Metapopulation SIS epidemic model

Abderrahman Iggidr, Gauthier Sallet, Berge Tsanou

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Iggidr Abderrahman
Sallet Gauthier
Tsanou Berge

project-team MASAIE
INRIA Grand Est
France
and
MAT IRD Laboratory
Yaounde
Cameroon
sallet@loria.fr, iggidr@loria.fr, bergetsanou@yahoo.fr

RÉSUMÉ.

ABSTRACT. We consider a metapopulation model with n patches. The migration model is with residents and travelers. The epidemic model is of SIS type. We confirm the conjecture of Arino and van den Driessche [4]. We prove that if $\mathcal{R}_0 \leq 1$ then the disease free equilibrium is globally asymptotically stable. If $\mathcal{R}_0 > 1$ we prove that there exists a unique endemic equilibrium which is globally asymptotically stable on the nonnegative orthant except the disease free equilibrium.

MOTS-CLÉS :

KEYWORDS : Metapopulation models; SIS models; Nonlinear dynamical systems; global stability; monotone systems.

1. Introduction

A basic assumption of many epidemic models is that populations are composed of a homegeneous group of randomly mixing individuals. Most actual populations are divided into a number of subpopulations, within which there may be random mixing, but among which there is nonrandom mixing. In ecological studies important developments occur in the last three decades as a consequence of the recognition that spatial distribution is not homogeneous, and consists of subpopulations. These developments have given origin to the theory of metapopulations [9, 10]. The metapopulation concept is to subdivide the entire population into distinct patches, each of which has independent dynamics, with limited interaction between the subpopulations. An SIS epidemic model is proposed to describe the dynamics of the disease spread among patches due to population dispersal. This mobility model is inspired by Arino and van den Driessche [4, 3]. In [4] Arino and van den Driessche considered a mobility model with residents and travelers adapted from Sattenspiel and Dietz [14] by adding demography. However to work with a constant overall population, the authors suppose that birth and death occurs with the same rate. Actually these authors study a SIS dynamic on each patch. The population is divided into two classes : susceptible individuals and infectious individuals. Susceptible individuals become infective after adequate contact with infective individuals. Infective individuals return to susceptible class when recovered. Gonorrhea and other sexually transmitted diseases or bacterial infections exhibit this phenomenon. In [4] they give a rigorous derivation of the basic reproduction number, $\mathcal{R}_0$, which is the average number of new infectives produced by one infective introduced into a susceptible population [7, 8]. They also give bounds on $\mathcal{R}_0$, as well as some numerical simulations indicating that $\mathcal{R}_0 = 1$ acts as a sharp threshold between the disease dying out ($\mathcal{R}_0 < 1$) and endemic disease ($\mathcal{R}_0 > 1$).

We confirm the conjecture of Arino and van den Driessche. We prove that if $\mathcal{R}_0 \leq 1$ then the disease free equilibrium is globally asymptotically stable. If $\mathcal{R}_0 > 1$ we prove that there exists a unique endemic equilibrium which is globally asymptotically stable on the nonnegative orthant except the disease free equilibrium (i.e., the origin).

2. The migration model

Suppose that the total number of patches is n. In the following we call *residents* of a patch i the individuals who were born in and normally live in this patch, and *travelers* the individuals who, at the time they are considered, are not in the patch they reside in. We denote the number of residents of patch i who are present in patch j at time t by N_{ij}. Letting N_i^r be the resident population of patch i at time t, then

$$N_i^r = \sum_{j=1}^{n} N_{ij}.$$

Also, letting N_i^p the population of city i at time t, i.e., the number of individuals who are physically present in patch i, both residents and travelers, then

$$N_i^p = \sum_{j=1}^{n} N_{ji}.$$

Residents of patch i leave the city at a capita rate g_i per unit time. A fraction m_{ji} of these outgoing individuals go to patch j. Thus if $g_i > 0$, then $\sum_{j=1}^{n} m_{ji} = 1$, with the convention $m_{ii} = 0$, and the $g_i\, m_{ji}$ is the travel rate from patch i to patch j. Residents of patch i who are in patch j return to i with a capita rate of r_{ij}, with $r_{ii} = 0$. The death rate, equal to the birth rate is denoted by d.

With these assumptions and notations the model considered in [4] is

$$\dot{N}_{ii} = d\,(N_i^r - N_{ii}) + \sum_{j=1}^{n} r_{ij}\, N_{ij} - g_i\, N_{ii} \tag{1}$$

and for $j \neq i$

$$\dot{N}_{ij} = g_i\, m_{ji}\, N_{ii} - r_{ij}\, N_{ij} - d\, N_{ij} \tag{2}$$

As the model describes travels, it is natural to assume that if individuals travel between one city and another, then at least some of these travelers return home. We define the return matrix R by $R(i,j) = r_{ij}$ and the outgoing matrix M by $M(i,j) = g_j\, m_{ji}$. Then we assume that these two matrices have the same zero/nonzero pattern, since they represent respectively the return to i from j and the outgoing travel from j to i. We also assume that these matrices are irreducible. This means that the n patches cannot be separated into two groups such that there is no immigration from one group to another group. It is always possible to reduce the global study to the study of irreducible components, thus our hypothesis does not reduce the generality of our results.

It is straightforward to check that $\dot{N}_i^r = 0$. In other words the population of resident in each patch is constant. It follows that the total population is constant. However the number of individuals present in a patch i is in general a variable quantity. The following result is proven in [4]

Theorem 1 *The system given by (1) and (2), for the initial value $N_{ij} > 0$, has the global asymptotically stable equilibrium*

$$\bar{N}_{ii} = \frac{1}{1 + g_i\, C_i}\, N_i^r$$

$$\bar{N}_{ij} = g_i \frac{m_{ji}}{d + r_{ij}}\, \frac{1}{1 + g_i\, C_i}\, N_i^r$$

where $C_i = \sum_{k=1}^{n} \frac{m_{ki}}{d + r_{ik}}$

The state of the system is given by n^2 components N_{ij}, hence an element of the nonnegative orthant $[0, +\infty)^{n^2}$. We denote by $\mathcal{N}$ the matrix N_{ij} and by N the "columnization" of the transpose of this matrix, i.e. in Scilab notations $N = \mathcal{N}^T(:)$, i.e., $N = (N_{11}, N_{12}, \ldots, N_{1n}, N_{21}, N_{22}, \ldots, N_{2n}, \ldots\ldots, N_{nn})^T$.

The migration model can be written

$$\dot{N} = \mathcal{M}\, N, \tag{3}$$

where $\mathcal{M} = \mathrm{diag}(\mathcal{M}_{ii})$ is a block-diagonal matrix, with the first block $\mathcal{M}_{11}$ given by

$$\mathcal{M}_{11} = \begin{bmatrix} -g_1 & r_{12}+d & r_{13}+d & \dots & r_{1n}+d \\ g_1\, m_{21} & -r_{12}-d & 0 & \dots & 0 \\ g_1\, m_{31} & 0 & -r_{13}-d & \dots & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ g_1\, m_{n1} & 0 & \dots & 0 & -r_{1n}-d \end{bmatrix},$$

and the other blocks similarly defined.

3. The complete model

In the case of mild diseases it may be reasonable to assume that the movement rates are independent of disease status, thus infectious and susceptible individuals have the same migration rate. With this assumption the demographic evolution is also given by the system (3). To obtain the complete epidemic system it is sufficient to add for example the differential equations for the infectious I_{ij} since $N_{ij} = S_{ij} + I_{ij}$. Disease transmission is modeled using standard incidence, which, for human diseases, is considered more accurate than mass action. We denote by β_{ijk} is the proportion of adequate contacts in city j between a susceptible of cit i and an infective from city k that results in transmission of the disease, and $\kappa_j > 0$ is the average number of such contacts in city j per unit of time. [11, 6]. We denote by γ the recovery rate. Note thet γ is assumed to be the same for all cities. Then we have

$$\dot{I}_{ii} = \sum_{k=1}^{n} r_{ik}\, I_{ik} - g_i\, I_{ii} + \sum_{k=1}^{n} \kappa_i\, \beta_{iki}\, (N_{ii} - I_{ii})\, \frac{I_{ki}}{N_i^p} - (\gamma + d)\, I_{ii}, \tag{4}$$

and for $j \neq i$,

$$\dot{I}_{ij} = g_i\, m_{ji}\, I_{ii} - r_{ij}\, I_{ij} + \sum_{k=1}^{n} \kappa_j\, \beta_{ikj}\, (N_{ij} - I_{ij})\, \frac{I_{kj}}{N_j^p} - (\gamma + d)\, I_{ij}. \tag{5}$$

We will vectorialize these equations. Let us define $\mathbf{N}^p$ the vector of $\mathbb{R}^{n^2}$ given by

$$\mathbf{N}^p = (N_1^p, N_2^p, \cdots, N_n^p, N_1^p, N_2^p, \cdots, N_n^p, \cdots\cdots, N_n^p)^T.$$

We remark that $\mathbf{N}^p \gg 0$.
Using the same ordering that for the N_{ij} we define the vector I. We define a vector κ, of size the dimension of I. The vector κ is defined by $\kappa_{i,j} = \kappa_j$.

The system given by (4) and (5) can be written

$$\dot{I} = \mathcal{D}\, I - (\gamma + d)\, I + \text{diag}(\kappa)\, \text{diag}(\mathbf{N}^p)^{-1}\, \text{diag}(N - I)\, B\, I \tag{6}$$

The matrix $\mathcal{D}$ is simply the migration term. In other words, the matrix $\mathcal{D}$ is a diagonal block matrix, $\mathcal{D} = \text{diag}(D_{ii})$, where the block diagonal matrices D_{ii} are defined by

$$D_{ii}(i,k) = r_{ik} \quad D_{ii}(k,i) = g_i\, m_{ik} \quad D_{ii}(k,i) = -g_i \quad D_{ii}(k,k) = -r_{ik}$$

For example

$$D_{11} = \begin{bmatrix} -g_1 & r_{12} & r_{13} & \cdots & r_{1n} \\ g_1\, m_{21} & -r_{12} & 0 & \cdots & 0 \\ g_1\, m_{13} & 0 & -r_{13} & \cdots & 0 \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ g_1\, m_{n1} & 0 & \cdots & 0 & -r_{1n} \end{bmatrix}$$

The matrix B is defined by the following relations. If we denote by e_{ij} the canonical basis of $\mathbb{R}^{n^2}$, then the matrix B is such that

$$B\, e_{ij} = \sum_{k=1}^{n} \beta_{ikj}\, e_{kj}$$

Finally the SIS system is given by

$$\begin{cases} \dot{N} = & \mathcal{M}\, N \\ \\ \dot{I} = & \mathcal{D}\, I - (\gamma + d)\, I + \mathrm{diag}(\kappa)\, \mathrm{diag}(\mathbf{N}^p)^{-1}\, \mathrm{diag}(N - I)\, B\, I \end{cases} \tag{7}$$

4. Properties of the model

We denote by $\leq$ the pointwise ordering in $\mathbb{R}^n$, i.e., the ordering generated by the cone $\mathbb{R}^n_{=}$. We also define the classical notations $x < y$ for $x \leq y$ and $x \neq y$ and $x \ll y$ if for any index i, $x_i < y_i$.

4.1. Positively Invariant set

We define the following vector

$$\mathbf{N}^r = (N_1^r, N_1^r, \cdots, N_1^r, N_2^r, N_2^r, \cdots, N_2^r, \cdots\cdots, N_n^r)^T.$$

Proposition 1 *Let us define the set*

$$K = \{(N, I) | 0 \leq N \leq \mathbf{N}^r; 0 \leq I \leq \mathbf{N}^r\}.$$

Then K is a compact positively invariant set of system (7)

This is straightforward on the expressions (1), (2), (4) and (5)

4.2. Reduction of the system

The system (7) is a triangular system. The following theorem will permit us to reduce the stability analysis to a smaller system

Theorem 2 (Vidyasagar [18], Theorem 3.1 and 3.4) *:*
Consider the following $\mathcal{C}^1$ system

$$\begin{cases} \dot{x} = f(x) & x \in \mathbb{R}^n\, , y \in \mathbb{R}^m \\ \dot{y} = g(x, y) \end{cases} \tag{8}$$

with an equilibrium point (x^*, y^*) i.e., $f(x^*) = 0$ and $g(x^*, y^*) = 0$.

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 (8). Moreover, if all the trajectories of (8) are forward bounded, then (x^*, y^*) is GAS for (8).

We consider the system in the positively invariant compact set K and we know that the first system $\dot{N} = \mathcal{M}\, N$ is globally asymptotically stable at the equilibrium defined in theorem. We denote by $\bar{N}$ this equilibrium, and by $\bar{\mathbf{N}}^p$ the corresponding vector. From the preceding theorem it is sufficient to study the stability of the reduced system

$$\dot{I} = \mathcal{D}\, I - (\gamma + d)\, I + \mathrm{diag}(\kappa)\, \mathrm{diag}(\bar{\mathbf{N}}^p)^{-1}\, \mathrm{diag}(\bar{N} - I)\, B\, I. \tag{9}$$

4.3. Expression for $\mathcal{R}_0$

We use the now classical framework of [16, 7, 8].
Let us define, as in [16]

$$\mathcal{F} = \mathrm{diag}(\kappa)\, \mathrm{diag}(\bar{\mathbf{N}}^p)^{-1}\, \mathrm{diag}(\bar{N} - I)\, B\, I,$$

the function of appearance of new infection in infectious compartments and by
$\mathcal{V} = \mathcal{D}\, I - (\gamma + dI$ the transfer in compartments by all other means.
The Jacobian F of $\mathcal{F}$ at the origin, i.e., where there is no infective (in other words at the disease free equilibrium) is $F = \mathrm{diag}(\kappa)\, \mathrm{diag}(\bar{N}^p)\, B$, and the Jacobian V of $\mathcal{V}$ is $V = \mathcal{D} - (\gamma + d)\, I_{n^2}$, with I_{n^2} the identity matrix of $\mathbb{R}^{n^2}$.
The matrix $\mathcal{D}$ is a Metzler matrix [13](nonnegative off diagonal terms) with a zero column sum. This imply that 0 is simple eigenvalue of $\mathcal{M}$, the other eigenvalues having a negative real part. Hence V is a stable Metzler matrix with stability modulus $-(\gamma+d)$. This implies that V is nonsingular.

Proposition 2 *The basic reproduction ratio is given by*

$$\rho\left(-F\, V^{-1}\right) = \rho\left(-diag(\kappa)\, diag(\bar{N})\, B(\mathcal{D} - (\gamma + d)\, I_{n^2})^{-1}\right).$$

where $\rho(A)$ denotes the spectral radius of a matrix A.

This is simply the application of the results of [3].

5. Main result

Theorem 3 *We consider system (7) on K.*

– If $\mathcal{R}_0 \leq 1$ then the system is globally asymptotically stable at the origin.

– If $\mathcal{R}_0 > 1$ then there exists a unique endemic equilibrium $(\bar{N}, \bar{I})$ with $\bar{I} \gg 0$ which is globally asymptotically stable on $K \setminus \{0\}$.

Proof
It is sufficient to study the reduced system (9). The system (9) can be rewritten

$$\dot{I} = (F + V)\, I - \mathrm{diag}(\kappa)\, \mathrm{diag}(I)\, B\, I$$

Let $X(I) = (F + V)\, I - \mathrm{diag}(\kappa)\, \mathrm{diag}(I)\, B\, I$ the $\mathcal{C}^1$ vector field in K. The flow preserve K for $t \geq 0$. The derivative DX is

$$DX(I) = \mathcal{D} - (\gamma + d)\, I_{n^2} + \text{diag}(\kappa)\, \text{diag}(\bar{N} - I)\, B - \text{diag}(\kappa)\, \text{diag}(B\, I).$$

This is an irreducible $n^2 \times n^2$ Metzler matrix, hence the flow of X is strongly monotone in K. Since each row of B is nonnegative and nonzero the matrix-valued map DX is strictly antimonotone, i.e., of $I_1 < I_2$ then $DX(I_1) < DX(I_2)$. Applying theorem 6, page 55 of [12], we deduce that either all the trajectories in $\mathbb{R}^{n^2}$ tend to the origin, or else there is a unique equilibrium in the interior of K and all trajectories in $\mathbb{R}^{n^2}$ tend to this equilibrium.
The stability modulus $\alpha(M)$ of a matrix M is the largest real part of the elements of the spectrum Spec(M) of M.

$$\alpha(M) = \max_{\lambda \in \text{Spec}(M)} \text{Re}(\lambda).$$

The Jacobian $J(0)$ of system (9) at the origin is $J(0) = F + V$. Since $F \geq 0$ and V is a nonsingular Metzler matrix, $F + V$ is a regular splitting of $J(0)$. Hence we have, from [17], $\rho(-FV^{-1}) < 1$ is equivalent to $\alpha(F + V) < 0$. Hence the origin is asymptotically stable. With the preceding result we have proven that the origin s GAS if $\mathcal{R}_0 < 1$. If $\mathcal{R}_0 > 1$, this is equivalent to $\alpha(J(0)) > 0$. Hence the origin is unstable, there exists a unique attracting endemic equilibrium $\bar{I} \gg 0$. This endemic equilibrium $\bar{I}$ satisfies

$$[\mathcal{D} - (\gamma + d)]\, \bar{I} + \text{diag}(\kappa)\, \text{diag}(\bar{N} - \bar{I})\, B\, \bar{I} = 0.$$

Using this relation, the properties of B and the fact that $\bar{I} \gg 0$ we get

$$DX(\bar{I})\, \bar{I} = -\text{diag}(\kappa)\, \text{diag}(B\, \bar{I})\, \bar{I} < 0.$$

Using the fact that $DX(\bar{I})$ is a Metzler matrix, this relation implies that this matrix is stable [20](criterion I_{28} of theorem 6.2.3).
Hence the stability modulus satisfies $\alpha(DX(I)) < 0$. This proves the asymptotic stability of $\bar{I}$.
To finish the proof it remains to consider the case $\mathcal{R}_0 = 1$, which is equivalent to
$\alpha(F + V) = 0$. Since $F + V$ is an irreducible Metzler matrix, there exists a positive vector $\mathbf{v}$ such that $(F + V)^T\, \mathbf{v} = 0$. We consider on K the following Lyapunov function

$$V(I) = \langle I | \mathbf{v} \rangle.$$

The derivative along the trajectories are

$$\dot{V} = -\langle \text{diag}(\kappa)\, \text{diag}(I)\, B\, I | \mathbf{v} \rangle \leq 0$$

This proves the stability of the origin. By the theorem of Hirsch we are necessarily in the case where the origin is attractive. Which ends the proof of the theorem.

■

6. Conclusion

In [4] a epidemic metapopulation model is given. The stability analysis of this model was addressed. We completely answer to this question. There are not so numerous results in this direction for general epidemic system. Moreover The complete analysis of stability

for epidemic metapopulation models are still fewr [15, 11, 19]. We use the monotonicity property of the Arino-van den Driessche model to obtain the stability analysis of the system.

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