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Mathematical analysis of a two-patch model of tuberculosis disease with staged progression

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ABSTRACT

The spread of tuberculosis is studied through a two-patch epidemiological system $SE_1 \cdots E_nI$ which incorporates migrations from one patch to another just by susceptible individuals. Our model is consider with bilinear incidence and migration between two patches, where infected and infectious individuals cannot migrate from one patch to another, due to medical reasons. The existence and uniqueness of the associated endemic equilibria are discussed. Quadratic forms and Lyapunov functions are used to show that when the basic reproduction ratio is less than one, the disease-free equilibrium (DFE) is globally asymptotically stable, and when it is greater than one there exists in each case a unique endemic equilibrium (boundary equilibria and endemic equilibrium) which is globally asymptotically stable. Numerical simulation results are provided to illustrate the theoretical results.

1. Introduction

For a given system, the focus in qualitative mathematical epidemiology is the long term dynamics. The simplest possible attractor is a globally asymptotically stable equilibrium. An equilibrium can be shown to be globally asymptotically stable, using Poincar–Bendixson theory [1], Bendixson's Negative Criterion [2,3], or the generalized version of Dulac [4]. Another method of Li and Muldowney [5–7] for demonstrating global stability global stability in n dimensions have been developed more recently, with applications in three [8–10] and four dimensions [11,12]. For higher-dimensional systems, the theory of quadratic forms [13] or Lyapunov's method can be used [14,15]. Lyapunov's method requires to find a function V such that the flow always crosses the level sets from higher values of V to lower values. When such a function can be found, then any isolated minimum of the function is a stable equilibrium of the flow.

In this paper, the stability of a $2n + 4$-dimensions system will be investigated using Lyapunov–LaSalle functions and quadratic forms. The function $V = \sum_{i=1}^{n} a_i(x_i - x_i^* \ ln \ x_i)$ has a long story in epidemiology [16–21] and in ecology [22,23]. This function was originally discovered by Volterra himself, although he did not use the vocabulary and the theory of Lyapunov functions. Since epidemic models are Lotka–Volterra like models, the pertinence of this function is not surprising.

The model studied in this paper is motivated by the issue of modeling tuberculosis. Several models of one population in the literature [24–28] have a common structure in that there is a single compartment of susceptible individuals, a single

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Table 1
Numerical values for the parameters of the model (1).

Parameters	Description	Estimated value/range	Reference
Λ_1	Recruitment rate into the S_1 class	100/yr	Assumed
Λ_2	Recruitment rate into the S_2 class	110/yr	Assumed
β_1	Transmission coefficient of infectious in the first sub-population	variable	Assumed
β_2	Transmission coefficient of infectious in the second sub-population	variable	Assumed
$\mu_1 = \mu_{1i}$	Force of mortality in the first sub-population	0.019896/yr	Estimated
$\mu_2 = \mu_{2i}$	Force of mortality in the second sub-population	0.019897/yr	Estimated
$\gamma_{11} = \gamma_{12}$	Rate of progression from the E_{11} class to the I_1 class	0.00013/yr	Assumed
$\gamma_{21} = \gamma_{22}$	Rate of progression from the E_{21} class to the I_2 class	0.00023/yr	Assumed
γ_{10}	Rate of effective therapy in the I_1 class	0.8182/yr	Estimated
γ_{20}	Rate of effective therapy of in the I_2 class	0.8183/yr	Assumed
a_1	Rate of migration of individuals from the susceptible class S_1 to the susceptible class S_2	0.07/yr	Assumed
a_2	Rate of migration of individuals from the susceptible class S_2 to the susceptible class S_1	0.0701/yr	Assumed
d_1	Additional death rate in the I_1 class	0.0575/yr	Assumed
d_2	Additional death rate in the I_2 class	0.05751/yr	Assumed

compartment of infectious, constant recruitment of new individuals into the susceptible individuals compartment, and mass action incidence. By allowing for an arbitrary number of latently infected compartments, the model allows for the approximation of a wide class of distributions of latency durations. This is of particular importance for tuberculosis since latency may last for years or even decades. In the model given here, the migration of only susceptible individuals has an influence on the spread of the disease in two populations.

Let us give now the outlines of the paper. In Section 2, the model is constructed; the variables and parameters of the model are explained. In Section 3, the mathematical properties of the model are given. We present the computation of the bifurcation parameters $\mathcal{R}_0^i$ using the method found in [29]. The equilibria of the model are computed: equilibrium without disease, boundary equilibria (it is an equilibrium without one population), endemic equilibrium or coexistence equilibrium. The complete stability of these equilibria are presented, using the bifurcation parameters $\mathcal{R}_0^i$. In Section 4, numerical simulations are done to illustrate the results. In Section 5, we give the conclusions and tree situations can be observed: the disease can disappear in the two populations, can disappear just in one population and persist in the other, can persist in both the two populations.

2. Model construction

The model is consisted by two sub-populations of a big one. For diseases like tuberculosis that confer temporary immunity, the individual returns to the first latent class E_1 after an immune period. The disease in each population can then be described by a $SE_1 \cdots E_nI$ compartmental model, with staged progression to the disease. We have one class of susceptible individuals (S_i), n classes of latently infected individuals (E_i) and one class of infectious individuals (I_i), with $i = 1, 2$. The subscript i stands for population i. We assume that the transmission does not occurs during migration. The recruitment in each population is only in the susceptible class and occurs at a constant rate Λ_i; only the susceptible individuals are concerned by migrations at rate a_i between the two populations. The infectious individuals does not migrate from one population to another, because of medical reasons. The force of mortality is a constant μ_i, $i = 1, 2$, for susceptible classes, μ_{ij}, $i = 1, 2$, $j = 1,2,\ldots,n$, for latently infected classes and μ_{I_i}, $i = 1, 2$, for infectious classes; the additional death rate due to disease affects only the classes I_i and has constant rates d_i, $i = 1, 2$. Once latently infected with M. Tuberculosis, an individual will remain so for life unless reactivation occurs. This is the reason of having n stages of progression. To account for treatment, we define r_iE_{in} as the fraction of infected individuals receiving effective chemoprophylaxis; then, $\gamma_{in} = k(1 - r_1)$. We assume that

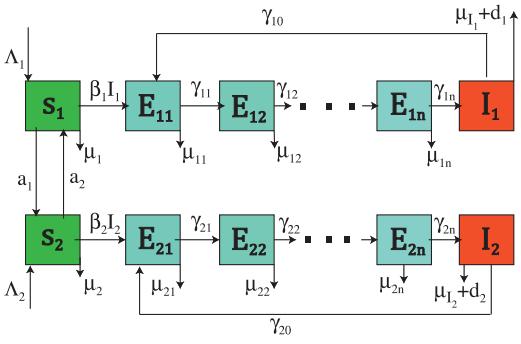

Fig. 1. Transfer diagram for a two-patch model of tuberculosis, with migrations only between susceptible individuals at rate a_i.