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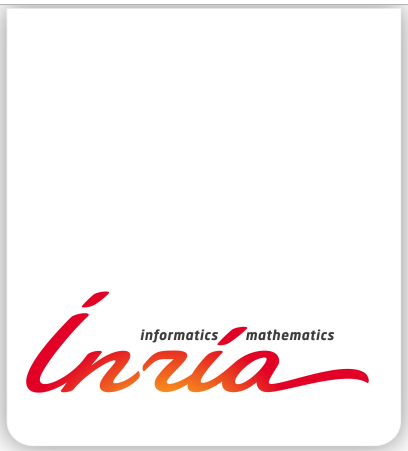

Analysis of the dynamics of a class of models for vector-borne diseases with host circulation

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Abstract: In this work we study the dynamics of a vector borne disease on a metapopulation model that accounts for host circulation. For such models, the movement network topology gives rise to a contact network topology, corresponding to a bipartite graph. Under the assumption that the contact network is strongly connected, we can define the basic reproductive number $\mathcal{R}_0$ and show that this system has only two equilibria: the so called disease free equilibrium (DFE); and a unique interior equilibrium that exists if, and only if, the basic reproduction number, $\mathcal{R}_0$, is greater that unity. We are also able to show that the DFE is globally asymptotically stable, if $\mathcal{R}_0 \leq 1$. If $\mathcal{R}_0 > 1$, the dynamics is uniformly persistent and, with further assumptions on the contact network structure, we also show that the endemic equilibrium (EE) is globally asymptotically stable.

Key-words: Vector-borne diseases, Metzler matrix, network models, global stability, Lyapunov functions.

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Analyse de la dynamique d'une maladie à transmission vectorielle en présence de mouvements humains

Résumé : Dans ce travail, nous étudions la dynamique d'une maladie vectorielle (transmise par vecteur) sur un modèle de métapopulation qui tient compte de la circulation humaine. Sous l'hypothèse que le réseau de contacts est fortement connecté, nous définissons le nombre de reproduction de base $\mathcal{R}_0$ et montrons que ce ce système a seulement deux équilibres: l'équilibre sans maladie (DFE), et un équilibre intérieur unique qui existe si , et seulement si, le nombre de reproduction de base, $\mathcal{R}_0$, est plus grand que l'unité. Dans ce cas, le système est également persistant. Nous sommes également en mesure de montrer que le DFE est globalement asymptotiquement stable, si $\mathcal{R}_0 \leq 1$, et que la dynamique est uniformément persistante si $\mathcal{R}_0 > 1$. Avec d'autres hypothèses sur la structure du réseau de contacts, nous montrons alors que l'équilibre endémique (EE) est globalement asymptotiquement stable, si $\mathcal{R}_0 > 1$.

Mots-clés : transmission vectorielle, mouvement humains, modèles de métapopulations, taux de reproduction de base, matrices de Metzler.

Contents

1 Introduction and outline

1.1 Background

Indirectly transmitted diseases are a growing concern for many countries, as diseases like Dengue and Chikunguya continues to spread all over the world, hand in hand with the spread of their associated vectors, see [25]. Thus, in the United States the *Aedes albopictus*, the tiger mosquito, is fixating very rapidly , while in Europe *Ae. albopictus* is also spreading at a fast rate—cf. [22]. This prompts for joint modeling of the disease dynamics together with the vector dynamics—cf. [14] for instance.

The disease dynamics can be largely dependent on whether one has a homogeneous or heterogeneous population—cf. [15, 11, 29]. In the case of a large city, or a large country with a good transportation system the movements from one location to another are fast, and the propagation of the disease will mostly likely happen either at its home region or at an usual destination location. Thus, in areas with significant movements of population, the epidemiological dynamics can be strongly determined by the movement of human hosts, and lead to a different type of heterogeneity than the typically studied spatial or temporal ones. This seems to be first pointed out by [1, 7, 32]. In this situation, it is natural to consider discrete spatial models, i.e, metapopulation models, the heterogeneity that arises from these circulation patterns. The population is distributed among discrete locations named patches. A metapopulation model involves movement of the individuals between discrete locations. This kind of model is actually a multi-group model. The assumptions are that there is no exchange of individuals between the subpopulations, and that individuals make short visits to other patches. For example, in the case of dengue, an individual can be infected at its work location, during daylight, and when becoming infectious can transmit the virus to the mosquitoes of its location of residence.

From the point of view of epidemiological mathematical modeling, the first natural question about a dynamical model is to what are its stability features as a function of the basic reproduction number, $\mathcal{R}_0$. The development of the models for indirectly transmitted diseases can be traced back to Ross malaria model as discussed in [26]—see also the recent review in [28] and the classical monographs [5, 10]. Nevertheless, the bulk of the theory in the literature is leaned towards directly transmitted diseases and uniform populations—see [3, 8] for instance. See [12] for a global stability analysis of the Bailey-Dietz model, and [38, 6] for later similar studies. See also [34] and [23] for various results on global stability of epidemiological models.

In the framework of multi-group endemic models for directly transmitted diseases, the first paper was probably by Rushton and Mauser [27], but seminal results are in Lajmanovich, Yorke [17] and the book of Hethcote and Yorke [17]. Stability was obtained by Thieme [34] and Hethcote and Thieme [16]. There is an important literature on this topic. See for example chapter 23 of [35]. For indirectly transmitted diseases, see [15, 19, 4] for modeling disease dynamics in spatially heterogeneous populations. See also [33] for empirical studies on the impact of human movement on the disease dynamics and [2] for complementary views to [1, 7].

1.2 Outline

In Section 2 we introduce the studied models and present some preliminary results. For the models discussed here, the existence and uniqueness of the Endemic Equilibrium (EE) for $\mathcal{R}_0 > 1$ is not obvious, and this is tackled in Section 3, where the local stability is also established. This result is obtained by first identifying the host-vector contact network as the relevant object, and assuming that it is strongly connected. As a byproduct, we observe that strong connectivity of the circulation is not enough to ensure strong connectivity of the host-vector contact network, and this is markedly different from directly transmitted diseases. In Section 4 we address global stability issues: with the same assumptions of the previous section, we show that the dynamics is uniformly persistent when $\mathcal{R}_0 > 1$. However, when $\mathcal{R}_0 \leq 1$, the global stability of the Disease Free Equilibrium (DFE) can be obtained with a weaker assumption on the topology of the network. We then address the global stability of the EE and, with an additional assumption, we show that it is globally asymptotically stable when $\mathcal{R}_0 > 1$ using a "vectorial" extension of the Lyapunov function used in [31]. Conclusions are presented in Section 5.

2 Model setup

In the following, we provide the basic set up for a class of multi-group models for indirectly transmitted diseases. These models are built upon the classical single-patch model by [5, 10], and include some of the models studied in [1] and the models studied in [2].

2.1 A one patch model

We consider the classical Bailey-Dietz model:

$$\begin{cases} \dot{S}_h = & \Lambda_h - \beta_1 \dfrac{S_h\, I_v}{N_h} - \mu_h\, S_h \\ \dot{I}_h = & \beta_1 \dfrac{S_h\, I_v}{N_h} - \gamma_h\, I_h - \mu_h\, I_h \\ \dot{R}_h = & \gamma_h\, I_h - \mu_h\, R_h \\ \dot{S}_v = & \Lambda_v - \beta_2 \dfrac{S_v\, I_h}{N_h} - \mu_v\, S_v \\ \dot{I}_v = & \beta_2 \dfrac{S_v\, I_h}{N_h} - \mu_v\, I_v, \end{cases} \tag{1}$$

where S_h, I_h, R_h denote, as usual, the number of, respectively, susceptible, infectious and removed host individuals and S_v, I_v the number of susceptible, infectious vectors.

The constant β_1 is a composite biological constant that embodies all the biological processes relating to transmission from mosquito to man, from the biting rate of the mosquitoes through the probability to develop and infection after a bite. Analogously β_2 captures the effect of transmission from man to mosquito. The constant μ_h is the per capita human mortality, γ

denotes the per capita rates at which infectious individual recover and are permanently immune. The parameter Λ_v is the constant recruitment of mosquitoes and μ_v is the per capita vector mortality.
It is not difficult to see that the compact K defined by

$$K = \{(S_h, I_h, R_h, S_v, I_v) \in \mathbb{R}^5_+ \mid S_h + I_h + R_h \leq \frac{\Lambda_h}{\mu_h} \quad S_v + I_v \leq \frac{\Lambda_v}{\mu_v}\},$$

is a positively invariant compact set for system (1). We can replace the two last equations of (1) by

$$\begin{cases} \dot{I}_v = & \beta_2 \dfrac{S_v\, I_h}{N_h} - \mu_v\, I_v \\ \dot{N}_v = & \Lambda_v - \mu_v\, N_v, \end{cases}$$

with $N_v = S_v + I_v$, so as to obtain an equivalent system. Notice that N_v does not appear in the preceding equations. We also denote the total host population by $N_h = S_h + I_h + R_h$, and replacing the equation for $\dot{R}_h$ by $\dot{N}_h = \Lambda_h - \mu_h\, N_h$, we finally obtain:

$$\begin{cases} \dot{S}_h = & \Lambda_h - \beta_1 \dfrac{S_h\, I_v}{N_h} - \mu_h\, S_h \\ \dot{I}_h = & \beta_1 \dfrac{S_h\, I_v}{N_h} - \gamma_h\, I_h - \mu_h\, I_h \\ \dot{N}_h = & \Lambda_h - \mu_h\, N_h \\ \dot{I}_v = & \beta_2 \dfrac{S_v\, I_h}{N_h} - \mu_v\, I_v, \\ \dot{N}_v = & \Lambda_v - \mu_v\, N_v. \end{cases} \tag{2}$$

System (2) is triangular. The following theorem will reduce the stability analysis to a smaller system:

Theorem 2.1 (Vidyasagar [37], Theorem 3.1)**.** *Consider the following $\mathcal{C}^1$ system :*

$$\begin{cases} \dot{x} = f(x) & x \in \mathbb{R}^n\ , y \in \mathbb{R}^m \\ \dot{y} = g(x, y) & \\ \text{ with an equilibrium point, } (x^*, y^*), \text{ i.e.,} & \\ f(x^*) = 0 \text{ and } g(x^*, y^*) = 0. & \end{cases} \tag{3}$$

If x^* is globally asymptotically stable (GAS) in $\mathbb{R}^n$for the system $\dot{x} = f(x)$, and if y^* is GAS in $\mathbb{R}^m$, for the system $\dot{y} = g(x^*, y)$, then (x^*, y^*) is (locally) asymptotically stable for (3). Moreover, if all the trajectories of (3) are forward bounded, then (x^*, y^*) is GAS for (3).

Applying Theorem 2.1, we see that the stability analysis of system (2) is equivalent to the stability analysis of the following system:

$$\begin{cases} \dot{S}_h = & \mu_h\, \mathbf{N} - \dfrac{\beta_1}{\mathbf{N}}\, S_h\, I_v - \mu_h\, S_h \\ \dot{I}_h = & \dfrac{\beta_1}{\mathbf{N}}\, S_h\, I_v - (\mu_h + \gamma_h)\, I_h \\ \dot{I}_v = & \dfrac{\beta_2}{\mathbf{N}}\, (\mathbf{V} - I_v)\, I_h - \mu_v\, I_v, \end{cases} \tag{4}$$

defined on

$$\bar{K} = \{(S_h, I_h, I_v) \in \mathbb{R}^3_+ \mid S_h + I_h \leq \mathbf{N} \quad I_v \leq \mathbf{V}\},$$

where we have defined $\mathbf{N} = \dfrac{\Lambda_h}{\mu_h}$ and by $\mathbf{V}$ the quantity $\mathbf{V} = \dfrac{\Lambda_v}{\mu_v}$.

It is not difficult, using the techniques in [36], to see that the reproduction number of (1) (or equivalently of (4)) is

$$\mathcal{R}_0^2 = \frac{\beta_1\,\beta_2\,\mathbf{V}}{\mu_v\,(\mu_h+\gamma)\,\mathbf{N}} = \frac{\beta_1\,\beta_2\,\mathbf{m}}{\mu_v\,(\mu_h+\gamma)}$$

With $\mathbf{m} = \dfrac{\mathbf{V}}{\mathbf{N}}$, the classical vectorial density. The basic reproduction ratio $\mathcal{R}_0$ is the same than for a classical Ross's model [3, 4, 5, 26].

As for Ross 's model we will use the prevalences, i.e., defining $x_1 = \dfrac{S_h}{N}$, $x_2 = \dfrac{I_h}{N}$ and $y = \dfrac{I_h}{V}$. Then the system is now defined on the compact set

$$\Omega = \{(x_1, x_2, z) \in \mathbb{R}^3 \mid x_1 + x_2 \leq 1 \quad y \leq 1\}$$

$$\begin{cases} \dot{x}_1 = & \mu_h - \beta_1\,\mathbf{m}\,x_1\,y - \mu_h\,x_1 \\ \dot{x}_2 = & \beta_1\,\mathbf{m}\,x_1\,y - (\mu_h+\gamma_h)\,x_2 \\ \dot{y} = & \beta_2\,(1-y)\,x_2 - \mu_v\,y. \end{cases} \tag{5}$$

Two equilibria can be defined : the disease free equilibrium $(\mathbf{1}, 0, \mathbf{0})$ and, when $\mathcal{R}_0 > 1$, an endemic equilibrium $(\bar{x}_1, \bar{x}_2, \bar{y}) \in \Omega$ given by

$$\bar{x}_1 = \frac{1 + \dfrac{1}{\mathcal{R}_0}\dfrac{\beta_1\,\mathbf{m}}{\mu_h}}{1 + \dfrac{\beta_1\,\mathbf{m}}{\mu_h}} \qquad \bar{x}_2 = \frac{\mu_h}{\mu_h+\gamma_h}\,\frac{1 - \dfrac{1}{\mathcal{R}_0}}{1 + \dfrac{\mu_h}{\beta_1\,\mathbf{m}}} \qquad \bar{y} = \frac{\mathcal{R}_0 - 1}{\mathcal{R}_0 + \dfrac{\beta_1\,\mathbf{m}}{\mu_h}}.$$

The global stability of (1) was originally studied by [12], who showed that the endemic equilibrium is globally asymptotically stable when $\mathcal{R}_0 > 1$, and that the disease-free is the global attractor when $\mathcal{R}_0 \leq 1$. using the so-called Poincaré-Bendixson theorem for competitive systems—cf. [30]. More recently, [31] has obtained a proof using only Lyapunov functions.

2.2 A patchy model for urban circulation

We consider a region divided in n patches, each patch i has a host population of $N_{h,i}$ and a vector population of $N_{v,i}$. Let $\bar{N} = \sum N_{h,i}$ and $\bar{V} = \sum N_{v,i}$ be respectively the total host and vector populations on the whole region.

We assume that the population can move between patches, but it cannot migrate.

A natural generalization of the one-patch model is then as follows:

$$\begin{cases} \dot{S}_{h,i} = & \Lambda_{h,i} - S_{h,i}\,\sum_{j=1}^n L_{i,j} I_{v,j} - \mu_h\,S_{h,i} \\ \dot{I}_{h,i} = & S_{h,i}\,\sum_{j=1}^n L_{i,j} I_{v,j} - \gamma_h\,I_{h,i} - \mu_h\,I_{h,i} \\ \dot{R}_{h,i} = & \gamma_h\,I_{h,i} - \mu_h\,R_{h,i} \\ \dot{S}_{v,i} = & \Lambda_{v,i} - S_{v,i}\,\sum_{j=1}^n M_{i,j} I_{h,j} - \mu_v\,S_{v,i} \\ \dot{I}_{v,i} = & S_{v,i}\,\sum_{j=1}^n M_{i,j} I_{h,j} - \mu_v\,I_{v,i}, \end{cases} \tag{6}$$

The nonnegative matrices L and M encode the movement information, as well as the transmission from vector to host and host to vector, respectively.
We can rewrite the preceding equation (6) as follows:

$$\left\{\begin{array}{ll} \dot{S}_{h,i} = & \Lambda_{h,i} - S_{h,i} \sum_{j=1}^{n} L_{i,j} I_{v,j} - \mu_h S_{h,i} \\ \dot{I}_{h,i} = & S_{h,i} \sum_{j=1}^{n} L_{i,j} I_{v,j} - \gamma_h I_{h,i} - \mu_h I_{h,i} \\ \dot{N}_{h,i} = & \Lambda_{h,i} - \mu_h N_{h,i} \\ \dot{N}_{v,i} = & \Lambda_{v,i} - \mu_v N_{v,i} \\ \dot{I}_{v,i} = & S_{v,i} \sum_{j=1}^{n} M_{i,j} I_{h,j} - \mu_v I_{v,i}, \end{array}\right. \tag{7}$$

where we denote by S_h, I_h, N_h, I_V and N_v the vectors of $\mathbb{R}_+^n$ whose components are respectively $S_{h,i}$, $I_{h,i}$, $N_{h,i}$, $N_{v,i}$ and $I_{v,i}$ for $i = 1, \cdots n$. It is clear that for (7), the set defined by

$$\Omega = \{(S_h, I_h, N_h, S_v, I_v) \in \mathbb{R}_+^{5n} |\ 0 \leq S_{h,i} + I_{h,i} \leq \frac{\Lambda_{h,i}}{\mu_h}\ \ 0 \leq S_{v,i} + I_{v,i} \leq \frac{\Lambda_{v,i}}{\mu_v}\}$$

is a compact positively invariant set.
Hence using Theorem 2.1 the stability study of 7 is reduced to the study of

$$\left\{\begin{array}{ll} \dot{S}_{h,i} = & \Lambda_{h,i} - S_{h,i} \displaystyle\sum_{j=1}^{n} L_{i,j} I_{v,j} - \mu_h S_{h,i} \\ \dot{I}_{h,i} = & S_{h,i} \displaystyle\sum_{j=1}^{n} L_{i,j} I_{v,j} - \gamma_h I_{h,i} - \mu_h I_{h,i} \\ \dot{I}_{v,i} = & S_{v,i} \displaystyle\sum_{j=1}^{n} M_{i,j} I_{h,j} - \mu_v I_{v,i}. \end{array}\right. \tag{8}$$

We write (8) in vector notation. We define $\bar{N}_{v,i} = \dfrac{\Lambda_{v,i}}{\mu_v}$, and we denote by S_h, I_h, I_v, Λ_h and $\bar{N}_v$ the corresponding vectors of $\mathbb{R}_+^n$. Then

$$\left\{\begin{array}{ll} \dot{S}_h = & \Lambda_h - \mathrm{diag}(S_h)\, L\, I_v - \mu_h S_h \\ \dot{I}_h = & \mathrm{diag}(S_h)\, L\, I_v - (\mu_h + \gamma_h)\, I_h \\ \dot{I}_v = & \mathrm{diag}(\bar{N}_v - I_v)\, M\, I_h - \mu_v I_v\,, \end{array}\right. \tag{9}$$

3 Equilibria and local stability

We will show that for our vectorial disease with subpopulations structure, System (9), the results of Thieme [16, 35] are conserved. Namely we obtain that the DFE is locally asymptotically stable, iff $\mathcal{R}_0 \leq 1$, and the existence and uniqueness of a strongly endemic equilibrium when $\mathcal{R}_0 > 1$. This equilibrium is locally asymptotically stable. For global results, see Section 4.
We shall need an assumption about the network topology in system (9). For a matrix A, we write $\Gamma(A)$ for the associated graph. We begin with a definition

Definition 3.1 (Host-Vector Contact Network)**.** *Given nonnegative matrices L and M, we write*

$$\mathcal{M} = \begin{pmatrix} 0 & L \\ M & 0 \end{pmatrix}.$$

The graph associated to $\mathcal{M}$, $\Gamma(\mathcal{M})$, is denoted the host-vector contact network, or contact network for short.

Hypothesis 3.1. *The contact network is strongly connected, i.e., $\mathcal{M}$ is nonnegative and irreducible.*

Remark 3.1. *Notice that irreducibility of L and M are neither necessary or sufficient for the irreducibility of $\mathcal{M}$. As an example, consider*

$$C = \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix} \text{ and } D = \begin{pmatrix} 1 & 0 \\ 1 & 1 \end{pmatrix}; \quad \mathcal{M}_1 = \begin{pmatrix} 0 & C \\ C & 0 \end{pmatrix} \text{ and } \mathcal{M}_2 = \begin{pmatrix} 0 & D^t \\ D & 0 \end{pmatrix}.$$

Then C is irreducible and D is reducible. Nevertheless, $\mathcal{M}_1$ is reducible and $\mathcal{M}_2$ is irreducible. The irreducibility of $\mathcal{M}$ is associated to the strong connectivity of the corresponding directed bipartite graph. This is a consequence of the infection process, when considered between hosts (or vectors) themselves, is a two step process. Thus, even when the circulation structure (the non-zero patterns of L and M) is strongly connected, this is not necessarily the case for an indirectly transmitted disease, and this a significant difference to directly transmitted ones.

We now describe a class of network topologies that are important for epidemiological modeling, for which hypothesis 3.1 can be easily verified in terms of L and M.

Definition 3.2. *We say that a host-vector contact network is specially connected, if L and M are nonnegative matrices with positive diagonal and such that $\Gamma(L+M)$ is strongly connected, i.e., $L+M$ is irreducible.*

Proposition 3.1. *Assume that the contact network is complete. Then $\mathcal{M}$ is irreducible.*

Proof. First, observe that

$$\mathcal{M}^{2k} = \begin{pmatrix} (LM)^k & 0 \\ 0 & (ML)^k \end{pmatrix} \quad \text{and} \quad \mathcal{M}^{2k+1} = \begin{pmatrix} 0 & M(LM)^k \\ L(ML)^k & 0 \end{pmatrix}$$

Since the diagonal of L is positive, let

$$c_L = \frac{1}{2} \min_i L_{ii}.$$

Then $L - c_L I$ has positive diagonal, and it is irreducible. Hence

$$L = c_L(I + \tilde{L}), \quad \tilde{L} = \frac{1}{c_L} L - I,$$

and $\tilde{L}$ is nonnegative and irreducible. Analogously, we write $M = c_M(I+\tilde{M}$, with $\tilde{M}$ nonnegative with positive diagonal. Moreover, $\tilde{L} + \tilde{M}$ is also irreducible. But then

$$LM = c_L c_M (I + \tilde{L})(I + \tilde{M}) \geq c_L c_M (I + \tilde{L} + \tilde{M}),$$

Since $\tilde{L} + \tilde{M}$ is irreducible there exists k_1 such that $(I + \tilde{L} + \tilde{M})^{k_1}$ is positive. The argument for ML is similar. This shows that $\mathcal{M}^{2k_1}$ has positive diagonal blocks. Finally, notice that, if $(LM)^k$ is positive, then $M(LM)^k$ is also positive, since M has positive diagonal. A similar argument holds for $L(ML)^k$. Thus $\mathcal{M}^{2k_1+1}$ has positive off-diagonal blocks. Hence $\mathcal{M}$ is irreducible as claimed. □

Theorem 3.1. *Assume 3.1. Then system 6 has a unique endemic equilibrium if, and only if,* $\mathcal{R}_0 > 1$. *Moreover this equilibrium is locally asymptotically stable.*

Proof. We have seen that the stability properties of system (6) are equivalent to the properties of system (9). Using, the now standard techniques [9, 36], it is clear that the basic reproduction ratio is

$$\mathcal{R}_0 = \rho \begin{pmatrix} 0 & \frac{1}{\mu_h+\gamma_h}\operatorname{diag}(\bar{S}_h)\, L \\ \frac{1}{\mu_v}\operatorname{diag}(\bar{N}_v)\, M & 0 \end{pmatrix}$$

We deduce immediately

$$\mathcal{R}_0^2 = \rho \left(\frac{1}{(\mu_h+\gamma_h)\,\mu_v} \operatorname{diag}(\bar{S}_h)\, L \operatorname{diag}(\bar{N}_v)\, M \right)$$

We will now prove the existence and uniqueness of an endemic equilibrium when $\mathcal{R}_0 > 1$.

We denote by S_k^*, I_h^* and I_v^* the expression of an endemic equilibrium. Recall that the notation $\mathbb{1}$ refers to the vector of $\mathbb{R}_+^n$ whose components are all equal to 1. We have the following relation, defining an endemic equilibrium:

$$\Lambda_h = \operatorname{diag}(\mu_h\, \mathbb{1} + L\, I_v^*)\, S_h^* \tag{10a}$$
$$(\mu_h+\gamma_h)\, I_h^* = \operatorname{diag}(S_h^*)\, L\, I_v^* \tag{10b}$$
$$\mu_v\, I_v^* = \operatorname{diag}(\bar{N}_v - I_v^*)\, M\, I_h^* \tag{10c}$$

From (10a) we obtain

$$S_h^* = \operatorname{diag}(\mu_h\, \mathbb{1} + L\, I_v^*)^{-1}\, \Lambda_h$$

Rewriting (10c) as

$$\mu_v\, I_v^* = \operatorname{diag}(M\, I_h^*)\, (\bar{N}_v - I_v^*)$$

Replacing the value of S_h^* in (10b) we obtain

$$I_h^* = \tfrac{1}{\mu_h+\gamma_h} \operatorname{diag}(\mu_h\, \mathbb{1} + L\, I_v^*)^{-1} \operatorname{diag}(L\, I_v^*)\, \Lambda_h \tag{11a}$$
$$I_v^* = \operatorname{diag}(\mu_v\, \mathbb{1} + M\, I_h^*)^{-1} \operatorname{diag}(M\, I_h^*)\, \bar{N}_v \tag{11b}$$

Hence (I_h^*, I_v^*) is a fixed point of the following application

$$F(x,y) = \begin{bmatrix} \frac{1}{\mu_h+\gamma_h} \operatorname{diag}(\mu_h\, \mathbb{1} + L\, y)^{-1} \operatorname{diag}(L\, y)\, \Lambda_h \\ \operatorname{diag}(\mu_v\, \mathbb{1} + M\, x)^{-1} \operatorname{diag}(M\, x)\, \bar{N}_v \end{bmatrix}$$

We will now use a result of Hethcote and Thieme [16]. For the convenience of the reader we recall this theorem:

Theorem 3.2 ([16] Theorem 2.1)**.**
Let $F(w)$ *be a continuous, monotone nondecreasing, strictly sublinear, bounded function which maps the nonnegative orthant* $\mathbb{R}_+^n = [0,\infty(^n$ *into itself. Let* $F(0) = 0$ *and* $F'(0)$ *exist and be irreducible. Then* $F(w)$ *does not have a nontrivial fixed point on the boundary of* $\mathbb{R}_+^n$. *Moreover,* $F(x)$ *has a positive fixed point iff* $\rho(F('0)) > 1$. *If there is a fixed point, then it is unique.*

We have to check, for our function F defined on $\mathbb{R}^n_+ \times \mathbb{R}^n_+$, the conditions of Hethcote-Thieme's Theorem.
It is immediate that F is continuous, bounded and maps the nonnegative orthant $\mathbb{R}^n_+ \times \mathbb{R}^n_+$ into itself.
The function F is monotone since the Jacobian of F is

$$JF(x,y) = \begin{bmatrix} 0 & A_1 \\ A_2 & 0 \end{bmatrix}$$

With

$$A_1 = \frac{1}{\mu_h + \gamma_h} \operatorname{diag}(\mu_h \mathbb{1} + L\,y)^{-1} \operatorname{diag}(\Lambda_h) \left[I_n - \operatorname{diag}(\mu_h \mathbb{1} + L\,y)^{-1} \operatorname{diag}(L\,y) \right] L.$$

and

$$A_2 = \operatorname{diag}(\bar{N}_v) \operatorname{diag}(\mu_v \mathbb{1} + M\,x)^{-1} \left[I_n - \operatorname{diag}(\mu_v \mathbb{1} + M\,x)^{-1} \operatorname{diag}(M\,x) \right] M.$$

Then $JF(x,y)$ is a Metzler matrix, i.e. a matrix whose off diagonal terms are nonnegative [20, 24]. These matrices are also known as quasi-positive matrix [30, 35]. This proves that F is monotone [30, 18]. Now, we have to check the strict sublinearity. We use the equivalent definition of [18], using the standard ordering of $\mathbb{R}^n$ and the classical notations $x \leq y$ if, for any index i, $x_i \leq y_i$; $x < y$ if $x \leq y$ and $x \neq y$; $x \ll y$ if $x_i < y_i$ for any index i ;
F is strongly sublinear if

$$0 < \lambda < 1, \quad w \gg 0 \Longrightarrow \lambda F(w) \gg F(\lambda w).$$

With $x \gg 0$ and $y \gg 0$, since L and M are irreducible nonnegative matrices, we have $L\,y \gg 0$ and $M\,x \gg 0$, hence $\mu_h \mathbb{1} + \lambda L\,y \ll \mu_h \mathbb{1} + L\,y$ and a similar inequality $\mu_v \mathbb{1} + \lambda M\,x \ll \mu_v \mathbb{1} + M\,x$. This proves the strict sublinearity. Using the formula for the Jacobian of F, we have

$$JF(0,0) = \begin{bmatrix} 0 & \frac{1}{\mu_h + \gamma_h} \operatorname{diag}(\frac{\Lambda_h}{\mu_h})\, L \\ \frac{1}{\mu_v} \operatorname{diag}(\bar{N}_v)\, M & 0 \end{bmatrix}$$

This matrix is irreducible and $\rho(JF(0,0)) = \mathcal{R}_0$. All the requirements of Hethcote-Thieme's Theorem are satisfied. This proves that there exists an unique positive endemic equilibrium in $\mathbb{R}^n_+$ when $\mathcal{R}_0 > 1$. Moreover, looking at the expression of F, it is clear that this equilibrium is in the compact Ω.

We will prove the asymptotic stability of this positive equilibrium. The proof is adapted from [16], using Krasnosel′skiĭ's trick [21] . The difference is that we have to vectorize this proof for the infective of human host and vectors.
We will show that the linearized equation has no solution of the form $X(t) = \exp(z\,t)\,X_0$ with $X_0 \in \mathbb{C}^{3n}$, $z \in \mathbb{C}$, $\Re z \geq 0$ for X_0 eigenvector and z corresponding eigenvalue of the Jacobian computed at the endemic equilibrium. Let $X_0 = (U, V, W) \in \mathbb{C}^{3n}$ such an eigenvector for the eigenvalue z . Then

$$z\,U = -\mu_h\,U - \operatorname{diag}(L\,I_v^*)\,U - \operatorname{diag}(S_h^*)\,L\,W \tag{12a}$$
$$z\,V = \operatorname{diag}(L\,I_v^*)\,U - (\mu_h + \gamma_h)\,V + \operatorname{diag}(S_h^*)\,L\,W \tag{12b}$$
$$z\,W = \operatorname{diag}(\bar{N}_v - I_v^*)\,M\,V - \mu_V\,W - \operatorname{diag}(M\,I_h^*)\,W \tag{12c}$$

Adding the sub-equations (12a) and(12b) we obtain the relation

$$(\mu_h + z)\, U = -(\mu_h + \gamma_h + z)\, V$$

Replacing U in (12b) and (12c) yields after some rearrangements

$$\begin{bmatrix} \operatorname{diag}\left(\mathbb{1} + \frac{z}{\mu_h+\gamma_h}\,\mathbb{1} + \frac{z+\mu_h+\gamma_h}{(z+\mu_h)\,(\mu_h+\gamma_h)}\, L\, I_v^*\right) V \\ \\ \operatorname{diag}\left(\mathbb{1} + \frac{z}{\mu_v}\,\mathbb{1} + \frac{1}{\mu_v}\, M\, I_h^*\right) W \end{bmatrix} =$$

$$\begin{bmatrix} 0 & \frac{1}{\mu_h+\gamma_h}\operatorname{diag}(S_h^*)\, L \\ \\ \frac{1}{\mu_v}\operatorname{diag}(\bar{N}_v - I_v^*)\, M & 0 \end{bmatrix} \begin{bmatrix} V \\ \\ W \end{bmatrix} \tag{13}$$

The matrix

$$H = \begin{bmatrix} 0 & \frac{1}{\mu_h+\gamma_h}\operatorname{diag}(S_h^*)\, L \\ \\ \frac{1}{\mu_v}\operatorname{diag}(\bar{N}_v - I_v^*)\, M & 0 \end{bmatrix}$$

is a nonnegative irreducible matrix, and from (10b) (10c), satisfying

$$H \begin{bmatrix} I_h^* \\ I_v^* \end{bmatrix} = \begin{bmatrix} I_h^* \\ I_v^* \end{bmatrix}.$$

Note that $\begin{bmatrix} I_h^* \\ I_v^* \end{bmatrix}$ is the positive Perron-Frobenius vector of H.
We suppose that $\Re z \geq 0$, we denote by $\eta(z)$ the minimum of the real part of the components of the two vectors

$$\frac{z}{\mu_h + \gamma_h}\,\mathbb{1} + \frac{z + \mu_h + \gamma_h}{(z + \mu_h)\,(\mu_h + \gamma_h)}\, L\, I_v^*$$

and

$$\frac{z}{\mu_v}\,\mathbb{1} + \frac{1}{\mu_v}\, M\, I_h^*$$

Since $\Re z \geq 0$, $I_v^* \gg 0$, $I_h^* \gg 0$, L and M irreducible nonnegative matrices we have $\eta(z) > 0$. Taking the absolute values in (13) gives

$$[1 + \eta(z)] \begin{bmatrix} |V| \\ |W| \end{bmatrix} \leq H \begin{bmatrix} |V| \\ |W| \end{bmatrix}$$

Let r the minimum number such that

$$\begin{bmatrix} |V| \\ |W| \end{bmatrix} \leq r \begin{bmatrix} I_h^* \\ I_v^* \end{bmatrix}.$$

We now have

$$[1 + \eta(z)] \begin{bmatrix} |V| \\ |W| \end{bmatrix} \leq H \begin{bmatrix} |V| \\ |W| \end{bmatrix} \leq r\, H \begin{bmatrix} I_h^* \\ I_v^* \end{bmatrix} = r \begin{bmatrix} I_h^* \\ I_v^* \end{bmatrix}.$$

Since $\eta(z) > 0$ if $\Re z \geq 0$, we obtain a contradiction to the minimality of r. Thus $\Re z < 0$, which proves the asymptotic stability at the endemic equilibrium.

□

4 Global Dynamics

In this section, we discuss a number of results concerning the global dynamics of system (9). It turns out that it is more convenient to work with system (9) rescaled so that the uninfected equilibrium for both host and vector populations in each patch is unity. Let

$$\begin{aligned} &D_h = \mathrm{diag}(N_h), D_v = \mathrm{diag}(N_v), \\ &(X, Y) = D_h^{-1}(S_h, I_h), \quad Z = D_v^{-1} I_v \\ &A = LD_v \text{ and } B = MD_h. \end{aligned}$$

In this case system (9) reads

$$\left\{ \begin{array}{rcl} \dot{X} &=& \mu_h(\mathbb{1} - X) - \mathrm{diag}(X)AZ \\ \dot{Y} &=& \mathrm{diag}(X)AZ - (\mu_h + \gamma)Y \\ \dot{Z} &=& \mathrm{diag}(\mathbb{1} - Z)BY - \mu_v Z \end{array} \right. \tag{14}$$

With this notation, the DFE is $(\mathbb{1}, 0, 0)$ and we shall write the EE as $(\bar{X}, \bar{Y}, \bar{Z})$. Notice that the next generation operator is now given by

$$\mathcal{N} = \begin{pmatrix} 0 & \frac{1}{\mu_h + \gamma} A \\ \frac{1}{\mu_v} B & 0 \end{pmatrix}.$$

We begin with a more general result about its persistence.

Theorem 4.1. *The system (14) is uniformly persistent, if $\mathcal{R}_0 > 1$.*

Proof. Let $E = \{\mathbf{Y} = \mathbf{Z} = 0\}$. Then, it is clear that E is the only invariant set of the flow defined by the system (9) that is contained in $\partial \bar{K}$. Therefore, the hypothesis (H) in [13] is satisfied. Recall that if $\mathcal{R}_0 > 1$, then the DFE equilibria is unstable. Hence, we have that the conditions for theorem 4.3 in [13] are satisfied and, therefore, system (14) is uniformly persistent. □

It turns out that we can ensure global stability of the DFE under weaker assumptions than of the Hypothesis 3.1:

Hypothesis 4.1. *The matrix $\mathcal{N}$ has a positive, left eigenvector associated to $\mathcal{R}_0$.*

Theorem 4.2. *Assume 4.1 holds and that $\mathcal{R}_0 \leq 1$. Then the DFE is globally asymptotically stable.*

Proof. Let (α, β) be a left, positive eigenvector of $\mathcal{N}$, associated to the eigenvalue $\mathcal{R}_0$. Let

$$V = \langle \alpha, Y \rangle + \frac{\mu_h + \gamma}{\mu_v} \langle \beta, Z \rangle \quad \text{and} \quad R = \langle \alpha, \mathrm{diag}(\mathbb{1} - X)AZ \rangle + \frac{\mu_h + \gamma}{\mu_v} \langle \beta, \mathrm{diag}(Z)BY \rangle.$$

Notice that $R \geq 0$, and that in the interior of $\bar{K}$, we have $R > 0$. Computing the derivative along the flow, we have:

$$\begin{aligned}
\dot{V} &= \langle \alpha, \dot{Y} \rangle + \frac{\mu_h + \gamma}{\mu_v} \langle \beta, \dot{Z} \rangle \\
&= \langle \alpha, \mathrm{diag}(X)AZ - (\mu_h + \gamma)\, Y \rangle + \frac{\mu_h + \gamma}{\mu_v} \langle \beta, \mathrm{diag}(\mathbb{1} - Z)BY - \nu_v Z \rangle \\
&= \langle \alpha, AZ - (\mu_h + \gamma)\, Y \rangle + \frac{\mu_h + \gamma}{\mu_v} \langle \beta, BY - \nu_v Z \rangle - R \\
&= (\mu_h + \gamma)\left[\mathcal{R}_0 \langle \beta, Z \rangle - \langle \alpha, Y \rangle + \mathcal{R}_0 \langle \alpha, Y \rangle - \langle \beta, Z \rangle\right] - R \\
&= (\mu_h + \gamma)\,(\mathcal{R}_0 - 1)\left[\langle \alpha, Y \rangle + \langle \beta, Z \rangle\right] - R \\
&\leq 0,
\end{aligned}$$

provided that $\mathcal{R}_0 \leq 1$.
Also, notice that when $\mathcal{R}_0 < 1$, we have that $\dot{V} = 0$ if, and only if, $Y = Z = 0$. Since the DFE is the unique invariant compact set in this latter case, LaSalle principle implies that it is globally asymptotically stable.
If $\mathcal{R}_0 = 1$, then $\dot{V}$ may vanish not only if $Y = Z = 0$, but also at $Z = 0$, and $\{(X, Y, Z) : \mathrm{diag}(\mathbb{1} - X)LZ = \mathrm{diag}(Z)BY = 0\,,\ Z \neq 0\}$. In the former case, with $Z = 0$ but $Y \neq 0$, it is easily seen directly from system (14), that we cannot have $\dot{Z} = 0$, and hence $Z = 0$, with $Y \neq 0$ cannot be invariant. Analogously, it can be seen that the latter case is also not invariant, and the result follows again by LaSalle principle.

□

Remark 4.1. *In particular, Theorem 4.2 shows that the only equilibrium when $\mathcal{R}_0 \leq 1$ is the DFE. Since 4.1 is weaker than 3.1, this result strengths the only-if part of Theorem 3.1. Thus, for reducible matrices that satisfy Hypothesis 4.1, there is no other equilibria than the DFE, if $\mathcal{R}_0 \leq 1$.*

Before we can tackle the global stability of the endemic equilibrium, when $\mathcal{R}_0 > 1$, we need further assumptions on the structure of the system, and some preliminary results.

Lemma 4.1. *Assume $\mathcal{N}$ is irreducible, and let*

$$T = \frac{1}{\mu_v(\mu_h + \gamma)} \mathrm{diag}(\bar{X}) A \mathrm{diag}(\mathbb{1} - \bar{Z}) B.$$

Then $\rho(T) = 1$, and T has a positive left eigenvector η such that $T^t \eta = \eta$.

Proof. Since $\mathcal{N}$ is irreducible, we have that

$$\bar{\mathcal{N}} = \begin{pmatrix} 0 & \frac{1}{\mu_h + \gamma} \mathrm{diag}(\bar{X}) A \\ \frac{1}{\mu_v} \mathrm{diag}(\mathbb{1} - \bar{Z}) B & 0 \end{pmatrix}$$

is irreducible, and from the equilibrium relationship we also have

$$\bar{\mathcal{N}} \begin{pmatrix} \bar{Y} \\ \bar{Z} \end{pmatrix} = \begin{pmatrix} \bar{Y} \\ \bar{Z} \end{pmatrix}.$$

Hence,

$$\rho(\bar{\mathcal{N}}) = 1.$$

Since $\bar{\mathcal{N}}$ has also a left Frobenius eigenvector, we have that there are positive vectors η and ξ such that

$$\frac{1}{\mu_v}B^t\text{diag}(\mathbb{1}-\bar{Z})\xi=\eta \quad \text{and} \quad \frac{1}{\mu_h+\gamma}A^t\text{diag}(\bar{X})\eta=\xi,$$

and hence

$$T^t\eta=\eta.$$

Since T is nonnegative and η is positive, the spectral radius of T must be one.

□

The entry-wise product for vectors, the Hadamard product, will be denoted by $\circ$. For a vector $X=(X_1,\dots,X_n)\in\mathbb{R}^n$ and for $f: I\subset\mathbb{R}\to\mathbb{R}$, we shall write $f(X)=(f(X_1),\dots,f(X_n))$. We collect some useful facts in the following Lemma:

Lemma 4.2. *If $X,\dots,X_m\in\mathbb{R}^n$ and $M\in M_n(\mathbb{R})$ then we have*

1. $X_1+\dots+X_m\geq m\sqrt[m]{X_1\circ\dots\circ X_m}$;
2. $X_1\circ(MX_2)=\text{diag}(X_1)MX_2=\text{diag}(MX_2)X_1$;
3. $f(\dot{X}_1)=\dot{X}_1\circ f'(X_1)$.

Lemma 4.3. *Let M be a non-negative square matrix with positive diagonal. Let $\epsilon\geq 0$ be given. Then there exists a vector $\zeta_\epsilon>>0$ such that*

$$Mv\geq\zeta_\epsilon\circ v$$

for all vectors $v>>\epsilon\mathbb{1}$.

Proof. Notice that

$$\frac{(Mv)_i}{v_i}=\frac{\sum_j M_{ij}v_j}{v_i}\geq\frac{M_{ii}v_i}{v_i}=M_{ii}>0.$$

Thus let

$$\zeta_i=\inf_{v>>\epsilon\mathbb{1}}\frac{(Mv)_i}{v_i}>0,$$

and the result follows. □

Proposition 4.1. *Assume that the host-vector contact network is specially connected. Then there exists an $\epsilon>0$ such that the set $\Omega_\epsilon=\{\epsilon\mathbb{1}\leq X,Y,Z\leq\mathbb{1}\}$ is forward invariant, and there are vectors $\delta>>0$ and $\sigma>>0$ such that*

$$\frac{1}{\mu_h+\gamma}\text{diag}(\bar{X})AZ\geq\delta\circ Z \quad \textit{and} \quad \frac{1}{\mu_v}\text{diag}(\mathbb{1}-\bar{Z})BY\geq\sigma\circ Y.$$

for $Y,Z\geq\epsilon\mathbb{1}$. In addition, δ can be chosen such that we also have

$$\frac{1}{\mu_h+\gamma}A^t\text{diag}(\bar{X})Z\geq\delta\circ Z.$$

Proof. The existence of $\epsilon > 0$ such that Ω_ϵ is forward invariant follows from Theorem 4.1. Since the network is specially connected both A and B have positive diagonal. Hence, this also holds for $\mathrm{diag}(\bar{X})A$ and $\mathrm{diag}(\mathbb{1} - \bar{Z})B$, and the existence of the vectors δ and σ follows from Lemma 4.3.
To see the claim for the transpose, notice that the lower bound in Lemma 4.3 is common both to a matrix and its transpose. □

Towards the proof of stability, we introduce the following assumption:

Hypothesis 4.2. *In addition to 3.1, we shall also assume that*

1. *The contact network is specially connected.*
2. *The vectors δ and σ, whose existence is assured by Proposition 4.1, satisfy:*

$$\delta \circ \sigma \geq \mathbb{1}.$$

Theorem 4.3. *Assume 4.2 holds and that $\mathcal{R}_0 > 1$. Then the EE is globally asymptotically stable.*

Proof. Let

$$V = \langle X - \bar{X} \circ \log(X), \eta \rangle + \langle Y - \bar{Y} \circ \log(Y), \eta \rangle + \langle Z - \bar{Z} \log(Z), \bar{\xi} \rangle, \quad \bar{\xi} = \frac{\mu_h + \gamma}{\mu_v} \xi.$$

Thus, from Lemma 4.1

$$A^t \mathrm{diag}(\bar{X})\eta = \mu_v \bar{\xi}. \quad \text{and} \quad B^t \mathrm{diag}(\mathbb{1} - \bar{Z})\bar{\xi} = (\mu_h + \gamma)\eta.$$

Then

$$\begin{aligned}
\dot{V} &= \langle \dot{X} \circ \left(\mathbb{1} - \bar{X} \circ X^{-1}\right), \eta \rangle + \langle \dot{Y} \circ \left(\mathbb{1} - \bar{Y} \circ Y^{-1}\right), \eta \rangle + \langle \dot{Z} \circ \left(\mathbb{1} - \bar{Z} \circ Z^{-1}\right), \bar{\xi} \rangle \\
&= \langle \mu_h(\mathbb{1} - X) - \mathrm{diag}(X)AZ - \mu_h(\mathbb{1} - X) \circ \bar{X} \circ X^{-1} + (\mathrm{diag}(X)AZ) \circ \bar{X} \circ X^{-1}, \eta \rangle \\
&\quad + \langle \mathrm{diag}(X)AZ - (\mu_h + \gamma)Y - (\mathrm{diag}(X)AZ) \circ \bar{Y} \circ Y^{-1} + (\mu_h + \gamma)\bar{Y}, \eta \rangle \\
&\quad + \langle \mathrm{diag}(\mathbb{1} - Z)BY - \mu_v Z - (\mathrm{diag}(\mathbb{1} - Z)BY) \circ \bar{Z} \circ Z^{-1} + \mu_v \bar{Z}, \bar{\xi} \rangle \\
&= \mu_h \langle \mathbb{1} + \bar{X} - X - \bar{X} \circ X^{-1}, \eta \rangle + \langle (AZ) \circ \bar{X}, \eta \rangle - \mu_v \langle Z, \bar{\xi} \rangle - (\mu_h + \gamma)\langle Y, \eta \rangle \\
&\quad + (\mu_h + \gamma)\langle \bar{Y}, \eta \rangle - \langle (\mathrm{diag}(X)AZ) \circ \bar{Y} \circ Y^{-1}, \eta \rangle + \langle \mathrm{diag}(\mathbb{1} - Z)BY, \bar{\xi} \rangle \\
&\quad - \langle (\mathrm{diag}(\mathbb{1} - Z)BY) \circ \bar{Z} \circ Z^{-1}, \bar{\xi} \rangle + \mu_v \langle \bar{Z}, \bar{\xi} \rangle.
\end{aligned}$$

Now observe that

$$\langle (AZ) \circ \bar{X}, \eta \rangle = \langle \mathrm{diag}(\bar{X})AZ, \eta \rangle = \langle Z, A^t \mathrm{diag}(\bar{X})\eta \rangle = \mu_v \langle Z, \bar{\xi} \rangle.$$

Also, from the equilibrium equations:

$$(\mu_h + \gamma)\bar{Y} = \mu_h(\mathbb{1} - \bar{X}) \quad \text{and} \quad \mathrm{diag}(\bar{X})A\bar{Z} = \mu_h(\mathbb{1} - \bar{X}).$$

Thus,

$$\mu_v \langle \bar{Z}, \bar{\xi} \rangle = \langle \bar{Z}, A^t \mathrm{diag}(\bar{X})\eta \rangle = \mu_h \langle \mathbb{1} - \bar{X}, \eta \rangle.$$

Combining all this information, we find that

$$\begin{aligned}\dot{V} &= \mu_h\langle 3\mathbb{1} - \bar{X} - X - \bar{X}\circ X^{-1}, \eta\rangle - (\mu_h+\gamma)\langle Y,\eta\rangle - \langle(\mathrm{diag}(X)AZ)\circ\bar{Y}\circ Y^{-1},\eta\rangle \\ &\quad + \langle \mathrm{diag}(\mathbb{1}-Z)BY,\bar{\xi}\rangle - \langle(\mathrm{diag}(\mathbb{1}-Z)BY)\circ\bar{Z}\circ Z^{-1},\bar{\xi}\rangle \\ &= \mu_h\langle 3\mathbb{1} - \bar{X} - X - \bar{X}\circ X^{-1}, \eta\rangle + \langle \mathrm{diag}(\mathbb{1}-\bar{Z})BY,\bar{\xi}\rangle - (\mu_h+\gamma)\langle Y,\eta\rangle \\ &\quad - \langle(\mathrm{diag}(X)AZ)\circ\bar{Y}\circ Y^{-1},\eta\rangle + \langle \mathrm{diag}(\bar{Z}-Z)BY,\bar{\xi}\rangle - \langle(\mathrm{diag}(\mathbb{1}-Z)BY)\circ\bar{Z}\circ Z^{-1},\bar{\xi}\rangle.\end{aligned}$$

We also have

$$\begin{aligned}\langle \mathrm{diag}(\mathbb{1}-\bar{Z})BY,\bar{\xi}\rangle &= \langle Y, B^t\mathrm{diag}(\mathbb{1}-\bar{Z})\bar{\xi}\rangle \\ &= (\mu_h+\gamma)\langle Y,\eta\rangle.\end{aligned}$$

and

$$\begin{aligned}&\langle \mathrm{diag}(\bar{Z}-Z)BY,\bar{\xi}\rangle - \langle(\mathrm{diag}(\mathbb{1}-Z)BY)\circ\bar{Z}\circ Z^{-1},\bar{\xi}\rangle \\ &\quad = \left\langle\left[(2\bar{Z} - Z - \bar{Z}\circ Z^{-1}\right]\circ BY,\bar{\xi}\right\rangle.\end{aligned}$$

Hence, we are left with

$$\begin{aligned}\dot{V} = \mu_h\langle 3\mathbb{1} - \bar{X} - X - \bar{X}\circ X^{-1},\eta\rangle + \left\langle\left[2\bar{Z} - Z - \bar{Z}\circ Z^{-1}\right]\circ BY,\bar{\xi}\right\rangle \\ - \langle(\mathrm{diag}(X)AZ)\circ\bar{Y}\circ Y^{-1},\eta\rangle.\end{aligned}$$

Now we write

$$\mathbb{1} = \bar{X} + \mathbb{1} - \bar{X} \quad \text{and} \quad \mathbb{1} = \bar{Z} + \mathbb{1} - \bar{Z}.$$

Then, we also have

$$-X - \bar{X}^2\circ X^{-1} \le -2\bar{X},$$

and analogously for $Z - \bar{Z}^2\circ Z^{-1}$.
Therefore, we find

$$\begin{aligned}\dot{V} &\le 3\mu_h\langle\mathbb{1}-\bar{X},\eta\rangle - \mu_h\langle\bar{X}\circ(\mathbb{1}-\bar{X})\circ X^{-1},\eta\rangle \\ &\quad - \langle\bar{Z}\circ(\mathbb{1}-\bar{Z})\circ Z^{-1}\circ(BY),\bar{\xi}\rangle - \langle(\mathrm{diag}(X)AZ)\circ\bar{Y}\circ Y^{-1},\eta\rangle. \\ &= 3\mu_h\langle\mathbb{1}-\bar{X},\eta\rangle - R,\end{aligned}$$

where

$$R = \mu_h\langle\bar{X}\circ(\mathbb{1}-\bar{X})\circ X^{-1},\eta\rangle + \langle\bar{Z}\circ(\mathbb{1}-\bar{Z})\circ Z^{-1}\circ(BY),\bar{\xi}\rangle + \langle(\mathrm{diag}(X)AZ)\circ\bar{Y}\circ Y^{-1},\eta\rangle.$$

Notice that the inequality above for $\dot{V}$ is strict, except when $X=\bar{X}$ and $Z=\bar{Z}$. Therefore, we have

$$\bar{\xi} = \frac{1}{\mu_v}A^t\mathrm{diag}(\bar{X})\eta \ge \frac{\mu_h+\gamma}{\mu_v}\delta\circ\eta,$$

in view of the second observation in Proposition 4.1.
Hence,

$$\langle\bar{Z}\circ(\mathbb{1}-\bar{Z})\circ Z^{-1}\circ(BY),\bar{\xi}\rangle \ge \frac{\mu_h+\gamma}{\mu_v}\langle\bar{Z}\circ(\mathbb{1}-\bar{Z})\circ Z^{-1}\circ(BY)\circ\delta,\eta\rangle.$$

Thus, we have that

$$
\begin{aligned}
R &\geq \left\langle 3\left[\frac{\mu_h(\mu_h+\gamma)}{\mu_v}\bar{X}\circ(\mathbb{1}-\bar{X})\circ\bar{Z}\circ(\mathbb{1}-\bar{Z})\circ Z^{-1}\circ(BY)\circ\delta\circ(AZ)\circ\bar{Y}\circ Y^{-1}\right]^{1/3},\eta\right\rangle \\
&= \left\langle 3\left[\frac{\mu_h^2}{\mu_v}(\mathbb{1}-\bar{X})^2\circ\bar{Z}\circ\bar{X}\circ(AZ)\circ Z^{-1}\circ(\mathbb{1}-\bar{Z})\circ(BY)\circ Y^{-1}\circ\delta\right]^{1/3},\eta\right\rangle \\
&= \left\langle 3\left[\frac{\mu_h^2}{\mu_v^2}(\mathbb{1}-\bar{X})^2\circ(\mathbb{1}-\bar{Z})\circ(B\bar{Y})\circ\bar{X}\circ(AZ)\circ Z^{-1}\circ(\mathbb{1}-\bar{Z})\circ(BY)\circ Y^{-1}\circ\delta\right]^{1/3},\eta\right\rangle \\
&\geq \left\langle 3\left[\frac{\mu_h^3}{\mu_v(\mu_h+\gamma)}(\mathbb{1}-\bar{X})^3\circ(\mathbb{1}-\bar{Z})\circ(B\bar{Y})\circ\bar{X}\circ(AZ)\circ Z^{-1}\circ(\mathbb{1}-\bar{Z})\circ(BY)\circ Y^{-1}\circ\sigma\circ\delta\right]^{1/3},\eta\right\rangle
\end{aligned}
$$

where we have used that

$$
\bar{Y}=\frac{\mu_h}{\mu_h+\gamma}(\mathbb{1}-\bar{X})\quad\text{and}\quad\bar{Z}=\frac{1}{\mu_v}(\mathbb{1}-\bar{Z})\circ(B\bar{Y})\geq\sigma\circ\bar{Y}=\frac{\mu_h}{\mu_h+\gamma}\sigma\circ(\mathbb{1}-\bar{X}).
$$

Therefore, on using Proposition 4.1, we find that

$$
R\geq\left\langle 3\mu_h(\mathbb{1}-\bar{X})\circ\left[\sigma^2\circ\delta^2\right]^{1/3},\eta\right\rangle.
$$

On using Hypothesis 4.2, we then conclude that $\dot{V}\leq 0$, with equality only when $X=\bar{X}$ and $Z=\bar{Z}$. □

5 Conclusions

We have considered a class of multi-group models for indirectly transmitted diseases.This class is a natural candidate for modeling the impact of fast urban movement in some vector transmitted diseases, as for instance, in the case of dengue fever. From the network movement topology, we have identified a bipartite graph that describes the host-vector contact topology. The irreducibility of such contact network then leads to a complete analysis of the basic reproductive number, $\mathcal{R}_0$, and the existence and local stability of both disease free and endemic equilibria. A very natural condition, under usual modeling assumptions, is derived as to characterize a broad family of models in this class. These conditions are also sufficient to show that the dynamics is uniformly persistent, when $\mathcal{R}_0>1$. It also turns out that a somewhat weaker assumption allows for a complete global stability analysis when $\mathcal{R}_0\leq 1$. In addition, this result also enlarges the class of models for which no endemic equilibrium can exist when R_0 does not exceed unity. Finally, with additional assumptions on the contact topology network, we have shown the global stability of the endemic equilibrium when $\mathcal{R}_0>1$.

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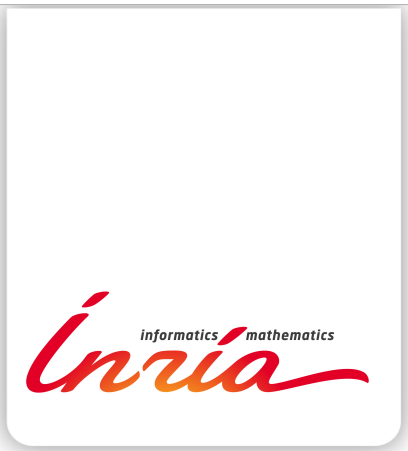

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