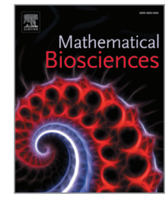
Mathematical Biosciences 258 (2014) 201–222

Contents lists available at ScienceDirect

Mathematical Biosciences

journal homepage: www.elsevier.com/locate/mbs



Large number of endemic equilibria for disease transmission models in patchy environment

D.H. Knipl [a,*], G. Röst [b]

[a] MTA–SZTE Analysis and Stochastic Research Group, University of Szeged, Aradi vértanúk tere 1, Szeged 6720, Hungary
[b] Bolyai Institute, University of Szeged, Aradi vértanúk tere 1, Szeged 6720, Hungary

ARTICLE INFO

Article history:
Received 31 March 2014
Revised 19 August 2014
Accepted 21 August 2014
Available online 16 September 2014

2010 MSC:
92D-30
58C-15

Keywords:
Differential equations
Large number of steady states
Compartmental patch model
Epidemic spread

ABSTRACT

We show that disease transmission models in a spatially heterogeneous environment can have a large number of coexisting endemic equilibria. A general compartmental model is considered to describe the spread of an infectious disease in a population distributed over several patches. For disconnected regions, many boundary equilibria may exist with mixed disease free and endemic components, but these steady states usually disappear in the presence of spatial dispersal. However, if backward bifurcations can occur in the regions, some partially endemic equilibria of the disconnected system move into the interior of the nonnegative cone and persist with the introduction of mobility between the patches. We provide a mathematical procedure that precisely describes in terms of the local reproduction numbers and the connectivity network of the patches, whether a steady state of the disconnected system is preserved or ceases to exist for low volumes of travel. Our results are illustrated on a patchy HIV transmission model with subthreshold endemic equilibria and backward bifurcation. We demonstrate the rich dynamical behavior (i.e., creation and destruction of steady states) and the presence of multiple stable endemic equilibria for various connection networks.

1. Introduction

Compartmental epidemic models have been considered widely in the mathematical literature since the pioneering works of Kermack, McKendrick and many others. Investigating fundamental properties of the models with analytical tools allows us to get insight into the spread and control of the disease, by gaining information about the solutions of the corresponding system of differential equations. Determining steady states of the system and knowing their stability is of particular interest if one thinks of the long term behavior of the solution as final epidemic outcome.

In most deterministic models for communicable diseases, there are two types of steady states: one is disease free, meaning that the disease is not present in the population, and the other one is endemic, when the infection persists with a positive state in some of the infected compartments. In such situation, the basic reproduction number ($\mathcal{R}_0$) usually works as a threshold for the stability of fixed points. Typically, the disease free equilibrium is locally asymptotically stable whenever this quantity—defined as the number of secondary cases generated by an index infected individual who was introduced into a completely susceptible population—is less than unity, and for values of $\mathcal{R}_0$ greater than one, the endemic fixed point emerging at $\mathcal{R}_0 = 1$ takes stability over by making the disease free state unstable. This phenomenon, known as forward bifurcation at $\mathcal{R}_0 = 1$, is in contrary to some other cases when more than two equilibria coexist in certain parameter regions. Backward bifurcation presents such a scenario, when there is an interval for values of $\mathcal{R}_0$ to the left of one where there is a stable and an unstable endemic fixed point besides the unique disease free equilibrium. Such dynamical structure of fixed points has been observed in several biological models considering multiple groups with asymmetry between groups and multiple interaction mechanisms (for an overview see, for instance, Gumel [8] and the references therein). However, examples can also be found in the literature where the coexistence of multiple nontrivial steady states is not due to backward transcritical bifurcation of the disease free equilibrium: in the age-structured SIR model analyzed by Franceschetti et al. [6] endemic equilibria arise through two saddle-node bifurcations of a positive fixed point, moreover Wang [17] found backward bifurcation from an endemic equilibrium in a simple SIR model with treatment.

In case of forward transcritical bifurcation, the classical disease control policy can be formulated. The stability of the endemic state is typically accompanied with the persistence of the disease in the population as long as the reproduction number is larger than one, and controlling the epidemic in a way such that $\mathcal{R}_0$ decreases below one successfully eliminates the infection, since every solution converges

* Corresponding author: Tel: +36 62 34 3310.
E-mail addresses: knipl@math.u-szeged.hu (D.H. Knipl), rost@math.u-szeged.hu (G. Röst).

http://dx.doi.org/10.1016/j.mbs.2014.08.012
0025-5564/

to the disease free equilibrium when $\mathcal{R}_0 < 1$. On the other hand, the presence of backward bifurcation with a stable non-trivial fixed point for $\mathcal{R}_0 < 1$ means that bringing the reproduction number below one is only necessary but not sufficient for disease eradication. Nevertheless, multiple endemic equilibria have further epidemiological implications, namely that stability and global behavior of the models that exhibit such structure are often not easy to analyze, henceforth little can be known about the final outcome of the epidemic.

Multi-city epidemic models, where the population is distributed in space over several discrete geographical regions with the possibility of individuals' mobility between them, provide another example for rich dynamics. In the special case when the cities are disconnected, the model possesses a large number of steady states (i.e., the product of the numbers of equilibria in the one-patch models corresponding to each city). However, the introduction of traveling has a significant impact on steady states, as it often causes substantial technical difficulties in the fixed point analysis and, more importantly, makes certain equilibria disappear. Some works in the literature deal with models where the system with traveling exhibits only two steady states, one disease free with the infection not present in any of the regions, and another one, which exists only for $\mathcal{R}_0 > 1$, corresponding to the situation when the disease is endemic in each region (see, for instance, Arino [1], Arino and van den Driessche [2]). Other studies which consider the spatial dispersal of infecteds between regions (Gao and Ruan [7], Wang and Zhao [18] and the references therein) do not derive the exact number for the steady states, but show the global stability of a single disease free fixed point for $\mathcal{R}_0 < 1$, and claim the uniform persistence of the disease for $\mathcal{R}_0 > 1$ which implies the existence of at least one (componentwise) positive equilibrium.

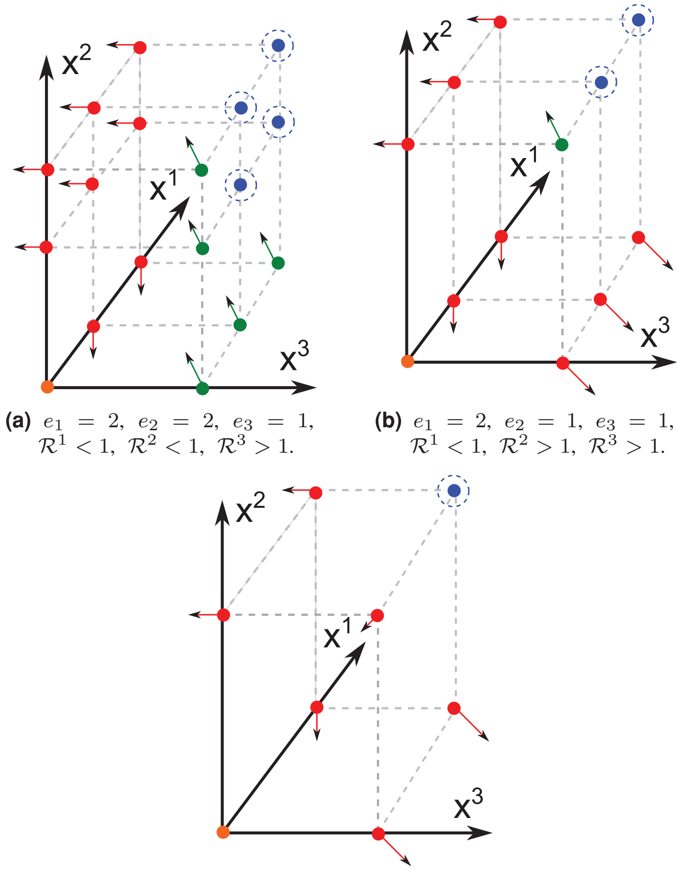
The purpose of this study is to investigate the impact of individuals' mobility on the number of equilibria in multiregional epidemic models. A general deterministic model is formulated to describe the spread of infectious diseases with horizontal transmission. The framework enables us to consider models with multiple susceptible, infected and removed compartments, and more significantly, with several steady states. The model can be extended to an arbitrary number of regions connected by instantaneous travel, and we investigate how mobility creates or destroys equilibria in the system. First we determine the exact number of steady states for the model in disconnected regions, then give a precise condition, in terms of the reproduction numbers of the regions and the connecting network, for the persistence of equilibria in the system with traveling. The possibilities for a three-patch scenario with backward bifurcations (i.e., when two endemic states are present for local reproduction numbers less than one) are sketched in Fig. 1 (cf. Corollary 10).

The paper is organized as follows. A general class of compartmental epidemic models is presented in Section 2, including multi-group, multistrain and stage progression models. We consider r regions which are connected by means of movement between the subpopulations, and use our setting as a model building block in each region. Section 3 concerns with the unique disease free equilibrium of the multiregional system with small volumes of mobility, while in Sections 4–6 we consider the endemic steady states of the disconnected system, and specify conditions on the connection network and the model equations for the persistence of fixed points in the system with traveling. We close Sections 4–6 with corollaries that summarize the achievements. The results are applied to a model for HIV transmission in three regions with various types of connecting networks in Section 7, then this model is used for the numerical simulations of Section 8 to give insight into the interesting dynamics with multiple stable endemic equilibria, caused by the possibility of traveling.

2. Model formulation

We consider an arbitrary (r) number of regions, and use upper index to denote region i, $i \in \{1, \ldots r\}$. Let $x^i \in \mathbb{R}^n$, $y^i \in \mathbb{R}^m$ and $z^i \in \mathbb{R}^k$ represent the set of infected, susceptible and removed (by means of immunity or recovery) compartments, respectively, for $n, m, k \in \mathbb{Z}^+$. The vectors x^i, y^i and z^i are functions of time t. We assume that all individuals are born susceptible, the continuous function $g^i(x^i, y^i, z^i)$ models recruitment and also death of susceptible members. It is assumed that g^i is $r-1$ times continuously differentiable. The $n \times n$ matrix $-V^i$ describes the transitions between infected classes as well as removals from infected states through death and recovery. It is reasonable to assume that all non-diagonal entries of V^i are non-positive, that is, V^i has the Z sign pattern [16]; moreover the sum of the components of $V^i u$ should also be nonnegative for any $u \geq 0$. It is shown in [16] that such a matrix is a non-singular M-matrix, moreover $(V^i)^{-1} \geq 0$. Furthermore, we let D^i be a $k \times k$ diagonal matrix whose diagonal entries denote the removal rate in the corresponding removed class.

Disease transmission is described by the $m \times n$ matrix function $\mathcal{B}^i(x^i, y^i, z^i)$, assumed C^{r-1} on $\mathbb{R}^n_+ \times (\mathbb{R}^m_+ \setminus \{0\}) \times \mathbb{R}^k_+$, an element $\beta^i_{p,q}(x^i, y^i, z^i)$ represents transmission between the pth



(a) $e_1 = 2,\ e_2 = 2,\ e_3 = 1,$ $\mathcal{R}^1 < 1,\ \mathcal{R}^2 < 1,\ \mathcal{R}^3 > 1.$

(b) $e_1 = 2,\ e_2 = 1,\ e_3 = 1,$ $\mathcal{R}^1 < 1,\ \mathcal{R}^2 > 1,\ \mathcal{R}^3 > 1.$

(c) $e_1 = 1,\ e_2 = 1,\ e_3 = 1,$ $\mathcal{R}^1 > 1,\ \mathcal{R}^2 > 1,\ \mathcal{R}^3 > 1.$

Fig. 1. We illustrate the behavior of steady states in the system of three regions connected to each other by a complete mobility network, for three different cases in the values of local reproduction numbers. Dots on the schematic diagrams depict infected components of equilibria of the disconnected system, and e_i denotes the number of positive fixed points in region i, $i = 1, 2, 3$. Mobility has no impact on the disease free equilibrium (orange dot). Componentwise positive steady states (blue dots) are preserved in the system with traveling, as they continuously depend on the mobility parameter α. A boundary endemic equilibrium moves out from the nonnegative octant with the introduction of traveling if the equilibrium has a component corresponding to a region, which is disease free in the absence of traveling and has local reproduction number ($\mathcal{R}$) greater than one (red dot). Other boundary steady states move into the interior of the nonnegative octant (green dots). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)