

Analysis of the steady states of a mathematical model for Chagas disease

> Mary Clauson, Albert Harrison, Laura Shuman, Meir Shillor and Anna Maria Spagnuolo





Analysis of the steady states of a mathematical model for Chagas disease

Mary Clauson, Albert Harrison, Laura Shuman, Meir Shillor and Anna Maria Spagnuolo

(Communicated by Suzanne Lenhart)

The steady states of a mathematical model for the dynamics of Chagas disease, developed by Spagnuolo et al., are studied and numerically simulated. The model consists of a system of four nonlinear ordinary differential equations for the total number of domestic carrier insects, and the infected insects, infected humans, and infected domestic animals. The equation for the vector dynamics has a growth rate of the blowfly type with a delay. In the parameter range of interest, the model has two unstable disease-free equilibria and a globally asymptotically stable (GAS) endemic equilibrium. Numerical simulations, based on the fourth-order Adams–Bashforth predictor corrector scheme for ODEs, depict the various cases.

1. Introduction

Chagas disease is wide spread in rural parts of South and Central America, where an estimated 10 million people are infected [Bilate and Cunha-Neto 2008; Cohen and Gürtler 2001; Schofield et al. 2006], and a search on the World Health Organization (WHO) web site yielded 1460 results. A summary of the state of the disease can be found at [WHO 2010]. Cases of the disease were also reported in Mexico and even a few in Southern California. The disease is transmitted by the insect *Triatoma infestans*, known as the "kissing bug", which bites the victim and then defecates around the bite wound. The parasites that cause the disease, *Trypanosoma cruzi*, which are in the bug's feces, enter the wound and spread throughout the body. The disease causes significant morbidity and eventually death, and there is no cure for the disease, after its initial stage. Currently the main way to control the spread of the disease is by insecticide spraying.

A mathematical model for the dynamics of the disease was developed in [Spagnuolo et al. 2011], where the main interest was to understand the disease spread

MSC2000: primary 92D30; secondary 34K28, 34K99, 37N25.

Keywords: Chagas disease, population dynamics, blowflies rate with delay, steady states. This research was partially supported by the NSF-REU Grant DMS 0649099.

and how to control it by using insecticide spraying. The model consists of four nonlinear ordinary differential equations (ODEs), describing the evolution of the total numbers of the insects or vectors and of the infected vectors, infected humans, and infected household mammals, which for the sake of simplicity we call dogs. It is of the MSEIR type, but with only S (susceptibles) and I (infectives) components for the insects, humans, and dogs. The model describes a typical rural village with humans, dogs, chickens, and the vectors. Although chickens cannot be infected nor are they carriers of Chagas disease, they are a blood source for the vectors, so they contribute essentially to the disease dynamics. We refer to [Spagnuolo et al. 2011] for a detailed description of the disease and the assumptions that underlie the model. An extensive literature can be found there, in [Coffield et al. 2010], and the references therein.

This work concentrates on the steady states of the model of Spagnuolo et al. and studies their stability. The time-dependent model coefficients, with their yearly oscillations are replaced by their yearly averages. Thus, the seasonal changes in the relevant system parameters are not included here. However, they were taken into account in [Coffield et al. 2010; Spagnuolo et al. 2011].

The interest in this work lies in understanding the mathematical structure of the model without spraying, and with time-independent coefficients.

We note that a somewhat different model was studied in [Spagnuolo et al. 2012; Coffield et al. 2010], where the analysis of the steady states can be found, too. There, the growth rate in the equation for the vectors was a logistic term with delay, while in [Spagnuolo et al. 2011] and here, the so-called "blowflies" term with a delay is used ([Nicholson 1954]; see also [Wei and Li 2005] and references therein).

In addition to the stability analysis of the steady states, Section 3, we present a scheme for the numerical solutions of the model and depict two sets of simulations, Section 4. The results depict the monotone ways the system approaches the endemic steady state.

2. The model

We briefly describe the mathematical model for Chagas disease developed in [Spagnuolo et al. 2011]. It describes the population dynamics of the total numbers of: vectors (bugs), infected vectors, infected humans, and infected domestic animals (dogs) in a representative village in South America. The model was used to study the effects of periodic insecticide spraying for the control of the disease. In this work we are interested in the stability of its disease-free and endemic equilibria, so we omit the terms related to insecticide spraying.

The populations are assumed to be large enough to be governed by differential equations. The total populations of humans (N), dogs (D), and chickens (C)

are assumed to remain constant over time. We denote by V = V(t) the number of carrier insects living in the houses at time t; the number of infective insects by $V_i = V_i(t)$, the number of infective humans by $N_i = N_i(t)$, and the number of infective dogs by $D_i = D_i(t)$. Each non-infected population, excluding C, is assumed to be susceptible. The rate coefficients $d_h = d_h(t)$, $d_m = d_m(t)$ and $b_i = b_i(t)$ are assumed to be periodic, with period of one year.

The *mathematical model for Chagas disease* of Spagnuolo et al., without insecticide spraying, is this:

$$V' = d_h V(t - \tau) e^{-aV(t - \tau)} - d_m V,$$
(2-1)

$$V'_{i} = b_{i}(V - V_{i}) \left(P_{NV}N_{i} + P_{DV}d_{f}D_{i} \right) - d_{m}V_{i}, \qquad (2-2)$$

$$N'_{i} = b_{i} P_{VN} (N - N_{i}) V_{i} - \gamma_{N} N_{i}, \qquad (2-3)$$

$$D'_i = b_i d_f P_{VD} (D - D_i) V_i - \gamma_D D_i, \qquad (2-4)$$

$$V_{i}(0) = V_{i0}, \quad N_{i}(0) = N_{i0}, \quad D_{i}(0) = D_{i0},$$

$$V(t) = V_{0}(t), \quad -\tau \le t \le 0.$$
(2-5)

Equation (2-1) describes the rate of change of the total vector population. The first term on the right-hand side is similar in form to Nicholson's *blowflies model* where the growth rate at time t (days) depends on the population size at time $t - \tau$ (days) [Gurney et al. 1980; Győri and Ladas 1991; Nicholson 1954]. However, in the Nicholson model $d_{h\tau}$ is a constant, since blowflies have only two stages of development: pupae and adult. In contrast, triatomines have six distinct stages of life: five instar stages and an adult stage. The egg hatching rate $d_{h\tau} = d_{h\tau}(t)$ at time t depends on the fraction of adult females at time $t - \tau$, as well as other factors including seasonal temperatures and blood supply. In particular, the growth term attains a maximum when the number of vectors in the village houses at time $t - \tau$ reaches the value of 1/a. The natural death rate coefficient of the vectors is d_m . We note that (2-1) is decoupled from the other equations and can be solved separately.

Equation (2-2) models the rate of change of the number of infected vectors. The first term represents the rate of growth of the infectives. The factor $b_i(t) = b/b_{sup}$ is the biting rate of the vectors *b* divided by the total available blood supply $b_{sup} = N + d_f D + c_f C$, where d_f and c_f are the blood supply weights of the dogs and the chickens, respectively. The susceptible vector population is $V - V_i$, and P_{NV} and P_{DV} are the respective probabilities of a vector becoming infected from biting a human or a dog.

The rate of change in the number of infected humans, (2-3), is determined by the biting rate of infected vectors $b_i(t)V_i$ and the probability $P_{VN}(N - N_i)$ of a susceptible human catching the disease in one bite. The death rate of infective humans is $\gamma_N N_i$, where γ_N is the death rate constant, and is known to be higher than that of the susceptibles, [Rassi et al. 2009]. Equation (2-4) for infected dogs is similar, but with the addition of the factor d_f to take into account the vectors' preference to feed on dogs.

The model has time-dependent coefficients that incorporate seasonal variations in the life cycles of the vectors. The oscillatory behavior of the solutions can be found in the simulations in [Spagnuolo et al. 2011]. However, to study the steady states, which we do in the next section, we replace them with their yearly averages.

3. The steady states

We now study the steady states of the problem. To this end, we first rewrite the system using time-independent averaged coefficients. We set

$$a_1 = d_h, \quad a_3 = b_i P_{NV}, \quad a_5 = b_i P_{VN},$$

 $a_2 = d_m, \quad a_4 = b_i d_f P_{DV}, \quad a_6 = b_i d_f P_{VD},$

where we take each a_i , i = 1, ..., 6 to be the average value, over 365 days, of its corresponding function in the *baseline* simulation case studied in [Spagnuolo et al. 2011]. These system parameters are positive constants. The definitions of the various coefficients and their values used in the baseline simulation case of the model can be found in Table 1.

To simplify the presentation, we rename the dependent variables as follows: v = V, $x = V_i$, $y = N_i$, $z = D_i$.

The problem in the new notation is: Find the functions $\{v, x, y, z\}$, defined on the time interval [0, *T*], such that,

$$v' = a_1 v(t - \tau) e^{-av(t - \tau)} - a_2 v, \qquad (3-1)$$

$$x' = a_3(v - x)y + a_4(v - x)z - a_2x, \qquad (3-2)$$

$$y' = a_5 (N - y) x - \gamma_N y,$$
 (3-3)

$$z' = a_6(D-z)x - \gamma_D z,$$
 (3-4)

$$\begin{aligned} x(0) &= V_{i0}, \quad y(0) = N_{i0}, \quad z(0) = D_{i0}, \\ v(t) &= V_0(t), \quad -\tau \le t \le 0. \end{aligned}$$
(3-5)

To study the long time behavior of the system (3-1)–(3-4) [Hethcote 2000; Thieme 2003], we note that the steady states or the fixed points are the solutions of the system

$$0 = a_1 \bar{v} e^{-av} - a_2 \bar{v}, \tag{3-6}$$

$$0 = a_3(\bar{v} - \bar{x})\bar{y} + a_4(\bar{v} - \bar{x})\bar{z} - a_2\bar{x}, \qquad (3-7)$$

$$0 = a_5(N - \bar{y})\bar{x} - \gamma_N \bar{y}, \qquad (3-8)$$

$$0 = a_6 (D - \bar{z})\bar{x} - \gamma_D \bar{z}.$$
 (3-9)

Symbol	Description	Units
V	total number of vectors	bugs/village
N	total number of humans	humans/village
D	total number of domestic dogs	dogs/village
C	total number of chickens	chickens/village
V_i	infected domestic triatomines	bugs/village
Ni	number of infected humans	humans/village
D_i	number of infected dogs	dogs/village
$d_{h au}$	egg hatching rate	1/day
d_m	death rate of bugs	1/day
τ	the delay factor	days
b	biting rate	1/day
P_{NV}	human to bug infection probability (per bite)	NA
P_{DV}	dog to bug infection probability (per bite)	NA
P_{VN}	bug to human infection probability (per bite)	NA
P_{VD}	bug to dog infection probability (per bite)	NA
d_f	human factor of one dog	NA
c_f	human factor of one chicken	NA
γ_N	mortality rate of infected humans	1/day
γD	mortality rate of infected dogs	1/day
a^{-1}	value of V at which growth rate the largest	bugs

Table 1. The model variables and coefficients.

The two solutions of the steady-state equation (3-6) for v are

$$\bar{v}_0 = 0$$
 and $\bar{v}_1 = \frac{1}{a} \log \frac{a_1}{a_2}$. (3-10)

We note that since $\bar{v}_1 > 0$, (because $a_1 > a_2$ in our setting), it follows from the results in [Wei and Li 2005] that the solution $\bar{v}_0 = 0$ is unstable. Also, when $\bar{v} = \bar{v}_0 = 0$, we have that $\bar{x} = \bar{y} = \bar{z} = 0$. So, (0, 0, 0, 0) is an unstable equilibrium point of the system. This corresponds to the observation that Chagas disease is endemic in Latin America.

We turn to the steady states with a positive number \bar{v}_1 , (3-10), of total vectors. In the baseline case we have $\bar{v}_1 \approx 31$, 500. It follows from [Wei and Li 2005] that \bar{v}_1 is locally asymptotically stable. Moreover, it is found that the condition for intrinsic oscillations in Equation (2) of [Wei and Li 2005],

$$a_2\tau e^{\tau a}\left(\log\frac{a_1}{a_2}-1\right) > \frac{1}{e},$$

is not satisfied, so the delay τ does not cause any oscillations of the solution. In this case, there are two nonnegative equilibria for \bar{x} , \bar{y} , and \bar{z} . One is the disease-free equilibrium (0, 0, 0), and the other, an endemic state, is approximately (9239, 86, 51), as computed numerically, using the baseline parameters.

The Jacobian matrix evaluated at the disease-free equilibrium is

$$J(0,0,0) = \begin{bmatrix} -a_2 & a_3 \bar{v}_1 & a_4 \bar{v}_1 \\ a_5 N & -\gamma_N & 0 \\ a_6 D & 0 & -\gamma_D \end{bmatrix}.$$

This matrix has three distinct real eigenvalues, one positive and the other two negative. Therefore, (31500, 0, 0, 0) is an unstable equilibrium. In Section 4 we simulate the model in cases when the initial conditions are near (31500, 0, 0, 0).

Finally, at the endemic equilibrium ($\bar{v}_1 = 31500, 9239, 86, 51$) the Jacobian matrix at ($\bar{x}, \bar{y}, \bar{z}$) is:

$$J(\bar{x}, \bar{y}, \bar{z}) = \begin{bmatrix} -a_3 \bar{y} - a_4 \bar{z} - a_2 & a_3(\bar{v}_1 - \bar{x}) & a_4(\bar{v}_1 - \bar{x}) \\ a_5(N - \bar{y}) & -a_5 \bar{x} - \gamma_N & 0 \\ a_6(D - \bar{z}) & 0 & -a_6 \bar{x} - \gamma_D \end{bmatrix}.$$

A straightforward computation shows that J(9239, 86, 51) has three real negative eigenvalues. Therefore, the endemic steady state (31500, 9239, 86, 51) is stable and attracting, or globally asymptotically stable (GAS). It follows from the model that under these conditions, without insecticide spraying or other interventions, the disease will persist. We note that we do not make a general statement on the conditions for the endemic steady state to be GAS, only that this is so in this case.

4. Simulations

We used the fourth-order Adams–Bashforth predictor corrector method to compute the numerical approximations of the model, equations (3-1)–(3-5). Due to the delay, a small step size of $\frac{1}{100}$ of a day was chosen. We also solved the system using other numerical schemes and they all matched our results for 1000 years of simulations. Moreover, Theorem 6.2.1 in [Bellen and Zennaro 2003, p. 156], guarantees the correctness of our numerical scheme.

The values of the parameters (with their references) used in the simulations are provided in Table 2. These were taken from [Spagnuolo et al. 2011]. The simulations were run using gfortran on a 3.0 GHz Intel Core 2 Duo CPU with Cent OS 5. A typical simulation of 100 years with 100 time steps per day $(3.65 \times 10^6$ time steps) took approximately 300 seconds. It was found that very long runs, over a few hundred years (tens of millions of time steps) were computationally reproducible, which indicates that the solution algorithm was stable.

Symbol	Baseline simulation value	Reference
d_f	2.45	[Gürtler et al. 2007]
c_f	4.8	[Gürtler et al. 2007]
d_m	0.00327	Estimate from [Castanera et al. 2003]
$d_{h\tau}$	0.00613	Estimate from [Castanera et al. 2003;
		Gorla and Schofield 1985]
b_i	0.0000215	Estimate from [Castanera et al. 2003;
		Catalá 1991]
γ_N	$0.7\frac{2\ln 2}{76.12\cdot 365} + 0.3\frac{\ln 2}{25\cdot 365}$	Estimate from [CIA 2009;
		Rassi et al. 2009]
γ _D	$\frac{\ln 2}{4.365}$	Estimated 8 years
C	100	This study
N	400	This study
D	100	This study
P_{NV}	0.03	[Cohen and Gürtler 2001]
P_{DV}	0.49	[Cohen and Gürtler 2001]
P_{VN}	0.00008	Estimate from [Cohen and Gürtler 2001]
P_{VD}	0.001	Estimate from [Cohen and Gürtler 2001]
a^{-1}	50,000	This study

Table 2. The parameters used in the baseline case.

We now present two numerical simulations of the model, with averaged coefficients, with different initial conditions, showing the convergence of the system to the endemic steady state (\bar{v}_1 , 9239, 86, 51). The first simulation has initial conditions that are considerably smaller than the steady state and chosen as V(0) = 2, $V_i(0) = 2$, $N_i(0) = 10$, and $D_i(0) = 0$. In the second example, the initial conditions were chosen to be larger than the steady state values, and the values were V(0) = 45, 000, $V_i(0) = 10$, 000, $N_i(0) = 100$, and $D_i(0) = 100$.

The results of both simulations are depicted in Figure 1. In each figure the heavy line represents the solution of the case with small initial conditions, i.e., starting near zero, and the thin line is the solution starting above the steady state. The convergence to the steady state of the total number of vectors can be seen at upper left; that of the infected vectors at upper right; infected humans at lower left; and infected dogs at lower right. It is seen clearly that each one of the populations, in both cases, converges monotonically to the steady state.

However, we stress that this monotone approach is characteristic of the system with averaged parameters. So it provides only qualitative insight at best. In the field, the parameters are affected by seasonal changes and are time dependent. This was taken into account in [Spagnuolo et al. 2011], since spraying is done once a year.

243

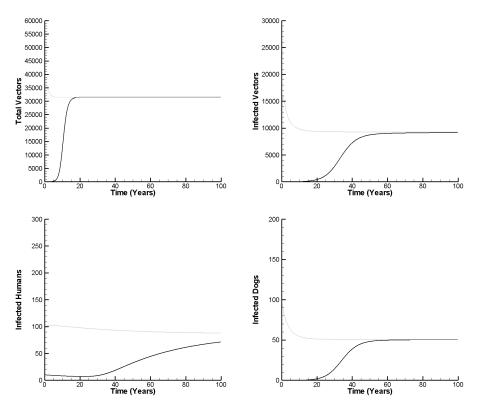


Figure 1. Convergence to the endemic state from above (thin line) and below (thick line).

5. Conclusions

A model for the dynamics of the Chagas disease, with averaged coefficients, was presented, following [Spagnuolo et al. 2012; 2011]. It consists of rate equations for the total numbers of vectors, and infected vectors, humans, and dogs (mammals). The model shows, within the conditions that seem to be observed in South America, an unstable disease-free equilibrium and a stable endemic equilibrium.

Then, our computer code was used to obtain numerical approximations of the model. In particular, we simulated the approach of the solutions to the endemic steady state. Two examples were presented, in the first one the initial conditions are below the values of the endemic equilibrium, and in the second they were above it. It was found, numerically, that the convergence to the endemic state was found to be monotone in both cases.

It may be of interest to prove that the convergence is monotone, however, the question is unresolved, yet.

Acknowledgements

The authors thank the referee for suggestions that helped improve the paper.

References

- [Bellen and Zennaro 2003] A. Bellen and M. Zennaro, Numerical methods for delay differential equations, Clarendon, Oxford, 2003. MR 2004i:65001 Zbl 1038.65058
- [Bilate and Cunha-Neto 2008] A. M. Bilate and E. Cunha-Neto, "Chagas disease cardiomyopathy: current concepts of an old disease", Rev. Inst. Med. Trop. São Paulo 50:2 (2008), 67-74.
- [Castanera et al. 2003] M. B. Castanera, J. P. Aparicio, and R. E. Gürtler, "A stage-structured stochastic model of the population dynamics of Triatoma infestans, the main vector of Chagas disease", Ecol. Model. 162 (2003), 33-53.
- [Catalá 1991] S. Catalá, "The biting rate of Triatoma infestans in Argentina", Med. Vet. Entomol. 5:3 (1991), 325-333.
- [CIA 2009] Central Intelligence Agency, The world factbook, Washington, DC, 2009.
- [Coffield et al. 2010] D. J. Coffield, A. M. Spagnuolo, M. Shillor, E. Mema, B. Pell, A. Pruzinsky, and A. Zetye, "A model for Chagas disease with vector consumption and congenital transmission", preprint, Oakland University, 2010.
- [Cohen and Gürtler 2001] J. E. Cohen and R. E. Gürtler, "Modeling household transmission of American trypanosomiasis", Science 293:5530 (2001), 694-698.
- [Gorla and Schofield 1985] D. E. Gorla and C. J. Schofield, "Analysis of egg mortality in experimental populations of Triatoma infestans under natural climatic conditions in Argentina", Bull. Soc. Vector Ecol. 10 (1985), 107-117.
- [Gurney et al. 1980] W. S. Gurney, S. P. Blythe, and R. M. Nisbet, "Nicholson's blowflies revisited", Nature 287 (1980), 17-21.
- [Gürtler et al. 2007] R. E. Gürtler, M. C. Cecere, M. A. Lauricella, M. V. Cardinal, U. Kitron, and J. E. Cohen, "Domestic dogs and cats as sources of Trypanosoma cruzi infection in rural northwestern Argentina", Parasitology 134 (2007), 69-82.
- [Győri and Ladas 1991] I. Győri and G. Ladas, Oscillation theory of delay differential equations: with applications, Clarendon, Oxford, 1991. MR 93m:34109 Zbl 0780.34048
- [Hethcote 2000] H. W. Hethcote, "The mathematics of infectious diseases", SIAM Rev. 42:4 (2000), 599-653. MR 2002c:92034 Zbl 0993.92033
- [Nicholson 1954] A. J. Nicholson, "An outline of the dynamics of animal population", Australian J. Zoology 2 (1954), 9-65.
- [Rassi et al. 2009] A. Rassi, Jr., A. Rassi, and J. A. Marin-Neto, "Chagas heart disease: pathophysiologic mechanisms, prognostic factors and risk stratification", Mem. Inst. Oswaldo Cruz. 104:Suppl 1 (2009), 152–158.
- [Schofield et al. 2006] C. J. Schofield, J. Jannin, and R. Salvatella, "The future of Chagas disease control", Trends Parasit. 22 (2006), 583-588.
- [Spagnuolo et al. 2011] A. M. Spagnuolo, M. Shillor, and G. A. Stryker, "A model for Chagas disease with controlled spraying", J. Biol. Dyn. 5:4 (2011), 299-317. MR 2012g:92205 Zbl 1219.92056
- [Spagnuolo et al. 2012] A. M. Spagnuolo, M. Shillor, L. Kingsland, A. Thatcher, M. Toeniskoetter, and B. Wood, "A logistic DDE model for Chagas disease with interrupted spraying schedules", J. Biol. Dyn. 6:2 (2012), 377-394.

245

[Thieme 2003] H. R. Thieme, *Mathematics in population biology*, Princeton University Press, Princeton, NJ, 2003. MR 2004m:92030 Zbl 1054.92042

[Wei and Li 2005] J. Wei and M. Y. Li, "Hopf bifurcation analysis in a delayed Nicholson blowflies equation", *Nonlinear Anal.* **60**:7 (2005), 1351–1367. MR 2005k:34279 Zbl 1144.34373

[WHO 2010] "Chagas disease (American trypanosomiasis)", fact sheet 340, World Health Organization, June 2010, http://www.who.int/mediacentre/factsheets/fs340/en.

Received: 2010-08-17	Revised: 2011-09-06 Accepted: 2012-01-04
maryclauson@gmail.com	Department of Biostatistics, Virginia Commonwealth University, Richmond, VA 23219, United States
aharris2351@yahoo.com	Department of Applied Mathematics, University of Pennsylvania, Indiana 15701, United States
lshuman@math.wsu.edu	Department of Mathematics, Washington State University, Pullman, WA 99164-3113, United States
shillor@oakland.edu	Department of Mathematics and Statistics, Oakland University, Rochester, MI 48309-4485, United States
spagnuol@oakland.edu	Department of Mathematics and Statistics, Oakland University, Rochester, MI 48309-4485, United States

involve

msp.org/involve

EDITORS

MANAGING EDITOR Kenneth S. Berenhaut, Wake Forest University, USA, berenhks@wfu.edu

BOARD OF EDITORS

BOARD OF EDITORS						
Colin Adams	Williams College, USA colin.c.adams@williams.edu	David Larson	Texas A&M University, USA larson@math.tamu.edu			
John V. Baxley	Wake Forest University, NC, USA baxley@wfu.edu	Suzanne Lenhart	University of Tennessee, USA lenhart@math.utk.edu			
Arthur T. Benjamin	Harvey Mudd College, USA benjamin@hmc.edu	Chi-Kwong Li	College of William and Mary, USA ckli@math.wm.edu			
Martin Bohner	Missouri U of Science and Technology, USA bohner@mst.edu	Robert B. Lund	Clemson University, USA lund@clemson.edu			
Nigel Boston	University of Wisconsin, USA boston@math.wisc.edu	Gaven J. Martin	Massey University, New Zealand g.j.martin@massey.ac.nz			
Amarjit S. Budhiraja	U of North Carolina, Chapel Hill, USA budhiraj@email.unc.edu	Mary Meyer	Colorado State University, USA meyer@stat.colostate.edu			
Pietro Cerone	Victoria University, Australia pietro.cerone@vu.edu.au	Emil Minchev	Ruse, Bulgaria eminchev@hotmail.com			
Scott Chapman	Sam Houston State University, USA scott.chapman@shsu.edu	Frank Morgan	Williams College, USA frank.morgan@williams.edu			
Joshua N. Cooper	University of South Carolina, USA cooper@math.sc.edu	Mohammad Sal Moslehian	Ferdowsi University of Mashhad, Iran moslehian@ferdowsi.um.ac.ir			
Jem N. Corcoran	University of Colorado, USA corcoran@colorado.edu	Zuhair Nashed	University of Central Florida, USA znashed@mail.ucf.edu			
Toka Diagana	Howard University, USA tdiagana@howard.edu	Ken Ono	Emory University, USA ono@mathcs.emory.edu			
Michael Dorff	Brigham Young University, USA mdorff@math.byu.edu	Timothy E. O'Brien	Loyola University Chicago, USA tobrie1@luc.edu			
Sever S. Dragomir	Victoria University, Australia sever@matilda.vu.edu.au	Joseph O'Rourke	Smith College, USA orourke@cs.smith.edu			
Behrouz Emamizadeh	The Petroleum Institute, UAE bemamizadeh@pi.ac.ae	Yuval Peres	Microsoft Research, USA peres@microsoft.com			
Joel Foisy	SUNY Potsdam foisyjs@potsdam.edu	YF. S. Pétermann	Université de Genève, Switzerland petermann@math.unige.ch			
Errin W. Fulp	Wake Forest University, USA fulp@wfu.edu	Robert J. Plemmons	Wake Forest University, USA plemmons@wfu.edu			
Joseph Gallian	University of Minnesota Duluth, USA jgallian@d.umn.edu	Carl B. Pomerance	Dartmouth College, USA carl.pomerance@dartmouth.edu			
Stephan R. Garcia	Pomona College, USA stephan.garcia@pomona.edu	Vadim Ponomarenko	San Diego State University, USA vadim@sciences.sdsu.edu			
Anant Godbole	East Tennessee State University, USA godbole@etsu.edu	Bjorn Poonen	UC Berkeley, USA poonen@math.berkeley.edu			
Ron Gould	Emory University, USA rg@mathcs.emory.edu	James Propp	U Mass Lowell, USA jpropp@cs.uml.edu			
Andrew Granville	Université Montréal, Canada andrew@dms.umontreal.ca	Józeph H. Przytycki	George Washington University, USA przytyck@gwu.edu			
Jerrold Griggs	University of South Carolina, USA griggs@math.sc.edu	Richard Rebarber	University of Nebraska, USA rrebarbe@math.unl.edu			
Sat Gupta	U of North Carolina, Greensboro, USA sngupta@uncg.edu	Robert W. Robinson	University of Georgia, USA rwr@cs.uga.edu			
Jim Haglund	University of Pennsylvania, USA jhaglund@math.upenn.edu	Filip Saidak	U of North Carolina, Greensboro, USA f_saidak@uncg.edu			
Johnny Henderson	Baylor University, USA johnny_henderson@baylor.edu	James A. Sellers	Penn State University, USA sellersj@math.psu.edu			
Jim Hoste	Pitzer College jhoste@pitzer.edu	Andrew J. Sterge	Honorary Editor andy@ajsterge.com			
Natalia Hritonenko	Prairie View A&M University, USA nahritonenko@pvamu.edu	Ann Trenk	Wellesley College, USA atrenk@wellesley.edu			
Glenn H. Hurlbert	Arizona State University,USA hurlbert@asu.edu	Ravi Vakil	Stanford University, USA vakil@math.stanford.edu			
Charles R. Johnson	College of William and Mary, USA crjohnso@math.wm.edu	Antonia Vecchio	Consiglio Nazionale delle Ricerche, Italy antonia.vecchio@cnr.it			
K. B. Kulasekera	Clemson University, USA kk@ces.clemson.edu	Ram U. Verma	University of Toledo, USA verma99@msn.com			
Gerry Ladas	University of Rhode Island, USA gladas@math.uri.edu	John C. Wierman	Johns Hopkins University, USA wierman@jhu.edu			
		Michael E. Zieve	University of Michigan, USA zieve@umich.edu			

PRODUCTION

Silvio Levy, Scientific Editor

See inside back cover or msp.org/involve for submission instructions. The subscription price for 2012 is US \$105/year for the electronic version, and \$145/year (+\$35, if shipping outside the US) for print and electronic. Subscriptions, requests for back issues from the last three years and changes of subscribers address should be sent to MSP.

Involve (ISSN 1944-4184 electronic, 1944-4176 printed) at Mathematical Sciences Publishers, 798 Evans Hall #3840, c/o University of California, Berkeley, CA 94720-3840, is published continuously online. Periodical rate postage paid at Berkeley, CA 94704, and additional mailing offices.

Involve peer review and production are managed by EditFLOW® from Mathematical Sciences Publishers.

PUBLISHED BY
mathematical sciences publishers

nonprofit scientific publishing

http://msp.org/

© 2012 Mathematical Sciences Publishers

2012 vol. 5 no. 3

Analysis of the steady states of a mathematical model for Chagas disease MARY CLAUSON, ALBERT HARRISON, LAURA SHUMAN, MEIR SHILLOR AND ANNA MARIA SPAGNUOLO	237
Bounds on the artificial phase transition for perfect simulation of hard core Gibbs processes MARK L. HUBER, ELISE VILLELLA, DANIEL ROZENFELD AND JASON XU	247
A nonextendable Diophantine quadruple arising from a triple of Lucas numbers A. M. S. RAMASAMY AND D. SARASWATHY	257
Alhazen's hyperbolic billiard problem Nathan Poirier and Michael McDaniel	273
Bochner (<i>p</i> , <i>Y</i>)-operator frames MOHAMMAD HASAN FAROUGHI, REZA AHMADI AND MORTEZA RAHMANI	283
<i>k</i> -furcus semigroups NICHOLAS R. BAETH AND KAITLYN CASSITY	295
Studying the impacts of changing climate on the Finger Lakes wine industry BRIAN MCGAUVRAN AND THOMAS J. PFAFF	303
A graph-theoretical approach to solving Scramble Squares puzzles SARAH MASON AND MALI ZHANG	313
The <i>n</i> -diameter of planar sets of constant width ZAIR IBRAGIMOV AND TUAN LE	327
Boolean elements in the Bruhat order on twisted involutions DELONG MENG	339
Statistical analysis of diagnostic accuracy with applications to cricket Lauren Mondin, Courtney Weber, Scott Clark, Jessica Winborn, Melinda M. Holt and Ananda B. W. Manage	349
Vertex polygons CANDICE NIELSEN	361
Optimal trees for functions of internal distance ALEX COLLINS, FEDELIS MUTISO AND HUA WANG	371

