Mathematical Models in Epidemiology

Several have been the classifications of models in infectious disease. So, for instance, Anderson and May (1991) use to classify models in microparasites (viruses, bacteria and protozoa) as *prevalence*-based models, and models in macroparasites (helminths, flat-worms, etc.) as *density*-based models. Other authors use a mathematical approach to classify models in *deterministic* and *stochastic* models (Bailey, 1975).

Current models take several forms, although most fall into two broad categories, which will be detailed further on: analytical and computer simulations. Compared to computer simulation models, analytical models tend to be relatively simple, usually sets of differential equations that keep track of a few important variables. In contrast, computer simulation models try to incorporate many more of the variables influencing transmission.

Analytical models are those which involve the association of a set of equations to each step individuals from the community take with the development of the natural history of the infection. Also called dynamical models, they capture the structure of the disease as this take their natural course. They can be of either deterministic or stochastic nature. Deterministic models are those which use difference, differential, integral or functional differential equations to describe the changes in time of the sizes of the epidemiological classes. So, consider, for instance, the picture described in figure 10, which describes the progress of a viral infection, such as measles, through a host.

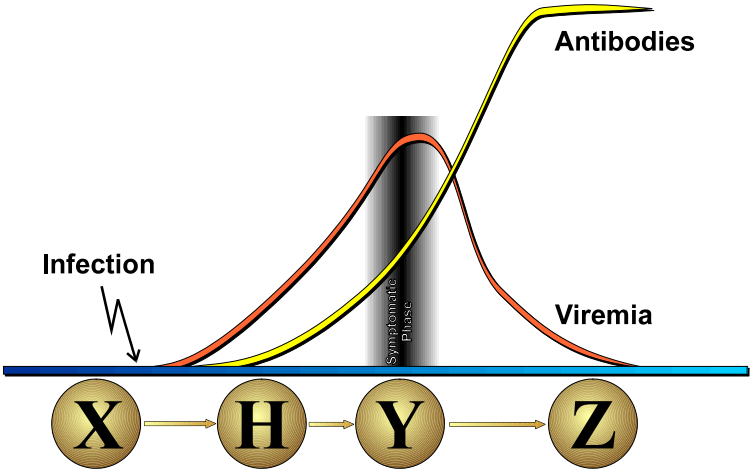

Figure 10

The curves above in the figure illustrate the growth of the virus population, the immune response to the virus, and the timing of acute disease. The block diagram below represents the flow of the transmission between infection categories. In this simple situation, the total population is considered to be constant, and therefore the birth and death rates are equal (μ). People are born susceptible X, are infected at a rate λ, passing by a latent state, H, before

developing the acute disease with a rate σ. Those infected and infectious, Y, recover from the infection at a rate γ, remaining immune, Z, for life.

The system illustrated by figure 1 is extremely simple but it captures the essence of the transmission chain between the involved categories. In general, systems like this, although still very simple in its biological assumptions are too complex to have analytical solution, i.e., the solution of the associated system of differential equations without the help of numerical simulations. This is the first problem posed by modelling biological phenomena: the highest the biological realism the lower the probability of analytical solution. Figure 11 illustrates, through a flow chart, the algorithm to solve infectious diseases problem by mathematical and computer modelling.

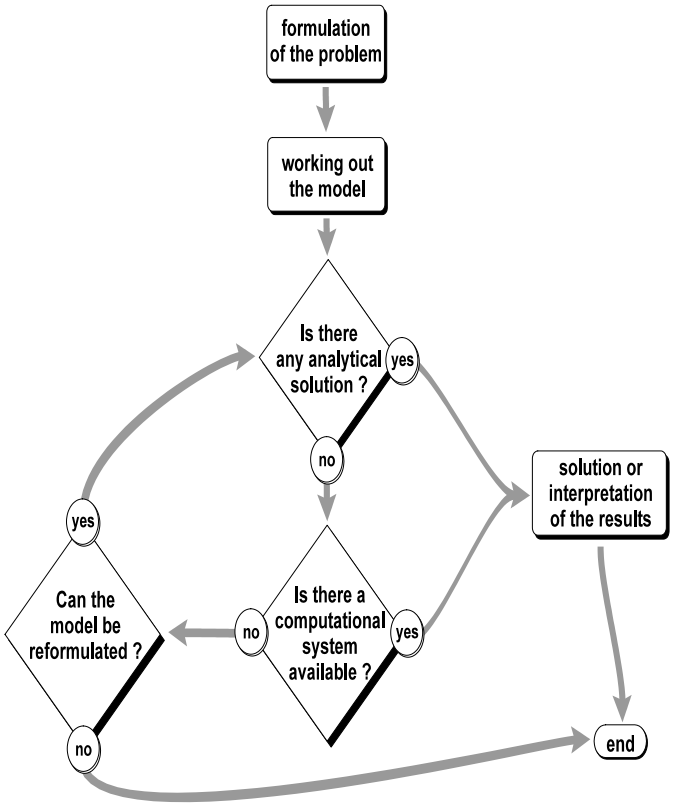

Figure 11

As can be noted from the figure, everything starts, as in any scientific approach, by defining the problem to be modelled. The next step is to design the model, in this case, the set of differential equations associated to the disease categories. If the system is simple enough then the analytical solution (by pencil and paper) is feasible. If so, then is just to interpret the results and the problem is finished. If, on the other hand, the problem is too complex, then it

is necessary the application of numerical methods for the computational solution. If the system to solve the model numerically is available, then is just to interpret the results and the problem is finished. If the computational system is not available, then the model needs to be reformulated, whenever possible, and the problem starts again. In case the model cannot be reformulated, then it is not possible to solve it and the system stop. Let us see some examples of the situation described above.

In figure 12, it is illustrated the simplest epidemic model as possible, involving only two categories, namely, susceptibles, X, and infected, Y. Individuals acquire the infection with a rate λ, normally denoted the *force of infection*. This later parameter is related to the incidence rate, *i.r.*, by the equation:

$$i.r. = \lambda X \tag{1}$$

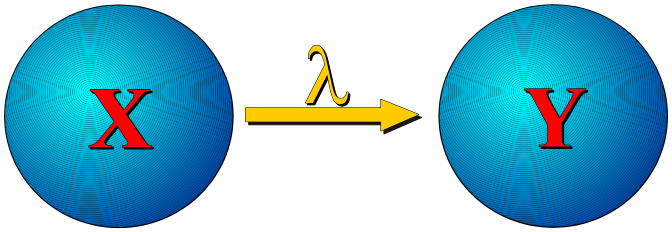

Figure 12

In this simple, and unrealistic model, it is associated the following system of ordinary differential equation (ODE):

$$\begin{array}{rcl} \frac{dX(t)}{dt} & = & -\lambda X(t) \\ \frac{dY(t)}{dt} & = & \lambda X(t) \end{array} \tag{2}$$

If we assume the total population as a constant, we can work with proportions, in the sense that $X(t) + Y(t) = 1$. The analytical solution of equations **??** is then straightforward:

$$\begin{array}{rcl} X(t) & = & X(0)\exp[-\lambda t] \\ \text{and} & & \\ Y(t) & = & 1 - \{X(0)\exp[-\lambda t]\} \end{array} \tag{3}$$