

INTRO TO EPIDEMIC MODELING



Introduction to epidemic modeling is usually made through one of the first epidemic models proposed by Kermack and McKendrick in 1927, a model known as the SIR epidemic model

When a disease spreads in a population it splits the population into nonintersecting classes. In one of the simplest scenarios there are 3 classes:

- The class of individuals who are healthy but can contract the disease. These people are called *susceptible individuals* or **susceptibles**. The size of this class is usually denoted by **S** .
- The class of individuals who have contracted the disease and are now sick with it, called **infected individuals**. In this model it is assumed that infected individuals are also *infectious*. The size of the class of infectious/infected individuals is denoted by **I** .
- The class of individuals who have recovered and cannot contract the disease again are called **removed/recovered individuals**. The class of recovered individuals is usually denoted by **R** .

The number of individuals in each of these classes changes with time, that is, $S(t)$, $I(t)$, and $R(t)$. The total population size N is the sum of these three classes

$$N(t) = S(t) + I(t) + R(t)$$

Assumptions: (1) Infected individuals are also infectious; (2) The total population size remains constant; (3) The population is closed (no immigration/emigration); (4) No births/deaths; (5) All recovered individuals have complete immunity

Epidemiological models consist of systems of ODEs which describe the dynamics in each class. To derive the differential equations, we consider how the classes change in time.

When a susceptible individual enters into a contact with an infectious individual, that susceptible individual becomes infected and moves from the susceptible class into the infected class. The susceptible population decreases in a unit of time by all individuals who become infected in this unit of time. At the same time the class of infectives increases by the same number of newly infected individuals.

The number of individuals who become infected per unit of time in epidemiology is called **incidence**.

The rate of change of the susceptible class is given by the incidence

$$S'(t) = -\text{incidence}$$

- cN is the number of contacts per unit of time this infectious individual makes. Here we assume that the number of contact one infectious individual makes is proportionate to the total population size with per capita contact rate c .
- S/N is the probability that a contact is with a susceptible individual.
- $cN S/N$ is number of contacts with susceptible individuals that one infectious individual makes per unit of time. Not every contact with a susceptible individual leads to transmission of the disease. Suppose p is the probability that a contact with susceptible individual results in transmission. Then,
- pcS is number of susceptible individuals who become infected per unit of time for each one infectious individual.
- βSI is the number of individuals who become infected per unit of time (incidence).

Here we have denoted by $\beta = pc$.

If we denote by $\lambda(t) = \beta I$, then the number of individuals who become infected per unit of time is equal to $\lambda(t)S$. The function $\lambda(t)$ is called *force of infection*. The coefficient β is the constant of proportionality called the *transmission rate constant*. The number of infected individuals in the population $I(t)$ is called *prevalence* of the disease.

We obtain the following equation for the susceptibles:

$$S'(t) = -\beta S(t)I(t)$$

There are different types of incidence depending on the assumption made for the form of the force of infection. This one is called **mass action incidence**.

The susceptible individuals who become infected move to the class I . Those individuals who recover leave the infective class at constant per capita probability per unit of time α called **recovery rate**. That is, αI is the number of infected individuals per unit of time who recover.

$$I'(t) = \beta S(t) I(t) - \alpha I(t)$$

Individuals who recover leave the infectious class and move to the recovered class

$$R'(t) = \alpha I(t)$$

To be well-defined mathematically, this system is equipped with given initial conditions $S(0)$, $I(0)$ and $R(0)$.

Loosely speaking, a differential equation model is **well posed** if through every point (initial condition) there exists a unique solution. Differential equations models must be well-posed to be mathematically acceptable and biologically significant. Because the dependent variables in the model denote physical quantities, for most models in biology and epidemiology we also require that solutions that start from positive (nonnegative) initial conditions remain positive (nonnegative) for all time.

Adding the three equations in the system, we obtain

$$N'(t) = S'(t) + I'(t) + R'(t) = 0$$

Thus, N remains a constant defined by the initial conditions:
 $N = S(0) + I(0) + R(0)$.

This model is called SIR model or SIR system. It is a special type of model called **compartmental model** because each letter is referring to a “compartment” in which an individual can reside. Each individual can reside in exactly one compartment and can move from one compartment to another. Compartmental models are schematically described by a diagram often called **flow chart**. Each compartment in a flow-chart is represented by a box indexed by the name of the class. Arrows indicate the direction of movement of individuals between the classes. The movement arrows are typically labeled by the transition rates

