

Basic Reproductive Rate of a Spatial Epidemic SEIR Model using Computer Algebra Software

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Abstract—

The use of computer algebra software has many applications in diverse fields like epidemiology. This work pretends to show how computer algebra software applications for symbolic computation have a very promissory future in mathematical epidemiology with a concrete problem of this kind.

In this case; the basic reproductive rate, corresponding to the propagation of a certain disease inside a circular habitat when the disease is endemic at the boundary is calculated using computer algebra software with the method of Laplace Transform Technique and residues calculus.

The results obtained, includes both the explicit form of the R_0 for the boundary condition that was considered, and the explicit symbolic solution of the model equations. The method used can be extended to more complex problems such as indirectly transmitted diseases with one or more intermediary hosts or effects of genetic, immunological, geographical or social heterogeneity in the human population.

Keywords— Basic reproductive rate, Computer algebra software, pan-epidemic threshold, pan-endemic threshold

Introduction

Some Mathematical Epidemiology problems can be solved using software to obtain numerical calculations, but certain epidemiological problems demand software for symbolic computations such as computer algebra systems. The object of the present work is to solve certain spatial epidemic model using computer algebra software. The chosen problem can not be solved using numerical software because the solution is the analytical formula for the basic reproductive rate which is a symbolic expression that can not be determined just with numerical experimentation.

Also, the manually solution of the chosen problem would not be an easy one, because of the algebraic manipulation. This epidemiological problem solved with the help of computer algebra system considers a circular habitat in which certain disease of SEIR kind, is endemic at the boundary.

That was obtained was the explicit expression for the basic reproductive rate of the disease at such configuration and the density profiles of infectious and latent individuals.

This work is enclosed within a line of symbolic computational epidemiology which was introduced by [7] and was extended in [8]. In [7] the spatial SIR model was considered and the respective basic reproductive rate was computed. In [8], the case of more complex disease like schistosomiasis, was affronted. The object of the present work is to display an original and unpublished example that is intermediate between [7] and [8].

I. Mathematical Model

This deterministic SEIR epidemic model [1], with spatial extension in form of the inclusion of terms about diffusion [2] consists of four coupled non-linear partial differential equations for the densities of susceptible, latent, infectious and removed individuals. But this non-linear model is non-tractable by computer algebra system. Despite, in the early stages of the pan-epidemic event it is possible to reduce the original non-tractable and non-linear model in one linear model, tractable by computer algebra system. Because of this, the four coupled and non-linear equations system is reduced to a two coupled but linear equations system for the densities of latent an infectious.

Then, we will look for the explicit symbolic solutions of these two equations and the explicit form of the basic reproductive rate of the disease.

The mathematical model is the following system of two coupled linear reaction-diffusion equations:

$$\left(\frac{\partial}{\partial t} u_E(r, t) \right) - \delta_E \left(\frac{\partial}{\partial r} u_E(r, t) + \left(\frac{\partial^2}{\partial r^2} u_E(r, t) \right) \right) = \beta S_0 u_I(r, t) - f_E u_E(r, t), \quad (1)$$

$$\left(\frac{\partial}{\partial t} u_I(r, t) \right) - \delta_I \left(\frac{\partial}{\partial r} u_I(r, t) + \left(\frac{\partial^2}{\partial r^2} u_I(r, t) \right) \right) - K u_E(r, t) + \gamma u_I(r, t) = 0 \quad (2)$$

with the initial conditions

$$u_E(r, 0) = 0, u_I(r, 0) = 0 \quad (3)$$

and with the boundary condition

$$u_I(a, t) = \mu_b \quad (4)$$

the equation (1) describes the dynamics of the density of latent individuals and the equation (2) gives the dynamics of the density of infectious individuals; where $u_E(r, t)$ represents the density of latent individuals at the point of polar coordinates (r, θ) in the time t and $u_I(r, t)$ represents the density of infectious individuals at (r, θ) in t . δ_E represents the diffusion constant of the latent individuals and similarly δ_I denotes the diffusion constant of the infectious individuals. The symbol β represents the infectiousness from the infectious to the susceptible that converts the susceptible to latent individual; K represents the rate of transition from the state of latent to the infectious state, f_E represents the removal rate of latent individuals and γ represents the removal rate of infectious individuals. Finally, S_0 represents the initial density of susceptible individuals.

The initial conditions shown at (3) represent neither infectious nor latent individuals inside the circular habitat initially. The boundary condition given in (4) corresponds to the case of endemic boundary, so, at the boundary of the circular habitat the disease is permanently present with a constant density of infectious individuals which is denoted μ_b .

II. Method

The method that is presented in this section was originally introduced in [7] and [8] and it is like follows. In order to solve the equations (1) and (2) with the conditions (3) and (4), a computer algebra algorithm was constructed. In such algorithm, the Laplace transform technique was applied and the Inverse Laplace transform was realized using calculus of residues. The algorithm of computer algebra that was used can be presented as:

Apply the Laplace Transform to the system (1), (2) with (3) to turn such partial equations in ordinary differential equations.

Solve such system of ordinary equations using the condition (4).

Calculate the Inverse Laplace Transform using the Bromwich integral and the residue theorem.

Extract from the solution the form of the basic reproductive rate of disease in a circular habitat with endemic boundary condition (Stability Analysis).

This algorithm can be implemented manually but the implied calculations are quite long and tedious. Fortunately, the accessible computer algebra software is able to realize such calculations in a very efficient way. Unfortunately, the algorithm can not be realized automatically, it requires constant command from the user. Maybe in the future the computer algebra software will incorporate the residue techniques for Inverse Laplace Transform so they can permit to make more direct algorithms for symbolic solution of partial differential equations systems with boundary conditions.

III. Results

The explicit solution for the density of infectious individuals and the density of latent individuals that are obtained using our algorithm for computer algebra software is

$$U_I(r, t) = \frac{\mu_b J_0(\lambda(0) r)}{J_0(\lambda(0) a)} + \left(\sum_{n=1}^{\infty} \left(\sum_{l=1}^2 \left(- \frac{\mu_b J_0\left(\frac{\alpha_n}{a}\right) e^{(S_{l,n} t)}}{S_{l,n} \left(\frac{\partial}{\partial s} \lambda(S_{l,n})\right) a J_l(\alpha_n)} \right) \right) \right) \quad (5)$$

where $\lambda(s)$ is defined according to

$$\frac{(s + f_E + \delta_E \lambda(s)^2) (s + \gamma + \delta_I \lambda(s)^2)}{\kappa} - \beta S_0 = 0 \quad (6)$$

and the parameters $S_{j,n}$ are the roots of the following quadratic equation

$$\frac{s^2}{\kappa} + \frac{\left(f_E + \frac{\delta_E \alpha_n}{a} + \gamma + \frac{\delta_I \alpha_n}{a}\right) s}{\kappa} + \frac{\left(f_E + \frac{\delta_E \alpha_n}{a}\right) \left(\gamma + \frac{\delta_I \alpha_n}{a}\right)}{\kappa} - \beta S_0 = 0 \quad (7)$$

being α_n are the roots of the Bessel function J_0 , it is to say, the solutions of the equation $J_0(x)=0$ [3].

IV. Analysis of Results

The equation (5) has two terms. The first term has no dependence on time. The other term that involve summations have exponential dependence on time. The first term can be named the pan-endemic state or configuration, corresponds to the stationary solution of (1)-(2). The pan-epidemic term is identified with the term with positive exponential dependence on time. In first instance we analyze the pan –endemic term. The pan-endemic state exists only if $\lambda(0) > 0$, it is to say when

$$\gamma f_E - K \beta S_0 < 0 \quad (8)$$

the pan-endemic threshold of the inequality (8) can be rewritten as $R_0 > 1$, where the pan-endemic basic reproductive rate R_0 is defined

$$R_0 := \frac{K \beta S_0}{\gamma f_E} \quad (9)$$

the formula (9) is the usual basic reproductive rate of disease in the case of purely temporal epidemic models that no incorporates spatial effects.

In the terms of (5) with exponential dependence on time, it can be observed that according to (7) and (8) only the first term that involves summation can have a positive exponential dependence on time which is determined by $s_{1,n}$ in (7) while for the second always has a negative exponential dependence on time which is determined by $s_{2,n}$ in (8). Then the pan-epidemic outbreak is possible only if $s_{1,n} > 0$, it is to say when $C_n < 0$ which implies that

$$-K \beta S_0 + \frac{\alpha_n^4 \delta_I \delta_E}{a^4} + \gamma f_E + \frac{\alpha_n^2 \delta_I f_E}{a^2} + \frac{\alpha_n^2 \delta_E \gamma}{a^2} < 0 \quad (10)$$

the pan-epidemic threshold inequality (10) can be rewritten as $R_{0,epi,n} > 1$ where the pan-epidemic basic reproductive rate $R_{0,epi,n}$ is defined like

$$R_{0,epi,n} = \frac{K \beta S_0}{\left(\gamma + \frac{\alpha_n^2 \delta_I}{a^2}\right) \left(f_E + \frac{\delta_E \alpha_n^2}{a^2}\right)} \quad (11)$$

as we can see from (9) and (11) we have the following relation

$$R_{0, \text{epin}, n} = \frac{R_0}{\left(1 + \frac{\alpha_n^2 \delta_I}{\gamma a^2}\right) \left(1 + \frac{\alpha_n^2 \delta_E}{f_E a^2}\right)} \quad (12)$$

V. Discussion and Conclusion

The spatial SEIR model that was considered in this work, can be applied to infectious diseases such as tuberculosis when the disease is endemic at the boundary of the circular habitat. The results that were obtained corresponds only to the early stages of the epidemic event when it is possible to consider as constant the density of susceptible, and then it is possible to have an linear model that permits the calculation of the basic reproductive rate of disease.

It is necessary to say now, that in this case, the computer algebra is a very useful tool to obtain the solution. From the other side, when the epidemic model refers to an indirectly transmitted disease [8] with one or more intermediary hosts or when the model refers to an directly transmitted disease but incorporates the effects of the genetic, geographical, immunological or social heterogeneity in the human population [4], then in such cases the manual procedure is very difficult to implement and then is necessary to use some computer algebra software that permits symbolic or analytical manipulations of the equations of the model.

Also is necessary to remark here that the numerical computer software that provides numerical solutions to boundary problems with partial differential equations including non-linear equations, can not proportionate explicit formulas of the solutions, and so, they can not give explicit formulas for R_0 . With these numerical software only we can realize numerical experimentation when the form of R_0 is previously given.

Finally is necessary to recognize that epidemic models that were considered are all linear models and the actual computer algebra software is not able to solve in general non-linear models; but it is possible, in the case of non-linear problems, to have approximate analytical or symbolic solutions using such computer algebra software which is an alternative with respect the numerical software [5]; all these, from the computational point of view.

From the epidemiological point of view the authors think that the formula in the equation (11) for the basic reproductive rate of the disease in pan-epidemic configuration is new in the literature and incorporates the effects of diffusion in a simple but not a priori evident form. The principal contribution of the present work is the introduction of a pan-epidemic threshold that it is different to the more conventional pandemic threshold [1]. It is possible that the equation (11) can be useful for the control of the propagation of the disease inside circular habitats when such disease is endemic at the boundary.

Finally from the computational epidemiology point of view, this work indicates that the computer algebra software for symbolic computation has a very promissory future in mathematical epidemiology.

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