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Structure and Analysis of Compartmental Epidemiological Models

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ABSTRACT

We study compartmental epidemiological models of the form $\dot{x} = A(x)x$, $x \in \mathbb{R}^n$, *where* $A(x)$ *is the so called Metzler matrix. We prove that for such systems there exist an energy function* $V(x)$ *which can be used to establish the stability of the critical points of the system.*

Mathematical models describing the evolutionary biological systems constitute a rich theory with a wide field of applications. It provides a way to examine the potential effects of the proximate biological and behavioral determinants of epidemic outbreak dynamics.

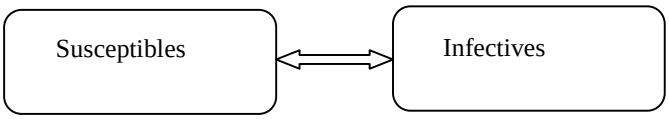
Epidemic outbreak is the occurrence in a community or region of cases of an illness clearly in excess of expectation. On the other hand the incidence of a disease is the number of new cases per unit time and plays an important role in the study of mathematical epidemiology. Thieme and Castillo-Chavez [1] have proposed that the general form of a population size dependent incidence should be written as $\beta C(N)\frac{S}{N}I$, where *S* and *I* are respectively the numbers of *susceptibles* and *infectives* at any given time *t*, β is the probability per unit time of transmitting the disease between two individuals taking part in a contact. $C(N)$, is the unknown probability for an individual to take part in a contact. $C(N)$ is usually called the contact rate, on the other hand $\beta C(N)$ represents the average number of contacts of an individual per unit time and is often referred to as the *adequate contact rate*. An adequate contact is a contact that is sufficient for transmission of the infection from and infective to a susceptible. In the popular literature the adequate contact rate is of two forms. One is linearly proportional to the total population size *N*, i.e. $C(N) = \beta N$, hence the corresponding incidence is bilinear and equals $\beta N\frac{S}{N}I = \beta SI$, the second form is a constant, say λ and the corresponding incidence is $\lambda\frac{S}{N}I$, called the standard form. When the total population size *N* is not too large, we expect the number of contacts made by an individual to increase as *N* increases. In this case the linear adequate contacts rate βN is suitable. However when the total population size is quite large, it is expected that the number of contacts made by an infective per unit time would be limited as *N* increases and as such the linear contacts rate βN is not suitable and the constant adequate contact rate λ may be more realistic.

Our objective is to show how mathematical modeling studies have contributed to our understanding of the dynamics and the disparities in the global spread of disease. We have standard convention labels for three major compartments; namely *S* (for susceptible), *I* (for infections) and *R* (for recovered). We therefore call this model the

SIR model. The SIR is dynamic in the sense that individuals are born susceptible, then may acquire the infections (move into the infections compartment) and finally recover (moved into the recovered compartment).

For the present study we consider the SIS model because it is easy to generalize it to an *n*-dimensional SIS group model.

1.1 THE SIS MODEL



We observe that certain infections do not confer long lasting immunity and as such do not have a recovered state [4]. This means that individuals in the population become susceptible again after infection. The mathematical model for the SIS model is written

$$\begin{cases} \dot{S} = -\beta SI + \gamma I \\ \dot{I} = \beta SI - \gamma I \\ I(0) = I_0 > 0,\ S(0) = S_0 > 0 \end{cases} \qquad 1.1$$

With $\dot{S} + \dot{I} = 0 \Rightarrow S(t) + I(t) = N$. Since the population is constant it suffices to know $I(t)$ which can be obtained from the first order ordinary differential equation;

$$\dot{I} = (\beta N - \gamma) I - \beta I^2 \qquad 1.2$$

The exact solution for the above is given by;

$$I(t) = \frac{1}{\frac{\beta}{\beta N - \gamma} + \left(\frac{1}{I_0} - \frac{\beta}{\beta N - \gamma}\right) e^{-(\beta N - \gamma)t}},\quad I_0 = I(0) \qquad 1.3$$

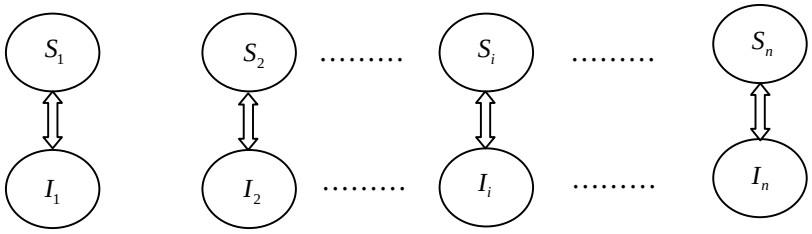
We observe that for this model;

(i) $\frac{\beta N}{\gamma} \le 1 \Rightarrow \lim_{t \to +\infty} I(t) = 0$ (ii) $\frac{\beta N}{\gamma} \ge 1 \Rightarrow \lim_{t \to +\infty} I(t) = \frac{\beta N - \gamma}{\beta}$ 1.4

2.0 Generalization of the SIS model

For many infectious diseases the transmission occurs in a heterogeneous population, in this case the epidemiological model must divide the population into subpopulations or groups, in which the members have similar characteristics. This division into groups can be based not only on mode of transmission, contact patterns, latent period, infectious period, genetic susceptibility or resistance, and amount of vaccination or chemotherapy, but also on social, cultural, economic, demographic, or geographic factors. This is the rationale for the introduction of multi-group models. In the epidemiological literature, the term “multi-group” usually refers to the division of a heterogeneous population into several homogeneous groups based on individual behaviour. The interest in multigroup endemic models originally stems from sexual transmitted diseases such as gonorrhea or HIV/AIDS.

We consider here a system consisting of *n* groups with constant population size and a disease which confer no immunity after recovery.



We model the contact by the mass action law. Let S_i and I_i be respectively the number of susceptible and infectives in the group *i*. Our model now reads;

$$\begin{cases} \dot{S}_i = -\sum_{j=1}^{n} \frac{\beta_{ij}}{N_i} S_i I_i + (\mu_i + \gamma_i) I_i \\ \dot{I}_i = \sum_{j=1}^{n} \frac{\beta_{ij}}{N_i} S_i I_i - (\mu_i + \gamma_i) I_i \\ N_i = S_i + I_i, \quad i = 1, 2, \ldots, n. \end{cases} \qquad 1.5$$

For the purpose of recasting the above systems in matrix form, we write;

$$\dot{S}_i = \mu_i N_i - \mu_i S_i - \sum_{j=1}^{n} \frac{\beta_{ij}}{N_i} S_i I_i + \gamma_i I_i$$

$$\dot{I}_i = \sum_{j=1}^{n} \frac{\beta_{ij}}{N_i} S_i I_i - (\mu_i + \gamma_i) I_i \qquad 1.6$$

and we let $x_i = \frac{I_i}{N_i}$, $\tilde{\beta}_{ij} = \beta_{ij} N_j$, $\alpha_i = \mu_i + \gamma_i$, giving the following systems of differential equations;

$$\dot{x}_i = (1 - x_i) \sum_{j=1}^{n} \tilde{\beta}_{ij} x_j - \alpha_i x_i \qquad i = 1, 2, \ldots, n. \qquad 1.7$$

If we define

$$\boldsymbol{B} = \left(\tilde{\beta}_{ij}\right)_{n \times n} = \begin{pmatrix} \tilde{\beta}_{11} & \tilde{\beta}_{12} & \cdots & \tilde{\beta}_{1n} \\ \tilde{\beta}_{21} & \tilde{\beta}_{22} & \cdots & \tilde{\beta}_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ \tilde{\beta}_{n1} & \tilde{\beta}_{n2} & \cdots & \tilde{\beta}_{nn} \end{pmatrix}, \qquad \boldsymbol{D} = -\operatorname{diag}(\alpha_i) = \begin{pmatrix} -\alpha_1 & 0 & \cdots & 0 \\ 0 & -\alpha_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & -\alpha_n \end{pmatrix},$$

the above equation can be recast in matrix form as;

$$\dot{\boldsymbol{x}} = \left[\boldsymbol{D} + \boldsymbol{B} - \operatorname{diag}(\boldsymbol{x})\boldsymbol{B}\right]\boldsymbol{x} \qquad 1.8$$

which can also be written;

$$\dot{\boldsymbol{x}} = \left[\boldsymbol{D} + \operatorname{diag}(\boldsymbol{1} - \boldsymbol{x})\boldsymbol{B}\right]\boldsymbol{x} \qquad 1.9$$

2.1 Definition

A matrix $\boldsymbol{A} = \left(a_{ij}\right)_{n \times n}$, $n \geq 2$ is called *irreducible* if for any proper subset $\Im$ of $\{1, \ldots, n\}$, there are $i \in \Im$, and $j \notin \Im$ such that $a_{ij} \neq 0$.

2.2 Definition

A Metzler matrix $\boldsymbol{A}=\left(a_{ij}\right)_{n\times n}$, $n\geq 2$ is a matrix such that $a_{ij}\geq 0,\forall i\neq j$ [3,5,9]. These matrices are also called quasi-positive matrices.

2.3 Remark

1. In the above model the matrix $\boldsymbol{B}$ describes the contact interaction between groups.
2. The irreducibility of the matrix $\boldsymbol{B}$ implies that no group is contact isolated in and out from the remaining groups.
3. In the system (1.9) the matrix $\boldsymbol{D}$ is a stable Metzler matrix and describes the transfer of individuals out of compartments.
4. The term $\boldsymbol{B}-\text{diag}\left(\boldsymbol{x}\right)\boldsymbol{B}$ represents the disease transmission, with $\boldsymbol{B}$ a nonnegative irreducible matrix.
5. Metzler matrices arise naturally in compartmental models and hence their preference in the present study.

2.4 Equilibrium

The equilibrium of the system is given by

$$\dot{\boldsymbol{x}}=\left[\boldsymbol{D}+\boldsymbol{B}-\text{diag}\left(\boldsymbol{x}\right)\boldsymbol{B}\right]\boldsymbol{x}=\boldsymbol{0}$$

$$\Rightarrow \boldsymbol{x}=0,\ \boldsymbol{D}+\boldsymbol{B}-\text{diag}\left(\boldsymbol{x}\right)\boldsymbol{B}=\boldsymbol{0}\quad\Rightarrow\quad \text{diag}\left(\boldsymbol{x}\right)=\boldsymbol{D}\boldsymbol{B}^{-1}+\boldsymbol{B}\boldsymbol{B}^{-1}=\boldsymbol{D}\boldsymbol{B}^{-1}+\boldsymbol{1} \qquad 1.10$$

Since $\boldsymbol{D}$ is diagonal then clearly the matrix $\boldsymbol{D}\boldsymbol{B}^{-1}+\boldsymbol{1}$ must be a diagonal matrix and hence the remaining equilibrium points can be picked out easily. We will also be interested in endemic equilibrium points which are essentially steady state solutions of (1.9) where the disease persists in the population (all state variables being positive).

2.5 The basic reproduction number

The basic reproduction number denoted $\Re_0$ is a key concept in epidemiology and is defined simply as the number of new cases of infection caused by a typical infected individual in a population of susceptible only. This terminology is quite common in most literature on the subject. [1,2,6]. For the purpose of giving a precise definition of $\Re_0$ we need to define the spectral radius $\rho\left(\boldsymbol{A}\right)$ of a matrix $\boldsymbol{A}$ given by;

$$\rho\left(\boldsymbol{A}\right)=\max\left\{\left|\lambda\right|:\lambda\in \text{Spec}\left(\boldsymbol{A}\right)\right\}$$

Where $\text{Spec}\left(\boldsymbol{A}\right)$ is the spectrum of $\boldsymbol{A}$.

Moreover the matrix $-\boldsymbol{D}^{-1}\boldsymbol{B}$ will be referred to as the next generation matrix according to [8]**.** We now define the basic reproduction number as $\Re_0=\rho\left(-\boldsymbol{D}^{-1}\boldsymbol{B}\right)$.

2.6 Theorem

Given $\Re_0>1$, *there exists a unique endemic equilibrium* $\bar{\boldsymbol{x}}$ *satisfying;*

$$\bar{\boldsymbol{x}}=-\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}+\text{diag}\left(\bar{\boldsymbol{x}}\right)\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}$$

Furthermore the search for an endemic equilibrium is equivalent to finding the fixed point of a map

$F:[0,1]^n\rightarrow[0,1]^n$ *where* $F\left(\boldsymbol{x}\right)=\left[\text{diag}\left(\boldsymbol{1}-\boldsymbol{D}^{-1}\boldsymbol{B}\boldsymbol{x}\right)\right]^{-1}\left(-\boldsymbol{D}^{-1}\boldsymbol{B}\right)\boldsymbol{x}$.

Proof

We observe that if an endemic equilibrium exists it must belong to the set $\left\{\bar{\boldsymbol{x}}:\text{diag}\left(\bar{\boldsymbol{x}}\right)=\boldsymbol{D}\boldsymbol{B}^{-1}+\boldsymbol{1}\right\}$. Hence

$$\bar{\boldsymbol{x}}=-\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}+\text{diag}\left(\bar{\boldsymbol{x}}\right)\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}$$

$$\Rightarrow \bar{\boldsymbol{x}}=-\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}+\left(\boldsymbol{D}\boldsymbol{B}^{-1}+\boldsymbol{1}\right)\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}$$

$$\Rightarrow \bar{\boldsymbol{x}}=-\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}+\boldsymbol{D}\boldsymbol{B}^{-1}\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}+\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}$$

We observe that since $\boldsymbol{D}$ is a diagonal matrix then;

$\boldsymbol{DB^{-1}D^{-1}B\bar{x} = B^{-1}DD^{-1}B\bar{x} = B^{-1}B\bar{x} = \bar{x}}$

And the result follows.

On the other hand an endemic equilibrium satisfies;

$(\boldsymbol{D}+\boldsymbol{B})\bar{\boldsymbol{x}} = \text{diag}(\bar{\boldsymbol{x}})\boldsymbol{B}\bar{\boldsymbol{x}}$

Equivalently,

$$\bar{\boldsymbol{x}} + \text{diag}(\bar{\boldsymbol{x}})\left(-\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}\right) = \bar{\boldsymbol{x}} + \text{diag}\left(-\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}\right)\bar{\boldsymbol{x}}$$
$$= -\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}$$

We can thus write;

$$\left[\boldsymbol{1} + \text{diag}\left(-\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}\right)\right]\bar{\boldsymbol{x}} = -\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}$$

It then follows that;

$$\bar{\boldsymbol{x}} = \left[\boldsymbol{1} + \text{diag}\left(-\boldsymbol{D}^{-1}\boldsymbol{B}\bar{\boldsymbol{x}}\right)\right]^{-1}\left(-\boldsymbol{D}^{-1}\boldsymbol{B}\right)\bar{\boldsymbol{x}}$$

If we define $F(\boldsymbol{x}) = \left[\text{diag}\left(\boldsymbol{1} - \boldsymbol{D}^{-1}\boldsymbol{B}\boldsymbol{x}\right)\right]^{-1}\left(-\boldsymbol{D}^{-1}\boldsymbol{B}\right)\boldsymbol{x}$ then the last equation becomes $F(\boldsymbol{x}) = \boldsymbol{x}$ as required. □

The proof of the uniqueness of the endemic equilibrium is provided in [9].

2.7 On the stability of the equilibrium

For arbitrary dimensional systems, the most efficient method is the Lyapunov method. In particular the Lyapunov function

$$V(\boldsymbol{x}) = \sum_{i=1}^{n} a_i\left(x_i - \bar{x}\ln x_i\right)$$

has been applied successfully to Lotka-Volterra (LV) models [7]. It turns out that epidemic models can be transformed to fit LV models and hence the above Lyapunov function can be applied in stability studies for such models. However for the general system $\dot{\boldsymbol{x}} = \boldsymbol{A}(\boldsymbol{x})\boldsymbol{x},\ \boldsymbol{x} \in \mathbb{R}^n$ where $\boldsymbol{A}(\boldsymbol{x})$ is a Metzler matrix we state and prove the following stability result.

2.8 Theorem (Lyapunov)

Given Ω *an open set containing the origin, which is positively invariant for the system* $\dot{\boldsymbol{x}} = \boldsymbol{A}(\boldsymbol{x})\boldsymbol{x},\ \boldsymbol{x} \in \mathbb{R}^n$ *where* $\boldsymbol{A}(\boldsymbol{x})$ *is a Metzler matrix, depending continuously on* $\boldsymbol{x}$. *We assume there exists* $\boldsymbol{c}^T \gg 0$ *such that* $\boldsymbol{c}^T\boldsymbol{A}(\boldsymbol{x}) \ll 0\ \forall \boldsymbol{x} \in \Omega, \boldsymbol{x} \neq 0$. *Then the origin is globally asymptotically stable on* Ω.

Proof

We consider on Ω the Lyapunov function

$$V(\boldsymbol{x}) = \sum_{i=1}^{n} c_i\left|x_i\right|$$

Furthermore we define $\varepsilon_x = \text{sign}(x)$, so that $\left|x_i\right| = \varepsilon_{x_i}x_i$.

Hence

$$V(\boldsymbol{x}) = \sum_{i=1}^{n} c_i\varepsilon_{x_i}x_i$$

The above function is locally Lipschitz and the Dini derivative [8] is given by

$$\begin{aligned}\dot{V}(\boldsymbol{x}) &= \sum_{i=1}^{n} c_i \varepsilon_{x_i} \dot{x}_i = \sum_{i=1}^{n} c_i \varepsilon_{x_i} \sum_{i=1}^{n} a_{ij} x_j \\ &= \sum_{i=1}^{n}\sum_{j=1}^{n} c_i \varepsilon_{x_i} a_{ij} x_j \\ &= \sum_{j=1}^{n} \varepsilon_{x_j} x_j \sum_{i=1}^{n} c_i \varepsilon_{x_j} \varepsilon_{x_i} a_{ij} \\ &= \sum_{j=1}^{n} \varepsilon_{x_j} x_j \left[c_j a_{jj} + \sum_{i \neq j} c_i \varepsilon_{x_j} \varepsilon_{x_i} a_{ij} \right] \\ &\leq \sum_{j=1}^{n} \varepsilon_{x_j} x_j \left[c_j a_{jj} + \sum_{i \neq j} c_i a_{ij} \right] = \sum_{j=1}^{n} \left| x_j \right| \left(\boldsymbol{c}^T \boldsymbol{A} \right)_j \leq 0\end{aligned}$$

Since $\boldsymbol{c}^T \boldsymbol{A}(\boldsymbol{x})$ 0 on Ω, then $\dot{V}$ is negative definite.

For the system (1.9), the global stability of the endemic equilibrium was proved in [9], and such it will not be considered here.

CONCLUSION

We have shown in this work how to generalize the SIS epidemic model to a multi group epidemiological model which divides the population into subpopulations for which the members have similar characteristics. The resulting mathematical model is an *n*-dimensional system of equations involving the so-called Metzler matrix. The equilibrium of the system and a stability result provided.

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