Assignment 1
Modeling an Epidemic

Assigned: Monday, September 9, 2013; Due: 5 PM Monday, September 16, 2013

This is an individual assignment

In this assignment you will experience the system dynamics modeling process by exploring the propagation of an infectious disease through a population of susceptible individuals. Infectious diseases present critical management and public policy challenges (consider SARS, MERS, Avian influenza, HIV, or the threat of bioterror attack). They also provide a useful setting to explore *feedback*—how the states of a system (the *levels* or *stocks*) influence (or "feed back" to) the *flows* that alter those states. The assignment also introduces you to the structure and behavior of fundamental feedback systems. These systems are the building blocks from which more complex systems are composed. In particular, the feedback structure governing the spread of contagious disease can also help to explain the growth of new products, the diffusion of innovations, the spread of financial panics, and other forms of social contagion important in business settings. The assignment gives you practice with the concepts of dynamic modeling and the modeling process while enabling familiarity with the modeling software we will use.

You are to work on this assignment individually, and submit your individual work and writeup via the course website.

A.   Get the Software

We've mentioned that there are several excellent software packages available for dynamic modeling. For our work this semester we will use the VensimPLE software. Your syllabus and Assignment 0 explained how to download and install the program.

B.   Become Familiar with the Software and Build and Explore the Base Model

Make sure to start your work early this week and attend the recitation if you have questions.

Download both <VensimPLE_Tutorial_F2013.pdf> and the datafile <SARSDATA.vdf>, which contains data for the Taiwanese SARS epidemic as a Vensim Data File (.vdf). Put the SARSDATA file in your Vensim directory. The tutorial walks you though the development of the epidemic model step by step and shows you how to use the data.

❑   denotes a question for which you must hand in an answer, a model, or a plot.
    ☐   denotes a tip to help you build the model or answer the question.

B1.   *2 points.* Do the tutorial and build the model it describes.

☐   *Be sure to document your model (both the diagram and the equations).* This means the following:

1.   Add sufficient commentary and explanation so that the meaning of each variable, the reasoning behind each formulation, and the data sources for each parameter value are clear to your audience. Do not wait until later to fill in the documentation, but document each equation as you create it. Doing so saves time in the long run. Forcing yourself to describe, in writing, the rationale for each formulation and sources for each parameter tests your understanding: if you can't write a concise, clear description of a formulation you probably don't understand it well enough.
2.   Label causal links with the correct polarities.
3.   Denote causal loops with appropriate names and labels.

☐   *Always provide the units of measure for every variable, and check that every equation is dimensionally consistent.* Vensim can test your model for dimensional consistency (see the tutorial). Models that fail the dimensional consistency test are meaningless. Dimensional errors are usually symptoms of more serious conceptual difficulties.

☐   As you finish the tutorial, you will have chosen base case parameter values for the exogenous parameters we asked you to select. Once you have a satisfactory overall pattern of behavior, don't worry too much about the exact values, but use the base case settings as a basis for comparison in the questions that follow.

❑   Include your model (the ".mdl" model file you created in Vensim) with your final submission.

B2.   *2 points.* Answer the following three questions.

❑ a.   What happens when you initialize the stock of infected people at zero? Briefly explain how you account for the behavior you observed with reference to the model's structure (remember, structure drives behavior). How do the dynamics change if you assume that one or more members of the population in question are already infected?

❑ b.   How do the dynamics change as the contact frequency increases? Does changing the contact frequency influence the total number of people who get SARS? Explain why or why not with reference to the structure of the model.

❑ c.   How do the dynamics change as infectivity varies? Explain.

☐   Submit your answers to the above questions in a brief writeup: each answer may be a few sentences and involve a handful of model runs. To back up your points, show only a few graphs, tables, or any form of result summary based on model output. You need not show all model runs you have done—just select the minimum you need to answer the questions concisely.

☐   Note: Place relevant selections of models and graphs next to your answers to a given question. Placing graphs in an appendix makes it harder to follow your logic (and to grade your work appropriately)

B3.   *2 points.* Critique your model.

❑   The model you have developed so far is very simple. Briefly critique its formulation and list the major assumptions you view as unrealistic. Aim for one paragraph or so.

C.   **Improve Your Model.**

In developing your critique of the model, you should have identified a range of unrealistic assumptions. In this section we will guide your exploration of what happens when one such assumption is relaxed.

C1.   *2 points.* So far we've assumed people remain infectious indefinitely. In epidemiology this is known as the "SI" (for Susceptible-Infectious) model. The SI model is appropriate for chronic infections that the body cannot clear and for which there is no cure, so that people remain infectious indefinitely. For most infectious diseases, including SARS, smallpox, chicken pox, measles, and influenza, patients either recover or die.

We'll help you reformulate your model to capture the notion that people eventually recover from SARS and are thus no longer infectious. The revised model is known in epidemiology as the "SIR" model (the "R" denotes "Removal" or "Recovery"). After following our instructions, your final model will look something like the following:
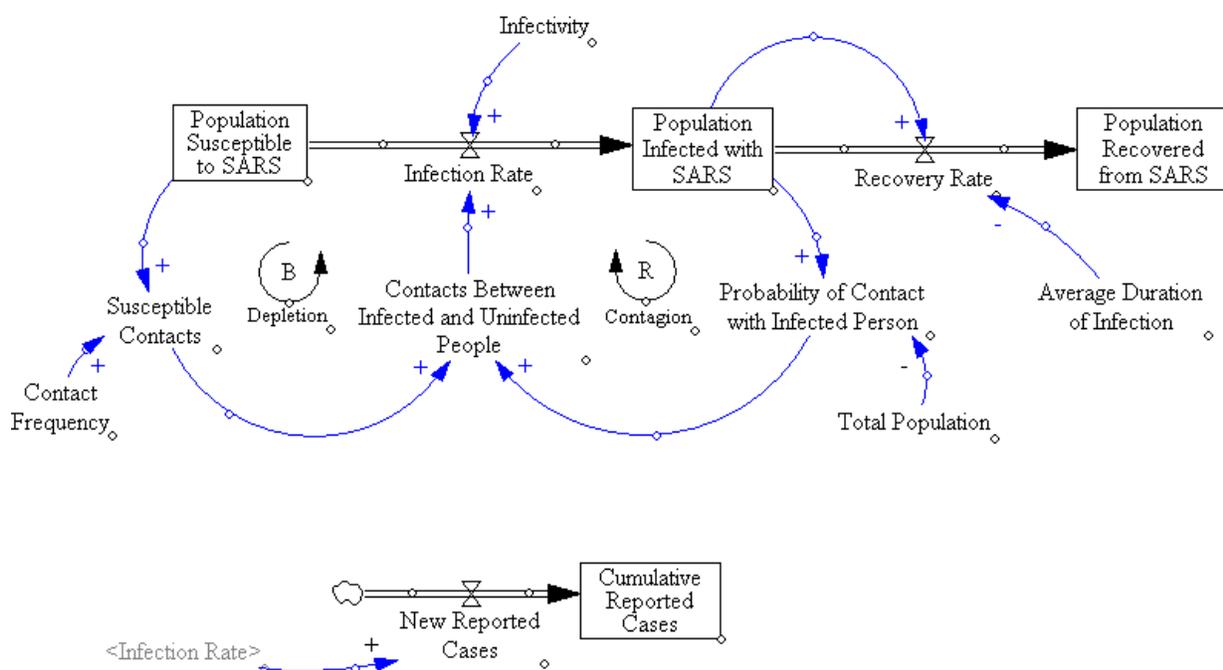
To modify your model, first create a new stock to represent the recovered population, placing it to the right of **Population Infected with SARS**. Next create a new flow, called the **Recovery Rate**, that moves people from the Infectious to the Recovered states (see the tutorial for help in creating stock and flow variables). Set the initial number of **Population Recovered from SARS** to zero.

☐   For simplicity, we will not distinguish death from recovery, so the recovery flow includes those recovering and those dying.

Next add an auxiliary variable representing the average duration of infection (that is, how long people remain infectious, on average).

Now you need to capture the feedback structure determining the rate at which people recover. The number of people who recover per day must depend on the number of people who are currently infected and the average duration of their infectivity. There are several ways to model the recovery process, but the simplest (and most widely used) is:

> Recovery Rate = Population Infected with SARS/Average Duration of Infectivity

To implement this formulation you need to add causal links connecting the infected stock and the average duration of infectivity to the recovery flow, as shown on the previous model diagram.

Next, change the equation for the infected population so that the recovery flow is now included as an outflow that drains the infected stock. Alter the equation for the **Population Infected with SARS** to read:

> Population Infected with SARS = INTEG(Infection Rate – Recovery Rate)

The equation states that the infectious population increases as people become infectious and decreases as people recover; the population infected with SARS accumulates the difference between infection and recovery.

Note that the infectious population is no longer equal to the cumulative number of cases.

Finally, you must estimate a value for **Average Duration of Infectivity**. Epidemiologists believe the infectious stage of SARS lasts about 1 to 3 weeks (7 – 21 days). Use your judgment to select a base case value.

Check that your diagram now resembles that on the previous page.

- ☐ Make sure your revised model is documented and dimensionally consistent.

- ❑ What kind of feedback loop have you added to your model? Make sure you have added an appropriate loop identifier and loop name to your diagram.

- ❑ Include your model (the ".mdl" model file you created in Vensim) with your final submission.

C2. *2 points.* Analyze your model to determine the effect of adding recovery.

- ❑ Explore how your model now behaves by running simulation tests. How do the dynamics change as the duration of infectivity is increased or decreased? What is different now? Explain in a brief discussion with reference to the structure of your model. You need not include many runs or tables, but do present a small selection of graphs or an overview of the data to back up your points.

Bonus Return to the questions you explored before. How does the epidemic change, once recovery is added? Now, what is the effect when contact frequency and infectivity change? Vary key parameters over a range to be sure you understand the possible dynamics of the system. Specifically, consider how the timing and severity of the epidemic change with parameters. How do the dynamics differ from those of the SI model in which there is no recovery?

D. What to hand in and how to submit your work

Write up your responses to the questions above in a word (.docx) document. In addition, you need to submit the various Vensim model (.mdl) files called for above in parts B1 and C1.

Upload your assignment by 5 PM on Sept 16, 2013. Submit your assignment as a single .zip file including your response document and models.

Name files with your last name, and for multiple files of the same type, the assignment section, e.g. *"Smith.docx"*, *"Smith-B1.mdl"*, and *"Smith-C1.mdl"*, all submitted as part of *"Smith.zip"*.

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15.871 Introduction to System Dynamics
Fall 2013