**SIR Model**

The SIR model is a mathematical model used to describe the spread of infectious diseases. It divides a population into three compartments: Susceptible (S) individuals who can become infected, Infected (I) individuals who have the disease and can spread it and Recovered (R) individuals who have recovered from the disease.

To develop this SIR model, certain simplifying assumptions are made, such as the population being mixed together in a confined area, and the model describing the temporal evolution of the disease rather than its spatial transport.

The simple SIR model uses a set of equations to describe how the number of individuals in each compartment (susceptible, infected, and recovered) changes over time. These equations take into account factors such as the number of contacts between individuals and the probability of infection, as well as the rate of recovery from the disease. They are converted into ordinary differential equations (ODEs) and then solved using the Runge Kutta 4 method, a numerical method that approximates the solutions of a system of differential equations using iterative calculations based on the function's values and derivatives at different points in time. This method is relatively simple to implement and provides accurate solutions, which is why it is popular for solving ordinary differential equations. These equations are used to predict the spread of the disease and inform public health interventions.

The extended version of the SIR model includes additional compartments such as exposed individuals who are infected but not yet contagious. These extensions can be made by adding additional equations and solving them in the same way as the simple SIR model. For instance, an SEIR model, which includes an additional compartment for exposed individuals (E) who are infected but not yet contagious, can be developed by adding an equation for the number of exposed individuals over time. Similarly, this extended model also includes a compartment for susceptible individuals who become infected again after recovery, can be developed by adding an equation for the number of individuals who move from the R compartment back to the S compartment over time. These models can provide more detailed and accurate predictions of the spread of a disease by taking into account the specific characteristics of the disease and the population being studied.