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SOME CORRECTIONS TO THE KERMACK-MCKENDRICK MODEL

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Summary

In the book "Mathematical Biology" written by J.D. Murray the Kermack-McKendrick model connected with epidemiological data is presented in the form of a system of differential equations in which fractions of individuals susceptible to illness (*S*), infected (*I*) and resistant (*R*) appear. From the equations Murray extracts the function $I(S) = 1 - S + \frac{1}{\delta} \ln \frac{S}{S_0}$, treating I_0 as fraction of infected in the initial time (δ is a parameter). In fact $I_0 = I(S_0)$, where S_0 is fraction of individuals susceptible to illness in the initial time and $I(S) = -S + \frac{1}{\delta} \ln \frac{S}{S_0} + I(S_0) + S_0$. In the paper differences resulting from both forms of I(S) are described.

Keywords and phrases: system of differential equations, the Kermack-McKendrick model connected with epidemiological data

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1. Introduction

Introduced in 1927 the Kermack-McKendrick model was proposed to explain the rapid rise and fall in the number of infected patients observed in epidemics such as the plague in London (1665-66), Bombay (1906) and cholera in London (1865). It is the so called SIR model, because a fixed population is considered with three compartments: susceptible (S(t)), infected (I(t)) and resistant (R(t)). Apart from the SIR model a lot of other models may be taken into consideration, e.g. SIS model (disease with no immunity), SIR endemic (including births and deaths), criss-cross infections (concerning malaria) and many others. The SIR model was forgotten for quite a long time and it was brought back to prominence by Anderson and May (1979). Since that time the Kermack-McKendrick model has been developed in many papers as in R.M Anderson (1991), F. Brauer (2005), J. Stepan and D. Hlubinka (2007), and we can note also some applications of that model, e.g. for AIDS epidemic (X.C. Huang and M. Villasana, 2005).

2. Murray's interpretation of the Kermack-McKendrick model

The Kermack-McKendrick model (1927) connected with epidemiological data is presented in the book "Mathematical Biology" written by J.D. Murray (2002). The same model is also described by Forys (2005).

Let us denote by S(t) fraction of individuals susceptible to illness, I(t) fraction of infected individuals, and R(t) - fraction of resistant ones, i.e. such individuals that have passed infection (they will not be infected in the future). The equations in the model are the following:

$$\begin{aligned} \frac{d}{dt}S(t) &= -\lambda S(t)I(t) \\ \frac{d}{dt}I(t) &= \lambda S(t)I(t) - \gamma I(t) \\ \frac{d}{dt}R(t) &= \gamma I(t) \,, \end{aligned}$$

where λ denotes the probability that contacts between individuals cause infection, and γ is the probability of recovering from infection. Let us take λ .

$$\delta = \frac{\pi}{\gamma}$$

Let us assume that $S_0 = S(0) > 0$, $I_0 = I(0) > 0$ and R(0) = 0. Analyzing the given equations we can state that S(t) is a decreasing function whereas I(t) also may be decreasing (when $S_0 < \frac{1}{\delta}$) but on the other hand it may initially increase (i.e. epidemic expands) to be decreasing then from a certain moment (see e.g. Foryś 2005).

Dividing the second equation by the first we get I as a function of S, namely

$$I(S) = -S + \frac{1}{\delta} \ln S + C \,.$$

Due to Murray the constant *C* is equal to $I_0 + S_0 - \frac{1}{\delta} \ln S_0$, where I_0 is treated as I(0). Still in this case I_0 is actually $I(S_0)$ and that is why we will continue with the following formula of I(S):

$$I(S) = -S + \frac{1}{\delta} \ln \frac{S}{S_0} + I(S_0) + S_0.$$

Of course $I_0 + S_0 = 1$ so Murray gave the following incorrect formula for I(S):

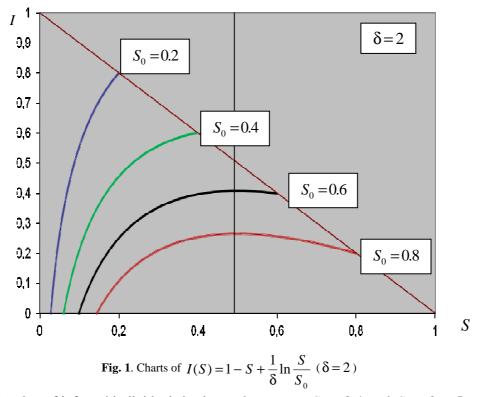
$$I(S) = 1 - S + \frac{1}{\delta} \ln \frac{S}{S_0}.$$

The figure 1 shows charts of $I(S) = 1 - S + \frac{1}{\delta} \ln \frac{S}{S_0}$ for $S_0 = 0.2, 0.4, 0.6, 0.8$. We assume that $\delta = 2$.

All the charts are located in the triangular area because $0 \le I(t) + S(t) \le 1$. Due to Figure 1 when more than half of population is initially susceptible to illness $(S_0 > \frac{1}{2})$ then epidemic expands in the beginning till S falls to $\frac{1}{2}$. Fraction of infected individuals is then the largest and equal to $\frac{1}{2}(1 - \ln 2S_0)$. Then epidemic is dying and I(t) tends to zero when S approaches to the solution of the equation $1 - S + \frac{1}{2} \ln \frac{S}{S_0} = 0$.

3.
$$I_0 = I(S_0)$$
 vs $I_0 = I(0)$

In effect $I(S_0) + S_0$ need not be equal to one. The next three figures show charts of $I(S) = -S + \frac{1}{\delta} \ln \frac{S}{S_0} + I(S_0) + S_0$ for the same values of S_0 and δ as in figure 1. Now $I(S_0)$ does not uniquely depend on S_0 . As we can see, now conclusions taking into account Figures 2, 3, and 4 are quite different from those resulting from Figure 1.



Fraction of infected individuals is almost the same at $S_0 = 0.4$ and $S_0 = 0.6$. It is always less than fraction at $S_0 = 0.8$ so the initial large number of susceptible to illness gives greater fraction of infected individuals. Epidemic may appear only when the fraction of infected individuals is rather small $(I(S_0) = 0.2)$ and, similarly as due to Figure 1, is dying after some moment and I(t) tends to zero when S approaches to the solution S_1 of the equation $I(S_0) + S_0 = S - \frac{1}{\delta} \ln \frac{S}{S_0}$. This solution is less than 0.2 and decreases if $I(S_0)$ increases.

Figures more similar to Figure 1 may be obtained when $I(S_0) = 0.2$ and $\delta = 1$ or $\delta = 1.5$ (see Figures 5 and 6).

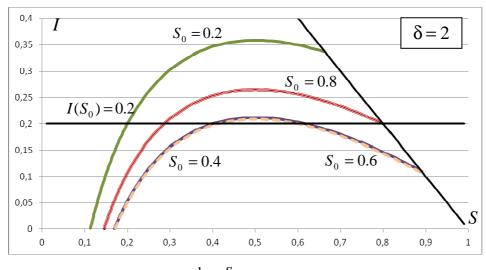


Fig. 2. Charts of $I(S) = -S + \frac{1}{\delta} \ln \frac{S}{S_0} + I(S_0) + S_0$ with $I(S_0) = 0.2$ ($\delta = 2$)

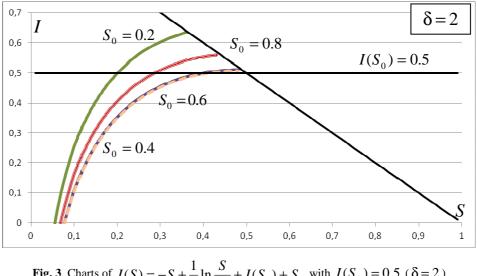
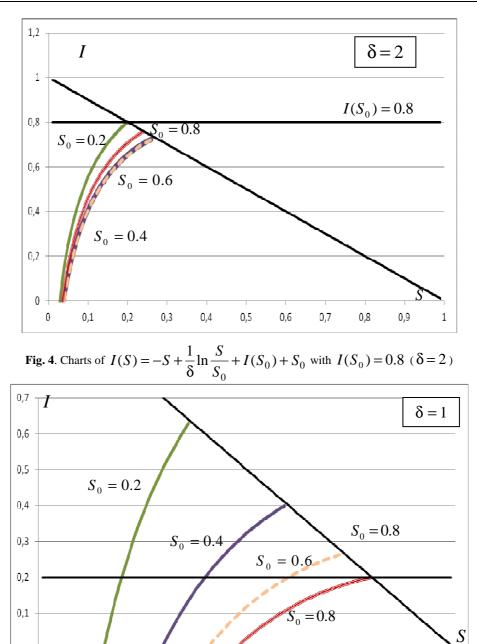
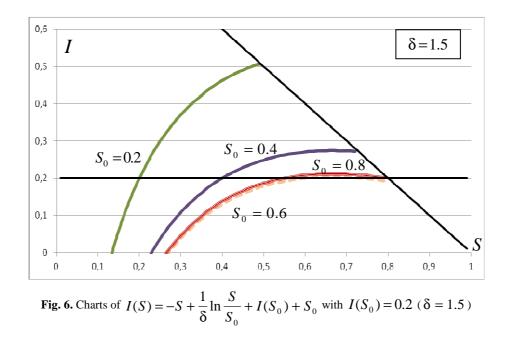


Fig. 3. Charts of $I(S) = -S + \frac{1}{\delta} \ln \frac{S}{S_0} + I(S_0) + S_0$ with $I(S_0) = 0.5 \ (\delta = 2)$



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