

# The Susceptible-Infectious-Recovered (SIR) model of disease expansion: a new approach

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## 1. Introduction

Mathematical modelling is helpful for prevention and control of emerging infectious diseases. It provides both information to health workers about the vaccination needed to protect a population and help to the public health decision making when new diseases potentially emerge on a large scale, such as Bird flu, measles, malaria, influenza and Ebola over the past few years [1]. After Bernoulli presented the first model for an infectious disease in 1760 [2], Kermack and McKendrick published papers on epidemic models and obtained the threshold that has to be exceeded for an epidemic outbreak can occur [3, 4]. Their model includes three states, the S (susceptible), I (Infectious) and R (Recovered) instead of the two, S and I, of the Bernoulli's model [5]. In the nineties, new paradigms spread out to better understand and model the impact of numerous variables that go beyond the micro host-pathogen level, such as ecological, social, economic, and demographic factors. Multidisciplinary approach is suitable for rapid assessment of urgent pandemic situations. The case of HIV/AIDS is a good example [6-9].

This paper presents a model to approach the dynamics of infectious diseases expansion by means of a set of neighbour rules between elements located in a square grid that represents the whole population. Following the introduction, Section 2 provides a brief summary of the Susceptible-Infectious-Recovered (SIR) model depicted by ordinary differential equations (ODE). Section 3 is entirely devoted to present our model. The contacts between people are set by the connectivity pattern of the grid. We consider different patterns such as 4-neighbours, 8-neighbours and horse jumping chess neighbourhood. The spread of the disease is performed by binary rules that are tailored to model different situations such as Susceptible, Infected, Recovered with or without capability to infect further. Section 4 presents the discussion and some concluding remarks.

## 2. The deterministic SIR model

The Kermack-McKendrick or SIR model concerns a number of people infected with a contagious illness in a closed population over time. It was proposed to explain the rapid rise and fall in the number of infected patients observed in epidemics such as the plague (London 1665, Bombay 1906) and cholera (London 1865). The model assumes that the population size,  $N$ , is fixed (i.e., no births, deaths due to disease, nor deaths by natural causes) and incubation period of the infectious agent is instantaneous. The population is divided into three health states: susceptible to the infection (denoted by  $S$ ), infected (denoted by  $I$ ) and recovered (denoted by  $R$ ). The SIR model provides immunity, so recovered people are no more able to infect nor transmit the disease. This model is depicted by a system of ODE shown in (1). Although the system has no analytical solution, in practice it can numerically be solved (Euler, Runge-Kutta). The rate at which susceptible hosts become infected is a product of the number of contacts each host has per unit time,  $r$ , and the probability of transmission of infection per contact,  $\beta$ . The recovery rate is  $\gamma$  (or, in other words, the mean infective period is  $1/\gamma$ ). The total population size is  $N = S + I + R$ . Figure

1 represents a generic simulation of the SIR model equations. Horizontal axis stands for the time, vertical axis stands for the number of individuals

$$\begin{aligned} \frac{dS}{dt} &= -\beta rSI \\ \frac{dI}{dt} &= \beta rSI - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned} \quad (1)$$

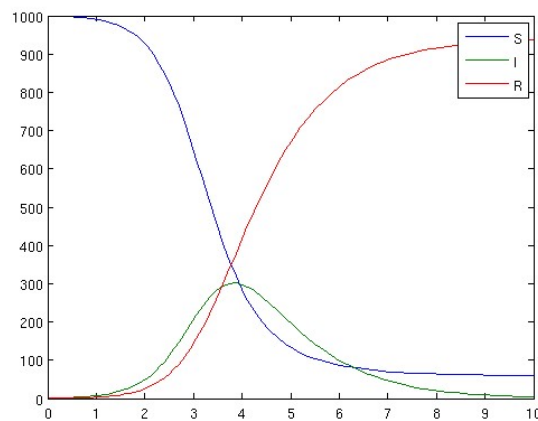
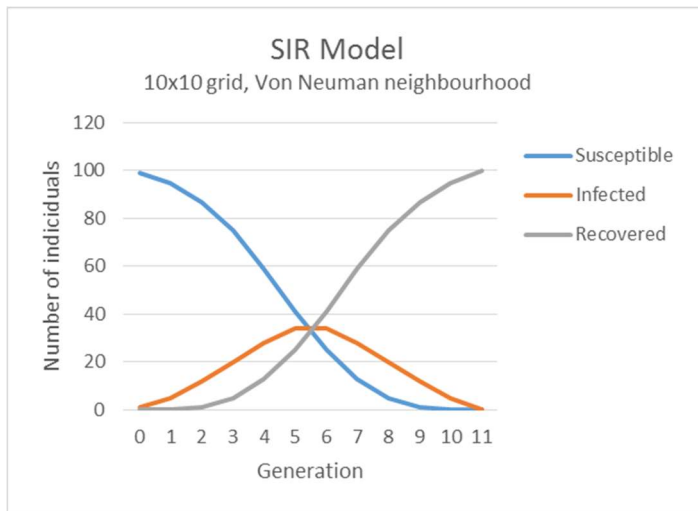


Figure 1. The deterministic SIR model (Wikipedia)

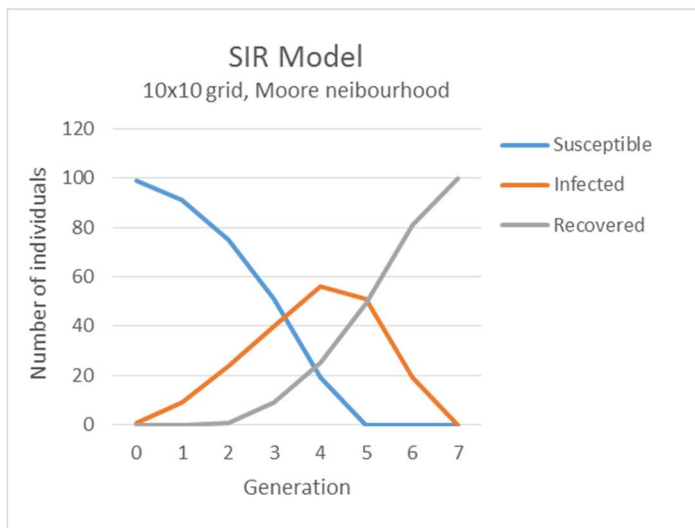
### 3. Our model

Our model is based on both a concrete connection between individuals set by particular neighbourhood pattern (4-neighbours or Von Neuman, 8-neighbours or Moore, chess horse jumping ...) which fixes the possible contacts between individuals, and a local binary rule that defines whether the contact is infective or not. This rule is implemented by a binary operation to set the results of the contacts between 0 and 1, 1 and 0, 0 and 0, 1 and 1, see [10-11]. Without loss of generality we consider a two-dimensional square grid where every cell represents a susceptible person, except the one at the centre which locates an infected one. When the infected person contacts with his/her neighbours he/she spreads the disease. The new infected people have then in turn the capability to infect their neighbours, a time later. When infected people recover from their illness they can no longer infect nor transmit the illness. They are immunized. As follows, Figure 2 represents the number of susceptible, infected and recovered people in the case of different neighbourhood patterns, for a 10x10 grid (100 people). For each case, we show a particular stage of the spread of the disease in the grid. For all them, at generation 0, the central cell is infected, at generation 1 the infected cell transmits the disease to its neighbour cells, at generation 2 the infected cells in previous generation infect their neighbour cells and the central recovered cell becomes immunized, and so on. In this experiment we have fixed the disease duration in two generations, but it can be variable depending of the concrete disease we have to model. White cells represent the susceptible people; numbers in the cells stand for the generation number: they are red when people are infected and green when they are recovered and immunized. The simulation has been run by Eclipse IDE 2 Release (4.5.2).



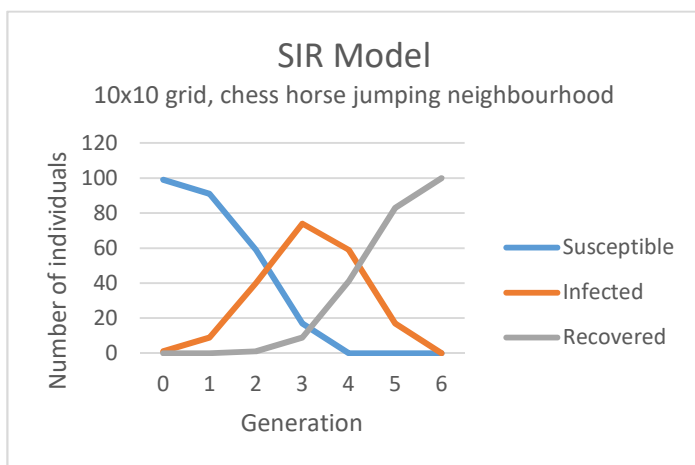

Generation 2 (out of 11)

Susceptible: 87  
 Infected: 12  
 Recovered: 1 (generation 0)




Generation 3 (out of 7)

Susceptible: 51  
 Infected: 40  
 Recovered: 9 (generations 0 and 1)




Generation 2 (out of 6)

Susceptible: 59  
 Infected: 40  
 Recovered: 1 (generation 0)

Figure 2. Simulation of our SIR model. Partial schedule of the disease expansion

#### 4. Discussion

Our model establishes a link between traditional simulation of the Susceptible-Infectious-Recovered (SIR) model of disease expansion based on ODE, and a very simple approach based on both connectivity between people and elementary binary rules that define the result of these contacts. The Susceptible-Infectious (SI) deterministic compartmental model has already been analysed and successfully modelled by our method in the case of different connectivity patterns [11]. In the present article, we observe the similarity between our graphics in Figure 2 and the generic graphic in Figure 1. We have assumed “time = generation” in order to allow flexibility for parameter fitting in real cases. We have also set  $10 \times 10 = 100$  people in the grid to obtain the rates of Susceptible, Infectious and Recovered people for easier comparison between different cases. We can also “identify” the connectivity pattern with the parameter  $\beta r$  (the number of effective infections per time unit) and the number of generations the disease lasts with the parameter  $\gamma$ . A more careful study of real cases is crucial to succeed in an accurate approximation, just as we do when simulating with the traditional ODE model.

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