THE BASIC REPRODUCTION NUMBER IN SIR MODELS – A PROBABILISTIC APPROACH

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Abstract: The SIR (susceptible; infected; recover) model has been extensively used to describe dynamics of a lot of diseases. We work with two types of the SIR model: one without and another with treatment of infection compartment. In this paper, we present the effect of uniform random perturbations in the basic reproduction number (R0) parameters using the Monte Carlo simulation technique, producing uncertainty in R0. The results show that the uncertainty related to the basic reproduction number R0, performed by the Monte Carlo simulation technique, is useful to describe the effects of the parameters changes in the SIR dynamic systems models.

Keywords: uncertainty, sensitivity analysis, Monte Carlo simulation.

1. INTRODUCTION

In the mathematical epidemiology an important concept is related to the basic reproduction number (R0). This is defined as the second expected number produced from just a one individual in a susceptible population. For any infectious disease, one of the most important concerns is its ability to invade a population (Heffernan & Smith, 2005). This can be expressed by a threshold parameter: if the disease free equilibrium is locally asymptotically stable, then the disease cannot invade the population and R0 < 1, whereas if the number of infected individuals grows, the disease can invade the population and R0 > 1 (van den Driessche & Watmough, 2008).

We work with two kind of the SIR model: one without and another with treatment of infection compartment. In this paper, we present for these models the effect of the uniform random perturbations in the basic reproduction number (R0) parameters using the Monte Carlo simulation technique. Sanchez & Blower (1997) assumed a uniform and triangular distribution to some parameters in SIR model. The recruitment parameter of the population Π is associated to the range between 1 and 20 individuals. As for the natural mortality rate μ (due to others factors without the studied disease) and for the recovery rate α (of infected individuals) the range is from 0 to 1. We opt that, because our object it isn’t study these parameters influence in the dynamic, but the disease transmission rate β, so we suggest three procedures to analyze: Procedure 1 has the interval between 0 and 0.1; Procedure 2 between 0.45 and 0.55; and Procedure 3 between 0.9 and 1. We proposed for the second model nine procedures, because we also have the treatment rate r (of infected individuals) with the same intervals as the disease transmission rate β of the other model. We perform 10,000 replicates for each procedure of the two models, thus obtaining values of R0, making possible to find the probability of epidemic occurrence, i.e., the probability of having R0>1. We use the scale transform taking the natural logarithm of R0 added one improving the display of the graphics to be built. Then we verify the disease transmission rate effect in R0 approximate probability distribution pattern, allowing us to obtain the empirical percentile and complementary percentile functions for the considered models.

2. THE PROPOSED METHOD

2.1. The model 1

The Model 1 is a SIR model without treatment in the infection compartment. The model dynamic system is as follows (see Figure 1):

\[
\begin{align*}
\frac{dS}{dt} &= \Pi - \mu S - \beta SI \\
\frac{dI}{dt} &= \beta SI - (\mu + \alpha)I \\
\frac{dR}{dt} &= \alpha I - \mu R 
\end{align*}
\]

where

\[
\begin{align*}
S &= \text{number of susceptible individuals}; \\
I &= \text{number of infected individuals}; \\
R &= \text{number of recovered individuals}; \\
N &= \text{total number of individuals}; \\
\Pi &= \text{recruitment parameter of the population}; \\
\mu &= \text{natural mortality rate (due to others factors without the studied disease)}; \\
\beta &= \text{disease transmission rate}; \text{ and} \\
\alpha &= \text{recovery rate of the infected individuals.}
\end{align*}
\]
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The diseases free equilibrium is:

\[ S^*, I^*, R^* = \left( \frac{\Pi}{\mu}, 0, 0 \right) \]  

(2)

The diseases equilibrium is:

\[ S^*, I^*, R^* = \left( \frac{\mu + \alpha}{\mu + \alpha + r}, \frac{\Pi}{\mu + \alpha + r} \cdot \frac{\mu}{\mu + \alpha + r} \cdot \frac{\mu}{\mu + \alpha + r} \right) \]  

(3)

With, \( N = S + I + R \Leftrightarrow \Pi = \mu N \): the system is closed, i.e., the total number of individuals is constant \( N = \frac{\Pi}{\mu} \).

The basic reproduction number is:

\[ R_0 = \frac{\beta \Pi}{\mu (\mu + \alpha + r)} \]  

(4)

\[ \| \]  

Figure 1 – Progression diagram for the SIR model without treatment.

The Monte Carlo Simulations:

We decided to divide our analyses into procedures, where the uniforms distributions are associated for each \( R_0 \) parameter of as follow:

a) recruitment parameter: \( \Pi \sim U(1 ; 20) \);

b) natural mortality rate: \( \mu \sim U(0 ; 1) \);

c) recovery rate: \( \alpha \sim U(0 ; 1) \); and

d) disease transmission rate \( \beta \) is divided in:

i. \( \beta \sim U(0 ; 0.1) \);

ii. \( \beta \sim U(0.45 ; 0.55) \);

iii. \( \beta \sim U(0.9 ; 1) \).

2.2. The model 2

The Model 2 is a SIR model with treatment in the infection compartment. The model dynamic system is as follows (see Figure 2):

\[
\begin{align*}
\frac{dS}{dt} &= \Pi - \mu S - \beta SI \\
\frac{dI}{dt} &= \beta SI - (\mu + \alpha + r)I \\
\frac{dR}{dt} &= (\alpha + r)I - \mu R
\end{align*}
\]  

(5)

where

\[ S = \text{number of susceptible individuals}; \]

\[ I = \text{number of infected individuals}; \]

\[ R = \text{number of recovered individuals}; \]

\[ N = \text{total number of individuals}; \]

\[ \Pi = \text{recruitment parameter of the population}; \]

\[ \mu = \text{natural mortality rate (due to others factors without the studied disease)}; \]

\[ \beta = \text{disease transmission rate}; \]

\[ \alpha = \text{recovery rate of the infected individuals}; \]

\[ r = \text{treatment rate of infected individuals}. \]

The diseases free equilibrium is:

\[ (S^*, I^*, R^*) = \left( \frac{\Pi}{\mu}, 0, 0 \right). \]  

(6)

The diseases equilibrium:

\[ (S^*, I^*, R^*) = \left( \frac{\mu + \alpha + r}{\mu + \alpha + r}, \frac{\Pi}{\mu + \alpha + r}, \frac{\mu}{\mu + \alpha + r} \cdot \frac{\mu}{\mu + \alpha + r} \right) \]  

(7)

\[ N = S + I + R \Leftrightarrow \Pi = \mu N \]: the system is closed, i.e., the total number of individuals is constant, \( N = \frac{\Pi}{\mu} \).

The basic reproduction number is:

\[ R_0 = \frac{\beta \Pi}{\mu (\mu + \alpha + r)} \]  

(8)

\[ \| \]  

Figure 2 – Progression diagram for the SIR model with treatment.

The Monte Carlo Simulations:

We decided to divide our analyses into procedures, where the uniforms distributions are associated for each \( R_0 \) parameter of as follow:

a) recruitment parameter: \( \Pi \sim U(1 ; 20) \);

b) natural mortality rate: \( \mu \sim U(0 ; 1) \);

c) recovery rate: \( \alpha \sim U(0 ; 1) \); and

d) disease transmission rate \( \beta \) is divided in:

i. \( \beta \sim U(0 ; 0.1) \);

ii. \( \beta \sim U(0.45 ; 0.55) \);

iii. \( \beta \sim U(0.9 ; 1) \); and

e) treatment rate \( r \) is divided in:

i. \( r \sim U(0 ; 0.1) \);

ii. \( r \sim U(0.45 ; 0.55) \);

iii. \( r \sim U(0.9 ; 1) \).

3. THE RESULTS

3.1. The Monte Carlo Simulation for the Model 1

The table 1 shows the empirical probabilities calculated for the basic reproduction number when \( R_0 < 1 \) and \( R_0 > 1 \) after 10,000 runs of the Monte Carlo simulation for each procedure we took.
Table 1 – The empirical probability values according the procedures of SIR model 1.

<table>
<thead>
<tr>
<th>Procedure</th>
<th>𝛽</th>
<th>% 𝑅0 &lt; 1</th>
<th>% 𝑅0 &gt; 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>U(0.00 ; 0.10)</td>
<td>52.90</td>
<td>47.10</td>
</tr>
<tr>
<td>2</td>
<td>U(0.45 ; 0.55)</td>
<td>2.61</td>
<td>97.39</td>
</tr>
<tr>
<td>3</td>
<td>U(0.90 ; 1.00)</td>
<td>0.37</td>
<td>99.63</td>
</tr>
</tbody>
</table>

The histograms of the empirical distribution of the basic reproduction number (𝑅0) are:

- **Figure 3** – Frequency distribution of 𝐿𝑛(𝑅0 + 1) (natural log of the basic reproduction number added one) for SIR model without treatment, Procedure 1: recruitment parameter of the population 𝑃 ∼ U(1 ; 20), natural mortality rate 𝜇 ∼ U(0 ; 1), recovery rate of the infected individuals 𝛼 ∼ U(0 ; 1); disease transmission rate 𝛽 ∼ U(0, 0.1). The red line is 𝐿𝑛(2), i.e. when 𝑅0 = 1.

- **Figure 4** – Frequency distribution of 𝐿𝑛(𝑅0 + 1) (natural log of the basic reproduction number added one) for SIR model without treatment, Procedure 2: recruitment parameter of the population 𝑃 ∼ U(1 ; 20), natural mortality rate 𝜇 ∼ U(0 ; 1), recovery rate of the infected individuals 𝛼 ∼ U(0 ; 1); disease transmission rate 𝛽 ∼ U(0.45 , 0.55). The red line is 𝐿𝑛(2), i.e. when 𝑅0 = 1.

- **Figure 5** – Frequency distribution of 𝐿𝑛(𝑅0 + 1) (natural log of the basic reproduction number added one) for SIR model without treatment, Procedure 3: recruitment parameter of the population 𝑃 ∼ U(1 ; 20), natural mortality rate 𝜇 ∼ U(0 ; 1), recovery rate of the infected individuals 𝛼 ∼ U(0 ; 1); disease transmission rate 𝛽 ∼ U(0.9 , 1). The red line is 𝐿𝑛(2), i.e. when 𝑅0 = 1.

3.2 The Monte Carlo Simulation for the Model 2

The table 1 shows the empirical probabilities calculated for the basic reproduction number when 𝑅0 < 1 and 𝑅0 > 1 after 10,000 runs of the Monte Carlo simulation for each procedure we took.
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Table 1 – The empirical probability values according the procedures of SIR model 2.

<table>
<thead>
<tr>
<th>Proc.</th>
<th>( \beta \sim )</th>
<th>( r \sim )</th>
<th>( R_0 &lt; 1 )</th>
<th>( R_0 &gt; 1 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>U(0.00 ; 0.10)</td>
<td>U(0.00 ; 0.10)</td>
<td>54.52</td>
<td>45.48</td>
</tr>
<tr>
<td>2</td>
<td>U(0.00 ; 0.10)</td>
<td>U(0.45 ; 0.55)</td>
<td>64.84</td>
<td>35.16</td>
</tr>
<tr>
<td>3</td>
<td>U(0.00 ; 0.10)</td>
<td>U(0.90 ; 1.00)</td>
<td>71.69</td>
<td>28.31</td>
</tr>
<tr>
<td>4</td>
<td>U(0.45 ; 0.55)</td>
<td>U(0.00 ; 0.10)</td>
<td>2.94</td>
<td>97.06</td>
</tr>
<tr>
<td>5</td>
<td>U(0.45 ; 0.55)</td>
<td>U(0.45 ; 0.55)</td>
<td>4.89</td>
<td>95.11</td>
</tr>
<tr>
<td>6</td>
<td>U(0.00 ; 0.10)</td>
<td>U(1.00 ; 1.00)</td>
<td>54.52</td>
<td>45.48</td>
</tr>
<tr>
<td>7</td>
<td>U(0.90 ; 1.00)</td>
<td>U(0.00 ; 0.10)</td>
<td>0.37</td>
<td>99.63</td>
</tr>
<tr>
<td>8</td>
<td>U(0.90 ; 1.00)</td>
<td>U(0.45 ; 0.55)</td>
<td>1.23</td>
<td>98.77</td>
</tr>
<tr>
<td>9</td>
<td>U(0.90 ; 1.00)</td>
<td>U(0.90 ; 1.00)</td>
<td>1.98</td>
<td>98.02</td>
</tr>
</tbody>
</table>

The histograms of the empirical distribution of the basic reproduction number (\( R_0 \)) are:

Figure 8 – Frequency distribution of \( \ln(R_0 + 1) \) (natural log of the basic reproduction number added one) for SIR model with treatment, Procedure 1: recruitment parameter of the population \( \Pi \sim U(1 ; 20) \), natural mortality rate \( \mu \sim U(0 ; 1) \), recovery rate of the infected individuals \( \alpha \sim U(0 ; 1) \); disease transmission rate \( \beta \sim U(0 , 0.1) \); treatment rate \( r \sim U(0 , 0.1) \). The red line is \( \ln(2) \), i.e. when \( R_0 = 1 \).

Figure 9 – Frequency distribution of \( \ln(R_0 + 1) \) (natural log of the basic reproduction number added one) for SIR model with treatment, Procedure 2: recruitment parameter of the population \( \Pi \sim U(1 ; 20) \), natural mortality rate \( \mu \sim U(0 ; 1) \), recovery rate of the infected individuals \( \alpha \sim U(0 ; 1) \); disease transmission rate \( \beta \sim U(0 , 0.1) \); treatment rate \( r \sim U(0.45 , 0.55) \). The red line is \( \ln(2) \), i.e. when \( R_0 = 1 \).

Figure 10 – Frequency distribution of \( \ln(R_0 + 1) \) (natural log of the basic reproduction number added one) for SIR model with treatment, Procedure 3: recruitment parameter of the population \( \Pi \sim U(1 ; 20) \), natural mortality rate \( \mu \sim U(0 ; 1) \), recovery rate of the infected individuals \( \alpha \sim U(0 ; 1) \); disease transmission rate \( \beta \sim U(0 , 0.1) \); treatment rate \( r \sim U(0.9 , 1) \). The red line is \( \ln(2) \), i.e. when \( R_0 = 1 \).

Figure 11 – Frequency distribution of \( \ln(R_0 + 1) \) (natural log of the basic reproduction number added one) for SIR model with treatment, Procedure 4: recruitment parameter of the population \( \Pi \sim U(1 ; 20) \), natural mortality rate \( \mu \sim U(0 ; 1) \), recovery rate of the infected individuals \( \alpha \sim U(0 ; 1) \); disease transmission rate \( \beta \sim U(0.45 , 0.55) \); treatment rate \( r \sim U(0 , 0.1) \). The red line is \( \ln(2) \), i.e. when \( R_0 = 1 \).

Figure 12 – Frequency distribution of \( \ln(R_0 + 1) \) (natural log of the basic reproduction number added one) for SIR model with treatment, Procedure 5: recruitment parameter of the population \( \Pi \sim U(1 ; 20) \), natural mortality rate \( \mu \sim U(0 ; 1) \), recovery rate of the infected individuals \( \alpha \sim U(0 ; 1) \); disease transmission rate \( \beta \sim U(0.45 , 0.55) \); treatment rate \( r \sim U(0.45 , 0.55) \). The red line is \( \ln(2) \), i.e. when \( R_0 = 1 \).
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Figure 13 – Frequency distribution of $\ln(R_0 + 1)$ (natural log of the basic reproduction number added one) for SIR model with treatment. Procedure 6: recruitment parameter of the population $\pi \sim U(1 ; 20)$, natural mortality rate $\mu \sim U(0 ; 1)$, recovery rate of the infected individuals $\alpha \sim U(0 ; 1)$; disease transmission rate $\beta \sim U(0.45 , 0.55)$; treatment rate $r \sim U(0.9 , 1)$. The red line is $\ln(2)$, i.e. when $R_0 = 1$.

Figure 14 – Frequency distribution of $\ln(R_0 + 1)$ (natural log of the basic reproduction number added one) for SIR model with treatment. Procedure 7: recruitment parameter of the population $\pi \sim U(1 ; 20)$, natural mortality rate $\mu \sim U(0 ; 1)$, recovery rate of the infected individuals $\alpha \sim U(0 ; 1)$; disease transmission rate $\beta \sim U(0.9 , 1)$; treatment rate $r \sim U(0.5 , 1)$. The red line is $\ln(2)$, i.e. when $R_0 = 1$.

Figure 15 – Frequency distribution of $\ln(R_0 + 1)$ (natural log of the basic reproduction number added one) for SIR model with treatment. Procedure 8: recruitment parameter of the population $\pi \sim U(1 ; 20)$, natural mortality rate $\mu \sim U(0 ; 1)$, recovery rate of the infected individuals $\alpha \sim U(0 ; 1)$; disease transmission rate $\beta \sim U(0.9 , 1)$; treatment rate $r \sim U(0.45 , 0.55)$. The red line is $\ln(2)$, i.e. when $R_0 = 1$.

The empirical percentile (figure 17) and complementary percentile (figure 18) functions for the first model are constructed from the values gotten in Monte Carlo simulation.
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4. CONCLUSION

The initial results show that the uncertainty related to the basic reproduction number, performed by the Monte Carlo simulation technique, are useful to describe the effects of the parameters changes in the SIR dynamic systems models.

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REFERENCES


