Modeling Simple Epidemics: SIS MODEL

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ABSTRACT

This poster examines the question of how to model an epidemic. There are two standard modeling procedures: Deterministic model and Stochastic model. Deterministic modeling considers a structured mathematical framework, where one takes the actual number of new cases in a short interval of time to be proportional to the number of both susceptible and infectious individuals, as well as the length of the time interval. Stochastic modeling considers conditional realizations, where one assumes that one new case in a short interval of time is proportional to both susceptibles and infectives, as well as the length of the time interval. Although both definitions sound similar, there is a subtle difference: the deterministic model considers a set mathematical structure, where the stochastic model works on conditional probability structure. Too few investigators realize that both models are crucial to the proper interpretation of the epidemic process. Provided that the sample size is not small, the deterministic model will provide sufficient understanding of the process; if at anytime population numbers do become too small, then the stochastic analysis is vital (Renshaw, 1991). Included in this presentation will be the syntax to compare stochastic realization, deterministic prediction, and comparison of the two modeling structures for simple epidemic.

INTRODUCTION

The common cold can be thought of as a simple epidemic. A person is healthy but susceptible to a cold. A sick person coughs around the healthy person, now infecting that person. The newly infected person can cause infection to possible susceptibles just as s/he was infected. After a period of time, with proper care and medical assistance, the infected person is healthy again and among the susceptible class of people. You could think of the process for a single individual as:

$$S \rightarrow I \rightarrow S \rightarrow \ldots$$

where a person can flow from susceptible to infectious back to susceptible status, hence the acronym SIS (Bailey, 1975).

DETERMINISTIC MODEL

If a constant population of size N is partitioned into X susceptibles and Y infected, then we can write the deterministic form of the SIS model as:

$$X' = -\lambda X(Y/N) + \delta Y$$
$$Y' = \lambda X(Y/N) - \delta Y$$

where:

- $\lambda = cB$.
- c is the average number of contacts per person unit time.
- B is the probability that any one such contact will transmit infection.
- δ is the rate of recovery.

Note that $1/\delta$ is the average duration of the disease before recovery.

A fundamental problem in predicting whether an epidemic will occur is that of finding a threshold parameter, which is denoted by R0. R0 is usually a scalar-valued function defined on some multidimensional space. In most formulations, for points in the parameter space such that R0 < 1,the epidemic dies out; but for points such that R0 > 1, infection spreads throughout the population. For the SIS epidemic we define R0 as such:

$$R0 = cB/\delta = \lambda/\delta.$$

Under this definition of R0, we can rewrite our deterministic model as:

$$Y' = \delta[R0(X/N) - 1]Y.$$

Examining the above equation illustrates that R0 = 1 is the threshold separating monotonic extinction of the disease. If R0 < 1 (Note: $X/N \leq 1$) then Y' < 0 and thus Y(t) decreases as t increases. On the other hand, if R0 > 1, a stable endemic equilibrium, where Y'=0, occurs at (X=N/R0, Y=N-N/R0).

DETERMINISTIC MODEL SYNTAX

New features in the MODEL procedure allow for estimation of systems of first-order differential equations (Erdman, 1996). The following syntax was used in solving the SIS deterministic model (SAS®, 1996).

```
PROC MODEL DATA=T;
        DEPENDENT X X0 Y Y0.;
        PARM LAM LAM0  N N0 G G0;
                DERT.X = - (LAM/N)*X*Y = G*Y;
                DERT.Y = (LAM/N)*X*Y – G*Y;
        SOLVE X Y /DYNAMIC OUT=DETERM;
RUN;
```

Where:

- X0 is the initial number of susceptibles.
- Y0 is the initial number of infectives.
- LAM0 is the infection rate.
- G0 is the recovery rate.

STOCHASTIC MODEL

We can think of the number of infectives as a random variable Y with realizations y where the range of Y is {0,1,2,3,…, N}, the rate of Y decreasing from y to y-1 is given by μ_y and the rate of Y increasing from y to y+1 is given by γ_y. The stochastic formulas are given as such:

$$P[Y(t+\Delta t)=y-1|Y(t)=y] = \mu_y(\Delta t) + o(\Delta t)$$
$$P[Y(t+\Delta t)=y+1|Y(t)=y] = \gamma_y + o(\Delta t)$$
$$P[Y(t+\Delta t)=k|Y(t)=y\} = o(\Delta t) \ (k \neq y+1, k \neq y-1)$$

It is natural to set:

$$\mu_y = \lambda y(1 - y/N)$$
$$\gamma_y = \delta y.$$

As is illustrated above, there is always a positive probability of infection and a positive probability of recovery regardless of the threshold parameter.

SIMULATIONS OF THE STOCHASTIC PROCESS

Information on the shape of the process may be realized by simulation of the process. Simulations of the process consist of:

- Interpreting the next event to occur. In the SIS model, event is defined as a susceptible becoming infected ((X,Y) $\rightarrow$ (X-1,Y+1)) or an infected recovering and becoming a susceptible ((X,Y) $\rightarrow$ (X+1, Y-1)). The probability of a susceptible becoming infected is:
  $$\lambda X(Y/N)/(\delta Y + \lambda X(Y/N)),$$
  and the probability of a recovery is:
  $$\delta Y /(\delta Y + \lambda X(Y/N)),.$$
- Interpreting the distribution of the time to the next event.

Using the uniform random number generator, whose realizations can be thought of as representing probability, this probability can be related to the time to the next event and the transition among states according to the distribution of the time to the next event and the probabilistic structure of the embedded Markov Chain, respectively. The use of realizations from a uniform random variable in this methodology is commonly called Monte Carlo simulation.

Simulation of our process is:

- If $W \leq ((\lambda/N)XY/(\delta Y + (\lambda/N)XY)$ then a new infection occurs; otherwise an infected recovers, where W is a uniform random variable.
- The time to the next event is distributed exponentially with parameter $(\delta Y + (\lambda/N)XY)$; therefore, simulation of the time to next event is given by $-(\log(W1)/ (\delta Y + (\lambda/N)XY))$, where W1 is a uniform random variable (Renshaw, 1991).

SIMULATION SYNTAX

The following syntax illustrates how to produce 1 simulation of the stochastic process.

```
DATA SIM1;
SET BASELINE;
DO WHILE (X NE 0 AND Y NE 0);
S = -LOG(RANUNI(0))/(G*Y + LAM*X*Y/N);
TIME = TIME + S;
RAND = RANUNI(0);
CHECK = ((LAM/N)*X*Y)/(G*Y + (LAM/N)*X*Y);
IF RAND LE CHECK THEN DO;
        X=X-1; Y=Y+1; ***INFECTION***; END;
IF RAND GT CHECK THEN DO;
        X=X+1; Y=Y-1; ***RECOVERY***; END;
SIM1 = Y;
OUTPUT;
END;
KEEP SIM1 TIME;
RUN;
```

COMPARISION OF THE MODELS

An investigation between the deterministic estimates and the realizations of the stochastic process will be made. As has been addressed by Mode (1980), a comparison of the deterministic estimates and the mean, minimum, and maximum of 50 simulations of the stochastic process at various time points (epochs) will illustrate the behavior of the epidemic and the importance of the two modeling methods.

A macro was written to perform the Monte-Carlo simulations of the Stochastic process. The macro graphically compares the deterministic solution via PROC MODEL, and the mean, minimum, and maximum of the 50 realizations of the stochastic process at 100 epochs, where the width of each epoch is the maximum time of the 50 simulations of the stochastic process divided by 100. The syntax is available upon request.

EXAMPLES

The following three examples will consider the spread of the epidemic when the threshold parameter is less than 1, slightly larger than 1, and much greater than 1. Our experiment will consider what happens when 1 infected rat is introduced to a population of 29 non-infected rats, where time will be measured in weeks. Will the epidemic spread throughout the entire population?

Example 1: R0 < 1 ($\lambda = 2.5$, $\delta = 3$).

If R0 < 1 the epidemic dies out with Y(t) decreasing monotonically to 0, where Y(t) represents the number of susceptibles at time=t.
As is indicated in Figure 1, the deterministic model and the stochastic realizations indicate that the epidemic dies out. However the stochastic realization illustrate that the number of infectives does not decrease monotonically.

Example 2 – R0 slightly greater than 1. ($\lambda = 4.0$, $\delta = 2.0$).

With R0 > 1, according to the deterministic model, the epidemic will increase monotonically to the endemic equilibrium of 15 infectives. As is illustrated in Figure 2A, the stochastic realizations indicate that the epidemic will die out, although caution must be used in the interpretation of the stochastic realizations. As is discussed by Jacquez (1993), the waiting time until the population is all susceptibles or all infectives goes to infinity exponentially in N and the lower bound is independent of the initial number of infectives; therefore, the waiting time may exceed the life expectancy of the members of the population. The maximum waiting time for at least one simulation is 945 weeks, which may exceed the life expectancy of our test subjects.; therefore it might be better to consider the observation time of the experiment as a more practical length of time. It would not be realistic to expect our test subjects to live for more than 1 year without at least one death or one birth. Figure 2B considers the same scenario but reduces the observation time of the epidemic to 52 weeks. The behavior of the system is as expected. The average and maximum stochastic simulation indicate that the epidemic does not die out during the 52 week observation period, but the epidemic does not infect all test subjects, although there is at least one simulation that indicates the epidemic dies out within the first week.

Example 3 – R0 > 1 ($\lambda = 3.0$, $\delta = 0.5$).

With R0 > 1, according to the deterministic model, the epidemic will increase monotonically to the endemic equilibrium of 25.0 infectives. As is illustrated by Figure 3, the stochastic realizations behave similar to the deterministic model, although 28% of the simulations indicate that the epidemic dies out.

CONCLUSIONS

Through PROC MODEL and the uniform random number generator, the deterministic and stochastic structures can be modeled and compared.
As is illustrated in the three figures, the deterministic model and stochastic realizations do not always agree. Clearly both structures are important to the proper interpretation of the spread of epidemics.

REFERENCES

Bailey, Norman T.J. (1975). *The Mathematical Theory of Infectious Diseases and its Applications*, 2nd ed. New York, NY: Oxford University Press.

Renshaw, E. (1991). *Modelling Biological Population in Space and Time*. New York, NY: Cambridge University Press.

Erdman, D., and Morelock, M.M., A Study of Kinetics: The Estimation and Simulation of Systems of First-Order Differential Equations, *Proceedings of the Twenty-First Annual SAS® Users Group International Conference*, 1407-1414.

Jacquez, J.A., and Simon, C.P. (1993). The Stochastic SI Model with Recruitment and Deaths – Comparison with the Closed SIS Model, *Mathematical Biosciences*, 117, 77-125.

Mode, C.J. (1980). *Stochastic Processes in Demography and Their Computer Implementation.* New York, NY: Springer-Verlag

SAS® (1996). *SAS® /ETS Software: Changes and Enhancements for Release 6.12*. Cary, NC: SAS® Institute Inc.

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FIGURE 1: R0 < 1
Number of Infectives versus Time

Mean of the Stochastic simulations behaves similarly to the Deterministic model. Maximum of the Stochastic simulations has a lot of variability, but the epidemic dies out by week 6. At least one of the simulations has all infectives recovering in the first epoch; therefore, the Minimum of the Stochastic simulations is always equal to 0.

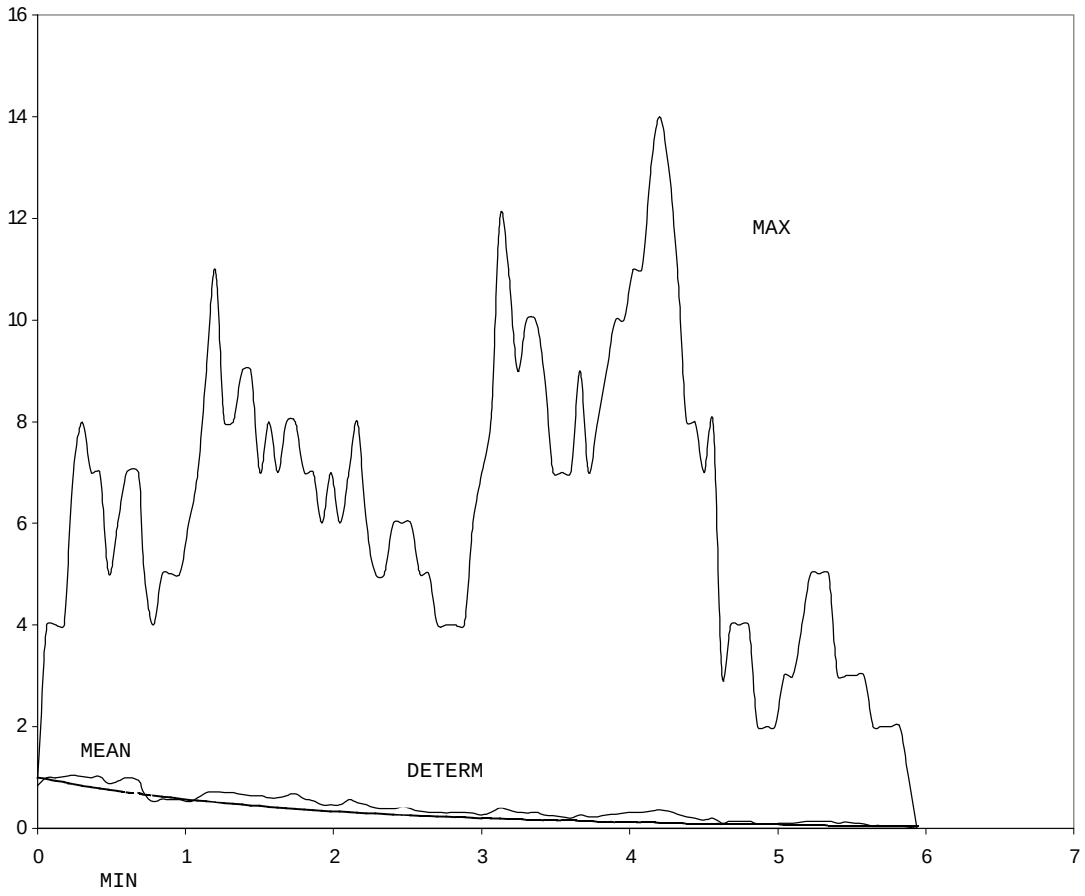

FIGURE 2A: R0 approximately 1 (R0 = 2)
Number of Infectives versus Time

The maximum waiting time until the end of the epidemic for the simulated stochastic process is 945 weeks. Time is segmented into 100 epochs each 9.45 weeks wide. Recovery time on average is 3.5 days; therefore, the number of events (Recovery on Infection) occurring within an epoch may be quite large. The Mean of the Stochastic simulations does not behave similarly to the Deterministic Model due to the large width of each epoch and the large waiting time for the epidemic. In at least one simulation, all infectives recover in the first epoch resulting in the Minimum of the Stochastic simulations equal to 0.

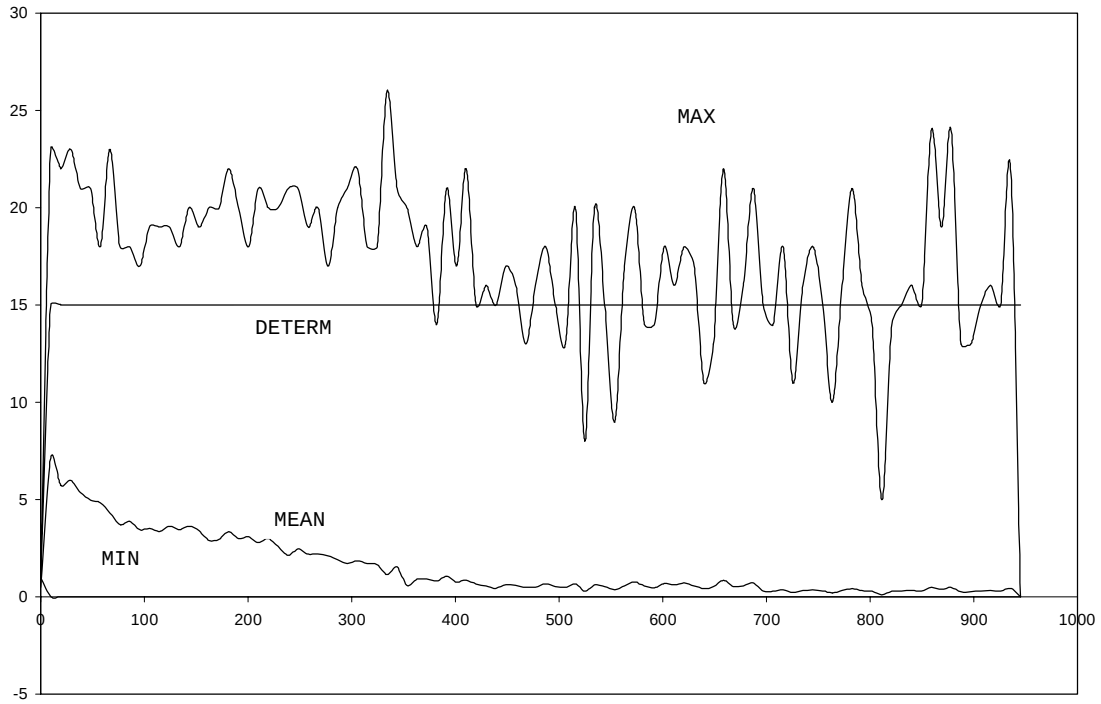

FIGURE 2B: R0 approximately 1 (R0 = 2)
Number of Infectives versus Time

When the observation time of the epidemic is reduced to 52 weeks the behavior between the Stochastic simulations and the Deterministic Model is as expected. The Deterministic Model estimates are between the Maximum Stochastic realization and the Mean Stochastic realization. Both the Mean of the Stochastic simulations and the Deterministic Model appear to achieve a state of equilibrium after week 10, with the equilibrium point of the Mean of the Stochastic simulations is around 8 infectives and the equilibrium point of the Deterministic Model is 15 infectives.

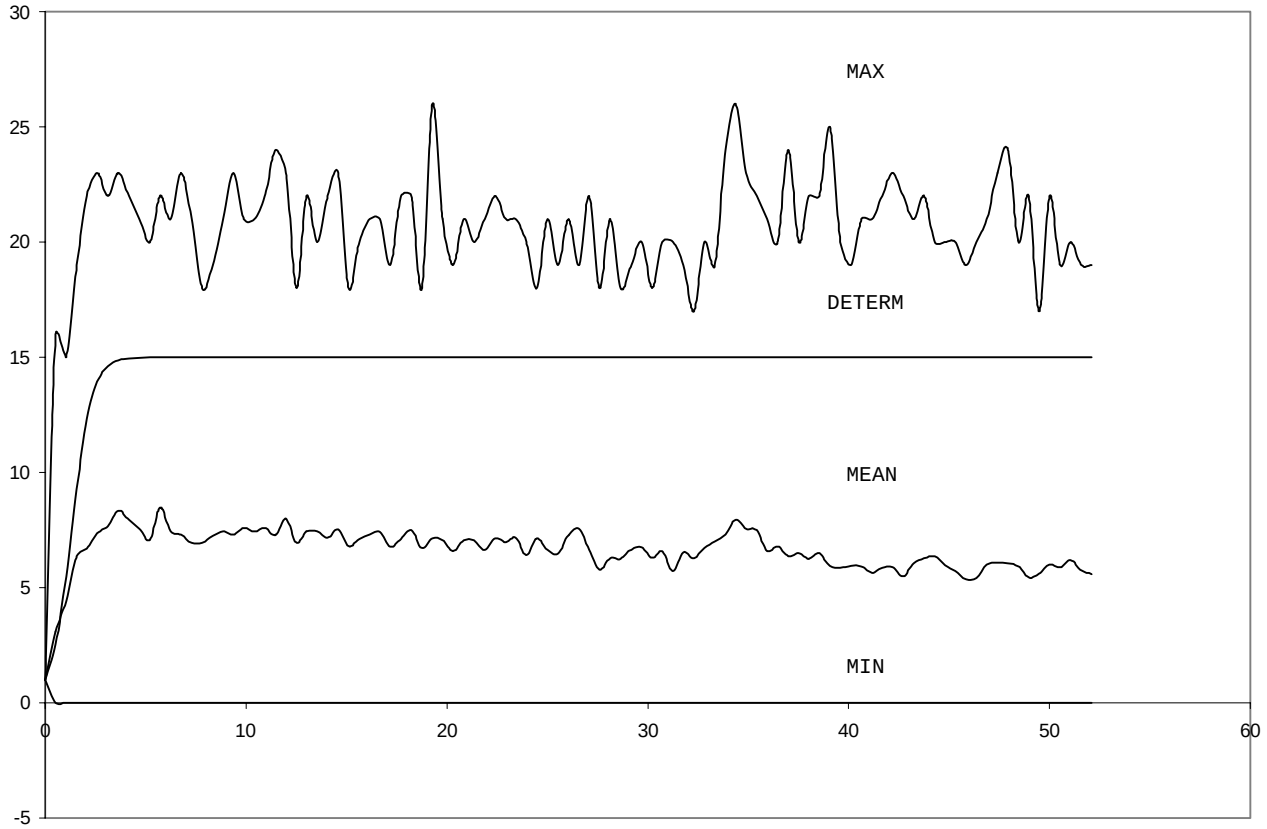

FIGURE 3: R0 > 1
Number of Infectives versus Time

The Mean of the Stochastic simulations behaves similarly to the Deterministic model. The Maximum of the Stochastic simulations indicates that the epidemic will infect all individuals. The Minimum of the Stochastic simulations indicates that in at least one simulation all infected individuals recover within the first epoch.