LYAPUNOV FUNCTIONS FOR DISEASE MODELS WITH IMMIGRATION OF INFECTED HOSTS

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Abstract. Recent work has produced examples where models of the spread of infectious disease with immigration of infected hosts are shown to be globally asymptotically stable through the use of Lyapunov functions. In each case, the Lyapunov function was similar to a Lyapunov function that worked for the corresponding model without immigration of infected hosts.

We distill the calculations from the individual examples into a general result, finding algebraic conditions under which the Lyapunov function for a model without immigration of infected hosts extends to be a valid Lyapunov function for the corresponding system with immigration of infected hosts.

Finally, the method is applied to a multi-group SIR model.

1. Introduction. The COVID-19 pandemic has made it clear that the importation of infection from one region to another can be unstoppable, particularly when there is a period of latency between the time of infection and the onset of symptoms. Accounting for this phenomenon requires models that account for the movement of infected individuals.

Mathematical models of infectious disease transmission that include immigration of infected hosts appear to have begun with [3]. The authors studied SIS and SIR models with immigration, showing that there was always a stable endemic equilibrium.

Recent papers [5, 8, 14] have used Lyapunov functions to establish the global asymptotic stability of an endemic equilibrium for compartmental disease models that include immigration of infected individuals. These models were all formulated as ordinary differential equations. In each case, the Lyapunov function that was used had the same form as the Lyapunov function that was used for a corresponding earlier model for which there was no such immigration. This suggests a pattern.

Models of disease-spread with infection-age structure that include immigration of infected individuals were studied in [13] and [15], providing Lyapunov functionals for the resulting partial differential equations. Once again, the Lyapunov functionals that were used were similar in nature to those that were used in the absence of immigration. This suggests a continuation of the pattern mentioned above, however infection-age models will not be analyzed in this paper.
In [1], the authors provided mild conditions under which immigration of infected hosts ensures the existence of an endemic equilibrium. That existence of an endemic equilibrium provides a context for determining conditions under which the equilibrium is globally asymptotically stable. That is the focus of this paper.

The approach used here is to distill the steps from [5, 8, 14] into a general method and to determine algebraic conditions under which global analysis of a system without immigration of infected individuals implies the existence of a globally asymptotically stable equilibrium for the corresponding system with immigration of infected individuals.

In Section 2, a low dimensional example is presented in order to set the stage for analyzing a general system. In Sections 3 and 4, the general result is developed. In Section 5, the method is applied to a multi-group SIR model to show that the results have non-trivial applications.

2. A motivating example - an SEI model. We begin by presenting an SEI model of disease transmission with fast and slow progression, that also allows for immigration of infected individuals. The transfer diagram is:

We assume that the parameters satisfy:
- \( \Lambda, \beta, k, \mu, d > 0 \),
- \( q \in [0,1) \),
- and \( W_E, W_I \geq 0 \).

The case where at least one of \( W_E \) and \( W_I \) is positive gives immigration of infected individuals, and leads to a situation where there is no disease-free equilibrium. The case where \( W_E = W_I = 0 \) is the more commonly studied situation, with no immigration of infected individuals; this case was studied previously in [2] and [12].

The differential equation corresponding to the transfer diagram above is:

\[
\begin{align*}
\frac{dS}{dt} &= \Lambda - \beta SI - \mu S \\
\frac{dE}{dt} &= W_E + (1-q)\beta SI - (\mu + k)E \\
\frac{dI}{dt} &= W_I + q\beta SI + kE - (\mu + d)I.
\end{align*}
\]

The initial conditions are \((S(0), E(0), I(0)) \in \mathbb{R}^3_{\geq 0}\).

2.1. SEI model without immigration of infected individuals: \((W_E, W_I) = (0,0)\). A detailed discussion of the model for this case can be found in [2], where it was first analyzed. The basic reproduction number \( R_0 \) is given by

\[
R_0 = \frac{\Lambda \beta k + q\mu}{\mu \mu + d k + \mu}.
\]
If $R_0 \leq 1$, then the only equilibrium is the disease-free equilibrium $X_0 = \left( \frac\Lambda\mu, 0, 0 \right)$.

If $R_0 > 1$, then $X_0$ is present as well as a unique endemic equilibrium $X^* = (S^*, E^*, I^*) \in \mathbb{R}^3_{>0}$.

In [12], the system was shown to have the traditional threshold behaviour. If $R_0 \leq 1$, then $X_0$ is globally asymptotically stable on $\mathbb{R}^3_{>0}$, and if $R_0 > 1$, then $X^*$ is globally asymptotically stable on $\mathbb{R}^3_{>0}$. In the case where $R_0 > 1$, the globally stability was shown by using the Lyapunov function

$$V = [S - S^* \ln(S)] + A[E - E^* \ln(E)] + B[I - I^* \ln(I)] \quad (2.3)$$

with coefficients $A, B > 0$ (discussed below). Note that $V$ is uniquely minimized at $X^*$. To show global stability it is necessary to show that $\frac{dV}{dt} \leq 0$. The calculation given in [12] is less direct than it could be. We provide an alternate version of the calculation here that better suits our purposes. We use the fact that $\frac{dS}{dt}, \frac{dE}{dt}$ and $\frac{dI}{dt}$ are all 0 at $X^*$. (This maneuver will be important in later sections of this paper.) We have

$$\frac{dV}{dt} = \frac{\partial V}{\partial S} \frac{dS}{dt} + \frac{\partial V}{\partial E} \frac{dE}{dt} + \frac{\partial V}{\partial I} \frac{dI}{dt}$$

$$= \left(1 - \frac{S^*}{S}\right) \left(\frac{dS}{dt} - \frac{dS}{dt}(X^*)\right) + A \left(1 - \frac{E^*}{E}\right) \left(\frac{dE}{dt} - \frac{E}{E^*} \frac{dE}{dt}(X^*)\right)$$

$$+ B \left(1 - \frac{I^*}{I}\right) \left(\frac{dI}{dt} - \frac{I}{I^*} \frac{dI}{dt}(X^*)\right)$$

Filling (2.1) into the right-hand side gives

$$\frac{dV}{dt} = \left(1 - \frac{S^*}{S}\right) \left(\Lambda - \beta SI - \mu S - \Lambda \beta S^* I^* - \mu S^*\right)$$

$$+ A \left(1 - \frac{E^*}{E}\right) \left((1 - q)\beta SI - (\mu + k)E - \frac{E}{E^*} (1 - q)\beta S^* I^* - (\mu + k)E^*\right)$$

$$+ B \left(1 - \frac{I^*}{I}\right) \left(q\beta SI + kE - (\mu + d)I - \frac{I}{I^*} q\beta S^* I^* + kE^* - (\mu + d)I^*\right)$$

$$= \left(1 - \frac{S^*}{S}\right) (\beta S^* I^* - \beta SI + \mu S^* - \mu S)$$

$$+ A \left(1 - \frac{E^*}{E}\right) \left((1 - q)\beta SI - (1 - q)\beta S^* I^* \frac{E}{E^*}\right)$$

$$+ B \left(1 - \frac{I^*}{I}\right) \left(q\beta SI - q\beta S^* I^* \frac{I}{I^*} + kE - kE^* \frac{I}{I^*}\right)$$

$$= \mu S^* \left(1 - \frac{S^*}{S}\right) \left(1 - \frac{S}{S^*}\right) + BkE^* \left(1 - \frac{I^*}{I}\right) \left(\frac{E}{E^*} - \frac{I}{I^*}\right)$$

$$+ \beta S^* I^* \left(1 - \frac{S^*}{S}\right) \left(1 - \frac{SI}{S^* I^*}\right) + A(1 - q) \left(1 - \frac{E^*}{E}\right) \left(\frac{SI}{S^* I^*} - \frac{E}{E^*}\right)$$

$$+ Bq \left(1 - \frac{I^*}{I}\right) \left(\frac{SI}{S^* I^*} - \frac{I}{I^*}\right)$$
Thus,
\[
\frac{dV}{dt} = \mu S^* \left( 2 - \frac{S^*}{S} - \frac{S}{S^*} \right) + BkE^* \left( \frac{E}{E^*} - \frac{1}{E^*} - \frac{E I^*}{E^*I} + 1 \right) \\
+ \beta S^* I^* \left[ \left( 1 - \frac{SI}{S^*I^*} - \frac{S^*}{S} + \frac{I}{I^*} \right) + A(1-q) \left( \frac{SI}{S^*I^*} - \frac{E}{E^*} - \frac{SI E^*}{S^*I^*E} + 1 \right) \\
+ Bq \left( \frac{SI}{S^*I^*} - \frac{I}{I^*} - \frac{S}{S^*} + 1 \right) \right].
\]
(2.4)

We now use \( A \) and \( B \) to combine some of these terms. In [12], these coefficients were given as \( A = \frac{k}{k+q} \) and \( B = \frac{k+\mu}{k+q} \), which is equivalent to what we will use here. However, rather than expressing \( A \) and \( B \) in terms of the original system parameters, we use the fact that \( A \) and \( B \) are the solution to
\[
1 = A(1-q) + Bq
\]
and
\[
BkE^* = A(1-q) \beta S^* I^*.
\]
(2.5)

We do this because it allows us to combine terms in (2.4). Equation (2.5) allows us to distribute the first group of terms multiplied by \( \beta S^* I^* \) into the second and third groups of terms, while (2.6) lets us replace \( BkE^* \). We obtain
\[
\frac{dV}{dt} = \mu S^* \left( 2 - \frac{S^*}{S} - \frac{S}{S^*} \right) + \beta S^* I^* A(1-q) \left( 3 - \frac{S^*}{S} - \frac{SI E^*}{S^*I^*E} - \frac{E I^*}{E^*I} \right) \\
+ \beta S^* I^* Bq \left( 2 - \frac{S^*}{S} - \frac{S}{S^*} \right).
\]
(2.7)

Using the Arithmetic-Mean-Geometric-Mean Inequality on each of the three groups of terms, it follows that \( \frac{dV}{dt} \leq 0 \), with equality if and only if \( S = S^* \) and \( \frac{E}{E^*} = \frac{I}{I^*} \). From here, an application of LaSalle’s Invariance Principle [11] shows that \( X^* \) is globally asymptotically stable on the set \( \mathbb{R}_3^3 \). Note that the only way in which the condition \( R_0 > 1 \) factored into the above calculation, was to ensure that the point \( X^* \) was strictly positive. We state the following result, which was first proved in [12].

**Theorem 2.1.** Suppose \( W_E = W_I = 0 \). Then \( X^* \) is globally asymptotically stable on the set \( \mathbb{R}_3^3 \), for any parameters for which \( X^* \) is present (which happens to be whenever \( R_0 > 1 \)).

2.2. **SEI model with immigration of infected individuals:** \((W_E, W_I) \neq (0,0)\). Using Brouwer’s Fixed Point Theorem [7] on \( \{(S,E,I) \in \mathbb{R}_3^3 : S + E + I \leq \frac{\Lambda + W_E + W_I}{n} \} \), it can be shown that there exists at least one equilibrium \( X^\Delta = (S^\Delta, E^\Delta, I^\Delta) \in \mathbb{R}_3^3 \).

We now consider the impact that having \((W_E, W_I) \neq (0,0)\) has on the Lyapunov calculation that was done in the previous subsection. We use the same function \( V \) that was given in (2.3), with \( A \) and \( B \) chosen as in (2.5) and (2.6), but with \( S^*, E^* \) and \( I^* \) replaced by \( S^\Delta, E^\Delta \) and \( I^\Delta \), respectively. Following the same sequence of
steps as before, we obtain
\[ \frac{dV}{dt} = \mu S^\triangle \left( 2 - \frac{S^\triangle}{S} - \frac{S}{S^\triangle} \right) + \beta S^\triangle I^\triangle A (1 - q) \left( 3 - \frac{S^\triangle}{S} - \frac{S I E^\triangle}{S^\triangle I E} - \frac{E I^\triangle}{E^\triangle I} \right) \\
+ \beta S^\triangle I^\triangle B q \left( 2 - \frac{S^\triangle}{S} - \frac{S}{S^\triangle} \right) \\
+ A W_E \left( 2 - \frac{E^\triangle}{E} - \frac{E}{E^\triangle} \right) + B W_I \left( 2 - \frac{I^\triangle}{I} - \frac{I}{I^\triangle} \right) \\
\leq 0, \quad (2.8) \]
with equality if and only if \((S, E, I) = (S^\triangle, E^\triangle, I^\triangle)\), giving the following result.

**Theorem 2.2.** If \((W_E, W_I) \neq (0, 0)\), then \(X^\triangle\) is positive and globally asymptotically stable on the set \(\mathbb{R}^3_{>0}\).

It follows from Theorem 2.2, that the equilibrium \(X^\triangle\) is unique. To our knowledge, Theorem 2.2 is a new result. It says that if there is immigration of infectives into a population with fast and slow progression (for which the other model assumptions apply), then the system should settle to an equilibrium, with a positive fraction of the population in each of the three classes \(S, E\) and \(I\).

It is noteworthy that this result is not merely a perturbation result. First, it is valid for both small and large values of \(W_E\) and \(W_I\). Furthermore, it extends to the case where \(R_0\) is less than one, even for very small values of \(W_E\) and \(W_I\), even though there was no positive equilibrium for the case where \(W_E = W_I = 0\).

In Section 3, we consider a general model with no immigration, which includes the case considered in Subsection 2.1. In Section 4, we consider a general model that includes the case considered in Subsection 2.2.

3. A general model without immigration of infected individuals. Consider a system
\[ \frac{dx}{dt} = f(x, \bar{p}), \quad (3.1) \]
where \(f : \mathbb{R}_{\geq 0}^N \times P \to \mathbb{R}^N\) and \(P \subseteq \mathbb{R}_{\geq 0}^k\) is the set of possible values for the system parameters \(\bar{p}\). We write \(f = [f_1, \ldots, f_N]^T\).

(A1) \(f\) is continuous in \(x\). Solutions to (3.1) are unique, bounded for \(t \geq 0\) and remain in \(\mathbb{R}_{\geq 0}^N\) for all \(t \geq 0\).

Note that solutions to (3.1) are unique if \(f\) is Lipschitz or differentiable, for example.

We assume that there exists a non-empty set \(P_0 \subseteq P\) such that, for each \(\bar{p} \in P_0\), there exists a positive equilibrium \(x^* = x^*(\bar{p}) \in \mathbb{R}_{\geq 0}^N\) for Equation (3.1). Then
\[ \bar{0} = f(x^*(\bar{p}), \bar{p}) \quad (3.2) \]
for each \(\bar{p} \in P_0\). (For a disease transmission model, the set \(P_0\) might be the set of parameter values that give \(R_0 > 1\), for example.)

Suppose there exists a differentiable function \(V : \mathbb{R}_{>0}^N \times \mathbb{R}_{\geq 0}^N \times P \to \mathbb{R}\) satisfying:

(A2) \(\text{sign} \left( \frac{dV}{dx_i}(x, y, \bar{p}) \right) = \text{sign} (x_i - y_i)\) for \(i = 1, \ldots, N\).
It follows from (A2) that for fixed \( y \) and \( \bar{p} \),
\[
V(x, y, \bar{p}) \geq V(y, y, \bar{p})
\]
for all \( x \in \mathbb{R}_{>0}^N \), with equality only if \( x = y \).

By considering \( V \) as a function of \( x \), we obtain the geometric interpretation of \( V \) as being “bowl-shaped” with the minimum at \( x = y \).

Let
\[
D_{(3.1)} = \frac{d}{dt}V(x(t), x^*, \bar{p}),
\]
where \( x(\cdot) \) is a solution of Equation (3.1). Then
\[
D_{(3.1)} = \sum_{i=1}^N \frac{\partial V}{\partial x_i} (x, x^*, \bar{p}) f_i(x, \bar{p}).
\]  
(3.3)

Next we assume that \( V \) is non-increasing along solutions to (3.1):
\[
D_{(3.1)} \leq 0.
\]  
(3.4)

In considering some recent examples where Lyapunov functions have been successfully used to prove the global stability of an equilibrium (see Section 2 or [4, 9, 10], for example), it becomes apparent that demonstrating (3.4) may involve some “tricks”. The equilibrium equations given in (3.2) are often used in order to assist in the calculation. Since \( f_i(x^*, \bar{p}) = 0 \) for each \( i \), we have
\[
D_{(3.1)} = \sum_{i=1}^N \frac{\partial V}{\partial x_i} (x, x^*, \bar{p}) f_i(x, \bar{p})
\]
(3.5)

where \( Q_i \) can be any function. Let
\[
F(x, x^*, \bar{p}) = \sum_{i=1}^N \frac{\partial V}{\partial x_i} (x, x^*, \bar{p}) [f_i(x, \bar{p}) - Q_i(x^*) f_i(x^*, \bar{p})].
\]  
(3.6)

Then (3.4) can be rewritten in terms of \( F \). In Subsection 2.1 and in each of the examples found in [4, 9, 10], the function \( F(x, x^*, \bar{p}) \) that arises is shown to be non-positive for any \( (x, x^*, \bar{p}) \in \mathbb{R}_{>0}^N \times \mathbb{R}_{>0}^N \times P \). That is, the fact that \( x^* \) depends on \( \bar{p} \) and the fact that \( \bar{p} \in P_0 \) are typically not part of the demonstration that \( F \) is non-positive (although they are almost certainly used in showing that \( D_{(3.1)} \) is equal to \( F \)). Thus, we assume:

\[\text{(A3)}\]  
\[
F(x, y, \bar{p}) \leq 0 \text{ for all } (x, y, \bar{p}) \in \mathbb{R}_{>0}^N \times \mathbb{R}_{>0}^N \times P.
\]

This assumption ensures that (3.4) is satisfied for any \( (x, x^*(\bar{p}), \bar{p}) \) with \( x \in \mathbb{R}_{>0}^N \) and \( \bar{p} \in P_0 \), but can also be used more generally.

Remark 1. For the SEI model that was discussed in Subsection 2.1, the function \( V \) is given in Equation (2.3). The functions \( Q_i \) that are used to show that \( \frac{dV}{dt} \leq 0 \) are \( Q_1 = 1 \), \( Q_2 = \frac{\Lambda}{\beta} \), and \( Q_3 = \frac{k}{I} \). The set \( P \) is \( \{ (\Lambda, \beta, \mu, q, k, d) \in \mathbb{R}_0^6 \} \) and \( P_0 \subseteq P \) is the set of parameter values that give \( R_0 > 1 \). The function \( F = F((S, E, I), (S^*, E^*, I^*), \bar{p}) \) is given by the right-hand side of Equation (2.7) with \( \bar{p} \in P \) and \( A, B \) being positive quantities.
4. **A general model with immigration of infected individuals.** Consider the system
\[
\frac{dx}{dt} = \tilde{W} + f(x, \tilde{p}),
\] (4.1)
where \(\tilde{W} \in \mathbb{R}^N_{\geq 0}\) is a non-zero constant vector and \(f\) satisfies the conditions given in Section 3. Assume the following:

(A4) Solutions to (4.1) are unique, bounded for \(t \geq 0\) and remain in \(\mathbb{R}^N_{\geq 0}\) for all \(t \geq 0\).

(A5) There exists a non-empty set \(P_1 \subseteq P\) such that for each \(\tilde{p} \in P_1\) there exists a solution \(x^\Delta = x^\Delta(\tilde{p}, \tilde{W}) \in \mathbb{R}^N_{> 0}\) to
\[
\tilde{0} = \tilde{W} + f(x^\Delta, \tilde{p}).
\] (4.2)

Following the examples that appear in Section 2 and in [8, 14], we aim to use the same Lyapunov function for (4.1) as for (3.1). Some care is needed, though, because the point \(x^*\) that is an equilibrium for (3.1), is not an equilibrium for (4.1). That is, \(x^*\) is not equal to \(x^\Delta\). However, the definition of the Lyapunov function makes use of the equilibrium. Thus, in mimicing the calculation that produced Equation (3.5), we use \(x^\Delta\) in place of \(x^*\).

Let
\[
U(x) = V(x, x^\Delta, \tilde{p})
\] (4.3)
and let
\[
D_{(4.1)} U = \frac{d}{dt} V(x(t), x^\Delta, \tilde{p}),
\] (4.4)
where \(x(\cdot)\) is a solution of Equation (4.1). We now calculate \(D_{(4.1)} U\) in a similar manner to how the function \(F\) was obtained in Section 3.

\[
D_{(4.1)} U = \sum_{i=1}^{N} \frac{\partial V}{\partial x_i} (x, x^\Delta, \tilde{p}) [W_i + f_i(x, \tilde{p})]
\]
\[
= \sum_{i=1}^{N} \frac{\partial V}{\partial x_i} (x, x^\Delta, \tilde{p}) \left[ \left(W_i + f_i(x, \tilde{p})\right) - Q_i(x, x^\Delta) \left(W_i + f_i(x^\Delta, \tilde{p})\right) \right]
\]
\[
= F(x, x^\Delta, \tilde{p}) + \sum_{i=1}^{N} \frac{\partial V}{\partial x_i} (x, x^\Delta, \tilde{p}) W_i \left[ 1 - Q_i(x, x^\Delta) \right].
\] (4.5)

By (A3), we have \(F(x, x^\Delta, \tilde{p}) \leq 0\), and so a sufficient condition for \(D_{(4.1)} U\) to be non-positive is
\[
\frac{\partial V}{\partial x_i} (x, x^\Delta, \tilde{p}) W_i \left[ 1 - Q_i(x, x^\Delta) \right] \leq 0 \quad \text{for } i = 1, \ldots, N.
\] (4.6)

By (A2), the sign of \(\frac{\partial V}{\partial x_i}\) is the same as the sign of \(x_i - x_i^\Delta\). Also, \(\tilde{W} \in \mathbb{R}^N_{\geq 0}\). Thus, to ensure that (4.6) is satisfied we assume the following:

(A6) For each \(i = 1, \ldots, N\), either \(W_i = 0\) or \(\left( Q_i(x, x^\Delta) - 1 \right) \left( x_i - x_i^\Delta \right) \geq 0\) for all \(\tilde{p} \in P_1\).

**Theorem 4.1.** Suppose (A1-A6) hold. Then \(D_{(4.1)} U \leq 0\) for all \(x \in \mathbb{R}^N_{> 0}, \tilde{p} \in P_1\).
If Theorem 4.1 can be applied to a particular model, then the Lyapunov function $V$ that worked for Equation (3.1) can be used as a Lyapunov function $U$ for Equation (4.1).

**Remark 2.** For the SEI model that was discussed in Section 2, we have $\dot{W} = (0, W_E, W_I)$, $x^\Delta = (S^\Delta, E^\Delta, I^\Delta)$ and $(Q_1, Q_2, Q_3) = (1, \frac{E}{E^\Delta}, \frac{I}{I^\Delta})$. The set $P_1$ is equal to the set $P$ since $x^\Delta \in \mathbb{R}^3_{>0}$ for any $\vec{p} \in P$. Since $W_1 = 0$, it follows that the criterion in (A6) is satisfied for $i = 1$. For $i = 2$,

$$
(Q_2(x, x^\Delta) - 1)(x_2 - x_2^\Delta) = \left(\frac{E}{E^\Delta} - 1\right)(E - E^\Delta) = \frac{(E - E^\Delta)^2}{E^\Delta} \geq 0,
$$

and so the criterion in (A6) is satisfied for this component too. A similar calculation works for $i = 3$. Thus, Theorem 4.1 applies.

In fact, by comparing (2.7) and (2.8), we can see that for this SEI model, the expression on the left-hand side of (4.6) is $AW_E \left(2 - \frac{E^\Delta}{E} - \frac{E}{E^\Delta}\right) + BW_I \left(2 - \frac{I^\Delta}{I} - \frac{I}{I^\Delta}\right)$, which is non-positive, as expected.

**Remark 3.** Common choices for $Q_i$ are 1 and $\frac{\beta_k}{\gamma_k}$. In fact, these are the types of choices that were used in Section 2, where we had $(Q_1, Q_2, Q_3) = (1, \frac{E}{E^\Delta}, \frac{I}{I^\Delta})$. For such choices, (A6) is satisfied.

5. **A complicated example - a multi-group SIR model.** We now apply our main result to a multi-group SIR model with immigration of infected hosts. The version without immigration of infected hosts was studied in [6], where the authors resolve the global dynamics. Of course, [6] was written without this current work in mind, and as a consequence it is necessary to modify a portion of their calculation so that the framework presented here can be used.

A heterogeneous population is divided into $n \geq 2$ groups. Superimposed on each group is an SIR structure with cross-infection between the groups. The system of differential equations is:

$$
\begin{align*}
\frac{dS_k}{dt} &= (1 - p_k) \Lambda_k - (d_k^S + \theta_k) S_k - \sum_{j=1}^{n} \beta_{kj} S_k I_j \\
\frac{dI_k}{dt} &= W_k + \sum_{j=1}^{n} \beta_{kj} S_k I_j - (d_k^I + \epsilon_k + \gamma_k) I_k \\
\frac{dR_k}{dt} &= p_k \Lambda_k + \theta_k S_k + \gamma_k I_k - d_k^R R_k,
\end{align*}
$$

for $k = 1, \ldots, n$. Let $\vec{W} = (W_1, \ldots, W_n) \in \mathbb{R}^n_{>0}$. For $k = 1, \ldots, n$, the parameter $W_k$ is the influx of infected hosts into group $k$. A full description of the model and parameters for the case where $\vec{W} = \vec{0}$ can be found in [6].

Let

$$
B = (\beta_{kj})_{n \times n}.
$$

The set $P$ of valid parameter sets (not including the immigration rates $W_k$) consists of $\Lambda_k, d_k^S, d_k^I, d_k^R, \theta_k, \epsilon_k, \gamma_k > 0$ for $k = 1, \ldots, n$, $p_k \in [0, 1)$ for $k = 1, \ldots, n$, and $\beta_{kj} \geq 0$ for $k, j = 1, \ldots, n$, with the matrix $B$ being irreducible. We will use the symbol $\vec{p}$ to refer to a point in $P$. 
immigration of infected hosts:

we rely on the remainder of the proof in [6] to establish that

then use our approach from Section 4 in order to get to [6, Equation 5.1]. Then

our Theorem 4.1 can be used.

necessary to reformulate a portion of their proof in order to obtain a setting where

X

a Lyapunov function to show the global stability of

and

X

There is a disease-free equilibrium

R

in [6], the authors provide a clever, though lengthy proof of this theorem, using

and let

R

∗

is globally asymptotically stable. For our purposes, it is

continuous, and solutions to the differential equation are unique, bounded for

t

≥ 0

and remain in

R

2n

for all

t

≥ 0

Thus, (A1) and (A4) are satisfied.

Multi-group model without immigration of infected hosts: \( \bar{W} = \bar{0} \).

There is a disease-free equilibrium \( \bar{X}^0 = (S_1^0, ..., S_n^0, I_1^0, ..., I_n^0) \) with

\[
S_k^0 = \frac{(1 - p_k) \Lambda_k}{d_k^S + \theta_k} \quad \text{and} \quad I_k^0 = 0 \quad \text{for } k = 1, ..., n.
\]

Let

\[
M_0 = \left( \frac{\beta_{kj} S_k^0}{d_k^S + \epsilon_k + \gamma_k} \right)_{n \times n}
\]

and let \( R_0 \) be the spectral radius of \( M_0 \). The following theorem appears as Theorem

3.3 in [6].

**Theorem 5.1.** If \( R_0 > 1 \), then there exists a unique endemic equilibrium \( X^* \in \mathbb{R}_{\geq 0}^n \)

and \( X^* \) is globally asymptotically stable in \( \bar{\Gamma} \).

In [6], the authors provide a clever, though lengthy proof of this theorem, using a

Lyapunov function to show the global stability of \( X^* \). For our purposes, it is

necessary to reformulate a portion of their proof in order to obtain a setting where

our Theorem 4.1 can be used.

We use the same Lyapunov function \( V \) that is given in [6, Equation 5.5]. We then use our approach from Section 4 in order to get to [6, Equation 5.11]. Then

we rely on the remainder of the proof in [6] to establish that \( \frac{dV}{dt} \leq 0 \) and that \( X^* \)

globally asymptotically stable.

Let \( X^* = (S_1^*, ..., S_n^*, I_1^*, ..., I_n^*) \) and \( \hat{\beta}_{kj} = \beta_{kj} S_k^* I_j^* \) for \( k, j = 1, ..., n \). Let

\[
\hat{B} = \begin{bmatrix}
\sum_{l \neq 1} \hat{\beta}_{1l} & -\hat{\beta}_{21} & \cdots & -\hat{\beta}_{n1} \\
-\hat{\beta}_{12} & \sum_{l \neq 2} \hat{\beta}_{2l} & \cdots & -\hat{\beta}_{n2} \\
\vdots & \vdots & \ddots & \vdots \\
-\hat{\beta}_{1n} & -\hat{\beta}_{2n} & \cdots & \sum_{l \neq n} \hat{\beta}_{nl}
\end{bmatrix}.
\]

Since the column sums of \( \hat{B} \) are all zero, the matrix is singular with at least one
eigenvalue equal to zero. The irreducibility of \( B \) implies the irreducibility of \( \hat{B} \)
and so all of the other eigenvalues are non-zero, and hence the nullspace of $\bar{B}$ is one-dimensional.

Consider the system

$$\bar{B}\vec{v} = \vec{0}. \quad (5.3)$$

It is shown in [6] that a solution of this system is given by $\vec{v} = (v_1, \ldots, v_n)^T = (C_{11}, \ldots, C_{nn})^T$, where $C_{kk} > 0$ is the $(k,k)$-cofactor of $\bar{B}$.

Let

$$V = V (X, X^*, \vec{p})$$

and so all of the other eigenvalues are non-zero, and hence the nullspace of $\bar{B}$ is one-dimensional.

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Let

$$V = V (X, X^*, \vec{p})$$

be defined on $\bar{\Gamma}$. It is straightforward to show that $(A2)$ is satisfied.

Thus far in this subsection, we have followed the work in [6, Section 5]. We now calculate $\frac{dV}{dt}$ a little differently than was done in [6].

$$\frac{dV}{dt} = \sum_{k=1}^{n} v_k \left[ \left( 1 - \frac{S_k^*}{S_k} \right) \left( \frac{dS_k}{dt} - \frac{dS_k}{dt} (X^*) \right) + \left( 1 - \frac{I_k^*}{I_k} \right) \left( \frac{dI_k}{dt} - \frac{I_k}{I_k} \frac{dI_k}{dt} (X^*) \right) \right]. \quad (5.4)$$

Filling $Q_{S_k}$ and $Q_{I_k}$ into the expression for $\frac{dV}{dt}$, and calculating $\frac{\partial V}{\partial S_k}$ and $\frac{\partial V}{\partial I_k}$ gives

$$\frac{dV}{dt} = \sum_{k=1}^{n} v_k \left[ \left( 1 - \frac{S_k^*}{S_k} \right) \left( \frac{dS_k}{dt} - \frac{dS_k}{dt} (X^*) \right) + \left( 1 - \frac{I_k^*}{I_k} \right) \left( \frac{dI_k}{dt} - \frac{I_k}{I_k} \frac{dI_k}{dt} (X^*) \right) \right]. \quad (5.5)$$

The choice for $Q_{S_k}$ allows for the constant terms $(1 - p_k) \Lambda_k$ in $\frac{dS_k}{dt}$ and $\frac{dS_k}{dt} (X^*)$ to cancel out. The choice for $Q_{I_k}$ results in the terms $(d_{k}^{*} + \epsilon_k + \gamma_k) \frac{dI_k}{dt}$ cancelling with corresponding terms in $\frac{dI_k}{dt} (X^*)$. This is similar to how Equations (5.6) and (5.7) of [6] were used. This gives

$$\frac{dV}{dt} = \sum_{k=1}^{n} v_k \left[ \left( 1 - \frac{S_k^*}{S_k} \right) \left( \frac{dS_k}{dt} + \theta_k \right) \left( S_k^* - S_k \right) + \sum_{j=1}^{n} \beta_{kj} \left( S_k^* I_j^* - S_k I_j \right) \right]$$

$$\quad + \left( 1 - \frac{I_k^*}{I_k} \right) \sum_{j=1}^{n} \beta_{kj} \left( S_k I_j - \frac{I_k}{I_k} S_k^* I_j^* \right).$$

Thus,

$$\frac{dV}{dt} = \sum_{k=1}^{n} v_k \left[ \left( d_{k}^{*} + \theta_k \right) S_k^* \left( 2 - \frac{S_k^*}{S_k} - \frac{S_k^*}{S_k} \right) + \sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* \left( 2 + \frac{I_k}{I_k} - \frac{I_k}{I_k} - \frac{S_k^*}{S_k} - \frac{S_k I_j I_j^*}{S_k^* I_j^* I_k} \right) \right]. \quad (5.5)$$

Note that $2 - \frac{S_k^*}{S_k} - \frac{S_k^*}{S_k} \leq 0$ with equality if and only if $S_k = S_k^*$. Thus,

$$\frac{dV}{dt} \leq \sum_{k,j=1}^{n} v_k \beta_{kj} \left( 2 + \frac{I_k}{I_k} - \frac{I_k}{I_k} - \frac{S_k}{S_k} - \frac{S_k I_j I_j^*}{S_k^* I_j^* I_k} \right). \quad (5.6)$$
In this expression, we now focus on the coefficients of $\frac{I_1}{I_k}, \ldots, \frac{I_n}{I_k}$. After a bit of work we obtain
\[
\begin{bmatrix}
\text{Coefficient of } \frac{I_1}{I_k} \\
\vdots \\
\text{Coefficient of } \frac{I_n}{I_k}
\end{bmatrix} = \bar{B}\bar{v}.
\]
From (5.3), we know that $\bar{B}\bar{v} = 0$ and so each of these coefficients is zero. Thus, (5.6) gives
\[
d\frac{dV}{dt} \leq \sum_{k,j=1}^n v_k\bar{\beta}_{kj} \left( 2 - \frac{S_k^*}{S_k} - \frac{S_k I_j I_k}{S_k^* I_j^* I_k} \right),
\] (5.7)
which is the same as [6, Equation 5.11].

Let $H_n$ be equal to the expression on the right-hand side of (5.7). At this point, we now rely on the remainder of [6, Section 5] (from the middle of page 273 to the middle of page 279), where the authors prove that $H_n \leq 0$ for any $n \geq 2$.

In the formulation of Section 3, the function $F$ from Equation (3.6) is given by the right-hand side of (5.5) so that
\[
F = F(X, X^*, \bar{p}) = \sum_{k=1}^n v_k \left[ (d_k^2 + \theta_k) S_k^* \left( 2 - \frac{S_k^*}{S_k} - \frac{S_k^* I_j^* I_k}{S_k^* I_j^* I_k} \right) + \sum_{j=1}^n \beta_{kj} S_k I_j^* \left( 2 + \frac{I_j}{I_j^*} - \frac{S_k^*}{S_k^*} - \frac{S_k I_j I_k}{S_k I_j I_k} \right) \right],
\] (5.8)
where $v_k > 0$ is the $(k,k)$-cofactor of $\bar{B}$.

In [6, Section 5], it is shown that $F \leq 0$ for all $(X, X^*(\bar{p}), \bar{p})$ such that $X \in \mathbb{R}^2_{\geq 0}$ and $R_0 > 1$, and that $F$ can only equal 0 if $S_k = S_k^*$ for $k = 1, \ldots, n$. Careful analysis of the proof in [6] shows that in fact, $F(X, Y, \bar{p}) \leq 0$ for all $X, Y \in \mathbb{R}^2_{\geq 0}$ and all $\bar{p} \in P$, and so (A3) is satisfied.

### 5.2 Multi-group model with immigration of infected hosts: $\tilde{W} \neq 0$.

The compact convex set $\Gamma$ is positively invariant. Thus, it follows from the Brouwer Fixed Point Theorem that $\Gamma$ contains an equilibrium. Since each $(1 - p_k)\Lambda_k$ is positive, it follows that each $S_k$ is positive at any equilibrium in $\Gamma$. The irreducibility of $B$ ensures that each $I_k$ is also positive at any equilibrium in $\Gamma$. Thus, for any $\tilde{W} \neq 0$, (A5) is satisfied with $P_1 = P$. Let such an equilibrium be denoted by $X^\Delta = \left( S_1^\Delta, \ldots, S_n^\Delta, I_1^\Delta, \ldots, I_n^\Delta \right)$.

A similar argument shows that solutions intersecting the boundary of $\mathbb{R}^2_{\geq 0}$ move to the interior and remain there.

We now verify (A6). From Equation (5.4), $Q_{S_k}(X, X^\Delta) = 1$ and $Q_{I_k}(X, X^\Delta) = \frac{I_k^\Delta}{I_k}$. Thus,
\[
\left( Q_{S_k} - 1 \right) \left( S_k - S_k^\Delta \right) = 0 \quad \text{and} \quad \left( Q_{I_k} - 1 \right) \left( I_k - I_k^\Delta \right) = \left( \frac{I_k^\Delta}{I_k} - 1 \right) \left( I_k - I_k^\Delta \right)
\]
\[
= \frac{\left( I_k - I_k^\Delta \right)^2}{I_k^\Delta} \geq 0.
\]
Thus, (A6) is satisfied. Let $U(X) = V(X, X^\Delta, \bar{p})$. Then Theorem 4.1 gives the following result.
Theorem 5.2. $D(5.2)U \leq 0$ for all $X \in \mathbb{R}^{2n}_{>0}$, $p \in P$, $\vec{W} \neq \vec{0}$.

It was shown in [6] that if $S_k = S^\Delta_k$ for $k = 1, \ldots, n$, then $H_n(X, X^\ast)$ is zero if and only if there exists a constant $a > 0$ such that $I_k = aI^\ast_k$ for $k = 1, \ldots, n$. This means that $D(5.2)U$ is zero only if $S_k = S^\Delta_k$ and $I_k = aI^\Delta_k$ for all $k$. Evaluating $\frac{dS_k}{dt}$ at these points where $D(5.2)U$ is zero, gives an affine function of $a$, which is only zero at $a = 1$, corresponding to $X = X^\Delta$. Thus, the largest invariant set for which $D(5.2)U$ is zero is the singleton $\{X^\Delta\}$ and so LaSalle’s Invariance Principle leads to the following result.

Theorem 5.3. $X^\Delta$ is globally asymptotically stable in $\Gamma$ for any $p \in P$ and $\vec{W} \neq \vec{0}$.

6. Discussion. In recent years, researchers have been able to demonstrate that many disease models exhibit a standard threshold behaviour. If the basic reproduction number $R_0$ is less than or equal to one, then there is a globally stable disease-free equilibrium $x_0$ (on the boundary), whereas if $R_0$ is greater than one, then there is a globally stable endemic equilibrium $x^\ast$. Often, the global stability for $R_0 > 1$ is shown by using a Lyapunov function $V$ along with a calculation showing that $\frac{dV}{dt}(x, x^\ast) \leq 0$ for all $x \in \mathbb{R}^n_{>0}$. Typically, one obtains an expression for $\frac{dV}{dt}$ that is non-positive for all $x \in \mathbb{R}^n_{>0}$ and for all $x^\ast \in \mathbb{R}^n_{>0}$ (often through an application of the Arithmetic-Mean-Geometric-Mean Inequality, for example).

For some of these examples, once immigration is added to the system, the same Lyapunov function works whether $R_0 \leq 1$ or $R_0 > 1$, even though this is not the case in the absence of immigration. It seems that the criterion for the Lyapunov function to work (for some class of systems) is that a positive equilibrium exists, rather than that $R_0$ be above a given threshold. This is the case, for example, for the SEI model discussed in Section 2, the multi-group model discussed in Section 5, and for the models studied in [5, 8, 14].

A lot of the recent success in applying Lyapunov theory to disease models is ad hoc in the sense that it is based on modifying Lyapunov functions that have worked previously on similar systems. Comparing these many successes, it is apparent that a similar sequence of calculations are used in many cases. This is indicative of a deeper structure.

In this paper we take a step towards finding a deeper understanding by studying how the Lyapunov calculations for one set of models (those without immigration) have implications for the corresponding calculations for a second set of models (those with immigration).

We prove a general result that gives sufficient conditions for a Lyapunov calculation for a model without immigration of infected hosts to still work when immigration of infected hosts is added to the model. This result is then applied to a multi-group SIR model studied in [6].

For those that may wish to apply the methods of this paper, it is important that the non-immigration version of the model have an interior equilibrium for at least part of the parameter space. Thus, a system which exhibits competitive exclusion (with some variables tending to zero) is not a natural candidate for straightforward application of these techniques.

Finally, this paper suggests that there is a class of systems (that includes some disease models) for which the existence of a strictly positive equilibrium implies global stability. This is worthy of further study.
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