On the Carrying and Evolution Matrices in Epidemic Models

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Abstract. This study presents a technical characterization of classical epidemic models of compartments by decomposing the state into an infectious sub-state (or infective compartment) and a non-infective sub-state (or non-infective compartment). Then, the linearized infective part of the model is discussed through a positivity /stability viewpoint from linear algebraic tools. Some relevant properties of the transition and transmission matrices are described in a general context. The main advantage of the given formalism is that the linearized behavior about the equilibrium steady-state is general in the sense that it is independent of the particular epidemic model due to the compartmental structure performed analysis. The performed study is made in the absence and in the presence of delayed dynamics.

1. Introductory Considerations

This study presents a formal and unified characterization of classical epidemic models of compartments by decomposing the state into an infectious sub-state (or infective compartment) and a non-infective sub-state (or non-infective compartment). Then, the linearised infective model-integrating part is discussed from a viewpoint of stability and positivity of the solution from linear algebraic tools. The Perron eigenvalue of a defined relevant so-called next generation matrix dictates the stability of the equilibrium steady-state in the absence of illness if it has a value strictly below unity. Such a Perron eigenvalue is the disease basic basic reproductive number1,2. It is assumed that the negative matrix of transition, that is the transition matrix with all its nonzero entries with opposed sign, of the infective components of the linearised epidemic model about the equilibrium point in the absence of infectious illness is a invertible matrix with positive inverse (then, a stable matrix) and the corresponding transmission matrix is also positive. It turns out that such matrices are the Jacobian matrices of the nonlinear system about the equilibrium point in the absence of infectious illness. It is used for stability analysis the feature that a Metzler matrix which is stable has a minus positive inverse and vice-versa. The problem is studied in the delay-free case and then extended to the presence of point delays in the dynamics and the calculation of a basic reproductive number in the delay-free case or bounds of it in the delayed case are key tools to evaluate the local stability about the disease-free equilibrium point. It is addressed in this research that the Perron eigenvalue of the auxiliary matrix $GH^{-1}$, which is the referred to as the next generation matrix is strictly less than unity, with the matrix $G$ being referred to as the carrying matrix of the illness while $(-H)$ is referred to as the evolution matrix. Thus, if its maximal real positive eigenvalue is below unity then the linearised epidemic model about the equilibrium point in the absence of illness is proved to be stable in the local...
asymptotic sense and conversely. It is also proved that the basic reproductive number is linked to the Perron eigenvalue of the above auxiliary matrix, which is coincident with its spectral radius in some well-known common examples of epidemic modeling ingredients based on differential equations. The appearance of delayed dynamics with either distributed or punctual delays is a relevant modeling tool in epidemiology in some cases when there are intermittent exploding expansions, or outbreaks, and eventual re-growing phenomena of the illness intensity caused by a certain positive increment of the amounts of transmission agents (namely, the transmission vector numbers) or due, may be, to outsiders immigration to the fixed environment under study in the epidemic model. The main results establish the local stability about the disease-free equilibrium point mainly based on the properties of the evolution and carrying matrices when linearised taking as basis the infective compartment structure. The basic study is made for the delay-free case but it is then extended to the case of presence of delayed dynamics. In a future research, it could be easily extended to epidemic models formulated in the discrete-time framework under constant or updated sampling period and under the potential presence of nonlinear disturbances$^{5-8}$. A numerical illustrative example involving three nodes is also discussed.

2. Delay-free Situation

$X > 0$ denotes that $X(> 0) = 0$, that is $> 0$ implies that the matrix $X$ has at least one positive entry. If $X, Y \in R^{p \times q}$ then $X > Y$ refers to $X - Y > 0$ (that is, $X - Y$ is a positive matrix) while $X < 0$ means that $-(X) > 0$, $X >> 0$ (in words: $X$ is a strictly positive matrix) has the meaning that $X_{ij} > 0$; $\forall i \in P, \forall j \in Q$. An alternative similar notation reads as $X \in R^{p \times q}$. In a parallel way, if $X, Y \in R^{p \times q}$ then $X \gg Y$ is equivalent to $X - Y$ to have all its entries being positive while $X << 0$ has the meaning that $-(X) > 0$. Close notations concern the positivity concepts of real vectors, $\rho(X) = \rho_{\text{max}}(X)$ is the spectral radius of $X \in R^{p \times p}$, $X \in R^{p \times p}$ is Metzler, which is in short referred to as $X \in M^{p \times p}$, if $X_{ij} > 0$; $\forall i, j(\neq i) \in P$, $X \in R^{p \times p}$ is an $M$-matrix if $X_{ii} \geq 0$ and $X_{ij} \leq 0$; $\forall i, j(\neq i) \in P$.

A generic compartmental disease model of dimension $(m + n)$ can be written as follows $^{1,2,7,8,9,10}$:

$$\dot{x}(t) = G(x(t), y(t)) - H(x(t), y(t)) = (G - H)x(t) - f(x(t), y(t)) ; \quad \dot{y}(t) = g(x(t), y(t))$$

(1)

with $g(x_1, x_2, ..., x_n, y_1, y_2, ..., y_m) = (f^T(x_1, x_2, ..., x_n), g(y_1, y_2, ..., y_m))^T$ for any fixed positive or null initial conditions $z^T(0) = (x(0), y(0))$, where $n$ and $m$ are the dimensions of the disease and non-disease compartments, respectively, being of state vectors $x(t)$ and $y(t)$, respectively; while $G$ and $(-H) \in R^{m \times n}$ are, respectively, the disease carrying and state evolution matrices of the linearised epidemic model about the equilibrium point in the absence of illness, and $f(x(t), y(t))$ takes into account the higher-order nonlinear contributions to the dynamics $\dot{(x(t), y(t))} = (G - H)x(t) - G(x(t), y(t)) + H(x(t), y(t))$ where $z^T(t) = (x(t), y(t))$ is the complete state vector which do not specifically contribute to the linearised dynamics about the steady-state. Analytical studies concerned the positivity framework in some alternative biologic problems of interest concerned the species evolution through time have been reported, for instance, in $^{8,9}$ and some references therein. Analytic studies of problems of carrying and evolutions in various kinds of epidemic models, in both the stochastic and the deterministic frameworks, have also been recently referred to in a set of references. See, for instance $^{11-27}$, and references therein.

Assumption 1. The following constraints are assumed:

$G_i(0, y(t)) = H_i(0, y(t)) = 0$ when $x_i = 0$, $\forall i \in \{1, 2, ..., n\}$, $G_i(x(t), y(t)) \geq 0$, $H_i(x(t), y(t)) \leq 0$, and $\sum_{i=1}^{n} H_i(x(t), y(t)) \geq 0$ for all $x(t), y(t) \geq 0$ (which refers to all the respective components of $x(t), y(t)$.

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being positive or null and with at least one of them being strictly positive). In Reference 1, the two matrices $G$ and $H$ are real square $n$-matrices while being defined as “ad-hoc” Jacobians about the equilibrium point in the absence of illness

$$x_{df} = [0^T, y_{df}^T]^T : G = \left[ \frac{\partial G_i(0,y_{df})}{\partial x_j} \right] ; H = \left[ \frac{\partial H_i(0,y_{df})}{\partial x_j} \right]$$

(2)

Assumption 2. $z_{df} = [0^T, y_{df}^T]^T$, that is, the equilibrium point in the absence of illness, is single (that is, unique) and the evolution matrix $(-H)$ of the states which are infective of the linearised epidemic model about the equilibrium point in the absence of illness is a invertible $M$-matrix under the constraint $H^{-1} > 0$ while the associate carrying matrix $G$ has non-negative entries, namely, $G \geq 0$.

Note that there is an intuitive physical interpretation of Assumption 2 concerned with the linearization about the disease-free equilibrium. Such an interpretation relays on the feature that there is no need of precisely calculating the concrete allocation of all the eigenvalues of the matrix $(-H)$. Also, it is usually seen that, in the situation when the epidemic model only possesses a constant and unique carrying coefficient rate of the disease $\beta$, then the reproduction number $R_0 = 0$ and $G = 0$.

This section establishes some elementary results on positivity and stability of the linearised epidemic model about the equilibria which are offered in a simplified format without their detailed technical proofs. The following assertions hold:

1. The linearised epidemic model about the disease-free equilibrium point possesses a positive or null trajectory solution of the sub-state of the infectious variables (that is, the infective sub-state) for any point initial conditions $x_0 \geq 0$ and $y_0 \geq 0$ if and only if $(G-H) \in M^{pos}_e$. An alternative statement of the sufficient and necessary condition is that $(-H) \in M^{pos}_e$ and $G \geq 0$.

2. A condition of necessary type for an epidemic model (1)-(2) to have a positive or null global solution of the state trajectory, independent of the fixed particular conditions of initialization $x(0) \geq 0, y(0) \geq 0$, is that $(G-H) \in M^{pos}_e$.

3. The linearised infective sub-state is uniformly bounded for all the instants of time with $x_L(t) \geq 0$; $\forall t \in R_{0+}$ and $x_L(t) \rightarrow 0$ exponentially as $t \rightarrow \infty$ for any given initial conditions $x_L(0) = x(0) \geq 0 , y_L(0) = y(0) \geq 0$ if and only if any of the equivalent conditions given below holds:

(1) $G-H \in M^{pos}_e$ is a stable matrix.

(2) $G-H \in M^{pos}_e$ (so that $G-H$ is a invertible $M$-matrix) while $(G-H)^{-1} > 0$.

(3) $(-H) \in M^{pos}_e$ (or $H$ is a invertible $M$-matrix) matrix, $H^{-1} > 0, G \geq 0$ and $\rho(GH^{-1})<1$.

4. The linearised infective sub-state is unstable if and only if any of the equivalent conditions given below holds:

(1) $(-H) \in M^{pos}_e$ and it exists $H^{-1} < 0, G \geq 0$ and $\rho(GH^{-1})>1$.

(2) $(G-H) \in M^{pos}_e$ is not a stable matrix.

(3) $(G-H) \in M^{pos}_e$ and it exists $G^{-1} < 0$.

5. The state-trajectory solution of the state of the whole non-linear epidemic model is either positive or null for all the instants of time, i.e. $z(t) = [x^T(t) , y^T(t)]^T \geq 0 ; \forall t \in R_{0+}$, supposed that $z(0) = [x^T(0) , y^T(0)]^T \geq 0$ is finite and arbitrary, if and only if the two subsequent constraints hold:

$$\int_0^t f(x(\tau), y(\tau))d\tau, y(\tau) \geq e^{(G-H)y}x(0) ; \forall t \in R_{0+} ; \limsup_{t \rightarrow \infty} \int_0^t g(x(\tau), y(\tau))d\tau \geq -y(0) ; \forall t \in R_{0+}$$

$$\liminf_{t \rightarrow \infty} \int_0^t f(x(\tau), y(\tau))d\tau \leq e^{(F-V)y}x(0) \leq 0 ; \liminf_{t \rightarrow \infty} \int_0^t g(x(\tau), y(\tau))d\tau \geq 0$$

(3)

(4)
6. Further assume that $(G-H)\in M_{m\times n}^+$ is a stable matrix, equivalently, that any of the two alternative equivalent restrictions of Property 3 holds. Then,
\[ \int_0^\infty f(x(t),y(t))dt = 0 \quad \text{as} \quad t \to \infty \]
provided that $f : \mathbb{R}^m \times \mathbb{R}^n \to \mathbb{R}^n$ is continuous everywhere function $A \gg B$ in its definition domain and $f(x(t),y(t)) \geq 0 \; \forall t \in \mathbb{R}_0^+$; and
\[ f(x(t),y(t)) \to 0 \quad \text{as} \quad t \to \infty \]
(but non-necessarily $\int_0^\infty f(x(t),y(t))dt = 0$ ) if
\[ f : \mathbb{R}^m \times \mathbb{R}^n \to \mathbb{R}^n \]
is uniformly continuous everywhere in its definition domain.

7. The state-trajectory solution of is positive or null for any instant of time, i.e. $z^T(t) = (x(t),y(t)) \geq 0 \; \forall t \in \mathbb{R}_0^+$, for any given initial condition $z(0) = (x(0),y(0)) \geq 0$ if and only if for all $i \in \pi$, $j \in \pi$ and all $t \in \mathbb{R}_0^+$:
\[
(x_i(t) = 0) \Rightarrow \left(f_i(x(t),y(t)) \leq \sum_{j=1}^m (G_{ij} - H_{ij})x_j(t) = \sum_{j=1}^m (G_{ij} - H_{ij})x_j(t) \right)
\]
\[
(y_j(t) = 0) \Rightarrow (g_j(x(t),y(t)) \geq 0).
\]

8. Property 7 also implies that $f_i(0,y_{df}) = g_j(0,0) = 0 \; \forall i \in \pi \; \forall j \in \pi$ if an equilibrium state $z_{df} = (0^T, y_{df}^T)^T$ exists in the disease-free situation.

Let us consider the function $g : \mathbb{R}^{n+m} \to \mathbb{R}^m$ being continuously differentiable in its whole definition domain with its associate Jacobian:
\[
J_{g.z}(z_0) = \left[ J_{g,z}(z_0) \mid J_{g,z}(z_0) \right] \quad \text{at any} \; z_0 = (x_0^T, y_0^T)^T \in \mathbb{R}^{n+m} \quad \text{with} \; x_0 \in \mathbb{R}^n \; \text{and} \; y_0 \in \mathbb{R}^m, \; \text{where} \; z = (x^T, y^T)^T \in \mathbb{R}^{n+m}, \; x \in \mathbb{R}^n, \; y \in \mathbb{R}^m. \; \text{Then, the following stability result holds:}
\]

**Proposition 1 (Global stability result).** Assume that $(-H) \in M_{n \times n}^+$, $H^{-1} \succ 0$, $G \succeq 0$ and $\rho(GH^{-1}) < 1$.

Further assume that $J_{g,z}(z(t))$ is invertible, $g_i(z(t)) \geq 0$ if $y_i(t) = 0$ for any $i \in \pi$ and $t \in \mathbb{R}_0^+$, and $f_j(z(t)) \leq e_i^T (G-H) z(t)$ if $x_i(t) = 0$ for any $i \in \pi$ and $t \in \mathbb{R}_0^+$ (it suffices that $f_j(z(t)) \leq 0$ if $x_i(t) = 0$), that the total population is bounded for all the instants of time.

Then, any trajectory solution is bounded and positive or null for all the instants of time for any finite given initial condition $x_0 \succeq 0$ and $y_0 \succeq 0$ while it is globally convergent to the disease-free equilibrium state, which is also the unique equilibrium point being attainable by the solution trajectory. Such an equilibrium point is a stable attractor in the global asymptotic sense.

3. Delayed Situation

The results which have been described the previously mentioned section can be broadened in some sense to the situation of existence of punctual delays in the model. A general disease model of compartmental type having a dimension $(m+n)$ with $r$ being constant, and in general, incommensurate, internal punctual delays (that is, not being integer multiple of a basic reference delay) $h_i (i \in \pi)$ satisfying $0 = h_0 < h_1 < h_2 < \ldots < h_r = h \leq \bar{h}$ might be generalized from the un-delayed standard situation as follows:
\[
\dot{x}(t) = \sum_{i=0}^{r} (G_i(x(t-h_i), y(t-h_i)) - H_i(x(t-h_i), y(t-h_i))) = \sum_{i=0}^{r} (G_i-H_i)x(t-h_i)
\]
\[
- f_i(x(t), y(t), x(t-h_i), y(t-h_i), \ldots, x(t-h_{i-1}), y(t-h_{i-1}))
\]
\[
y(t) = g(x(t), y(t)) = g(x(t), y(t), x(t-h_i), y(t-h_i), \ldots, x(t-h_{i-1}), y(t-h_{i-1}))
\]

(6)
being subject to any prefixed absolutely continuous function of initial conditions \( \varphi : [-h, 0] \rightarrow \mathbb{R}^{n+m} \) with eventual finite jumps on a subset of \([-h, 0]\) of zero measure with \( \varphi(0) = (x^T(0), y^T(0))^T \). It turns out that the solution is unique on \([-h, \infty)\) for any such initial conditions from the well-known Cauchy-Peano theorem of differential equations. The integers \( n \) and \( m \) are the dimensionalities of the disease and non-disease compartments of respective state vectors \( x(t) \) and \( y(t) \), and

\[
\begin{align*}
f(x(t), y(t)) &= f(x(t), y(t), x(t-h_1), y(t-h_1), \ldots, x(t-h_r), y(t-h_r))
\end{align*}
\]

\[
\begin{align*}
&= \sum_{i=0}^{r} (G_i - H_i) x(t-h_i) - \sum_{i=0}^{r} (G_i (x(t-h_i), y(t-h_i)) - H_i (x(t-h_i), y(t-h_i)))
&= \rho(\hat{z}(t)) W(\hat{z}(t))
\end{align*}
\]

(7)

where \( G \) and \((- H)\) \( \in \mathbb{R}^{n \times n} \) are, respectively, the disease carrying matrix and the state evolution matrix of the linearised epidemic model about the equilibrium point in the absence of illness, and \( f(x(t), y(t)) \) takes care of evaluating the influence of the dynamics of higher-order contribution nonlinear phenomena.

\[
\hat{z}(t) = [\hat{x}(t), \hat{y}(t)] = [z^T(t), \ldots, z^T(t-h_r)]
\]

where \( z(t) = [y^T(t), x^T(t)]^T \) and \( \rho(\hat{z}(t)) \) is the quantified bounded and positive illness incidence rate, and \( W(\hat{z}(t)) = \sum_{i=0}^{r} G_i (z(t-h_i)) z(t-h_i) \) where \( W(\hat{z}(t)) \) is a partitioned block matrix function of order \((n+m)\) of the form

\[
W(\hat{z}(t)) = \sum_{i=0}^{r} \begin{bmatrix} W_{yx}(y(t-h_i)) & W_{yx}(x(t-h_i)) \\ W_{xy}(x(t-h_i)) & W_{xx}(x(t-h_i)) \end{bmatrix}
\]

(8)

Note that

\[
\begin{align*}
\dot{x}(t) &= \sum_{i=0}^{r} (G_i - H_i) x(t-h_i) - f(\hat{x}(t), \hat{y}(t))
&= (G_0 - H_0) x(t) + \sum_{i=1}^{r} (G_i - H_i) x(t-h_i) - f(\hat{x}(t), \hat{y}(t))
&= (G - H) x(t) + \sum_{i=1}^{r} (G_i - H_i) (x(t-h_i) - x(t)) - f(\hat{x}(t), \hat{y}(t))
\end{align*}
\]

\[
\dot{y}(t) = g(\hat{x}(t), \hat{y}(t))
\]

(9)

(10)

where

\[
\begin{align*}
f(\hat{x}(t), \hat{y}(t)) &= \sum_{i=0}^{r} (G_i - H_i) x(t-h_i) - \sum_{i=0}^{r} (G_i (x(t-h_i), y(t-h_i)) - H_i (x(t-h_i), y(t-h_i)))
&= (G_0 - H_0) x(t) + \sum_{i=1}^{r} (G_i - H_i) x(t-h_i) - \sum_{i=0}^{r} (G_i (x(t-h_i), y(t-h_i)) - H_i (x(t-h_i), y(t-h_i)))
&= (G - H) x(t) + \sum_{i=1}^{r} (G_i - H_i) (x(t-h_i) - x(t)) - \sum_{i=0}^{r} (G_i (x(t-h_i), y(t-h_i)) - H_i (x(t-h_i), y(t-h_i)))
\end{align*}
\]

(11)

with \( G = \sum_{i=0}^{r} G_i \) , \( H = \sum_{i=0}^{r} H_i \) with

\[
\begin{align*}
G_j &= \left[ \frac{\partial G_{j}}{\partial x} (x(t-h_i), y(t-h_i)) \right] ; \ H_j &= \left[ \frac{\partial H_{j}}{\partial x} (x(t-h_i), y(t-h_i)) \right] ; \ j \in \mathcal{F} \cup \{0\}
G_{ej} &= \left[ \frac{\partial G_{e_j}}{\partial x} (x_{end}, y_{end}) \right] ; \ H_{ej} &= \left[ \frac{\partial H_{e_j}}{\partial x} (x_{end}, y_{end}) \right] ; \ j \in \mathcal{F} \cup \{0\}
\end{align*}
\]

(12)

(13)

, respectively, at the equilibrium point in the absence of illness \( z_{df} = (0^T, y_{df}^T)^T \) and at the endemic one \( z_{end} = (x_{end}^T, y_{end}^T)^T \) and the re-taken new definitions:
\[ G = \sum_{i=0}^{r} G_i, \quad H = \sum_{i=0}^{r} H_i, \quad (14) \]

Some sufficiency-type conditions to guarantee the stability of the linearised epidemic model about the disease-free equilibrium point can be got irrespective of the sizes of the delay for the relevant illustrative situations that \( G_0 \) or \( G \) are a stable matrices.

Generalized versions of the preceding Assumption 1 and Assumption 2 are maintained related to the epidemic models in the existence of delays as follows:

**Assumptions 4.** \( \sum_{j=0}^{r} G_j(0, y(t-h_j)) = \sum_{j=0}^{r} H_j(0, y(t-h_j)) = 0; \forall i \in \bar{\pi} = \{1, 2, ..., n\}, G_j(y(t-h_j), y(t-h_j)) \geq 0, H_j(y(t-h_j), y(t-h_j)) \leq 0 \) when \( x_i(t-h_j) = 0, \) and \( \sum_{j=0}^{n} \sum_{j=0}^{r} H_j(x(t), y(t)) \geq 0 \) for all \( x(t), y(t) \geq 0. \)

**Assumptions 5.**

a) \( (-H_0) \in M^{\infty}_{\rho}, H_0^{-1} > 0, \) \( G_i \geq H_i; \forall i \in \bar{\pi}. \)
b) The equilibrium point in the absence of illness \( z_{df}' = (0^T, y_{df})^T \) fulfils uniqueness while the non-infective subsystem \( y(t) = g(0, y(t)) \) is stable in the local asymptotic sense.

**Proposition 2.** The subsequent assertions hold:

(i) If \( H_0 \) is non-singular then
\[
\dot{x}_L(t) = -H_0 \left( I_n - H_0^{-1} G_0 \right) x_L(t) + \sum_{i=0}^{r} \left( G_i - H_i \right) x_L(t - h_i) \quad (15)
\]

(ii) If \( H \) is invertible then
\[
\dot{x}_L(t) = -\left( \sum_{i=0}^{r} (H_i) \right) \left[ I_n - \left( \sum_{i=0}^{r} (H_i) \right)^{-1} \sum_{i=0}^{r} (G_i) \right] x_L(t) + \sum_{i=0}^{r} \left( G_i - H_i \right) (x_L(t - h_i) - x_L(t)) \quad (16)
\]

(iii) If \( H_0 \) and \( H \) are invertible then the linearised epidemic model about the equilibrium point in the absence of illness is described by both (12) and (13) and also by
\[
\dot{x}_L(t) = -H_0 \left( I_n - H_0^{-1} \left( \sum_{i=1}^{r} (H_i) \right) \right) \left[ I_n - \left( H_0 \left( I_n - H_0^{-1} \left( \sum_{i=1}^{r} (H_i) \right) \right) \right)^{-1} \sum_{i=0}^{r} (G_i) \right] x_L(t) + \sum_{i=0}^{r} \left( G_i - H_i \right) (x_L(t - h_i) - x_L(t)) \quad (17)
\]

The state vectors \( x(t) \) and \( y(t) \) of the disease and non-disease compartments can be re-named as the infective and non-infective sub-states of the epidemic model.

**Proposition 3.** The following assertions hold:

(i) The linearised epidemic model with several input incommensurate delays about the disease-free equilibrium steady-state has either a null or a positive solution of the infective sub-state which is independent of the delays for any finite function of admitted initial conditions \( \phi(t) \geq 0; \forall t \in [-h, 0] \) if and only if \( (G_0 - H_0) \in M^{\infty}_{\rho} \) (equivalently, \( (-H_0) \in M^{\infty}_{\rho} \) and \( G_0 \geq 0 \)) and \( G_i \geq H_i; \forall i \in \bar{\pi} \). Those conditions are also jointly necessary for the epidemic model to have a positive or null solution trajectory independent of the delays for any admissible function of initial conditions \( \phi(t) \geq 0; \forall t \in [-h, 0] \) if and only if any of the similar restrictions listed below holds:

(1) \( (G_0 - H_0) \in M^{\infty}_{\rho} \) is a matrix which is stable(equivalently, it exists \( (G-H)^{-1} > 0 \); equivalently \((-H_0) \in M^{\infty}_{\rho}, \) it exists \( H_0^{-1} > 0, \) \( G_0 \geq 0 \) and \( \rho(G_0 H_0^{-1}) < 1), \) \( G_i \geq H_i; \forall i \in \bar{\pi}, \) and
\[
\left\| (sI_n + H_0 - G_0)^{-1} \left( \sum_{i=0}^{r} (G_i - H_i) e^{-s h_i} \right) \right\|_\infty = \sup_{\omega \in \mathbb{R}_+} \left| \int_0^{\infty} (sI_n + H_0 - G_0)^{-1} \left( \sum_{i=0}^{r} (G_i - H_i) e^{-i \omega h_i} \right) \right| < 1 \quad (18)
\]
\[ \sum_{i=0}^{r'} (G_i - H_i) \] is a stable matrix, \((G_0 - H_0) \in M_{n \times n}^e\) (equivalently, \((- H_0) \in M_{n \times n}^e\) and \(G_0 \geq 0\)), \(G_i \geq H_i\); \(\forall i \in \mathcal{I}\), and

\[
\sup_{\omega \in \mathbb{R}_+} \left\| \left( \text{io} \text{I}_n + \sum_{i=0}^{r'} (G_i - H_i) e^{-\omega h_i} \right)^{-1} \right\| < 1 \]

where the argument \(s\) is the Laplace transform variable.

**(iii)** The linearised infective sub-state is unstable if and only if any of the constraints given below, which are equivalent to each other, holds:

1. \((G - H) \in M_{n \times n}^e\) is not a stable matrix.
2. \((G - H) \in M_{n \times n}^e\) and it exists \((H - G)^{-1} < 0\).
3. \((- H) \in M_{n \times n}^e\) and it exists \(H^{-1} < 0\), \(G \geq 0\) and \(\rho\left(GH^{-1}\right) > 1\).

**(iv)** The linearised infective sub-state about the equilibrium steady-state in the absence of illness is positive and, in the global exponential sense independent of the set of any set of \(r\) commensurate delays \(h_i = h_1\) \(\forall i \in \mathcal{I}\), for any bounded admissible function of initial conditions \(\phi(t) \geq 0\); \(\forall t \in [-h, 0]\) if and only if \(\sum_{i=0}^{r'} (G_i - H_i)\) is a stable matrix, \((G_0 - H_0) \in M_{n \times n}^e, G_i \geq H\); \(\forall i \in \mathcal{I}\), and

\[
\det\left( \text{io} \text{I}_n + \sum_{i=0}^{r'} (H_i - G_i) z^i \right) \neq 0 \quad \forall \omega \in \mathbb{R}_+, \forall z \in \mathbb{C}(0, 1).
\]

In the event that \(S = \{(\omega, z) \in \mathbb{R}_+ \times \mathbb{C}(0, 1) \neq \emptyset\) then the infective sub-state about the free of illness equilibrium steady-state is not stable at exponential rate for the following constraint for the sets of commensurate delays \(S_H = \left\{ h_i = \frac{\ln z}{\omega} : (\omega, z) \in S \right\}\).

**(v)** The linearised infective sub-state about the steady-state in the illness-free case is stable with exponential convergence rate independent of the set of \(r\) incommensurate delays \(h_i\); \(\forall i \in \mathcal{I}\) if:

\[
\mathcal{F}_{00} = 2 \left\| \sum_{i=0}^{r'} (G_i - H_i) \right\|_2 \sup_{\omega \in \mathbb{R}_+} \left\| \text{io} \text{I}_n - \left( \sum_{i=0}^{r'} (G_i - H_i) \right)^{-1} \right\|_2 < 1
\]

provided that \(\sum_{i=0}^{r'} (G_i - H_i)\) is a stable matrix, which holds if and only if

\[
\rho_{00} = \rho\left( \left( \sum_{i=0}^{r'} G_i \right) \left( \sum_{i=0}^{r'} H_i \right)^{-1} \right) < 1.
\]

The infective linearised epidemic model about the steady-state equilibrium in the complete absence of illness has two relevant particular situations of interest which define two corresponding auxiliary linearised epidemic models. Those mentioned systems are useful for stability analysis in the local sense being independent of the sizes of the delays, namely:

a) **Linearised infective free-of-delay system (AILDFS)** with \(h_i = 0\); \(\forall i \in \mathcal{I}\):

\[
\dot{x}_L(t) = \sum_{i=0}^{r'} (G_i - H_i) x_L(t)
\]

for \(t > 0\) for admissible initial conditions \(\phi: [-h, 0] \rightarrow \mathbb{R}_{0+}^n\) with \(\phi(0) = x(0) = x_0\) and \(h = h_i\);

b) **Linearised infective free of delayed system (AILDDFS)** with \(G_i - H_i = 0\); \(\forall i \in \mathcal{I}\):

\[
\dot{x}_L(t) = (G_0 - H_0) x_L(t)
\]

for \(t > 0\) for admissible initial conditions \(\phi: [-h, 0] \rightarrow \mathbb{R}_{0+}^n\) with \(\phi(0) = x(0) = x_0\) and a given maximum delay \(h = h_i \leq +\infty\). This particular system can also be interpreted for the situation of point initial
conditions \( \phi(t) = 0 \) for \( t \in [-\infty, 0) \) and \( \phi(0) = x(0) = x_0 \) as defined under any quantified levels of delayed dynamics associated with infinity delays \( h_i = +\infty \); \( \forall i \in \mathcal{F} \).

Note that the disease basic reproductive number \( R_0(0, h_1, h_2, \ldots, h_r) \) is, in general, delay-dependent under specific values \( R_0 = R_0(\theta) \) with \( \theta \in \mathbb{R}^{n+1} \), which is the basic reproductive number of the AILDPS, and \( R_{0,\infty} = R_0(0, \infty) \), where \( \infty \in \mathbb{R}^r \) has all components equal to \( +\infty \), which is the basic reproductive number of the AILDDDFS. Define the maximum and minimum reproductive-like numbers for any given finite set of incommensurate delays:

\[
R_{M0} = \max_{0 \leq h_i \leq \infty} R_0(0, h_1, h_2, \ldots, h_r) ; \quad R_{m0} = \min_{0 \leq h_i \leq \infty} R_0(0, h_1, h_2, \ldots, h_r)
\]

where \( R_{00} = \max(\rho_{00}, \bar{\rho}_{00}) \), \( R_{0,\infty} = \max(\rho_{0,\infty}, \bar{\rho}_{0,\infty}) \). Note that \( \rho_{00} \) and \( \rho_{0,\infty} \) are the respective basic reproductive numbers of the AILDPS and the AILDDDFS which are auxiliary free of delay linearised epidemic models and the amounts \( \bar{\rho}_{00} \) and \( \bar{\rho}_{0,\infty} \) quantify the tolerance in the absence of illness to stability independent of the delays of the linearised epidemic models about the equilibrium steady-state being compatible with ensuring the stability property independent of the delay sizes provided that those amounts are under unity. Let us consider \( \bar{R}_0 = \min(\rho_{00}, \rho_{0,\infty}) \) while noting that \( R_{m0} \leq R_0(0, h_1, h_2, \ldots, h_r) \leq \bar{R}_0 \leq R_{M0} \); \( \forall h_i \in R_{00}, \forall i \in \mathcal{F} \), \( R_{00} \subseteq [R_{m0}, R_{M0}] \), \( R_{0,\infty} \in [R_{m0}, R_{M0}] \) (24)

Thus, the stability in the asymptotic sense independent of the sizes of the incommensurate delays of the linearised epidemic model about the steady-state equilibrium in the absence of illness holds if \( R_{M0} \leq 1 \) which is ensured if \( \bar{R}_0 \leq 1 \). The subsequent situations can be discussed:

1) For a given set of incommensurate delays \( h_i \); \( \forall i \in \mathcal{F} \), it turns out that \( R_0(0, h_1, h_2, \ldots, h_r) \leq 1 < \bar{R}_0 \leq R_{M0} \). So, it is concluded that the disease-free equilibrium steady-state presents stability in the local asymptotic sense while the endemic steady-state behavior is not attainable for this amount of the basic reproductive number \( R_0(\cdot) \). Since \( R_{M0} \geq 1 \), one might conclude that there exist some potential combinations of delays, all of them with the same associated quantified levels of delayed dynamics, for which the disease results to be endemic, that is, it is persistent through time. However, it also holds that there exist some concrete after-effects for which the disease is able to asymptotically extinguish. On the other hand, and since \( R_{M0} > 1 \), it turns out that there exist alternative sets of incommensurate after-effect amounts \( \bar{h}_i \); \( \forall i \in \mathcal{F} \) for the same previously mentioned matrices of dynamics such that the disease-free equilibrium becomes unstable while the endemic one is both attainable and stable.

2) For a set of delays \( h_i \); \( \forall i \in \mathcal{F} \), it holds that \( R_0(0, h_1, h_2, \ldots, h_r) \leq \bar{R}_0 < 1 < R_{M0} \). We might get the interesting practical concluding remark which establishes that the disease-free steady-state equilibrium becomes stable in the local asymptotic sense and that the endemic one has some negative component so that is not-attainable. However, the basic reproductive number range on values for which the above concern holds is larger than the reproductive number lower-bound given by \( R_{m0} \).

Furthermore, there exist other potentially distinct sets of point delays \( \bar{h}_i \); \( \forall i \in \mathcal{F} \), being associated with the same quantified levels of delayed dynamics, for which that the disease-free steady-state becomes unstable while the endemic equilibrium point becomes jointly attainable and stable.

4. Example

One considers now a delay-free model in a complex habitat of three mutually influencing nodes which interchange mutually travelling subpopulations each with susceptible, infectious and recovered subpopulations under null or constant vaccination efforts through time. Such a model is as follows:

\[
S_i(t) = A_i - \beta_i S_i(t) I_i(t) - d_i^S S_i(t) + \sum_{j(\omega_i) = 1} \rho_{ij} S_j(t) - a_i S_i(t) - V_i(t)
\]
\[ I_i(t) = \beta_i S_i(t) I_i(t) - \left( d_i + \gamma_i \right) I_i(t) + \sum_{j=1}^{n} \left( b_{ij} I_j(t) - c_{ij} R_j(t) \right) \]
\[ R_i(t) = \gamma_i I_i(t) - d_i R_i(t) + \sum_{j=1}^{n} \left( c_{ij} R_j(t) - c_{ij} R_j(t) \right) + V_i(t) \]

The three nodes can describe, for instance, three neighboring villages which interchange population and whose respective Health Centers can eventually vaccinate travelers from the other villages. The model parameterization is:

\[
\begin{align*}
\beta &= \begin{bmatrix} 3.24 & 3.08 & 3.16 \end{bmatrix} \text{years}^{-1} \\
A &= 30d, \quad \gamma = \begin{bmatrix} 1.78 & 1.82 & 1.75 \end{bmatrix}
\end{align*}
\]

The travelling matrices \( A = \{a_{ij}\}, \ B = \{b_{ij}\} \) and \( C = \{c_{ij}\} \) are:

\[
A = \begin{bmatrix} 1 & 1.2 & 0.3 \\ 1.1 & 0.6 & 1 \\ 1.2 & 1.4 & 0.9 \end{bmatrix}, \quad B = \begin{bmatrix} 0.4 & 1.12 & 0.4 \\ 1.22 & 0.7 & 0.85 \\ 1 & 1.14 & 0.7 \end{bmatrix}, \quad C = \begin{bmatrix} 0.8 & 0.78 & 0.56 \\ 1.16 & 0.95 \\ 1.2 & 0.94 & 0.8 \end{bmatrix}
\]

The dynamics of the susceptible and infectious subpopulation in the absence of vaccination are depicted in Figures 1-2:

**Figure 1.** Susceptible time-evolution in the vaccination-free situation.

**Figure 2.** Infectious time-evolution in the vaccination-free situation.

We incorporate now a feedback vaccination effort \( V_0 = 0.9A \), \( K = A \) so that evolution of the susceptible and infectious subpopulations along time with this control action are displayed in Figures 3-4. Note that the infectivity decreases at a faster rate regarding the vaccination-free situation as well as the limit susceptible subpopulations as time tends to infinity.
Figure 3. Susceptible time-evolution with vaccination.

Figure 4. Infectious time-evolution with vaccination.

5. Concluding Remarks
This study has given a formal and unified characterization of classical epidemic models of compartments in the absence of presence of punctual incommensurate delays in a general context, not just independently for each particular stated model by decomposing the state into an infectious sub-state (or infective compartment) and a non-infective sub-state (or non-infective compartment). Thus, the linearised infective part of the model is formally discussed through a positivity and stability viewpoint from linear algebraic tools. Some relevant properties of the carrying and evolution matrices are described in such a general context. A numerical example concerned with three interacting nodes of the epidemics has been also discussed.

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