Urn, Baby, Urn: A simpler approach to studying epidemic models and the efficacy of disease-prevention policies

BU-1521-M

Michael Stuart Montgomery Lanham
Centre College

Desiree Mesa
California State Polytechnic University, Pomona

Jesús Francisco Rodríguez
Cornell University

Dianna Soliz Torres
Westminster College

August 11, 1999

Abstract

In this paper, we explore the use of urn models to describe and analyze the long-term effects of various disease-controlling policies on the spread of an infection through a population. These policies include vaccination with all/nothing vaccines or leaky vaccines, ring vaccination with the all/nothing vaccine, and contact tracing. The populations are described via the Susceptible-Infected-Susceptible (SIS) model with demography, the SIS model without demography and the Susceptible-Infected-Recovered (SIR) and Susceptible-Infected-Recovered-Susceptible ($SIRS$) models. We show that these urn models, often simpler than their respective deterministic and stochastic

counterparts, yield, in most cases, the same average qualitative dynamics. We also examine the definitions and implications of equilibria and stability in these systems.

1 An Introduction to the Simple SIS Urn Model

In this section, we describe a Susceptible-Infected-Susceptible (SIS) epidemic structure as an urn model. The SIS structure was first analyzed by Bailey and Bartlett via deterministic and stochastic methods[1]. In our approach, we imagine an urn full of white (S) and black (I) balls, which represent susceptibles and infectives, respectively. We assume there is a constant number of balls; that is, the total population size, N, is constant. We also assume there are no births or deaths in the system. We assume all infected individuals become instantly infectious and when an infected person recovers he/she becomes a susceptible individual immediately; in other words, he/she gains no immunity from the disease. We further assume there is a constant per-infective (or per black ball) recovery rate μ, and a per-ball contact rate λ.

As is customary in other SIS epidemic models, we use the standard notation R_0 to denote the average number of secondary cases of an infectious disease that one case generates in a completely susceptible population. To determine this R_0, we seek the disease-free and endemic equilibria of the system. That is, we study the long-term dynamics of the system and attempt to find the numbers of black and white balls in the urn such that the probability of an infection occurring is equal to the probability of a recovery occurring. In order to do this, we let X_n be a random variable defined as the number of black balls in the urn after the n^{th} event and look at the expected number of black balls in the urn after the $(n+1)th$ event. We then evaluate when $E[X_{n+1}|X_n]$ is equal to the observed value of black balls in the urn after the n^{th} event, X_n. After this expected value is computed, we look for the R_0 value, which determines whether a specific λ and μ give rise to a system with a disease-free equilibrium or with an endemic equilibrium.

1.1 The SIS Urn Model Unplugged

For this model we imagine our urn with white and black balls where white balls represent the susceptibles in our population and the black balls repre-

sent the infectives in our population. We also imagine two people, A and B, drawing balls from the urn. A will be selecting a ball at random from the population of black balls in the urn at the rate μ. Each drawn black ball is then replaced with a white ball, and this ball is placed back into the urn. B will be drawing two balls at a time at the rate λ. If both balls are white or both balls are black, they will be put back into the urn. However, if one ball is black and one ball is white (we think of this event as a susceptible coming in contact with an infective and causing an infection), the white ball will be replaced with a black ball and both black balls will be placed back into the urn.

Thus far, we have described the following system:

Variables

$$\begin{aligned} \text{Number of white balls} &= S \\ \text{Number of black balls} &= I \end{aligned}$$

Constants

$$\begin{aligned} \text{Recovery rate per black ball} &= \mu \\ \text{Contact rate per ball} &= \lambda \\ \text{Total number of individuals} &= N = S + I \end{aligned}$$

From these, we derive the following total rates:

$$\begin{aligned} \text{Total recovery rate} &= \mu I \\ \text{Total infection rate} &= \lambda I \frac{S}{N} \end{aligned}$$

The total recovery rate is found by taking the product of the per-black-ball recovery rate and the number of infectives in the system. The total infection rate is found by first determining the rate of contact of infectives (λI), and then by taking the fraction of that contact rate that involves collisions with susceptibles ($\frac{S}{N}$). These rates are identical to those used in the deterministic or stochastic SIS models. We assume the balls in the urn are uniformly

mixed.

We now determine the probability that one of the two events will happen next. In defining our rates, we assume the time between each event is exponentially distributed; however, we are interested only in what event occurs next, not in the actual time between events.

Property 1 *If n events, $A_1, A_2, ..., A_n$, exhibit exponentially distributed time intervals between them governed by rates $\alpha_1, \alpha_2, ..., \alpha_n$, then the probability that A_i occurs next is given by*

$$P[A_i \text{ occurring next}] = \alpha_i (\sum_{j=1}^{n} \alpha_j)^{-1}.$$

Defining the following,

$$\begin{aligned} \text{Infec} &= \text{an infection occurs next,} \\ \text{Rec} &= \text{a recovery occurs next,} \end{aligned}$$

for our SIS system we have the following probabilities, typical of SIS stochastic models:

$$\begin{aligned} P[\text{Infec}|I,S] &= \frac{\frac{\lambda SI}{N}}{\mu I + \frac{\lambda SI}{N}} = \frac{\lambda S}{\mu N + \lambda S}, \\ P[\text{Rec}|I] &= \frac{\mu I}{\mu I + \frac{\lambda SI}{N}} = \frac{\mu N}{\mu N + \lambda S}. \end{aligned}$$

Having determined these probabilities, we present the following terms and notation:

- **Definition 1.1** X_n*: The random variable* $\underline{X_n}$ *represents the number of infectives in the urn after the* n^{th} *step.*
- **Definition 1.2 Equilibria**: *Any number* $\widehat{X}_n$*, such that when* $X_n = \widehat{X}_n$*, the expected change in* X_n *in the next time step is zero is called an* $\underline{\text{equilibrium}}$*. We notate the expected change in the value of* X_n *as* $\underline{\Delta X_n}$*.*

- **Definition 1.3 Stability**: *We say an equilibrium $\widehat{X}_n$ is stable if, given any $X_0 \notin \{0, \widehat{X}_n\}$, the expected change in X_n in the direction of $\widehat{X}_n$ in the next step is greater than the expected change in X_n in the direction away from $\widehat{X}_n$ in that step. (When we are dealing with only infection and recovery – since each event only adds or subtracts one infective individual, respectively – we say that an $\widehat{X}_n$ is stable if, for all $X_0 \notin \{0, \widehat{X}_n\}$, the probability of moving in the direction of the equilibrium in the next step is greater than the probability of moving away from the equilbrium in the same step.)*

Thus, in order to determine an equilibrium for our system, we compute an expression for the expected value of our random variable X at generations n and generation $n+1$. Substituting X_n for I, and $N - X_n$ for S, the expression for the expected value of X_{n+1}, given X_n, is

$$\begin{aligned} E[X_{n+1}|X_n] &= X_n + (P[\text{Inf}])(1) + (P[\text{Rec}])(-1) \\ &= X_n + \frac{\lambda(N - X_n)}{\mu N + \lambda(N - X_n)} - \frac{\mu N}{\mu N + \lambda(N - X_n)} \\ &= X_n + \frac{(\lambda - \mu)N - \lambda X_n}{\mu N + \lambda(N - X_n)}. \end{aligned} \tag{1}$$

At equilibrium, $\Delta X_n = 0$, so $E[X_{n+1}|\widehat{X}_n] = \widehat{X}_n + \Delta X_n = \widehat{X}_n$. From (1) this equation holds when

$$\begin{aligned} \widehat{X}_n &= \widehat{X}_n + \tfrac{(\lambda-\mu)N - \lambda\widehat{X}_n}{\mu N + \lambda(N - \widehat{X}_n)} \\ \implies 0 &= \tfrac{(\lambda-\mu)N - \lambda\widehat{X}_n}{\mu N + \lambda(N - \widehat{X}_n)} \\ \implies \widehat{X}_n &= \tfrac{(\lambda-\mu)}{\lambda} N. \end{aligned}$$

We now introduce the concept of the reproductive number R_0. Heesterbeek defines R_0 as the "expected number of secondary cases (new infected individuals) produced by one infectious individual during its entire infectious life in a [totally] susceptible population ... " [3]. It is simple to see that the $R_0 = 1$ value is an important threshold in the epidemic model. If each infective individual causes more than one secondary infection during his infectious life-span ($R_0 > 1$), it is intuitive that the epidemic will sustain itself. Likewise, if each infective does not cause more than one secondary infection

during his infectious life-span ($R_0 < 1$), the number of infectives in the population will tend toward zero, *i. e.*, there is no endemic equilibrium. It is from the relationship between R_0 and the existence of an endemic equilibrium that we determine R_0 for our systems.

We define the reproductive number of this system as $R_0 = \frac{\lambda}{\mu}$. Rewriting our equilibrium as

$$\widehat{X}_n = \left(1 - \frac{1}{R_0}\right) N,$$

we see when $R_0 > 1$, $\widehat{X}_n$ is positive (an endemic equilibrium exists), but when $R_0 < 1$, $\widehat{X}_n$ is negative (only a disease-free equilibrium exists).

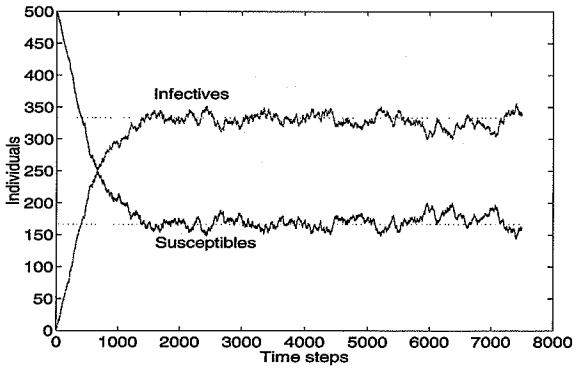

Figure 1.1.1: A sample SIS, no vaccination simulation ($S_0 = 499$, $I_0 = 1$, $\lambda = .75$, and $\mu = .25$; using sis.m, Appendix, p. 430) with the two expected equilibria, $\widehat{X}_n = 333.\overline{3}$ and $\widehat{S}_n = 166.\overline{6}$, graphed with dotted lines.

Having found $\widehat{X}_n$ and R_0 for the simple SIS system, we seek proof that the system tends toward its equilibria for various X_0 and R_0 values. In other words, if we start with a number of black balls less than the endemic equilibrium value ($X_0 < \widehat{X}_n$, $X_0 \neq 0$) and $R_0 > 1$, we want the expected change in the number of black balls to be positive, moving the number of black balls towards equilibrium in the next step. Similarly, if we begin with a number of black balls above the equilibrium value, to estabilish our stability we want the expected change in the number of black balls to be negative, moving the number of black balls in the urn in the direction of the equilibrium.

From (1), we see that the expected change in one step is

$$\Delta X_n = \frac{(\lambda - \mu)N - \lambda X_n}{\mu N + \lambda(N - X_n)}. \tag{2}$$

If we begin with any $X_0 < \widehat{X}_n$, $X_0 \neq 0$, then

$$\begin{array}{rrcl} & X_0 & < & \frac{\lambda-\mu}{\lambda}N \\ \Longrightarrow & \lambda X_0 & < & \lambda N - \mu N \\ \Longrightarrow & 0 & < & \lambda(N - X_0) - \mu N \\ \Longrightarrow & 0 & < & \frac{\lambda(N-X_0)-\mu N}{\mu N+\lambda(N-X_n)} \\ \Longrightarrow & 0 & < & \Delta X_n. \end{array}$$

If we begin with $X_0 > \widehat{X}_n$, the inequalities are reversed, and the expected change in the number of black balls is negative, moving the system back towards equilibrium. Thus, for $R_0 > 1$ and all $X_0 \notin \{0, \widehat{X}_n\}$, ΔX_n tends towards the equilibrium.

At this point in our discussion, it is important that we examine the fundamental differences between equilibria and stability in the deterministic models and equilibria and stability as we have defined them in this model. In both the differential and difference equiation SIS models, deterministic equilibria (notated X^*) are defined as the values from which there is no movement over time, *e. g*, beginning at $X_0 = X^*$, we know $X_1, X_2, X_3, \ldots = X^*$ or $X(t) = X^*$ for all $t > 0$, depending on the model. However, in our system, if we begin at $X_0 = \widehat{X}_n \neq 0$, stable or unstable, we understand that either an infection or a recovery must occur next ($P[\text{nothing occurs}] = 0$), and we know $X_1 \neq \widehat{X}_n$; however, this does not violate our conditions for $\widehat{X}_n$.

As for stability, it could be said that for any R_0, X_0, and $\widehat{X}_n$, if we look at the value of X_n as $n \to \infty$, we will see that X_n will always have one final value, namely $X_f = 0$. The fact that there is a non-zero probability of reaching zero in finite time and the fact that, once there, X_n never moves from zero combine to force all X_f to zero. However, our definition of stability does not require that all $X_f = \widehat{X}_n$, or that the movement of the $(n+1)th$ step be in the direction of $\widehat{X}_n$ for any n. Rather, we require that there be a tendency towards the equilibrium for all values $X_0 \notin \{0, \widehat{X}_n\}$ (with appropriate corresponding R_0 values).

It is important to note that this expected change in X_n is not dependent on the proximity of X_0 to $\widehat{X}_n$, meaning this system of inequalities proves $\widehat{X}_n = \frac{\lambda-\mu}{\lambda}N = (1 - \frac{1}{R_0})N$ is both locally and globally stable for $R_0 > 1$. For $R_0 < 1$, however,

$$\begin{array}{rcl} R_0 = \frac{\lambda}{\mu} & < & 1 \\ \Longrightarrow \quad \lambda & < & \mu \\ \Longrightarrow \quad \lambda - \mu & < & 0 \\ \Longrightarrow \quad (\lambda - \mu)N & < & 0 \\ \Longrightarrow \quad (\lambda - \mu)N - \lambda X_0 & < & 0, \text{for any } X_0 \\ \Longrightarrow \quad \frac{(\lambda-\mu)N-\lambda X_n}{\mu N+\lambda(N-X_n)} & < & 0 \\ \\ \Delta X_n & < & 0, \end{array}$$

so X_n tends towards zero.

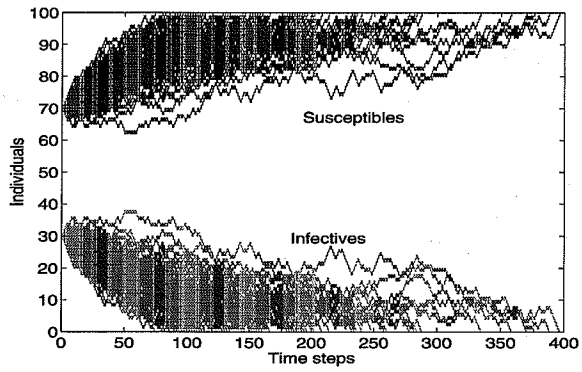

Figure 1.1.2: One hundred sample SIS simulations ($S_0 = 70$, $I_0 = 30$, $\lambda = .75$, $\mu = .9$; $R_0 = .8\overline{3}$; using sis.m, Appendix, p. 430) illustrating the stability of $\widehat{X}_n = 0$ when $R_0 < 1$.

Figures 1.1.1 and 1.1.2 demonstrate the evolution in the numbers of black and white balls and their tendencies towards their respective equilibria. The figures were obtained from simulations run using the MATLAB[1] code found in the Appendix.

[1]MATLAB is a registered trademark of *The MathWorks, Inc.*, All Rights Reserved.

2 SIS Urn Models with Vaccination

In this section we incorporate and analyze different vaccination strategies in the SIS model of section 1.1. These include the all/nothing vaccine, the leaky vaccine, and ring vaccination. The all/nothing vaccine SIS system can be thought of as an urn in which a fraction f of the the white balls are vaccinated against the disease. Of those vaccinated, only a fraction are protected againt the disease, and those are colored blue. This blue fraction is completely protected. This fraction is also called the vaccine efficacy (VE) and is equal to $1 - \beta$, where β is the probability that the vaccine takes no effect when applied to a susceptible. After vaccination, A and B are still drawing balls at their respective rates with the same effects on the population of balls as before, but if B draws a black ball and a blue ball, then both balls are both put back into the population unchanged (Section 2.1).

In the leaky vaccine, SIS urn model, we say instead that we color an entire fraction f of the susceptible population blue, and that each blue ball now has a lower probability of infection β, $0 \leq \beta < 1$, when drawn with a black ball [4] (Section 2.2). With this type of vaccine, no one is ever completely protected from infection.

For ring vaccination, we introduce the concept of random screening for the disease at a constant rate r. For every black ball that is discovered via screening, we apply an all/nothing vaccine to k balls surrounding it regardless of their color, in an attempt to contain the disease. (See page 408 for a discussion of the implications of and problems with the "ring" aspect of this model.) However, we assume the vaccine has no effect on infective or previously-vaccinated individuals. Therefore, the only balls that change color when the vaccine is applied are the white ones, and the number of balls that are changed from white to blue during each ring vaccination attempt is proportional to the fraction of the population that remains unvaccinated and susceptible. We vaccinate the entire "ring" without checking for infection or previous vaccination first, and we must keep track of those susceptibles who were vaccinated but in whom the vaccine had no effect. They are classified in the same way as those susceptibles who have received no vaccine (Section 2.3).

2.1 All or Nothing Vaccine

In this section we use the SIS urn model to examine the effects of all or nothing vaccines on epidemics. An all or nothing vaccine, when applied to an individual will provide either total protection or no protection at all from a given disease. As in the previous section, N represents the total constant population size, λ represents the contact rate, and μ represents the recovery rate. There is a probability β, of the vaccination not providing any protection to a vaccinated individual. We must also take into account that only a fraction f, of the total population, N, will be vaccinated before our initial infected is introduced to the system. Thus, our maximum number of susceptibles S^*, is found by adding the total number of protected vaccinated susceptibles and the number of unprotected vaccinated susceptibles before the epidemic. Therefore,

$$S^* = S_0(1-f) + S_0 f\beta,$$

and the following rates hold for the total population:

$$\begin{aligned} \text{Rate of recovery} &= \mu X_n \\ \text{Rate of infection} &= \frac{\lambda X_n (S^* - X_n)}{N}. \end{aligned}$$

From Property (1) we have

$$\begin{aligned} P[\text{Infec}|X_n] &= \frac{\lambda(S^* - X_n)}{\lambda(S^* - X_n) + \mu N} \\ P[\text{Rec}|X_n] &= \frac{\mu N}{\lambda(S^* - X_n) + \mu N}. \end{aligned}$$

Since

$$E[X_{n+1}|X_n] = X_n + (P[\text{Infec}|X_n])(1) + (P[\text{Rec}|X_n])(-1)$$

and $E[X_{n+1}|\widehat{X}_n] = \widehat{X}_n$, then

$$0 = \frac{\lambda(S^* - \widehat{X}_n)}{\lambda(S^* - \widehat{X}_n) + \mu N} - \frac{\mu N}{\lambda(S^* - \widehat{X}_n) + \mu N}$$

which implies

$$\widehat{X}_n = S^* - \frac{\mu N}{\lambda}.$$

Now, substituting our value of S^* we find our equilibrium exists at

$$\widehat{X}_n = S_0(1-f) + S_0 f\beta - \frac{\mu N}{\lambda}$$

If we solve for $\widehat{X}_n > 0$, we find an expression for the reproductive value:

$$R_0 = \frac{S_0(1-f+f\beta)\lambda}{\mu N} > 0.$$

If we assume $I_0 = 1$, then $S_0 \approx N$ for large N, and it follows that

$$\widehat{X}_n = \frac{\lambda(1-f+f\beta)-\mu}{\lambda}N = \frac{\lambda-\mu}{\lambda}N - f(1-\beta)N$$

and

$$R_0 = \frac{(1-f+f\beta)\lambda}{\mu} = \frac{\lambda}{\mu}\left(1-(1-\beta)f\right).$$

Both the equilibrium and the R_0 for the all/nothing vaccine, SIS system are less than those for the no vaccine, SIS system. Biologically, this means the vaccine is reducing both the average number of infectives each infectious individual produces during its infected lifespan and the number of individuals in the infected class at equilibrium. As before, this expression for R_0 allows us to write the equilibrium point as

$$\widehat{X}_n = (1 - \frac{1}{R_0})N.$$

We see that given $X_0 < \widehat{X}_n$, $X_0 \neq 0$,

$$\begin{array}{rrl} & X_0 & < \frac{\lambda(1-f+f\beta)-\mu}{\lambda}N \\ \Longrightarrow & 0 & < \frac{\lambda((1-f+f\beta)N-X_0)-\mu N}{\lambda(N-X_0)+\mu N} = \Delta X_n. \end{array}$$

The corresponding analysis for $X_0 > \widehat{X}_n$ leads to a negative expected change in the number of black balls in the urn. Therefore, for all $R_0 = \frac{(1-f+f\beta)\lambda}{\mu} > 1$,

and $X_0 \notin \{0, \widehat{X}_n\}$, $\widehat{X}_n = (1 - \frac{1}{R_0})N$ is stable. However, for $R_0 < 1$,

$$\begin{aligned} & \frac{(1-f+f\beta)\lambda}{\mu} && < && 1 \\ \Longrightarrow \quad & \lambda(1-f+f\beta) - \mu && < && 0 \\ \Longrightarrow \quad & (\lambda(1-f+f\beta) - \mu)N && < && 0 \\ \Longrightarrow \quad & (\lambda(1-f+f\beta) - \mu)N - \lambda X_0 && < && 0 \\ \Longrightarrow \quad & \Delta X_n = \frac{\lambda((1-f+f\beta)N - X_0) - \mu N}{\lambda(N - X_0) + \mu N} && < && 0. \end{aligned}$$

As in the SIS model without vaccination, when $R_0 < 1$, $\widehat{X}_n = 0$ is a stable equilibrium for all X_0.

2.2 Leaky Vaccine

To examine the SIS urn model with a leaky vaccine, we keep our definitions of N, f, S^*, S_0, X_n, $\widehat{X}_n$, R_0, λ, and μ, as before. However, the β in the leaky vaccine has a different meaning than the β in the all or nothing system. Everyone who is vaccinated has a reduced chance of infection at each contact with an infective individual; we call this probability β [2]. To model the impact of a leaky vaccine, we must introduce new constants and variables to account for the susceptibility of both vaccinated and unvaccinated people to infection. The susceptible class must be split into two separate classes, unvaccinated susceptibles S_u, and vaccinated susceptibles S_v. We define S_u^* and S_v^* as the maximum number of unvaccinated susceptibles and the maximum number of vaccinated susceptibles, respectively, and we see that $S^* = S_u^* + S_v^*$. The infective class must also be split into two separate classes, unvaccinated infectives I_u, and vaccinated infectives I_v, where the total number of infectives $I_{total} = I_u + I_v$. We assume that the vaccine does not affect an individual's infection potential.

We must now consider a number of different random variables in the system. After the n^{th} step, we denote the values of S_u, S_v, I_u, and I_v as S_{u_n}, S_{v_n}, I_{u_n}, and I_{v_n}, respectively. We see that $N = S_{u_n} + S_{v_n} + I_{u_n} + I_{v_n}$ and $I_{total_n} = I_{u_n} + I_{v_n}$. In deriving our rates, we must separate infections of vaccinated and unvaccinated susceptibles, such that, instead of involving the proportion of total susceptibles in the system to the total population, we now involve the total number of individuals from each sub-class in the rate for that sub-class' respective infection. Where we used S or $N - X_n$ for the number of susceptibles in the rate of infection, we now use $S_u^* - I_{u_n}$ and

$S_v^* - I_{v_n}$ for the number of susceptibles available for infection in the appropriate expressions. Also, we see that the rate of collision of infectives with vaccinated susceptibles is not the rate of infection of vaccinated susceptibles, since each collision results in an infection only with probability β.

Using these terms, we derive the following rate definitions:

$$\begin{aligned}
\text{Rate of recovery of } I_u &= \mu I_u \\
\text{Rate of recovery of } I_v &= \mu I_v \\
\text{Rate of infection of } S_u &= \frac{\lambda I_{total}(S_u^* - I_u)}{N} \\
\text{Rate of collision of } S_v \text{ with } I_{total} &= \frac{\lambda I_{total}(S_v^* - I_v)}{N}.
\end{aligned}$$

Because these rates are exponentially distributed we know by Property (1) that the probability of any of these events occuring next is given by:

$$\begin{aligned}
P[\text{Infec of } S_u | I_{u_n}, I_{v_n}] &= \frac{\lambda(S_u^* - I_{u_n})}{\lambda((S_u^* - I_{u_n}) + (S_v^* - I_{v_n})) + \mu N} \\
P[\text{Infec of } S_v | I_{u_n}, I_{v_n}] &= \beta\left(\frac{\lambda(S_v^* - I_{v_n})}{\lambda((S_u^* - I_{u_n}) + (S_v^* - I_{v_n})) + \mu N}\right) \\
P[\text{Rec of } I_u | I_{u_n}, I_{v_n}] &= \frac{\mu I_{u_n} N}{\lambda I_{total_n}((S_u^* - I_{u_n}) + (S_v^* - I_{v_n})) + \mu N I_{total_n}} \\
P[\text{Rec of } I_v | I_{u_n}, I_{v_n}] &= \frac{\mu I_{v_n} N}{\lambda I_{total_n}((S_u^* - I_{u_n}) + (S_v^* - I_{v_n})) + \mu N I_{total_n}}
\end{aligned}$$

We involve β by multiplying the probability that a collision between an infective and a vaccinated susceptible and the probability that this collision results in an infection to obtain the probability that the next event is the infection of a vaccinated susceptible.

In order to study the long-term dynamics of the infective population, we must find the equilibria, $\widehat{X}_n$. Since

$$\begin{aligned}
E[X_{n+1} | X_n, I_{u_n}, I_{v_n}] &= X_n + (P[\text{Infec of } S_u] + P[\text{Infec of } S_v])(1) \\
&\quad + (P[\text{Rec of } I_u] + P[\text{Rec of } I_v])(-1),
\end{aligned}$$

it follows that at equilibrium

$$P[\text{Infec of } S_u] + P[\text{Infec of } S_v] = P[\text{Rec of } I_u] + P[\text{Rec of } I_v].$$

Simplifying this, we need only solve:

$$\lambda(S_u^* - I_{u_n})I_{total_n} + \lambda\beta(S_u^* - I_{u_n})I_{total_n} = \mu I_{u_n}N + \mu I_{v_n}N.$$

The assumption $S_0 \approx N$ leads to

$$((1-f)S_0 - I_{u_n}) + \beta(fS_0 - I_{v_n}) = \frac{\mu N}{\lambda}.$$

Using this equation we solve for an expression for I_{total_n}, given by

$$\widehat{X}_n = \widehat{I}_{total_n} = \frac{\frac{N(\lambda(1-f+f\beta)-\mu)}{\lambda}}{1-(1-\beta)\frac{I_{v_n}}{I_{total_n}}}.$$

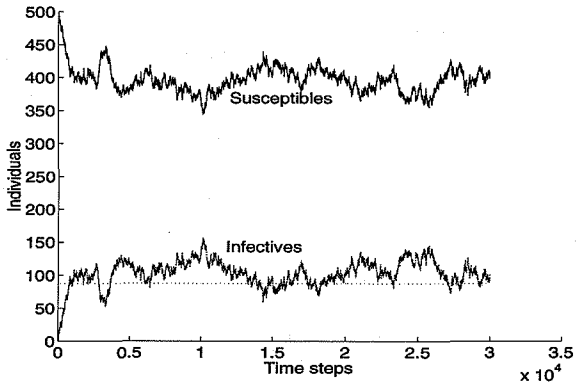

Figure 2.2.1: A sample SIS simulation with leaky vaccination ($S_0 = 499$, $I_{v_0} = 0$, $I_{u_0} = 1$, $\lambda = 1$, $\mu = .5$, $f = .5$, $\beta = .35$; using sisleaky.m, Appendix p. 431), demonstrating the tendency for I_{total_n} to remain above the calculated $I_{min} = 87.5$ (dotted line).

From this expression we conclude there is a minimum X_n because I_{total_n} will always be greater than

$$\widehat{I}_{min} = \widehat{X}_{n_{min}} = \frac{N(\lambda(1-f+f\beta)-\mu)}{\lambda},$$

the expression for $\widehat{X}_n$ for the all or nothing vaccine SIS model with the same f and β.

We then set $\widehat{I}_{total_n} > 0$ to find R_0 and see that

$$R_0 = \frac{\lambda}{\mu}(1-f+f\beta) > 1.$$

$\widehat{I}_{min}$ can therefore be written in the form

$$\widehat{I}_{min} = (1 - \frac{1}{R_0})N.$$

This analysis of the leaky vaccine shows us that $\widehat{X}_n$ in this system will be equal to $\widehat{X}_n$ in the all-or-nothing system only when $\beta = 0$ or when $I_{v_n} = 0$, both of which are equivalent to having an all or nothing system where everyone who is vaccinated is protected.

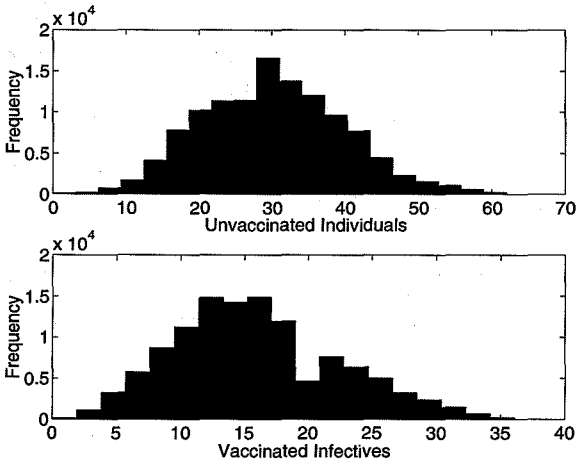

Figure 2.2.2: The histograms for the I_{u_n} and I_{v_n} values for some number of simulations with the same parameters ($S_0 = 499$, $I_0 = 1$, $\lambda = 1$, $\mu = .45$, $\beta = .25$, $f = .65$; $R_0 \approx 1.1389$; using sisleaky.m, Appendix p. 431); the distribution of the points provide some support for our assumption that I_u and I_v independently seek equilibria values for some $R_0 > 1$.

It would be useful if we could solve for an equilibrium of both I_v and I_u, allowing us to solve for an expression for I_{total} using only the constants in the system. The solutions to $E[I_{u_{n+1}}|\widehat{I}_{u_n}, \widehat{I}_{v_n}] = \widehat{I}_{u_n}$ and $E[I_{v_{n+1}}|\widehat{I}_{u_n}, \widehat{I}_{v_n}] = \widehat{I}_{v_n}$, though not explicitly derived here, are calculated as are other equilibria in this paper. Figure (2.2.2) implies that there is a tendency towards them for at least some $R_0 > 1$.

2.3 Ring Vaccination

Our model for ring vaccination is based on a policy such that each discovery of an infective individual leads to the vaccination of a ring of susceptible individuals surrounding them. This ring of individuals in the model is of constant size and consists of friends, relatives, etc. Theoretically, in the real world this policy could lead to containment of the disease, followed by erradication or prevention of an epidemic.

In our model, however, this ring of vaccinated individuals is simply represented by a change in classification of a certain number of individuals in the urn from unvaccinated susceptibles to vaccinated susceptibles. We see that the urn model description of ring vaccination removes the spatial aspects of the actual policy. Our model would work just as well for a policy that vaccinates a number of random people in the population each time a screened individual is found to be infected. Yet, because the balls in the urn are uniformly mixed, a description of our kind is required. When an infected person is randomly discovered in this model, we automatically apply a vaccine to k people in the system. Because not all people in the ring are unvaccinated susceptibles, and because we assume application of the vaccine to an infective or a previously vaccinated and protected individual will not have any effect on those individuals' classifications, we must adjust the number of individuals who are actually moved from the unvaccinated susceptibles to the vaccinated susceptibles class to reflect this. We also analyze only ring vaccination with an all/nothing vaccine, simplifying the model.

As in all of the above models, we have the usual constants N, λ, and μ. In this model, we also introduce two other constants: r, the rate at which all individuals are randomly screened for infection – a positive test result triggering ring vaccination, and β, the probability that the vaccine does not work at all, equal to $1 - \text{VE}$, where VE is the vaccine efficacy.

In this model, we must keep track of both the vaccinated susceptibles and the unvaccinated susceptibles, as well as the infectives; so, we again have random variables S_{u_n}, S_{v_n}, and X_n. If we let "Ring" denote the event the next occurrence is the triggering of ring vaccination, then we define the

following rates, probabilities, and expected values:

$$\begin{aligned}
\text{Rate of recovery} &= \mu X_n \\
\text{Rate of infection} &= \frac{\lambda S_{u_n} X_n}{N} \\
\text{Rate of initiation of ring vaccination} &= r\frac{X_n}{N}
\end{aligned}$$

$$\begin{aligned}
P[\text{Rec}|X_n] &= \frac{\mu X_n}{\mu X_n + \frac{\lambda S_{u_n} X_n}{N} + r\frac{X_n}{N}} = \frac{\mu N}{\mu N + \lambda S_{u_n} + r}, \\
P[\text{Infec}|X_n, S_{u_n}] &= \frac{\frac{\lambda S_{u_n} X_n}{N}}{\mu X_n + \frac{\lambda S_{u_n} X_n}{N} + r\frac{X_n}{N}} = \frac{\lambda S_{u_n}}{\mu N + \lambda S_{u_n} + r}, \\
P[\text{Ring}|X_n] &= \frac{r\frac{X_n}{N}}{\mu X_n + \frac{\lambda S_{u_n} X_n}{N} + r\frac{X_n}{N}} = \frac{r}{\mu N + \lambda S_{u_n} + r},
\end{aligned}$$

$$\begin{aligned}
E[X_{n+1}|X_n, S_{u_n}] &= X_n + (P[Infec])(1) + (P[Rec])(-1) + (P[Ring])(0) \\
&= X_n + \frac{\lambda S_{u_n}}{\lambda S_{u_n} + \mu N + r} - \frac{\mu N}{\lambda S_{u_n} + \mu N + r}, \\
E[S_{u_{n+1}}|X_n, S_{u_n}] &= S_{u_n} + P[Infec](-1) + P[Rec](1) + P[Ring]\left(-k\frac{S_{u_n}}{N}\right)(1-\beta), \\
&= S_{u_n} - \frac{\lambda S_{u_n}}{\lambda S_{u_n} + \mu N + r} + \frac{\mu N}{\lambda S_{u_n} + \mu N + r} - \frac{(1-\beta) r k \frac{S_{u_n}}{N}}{\lambda S_{u_n} + \mu N + r}, \\
E[S_{v_{n+1}}|X_n, S_{u_n}, S_{v_n}] &= S_{v_n} + P[Ring]\left(k\frac{S_{u_n}}{N}(1-\beta)\right) \\
&= S_{v_n} + \frac{(1-\beta) r k \frac{S_{u_n}}{N}}{\lambda S_{u_n} + \mu N + r}.
\end{aligned}$$

As before, we consider the equilibria of this system to be the $\widehat{X}_n$, $\widehat{S}_{u_n}$, and $\widehat{S}_{v_n}$ that satisfy the expression $E[X_{n+1}|\widehat{X}_n, S_{u_n}] = \widehat{X}_n$. This leads us to

$$0 = \frac{\lambda S_{u_n}}{\lambda S_{u_n} + \mu N + r} - \frac{\mu N}{\lambda S_{u_n} + \mu N + r},$$

or

$$S_{u_n} = \frac{\mu}{\lambda} N.$$

This result says nothing about the value of $\widehat{X}_n$, only that if $S_{u_n} = \frac{\mu}{\lambda} N$, then the expected change in X_n in the next step is zero. We need to determine if S_{u_n} stays constant and equal to $\frac{\mu}{\lambda} N$ in the long run. Thus, we seek solutions to the system

$$\widehat{S}_{u_n} = \widehat{S}_{u_n} - \frac{\lambda \widehat{S}_{u_n}}{\lambda \widehat{S}_{u_n} + \mu N + r} + \frac{\mu N}{\lambda \widehat{S}_{u_n} + \mu N + r} - \frac{(1-\beta) r k \frac{\widehat{S}_{u_n}}{N}}{\lambda \widehat{S}_{u_n} + \mu N + r},$$

from which we have

$$0 = -\frac{\lambda \widehat{S}_{u_n}}{\lambda \widehat{S}_{u_n} + \mu N + r} + \frac{\mu N}{\lambda \widehat{S}_{u_n} + \mu N + r} - \frac{(1-\beta) r k \frac{\widehat{S}_{u_n}}{N}}{\lambda \widehat{S}_{u_n} + \mu N + r}$$

or

$$\widehat{S}_{u_n} = \frac{\mu N^2}{\lambda N + (1-\beta) r k}.$$

However, we see the two expressions we have obtained for S_{u_n} are equal only if $N = 0$, $\mu = 0$, $\beta = 1$, $r = 0$, or $k = 0$, the last three of which correspond to no ring vaccination being implemented in the system. This shows that there is not a constant $\widehat{X}_n$ towards which the value of X_n tends in the long-run. Rather, there is a constant $\widehat{S}_{u_n}$ toward which the value of S_{u_n} tends in the long-run.

Before we can continue analyzing $\widehat{X}_n$ in this system, we first need to see if the $\widehat{S}_{u_n}$ we found is a stable equilibrium. As before, we see that if

$$S_{u_0} < \frac{\mu N^2}{\lambda N + (1-\beta) r k} = \widehat{S}_{u_n},$$

then,

$$\begin{aligned} \lambda S_{u_0} N + S_{u_0}(1-\beta) r k &< \mu N^2 \\ \implies 0 &< -\lambda S_{u_0} - (1-\beta) r k S_{u_0} + \mu N^2 \\ \implies 0 &< \frac{-\lambda S_{u_0} - (1-\beta) r k \frac{S_{u_0}}{N} + \mu N}{\lambda S_{u_0} + \mu N + r}. \end{aligned} \tag{3}$$

Yet we see that the right side of expression (3) is the portion of the $E[S_{u_{n+1}}]$ equation which refers to the expected change in the S_{u_n} value from the n^{th} step to the $(n+1)th$ step, ΔS_{u_n}. In other words, if $S_{u_0} < \widehat{S}_{u_n}$, the expected change in the number of white balls in the system is positive, moving up in the direction the equilibrium. Similarly, we see if we begin with an $S_{u_0} > \widehat{S}_{u_n}$, we find the expected change in the number of white balls is negative, moving again in the direction of our equilibrium.

Now we can begin to examine the dynamics of X_n in this system. We know in the long run, S_{u_n} tends towards $\frac{\mu N^2}{\lambda N+(1-\beta)rk}$, but we also know $N = S_{u_n} + S_{v_n} + X_n$ is a constant. It then follows that

$$N - S_{u_n} = X_n + S_{v_n},$$

and

$$N - S_{u_n} = N - \frac{\mu N^2}{\lambda N + (1-\beta)rk}.$$

We then see that at the n^{th} step,

$$\begin{aligned} X_n + S_{v_n} &= \left(1 - \frac{\mu N}{\lambda N + (1+\beta)rk}\right) N \\ \Longrightarrow\ X_n + S_{v_n} &= \left(\frac{(\lambda-\mu)N + (1-\beta)rk}{\lambda N + (1-\beta)rk}\right) N \\ \Longrightarrow\ X_n &= \left(\frac{(\lambda-\mu)N + (1-\beta)rk}{\lambda N + (1-\beta)rk}\right) N - S_{v_n}. \end{aligned} \tag{4}$$

From the analysis of the stability of S_{u_n} above, we know the S_{v_n} and X_n that satisfy these equations are also locally stable. We see that as soon as

$$S_{v_n} \geq \left(\frac{(\lambda-\mu)N + (1-\beta)rk}{\lambda N + (1-\beta)rk}\right) N,$$

X_n will be forced to zero as S_{u_n} is forced towards equilibrium.

This analysis yields two interesting results: first, we see that for any constant, non-zero population system employing ring vaccination with $\mu \neq 0$, $\beta \neq 1$, $r \neq 0$, and $k \neq 0$, $\widehat{X}_n = 0$ is a globally stable equilibrium; second, we see from (4) that if $(\lambda - \mu)N + (1-\beta)rk < 0$, X_n will not be forced to

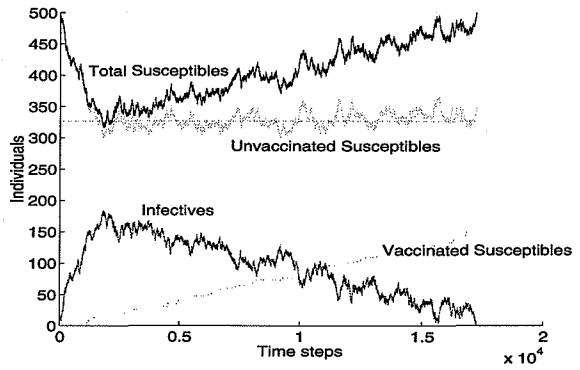

Figure 2.3.1: A sample ring vaccination simulation ($S_0 = 499$, $I_0 = 1$, $\lambda = .75$, $\mu = .5$, $r = 2$, $\beta = .25$, $k = 5$; using sisring.m, Appendix p. 432), demonstrating the steady descent of X_n to 0.

a positive value for any S_{u_n}. We see this in figures 2.3.1 and 2.3.3. Though there are no non-negative $\widehat{X}_n$, we describe the dynamics of the system for very small S_{v_n} by defining $\bar{R}_0 = \frac{\lambda N+(1-\beta)rk}{\mu N}$. However, for this system $\bar{R}_0 > 1$ does not mean there is an endemic equilibrium, but rather for small S_{v_n}, before its decline towards zero, X_n will approach a positive maximum value, namely $\left(\frac{(\lambda-\mu)N+(1-\beta)rk}{\lambda N+(1-\beta)rk}\right) N$.

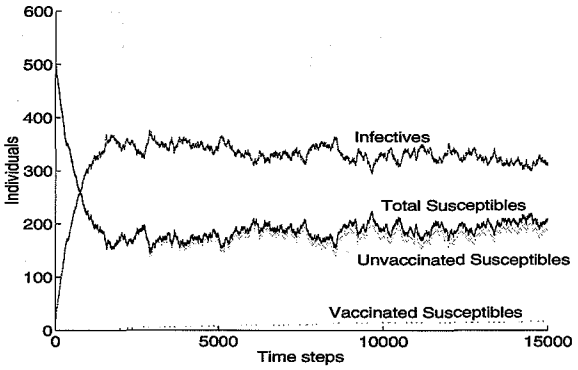

Figure 2.3.2: The first 15000 steps of another ring vaccination simulation ($S_0 = 500$, $I_0 = 20$, $\lambda = .75$, $\mu = .25$, $r = 2$, $\beta = .80$, $k = 2$; using sisring.m, Appendix p. 432), showing the $X_{n_{max}}$ at 376 individuals with $X_{n_{max}} \approx 347$ predicted. Though it seems that the number of infectious individuals is hovering around a constant value throughout this portion of the simulation, after 350,000 steps, this simulation, too, went to $\widehat{X}_n = 0$.

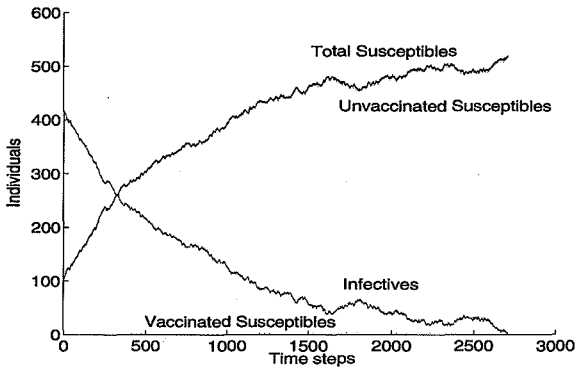

Figure 2.3.3: A sample ring vaccination simulation ($S_0 = 100$, $I_0 = 420$, $\lambda = .75$, $\mu = .8$, $r = 2$, $\beta = .80$, $k = 2$; $\bar{R}_0 \approx .9394$; using sisring.m, Appendix p. 432), illustrating that when $\bar{R}_0 < 1$, the infectives die out much faster than when $\bar{R}_0 > 1$ (see Figure 2.3.1). Notice, too, that the first noticable increase in numbers of vaccinated individuals occurs around time step 1200, indicating that ring vaccination was not needed to avoid an endemic equilibrium.

3 A Non-vaccination Disease-erradication Policy: Contact Tracing

Here we study a disease prevention policy without using vaccines. In contact-tracing we find black balls at a certain rate and proceed to search for the ball's k previous contacts which can only be found with a certain probability p. Once found, the contact balls have an average probability of being black equal to the fraction of balls left in the urn that are still black, $\frac{X_n}{N}$. If any contacts found are black, they are removed and replaced by white balls. Otherwise, nothing happens and the next event occurs.

In this section we analyze disease control by a variation on the method of contact tracing. The premise behind our approach is that a person is tested for the infection with an exponential rate, r, and if discovered to possess the disease, the infective proceeds to supply us with k contacts. However, we can only locate each contact with probability p. Therefore, on average, we find kp contacts for each discovered infective. Thus, if we let X_n be a random variable representing the number of infectives at step n, the average number of infectives found from the contacts given to us by the first discovered

infective in the $(n+1)th$ step is given by

$$kp\frac{X_n - 1}{N - 1},$$

since $\frac{X_n-1}{N-1}$ is the probability that any one contact found is infected. (Remember that when we examine the behavior of the system in the $(n+1)th$ step, we already know the value of X_n from the previous step.) In theory, we would continue this policy with our new infectives, each of whom would lead us to an average of kp people, and only a portion of those would be infected.

Our system has the following rate definitions:

$$\begin{aligned} \text{Screening Rate} &= r \\ \text{Rate at infectives are screened and discovered} &= r\frac{X_n}{N} \\ \text{Rate of infection} &= \lambda X_n \frac{N - X_n}{N} \\ \text{Rate of recovery} &= \mu X_n. \end{aligned}$$

Now let

$$\begin{aligned} \text{Infec} &= \text{the event that the next occurrence is an infection of a susceptible} \\ \text{Rec} &= \text{the event that the next occurrence is a recovery} \\ \text{Dis} &= \text{the event that the next occurrence is a random discovery of an infective.} \end{aligned}$$

Since these rates exhibit exponential distribution we can apply Property 1 to find the probabilities of the following events:

$$\begin{aligned} P[\text{Infec}] &= \frac{\lambda X_n \frac{N-X_n}{N}}{\lambda X_n \frac{N-X_n}{N} + \mu X_n + r\frac{X_n}{N}} = \frac{\lambda(N - X_n)}{\lambda(N - X_n) + \mu N + r} \\ P[\text{Rec}] &= \frac{\mu X_n}{\lambda X_n \frac{N-X_n}{N} + \mu X_n + r\frac{X_n}{N}} = \frac{\mu N}{\lambda(N - X_n) + \mu N + r} \\ P[\text{Dis}] &= \frac{r\frac{X_n}{N}}{\lambda X_n \frac{N-X_n}{N} + \mu X_n + r\frac{X_n}{N}} = \frac{r}{\lambda(N - X_n) + \mu N + r}. \end{aligned}$$

In our model we will assume that for every discovery of infection we will instantaneously cure the discovered infective and every infective individual our original infective leads us to. On the average, the number of people that

each infected individual is able to lead us to must be a fraction less than one. If this were not so, meaning an infected person leads us to more than one other infected person on the average, then it is conceivable that the first person we trace will lead us to the majority of the infected people in the population. We see that the time constraints and practicality of a model that predicts this type of behavior force us to assume each tracing leads to only a fraction of a new infective on the average. This assumption allows us to estimate the total number of people we find per contact tracing by ignoring the higher order terms. Simply, the number of people we cure per contact tracing (including the initial infective) is

$$1+kp\frac{X_n-1}{N-1}+kp\frac{X_n-1}{N-1}\left(kp\frac{X_n-\left(1+kp\frac{X_n-1}{N-1}\right)}{N-\left(1+kp\frac{X_n-1}{N-1}\right)}\right)\ldots\approx 1+kp\frac{X_n-1}{N-1}.$$

As before, to study the number of infectives as time goes to infinity we need to find when $E[X_{n+1}|X_n]=X_n$. But since

$$\begin{aligned}E[X_{n+1}|X_n] &= X_n+(1)(\frac{\lambda(N-X_n)}{\lambda(N-X_n)+\mu N+r})-(1)(\frac{\mu N}{\lambda(N-X_n)+\mu N+r})\\ &\quad -(1+kp\frac{X_n-1}{N-1})(\frac{r}{\lambda(N-X_n)+\mu N+r}),\end{aligned}$$

it follows that

$$(N-1)[\lambda(N-X_n)-\mu N]=(r)[N-1+kp(X_n-1)].$$

Therefore, if we solve for X_n we get

$$\widehat{X}_n=\frac{(\lambda-\mu)N(N-1)-r((N-1)-kp)}{\lambda(N-1)+kpr}.$$

Hence, as before, we show $\widehat{X}_n$ is globally stable for

$$R_0=\frac{(\lambda(N-1)+kpr)N}{(\mu N+r(1+kp))(N-1)}>1:$$

Given

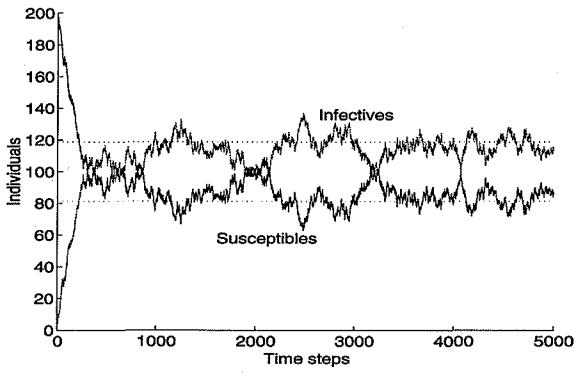

Figure 3.0.4: An example *SIS* contact-tracing simulation ($S_0 = 99$, $X_0 = 1$, $\lambda = 1$, $\mu = .4$, $r = .75$, $k = 3$, $p = .35$; using sistrace.m, Appendix p. 435), with the equilibria, $\widehat{S}_n = 81.2$ and $\widehat{X}_n = 118.8$ graphed with dotted lines.

$$X_0 < \widehat{X}_n,$$

we have

$$\begin{array}{rrcl} & X_0 & < & \frac{(\lambda-\mu)N(N-1)-r((N-1)-kp)}{\lambda(N-1)+kpr} \\ \Longrightarrow & \lambda X_0(N-1)+kprX_0 & < & (\lambda-\mu)N(N-1)-r((N-1)-kp) \\ \Longrightarrow & 0 & < & (N-1)[\lambda(N-X_0)-\mu N-r]-kpr(X_0-1) \\ \Longrightarrow & 0 & < & \lambda(N-X_0)-\mu N-r\left(1+kp\frac{X_0-1}{N-1}\right) \\ \Longrightarrow & 0 & < & \frac{\lambda(N-X_0)-\mu N-r\left(1+kp\frac{X_0-1}{N-1}\right)}{\lambda(N-X_n)+\mu N+r}. \end{array}$$

Reversing the inequalities, we see that for $R_0 > 1$, all X_0 tend toward $\widehat{X}_n$. To show that $R_0 < 1$ creates a globally stable disease-free equilibrium we use the same method. While it is difficult to ascertain from the equations how effective a policy like contact tracing could be when in effect, the expressions for $\widehat{X}_n$ and R_0 can give health professionals who have estimates for λ and μ a way to determine what k, p, and r will be required to prevent or erradicate a developing disease.

4 SIS Model with Non-constant Populations

To further explore the use of urns as realistic epidemic model, we begin examining urn models with non-constant populations. We present three models of this type, followed by the combination of the three. None of the following

SIS non-constant population models employ vaccination; rather, they are presented as the preliminary steps of further, more complicated research in epidemics via urn models.

4.1 Vital Statistics

We begin our study of non-constant populations in urn models by jumping directly to a model that involves a birth rate η, a natural death rate δ, and a disease-related death rate σ. We assume both susceptibles and infectives produce new individuals at the same rate, all births to susceptibles lead to new susceptibles, and all births to infectives lead to new infectives. We will see that the final equilibrium does not depend directly on the rate at which new susceptibles enter the system, so a variation on this model that either employs different susceptible and infective birth rates or changes the assumption that all births to infectives create new infectives could easily be analyzed using a similar approach.

The most obvious differences between this system and all others we have studied thus far are there are many more events that can occur and the total population in the urn is now another random variable N_n. We must include a few additional assumptions in the model with vital statistics: births to infected individuals result in the addition of infected individuals to the population; births to susceptible individuals result in the addition of susceptible individuals to the population; all individuals have the same per-capita reproductive rate, regardless of their infective state. By including both δ and σ in the system, our solution will include solutions for both the case when the per-capita death rate is affected by the infection and for the case when the per-capita death rate of infectives is equal to the per-capita death rate of susceptibles (the latter is found by letting $\sigma = 0$).

$$\begin{aligned}
\text{Recovery rate} &= \mu X_n \\
\text{Infection rate} &= \frac{\lambda X_n (N_n - X_n)}{N_n} \\
\text{Infected birth rate} &= \eta X_n \\
\text{Susceptible birth rate} &= \eta (N_n - X_n) \\
\text{Infectives' natural death rate} &= \delta X_n \\
\text{Susceptibles' natural death rate} &= \delta (N_n - X_n) \\
\text{Disease-related death rate} &= \sigma X_n
\end{aligned}$$

Let

$$\begin{aligned}
\text{B} &= \text{the event that the next occurrence is an infective birth} \\
\text{ND} &= \text{the event that the next occurrence is an infectives' natural death} \\
\text{DRD} &= \text{the event that the next occurrence is a disease-related death}
\end{aligned}$$

We begin to look for $\widehat{X}_n$ by determining an expression for $E[X_{n+1}|X_n]$:

$$\begin{aligned}
E[X_{n+1}|X_n] &= X_n + (P[\text{Infec}] + P[\text{B}])\,(1) + (P[\text{Rec}] + P[\text{ND}] + P[\text{DRD}])\,(-1) \\
&= X_n + \frac{-\mu X_n + \frac{\lambda X_n (N_n - X_n)}{N_n} + \eta X_n - \delta X_n - \sigma X_n}{\mu X_n + \frac{\lambda X_n (N_n - X_n)}{N_n} + \eta X_n + \eta (N_n - X_n) + \delta N_n + \sigma X_n} \\
&= X_n + \frac{-\mu N_n + \lambda (N_n - X_n) + \eta N_n - \delta N_n - \sigma N_n}{\mu N_n + \lambda (N_n - X_n) + \eta \frac{N_n^2}{X_n} + \delta \frac{N_n^2}{X_n} + \sigma N_n}. \qquad (5)
\end{aligned}$$

To find the equilibrium, we need to solve $E[X_{n+1}|\widehat{X}_n, N_n] = \widehat{X}_n$ for $\widehat{X}_n$. But from (5), we see this holds when

$$\lambda \widehat{X}_n = -\mu N_n + \lambda N_n + \eta N_n - \delta N_n - \sigma N_n$$

and

$$\widehat{X}_n = \left(\frac{\lambda - \mu + \eta - \delta - \sigma}{\lambda} \right) N_n. \qquad (6)$$

However, we see that there is no constant $\widehat{X}_n$, as N_n is no longer constant. In order to describe the dynamics of the system, we instead define a new

random variable $Y_n = \frac{X_n}{N_n}$. From expression (6) we know that $\Delta X_n = 0$ when the number of infecteds in the system is equal to $\widehat{X}_n$. It follows that ΔY_n, defined as the expected change in X_n divided by the expected change in N_n would also equal zero for any ΔN_n. Thus, the expression $\widehat{Y}_n = \frac{\widehat{X}_n}{N_n}$ satisfies our definition for equilibria of a system. In other words, $E[Y_{n+1}|\widehat{Y}_n] = \widehat{Y}_n$. Thus, we have

$$\widehat{Y}_n = \frac{\widehat{X}_n}{N_n} = \frac{\lambda - \mu + \eta - \delta - \sigma}{\lambda}.$$

We expect the long-run dynamics of this system to force the ratio $\frac{X_n}{N_n}$ to $\widehat{Y}_n$, and we observe this in the sample simulation in figure 4.4.1. We define

$$R_0 = \frac{\lambda + \eta}{\mu + \delta + \sigma}.$$

and show stability of the disease-free and endemic equilibria for $R_0 > 1$ and $R_0 < 1$, respectively.

We know that when $R_0 > 1$,

$$\begin{aligned} E[Y_{n+1}|Y_0] &= Y_0 + \frac{-\mu Y_0 + \lambda Y_0(1 - Y_0) + \eta Y_0 - \delta Y_0 - \sigma Y_0}{\mu Y_0 + \lambda Y_0(1 - Y_0) + \eta Y_0 + \eta(1 - Y_0) + \delta + \sigma Y_0} \\ &= Y_0 + \frac{Y_0(-\mu + \lambda - \lambda Y_0 + \eta - \delta - \sigma)}{\mu Y_0 + \lambda Y_0(1 - Y_0) + \eta Y_0 + \eta(1 - Y_0) + \delta + \sigma Y_0}, \end{aligned}$$

and

$$\Delta Y_n = \frac{Y_0(-\mu + \lambda - \lambda Y_0 + \eta - \delta - \sigma)}{\mu Y_0 + \lambda Y_0(1 - Y_0) + \eta Y_0 + \eta(1 - Y_0) + \delta + \sigma Y_0}.$$

We expect the ratio of infecteds to the total population to increase when

$$-\mu + \lambda - \lambda Y_0 + \eta - \delta - \sigma > 0$$

$$\implies Y_0 < \frac{\lambda - \mu + \eta - \delta - \sigma}{\lambda} = \widehat{Y}_n,$$

and we expect the ratio of infecteds to the total population to decrease when

$$-\mu + \lambda - \lambda Y_0 + \eta - \delta - \sigma < 0 \tag{7}$$

$$\Longrightarrow Y_0 > \frac{\lambda - \mu + \eta - \delta - \sigma}{\lambda} = \widehat{Y}_n$$

Thus, $\widehat{Y}_n$ is for $R_0 > 1$.

For $R_0 < 1$, we see expression (7) is true for all Y_0. This implies that the Y_n tends towards zero for all Y_0; *i. e*, $\widehat{Y}_n = 0$ is stable for $R_0 < 1$.

4.2 IMMIGRATION

Here we wish to study the long-term effects of immigration on our previously studied SIS model. We now incorporate a constant immigration rate Λ. We assume that immigration adds individuals to only the susceptible class.

As before, we wish to study the equilibria by determining when $E[X_{n+1}|\widehat{X}_n, N_n] = \widehat{X}_n$. We have an equilibrium when

$$0 = \frac{\frac{\lambda \widehat{X}_n (N_n - \widehat{X}_n)}{N_n}}{\mu \widehat{X}_n + \frac{\lambda \widehat{X}_n (N_n - \widehat{X}_n)}{N_n} + \Lambda} - \frac{\mu \widehat{X}_n}{\mu \widehat{X}_n + \frac{\lambda \widehat{X}_n (N_n - \widehat{X}_n)}{N_n} + \Lambda}.$$

That is,

$$\widehat{X}_n = \left(\frac{\lambda - \mu}{\lambda}\right) N_n,$$

and using our definition of Y_n from the previous section, we have

$$\widehat{Y}_n = \frac{\lambda - \mu}{\lambda}.$$

Note that $\widehat{Y}_n$ is unaffected by Λ, but that $\widehat{X}_n$ will increase at a constant rate $\Lambda \left(\frac{\lambda - \mu}{\lambda}\right)$.

4.3 EMIGRATION

We now examine a simple SIS model with emigration. We assume there is a constant rate of emigration Θ, and that infectives and susceptibles have

the same rates of emigration, *i. e.*, emigration is not selective towards either infectives or susceptibles. If we define

$$\begin{aligned} \text{E} &= \text{the event that an emigration occurs next} \\ \text{EI} &= \text{the event that an emigration of an infected occurs next} \end{aligned}$$

and we remember that

$$P[\text{Emmigré is infected}] = \frac{X_n}{N_n},$$

then in addition to our usual infection and recovery rates and probabilities, we also have

$$P[E] = \frac{\Theta}{\mu X_n + \frac{\lambda X_n (N_n - X_n)}{N_n} + \Theta}$$

and

$$P[\text{EI}] = \left(\frac{X_n}{N_n}\right) \frac{\Theta}{\mu X_n + \frac{\lambda X_n (N_n - X_n)}{N_n} + \Theta}.$$

Solving for $E[X_{n+1} | \widehat{X}_n, N_n] = \widehat{X}_n$, we obtain

$$\begin{aligned} \widehat{X}_n &= \widehat{X}_n + \frac{\lambda(N_n - \widehat{X}_n) - \mu N_n - \Theta}{\mu N_n + \lambda(N_n - \widehat{X}_n) + \Theta \frac{N_n}{\widehat{X}_n}} \\ \Longrightarrow \widehat{X}_n &= \frac{(\lambda - \mu)N_n - \Theta}{\lambda} \\ \Longrightarrow \widehat{Y}_n &= \frac{\lambda - \mu}{\lambda} - \frac{\Theta}{\lambda N_n}. \end{aligned}$$

If we analyze these equations with our original assumption that Θ is positive, *i. e.*, N_n is never decreasing, we see that we have created a trivial system: for all λ, μ, and Θ, there will be a point at which $\frac{\Theta}{\lambda N_n} > \frac{\lambda - \mu}{\lambda}$, and both $\widehat{Y}_n$ and $\widehat{X}_n$ will be pushed to zero. However, if we say that Θ can be negative (people are coming into the system at a constant rate, with the ratio of infectives to susceptibles in the inflow equal to the ratio of infectives to susceptibles already in the population), we see that $\widehat{Y}_n = \frac{\lambda - \mu}{\lambda}$ becomes a stable equilibrium, as the $\frac{\Theta}{\lambda N_n}$ term goes to zero as N_n goes to infinity.

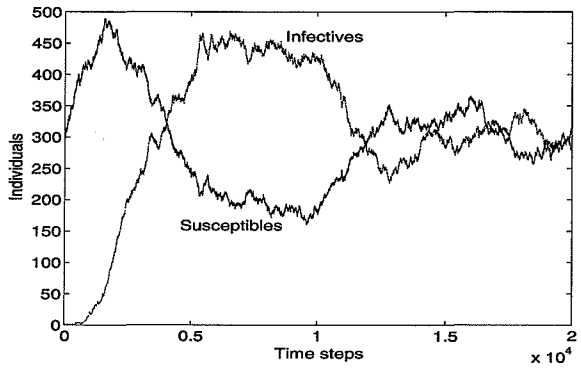

Figure 4.4.1: An urn model *SIS* simulation incorporating vital statistics, immigration, and emigration ($S_0 = 299$, $I_0 = 1$, $\lambda = 1.25$, $\mu = .5$, $\eta = .5$, $\delta = .35$, $\sigma = .25$, $\Lambda = 3$, $\Theta = 1$; using sisvitals.m, Appendix p. 434).

4.4 The complete SIS model without vaccination: vital statistics, immigration, and emigration

We combine the results of the previous three sections and find an expression for $\widehat{Y}_n$ that predicts the infective to total population ratio for any given λ, μ, η, δ, σ, Λ, and Θ. Remembering all of the assumptions from sections (4.1), (4.2), and (4.3), we can write

$$\widehat{Y}_n = \frac{\widehat{X}_n}{N_n} = \frac{\lambda - \mu + \eta - \delta - \sigma}{\lambda} - \frac{\Theta}{\lambda N_n}$$

and

$$R_0 = \frac{\lambda + \eta}{\mu + \delta + \sigma}.$$

The relative ease by which the urn model facilitates the addition of new parameters is clearly evidenced here and should be noted.

5 Epidemic Urn Models with Aquired Immunity

In these models, we must again introduce a third ball color into our urn system. We will again use blue balls, but this time they represent the people in the population who have recovered from the disease and cannot be

infected. However, this natural immunity they have acquired can be either temporary or permanent, and after a certain amount of time the blue balls may turn into white balls again and rejoin the susceptible class. The two models we will examine that incorporate this acquired immunity class are the Susceptible-Infective-Recovered (SIR) model and the Susceptible-Infective-Recovered-Susceptible ($SIRS$) model. The $SIRS$ model assumes that a recovered individual obtains a temporary immunity, lost by the recovered class at an average per-capita rate γ. The SIR model, on the other hand, assumes that anyone recovering from the disease is granted permanent immunity.

It is intuitive that there is no endemic equilibrium for the SIR system with constant population and neither births nor deaths, because if there are any black balls in the population after a step n, then after the $(n+1)th$ step, either the number of white balls or the number of blue balls will have gone up, and since infection and recovery are the only ways for the white and blue balls, respectively, to change their numbers, their numbers are constantly changing until all of the balls are either white or blue. At this point, events no longer occur, as no more infections or recoveries are occurring in the system. We give this as our purpose for presenting the SIR model immediately with vital statistics, rather that presenting the trivial constant population case first. We follow this with the $SIRS$ model with vital statistics, though we can find the solution for the constant population $SIRS$ model by allowing γ to be zero.

5.1 SIR Model with Vital Statistics

Using the constants from the SIS model with vital statistics (section 4) and the new random variable R_n, representing the number of recovered individuals (blue balls) in the urn after the n^{th} step, we present the following:

$$\begin{aligned}
\text{Recovery rate} &= \mu X_n \\
\text{Infection rate} &= \frac{\lambda X_n (N_n - X_n - R_n)}{N_n} \\
\text{Birth rates} &= \eta X_n, \quad \eta(N_n - X_n) \\
\text{Nat. death rates} &= \delta X_n, \quad \delta(N_n - X_n - R_n), \quad \delta R_n \\
\text{D.-R. death rate} &= \sigma X_n.
\end{aligned}$$

At equilibrium,

$$\widehat{X}_n = E[X_{n+1}|\widehat{X}_n, \widehat{R}_n] = \widehat{X}_n + \frac{\lambda(N_n - \widehat{X}_n - \widehat{R}_n) - \mu N_n - \delta N_n - \sigma N_n + \eta N_n}{\lambda(N_n - \widehat{X}_n - \widehat{R}_n) + \mu N_n + \frac{\delta N_n^2}{\widehat{X}_n} + \sigma N_n + \frac{\eta N_n^2}{\widehat{X}_n}}.$$

Then,

$$\begin{aligned} 0 &= (\lambda - \mu - \delta - \sigma + \eta)N_n - \lambda\widehat{X}_n - \lambda\widehat{R}_n \\ \implies \widehat{X}_n &= \frac{(\lambda - \mu - \delta - \sigma + \eta)N_n}{\lambda} - \widehat{R}_n, \end{aligned} \tag{8}$$

and

$$\begin{aligned} \widehat{R}_n = E[R_{n+1}|\widehat{X}_n, \widehat{R}_n] &= \widehat{R}_n + \frac{\mu N_n - \delta\widehat{R}_n(\frac{N_n}{\widehat{X}_n})}{\lambda(N_n - \widehat{X}_n - \widehat{R}_n) + \mu N_n + \frac{\delta N_n^2}{\widehat{X}_n} + \sigma N_n + \frac{\eta N_n^2}{\widehat{X}_n}} \\ \implies 0 &= \mu N_n - \delta\widehat{R}_n(\frac{N_n}{\widehat{X}_n}) \\ \implies \widehat{R}_n &= \frac{\mu}{\delta}\widehat{X}_n. \end{aligned} \tag{9}$$

Therefore, if we combine (8) and (9) we get

$$\widehat{X}_n = \left(\frac{\lambda - \mu - \delta - \sigma + \eta}{\lambda}\right)\left(\frac{\delta}{\delta + \mu}\right)N_n$$

and

$$\widehat{R}_n = \left(\frac{\lambda - \mu - \delta - \sigma + \eta}{\lambda}\right)\left(\frac{\mu}{\delta + \mu}\right)N_n.$$

Thus, if we define Z_n as the ratio of the number of blue balls to the total number of balls in the urn, $\frac{R_n}{N_n}$, we have

$$\widehat{Y}_n = \left(\frac{\lambda - \mu - \delta - \sigma + \eta}{\lambda}\right)\left(\frac{\delta}{\delta + \mu}\right) \tag{10}$$

and

$$\widehat{Z}_n = \left(\frac{\lambda - \mu - \delta - \sigma + \eta}{\lambda}\right)\left(\frac{\mu}{\delta + \mu}\right). \tag{11}$$

We find that expressions (10) and (11) are positive ($\widehat{Y}_n$ and $\widehat{R}_n$ exist) for $R_0 > 1$ if we define

$$R_0 = \frac{\lambda + \eta}{\mu + \delta + \sigma}.$$

5.2 *SIRS* Model with Vital Statistics

As in the *SIR* model, we assume all births to infectives lead to the addition of infectives to the population, and that all births to either susceptible or recovered individuals lead to the addition of susceptibles to the population. Given γ as the rate at which recovered patients return to the susceptible class, we have

$$\begin{aligned}
\text{Recovery rate} &= \mu X_n \\
\text{Infection rate} &= \frac{\lambda X_n(N_n - X_n - R_n)}{N_n} \\
\text{Loss of immunity rate} &= \gamma R_n \\
\text{Birth rates} &= \eta X_n, \quad \eta(N_n - X_n) \\
\text{Nat. death rates} &= \delta X_n, \quad \delta(N_n - X_n - R_n), \quad \delta R_n \\
\text{D.-R. death rate} &= \sigma X_n.
\end{aligned}$$

At equilbrium,

$$\widehat{X}_n = E[X_{n+1}|\widehat{X}_n, \widehat{R}_n] = \widehat{X}_n + \frac{\frac{\lambda X_n(N_n - X_n - R_n)}{N_n} - \mu X_n + \eta X_n - \delta X_n - \sigma X_n}{\mu X_n + \frac{\lambda X_n(N_n - X_n - R_n)}{N_n} + \eta N_n + \delta N_n + \sigma X_n} \quad \text{and}$$

$$\widehat{R}_n = E[R_{n+1}|\widehat{X}_n, \widehat{R}_n] = \widehat{R}_n + \frac{\mu \widehat{X}_n - \gamma \widehat{R}_n - \delta \widehat{R}_n + \eta \widehat{R}_n}{\mu X_n + \frac{\lambda X_n(N_n - X_n - R_n)}{N_n} + \eta N_n + \delta N_n + \sigma X_n}.$$

Solving these two equations, we obtain

$$\begin{aligned}
\widehat{X}_n &= \left(\tfrac{\lambda - \mu - \sigma - \delta + \eta}{\lambda}\right)\left(\tfrac{\gamma + \delta}{\gamma + \delta + \mu}\right) N_n, \quad \text{and} \\
\widehat{R}_n &= \left(\tfrac{\lambda - \mu - \sigma - \delta + \eta}{\lambda}\right)\left(\tfrac{\mu}{\gamma + \delta + \mu}\right) N_n.
\end{aligned}$$

Therefore,

$$\begin{aligned}
\widehat{Y}_n &= \left(\frac{\lambda - \mu - \sigma - \delta + \eta}{\lambda}\right)\left(\frac{\gamma + \delta}{\gamma + \delta + \mu}\right) \\
\widehat{Z}_n &= \left(\frac{\lambda - \mu - \sigma - \delta + \eta}{\lambda}\right)\left(\frac{\mu}{\gamma + \delta + \mu}\right).
\end{aligned}$$

Finally, we see that

$$R_0 = \frac{\lambda + \eta}{\mu + \sigma + \delta}.$$

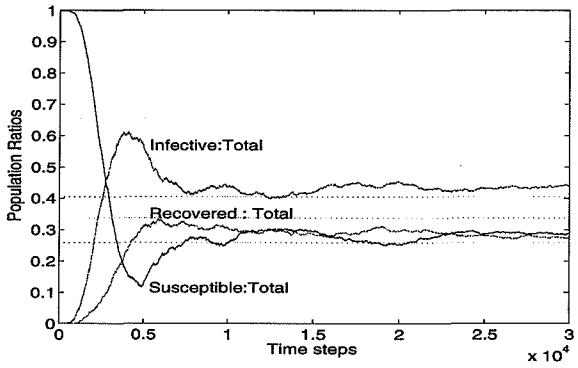

Figure 5.2.1: A plot of the ratios S_n:N_n, Y_n, and Z_n for an $SIRS$ urn model simulation ($S_0 = 499$, $X_0 = 1$, $\lambda = 3$, $\mu = 1$, $\eta = .02$, $\delta = .01\bar{3}$, $\sigma = .\bar{3}$, $\gamma = .08\bar{3}$; using sirsvitals.m, Appendix p. 441) with their expected equilibria ratio values.

It is interesting to note that our value for R_0 is the same in both our SIR and $SIRS$ models. But after careful inspection, we can see that whether or not a black ball produces another black ball is independent of γ, and therefore γ should play no role when we go from studying the SIR model to the $SIRS$ model. If we also compare the $\widehat{Y}_n$ and $\widehat{Z}_n$ of the two models without vital statistics (most importantly, $\delta = 0$), we observe that, as expected, $\widehat{Y}_n$ in the SIR model is zero, while in the $SIRS$ model, it still exists.

As before, we find stability for the disease-free equilibrium for $R_0 < 1$, but we do not present proof of stability for the endemic equilibrium with $R_0 > 1$.

6 Conclusions

We have shown that analyzing the SIS, SIR, and $SIRS$ models with an urn model is a straightforward, simple approach to studying the long-range dynamics of these systems. Without the use of differential equations or stochastic simulations, we have calculated $\widehat{X}_n$ and R_0 for a number of different systems, some of which have not been previously studied with other models. Proving stability in these models also involves only the use of a simple set of inequalities, unlike the better-studied methods. Thus, this type of approach could be used as an educational tool to describe and study epidemiological phenomena by students and teachers who lack the background or the exper-

tise to study the systems via the deterministic or stochastic approaches.

As a teaching tool, the urn model is appropriate because it employs the simple concepts of the probability of drawing a certain combination of colored balls, yet provides powerful insight into the workings of epidemics and disease-prevention policies. The simulations (see Appendix) can also provide students with a visual interpretation of what is occurring, showing that their assumptions about $\widehat{X}_n$, R_0, and the tendencies towards the equilibria hold. Also important in this model is the ease with which one can add more parameters (vital statistics, immigration, emigration, class-related births and deaths, etc.) and still obtain a solvable system of equations for the equilibria.

Within the urn models themselves, we also obtained a number of interesting results. After determining the equilibria for the simple SIS model, we solved for the equilibria of the three vaccination policies. We showed that the equilibrium of the leaky vaccine is always larger than that of the all or nothing vaccine; therefore, an all-or-nothing vaccine is a more efficient and more effective epidemic controller. The universally-stable disease-free equilibrium for the ring vaccination, SIS model shows that a vaccination policy based on the discovery of infectives may be efficient, if the screening rate is large enough to push the X_n towards the zero equilibrium in a reasonable amount of time.

The equation we obtained for the equilibrium and R_0 of a system undergoing contact tracing is significant in that, while it does not show us that there is always a disease-free equilibrium, it does give us a starting point for implementing this type of policy. For a disease with a known λ and μ, we can attempt to adjust k, r, and p, as much as is within our control in order to force R_0 below 1.

Finally, the ease with which the urn model could be manipulated to handle vital statistics, immigration, and emigration, and to incorporate a recovered class was amazing. Though the stabilities of the SIR and $SIRS$ models have yet to be proven, obtaining expressions for the two models' equilibria and R_0 values was as simple as determining what events were occurring and at what rates they were occurring.

7 Future Research

Further work must be done before the urn model can be widely used as a standard epidemiological tool. Though proving the stability of the equilibria in a one-dimensional model (SIS, for example) has not proven difficult, proving the stability for a two-dimensional model like SIR is more complicated. The next step in epidemiological urn model research would be to determine a method by which this type of stability could be determined in models of two- and higher dimensions.

Our urn model vaccination policies would better describe real-life policies if they included some vital dynamics, immigration, and/or emigration. This would especially make the role of a ring vaccination policy in an epidemic more clear, as it would allow for removal from the S_v class, perhaps preventing the disease-free equilibrium from always being stable.

Finally, this preliminary research in biological urn models may lead to research demonstrating that any number of different events or biological phenomena may be systematically analyzed and better understood using this type of approach. Though stability cannot yet be proven for more complex systems, urn models may be well suited to model any phenomenon in which you can assume average group dynamics for a discrete number of subgroups of a population who exhibit behaviors that are either related to the numbers of individuals in the group or are constant. Many biological problems deal with systems of this type, and they may soon prove to be more simply explained and analyzed for average qualitative dynamics via urn models.

8 Acknowledgements

This study was supported by the following institutions and grants: National Science Foundation (NSF Grant DMS 9977919); National Security Agency (NSA Grant MDA 9049710074); Presidential Faculty Fellowship Award (NSF Grant DEB 9724850) and Presidential Mentoring Award (Grant HRD 9724850) to Carlos Castillo-Chavez; the office of the provost of Cornell University; and the Intel Technology for Education 2000 Equipment Grant. Special thanks to Ted Greenwood of the Sloan Foundation; and to our advisor, Car-

los Hernández, for presenting the idea for this project, as well as for his guidance and support.

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Appendix – MATLAB[1] files

sis.m

```
function sis(filename,ap,TT,s0,i0,l,u)
% sis(filename,ap,TT,s0,i0,l,u)
% Simulates a simple SIS epidemic model with constant population
% s0 is the initial susceptible population
% i0 is the initial infected population
% l is the individual contact rate
% u is the individual recovery rate
% TT is the number of steps to run this time
% ap = 0 for new file; ap = 1 to append an old one
% filename is the name of the file to create or to be appended
% only filename, ap, and TT parameters are always needed in order to append
%   a file;
% all other parameters will be ignored unless ap = 0
initrnd;
id=1;
if ap==0
Nused = [s0,i0,0,l,u;0,0,0,0,id;0,0,0,0,0;0,i0,0,s0,0];
save(filename,'Nused')
end
[t t0 T s0 i0 iu0 iv0 su0 sv0 r k u l B f]=apinit(filename,id,TT);
load(filename,'Nused')
S=s0; %set initial values
I=i0;
t=t0;
%set initial time
Nplot=[t,I,0,S,0]; %create matrix to remember points by making first entry
while (t<=T) & (I>0);
N=S+I;
t=t+1; %calculate next time
Nplot=[Nplot; [t,I,0,S,0]];event=wheel([l*S*I/N,u*I]);
if event==1
S=S-1;
I=I+1; %infection
else
S=S+1;
I=I-1; %recovery
end
Nplot=[Nplot;[t,I,0,S,0]]; %next point
end
Nused=[Nused;Nplot];
Nsize=size(Nused);
```

```
if Nused(3,2)==0
Nadd=[zeros(2,5);0,T,0,0,0;zeros(Nsize(1)-3,Nsize(2))];
else
Nadd=[zeros(2,5);T,T,0,0,0;zeros(Nsize(1)-3,Nsize(2))];
end
Nused=Nused+Nadd;
save(filename,'Nused')
```

sisleaky.m

```
function sisleaky(filename,ap,TT,s0,iv0,iu0,f,B,l,u)
% sisleaky(filename,ap,TT,s0,iv0,iu0,f,B,l,u)
% Simulates a simple SIS epidemic model with constant population and
%   application of a leaky vaccine
% s0 is the initial total susceptible population
% iv0 is the initial infected, vaccinated population
% iu0 is the initial infected, non-vaccinated population
% f is the proportion of the susceptibles who are vaccinated
% B is the probability that the vaccine will not work, i.e.  B = (1 - Vaccine
%   Efficacy)
% l is the individual contact rate
% u is the individual recovery rate
% TT is the number of events that will occur this time
% ap = 0 for new file; ap = 1 to append an old one
% filename is the name of the file to create or to be appended
% only filename, ap, and TT parameters are always needed in order to append
a file;
% all other parameters will be ignored unless ap = 0 initrnd;
id=3;
if ap==0
Nused=[s0,iu0,iv0,l,u;f,B,0,0,id;0,0,0,0,0;0,iu0,iv0,(1-f)*s0,f*s0];
save(filename,'Nused')
end
[t t0 T s0 i0 iu0 iv0 su0 sv0 r k u l B f L]=apinit(filename,id,TT);
load(filename,'Nused')
S=Nused(1,1)*(1-f*B); %set initial values (constants)
SV=Nused(1,1)*f;
SU=Nused(1,1)*(1-f);
Iv=iv0; %set initial values (variables)
Iu=iu0;
Sv=sv0;
Su=su0;
t=t0; %set initial time
Nplot=[t,Iu,Iv,Su,Sv]; %create matrix to remember points by making first entry
while (t<T+1) & (Iv+Iu>0) & (Sv>0) & (Su>0);
```

```
Itot=Iv+Iu;
N=Su+Iu+Sv+Iv;
t=t+1;
Nplot=[Nplot; [t,Iu,Iv,Su,Sv]]; %event does not occur until t, so N remains
constant until t
event=wheel([l*Itot*(SU-Iu)/N,l*Itot*(SV-Iv)/N,u*Iu,u*Iv]);
if event==1
Su=Su-1;
Iu=Iu+1; %infection of unvaccinated individual elseif event==2
infif=wheel([B,1-B]);
if infif==1 %with probability B . .  .
Sv=Sv-1;
Iv=Iv+1; %an infection occurs in a vaccinated individual
end
elseif event==3
Su=Su+1;
Iu=Iu-1; %recovery of unvaccinated individual
else
Sv=Sv+1;
Iv=Iv-1; %recovery of vaccinated individual
end
Nplot=[Nplot;[t,Iu,Iv,Su,Sv]]; %next point
end
Nused=[Nused;Nplot];
Nsize=size(Nused);
Nadd=[zeros(2,5);0,T,0,0,0;zeros(Nsize(1)-3,Nsize(2))];
Nused=Nused+Nadd;
save(filename,'Nused')
```

sisring.m

```
function sisring(filename,ap,TT,s0,i0,k,B,l,u,r)
%sisring(filename,ap,TT,s0,i0,k,B,l,u,r)
%Simulates a simple SIS model
% s0 is the initial total susceptible population
% iv0 is the initial infected, vaccinated population
% iu0 is the initial infected, non-vaccinated population
% f is the proportion of the susceptibles who are vaccinated
% B is the probability that the vaccine will not work, i.e.  B = (1 - Vaccine
Efficacy)
% l is the individual contact rate
% u is the individual recovery rate
% TT is the number of events that will occur this time
% ap = 0 for new file; ap = 1 to append an old one
% filename is the name of the file to create or to be appended
% only filename, ap, and TT parameters are always needed in order to append
```

```
%   a file;
% all other parameters will be ignored unless ap = 0
initrnd;
id=4;
if ap==0
ratio=u/l;
Nused=[s0,i0,0,l,u;0,B,r,k,id;0,0,0,0,0;0,i0,ratio,s0,0];
save(filename,'Nused')
end
[t t0 T s0 i0 iu0 iv0 su0 sv0 r k u l B f]=apinit(filename,id,TT);
ratio=u/l;
load(filename,'Nused')
I=i0; %set initial values (variables)
Sv=sv0;
Su=su0;
N=su0+sv0+i0;
t=t0; %set initial time
Nplot=[t,I,ratio,Su,Sv]; %create matrix to remember points by making first entry
while (t<T) & (I>0) & (Su>0);
t=t+1;
Nplot=[Nplot;[t,I,ratio,Su,Sv]];event=wheel([l*I*Su/N,u*I,r*I/N]);
if event==1
Su=Su-1;
I=I+1; %infection of unvaccinated individual
elseif event==2
Su=Su+1;
I=I-1; %an infection occurs in an unvaccinated individual
elseif event==3
for ring =1:k
ring;
type=wheel([Su/N,(N-Su)/N]);
if type==1 %if the person in the ring is an non-vaccinated, susceptible individual
vaccine=wheel([1-B,B]);
if vaccine==1 % try to vaccinate her; it will work 1-B of the time
Su=Su-1;
Sv=Sv+1; %vaccination with all part of an all-nothing vaccine
end
end
end
end
Nplot=[Nplot;[t,I,ratio,Su,Sv]]; %next point
end
Nused=[Nused;Nplot];
Nsize=size(Nused);
if Nused(3,2)==0
```

```
Nadd=[zeros(2,5);0,T,0,0,0;zeros(Nsize(1)-3,Nsize(2))];
else
Nadd=[zeros(2,5);T,T,0,0,0;zeros(Nsize(1)-3,Nsize(2))];
end
Nused=Nused+Nadd;
save(filename,'Nused')
```

sisvitals.m

```
function sisvitals(filename,ap,TT,s0,i0,l,u,n,d,s,L,Th)
%sisvitals(filename,ap,TT,s0,i0,l,u,n,d,s,L,Th)
%Simulates an SIS model with vital statistics, immigration, and emigration
% s0 is the initial total susceptible population
% iv0 is the initial infected, vaccinated population
% iu0 is the initial infected, non-vaccinated population
% l is the individual contact rate
% u is the individual recovery rate
% n is the birth rate
% d is the natural death rate
% s is the disease-related death rate
% L is the immigration rate
% Th is the emigration rate
% TT is the number of events that will occur this time
% ap = 0 for new file; ap = 1 to append an old one
% filename is the name of the file to create or to be appended
% only filename, ap, and TT parameters are always needed in order to append
%   a file;
% all other parameters will be ignored unless ap=0
initrnd;
id=8;
if ap==0
Nused=[s0,i0,0,l,u;0,0,0,0,id;0,0,L,0,0;n,d,s,0,Th;0,i0,0,s0,0];
save(filename,'Nused')
end
[t t0 T s0 i0 iu0 iv0 su0 sv0 r k u l B f L p n d s Th]=apinit(filename,id,TT);
load(filename,'Nused')
I=i0; %set initial values (variables)
S=s0;
N=s0+i0;
t=t0; %set initial time
Nplot=[t,I,0,S,0]; %create matrix to remember points by making first entry
while (t<T) & (I>0) & (S>0);
t=t+1;
Nplot=[Nplot;[t,I,0,S,0]];event=wheel([l*I*S/N,u*I,n*I,n*S,d*I,d*S,s*I]);
if event==1
S=S-1;
```

```
I=I+1; %infection
elseif event==2
S=S+1;
I=I-1; %a recovery
elseif event==3
I=I+1;
elseif event==4
S=S+1;
elseif event==5
I=I-1;
elseif event==6
S=S-1;
elseif event==7
I=I-1;
end
Nplot=[Nplot;[t,I,0,S,0]]; %next point
end
Nused=[Nused;Nplot];
Nsize=size(Nused);
Nadd=[zeros(2,5);0,T,0,0,0;zeros(Nsize(1)-3,Nsize(2))];
Nused=Nused+Nadd;
save(filename,'Nused')
```

sistrace.m

```
function sistrace(filename,ap,TT,s0,i0,k,p,l,u,r)
%sistrace(filename,ap,TT,s0,i0,k,p,l,u,r)
%Simulates a simple SIS model with contact tracing to one degree
% s0 is the initial total susceptible population
% iv0 is the initial infected, vaccinated population
% iu0 is the initial infected, non-vaccinated population
% f is the proportion of the susceptibles who are vaccinated
% B is the probability that we find each traced person
% l is the individual contact rate
% u is the individual recovery rate
% k is the number of people traced to
% TT is the number of events that will occur this time
% ap = 0 for new file; ap = 1 to append an old one
% filename is the name of the file to create or to be appended
% only filename, ap, and TT parameters are always needed in order to append
%   a file;
% all other parameters will be ignored unless ap=0
initrnd;
id=5;
if ap==0
```

```
Nused=[s0,i0,0,l,u;0,0,r,k,id;0,0,0,p,0;0,i0,0,s0,0];
save(filename,'Nused')
end
[t t0 T s0 i0 iu0 iv0 su0 sv0 r k u l B f p]=apinit(filename,id,TT);
load(filename,'Nused')
I=i0; S=s0;
N=s0+i0;
t=t0; %set initial time
Nplot=[t,I,0,S,0]; %create matrix to remember points by making first entry
while (t<T) & (I>0) & (S>0);
t=t+1;
Nplot=[Nplot;[t,I,0,S,0]];%event does not occur until t, so N remains constant
until t
event=wheel([l*I*S/N,u*I,r*I/N]);
if event==1
S=S-1;
I=I+1; %infection of unvaccinated individual
elseif event==2
S=S+1;
I=I-1; %an infection occurs in an unvaccinated individual
elseif event==3
for trace=1:k
find=wheel([p,1-p]);
if find==1 %if the traced individual is found
type=wheel([(I-1)/(N-1),S/(N-1)]);
if type==1 %if the traced inidividual is infected
I=I-1; %cure her
S=S+1;
end
end
end
I=I-1; %cure the initial infected
S=S+1;
end
Nplot=[Nplot;[t,I,0,S,0]]; %next point
end
Nused=[Nused;Nplot];
Nsize=size(Nused);
Nadd=[zeros(2,5);0,T,0,0,0;zeros(Nsize(1)-3,Nsize(2))];
Nused=Nused+Nadd;
save(filename,'Nused')
```

sisplot.m

```
function [k1,k2]=sisplot(filename,fig,Trange,b)
%for sisimm, sis, sisallornothing, sisleaky, sisring, or sistrace
```

```
%Trange is a vector [T0,Tf]; Use [0,0] to plot the entire matrix
% filename is the name of the file that was run by the sis . . . program
% fig is the number of the figure where the plot will be
% b is an option for some graphs, see code for details
% The vector [k1,k2] gives the rows where the values T0 and Tf reside.
load(filename,'Nused')
s0=Nused(1,1);
if Nused(1,3)==0
i0=Nused(1,2);
else
iu0=Nused(1,2);
iv0=Nused(1,3);
end
l=Nused(1,4);
u=Nused(1,5);
f=Nused(2,1);
B=Nused(2,2);
r=Nused(2,3);
k=Nused(2,4);
id=Nused(2,5);
T0=Nused(3,1);
Tf=Nused(3,2);
L=Nused(3,3);
p=Nused(3,4);
n=Nused(4,1);
d=Nused(4,2);
s=Nused(4,3);
Th=Nused(4,5);
if id==4
figure(fig);
H=xlabel('Time steps');
HH=ylabel('Individuals');
legend('Unvaccinated Susceptibles','Total Susceptibles','Infectives','Vaccinated
Susceptibles',2)
set(H,'FontSize',12);
set(HH,'FontSize',12);
hold on;
elseif id==5
figure(fig);
H=xlabel('Time steps');
HH=ylabel('Individuals');
legend('Susceptibles','Infectives')
set(H,'FontSize',12);
set(HH,'FontSize',12);
hold on;
```

```
elseif id==3
figure(fig)
H=xlabel('Time steps');
HH=ylabel('Individuals');
legend('Susceptibles','Infectives')
set(H,'FontSize',12);
set(HH,'FontSize',12);
hold on;
figure(fig+1)
H=xlabel('Time steps');
HH=ylabel('Individuals');
legend('Vaccinated Infectives','Unvaccinated Infectives')
set(H,'FontSize',12);
set(HH,'FontSize',12);
end
if (Trange(1)==0) & (Trange(2)==0)
Nsize=size(Nused);
Nrows=Nsize(1);
if id==8
Ntop=-95;
Nbottom=4;
else
Ntop=-96;
Nbottom=3;
end
else
for k=4:size(Nused)
if Trange(1)==Nused(k,1)
Ntopp=k;
k1=k
end
if Trange(2)==Nused(k,1)
Nbottomm=k;
k2=k
end
end
Nrows=Nbottomm-Ntopp+1;
Ntop=Ntopp-100;
Nbottom=Ntopp+99;
end
Ntimes=ceil(Nrows/100);
Nrem=rem(Nrows,100);
for Nrep = 1:Ntimes
if (Nrep<Ntimes)
Ntop=Ntop+100;
```

```
Nbottom=Nbottom+100;
else
Ntop=Ntop+100;
Nbottom=(Nrep-1)*100+Nrem;
end
Nsize=size(Nused);
if Nbottom>Nsize(1)
Nbottom=Nsize(1);
end
Nplot=Nused(Ntop:Nbottom,:);
if id==1 %% sis
figure(fig) %this figure will hold the time plots
plot(Nplot(:,1),Nplot(:,4)); %plot susceptibles with a blue line
hold on; %superimposes time plots
plot(Nplot(:,1),Nplot(:,2),'-r');%plots infecteds with a red line
elseif id==2 %% sisallornothing
if b==1
figure(fig) %this figure will hold the time plots
plot(Nplot(:,1),Nplot(:,4)+Nplot(:,5)); %plot total susceptibles with a blue
line
hold on; %superimposes time plots
plot(Nplot(:,1),Nplot(:,2)+Nplot(:,3),'-r') %plots total infecteds with a red
line
elseif b==2
figure(fig) %this figure will plot Itot, Iv, and Iu
plot(Nplot(:,1),Nplot(:,2)+Nplot(:,3),'-r')
hold on;
plot(Nplot(:,1),Nplot(:,2),'-g') %vaccinateds are green
plot(Nplot(:,1),Nplot(:,3),'-y'); %unvaccinateds are yellow
end
elseif id==3 %% sisleaky
figure(fig) %this figure will hold the time plots
plot(Nplot(:,1),Nplot(:,4)+Nplot(:,5),'-b'); %plot total susceptibles with a
blue line
hold on; %superimposes time plots
plot(Nplot(:,1),Nplot(:,2)+Nplot(:,3),'-r')%plots total infecteds with a red
line
figure(fig+1) plot(Nplot(:,1),Nplot(:,2)+Nplot(:,3),'-r')
hold on;
plot(Nplot(:,1),Nplot(:,3),'-g') plot(Nplot(:,1),Nplot(:,2),'-y'); elseif id==4
%% sisring
figure(fig) %this figure will hold the time plots
plot(Nplot(:,1),Nplot(:,4),'-y',Nplot(:,1),Nplot(:,4)+Nplot(:,5),
'b',Nplot(:,1),Nplot(:,2),'-r',Nplot(:,1),Nplot(:,5),':g'); %plot total susceptibles
with a blue line
```

```
hold on; %superimposes time plots
elseif id==5 %% sistrace
figure(fig)
plot(Nplot(:,1),Nplot(:,4),'-b')
hold on;
plot(Nplot(:,1),Nplot(:,2),'-r')
elseif id==6 %% sisimm
if b==1
figure(fig) %this figure will hold the time plots
plot(Nplot(:,1),Nplot(:,2)+Nplot(:,3)); %plot total population with a blue line
hold on; %superimposes time plots
plot(Nplot(:,1),Nplot(:,2),'-r')%plots infecteds with a red line
plot(Nplot(:,1),Nplot(:,4),'-g')%plots susceptibles with a green line
plot(Nplot(:,1),Nplot(:,3).*(Nplot(:,2)+Nplot(:,4)),'-y')%plots expected value
of infecteds
plot(Nplot(:,1),Nplot(:,5),'-b')%plots expected value of susceptibles
title('SIS Urn Model Simulation with Immigration, Population Values');
elseif b==2
figure(fig) %this figure will plot the ratios I/N and S/N
plot(Nplot(:,1),Nplot(:,2)/(Nplot(:,2)+Nplot(:,4)),'-r') %Infected ratio is
red
hold on;
plot(Nplot(:,1),Nplot(:,4)/(Nplot(:,2)+Nplot(:,4)),'-g') %Susceptible ratio
is green
plot(Nplot(:,1),Nplot(:,3),'-y'); %expected ratio I:N is yellow
title('SIS Urn Model Simulation with Immigration, Population Ratios')
elseif b==3
figure(fig) %This figure will hold two subplots, one with the Total and Inf,
and the other with I/N
subplot(2,1,1)
%plot(Nplot(:,1),(Nplot(:,2)+Nplot(:,3))); %plot total population with a blue
line hold on; plot(Nplot(:,1),Nplot(:,2),'r-')%plots infecteds with a red line
title('SIS Urn Model Simulation with Immigration, Population Values');
subplot(2,1,2)
plot(Nplot(:,1),Nplot(:,2)/(Nplot(:,2)+Nplot(:,4)),'r-') %Infected ratio is
red
hold on;
plot(Nplot(:,1),Nplot(:,3),'y-'); %expected ratio I:N is yellow
title('SIS Urn Model Simulation with Immigration, Population Ratios');
end
end
if id==7
figure(fig)
plot(Nplot(:,1),Nplot(:,3)/(Nplot(:,2)+Nplot(:,3)),':k')
hold on;
```

```
end
if id==8
if b==1
figure(fig)
plot(Nplot(:,1),Nplot(:,4),'b',Nplot(:,1),Nplot(:,2),'r')
hold on;
elseif b==2
figure(fig)
plot(Nplot(:,1),-s0-i0+Nplot(:,2)+Nplot(:,4),'g')
hold on;
elseif b==3
figure(fig)
plot(Nplot(:,1),Nplot(:,2)/(Nplot(:,2)+Nplot(:,4)))
hold on;
plot(Nplot(:,1),(l-u+n-d-s)/l*(1+Nplot(:,1)-Nplot(:,1)),':k')
elseif b==4
figure(fig)
plot(Nplot(:,1),Nplot(:,2)/(Nplot(:,2)+Nplot(:,4)))
hold on;
plot(Nplot(:,1),(l-u+n-d-s)/l-Th/(l*(Nplot(:,2)+Nplot(:,4))))
end
end
end
```

sirsvitals.m

```
function sisrsvitals(filename,ap,TT,s0,i0,r0,l,u,n,d,s,L,Th,g)
%sirsvitals(filename,ap,TT,s0,i0,r0,l,u,n,d,s,L,Th,g)
%Simulates an SIRS model with vital statistics, immigration, and emigration
% s0 is the initial total susceptible population
% i0 is the initial infective population
% r0 is the initial recovered population
% l is the individual contact rate
% u is the individual recovery rate
% n is the birth rate
% d is the natural death rate
% s is the disease-related death rate
% g is the loss-of-immunity rate
% L is the immigration rate
% Th is the emigration rate
% TT is the number of events that will occur this time
% ap = 0 for new file; ap = 1 to append an old one
% filename is the name of the file to create or to be appended
% only filename, ap, and TT parameters are always needed in order to append
%   a file;
initrnd;
```

```
id=51;
if ap==0
Nused=[s0,i0,0,l,u,r0,0;0,0,0,0,0,id,0,0;0,0,L,0,0,0,0,0;n,d,s,g,Th,0,0;0,i0,0,s0,0,r0,0];
save(filename,'Nused')
end
[t t0 T s0 i0 iu0 iv0 su0 sv0 r k u l B f L p n d s Th g r0]=apinit(filename,id,TT);
load(filename,'Nused')
I=i0; %set initial values (variables)
S=s0;
R=r0;
N=s0+i0+r0;
t=t0; %set initial time
Nplot=[t,I,0,S,0,R,0]; %create matrix to remember points by making first entry
while (t<T) & (I>0) & (S>0);
t=t+1;
Nplot=[Nplot;[t,I,0,S,0,R,0]];%event does not occur until t, so N remains constant
until t
event=wheel([l*I*S/N,u*I,g*R,n*I,n*S,n*R,d*I,d*S,d*R,s*I,L,Th]);
if event==1
S=S-1;
I=I+1; %infection
elseif event==2
R=R+1;
I=I-1; %a recovery
elseif event==3
R=R-1;
S=S+1; %loss of immunity
elseif event==4
I=I+1; %birth of an infective
elseif event==5
S=S+1; %birth of a susceptible to a susceptible
elseif event==6
S=S+1; %birth of a susceptible to a recovered
elseif event==7
I=I-1; %natural death of an infective
elseif event==8
S=S-1; %death of a susceptible
elseif event==9
R=R-1; %death of a recovered
elseif event==10
I=I-1; %disease-related death of an infective
elseif event==11
S=S+1; %immigration
elseif event==12
type=wheel([I,S,R]); %emigration
```