THE BASIC REPRODUCTION NUMBER IN SI STAGED PROGRESSION MODEL: A PROBABILISTIC APPROACH

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Abstract: The SI (susceptible; infected) staged progression model is used for many diseases where the transmission probabilities vary as the viral load in an infected individual changes. We work with a version of the SI staged progression model proposed by van den Driessche & Watmough (2002). In this paper, we present the effect of uniform random perturbations in the basic reproduction number (R_0) parameters using the Monte Carlo simulation technique, producing uncertainty in R_0. The idea of perturbation is due to the fact that in nature these parameters aren't constant. The results show that the uncertainty related to the basic reproduction number R_0, performed by the Monte Carlo simulation technique, is useful to describe the effects of the parameters changes in the SI staged progression dynamic system model.

keywords: uncertainty, sensitivity analysis, Monte Carlo simulation.

1. INTRODUCTION

In the mathematical epidemiology an important concept is related to the basic reproduction number (R_0). This is defined as the expected number of secondary infection produced by an index case in a completely 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 $R_0 < 1$, whereas if the number of infected individuals grows, the disease can invade the population and $R_0 > 1$ (van den Driessche & Watmough, 2008).

We work with the SI staged progression model, which has a single uninfected compartment and infected individuals progress through several stages of the disease with changing infectivity. We present for this model the effect of the uniform random perturbations in the basic reproduction number (R_0) parameters using the Monte Carlo simulation technique. The idea of perturbation is due to the fact that in nature these parameters aren't constant. Sanchez & Blower (1977) as-

sumed a uniform and triangular distribution to some parameters in SIR model.

2. THE PROPOSED METHOD

2.1. The model

The SI (susceptible; infected) staged progression model has a single uninfected compartment and infected individuals progress through several stages of the disease with changing infectivity. It is used for many diseases where the transmission probabilities vary as the viral load in an infected individual changes, for example HIV/AIDS. The model dynamic system is as follows (see Figure 1):

$$
\begin{cases}
\dfrac{dS}{dt} &= \Pi - \mu S - S \sum_{i=1}^{n} \beta_i I_i \\[2mm]
\dfrac{dI_1}{dt} &= S \sum_{i=1}^{n} \beta_i I_i - (\mu + \nu_1) I_1 \\[2mm]
\dfrac{dI_k}{dt} &= \nu_{k-1} I_{k-1} - (\mu + \nu_k) \\[2mm]
\dfrac{dI_n}{dt} &= \nu_{n-1} I_{n-1} - \mu I_n
\end{cases}
\tag{1}
$$

$k = 2, 3, \ldots, n - 1$
where

S = number of susceptive individuals;
I_k = number of infected individuals in the k stage of the disease, $k = 1, \ldots, n$;
N = total number of individuals;
Π = recruitment parameter of the population;
μ = natural mortality rate (due to others factors without the studied disease;
β_i = disease transmission rate for i stage of the disease;
ν_i = disease evolution rate from i to $i + 1$ stage of the disease, $i = 1, 2, \ldots$; and
n = number of infected compartments.

With $N = S + I_1 + I_2 + \ldots + I_n \iff \Pi = \mu N$: the system is closed, i.e., the total number of individuals is constant, then $N = \frac{\Pi}{\mu}$.

The basic reproduction number is:

$$R_0 = \frac{\Pi}{\mu(\mu+\nu_1)} \left[\beta_1 + \frac{\beta_2 \nu_1}{\mu+\nu_2} + \frac{\beta_3 \nu_1 \nu_2}{(\mu+\nu_2)(\mu+\nu_3)} \right. $$
$$\left. + \ldots + \frac{\beta_n \nu_1 \nu_2 \ldots \nu_{n-1}}{(\mu+\nu_2)\ldots(\mu+\nu_{n-1})\mu} \right] \quad (2)$$
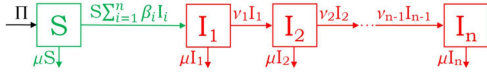

Figure 1 – Progression diagram for SI staged model

2.2. *The Monte Carlo Simulation*

We decided to divide our analysis into procedures, where the uniforms distributions are associated for each R_0 parameter as follow:

a) recruitment parameter of the population: $\Pi \sim U(1; 20)$;
b) natural mortality rate: $\mu \sim U(0; 1)$;
c) disease evolution rate: $\nu_i \sim U(0; 1), \forall i = 1, \ldots, n$;
d) disease transmission rate β_i is divided in:

- $\beta_i \sim U(0; 0.1)$;
- $\beta_i \sim U(0.45; 0.55)$;
- $\beta_i \sim U(0.9; 1)$;

We opt these intervals, because our object it's study the disease transmission rates influences in the dynamic, and not of the others parameters.

3. DISCUSSION

10,000 replicates were performed for each procedure of the two models, thus obtaining values of R_0, making possible to find the probability of an epidemic, i.e., when $R_0 > 1$. We developed a scale transformation taking the natural logarithm of R_0 added by unity with the goal of improving the graphics display to be constructed. Thus we see the effect of the disease transmission rate in the pattern of the approximate probability distribution of R_0, allowing to obtain the empirical percentile and complementary percentile functions for the cases with one, two and three stages of the infected compartment of the consider models.

For the case with one compartment of disease we have the famous SI model. We observed that when the range of disease transmission rate is close to zero, the empirical probability of $R_0 > 1$ is about 60%. For the others two intervals is greater than 90%. When we have two compartments of the disease, if one of the disease transmission rates is not close to zero, the empirical probability of $R_0 > 1$ is greater than 90%, otherwise, this probability is almost 70%. Now, for three compartments, when all the disease transmission rate are close to zero, the empirical probability of $R_0 > 1$ is more

than 70%, and for the others combinations, this probability is around or greater than 90%.

So, with these results we verify the importance of dividing the disease into stages, if, of course, the disease under study allow this use. But also know in how many stages classify.

4. CONCLUSION

The initial results show that the uncertainty related to the basic reproduction number (R_0) performed by the Monte Carlo simulation technique, is useful to describe the effects of the parameters changes in the SI staged progression dynamic system model.

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