SIR Model for Spread of Disease

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1   Introduction

An SIR model is an epidemiological model that computes the theoretical number of people infected with a contagious illness in a closed population over time. One of the simplest SIR models is the Kermack-McKendrick model. It assumes that the population size is fixed (i.e., no births, deaths due to disease, or deaths by natural causes), incubation period of the infectious agent is instantaneous, and duration of infectivity is same as length of the disease. It also assumes a completely homogeneous population with no age, spatial, or social structure.

2   The Differential Equations

2.1   Variables

S = **S(t)** is the number of *susceptible* individuals

I = **I(t)** is the number of *infected* individuals

R = **R(t)** is the number of *recovered* individuals

$\boldsymbol{\beta}$ = rate of infection

$\boldsymbol{\gamma}$ = 1/d where d is the average duration of infection

2.2   Equations

The Susceptible Equation

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

The Infected Equation

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$

1

The Recovered Equation

$$\frac{dR}{dt} = \gamma I \tag{3}$$

2.3 R_0, the Epidemiological Threshold

R_0 is probably the single most important quantity in epidemiology.

$$R_0 = \frac{\beta S}{\gamma} \tag{4}$$

Although different SIR models have different formulas to calculate it, the underlying principle is the same. When $R_0 < 1$, each person who contracts the disease will infect fewer than one person before dying or recovering, so the outbreak will die out. If $R_0 > 1$, each infected person will infect more than one person and an epidemic will form.
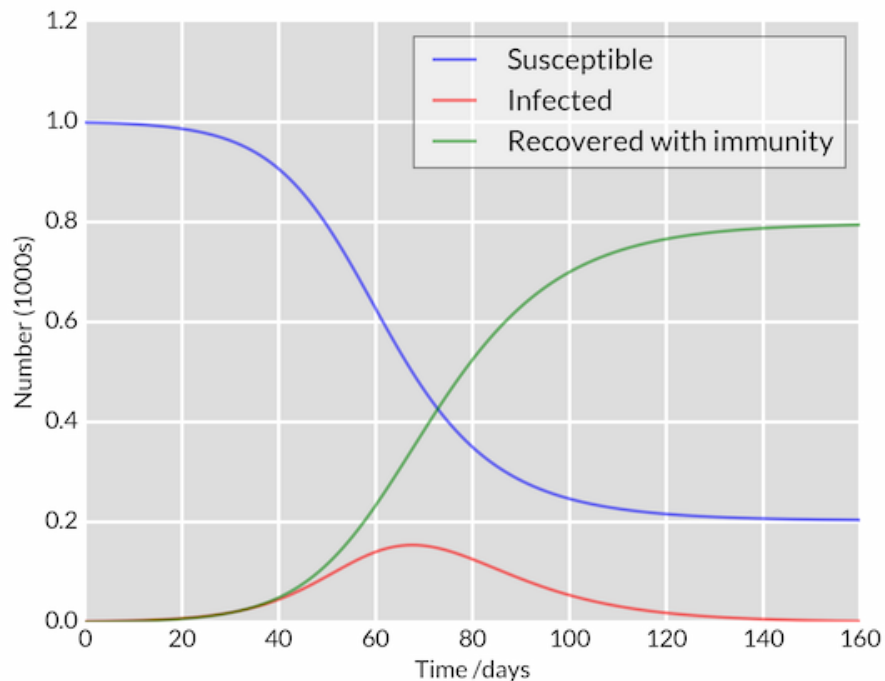
3 Graphing the SIR Model

Figure 1: Change of epidemic populations in SIR.