrid,doggrid,out(:, :, 13))
colormap([0 0 0])
title('spring feeding contacts with dogs','FontSize',fnt)

```

```

xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('fraction of feeding contacts with dogs','FontSize',fnt)
set(gca,'fontsize',fntic)
%print
print -deps -tiff springdogbloodmeals.eps

%Figure 2E prevrateinspringbugs
figure(6)
mesh(chigrd,doggrid,out(:, :, 6))
colormap([0 0 0])
title('prevalence rate in spring bugs','FontSize',fnt)
xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('prevalence rate in bugs','FontSize',fnt)
set(gca,'fontsize',fntic)
%print
print -deps -tiff prevrateinspringbugs.eps

%Figure 2F infectedspringbugs
figure(8)
mesh(chigrd,doggrid,out(:, :, 8))
colormap([0 0 0])
title('infected spring bugs','FontSize',fnt)
xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('number of infected bugs','FontSize',fnt)
set(gca,'fontsize',fntic)
%print
print -deps -tiff infectedspringbugs.eps

%Figure 2G infectedsummerbugs

```

```

figure(9)
mesh(chigrid,doggrid,out(:, :, 9))
colormap([0 0 0])
title('infected summer bugs','FontSize',fnt)
xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('number of infected bugs','FontSize',fnt)
set(gca,'fontsize',fntic)
%print
print -deps -tiff infectedsummerbugs.eps

%Figure 2H feedingsperhumanyear
figure(10)
mesh(chigrid,doggrid,out(:, :, 10))
colormap([0 0 0])
title('feeding contacts per human','FontSize',fnt)
xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('feeding contacts per human','FontSize',fnt)
set(gca,'fontsize',fntic)
%print
print -deps -tiff feedingsperhumanyear.eps

%Figure 2I humanprevalencerate
figure(12)
mesh(chigrid,doggrid,out(:, :, 3))
colormap([0 0 0])
title('human prevalence rate','FontSize',fnt)
xlabel('chickens','FontSize',fnt),ylabel('dogs','FontSize',fnt),z
    label('human prevalence rate','FontSize',fnt)
set(gca,'fontsize',fntic)

```

```
%print  
print -deps -tiff humanprevalencerate.eps  
return
```

Web table 1. Parameters, calculated variables and descriptive statistics of the model.

Symbol	Meaning	Formula or illustrative value in base case at equilibrium
a	Age groups of humans in household (vector of midpoints of ages, measured in years)	[2.5 7.5 12.5 17.5 22.5 27.5 32.5]
Ha	Number of humans in each age group (vector of values)	[1 1 1 0 0 1 1] (meaning 1 person aged 2.5 years, 1 aged 7.5 years, 1 aged 12.5 years, etc.)
H	Number of humans in household	sum of Ha Ha = 5 people
DI	Number of dogs infected with <i>T. cruzi</i>	DI = 2 infected dogs
DU	Number of dogs uninfected with <i>T. cruzi</i>	DU = 0 uninfected dogs
D	Number of household dogs	DI + DU D = 2 dogs
C	Number of household chickens	C = 2 chickens
R	Relative feeding index of dogs and chickens as sources of feeding contacts compared to humans	R = 3 dog or chicken feedings per human feeding
Vg, Vr	Number of vertebrate blood sources, in human equivalents, in spring (Vg) and summer (Vr)	Vg = H+R*(D+C), Vr = H+R*D Vg = 17 vertebrates in spring, Vr = 11 vertebrates in summer
Blimit	Maximum number of fourth- and fifth-instar nymphs and adult bugs the physical infrastructure of the house will support, given an unlimited food supply	Blimit = 500 large and late-stage bugs

Vhalf	Number of vertebrate blood sources (in human equivalents) sufficient to support Blimit/2 bugs	Vhalf = 7 vertebrates
Bg, Br	Number of fourth- and fifth-instar nymphs and adult bugs in spring (Bg) and summer (Br) that can be supported at steady-state by the vertebrate blood sources in the household	$Br = Blimit * Vg / (Vg + Vhalf)$ $Bg = Blimit * Vr / (Vr + Vhalf)$ Br = 354.2 bugs in summer, Bg = 305.6 bugs in spring
M	Number of feeding contacts per fourth- or fifth-instar nymph or adult bug per spring and summer combined	M = 5 feeding contacts per bug per summer and spring
pH0	Human prevalence rate in late winter (fraction of all humans infected with <i>T. cruzi</i>)	initial pH0=0.8 pH0=pH1 at equilibrium
t _{B→H}	Transmission probability to human = probability that, in one feeding by one infected bug on an initially uninfected human, the human acquires infection	t _{B→H} = 0.0008
t _{H→B}	Probability that, in one feeding by an initially uninfected bug on an infected (seropositive) human, the bug acquires infection	t _{H→B} = 0.03
t _{D→B}	Probability that, in one feeding by an initially uninfected bug on an infected (seropositive) dog, the bug acquires infection	t _{D→B} = 0.49
Tg, Tr	Transmission probability to bug in spring (Tg) and summer (Tr) = probability that, in one blood meal, an initially uninfected bug acquires infection	$Tg = (0.03 * NH + 0.49 * R * DI) / Vg$, $Tr = (0.03 * NH + 0.49 * R * DI) / Vr$
α	Fraction of feedings a bug takes in the season the bug is in instar 4 or 5 or adult	α = 0.75
pBg, pBr	Bug prevalence rates in spring (pBg) and summer (pBr) (fractions of bugs infected with <i>T. cruzi</i> in spring and summer)	$pBg = 1 - ((1 - Tg)^{\alpha * M}) * ((1 - Tr)^{(1 - \alpha) * M})$ $pBr = 1 - ((1 - Tr)^{\alpha * M}) * ((1 - Tg)^{(1 - \alpha) * M})$ pBg=0.6839 in spring pBr=0.7702 in summer

NBg, NBr	Number of infected bugs in spring (NBg) and summer (NBr)	$NBg = Bg * pBg$, $NBr = Br * pBr$ NBg=209.0 infected bugs in spring, NBr=272.8 infected bugs in summer
Bitespy	Number of feeding contacts per human per year	$(Bg * \alpha + Br * (1 - \alpha)) * M / Vg +$ $(Bg * (1 - \alpha) + Br * \alpha) * M / Vr$ Bitespy=248.9 feeding contacts per human per year
Infbitespy	Number of potentially infective feeding contacts per human per year	$(NBg / Vg + NBr / Vr) * \alpha * M +$ $(NBg / Vr + NBr / Vg) * (1 - \alpha) * M$ Infbitespy=182.9 infective feeding contacts per human per year
Ca	Contacts by age a = average number of times a human in each age-group a has had a feeding contact with an infected bug (vector of values)	$a * Infbitespy$
pHa	Prevalence rate in humans in each age-group a (vector of values)	$pHa = 1 - (1 - t_{B \rightarrow H})^{Ca}$
Nha	Expected number of infected humans in each age-group a (vector of values)	$Ha * pHa$
NH	Total number of infected humans	Sum of Nha
pH1	Human prevalence rate calculated through one cycle of the model	$pH1 = NH / H$ pH1=0.7572 at end of summer if pH0=0.8 at onset of spring
Humbloodg	Fraction of feeding contacts from humans in bugs collected in spring	$Humbloodg = \alpha * H / Vg + (1 - \alpha) * H / Vr$

Dogbloodg	Fraction of feeding contacts from dogs in bugs collected in spring	$\text{Dogbloodg} = \alpha * R * D / Vg + (1 - \alpha) * R * D / Vr$
Chibloodg	Fraction of feeding contacts from chickens in bugs collected in spring	$\text{Chibloodg} = \alpha * R * C / Vg$
Humbloodr	Fraction of feeding contacts from humans in bugs collected in summer	$\text{Humbloodr} = \alpha * H / Vr + (1 - \alpha) * H / Vg$
Dogbloodr	Fraction of feeding contacts from dogs in bugs collected in summer	$\text{Dogbloodr} = \alpha * R * D / Vr + (1 - \alpha) * R * D / Vg$
Chibloodr	Fraction of feeding contacts from chickens in bugs collected in summer	$\text{Chibloodr} = (1 - \alpha) * R * C / Vg$
Abar	Average age of humans (years)	$\text{Abar} = \text{Sum}(a * Ha) / H$ Abar = 16.5 years old
AI	Average age of infected humans (years)	$\text{AI} = \text{Sum}(a * Nha) / NH$ AI = 19.9391 years old

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