Simulating the SIR Model and its Derivatives

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The aim of this report is to present an implementation of the $\mathbf{SI}^K\mathbf{RD}$ Model of epidemics written in Python with all parameters being variable. This report will first present a review of the **SIR** model, followed by the extension of the **SIR** model into the **SIRD** and $\mathbf{SI}^K\mathbf{RD}$ models. Then, the time-discrete **SIR**, **SIRD** and $\mathbf{SI}^K\mathbf{RD}$ models actually used in the simulations will be presented. Finally, an introduction the simulation program and its features will be presented, along with a short instruction manual on how to use the program and example graphs produced by the program illustrating the various situations encountered in the first four sections.

1 The SIR Model

The **SIR** model is a model simulating the spread of infection over a homogeneous populace (of total size 1). The populace are separated into three compartments: **S** (the *susceptible*), **I** (the *infected*) and **R** (the *recovered*) of sizes s, ι, and r respectively. Since the size of the populace is 1, the three variables must satisfy

$$s + \iota + r = 1.$$

Here, we assume that the size of the populace never grows or shrinks due to immigration, births, deaths, etc. The three variables have time evolution that depends on the other variables (and/or itself). In the **SIR** model, the time evolutions of s, ι and r are given by the following equations:

$$\frac{\mathrm{d}s}{\mathrm{d}t} = -\beta s\iota, \qquad \frac{\mathrm{d}\iota}{\mathrm{d}t} = \beta s\iota - \gamma\iota, \qquad \frac{\mathrm{d}r}{\mathrm{d}t} = \gamma\iota.$$

Here, β is the *transmission coefficient*, which represents the rate in which the infected populace ι can infect the susceptible populace s. γ represents the *recovery rate*: the rate in which the infected populace recover from the infection. The ratio $R_0 = \beta/\gamma$ plays a very important role in the **SIR** model, since it solely determines whether or not an epidemic occurs; if $R_0 > 1$, an epidemic occurs, while if $R_0 < 1$, no epidemic occurs.

The **SIR** model is perhaps the most simple model of infection that can predict if an epidemic occurs (unlike the **SI** model which always predicts 100% of the populace to be in **I** after some time regardless of the size of infected populace or the value of β). However, even with the simplicity of the **SIR** model, there is no analytical solution to the equations defining the time evolutions of s, ι and r; one must rely on numerical solutions to study the behavior of the three components under different values of β, γ and $\iota(0)$.

2 The SIRD Model

The **SIRD** model is an extension of the **SIR** model with one difference: it models deaths in the population alongside a possibility of modelling the relatively increased mortality rate of the infected populace. In this case, a fourth compartment **D** of size ω representing the deceased. As such, one has that

$$s + \iota + r + \omega = 1.$$

The time evolutions of the four variables are modelled by the following equations:

$$\frac{\mathrm{d}s}{\mathrm{d}t} = -\beta s\iota - \delta s, \qquad \frac{\mathrm{d}\iota}{\mathrm{d}t} = \beta s\iota - \gamma\iota - \delta f\iota, \qquad \frac{\mathrm{d}r}{\mathrm{d}t} = \gamma\iota - \delta r, \qquad \frac{\mathrm{d}\omega}{\mathrm{d}t} = \delta(s + f\iota + r).$$

Here, δ represents the *baseline death rate*, representing how likely a susceptible (or recovered) individual is to die. The other new parameter is f, the *fatality factor* of the infection. f is the ratio of death rate among the infected over the death rate among the non-infected (which is extremely high in the case of fatal diseases).

While this model is a step up from the **SIR** model in terms of complexity (and thus models real situations better), it still suffers from a few issues. One big issue is that an infected individual is most likely to recover right after infection; this is unrealistic, since in reality diseases take some time to incubate and recover from.

3 The SI^{K}RD Model

The **SI^{K}RD** model seeks to improve the **SIRD** model by sub-dividing the compartment containing the infected **I** into K compartments, with recovery only being possible from the K-th compartment of **I**. This tries to model how in reality, all diseases take some time before recovery is possible. We have that

$$s + \iota + r + \omega = 1,$$

where ι is partitioned into k components, namely:

$$\iota = \sum_{i=1}^{k} \iota_i$$

with each ι_i being the size of a sub-compartment $\mathbf{I}_i$ of the compartment representing the infected **I**.
The time evolutions of the variables satisfy the following equations:

$$\frac{\mathrm{d}s}{\mathrm{d}t} = -\beta s\iota - \delta s, \quad \frac{\mathrm{d}\iota_1}{\mathrm{d}t} = \beta s\iota - k\gamma\iota_1 - \delta f\iota_1, \quad \frac{\mathrm{d}\iota_i}{\mathrm{d}t} = k\gamma\iota_{i-1} - k\gamma\iota_i - \delta f\iota_i, \quad (i \neq 1, k)$$

$$\frac{\mathrm{d}\iota_k}{\mathrm{d}t} = k\gamma\iota_{k-1} - \gamma\iota_k - \delta f\iota_k, \quad \frac{\mathrm{d}r}{\mathrm{d}t} = \gamma\iota_k - \delta r, \quad \frac{\mathrm{d}\omega}{\mathrm{d}t} = \delta(s + f\iota + r).$$

The time evolution equations in the **SI^{K}RD** model is very similar to the **SIRD** model, with one key difference, namely the process which one must go through from infection to recovery. Upon infection, one moves from **S** to $\mathbf{I}_1$, followed by $k-1$ sequential moves from $\mathbf{I}_1$ to $\mathbf{I}_2$ until one reaches $\mathbf{I}_k$, from which one can then finally move to **R** (i.e., recover from the disease). Note that one is infectious regardless of which subcompartment of **I** that one belongs to, yet can only recover from $\mathbf{I}_k$. This approach results in a longer time before one recovers.

4 The Discrete SIR(D) Model

Due to the nature of numerical simulations, it is impossible for a continuous time simulation to be done, and as such, the model(s) mentioned above must be adapted to a discrete-time setting to allow for simulations. The discrete-time model **SIRD** model is defined by the following equations:

$$\begin{aligned}
s_{t+1} &= \Delta t\left(-\beta s_t\iota_t - \delta s_t\right), \\
\iota_{t+1} &= \Delta t\left(\beta s_t\iota_t - \gamma\iota_t - \delta f\iota_t\right), \\
r_{t+1} &= \Delta t\left(\gamma\iota_t - \delta r_t\right), \\
\omega_{t+1} &= \Delta t\delta(s_t + f\iota_t + r_t).
\end{aligned}$$

Here, Δt represents the time step after which we re-calculate the value of s, ι, r and ω. As $\Delta t \to 0$, the discrete-time equations converges to the continuous time version. The discrete-time **SIR** model can be obtained from these equations by setting $\delta = 0$. On the other hand, the discrete-time **SI^{K}RD** model is defined by:

$$\begin{aligned}
s_{t+1} &= \Delta t\left(-\beta s_t\iota_t - \delta s_t\right), \\
(\iota_1)_{t+1} &= \Delta t\left(\beta s_t\iota_t - k\gamma(\iota_1)_t - \delta f(\iota_1)_t\right), \\
(\iota_i)_{t+1} &= \Delta t\left(k\gamma(\iota_{i-1})_t - k\gamma(\iota_i)_t - \delta f(\iota_i)_t\right), \quad (i \neq 1, k) \\
(\iota_k)_{t+1} &= \Delta t\left(k\gamma(\iota_{k-1})_t - k\gamma(\iota_k)_t - \delta f(\iota_k)_t\right), \\
r_{t+1} &= \Delta t\left(\gamma(\iota_k)_t - \delta r_t\right), \\
\omega_{t+1} &= \Delta t\delta(s_t + f\iota_t + r_t).
\end{aligned}$$

The quantity ι_t can be found by summing all ι_i $(i = 1, \ldots k)$ at time t:

$$\iota_t = \sum_{i=1}^{k} (\iota_i)_t.$$

5 The Program

The program can be accessed at

https://colab.research.google.com/drive/15Wpzu5fu79SbbYdF4B9XmQU_dtP9oFUL?usp=sharing

Upon clicking, one will be able to view but not edit the program. Please save a copy to one's own drive before editing (since one can't edit otherwise). To run the program, (in order) run the first and fourth cell first:

```
[ ] %%capture

    !pip install ipywidgets
    !pip install matplotlib
    !pip install numpy

    import ipywidgets as widgets
    import matplotlib.pyplot as matplotlib
    from IPython.display import clear_output
    import numpy as np
```

```
[ ] class sirmodel:
      def __init__(self):
        print("Beta value")
        self.betaslider = widgets.FloatSlider(min=0,
        display(self.betaslider)
        print("Gamma value (set to 0 for SI model)")
        self.gammaslider = widgets.FloatSlider(min=0,
        display(self.gammaslider)
        print("R0 (will be automatically updated with
        self.r0= widgets.FloatText(value = 1)
        display(self.r0)
```

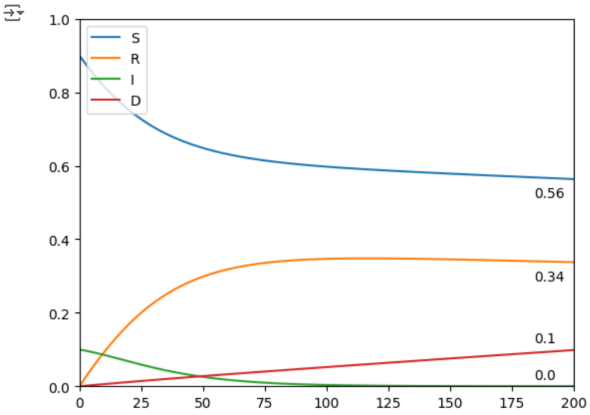
Then, run the second cell and the following user interface should appear:

```
[ ] test = sirmodel()
```

Beta value
0.10
Gamma value (set to 0 for SI model)
0.10
R0 (will be automatically updated with beta/gamma value)
1
Death factor (set to 0 for SI/SIR model), default = 0.001
0.001
Fatality factor (how likely an infected person is to die vs. a noninfected)
3
Initial value of infected population
0.10
Timestep (default = 0.01)
0.01
Iteration (default = 20000)
20000
Number of k (for SI^KRD model).
1.00

One then edits the parameters as one desires using this user interface. Editable parameters include β, γ, δ, f, ι_0, timestep, iteration and the value of k. Then, run the third cell and one should get:

```
[ ] test.make()
```



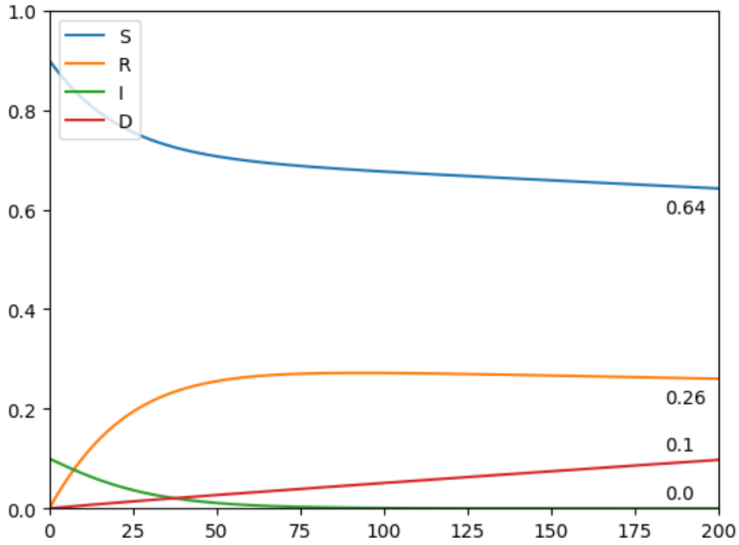
By changing the value of the parameters, one will obtain different behaviors, so please play around with it!

6 Select Examples

All graphs below use default values of parameters unless stated.

6.1 A Non-epidemic

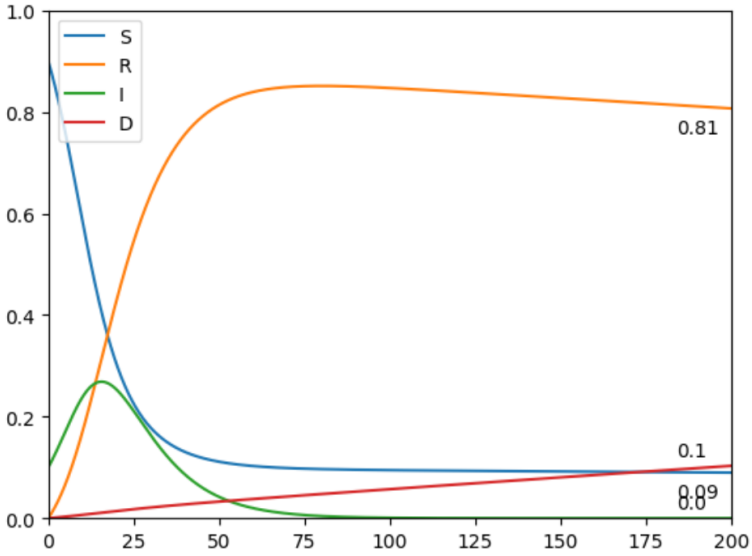
In the simulations of both **SIRD** and **SI^{K}RD** models, when $\beta/\gamma < 1$, the infected populace never shows a peak number, but instead simply decreases. A typical graph of the situation is given below:



($\beta = 0.1$, $\gamma = 0.2$)

6.2 An Epidemic

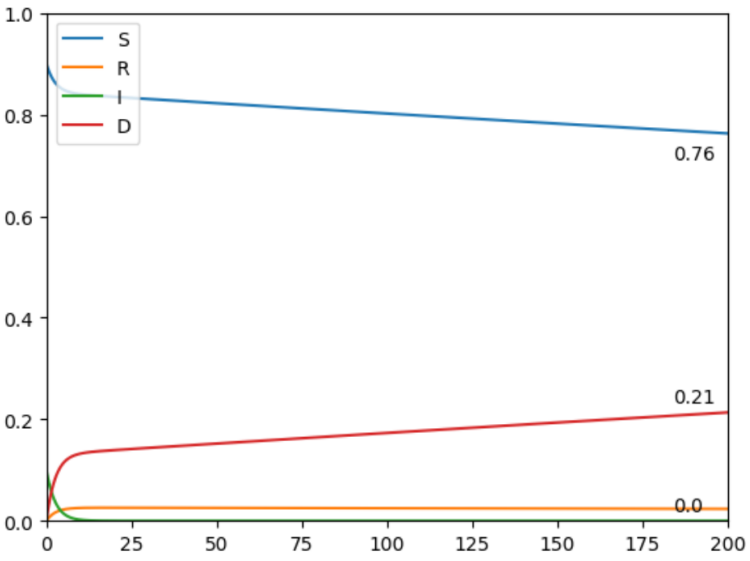
In both the **SIRD** and **SI^{K}RD** model, when $\beta/\gamma > 1$, an epidemic occurs, characterized by the presence of a peak number of infected individuals. A typical graph of the situation is given below:



($\beta = 0.25$, $\gamma = 0.1$)

6.3 A Fatal Disease

Another situation is that the disease is too fatal for it to spread. This is the situation of Ebola, which kills almost all of its hosts, leaving almost none alive. Here, the fatality factor f is very high.

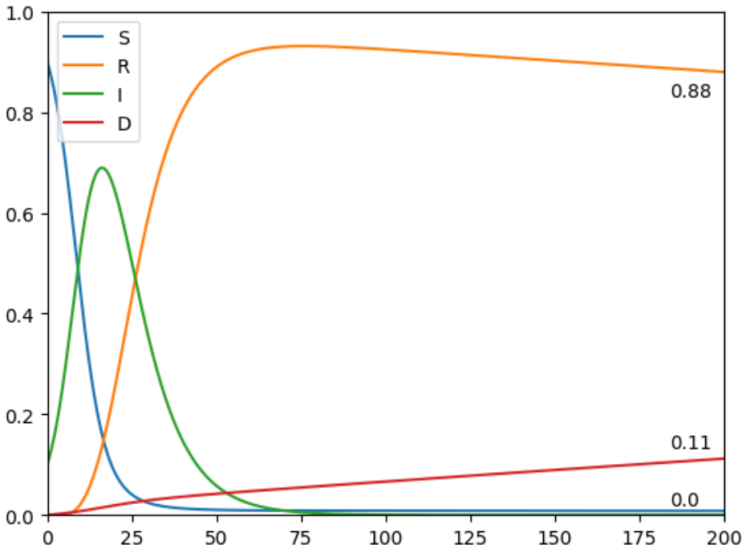


($\beta = 0.25$, $\gamma = 0.1$, $f = 1000$)

We observe that no pandemic occurs since almost all infected die very quickly.

6.4 The Difference between SIRD and SI^{K}RD Models

The **SI^{K}RD** model, as previously mentioned, ensures that the populace in **I** stays infected longer than the **SIRD** model. This graph is the same graph in **Section 6.2** but with $k = 9$.



($\beta = 0.25$, $\gamma = 0.1$, $k = 9$.)

If there are any questions/remarks about the program, please email me or hit me up on messenger.