Multiple State Models

In the previous models, populations only existed one state. That is to say that, while their numbers may change, individuals did not move from one group to another. For example, in the competition models, species 1 might be affected by species 2. However, individuals never changed species.

In the models discussed in this section, individuals are allowed to move from one group to another. Two specific cases will be considered. In infectious diseases, individuals can be at multiple states, such as sick or healthy. In the second case, spatially separated populations, individuals move from one location to another.

Epidemiological Modeling

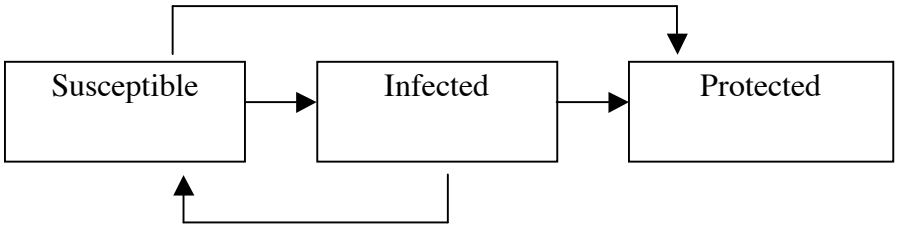
In epidemiological models the goal is to examine the spread of diseases through a population. The goal of these models is not to track the effect of a disease on an individual. Instead, the goal is to track the effect of the disease on the population as a whole. These models are used to examine a variety of factors on the progress of the disease, including:

- Number of sick individuals – allows the planning of hospital facilities, morgue facilities, and medical staffing
- The effect of immunization – allows determination of immunization strategy
- The effect of quarantine – allows cost benefit analysis on this strategy for minimizing disease spread

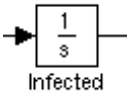
Living individuals within the population can be considered to be in one of the following conditions [1]

- Susceptible – These individuals do no currently have the disease *and* are capable of contracting the disease
- Infected – These individuals are currently infected with the disease *and* are capable of transmitting the disease to others.
- Protected – These individuals are those who do not fall into either of the above models. Typically, they fall into one or more of the following categories, naturally immune to the disease, immune to the disease due to immunization, immune to the disease due to previous exposure, and currently ill with the disease but not contagious.

The relationships between these three states are shown below.



Note that we have three "states" for the individuals in the model, susceptible (S), infected (I) , and protected (P). In Simulink, each state will be represented as an integrator.



It is also important to note that the total number of individuals is constant. This provides a means of checking the model as it is developed. If S + I + P is not constant, an error has been made The flows of individuals between these states are governed by the four equations. Each flow is represented by an arrow in the above diagram, but will be represented as a subsystem in the Simulink model. These four equations govern the flows of all subjects from one state to another for any given disease. By defining the values and constants involved, this model can be adapted to mimic the behavior of a defined disease through a population.

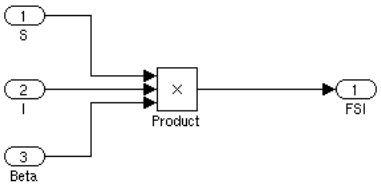
1. Flow from a susceptible to an infected host. If every host has an equal chance of interacting with any other host, the rate of interaction is then proportional to the product of the number of hosts in both the susceptible and infected states [2].

$$F_{S\text{-}I} = ß \bullet S \bullet I$$

Where: $F_{S\text{-}I}$ = The flow from a susceptible host to an infected host [Fraction of individuals / Day]

ß = Infectious contact rate [1 / (Fraction of individuals • Days)]

The inside of the subsystem for this flow is shown below:



The inputs and the output have been labeled. When they are labeled in this way, the ports into and out-of the subsystem are automatically labeled by Simulink.

The contact rate ß is the average number of events of possible transmission per unit of time [3]. It should be noted that there are significant diseases where the disease's transmission is not based on an equal chance of transmission by every host. One such example is sexually transmitted diseases, such as AIDS. In these diseases, transmission may be dominated by a small number of infected individuals, who are very sexually active [4].

2. *Flow from an infected to a protected host*. The second flow describes the flow of individuals from the infected population to the protected, as would occur when the user, after infection, acquires immunity to the disease. The flow from infected to protected is proportional to the total infected population and the recovery rate following infection over the total time from infection to recovery. The recover rate is the proportion of the infected to be cured and successfully converted to the protected status. The total time from infection can be described as the sum of the time from infection to discovery and the time between discovery and cure [2]. The total time can also be expressed as latency, ρ, which is the inverse of the time taken from discovery of infection to removal of the disease.

$$F_{I-P} = \frac{I \bullet \gamma}{\sigma + \delta}$$

Where: F_{I-P} = The flow from an infected host to a protected host
γ = Recovery rate [non-dimensional]
σ = Time taken from infection to discovery [Days]
δ = Time taken from discovery to cure [Days]

If we note the total time from infection to cure is $\sigma + \delta$, we can define a response latency,

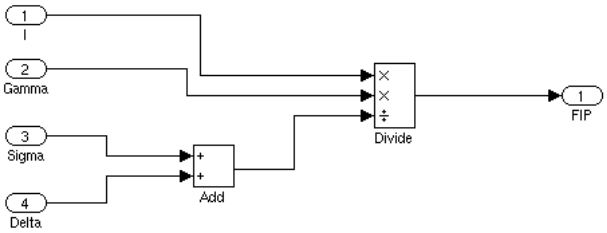
$$\rho = \frac{1}{(\sigma + \delta)}$$

and can rewrite this flow as follows:

$$F_{I-P} = I \bullet \gamma \bullet \rho$$

Where: ρ = Response latency [1 / Days]

The inside of the subsystem for this flow is shown below:

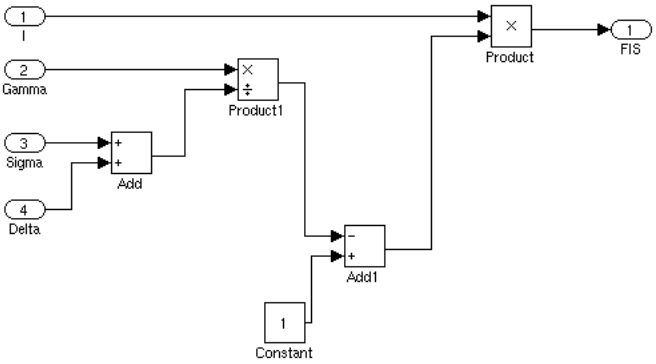


3. Flow from an infected to a susceptible host. This flow represents a situation where an infected individual is fully recovered by a one-time healing process without the full protection or immunization. Therefore, the individuals within this state are still vulnerable to future disease attack. This flow is proportional to the total infected population and the probability of cleaning the infection without complete immunization from the time of infection to recovery.

$$F_{I\text{-}S} = I \bullet (1 - (\gamma \bullet \rho))$$

Where: $F_{I\text{-}S}$ = The flow from an infected host to a susceptible host

The inside of the subsystem for this flow is shown below:



4. Flow from a susceptible to protected host. This fourth flow is an extension of the basic SIP model, and represents the possibility that individuals will learn about a new disease afflicting others and become immunized in anticipation of possible infection, protecting him/her from the disease without having gone through the infected stage. This is particularly appropriate for an institutional setting where a single agency administers control over a number of individuals, for example a school system.

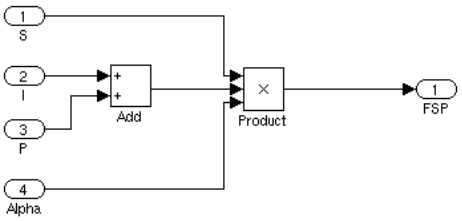
It assumes that the flow of information upon which action will be taken is proportional to the susceptible population who stand at risk multiplied by the number of individuals who have learned of the disease, which is assumed to be the sum of the infected and protected populations, those that have come in contact with or reacted to the disease.

$$F_{S\text{-}P} = \alpha \bullet (I + P) \bullet S$$

Where: $F_{S\text{-}P}$ = The flow from a susceptible host to a protected host
α = Immunization/communication rate [non-dimensional]

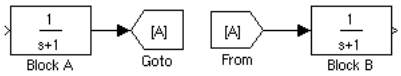
The immunization/communication rate is based on the probability that information concerning the disease will be conveyed to the susceptible population and that the information will be acted upon.

The inside of the subsystem for this flow is shown below:



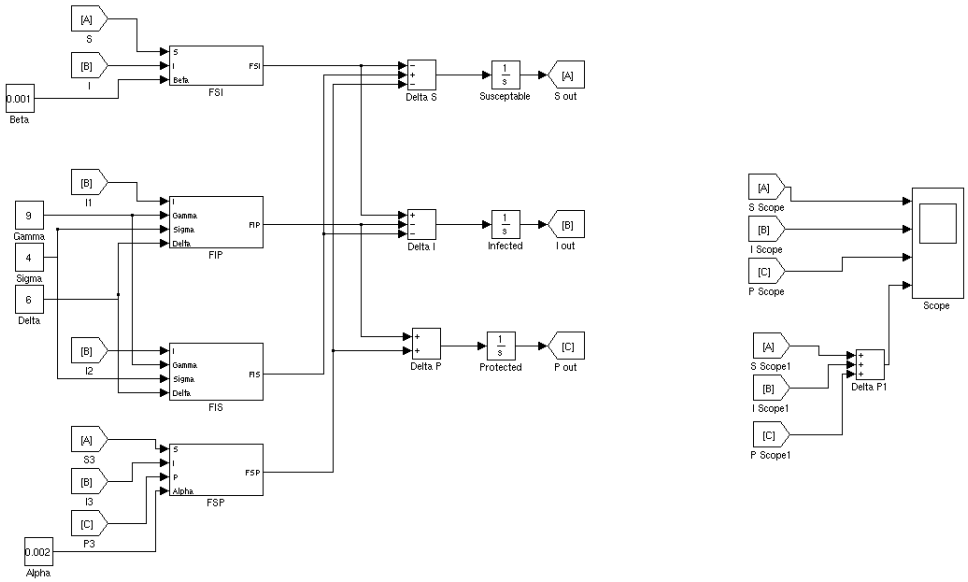
Assembling the Model. This model involves a large number of flows and blocks (even simplifying using subsystems). To further reduce the clutter and confusion, the "goto" and "from" blocks have been used. These blocks allow you to connect two blocks. For example, the connection between Block A and Block B shown below:

can be replaced with



There can be multiple "from"s linked to a single "goto." However, there can not be multiple "goto"s linked to a single "from".

When assembled the model looks like that shown below:



References

[1] F. C. Hoppensteadt and C. S. Perkin, *Modeling and simulation in medicine and the life sciences*, 2nd ed. New York, NY: Springer-Verlag, 2002.

[2] R. M. Anderson and R. M. May, *Infectious Diseases of Humans Dynamics and Control*. New York, NY: Oxford University Press, 1991.

[3] J. C. Frauenthal, *Mathematical modeling in epidemiology*. New York, NY: Springer-Verlag, 1980.

[4] A. Schneeberger, C. H. Mercer, S. A. Gregson, N. M. Ferguson, C. A. Nyamukapa, R. M. Anderson, A. M. Johnson, and G. P. Garnett, "Scale-free networks and sexually transmitted diseases: a description of observed patterns of sexual contacts in Britain and Zimbabwe," *Sex Transm Dis*, vol. 31, pp. 380-7, 2004.