

A note on Exact solution of SIR and SIS epidemic models

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Abstract

In this article we have successfully obtained an exact solution of a particular case of SIR and SIS epidemic models given by Kermack and Mckendrick [1] for constant population, which are described by coupled nonlinear differential equations. Our result has no limiting conditions for any parameter involved in the given models. In epidemiology many researchers believe that it is very hard to get an exact solution for such models. We hope this solution will be an opening window and good addition in the area of epidemiology.

Key Words: SIR and SIS, Epidemiology, Exact Solution.

1 Introduction

The mathematical modelling of spread of diseases is an area of biology named as epidemiology. Physical real life problems arising in epidemiology may be described, in a first formulation, using differential equations. As far as our knowledge is concerned the first mathematical model of epidemiology was formulated and solved by Daniel Bernoulli in 1760. Since the time of Kermack and McKendrick [1], the study of mathematical epidemiology has grown rapidly, with a large variety of models having been formulated and applied to infectious diseases [2]-[4].

The dilemma with models in epidemiology is, sometimes even the simplest mathematical model of natural phenomena with sets of first-order ordinary differential equations are non-integrable. Nucci and Leach [5] have discussed these features and obtained an integrable SIS model by applying Lie analysis. According to Nucci and Leach [5] *It would seem that a fatal disease which this models is also not good for mathematics!* Khan et.al., [6] has obtained the convergent series solutions for SIR and SIS models using homotopy analysis method. Considerable attention has been given to

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these models by several authors using stability, bifurcation theory, Lyapunov method, Poincaré-Bendixson type theorems, index and topological concepts see ([2]-[16]).

To understand what SIS and SIR stands for let us consider some constant population, let divide them into three components: the susceptible component, S, who can catch the disease; the infective component, I, who are infected and can transmit the disease to susceptible, and the removed component, R, who either had the disease and recovered, died or have developed immunity, or have been removed from contact with other components. SIR model contains all three classes, while, in SIS model the infectives return to the susceptible class on recovery because the disease confers no immunity against reinfection. Such models are more effective for disease caused by bacteria or helminth agents and also for most sexually transmitted disease.

In fact closed-form solutions to mathematical models play a vital role in the proper understanding of qualitative features of natural science. In epidemiology mathematical models describes some effects of disease in some population so one need to be very careful while analyzing such models. Keeping this view of point, here in this article our main goal is to obtain pure analytic exact solution to the SIS and SIR epidemic model which is a particular case of the model given by Kermack and McKendrick [1].

In second section we present the solution for SIS model while in third section we present solution for SIR model.

2 Mathematical Analysis for SIS model

The SIS model by Kermack and Mckendrick [1] is given as follows

$$s'(t) = -rsi + \alpha i, \quad (1)$$

$$i'(t) = rsi - \alpha i, \quad (2)$$

subject to Initial conditions,

$$i(0) = I_0, \quad s(0) = S_0, \quad (3)$$

where $r > 0$, $I_0 > 0$ and $S_0 > 0$. Here r is the infectivity coefficient of the typical Lotka-Volterra interaction term and α the recovery coefficient. From equation (1) and (2) one can easily observe that $s(t) + i(t) = k$, where k is total population. This model is different from SIR model as in this model the recovered members return to the class S at a rate of $i\alpha$ instead of moving to class R.

Now using $s(t) = k - i(t)$ in equation (2),

$$i' = r(k - i)i - \alpha i. \quad (4)$$

Integrating the above equation (4) with substitution $y = i^{-1}$, we get

$$ye^{(rk-\alpha)t} = \int re^{(rk-\alpha)t} dt + C, \quad (5)$$

where C is integrating constant. After simplifying equation. (5) and letting $\beta = rk - \alpha$, we get,

$$y = \frac{r + \beta C e^{-\beta t}}{\beta}. \quad (6)$$

Using back substitution $y = i^{-1}$,

$$i(t) = \frac{\beta}{r + \beta C e^{-\beta t}}. \quad (7)$$

After applying initial condition $i(0) = i_0$ on equation (7) we get,

$$C = \frac{\beta - i_0 r}{\beta i_0}.$$

The exact solution for $s(t)$ obtained by using the fact $s(t) + i(t) = k$ is,

$$s(t) = k - \frac{\beta}{r + \beta \left(\frac{\beta - i_0 r}{\beta i_0}\right) e^{-\beta t}}.$$

3 Mathematical Analysis for SIR model

The SIR model by Kermack and Mckendrick [1] is given as follows

$$s'(t) = -\beta s(t)i(t) - \mu s(t) + \mu, \quad (8)$$

$$i'(t) = \beta s(t)i(t) - \mu i(t), \quad (9)$$

subject to Initial conditions,

$$i(0) = i_0, \quad s(0) = s_0, \quad (10)$$

($'$) denotes the derivative with respect to time, where $\beta > 0$, $i_0 > 0$ and $s_0 > 0$. Here β is the infectivity coefficient of the typical Lotka-Volterra interaction term and μ the recovery coefficient. Now adding equation (8) and equation (9),

$$(s + i)' = -\mu (s + i) + \mu. \quad (11)$$

Integrating the above equation 11, we get

$$s(t) = 1 + C e^{(-\mu)t} - i(t), \quad (12)$$

where C is an integrating constant. Now using equation (12) in equation (9), we get,

$$i'(t) = (\beta - \mu + \beta C e^{-\mu t})i(t) - \beta i^2(t). \quad (13)$$

Integrating the above equation with substitution $z = i^{-1}$, we get

$$z e^{(\beta - \mu)t - (\frac{\beta C}{\mu})e^{-\mu t}} = \int \beta e^{(\beta - \mu)t - (\frac{\beta C}{\mu})e^{-\mu t}} dt + D. \quad (14)$$

Where D is an integrating constant. Now observing that $e^{-\mu t}$ approaches to zero as $t \rightarrow \infty$, here we take series expansion for $e^{-\mu t}$ and neglecting square and higher terms we get $e^{-\mu t} = 1 - \mu t$. Substituting back in equation (14) one gets,

$$z e^{(\beta - \mu)t - (\frac{\beta C}{\mu})(1 - \mu t)} = \int \beta e^{(\beta - \mu)t - (\frac{\beta C}{\mu})(1 - \mu t)} dt + D, \quad (15)$$

$$z = \frac{\beta}{\beta - \mu + \beta C} + D e^{-(\beta - \mu + \beta C)t} e^{\frac{\beta C}{\mu}}, \quad (16)$$

Substituting $z = i^{-1}$ and $\beta - \mu + \beta C = \lambda$, in equation (16) we get

$$i(t) = \frac{\lambda}{\beta + \lambda D e^{-\lambda t} e^{\frac{\beta C}{\mu}}}. \quad (17)$$

Applying initial condition $i(0) = i_0$ and $s(0) = s_0$ in equation (12) and (20) we get,

$$D = \frac{\lambda - i_0 \beta}{\lambda i_0 e^{\frac{\beta C}{\mu}}}$$

$$C = s_0 + i_0 - 1. \quad (18)$$

The exact solution for $s(t)$ obtained by using the value of $i(t)$ in equation (12) which is,

$$s(t) = 1 + (s_0 + i_0 - 1)(1 - \mu t) - \frac{\lambda}{\beta + \lambda \left(\frac{\lambda - i_0 \beta}{\lambda i_0 e^{\frac{\beta C}{\mu}}} \right) e^{-\lambda t + \frac{\beta(s_0 + i_0 - 1)}{\mu}}}, \quad (19)$$

$$i(t) = \frac{\lambda}{\beta + \lambda \left(\frac{\lambda - i_0 \beta}{\lambda i_0 e^{\frac{\beta C}{\mu}}} \right) e^{-\lambda t + \frac{\beta(s_0 + i_0 - 1)}{\mu}}}. \quad (20)$$

4 Conclusion

In this paper an exact analytic solution to a particular case of SIR and SIS models with constant population is obtained with the help of direct integration tools. As these models have already been observed by different researchers with different techniques

but we know the importance of exact solution, that exact solutions allow researchers to run experiments, by introducing natural initial or boundary conditions, to observe the behavior of functions involved in equations. This present work will be of great support to the epidemiology to investigate the hidden phenomenon and validity of these models which is already being considered and used by different researchers. This kind of approach will attract other nonlinear models as well having been analyzed again for the possible existence of exact solution.

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