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Global stability for an epidemic model with applications to feline infectious peritonitis and tuberculosis

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ABSTRACT

A general compartmental model of disease transmission is studied. The generality comes from the fact that new infections may enter any of the infectious classes and that there is an ordering of the infectious classes so that individuals can be permitted (or not) to pass from one class to the next. The model includes staged progression, differential infectivity, and combinations of the two as special cases.

The exact etiology of feline infectious peritonitis and its connection to coronavirus is unclear, with two competing theories – mutation process vs multiple virus strains. We apply the model to each of these theories, showing that in either case, one should expect traditional threshold dynamics. A further application to tuberculosis with multiple progression routes through latency is also presented.

1. Introduction

In this paper, we study a model of infectious disease transmission that is flexible enough to allow for staged progression [3], differential infectivity [6] or some combination of the two. The system also allows for fast and slow progression to infectivity, as is sometimes included in models of tuberculosis [1,8].

An important benefit in being able to study such a general model is that it allows analysis to be performed in the presence of uncertainty in the underlying etiology of a disease, as is the case with feline infectious peritonitis.

Feline coronavirus (FCoV) infection is ubiquitous amongst domestic and feral cats [9]. Cats that are infected with FCoV are usually asymptomatic; for those that are symptomatic, the clinical signs are mild [2].

Feline infectious peritonitis (FIP) is a fatal disease that affects cats and is associated with FCoV infection [9]. Although FCoV infection is common, not all FCoV infected cats develop FIP [9]. Although the exact etiology is not completely understood, there are two theories that are currently being debated amongst biologists [9].

One theory is that once FCoV infection occurs, it has the potential to mutate within the host. After mutation, the result is feline infectious peritonitis virus (FIPV) which then causes FIP [10].

The alternative theory is that there are virulent and avirulent strains of the coronavirus circulating in the feline population [2]. The virulent strain manifests itself as FIPV giving rise to the fatal condition, FIP. The avirulent strain causes mild enteritis and is relatively harmless.

In either case, FIPV itself is not transmitted from cat to cat. Although FIPV can be isolated in feces, it is shed at very low levels [9]. Hence, the main focus of research rests upon investigating the primary FCoV infection, which is readily and commonly transmitted with the potential for FIP.

The mathematical system studied here is presented in Section 2, with preliminary analysis given in Section 3. Mathematical theorems related to global dynamics are stated in Section 4, with the proofs appearing in the appendices. Special cases of

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the model, including staged progression, differential infectivity and a combination of the two are discussed in Section 5. Applications to feline infectious peritonitis and tuberculosis, are studied in Section 6. The results are discussed in Section 7.

2. The model

A population is divided into susceptibles S and infectives. The infective population is further divided into n subgroups $I_1, \ldots, I_n$ based on the disease status of the individuals.

All recruitment of new individuals is assumed to be into the susceptible class. Thus, there is no vertical transmission and no immigration of infectives. This recruitment occurs at the constant rate $\Lambda > 0$.

Mass action incidence is assumed, but it is allowed that the different infective classes may have different levels of infectivity. Thus, individuals leave the susceptible class due to infections at rate $\sum_{m=1}^{n}\beta_m SI_m$. We assume that $\beta_m \geqslant 0$, for $m = 1, \ldots, n$, and that $\beta_1 + \cdots + \beta_n > 0$. For $j = 1, \ldots, n$, a fraction q_j of the new infections appear in class I_j, where $q_j \in [0, 1]$, and $q_1 + \cdots + q_n \leqslant 1$. (Normally, we would have equality here, but we allow that a fraction of the new infections may result in rapid death, and therefore the sum may be less than one.)

For $j = 1, \ldots, n-1$, individuals in class I_j may progress to class I_{j+1} with per capita rate coefficient $k_j \geqslant 0$. Thus, for those that leave I_j by progressing rather than by dying, the average time spent in I_j before progression occurs is $\frac{1}{k_j} \leqslant \infty$.

We assume that $q_1 > 0$ and that $q_j + k_{j-1} > 0$ for $j = 2, \ldots, n$. This ensures that there is a mechanism by which individuals can enter each of the infective classes.

The per capita death rate coefficient for susceptibles is $\mu > 0$ and for infective class I_j is $d_j \geqslant \mu$, for $j = 1, \ldots, n$. We obtain the following system of ordinary differential equations:

$$\begin{aligned} \frac{dS}{dt} &= \Lambda - \mu S - \sum_{m=1}^{n}\beta_m SI_m, \\ \frac{dI_j}{dt} &= q_j\sum_{m=1}^{n}\beta_m SI_m + k_{j-1}I_{j-1} - (k_j + d_j)I_j, \quad \text{for } j = 1, \ldots, n, \end{aligned} \tag{2.1}$$

where $k_0 = I_0 = 0$, so that the identically zero term $k_0 I_0$ in the equation for $\frac{dI_1}{dt}$ is permitted for notational convenience.

It is useful, at times, to rewrite Eq. (2.1) in a more concise form. To do this, we define $\bar{I} = [I_1, \ldots, I_n]^T$, $\Gamma(\bar{I}) = \sum_{m=1}^{n}\beta_m I_m$, $\bar{Q} = [q_1, \ldots, q_n]^T$ and

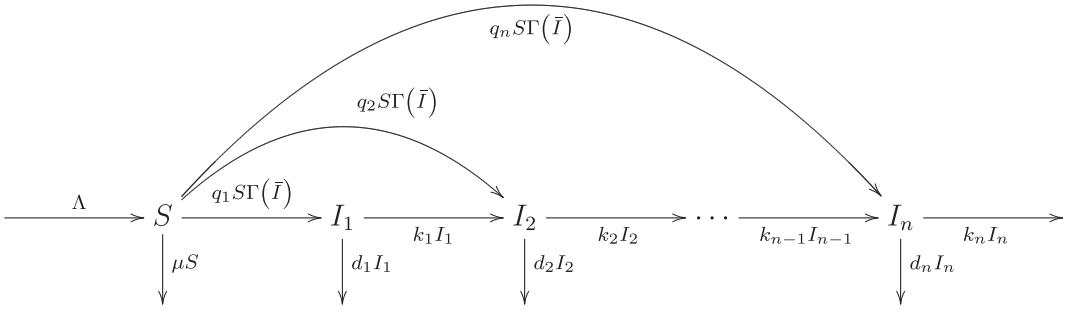
$$M = \begin{bmatrix} k_1 + d_1 & & & & \\ -k_1 & k_2 + d_2 & & & \\ & -k_2 & k_3 + d_3 & & \\ & & \ddots & \ddots & \\ & & & -k_{n-1} & k_n + d_n \end{bmatrix}_{n\times n},$$

where each of the omitted entries is zero. We note that M is invertible and that M^{-1} is a non-negative lower triangular matrix [5, Theorem 2.5.3].

Then Eq. (2.1) takes the form

$$\begin{aligned} \frac{dS}{dt} &= \Lambda - \mu S - S\Gamma(\bar{I}), \\ \frac{d\bar{I}}{dt} &= S\Gamma(\bar{I})\bar{Q} - M\bar{I}. \end{aligned} \tag{2.2}$$

The following transfer diagram describes the flow of individuals between the compartments.



Standard theory implies that solutions exist for all time and are unique.

Let $D \subseteq \mathbb{R}^{n+1}_{\geqslant 0}$ be defined by $D = \left\{(S, I_1, \ldots, I_n) \in \mathbb{R}^{n+1}_{\geqslant 0} : S + I_1 + \cdots + I_n \leqslant \frac{\Lambda}{\mu}\right\}$.