BU-1320-M February, 1996

Recruitment into a core group and its effect on the spread of a sexually-transmitted disease

Fred Brauer
Department of Mathematics, University of Wisconsin

Carlos Castillo-Chavez
Biometrics Unit, Cornell University

Jorge X. Velasco-Hernández
Departamento de Matemáticas UAM-Iztapalapa
and Biometrics Unit, Cornell University.

Running title: Prevalence-dependent recruitment.

Please send correspondence to the second author to:

322 Warren Hall
Biometrics Unit, Cornell University
Ithaca, NY. 14853-7801
Tel: 607-255-5488
Fax: 607-255-4698
E-mail: cc32@cornell.edu

Recruitment into a core group and its effect on the spread of a sexually transmitted disease

Fred Brauer
Department of Mathematics, University of Wisconsin

Carlos Castillo-Chavez
Biometrics Unit, Cornell University

Jorge X. Velasco-Hernandez
Departamento de Matemáticas UAM-Iztapalapa
and Biometrics Unit, Cornell University

Abstract

Heterogeneity plays a central role in disease dynamics. A challenge to the theoretician is best sumarized with the question: how does one model incorporate just 'enough' heterogeneity to capture the essential features needed to understand the transmission dynamics of a disease? A partial answer in the study of the role of hetereogeneity on the dynamics of sexually transmitted diseases (STDs) is provided by the introduction of a core group–those members of the population who are extremely sexually-active. Earlier research focussed on models with a fixed core, that is, it was assumed that the size of the core was not a dynamic variable. The weakening of this asssumption has generated new insights in the study of the dynamics of STDs. In our recent work, we looked at the effects of disease prevalence-dependent recruitment rates into the core group in the simplest situation, that is, when only sexual contacts within the core population are considered. In this article, we incorporate contacts involving non-core members as well. The simplest model is recovered as a limiting case when the non-core sexual activity tends to zero. Numerical simulations indicate that the less restrictive model can exhibit counter-intuitive behavior.

1 Introduction

A partial and sometimes satisfactory answer in the study of the role of hetereogeneity on the dynamics of sexually transmitted diseases is

provided by the subdivision of a population into a core group– those members of the population who are extremely sexually-active and a non-core. Earlier research focussed on models with a fixed core. This approach first introduced by *Nold* [9]) and *Hethcote & Yorke*[7] has had a strong impact on the development of innovative public health measures and has instigated new research on the role of core subpopulations in disease evolution. The weakening of the asssumption of a fixed core group size was introduced–in a particular form–by *Blythe, Brauer, & Castillo-Chavez*[1] and later developed by others (see *Blythe, Brauer & Castillo-Chavez*,[1], *Hadeler & Castillo-Chavez* [5]). The introduction of a core group with variable population size –even in the simplest case–gave rise to 'simpler' models that revealed the inherent limitations of 'classical' epidemic models with multiple interacting subgroups. The key limiting factor was 'hidden' on the assumption that all interacting subpopulations had reached a steady state. Therefore it was argued that it was safe to ignore the population dynamics of each subgroup (for some critique of this assumption see *Huang, Cooke & Castillo-Chavez* [8] as well as *Castillo-Chavez, Velasco-Hernandez & Fridman* [3]). The introduction of a core group with disease prevalence-dependent recruitment rates allowed for a dynamic core population. These new models with varying core goup size are capable of generating new insights into the effects of heterogeneity in disease dynamics.

We have shown that it is possible to destabilize the unique (whenever it exists) endemic equilibrium and in fact generate sustained oscillations about this equilibrium using an extremely simple model. This model includes a sexually-active core and a sexually incative non-core that only serves as a potential source for the recruitment of core individuals. We have shown that this instability is possible whenever the recruitment rate depends on the proportion of the core population which is infective, but not if the recruitment rate depends on the number of infective members. As these oscillations are generally of rather large period, instability makes prediction of the course of the disease difficult and complicates the development of effective health policy measures. Our results suggest, for example, that education programs might be more successful if they focus on the number of cases of an STD rather than on the proportion of individuals infected (see [1]).

This work begins by adding a little more realism to our earlier caricature core-non core model. We introduce sexual contacts between core and non core members. Hence, instead of viewing the non-core population as merely a reservoir for recruitment of new members into the core, we consider the possibility of having two different (positive) activity rates, higher for the core and smaller for the non-core members.

Our first caricature model *Blythe, Brauer and Castillo-Chavez*[1] is then just a limiting case, that is, our first model is recovered when the activity rate of the non-core population approaches zero. Hence, the qualitative behavior of the simple model extends–by continuity–to the new-model provided that the non-core population exhibits sufficiently low rates of sexual activity. Thus the simplifying assumption of the earlier model, that is, the absence of sexual activity outside the core, though obviously unrealistic, may not be aserious flaw in the formulation of qualitative models. However, as we shall see, the extended model may also behave in ways not suggested by the simpler model.

Our model uses gonorrhea as example and hence, we shall consider only SIS models in which all infectives recover with no immunity against re-infection. A similar approach could be used to study SIR models in which all infectives recover with full permanent immunity against re-infection, but such models would require additional variables for the recovered classes in the core and non-core subpopulations making the analysis more complex. Since, we only wish to study the role of non-core activity on our previous framework, it is enough to look at the simplest generalization, which is given by SIS models. We further assume the lack of disease induced mortality in order to keep the *total population* (core plus non-core) constant and thus allow a reduction in the number of variables. Again, this simplifying assumption while restrictive does not infringe on what we want to acomplish, namely that, as our numerical simulations have shown the less restrictive model can exhibit counter-intuitive behavior. Obviously, it is important to study models with disease induced mortality in the context of STDs. Such an extension would be necessary because of their relevance to models for HIV/AIDS. Other natural extensions which we shall leave for future study include those that model infective periods which are not exponentially distributed and delays in recruitment response to the disease state (see [6])

2 The basic core non-core model

We consider a closed population of constant total size Λ which is divided into a core population of size N_1 consisting of S_1 susceptibles and I_1 infectives ($N_1 = S_1 + I_1$), and a non-core population of size $N_2 = \Lambda - N_1$ consisting of S_2 susceptibles and I_2 infectives ($N_2 = S_2 + I_2$). Our basic model is

$$\begin{aligned} S_1' &= S_2 r(\frac{I_1}{N_1}) - \mu S_1 - a_1 S_1(p_{11}\frac{I_1}{N_1} + p_{12}\frac{I_2}{N_2}) + \sigma I_1, \\ I_1' &= a_1 S_1(p_{11}\frac{I_1}{N_1} + p_{12}\frac{I_2}{N_2}) - \sigma I_1, \end{aligned}$$

$$
\begin{aligned}
N_1' &= S_2 r(\frac{I_1}{N_1}) - \mu S_1, \qquad (1)\\
S_2' &= -S_2 r(\frac{I_1}{N_1}) + \mu S_1 - a_2 S_2(p_{21}\frac{I_1}{N_1} + p_{22}\frac{I_2}{N_2}) + \sigma I_2,\\
I_2' &= a_2 S_2(p_{21}\frac{I_1}{N_1} + p_{22}\frac{I_2}{N_2}) - \sigma I_2,\\
N_2' &= -S_2 r(\frac{I_1}{N_1}) + \mu S_1.
\end{aligned}
$$

The model as stated is redundant; any two of the first three equations and any two of the last three equations would be sufficient. Computations with the model are usually simplest if I_1, N_1, I_2, N_2 are used as variables, with S_1 replaced by $N_1 - I_1$ and S_2 replaced by $N_2 - I_2$. In addition, since $(N_1 + N_2)' = 0$, $N_1 + N_2$ is a constant Λ and we may replace N_2 by $\Lambda - N_1$, so that $S_2 = N_2 - I_2 = \Lambda - N_1 - I_2$. Thus the model is equivalent to

$$
\begin{aligned}
I_1' &= a_1(N_1 - I_1)(p_{11}\frac{I_1}{N_1} + p_{12}\frac{I_2}{\Lambda - N_1}) - \sigma I_1,\\
N_1' &= (\Lambda - N_1 - I_2) r(\frac{I_1}{N_1}) - \mu(N_1 - I_1), \qquad (2)\\
I_2' &= a_2(\Lambda - N_1 - I_2)(p_{21}\frac{I_1}{N_1} + p_{22}\frac{I_2}{\Lambda - N_1}) - \sigma I_2.
\end{aligned}
$$

The model (2) is a consequence of the following assumptions:

1. Susceptibles are recruited into the core from the non-core at a rate $S_2 r(I_1/N_1)$ in unit time, where $r(\eta)$ is a non-negative, non-increasing function on $0 \le \eta \le 1$.
2. A fraction μ of the susceptibles in the core choose to leave and move to the non-core in unit time.
3. Core members make an average of a_1 sexual contacts in unit time, while non-core members make an average of a_2 sexual contacts in unit time. The fraction of contacts of group i members that are with group j members is p_{ij} $(i, j = 1, 2)$, so that $p_{11} + p_{12} = p_{21} + p_{22} = 1$.
4. In unit time a fraction σ of infectives recover and return to the susceptible class.

These assumptions describe an SIS model in which each class is homogeneous but which allows for preference in the choice of class for sexual contacts. As core members make a total of $a_1 p_{12} N_1$ contacts with non-core members while non-core members make a total of $a_2 p_{21} N_2$ contacts with core members in unit time, we have a balance condition

$$
a_1 N_1 p_{12} = a_2 N_2 p_{21}. \qquad (3)
$$

If both groups are sexually active ($a_1 > a_2 > 0$), then either p_{12} and p_{21} are both positive or both are zero.

We will assume now that p_{ij} are of the form

$$p_{ij} = \bar{p}_j = \frac{a_j N_j}{a_1 N_1 + a_2 N_2}.$$

This type of frequency-dependent mixing probabilities satisfy (3). Further, we have that

$$p_{11} = 1 - \bar{p}_2, \quad p_{22} = 1 - \bar{p}_1.$$

Our analysis and discusion of this section is based on model (2) with these mixing probabilities.

Thus, we consider the model

$$\begin{aligned} I_1' &= a_1(N_1 - I_1)((1-\bar{p}_2)\frac{I_1}{N_1} + \bar{p}_2\frac{I_2}{\Lambda - N_1}) - \sigma I_1, \\ N_1' &= (\Lambda - N_1 - I_2)r(\frac{I_1}{N_1}) - \mu(N_1 - I_1), \\ I_2' &= a_2(\Lambda - N_1 - I_2)(\bar{p}_1\frac{I_1}{N_1} + (1-\bar{p}_1)\frac{I_2}{\Lambda - N_1}) - \sigma I_2. \end{aligned} \tag{4}$$

The new assumption made in the formulation of the model (4) is that the rate of contacts between core and non-core members is determined by the conservation law (3) with freuqency dependent mixing probabilities. Other scenarios are plausible [4], but would lead to different models.

In the limiting case where the non-core population is inactive, we take $a_2 = 0$, and (4) becomes

$$\begin{aligned} I_1' &= a_1(N_1 - I_1)\frac{I_1}{N_1} - \sigma I_1, \\ N_1' &= (\Lambda - N_1 - I_2)r(\frac{I_1}{N_1}) - \mu(N_1 - I_1), \\ I_2' &= -\sigma I_2. \end{aligned} \tag{5}$$

Then $I_2(t) = I_2(0)e^{-\sigma t} \to 0$ as $t \to \infty$, and (5) is equivalent to

$$\begin{aligned} I_1' &= a_1(N_1 - I_1)\frac{I_1}{N_1} - \sigma I_1, \\ N_1' &= (\Lambda - N_1 - I_2(0)e^{-\sigma t})r(\frac{I_1}{N_1}) - \mu(N_1 - I_1), \end{aligned}$$

which is asymptotically equivalent to

$$\begin{aligned} I_1' &= a_1(N_1 - I_1)\frac{I_1}{N_1} - \sigma I_1, \\ N_1' &= (\Lambda - N_1)r(\frac{I_1}{N_1}) - \mu(N_1 - I_1). \end{aligned} \tag{6}$$

Indeed, it is reasonable to impose the initial condition $I_2(0) = 0$; then (5) is equivalent to (6). The system (6) models a core-noncore population in which the non-core is sexually inactive and serves merely as an inert reservoir for recruitment into the core. A model analogous to (6) for a universally fatal SIR disease has been studied in [1]. Application of the same methods there yields the following result.

Theorem 1 *The system (6) has a disease free equilibrium* $I_1 = 0$, $N_1 = \frac{\Lambda r(0)}{\mu + r(0)}$ *which is (globally) asymptotically stable if* $R_0 = a_1/\sigma < 1$, *and unstable if* $R_0 > 1$. *If* $R_0 > 1$, *there is an endemic equilibrium defined by*

$$\eta = \frac{I_1}{N_1} = 1 - \frac{\sigma}{a_1} = 1 - \frac{1}{R_0},$$

$$I_1 = \frac{\Lambda \eta r(\eta)}{r(\eta) + \mu(1-\eta)}, \quad N_1 = \frac{\Lambda r(\eta)}{r(\eta) + \mu(1-\eta)},$$

and this equilibrium is asymptotically stable if and only if

$$-\mu(1-\eta)\frac{r'(\eta)}{r(\eta)} < \frac{\mu + r(\eta)}{\eta} + \frac{\sigma}{1-\eta}. \tag{7}$$

The condition (7) is necessarily satisfied as $\eta \to 0+$ (corresponding to $R_0 \to 1+$) and as $\eta \to 1-$ (corresponding to $R_0 \to \infty$), but may be violated for intermediate values of η. For example, if $r(\eta) = r(0)e^{-b\eta}$ so that $-r'(\eta)/r(\eta) = b$, the condition (7) is violated for some values of η if b is sufficiently large. Thus it is possible for the system (6) to have an endemic equilibrium which is unstable. As all solutions of (6) are bounded as $t \to \infty$, the Poincarè-Bendixon theorem implies that if the endemic equilibrium is unstable the system (6) must have a periodic orbit.

3 Analysis of the disease-free equilibrium

An equilibrium (I_1, N_1, I_2) of system (4) is a solution of the equations determined by setting the right-hand-side of (4) equal to zero.

Thus there is a disease-free equilibrium with $I_1 = 0$, $I_2 = 0$ and N_1 so that

$$N_1 = \frac{\Lambda r(0)}{\mu + r(0)}, \quad \Lambda - N_1 = \frac{\Lambda \mu}{\mu + r(0)}.$$

Our intuitive idea of a small core and a large non-core population suggest that we should assume $r(0) < \mu$.

The matrix of the next-generation operator corresponding to (4) at the disease-free equilibrium $(0, \frac{\Lambda r(0)}{\mu+r(0)}, 0)$ is given by

$$\begin{pmatrix} \frac{{a_1}^2 r(0)}{(a_2\mu+a_1 r(0))\sigma} & 0 & \frac{a_1 a_2 r(0)}{(a_2\mu+a_1 r(0))\sigma} \\ 1-k & -\frac{r(0)}{\mu} & -\frac{r(0)}{\mu} \\ \frac{a_1 a_2 \mu}{(a_2\mu+a_1 r(0))\sigma} & 0 & \frac{{a_2}^2 \mu}{(a_2\mu+a_1 r(0))\sigma} \end{pmatrix}.$$

The basic reproductive number $\mathcal{R}_0$ is the dominant eigenvalue of the above matrix and can be written as

$$\mathcal{R}_0 = \frac{a_1^2 r(0) + a_2^2 \mu}{\sigma(a_1 r(0) + a_2 \mu)}.$$

Note that when a_2 is small, $\mathcal{R}_0 \approx a_1/\sigma$.

This translates into a (local) asymptotic stability criterion for the disease-free equilibrium, and by a standard approach involving a priori estimates (see for example *Castillo-Chavez & Thieme* [2]), we can obtain global asymptotic stability. We may summarize our results as follows:

Theorem 2. *The disease-free equilibrium of the system (4) is globally asymptotically stable if* $\mathcal{R}_0 < 1$ *and it is unstable if* $\mathcal{R}_0 > 1$

It is important to note that $\mathcal{R}_0$ depends not only on the contact rates a_1 and a_2 but also on the probabilities $\bar{p}_j$ at the disease-free equilibrium, that measure the mixing between groups.

4 Non-interacting groups

We now describe the situation in which all sexual contacts are between members of the same group and the only interaction between the groups is in recruitment. Model (4) with $p_{11} = p_{22} = 1$, $p_{12} = p_{21} = 0$ is reduced to the following case (as the balance condition (3) is vacuous):

$$\begin{aligned} I_1' &= a_1 \frac{(N_1 - I_1)I_1}{N_1} - \sigma I_1, \\ N_1' &= (\Lambda - N_1 - I_2) r(I_1/N_1) - \mu(N_1 - I_1), \\ I_2' &= a_2(\Lambda - N_1 - I_2)\frac{I_2}{\Lambda - N_1} - \sigma I_2. \end{aligned} \tag{8}$$

Because we are thinking of the core as more active than the non-core, we assume $a_1 > a_2$. Equilibria of (8) are given by

$$I_1 = 0, \text{ or } 1 - \eta_1 = 1 - \frac{I_1}{N_1} = \frac{\sigma}{a_1},$$

$$I_2 = 0, \text{ or } 1 - \eta_2 = 1 - \frac{I_2}{\Lambda - N_1} = \frac{\sigma}{a_2},$$
$$(\Lambda - N_1 - I_2 - r(\eta_1) = \mu N_1(1 - \eta_1).$$

If $I_1 \neq 0$ then $0 < \eta_1 \leq 1$ and $a_1/\sigma > 1$. If $I_2 \neq 0$ then $0 < \eta_2 \leq 1$ and $a_2/\sigma > 1$. According to Theorem 2, the disease free equilibrium, with $I_1 = I_2 = 0$, is asymptotically stable if and only if $R_0 < 1$ and since $p = 1$ we have:

$$R_0 = \frac{1}{2\sigma}(a_1 + a_2 + |a_1 - a_2|) = a_1/\sigma.$$

The matrix of the linearization of (8) at an equilibrium (I_1, N_1, I_2) is

$$\begin{pmatrix} a_1(1-2\eta_1) - \sigma & a_1\eta_1^2 & 0 \\ \frac{\Lambda - N_1 - I_2}{N_1} r'(\eta_1) + \mu & -\frac{\Lambda - N_1 - I_2}{N_1}\eta_1 r'(\eta_1) - \mu & -r(\eta_1) \\ 0 & -\eta_2(\Lambda + N_1) - a_2\eta_2^2 & a_2(1-2\eta_2) - \sigma \end{pmatrix}.$$

It is easy to see that an equilibrium with $I_1 = 0$, $I_2 \neq 0$ cannot be stable, because existence of such an equilibrium requires $a_2 > \sigma$, and stability requires $a_1 < \sigma$, contradicting the assumption $a_1 > a_2$. However, it is possible to have an equilibrium with $I_1 > 0$, $I_2 = 0$, such an equilibrium the linearization matrix is:

$$\begin{pmatrix} a_1(1-2\eta_1) - \sigma & a_1\eta_1^2 & 0 \\ \frac{\Lambda - N_1}{N_1} r'(\eta_1) + \mu & -\frac{\Lambda - N_1}{N_1}\eta_1 r'(\eta_1) - r(\eta_1) - \mu & -r(\eta_1) \\ 0 & 0 & a_2 - \sigma \end{pmatrix}.$$

Stability of the equilibrium requires $a_2 < \sigma$ and also that the real part of the eigenvalues of

$$\begin{pmatrix} a_1 p(1-2\eta_1) - \sigma & a_1\eta_1^2 \\ \frac{\Lambda - N_1}{N_1} r'(\eta_1) + \mu & -\frac{\Lambda - N_1}{N_1}\eta_1 r'(\eta_1) - r(\eta_1) - \mu \end{pmatrix}$$

are negative. This 2×2 matrix is the same matrix that enters into the stability analysis of the two-dimensional inactive non-core model (6).

We conclude that if $R_0 > 1$ and $a_2 < \sigma$, so that $a_1 > \sigma > a_2$, there is an endemic equilibrium with $I_1 > 0$, $I_2 > 0$. These equilibria may be either asymptotically stable or unstable, depending on a condition (ommited) analogous to (7).

If $a_1 > a_2 > \sigma$, then there is an unstable equilibrium with $I_1 > 0$, $I_2 = 0$. In addition, there is an endemic equilibrium with $I_1 > 0$, $I_2 = 0$ whose stability is complicated to analyze. This analysis is possible but does not give new 'insights' and , more importantly, it goes against our characterization of core group. Hence, we ommit it. Thus, if $a_2 > \sigma$, the basic reproduction number $R_0 = a_1/\sigma$ must be very large indeed since a_1 is much larger than a_2.

We have carried out some numerical simulations for Model (8) using $r(\eta) = \exp(-\kappa\eta)$, for $\eta > 0$. Figure 1 illustrates the behavior of the model in the region of parameter space where periodic behavior occurs. We have decreased the value of a_2 to show that model (8) 'approximates' the behavior of the two-dimensional system (6)–for a sexually inactive non-core model. Note that as a_2 changes from 0.2 to 0.1 the asymptotic stability of the endemic equilibrium point is lost and periodic orbits appear. Another way to stabilize this system is to make the function r less responsive to prevalence levels within the core group. In our particular example this amounts to decreasing the magnitude of κ.

In summary, our numerical results indicate that increasing a_2 stabilizes oscillations, decreases period and the maximum number of infectives, and increases the core group size at equilibrium. Also, reducing κ in r stabilizes oscillations.

These results suggest that for reasonable low values of sexual activity for non-core members, the reduced model (6) is a very good predictor provided that there is no interaction between core and non-core subpopulations. By continuity, if there is 'little' interaction between core and non-core groups the same qualitative dynamics will be true. Thus, our original simple model (4) is applicable in more realistic situations provided there is little mixing between groups. As we have seen, if there is substantial mixing between groups, the effect of increased activity by non-core group members gives complicated and less predictable dynamics.

Finally, we have assumed that both populations of homosexually-active individuals mixed according to the proportionate mixing model. Obviously, preference must play a role. The dynamics will not differ if a_1 is small. However, large values of a_1 with preferential mixing need to be studied. We have no clear idea of what the dynamics will be in the most general case.

Acknowledgements This research has been supported by grant DEB-9253570 (Presidential Faculty Award) to Carlos Castillo-Chavez. JXVH also acknowledges the support of CONACYT grant 400200-5-3551E. This work was developed and finished while JXVH was a Postdoctoral Fellow at the Biometrics Unit of Cornell University.

References

[1] Stephen P. Blythe, Fred Brauer, and Carlos Castillo-Chavez. Demographic recruitment in sexually transmitted diseases. Technical Report BU-1154-M, Biometrics Unit, Cornell University, 1992.

[2] Carlos Castillo-Chavez and Horst R. Thieme. *Asymptotically autonomous epidemic models*, volume 2 of *Mathematical population dynamics: analysis of heterogeneity*, pages 33–50. Wuerz Publishing Ltd, Canada, 1995.

[3] Carlos Castillo-Chavez, Jorge X. Velasco-Hernandez, and Samuel Fridman. *Modeling contact structures in biology*, volume 100 of *Lecture Notes in Biomasthematics*, pages 454–492. Springer Verlag, Berlin, 1995.

[4] Shwu fang Hsu-Schmitz. Some theories, estimation methods, and applications of marriage functions for non-closed social networks. Ph.D. dissertation Ithaca, N.Y., Biometrics Unit, Cornell University, 1994.

[5] Karl P. Hadeler and Carlos Castillo-Chavez. A core group model for disease transmission. *Mathematical Biosciences*, 128:41–55, 1995.

[6] Karen Heiderich, Carlos Castillo-Chavez, and Wenzhang Huang. Nonlocal response in a simple epidemiological model. Technical Report 94–29, Mathematical Sciences Institute, Cornell University, 1994.

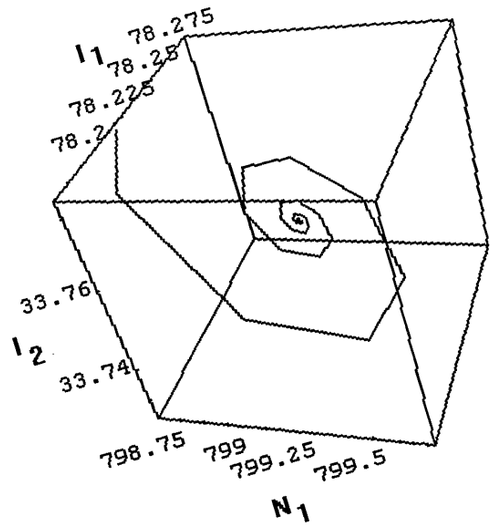
[7] Herbert W. Hethcote and James A. Yorke. *Gonorrhea: transmission dynamics and control.* Springer Verlag, New York, 1984. Lecture Notes in Biomathematics 56.

[8] Wenzhang Huang, Kenneth Cooke, and Carlos Castillo-Chavez. Stability and bifurcation for a multiple group model for the dynamics of hiv/aids transmission. *SIAM Journal of Applied Mathematics*, (52):835–854, 1992.

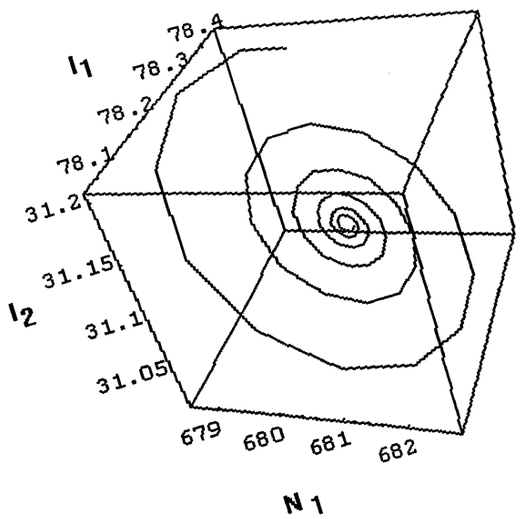
[9] A. Nold. Heterogeneity in disease transmission modeling. *Mathematical Biosciences*, (52):227–240, 1980.

Figure Captions

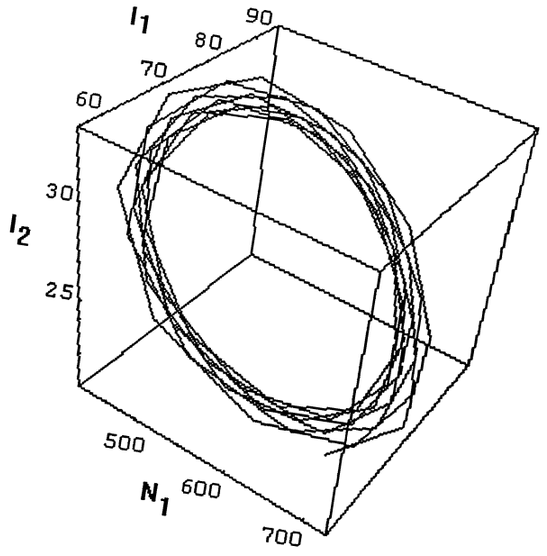
Figure 1. Numerical simulations of model (8) for the parameter values $a_1 = 3$, $\mu = 1$, $\sigma = 2$, $\kappa = 12$, $r(0) = 0.5$. a) Simulation with $a_2 = 0.2$ corresponding to $R_0 = 1.33$. The endemic equilibrium point is asymptotically stable; b) Simulation with $a_2 = 0.15$, corresponding to $R_0 = 1.37$. The endemic equilibrium still shows asymptotic stability but the value of a_2 is close to the Hopf bifurcation point; c) Simulation with $a_2 = 0.1$ corresponding to $R_0 = 1.4$. The endemic equilibrium is no longer asymptotically stable. The existence of periodic solutions is shown.



1a



1b



1c