Epidemic spreading by indirect transmission in a compartmental farm

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Abstract

In this paper, we present a discrete dynamic system which describes an epidemic spreading within a single farm, where animals are separated into batches. In this model, we consider an indirect transmission of the disease coming from the bacteria remaining in the reservoir and taking into account the transfer of bacteria between adjacent compartments. In our model, tridiagonal matrices of non-negative blocks are involved. The development of the matrix spectral properties allows us to improve our understanding of the epidemic spreading within a farm with the above mentioned characteristics. Based on the results obtained, we have determined some bounds to obtain the maximum number of batches and the maximum population in each batch to ensure that the disease dies out.

Keywords: Epidemic process, discrete-time system, block tridiagonal matrix, non-negative matrix, stability.

1. Introduction

Block tridiagonal matrices appear frequently in models of biological processes when different compartments are connected. These compartments are not independent, they have interconnections among them which depend on the type of problem studied. For example, in population dynamics, it is common to organize individuals by age range classes or cubicles with transfers between the compartments when they reach the age corresponding to the next compartment, [1, 2, 3, 4]. Moreover, compartmental models are also used when modeling virus transmission between computers connected

to each other [5] and in a wide range of processes involving networks. There is a vast literature on compartmental models on networks, see [6] and the references given there.

Usually, when performing a linear approach of a model with interconnected compartments the matrices which appear are block-structured matrices. If the connections are between the adjacent compartments, the structured matrix is a block tridiagonal matrix, see for example [7, 8].

On the other hand, when it comes to biological processes the variables involved in the model are non-negative because the state variable represents individuals, bacteria, viruses, etc. In this case we have a positive system.

Now, we recall, some results related with the Non-Negative Matrix Theory. A matrix A of size n is defined as non-negative, $A \geq O$, if all entries of A are non-negative and the fundamental results on them are collected in [9]. In particular, the spectral radius of a non-negative matrix A given by $\rho(A) = \max\{|\lambda|,\ |\lambda I_n - A| = 0\}$, where I_n denotes the identity matrix of size n, is a non-negative eigenvalue of A, and if $O \leq A \leq B$ then $\rho(A) \leq \rho(B)$. Moreover, if we consider $A,\ B \geq 0$, with $\rho(A) < 1$, then one of the following holds, see Theorem 3.3. of [10]:

$$\begin{aligned} &\rho(A+B) = \rho(B(I_n - A)^{-1}) = 1, \\ &\text{or } 1 < \rho(A+B) \leq \rho(B(I_n - A)^{-1}), \\ &\text{or } 0 \leq \rho(B(I_n - A)^{-1}) \leq \rho(A+B) < 1. \end{aligned} \tag{1}$$

Furthermore, if a matrix A is stable, that is $\rho(A) < 1$, then the discrete time system $x(t+1) = Ax(t)$ is asymptotically stable. Hence, the trajectory of the solution of the system tends to zero.

Several authors have studied tridiagonal or band matrices obtaining results on eigenvalues and eigenvectors, see for instance [11] and [12] for a discrete model with a tridiagonal transition matrix. In block tridiagonal case, some results on its application to solve systems with special block matrices are given in [13] and some results on non-singular block triangular matrices in [14, 15].

The paper is structured as follows. In Section 2, we give an epidemiological model whose linear approximation involves a non-negative block tridiagonal matrix. In Section 3, we discuss the propagation of the infectious disease and the analysis of the spectrum of a non-negative block triangular matrix due to relevance in this epidemiological model. In particular, we study spectral properties of these matrices. We give some bounds on the number of

compartments in the model and on the size of the population in order to eradicate the disease.

Lastly, in the Appendix, we shown some properties of non-negative block tridiagonal matrices which allow us to establish the results on the stability of the epidemiological model considered in this work.

2. Epidemiological dynamic in a compartmental farm

Several mathematical models are used, both in continuous and discrete time, to analyze the evolution of an infectious disease, see [16, 17]. When modeling livestock farming processes, it is interesting to know how animals are organized on the farm. For example, if they are in independent pens or semi-isolated in poultry houses or cages. This is particularly important in poultry sector where the environmental and epidemiological implications are different if the chickens are raised by several small households or in a single industrial unit, [18, 19, 20]. It is clear that in many livestock farming processes the transmission of a disease can not only be by directly but also indirectly transmitted. Thus, an infectious disease, as example salmonella or avian influenza, can spread by indirect transmission, see [21, 22, 23, 24] and [25] for a PDE model.

We are interested in studying epidemic models that include the indirect transmission of the disease due to the underlying contamination in the space where we have the animals. For that, we take into account that the animals are raised in several semi-isolated poultry houses which is frequent in small farms or livestock farming. In this case, the animals or poultry are organized in reservoirs or households, in order to improve the optimal environmental conditions. But, as total isolation does not occur, the sediments contaminated with feces from the individuals may flow through the water being a source of infection for animals. When an infected animal is introduced into the farm, it produces bacteria which dissipates through the air, or through water. For example, individuals can be separated into boxes but share the air space or water troughs. That is, the contaminant can be found in the food or beverage distribution system supplied to animals. So, an indirect transmission of the disease occurs. Individuals are not only in contact with the bacteria produced by the individuals in their compartment, but also with part of the bacteria produced by the infected individuals in the adjacent cubicles.

We consider the individuals organized in m compartments, and we denote by S_i the susceptible individuals, by I_i the infected individuals and by B_i bacteria amount at the ith-compartment, for $i = 1, \ldots, m$. At any time and in each compartment, we want the population size (i.e. total number of individuals except the bacteria) to remain constant equal to P. We are working in a livestock farm where resources and infrastructure determine the size of the population in order to optimize the results, that is, the benefits of the farm. As we have already mentioned, this livestock farm has cubicles with a capacity for P individuals. Ideally, there should be the same number of individuals in all cubicles, which facilitates and homogenizes the distribution of food and water, and allows to establish the same climatic conditions in all compartments. The individuals can become infected with residuals found in those compartments and with bacteria coming from adjacent compartments. The bacteria can be transmitted between compartments through water or another element keeping the bacteria alive. To replace dead individuals, we introduce an amount of new susceptible individuals equal to $\mu_i(t)P$, $i = 1, \ldots, m$.

The parameters involved in the model are: the survival probabilities of individuals, susceptible and infected; the survival probability, in the environment, of the bacteria; the coefficient of infection transmission of the disease; the amount of bacteria production by an infected individual; and finally, the transition probability of bacteria that escapes forward and backward from a compartment, passing into adjacent compartments since the boxes are not isolated. Note that, for the model to have biological meaning, all parameters are non-negative and some relationships between them have to be satisfied. A description of the parameters of the model is given in following Table 1.

p, q, s	*Survival probabilities of susceptible individuals, infected individuals and bacteria, respectively.*
α	*Infection transmission coefficient (1/bacteria).*
β	*The amount of bacteria produced by each infected individual (bacteria/ind).*
γ	*Transition probability from adjacent compartments, with* $2\gamma < s < 1$.

Table 1: Parameters in a compartment structured SIB model.

The mathematical representation of this SIB epidemiological model is given by the nonlinear discrete-time system:

$$\begin{aligned} S_i(t+1) &= -\alpha\left((1-2\gamma)B_i(t)+\gamma(B_{i-1}(t)+B_{i+1}(t))\right)S_i(t)+pS_i(t)+\mu_i(t)P \\ I_i(t+1) &= \alpha\left((1-2\gamma)B_i(t)+\gamma(B_{i-1}(t)+B_{i+1}(t))\right)S_i(t)+qI_i(t) \\ B_i(t+1) &= \gamma B_{i-1}(t)-2\gamma B_i(t)+\gamma B_{i+1}(t)+\beta I_i(t)+sB_i(t), \end{aligned} \tag{2}$$

with $i = 1, \ldots, m$, and $B_0(t) = B_{m+1}(t) = 0$.

In general, this system is $z(t+1) = f(z(t), \mu(t))$, where $z(t)$ is the state variable recollecting the variables corresponding to susceptible, infected population and bacteria, $S_i(t)$, $I_i(t)$, $B_i(t)$, and $\mu(t)$ is the vector whose entries are the functions $\mu_i(t)$. If we consider the equilibrium points of this system, we are looking for $(z^\star, \mu^\star = (\mu_i^\star))$ such that $z^\star = f(z^\star, \mu^\star)$. That said, we cannot forget that we are working with a model subject to a particular condition: the size of the population is constant P in each compartment. Thus, for all time t, $S_i(t+1) + I_i(t+1) = S_i(t) + I_i(t) = P$ lead us to

$$\mu_i(t)P = P - pS_i(t) - qI_i(t), \quad i = 1, \ldots, m. \tag{3}$$

Note that by replacing the relation (3) in the first equation of the system (2), we obtain a model where p, the survival probability of the susceptible individuals, does not appear explicitly. This model is

$$\begin{aligned} S_i(t+1) &= -\alpha\left((1-2\gamma)B_i(t)+\gamma(B_{i-1}(t)+B_{i+1}(t))\right)S_i(t)+P-qI_i(t) \\ I_i(t+1) &= \alpha\left((1-2\gamma)B_i(t)+\gamma(B_{i-1}(t)+B_{i+1}(t))\right)S_i(t)+qI_i(t) \\ B_i(t+1) &= \gamma B_{i-1}(t)-2\gamma B_i(t)+\gamma B_{i+1}(t)+\beta I_i(t)+sB_i(t), \end{aligned} \tag{4}$$

The system is $z(t+1) = \bar{f}(z(t))$ and the equilibrium points $z^\star = \bar{f}(z^\star)$.The disease-free equilibrium is given by $S_i^\star = P,\ I_i^\star = 0,\ B_i^\star = 0,\ i = 1, \ldots, m$ and we can observe that the relation given in (3) leads us to $1 = p + \mu^\star$.

Now, denoting $\bar{z}(t) = (\bar{z}_1(t)\ \bar{z}_2(t))^T$ where $\bar{z}_1(t) = (S_1(t) \cdots S_m(t))^T$, and $\bar{z}_2(t) = (I_1(t)\ B_1(t)\ \cdots I_m(t)\ B_m(t))^T$, we reorder the model (4) obtaining

$$\begin{pmatrix} \bar{z}_1(t+1) \\ \bar{z}_2(t+1) \end{pmatrix} = \begin{pmatrix} g_1(\bar{z}(t)) \\ g_2(\bar{z}(t)) \end{pmatrix}, \tag{5}$$

and we consider its linear approach around the disease-free equilibrium point $\bar{z}^\star = \begin{pmatrix} \tilde{P} \\ O \end{pmatrix}$ with $\tilde{P}$ a column vector of size m whose entries are equal to P.

Taking $B_j(t)S_i(t) \approx B_j(t)P$, $j = i-1,\ i,\ i+1$, $i = 1,\ \ldots,\ m$, we have

$$\begin{pmatrix} z_1^l(t+1) \\ z_2^l(t+1) \end{pmatrix} = \begin{pmatrix} O & * \\ O & E_{[m]} \end{pmatrix} \begin{pmatrix} z_1^l(t) \\ z_2^l(t) \end{pmatrix} \tag{6}$$

where $z_1^l(t) = \bar{z}_1(t) - \tilde{P}$, and $z_2^l(t) = \bar{z}_2(t)$, and $E_{[m]}$ a block matrix given by

$$E_{[m]} = \left(\begin{array}{cc|cc|c|c|c} q & g & 0 & \alpha\gamma P & & & \\ \beta & s-2\gamma & 0 & \gamma & & & \\ \hline 0 & \alpha\gamma P & q & g & 0 & \alpha\gamma P & \\ 0 & \gamma & \beta & s-2\gamma & 0 & \gamma & \\ \hline \multicolumn{2}{c|}{\vdots} & \multicolumn{2}{c|}{\vdots} & \multicolumn{2}{c|}{\ddots} & \ddots & \multicolumn{2}{c}{\vdots} \\ \hline \multicolumn{2}{c|}{O} & \multicolumn{2}{c|}{O} & \multicolumn{2}{c|}{O} & \ddots & 0 & \alpha\gamma P \\ & & & & & & & 0 & \gamma \\ \hline \multicolumn{2}{c|}{O} & \multicolumn{2}{c|}{O} & \multicolumn{2}{c|}{O} & \cdots & q & g \\ & & & & & & & \beta & s-2\gamma \end{array}\right), \tag{7}$$

where $g = \alpha(1-2\gamma)P$, $i = 1, \ldots, m$, $m \geq 2$, and all parameters are given in Table 1. It is clear that the analysis of the stability of the system (6) is closely related with the stability of the matrix $E_{[m]}$.

So, considering the variables of infected individuals and bacteria, we have the linear subsystem

$$z_2^l(t+1) = E_{[m]} z_2^l(t). \tag{8}$$

It is well known that we can analyze the evolution of the infectious disease from the subsystem which relates, in the linear approximation, the infected individuals and the bacteria, in our case, the system given in (8). Remember that it is usual to decompose the matrix of the system in two matrices, $E_{[m]} = T + F$, where T corresponds to the transition term and F corresponds to the infection term. From these matrices, the basic reproduction number is defined by $R_0 = \rho(F(I-T)^{-1})$ and it is a measure or indicator to know whether the disease will disappear, for instance, see [10, 25]. If $R_0 < 1$ the disease tends to disappear around the disease-free equilibrium point and otherwise it remains. However, the decomposition of the matrix of the system is not unique, see for instance the discussion shown in [26].

Throughout the work, an $m \times l$ block matrix is denoted by $A_{[m,l]}$ and $m \times m$ block matrix by $A_{[m]}$. Some matrices with this structure are analyzed in the Appendix. In the next Section, we use the result given in this Appendix on spectral properties to analyze the stability of the system (8).

3. Stability in the epidemiological model

Note that if the subsystem (8) is asymptotically stable, the state variables $I_i(t)$ and $B_i(t)$ will tend to zero and the disease will be controlled, tending to disappear. Moreover, the linear system given in (6) it is also asymptotically stable. It is known that a system is asymptotically stable if the state matrix is stable, that is, its spectral radius is less than 1. Note that matrix $E_{[m]}$ is a non-negative matrix and it has a block tridiagonal structure as in (A.1). Thus, we can apply the results of Appendix. Note that $E_{[m]}$ has an $m \times m$ block tridiagonal structure and from notation introduced in (A.1). From now on, $E_{[m]} = E_{[m]}(X, Y, Y)$ with

$$X = \begin{pmatrix} q & g \\ \beta & s - 2\gamma \end{pmatrix}, \; Y = \begin{pmatrix} 0 & \alpha\gamma P \\ 0 & \gamma \end{pmatrix}. \tag{9}$$

First, we focus our attention on the case where there is no loss of bacteria and therefore, it can not spread between adjacent compartments. In this case, $\gamma = 0$ and $E_{[m]} = E_{[m]}(X, O, O)$ with $g = \alpha P$. Then, the system will be stable if and only if

$$\rho(X) = \rho\left(\begin{pmatrix} q & \alpha P \\ \beta & s \end{pmatrix}\right) = \frac{q + s + \sqrt{(q-s)^2 + 4\alpha\beta P}}{2} < 1.$$

Solving for P, see [27], we obtain that this condition is equivalent to

$$P < \frac{(1-q)(1-s)}{\beta\alpha}. \tag{10}$$

However, we are interested in the case of transferring contaminant between adjacent batches. When the loss of bacteria in each compartment (given by the parameter γ) is coming to the adjacent compartments producing new infected individuals, the structure of matrix $E_{[m]}$ allows us to ensure that the condition given in (10) is not a stability condition.

In order to simplify the calculations and to make it easier to see the process, we consider a farm with two reservoirs, $m = 2$. In each compartment, if we do not consider infected individuals from bacteria of other compartment, the matrix of the system is $\begin{pmatrix} X & O \\ O & X \end{pmatrix}$, then, we have the stability of the model from the stability of matrix X defined in (9). Solving for P, we have

that the stability condition

$$\rho(X) = \frac{q + s - 2\gamma + \sqrt{(q - s + 2\gamma)^2 + 4\alpha(1 - 2\gamma)\beta P}}{2} < 1$$

it is equivalent to the size of the population satisfying

$$P < \frac{(1 - q)(1 - (s - 2\gamma))}{\beta\alpha(1 - 2\gamma)}. \tag{11}$$

In general, we consider that susceptible individuals can be infected by contact with bacteria spreading between adjacent batches. The system (8) with $m = 2$ is asymptotically stable if $\rho(E_{[2]}) < 1$, where $E_{[2]} = \begin{pmatrix} X & Y \\ Y & X \end{pmatrix}$, with X and Y given in (9). We define $V_{[2]}(M, M)$ from $E_{[2]}$ as in (A.2). Then, using Theorem 3 given in Appendix, we have that $\rho(E_{[2]}) < 1$ if and only if $\rho(V_{[2]}(M, M)) < 1$, with

$$\rho(V_{[2]}(M, M)) = \rho(Y(I_2 - X)^{-1}) = \frac{\gamma(1 + \beta\alpha P - q)}{(1 - q)(1 - (s - 2\gamma)) - \beta\alpha P(1 - 2\gamma)} < 1.$$

Thus, the size of the population has to satisfy

$$P < \frac{(1 - q)(1 - (s - \gamma))}{\beta\alpha(1 - \gamma)}. \tag{12}$$

It is clear that condition (12) is stronger than condition (11).

In the following Theorem, we assume a stable model in the case of independent compartments, that is satisfying (11), and we give two results when there is transfer of bacteria between the compartments: an upper bound for the population size when the number of compartments is fixed, and reciprocally, a bound for the number of compartments if the population P is given.

Theorem 1. *Consider the epidemic spreading given in model (4) with m compartments, $m \geq 2$, and we assume that the size of population P in each one satisfies (11). Then,*

(i) The state variable of the system tends to the disease free equilibrium if and only if

$$P < \frac{(1 - q)(1 - (s - k_m))}{\beta\alpha(1 - k_m)} \tag{13}$$

with $k_m = 2\gamma(1 - \cos(\frac{\pi}{m+1}))$.

(ii) If we consider a size P fixed, the state variable of the system tends to the disease free equilibrium if and only if the number of the compartments m is less than

$$m_0 = \frac{\pi}{\arccos\left(1 - \frac{\beta\alpha P - (1-q)(1-s)}{2\gamma(1+\beta\alpha P - q)}\right)} - 1 \tag{14}$$

Proof. Under Theorem assumptions, matrix $E_{[m]}$ is an $m \times m$ block tridiagonal matrix as in (A.1) with $X_i = X$, $Y_i = Z_i = Y$, for all i, being X and Y given in (9) and $\rho(X) < 1$.
(i) From Theorem 4, $E_{[m]}$ is a stable matrix if and only if $\rho\left(Y(I_2 - X)^{-1}\right) < \frac{1}{t_m}$. That is, $\rho\left(t_m Y(I_2 - X)^{-1}\right) < 1$. From (1) we can ensure that it is equivalent to $\rho\left(X + t_m Y\right) < 1$. Calculating the eigenvalues of $X + t_m Y$, we obtain the stability condition

$$\rho\left(X + t_m Y\right) = \tfrac{1}{2}\left(q + s - k_m + \sqrt{(q - s + k_m)^2 + 4\beta\alpha(1 - k_m)P}\right) < 1 \tag{15}$$

where $k_m = 2\gamma(1 - \cos(\frac{\pi}{m+1}))$. Hence, solving this inequality for the population size P, we obtain the upper bound given in (13).
(ii) Using, Corollary 1 and (15), it is straightforward that expression (14) gives the maximum number m_0 of compartments maintaining asymptotically stable the process. □

In Theorem 1 we have given conditions to ensure local stability of the disease free equilibrium of the system (4). Now, in the next result, we discuss if the disease free equilibrium is globally stable.

Theorem 2. *Consider the epidemic spreading given in model (4) with m compartments, $m \geq 2$, and we assume that the size of population P in each one satisfies (11). Then, the disease free equilibrium of model (4) is globally asymptotically stable if the population P satisfies (13).*

Proof. Under Theorem assumptions, matrix $E_{[m]}$ is stable which implies that matrix of linear model (6) is also stable and the disease free equilibrium point of (4) is locally asymptotically stable. From the two last equations of (4) and the fact $S_i(t) \leq P$ we have

$$I_i(t+1) \leq \alpha\left((1 - 2\gamma)B_i(t) + \gamma(B_{i-1}(t) + B_{i+1}(t))\right)P + qI_i(t)$$

$$B_i(t+1) = \gamma B_{i-1}(t) - 2\gamma B_i(t) + \gamma B_{i+1}(t) + \beta I_i(t) + sB_i(t),$$

$i = 1, \ldots, m$. Then, using the representation given in (5), we obtain the inequality

$$\bar{z}_2(t+1) \leq E_{[m]}\bar{z}_2(t), \ t \geq 0.$$

For any initial condition $\bar{z}_2(0)$ and by recurrence, we obtain

$$0 \leq \bar{z}_2(t) \leq E^t_{[m]}\bar{z}_2(0), \ t \geq 0.$$

Then, from the stability matrix $E_{[m]}$ we have $\rho(E_{[m]}) < 1$, this implies that for any initial condition $\bar{z}_2(0)$ we have $\lim_{t\to\infty} E^t_{[m]}\bar{z}_2(0) = 0$. Since $0 \leq \bar{z}_2(t) \leq E^t_{[m]}\bar{z}_2(0)$ we have $\lim_{t\to\infty} \bar{z}_2(t) = 0$. Hence, $\lim_{t\to\infty} I_i(t) = \lim_{t\to\infty} B_i(t) = 0, \ i = 1, \ldots, m$. Moreover, as $S_i(t) + I_i(t) = P$ then $\lim_{t\to\infty} S_i(t) = P, \ i = 1, \ldots, m$. Thus, $\lim_{t\to\infty} \bar{z}(t) = \bar{z}^\star$. This implies that the disease free equilibrium point of (4) is globally asymptotically stable. □

In order to illustrate the usefulness of the results obtained, we present the following academic example.

Example 1. We consider a farm where the animals are distributed in cubicles. These cubicles are not totally isolated. The animals of different boxes do not come into contact with each other, but they share the airspace and also share the drinking fountain and feeding trough. We consider that there is an outbreak of an infectious disease, which is transmitted by indirect contact. That is, susceptible individuals are infected by contact with the bacteria coming from infected animals and staying alive in the environment. The following parameters are considered: $q = 0.6$, $\alpha = 10^{-4}$ Bacteria^{-1}, $\beta = 10^2$ Bacteria.Indiv^{-1} colony-forming unit (c.f.u.) and a loss of bacteria in each compartment with transition probability $\gamma = 0.07$; and we consider two scenarios. In the first, the bacterium has a survival probability in the environment $s = 0.4$, and in the second case, the bacterium is more resistant and has a survival probability $s = 0.8$.

If the cubicles were totally isolated and with a loss of bacteria equal to 2γ, in each scenario, the bound given in (11) provides that a population less than or equal to 34 individuals and 15 individuals, respectively, assures us that matrix X is stable and the disease dies out.

Now, we consider the case where an amount of the contaminated solid waste is transferring to the adjacent compartments and we study the two scenarios. According to (13) and (14), Table A.2 shows the relationship between the maximum number of compartments and the maximum population

in each one to eradicate the disease. Moreover, for each option, the spectral radius of $M = Y(I_2 - X)^{-1}$, $E_{[1]} = X$ and $E_{[m]}$ with $m \geq 2$ are shown.

In order to illustrate in more detail the results obtained from the proposed test, we graphically present the evolution of the infectious process in the following cases. We consider a farm with $s = 0.4$. If we have 56 individuals in a single reservoir, the Figure A.1 shows that the disease remains, that is, the population of infected individuals grows. However, if we have these individuals distributed in two cubicles with 28 individuals in each of them, Figure A.2 shows that the disease tends to disappear. Finally, we check that if we add a third cubicle with 28 individuals, the process becomes unstable again, as shown in Figure A.3. From here, we conclude that if cubicles have a capacity for 28 individuals, we can only have two of them. According to Table A.2, the ideal number of individuals in each cubicle is 24, since in that case we can connect as many cubicles as we want.

As it is deduced in the example, if we intend to eradicate the disease, the virulence and the resistance of the bacteria are important to establish the size of the maximum population that we can have in each cubicle. Thus, in the second scenario where the survival probability of the bacterium is $s = 0.8$, the population of each cubicle must be reduced considerably so that the disease can be eradicated. Based on the obtained results it is possible to determine the population size which prevents that the disease dies out.

4. Conclusions

A mathematical model that represents the evolution of a disease through indirect transmission in a compartmental farm has been considered. The linear approximation of this model around the disease-free equilibrium point involves some special non-negative structured matrices. This special structure has motivated us to study some spectral properties of non-negative block tridiagonal matrices. In particular, we analyze the propagation of the infectious disease by using a relationship between the stability of the initial tridiagonal block matrix and the stability of a bidiagonal block matrix with a special structure. The spectral radii of the matrices that appear in the model are fundamental to determine if the disease is going to be eradicated. For that, we obtain an explicit expression of the spectral radius of the bidiagonal block matrix that allows us to give the bounds that determine the maximum number of compartments and the maximum population in each compartment. These bounds assure us that the disease is eradicated. Fi-

nally, an example has been used to clarify the results obtained. Specifically, the outbreak of two diseases with different probability of survival of the bacteria s has been compared and we have obtained the following conclusions. When s is low ($s = 0.4$) we can have any number of compartments with the condition that no more than 24 individuals are located in any of the compartments. However, if the bacteria are more resistant ($s = 0.8$) , the maximum number allowed per compartment decreases to 8 individuals. The method proposed in this work also indicates (see Table A.2) that a cubicle with more than 34 individuals (if $s = 0.4$) and with more than 15 (if $s = 0.8$), is not viable, as the disease remains. Other intermediate cases with several compartments and with the disease disappearing are shown in the Table A.2.

Acknowledgment The authors would like to thank the referees for their valuable comments which helped to improve the manuscript.

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Appendix A. Spectral properties of non-negative block tridiagonal matrices

We consider a non-negative $m \times m$ block tridiagonal matrix given by

$$T_{[m]}(X_i, Y_i, Z_i) = \begin{pmatrix} X_1 & Y_2 & O & \cdots & O & O \\ Z_1 & X_2 & Y_3 & \cdots & O & O \\ O & Z_2 & X_3 & \cdots & O & O \\ \vdots & \vdots & \vdots & \cdots & \vdots & \vdots \\ O & O & O & \cdots & X_{m-1} & Y_m \\ O & O & O & \cdots & Z_{m-1} & X_m \end{pmatrix}, \ m \geq 2, \qquad \text{(A.1)}$$

where $X_i,\ Y_i,\ Z_i \geq O$ are non-negative matrices of size $n \times n$, $i = 1, \ldots, m$. First, we have the following result.

Theorem 3. *Consider $T_{[m]}(X_i, Y_i, Z_i)$ defined as (A.1) with X_i a stable matrix, $i = 1, \ldots, m$. Then, $T_{[m]}(X_i, Y_i, Z_i)$ is a stable matrix if and only if the $m \times m$ block matrix*

$$V_{[m]}(M_i, N_i) = \begin{pmatrix} O & M_2 & O & \cdots & O & O \\ N_1 & O & M_3 & \cdots & O & O \\ O & N_2 & O & \cdots & O & O \\ \vdots & \vdots & \vdots & \cdots & \vdots & \vdots \\ O & O & O & \cdots & O & M_m \\ O & O & O & \cdots & N_{m-1} & O \end{pmatrix}, \qquad \text{(A.2)}$$

with $M_i = Y_i(I_n - X_i)^{-1}$, $i = 2, \ldots, m$ and $N_i = Z_i(I_n - X_i)^{-1}$, $i = 1, \ldots, m-1$, is stable.

Proof. The matrix $T_{[m]}(X_i, Y_i, Z_i)$ can be writen as $T_{[m]}(X_i, Y_i, Z_i) = G_{[m]} + H_{[m]}$ with $G_{[m]} = \operatorname{diag}(X_1 \ldots X_n) \geq O$ and $H_{[m]} \geq O$ is the rest of initial matrix. By a simple calculation, we prove that $H_{[m]}(I_{nm} - G_{[m]})^{-1}$ is equal to matrix $V_{[m]}(M_i, N_i)$ given in (A.2). Note that $G_{[m]}$ is a stable non-negative matrix, then, we can to apply the result given in (1) obtaining that $\rho(T_{[m]}(X_i, Y_i, Z_i)) < 1$ if and only if $\rho(H_{[m]}(I_{nm} - G_{[m]})^{-1}) < 1$. □

Note that, the relationship obtained in the previous theorem may be useful when studying the stability of matrices $V_{[m]}(M_i, N_i)$. In particular, if a matrix $V_{[2k]}(M_i, N_i)$ is not stable it would imply that the matrix $V_{[2k+1]}(M_i, N_i)$ is neither. This is due to the relationship obtained in the theorem and to the fact that the matrices are non-negative.

Now, we study the particular case in which only two different matrices form the blocks of the matrix $T_{[m]}(X_i, Y_i, Z_i)$, given in (A.1), that is, we consider the blocks

$$X_i = X,\ Y = Y_i = Z_i,\ \text{for all } i, \tag{A.3}$$

and, then we have that matrix $T_{[m]}(X, Y, Y)$ deserves a particular analysis. Now, $M = N = Y(I_n - X)^{-1}$ and an approach to characterize the stability of the matrix $T_{[m]}(X, Y, Y)$ is given using the Kronecker product to define matrix $V_{[m]}(M, M)$, $m \geq 2$. This characterization is given in the following theorem.

Theorem 4. *Consider $T_{[m]}(X, Y, Y)$ with $m \geq 2$, defined as (A.1) satisfying condition (A.3) with X a stable matrix. Then, $T_{[m]}(X, Y, Y)$ is a stable matrix if and only if $\rho\left(Y(I_n - X)^{-1}\right) < \dfrac{1}{t_m}$, with $t_m = 2\cos\left(\frac{\pi}{m+1}\right)$.*

Proof. From Theorem 3, $T_{[m]}(X, Y, Y)$ is a stable matrix if and only if $V_{[m]}(M, M)$, given in (A.2), is also stable. In this case,

$$V_{[m]}(M, M) = H_{[m]}(I_{nm} - G_{[m]})^{-1} = \begin{pmatrix} O & M & O & \cdots & O & O \\ M & O & M & \cdots & O & O \\ O & M & O & \cdots & O & O \\ \vdots & \vdots & \vdots & \cdots & \vdots & \vdots \\ O & O & O & \cdots & O & M \\ O & O & O & \cdots & M & O \end{pmatrix},\ m \geq 2,$$

with $M = Y(I_n - X)^{-1}$. We rewrite the matrix $V_{[m]}(M, M)$ using the Kronecker product (see for instance [28]) to get more information about this spectral radius.

Moreover, the eigenvalues of the Kronecker product of two matrices, $C_m \otimes M$, are the pairwise products of the respective eigenvalues of C_m and M. Then, it is clear that the spectral radius of $V_{[m]}(M, M)$ is the product of the spectral radii of C_m and M, [28],

$$\rho(V_{[m]}(M, M)) = \rho(C_m)\rho(M).$$

As C_m is an $m \times m$ tridiagonal matrix, using the results given in [11], we obtain the spectrum of C_m, $\sigma(C_m) = \{2\cos\left(\dfrac{k\pi}{m+1}\right),\ k = 1, \ldots, m\}$. Hence, $\rho(C_m) = t_m$ with $t_m = 2\cos\left(\frac{\pi}{m+1}\right)$.

Hence, the condition $\rho(V_{[m]}) = \rho(H_{[m]}(I_{nm} - G_{[m]})^{-1}) < 1$ is $\rho(M) = \rho\left(Y(I_n - X)^{-1}\right) < \dfrac{1}{t_m}$. □

Note that if we construct the sequence of block tridiagonal matrices $\{T_{[m]}(X, Y, Y),\ m \geq 2\}$ satisfying (A.3), the above result allows us to establish a relationship between the stability property of these matrices. First, we denote by $m_0 = \max\{m \,/\, \rho\left(Y(I_n - X)^{-1}\right) < \dfrac{1}{t_m}, m \geq 2\}$. From the relationship between the spectral radii of the matrices, $\rho(V_{[m]}(M, M)) = \rho(C_m)\rho(M)$, and using that the sequence $\{\dfrac{1}{t_m},\ m \geq 2\}$ is decreasing, we obtain the result given in the next Corollary.

Corollary 1. *Consider X and Y square non-negative matrices with X stable, m_0 and $T_{[m]}(X, Y, Y)$ defined as (A.1) satisfying condition (A.3). Then, $T_{[m]}(X, Y, Y)$ is a stable matrix if $m \leq m_0$ and it is an unstable matrix otherwise.*

Bacteria probability s	P	m	$\rho(M)$	$\rho(E_{[m]})$
0.4	$P \geq 35$	–	–	*Disease remains*
	34	1	–	0.996
	28	2	0.8623	0.8623
	27	2	0.7351	0.7351
	26	3	0.6381	0.9024
	25	5	0.5617	0.9729
	24	any m	≤ 0.5	*Disease dies out*
0.8	$P \geq 16$	–	–	*Disease remains*
	15	1	–	0.99
	11	2	0.8623	0.8623
	10	3	0.7	0.9899
	9	4	0.5853	0.947
	8	any m	≤ 0.5	*Disease dies out*

Table A.2: Analysis of an infectious disease with $q = 0.6$, $\alpha = 10^{-4}$ Bacteria^{-1}, $\beta = 10^2$ Bacteria.Indiv^{-1} c.f.u. and $\gamma = 0.07$, for $s = 0.4$ and $s = 0.8$.

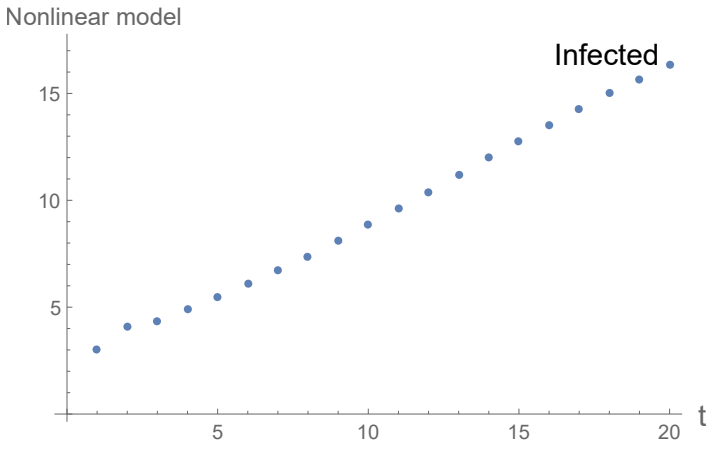

Figure A.1: *Infected population in a farm with* $P = 56$ *individuals in an enclosure from the data of the Example 1 with* $s = 0.4$ *and from the initial conditions: 51 susceptible individuals, 5 infected individuals and without bacteria.*

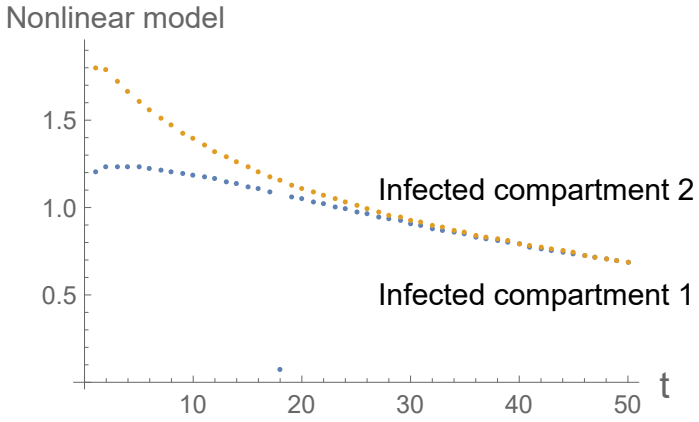

Figure A.2: *Infected population in a farm with* $P = 56$ *individuals in two cubicles with 28 individuals in each one from the data of the Example 1 with* $s = 0.4$ *and from the initial conditions: 26 susceptible individuals and 2 infected individuals in the compartment 1; 25 susceptible individuals and 3 infected individuals in the compartment 2 and without bacteria.*

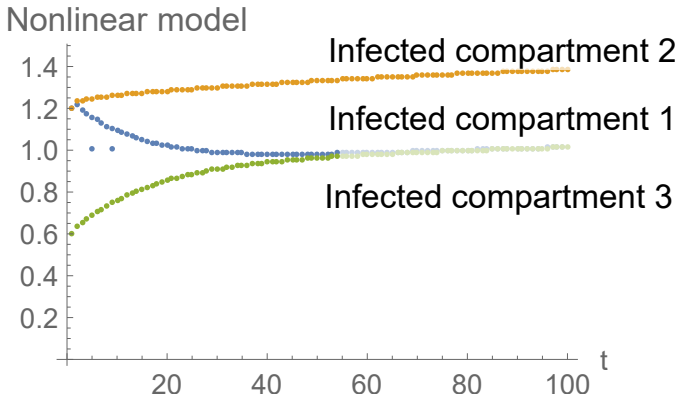

Figure A.3: *Infected population in a farm with* $P = 84$ *individuals in three cubicles with 28 individuals in each one from the data of the Example 1 with* $s = 0.4$ *and from the initial conditions: 26 susceptible individuals and 2 infected individuals in the compartment 1; 26 susceptible individuals and 2 infected individuals in the compartment 2; 27 susceptible individuals and 1 infected individuals in the compartment 3 and without bacteria.*