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Disease Models with Immigration

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by

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1. Abstract

In this thesis we focus first on studying the susceptible, exposed, and infected (SEI) disease model without immigration. We determine the basic reproduction number $\mathcal{R}_0$, which can be interpreted as the expected number of new cases that can be produced by a single infection in a completely susceptible population. Further, by using the Jacobian matrix, we determine the local stability of the disease model. Then we have the result that when $\mathcal{R}_0 < 1$ the DFE point is locally asymptotically stable(L.A.S). In contrast, when $\mathcal{R}_0 > 1$ we find that the endemic equilibrium is L.A.S. After that, we analyze the SEI model with immigration of infected individuals. Furthermore, we investigate the direction that the disease-free equilibrium moves, as a function of $\mathcal{R}_0$, when this immigration rate increases from zero. There are implications for what must happen to the disease-free equilibrium as the immigration rate increases away from zero:

- If $\mathcal{R}_0 < 1$, then the disease-free equilibrium moves to the interior of $\mathbb{R}^n_{\geq 0}$
- If $\mathcal{R}_0 > 1$, then the disease-free equilibrium moves away from $\mathbb{R}^n_{\geq 0}$.

This is an interesting phenomenon. In fact, we also study the susceptible, infectious, vaccination, and recovered (SIYR) disease model with immigration of infection individuals, with the same mathematical procedure as for the SEI model. Our study shows that the phenomenon is continuing. Then, we will consider the phenomenon for a general model, using matrix theory.

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Author

Reem Almarashi

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2. Introduction

When mathematical equations describe real life problems and their associated behaviours, this is known as mathematical modeling. In epidemiology, mathematical models help scientists to understand and control the spread of infectious diseases. Further, disease models address the transmission of infectious diseases among the population. The disease pathogen can be viruses, bacteria, or parasites [3].

Through basic pestilence models, scientists classify the human population into three categories : susceptible, infectious, or recovered (SIR model). However, certain types of diseases have incubation periods that contain the disease for a period of time. For example, "measles has an 8 to 13 days exposed period" [20]. For these types of diseases, the basic model needs to be formulated to address this exposed class. As a result, the $SEIR$ model is used to classify the population into susceptible, exposed, infectious, and recovered [20]. Indeed, a disease model may also include the vaccination class (Y) that shows effectiveness of a vaccination, so that an SIR model becomes an $SIYR$ model as in [10]. However, disease models can include many different compartments. In fact, disease models can take more general formula that includes many infected and uninfected classes.

Also, in the disease models there are individuals who enter from outside the population and may be infected with infectious disease. These individuals known as immigration [2]. It is significant to consider the diseases transmission models with immigration. In particular, study the impact of the immigration that has on the disease free state which is no infected individual in the population.

2.1. **Motivation.**

An understanding of the stability of equilibria of disease-transmission models is an important concept in biomathematics. Recently, much focus has been given to the analysis of the stability of disease models. The global stability and the basic reproduction number were the main areas of study in [10], [18], and [19]. Since there are a lot of studies that have been done on disease models without considering immigration of infected individuals, analysis of the spread of infectious disease with immigration becomes an important branch in understanding the relation between infected and susceptible individuals in disease modeling.

For models without immigration, we often find the following common results that are stated in terms of the basic reproduction number $\mathcal{R}_0$:

- If $\mathcal{R}_0 < 1$, then the only equilibrium is the disease-free equilibrium, on the boundary of $\mathbb{R}^n_{\geq 0}$.
- If $\mathcal{R}_0 > 1$, then there is the disease-free equilibrium and a unique endemic equilibrium $X^* \in \mathbb{R}^n_{>0}$.

There is not a disease-free equilibrium (DFE) nor a basic reproduction number $\mathcal{R}_0$ in models with immigration. In fact, for the models studied in [10] and [18], each of which included immigration of infectives, it was found that for all parameter values there was a unique equilibrium X^*, with $X^* \in \mathbb{R}^n_{>0}$. Therefore, the immigration can change the qualitative structure of the disease model.

In this work we investigate infectious disease models that account for the immigration of infected individuals.

3. Mathematical Models

3.1. **The SEI Disease Model.** The susceptible, exposed, and infectious individuals (SEI) disease model addresses a disease that has latent period between being infected and becoming infectious. In the SEI model the total population divides into three compartment S, E, and I.

The SEI model without immigration was studied first as a special case ofthe more complex model in [14]. It shows that the stability of the model when the threshold $\mathcal{R}_0$ becomes less than one the disease dies out and the DFE is locally asymptotically stable. Otherwise, when it becomes greater than one, the disease approaches an endemic equilibrium and is locally asymptotically stable.

In fact, it shows that the new individuals enter the S class at rate Λ and they move to E according to the incidence function βSI that shows the rate at which susceptible individuals become infected. Next, a fraction $\frac{\alpha}{\alpha+\mu_2}$ of latently infected individuals become infections; thoes individuals that become infectious do so after spending, on average, at time $\frac{1}{\alpha}$ in compartment E.

However, the exposed and infectious face death rate $\mu_2 E$, $\mu_3 I$, and susceptible individual face death rate $\mu_1 S$, with $0 < \mu_1 \leq \mu_2, \mu_3$. The disease transfer diagram in Figure 1 shows the movement of individuals.

The SEI model without immigration is

$$\begin{aligned} \frac{dS}{dt} &= \Lambda - \beta SI - \mu_1 S \\ \frac{dE}{dt} &= \beta SI - (\alpha + \mu_2)E \\ \frac{dI}{dt} &= \alpha E - \mu_3 I \end{aligned} \tag{1}$$

We assume that $\Lambda, \beta, \alpha, \mu_1, \mu_2, \mu_3 > 0$. The initial condition is X_0= (S(0),E(0),I(0)) $\in R^3_{\geq 0}$.

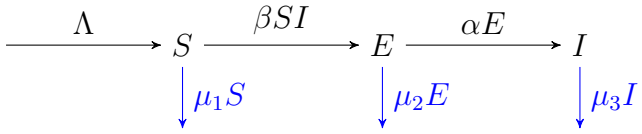

FIGURE 1. The Disease Transfer Diagram of the SEI Model

SEI model of disease transmission with immigration was studied first in [18] . It showed that there is no basic reproduction number. Also, the model has an endemic equilibrium as immigration becomes positive.

In the SEI model with immigration, it arrives at rate W distributed in compartments according to the fractions p, q, and r. Thus, we revisit the SEI model, where $p, q, r \in [0, 1]$ are the fraction of immigrants that enter the relevent groups as shown in Table 1. Thus $p + q + r = 1$. In fact, the model with immigration is a special case of the model without immigration with $p = 1$. To ensure there are infected immigration, we assume at least one of q or r is positive. That is, $q + r > 0$, and the disease model becomes:

$$\begin{aligned} \frac{dS}{dt} &= pW + \Lambda - \beta SI - \mu_1 S \\ \frac{dE}{dt} &= qW + \beta SI - (\alpha + \mu_2)E \\ \frac{dI}{dt} &= rW + \alpha E - \mu_3 I \end{aligned} \tag{2}$$

Then the transfer diagram can address the change as showsnin Figure 2.

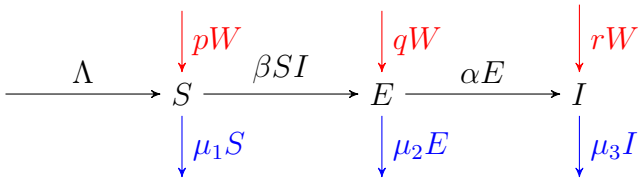

FIGURE 2. The Disease Transfer Diagram of the SEI Model with Immigration

TABLE 1. Parameters and Variables of SEI Models

symbols	Meaning
S	Susceptible individuals
E	Exposed individuals
I	Infected individuals
W	Total immigration rate
Λ	The rate that individuals enter the susceptible class
β	Mass action incidence cofficient
μ_1	Per capita death rate of susceptible individuals
μ_2	Per capita death rate of exposed individuals
μ_3	Per capita death rate of infected individuals
α	Per capita rate of movement from E to I
p	Fraction of immigrants that enter the susceptible class
q	Fraction of immigrants that enter the exposed class
r	Fraction of immigrants that enter the infective class

3.2. **The SIYR Disease Model.** In the disease model with vaccination and immigration in [10], it shows that there is no disease-free equilibrium nor basic reproduction number due to the infected immigration. However, there is a unique an endemic equilibrium for the $SIYR$ model of disease transmission with immigration.

In the SIYR model without immigration individuals who enter the susceptible class at rate Λ may leave the class if they are vaccinated at rate αS or become infected. The vaccine does not necessarily provide full immunity, so some vaccinated individuals may still become infected at rate $Yg(I)$.

However, under the vaccination effect some individuals may go to the recovered class at rate $\gamma_1 Y$ as the disease transfer diagram (3) shows. Also, the susceptible individuals who leave the class because they become infected at rate $Sf(I)$, they spending on average $\frac{1}{\delta}$ in the infections compartment I, then the infected individuals may recover from the disease or face death at rate $(\mu+\gamma)I$. Further, all S, Y, R class face death at rate $\mu S, \mu Y, \mu R$. Also, we assume (H1) the function f and g satisfy the criteria given in (5), and we have the assumption that force of infection for vaccinated individuals (H2) $g(I) \leq f(I)$ the force of infection for susceptible individuals for all $I \geq 0$. The disease model is:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - Sf(I) - (\alpha+\mu)S \\
\frac{dI}{dt} &= Sf(I) + Yg(I) - (\gamma+\mu+\delta)I \\
\frac{dY}{dt} &= \alpha S - Yg(I) - (\mu+\gamma_1)Y \\
\frac{dR}{dt} &= \gamma_1 Y + \delta I - \mu R
\end{aligned} \tag{3}$$

The initial condition is $X_0 = (S(0), I(0), Y(0), R(0)) \in R^4_{\geq 0}$. Table 2 defines all of the variables and the parameters of the $SIYR$ models.

The susceptible, infected, vaccinated, and recovered individuals (SIYR) diease model transfer diagram without immigration in (3):

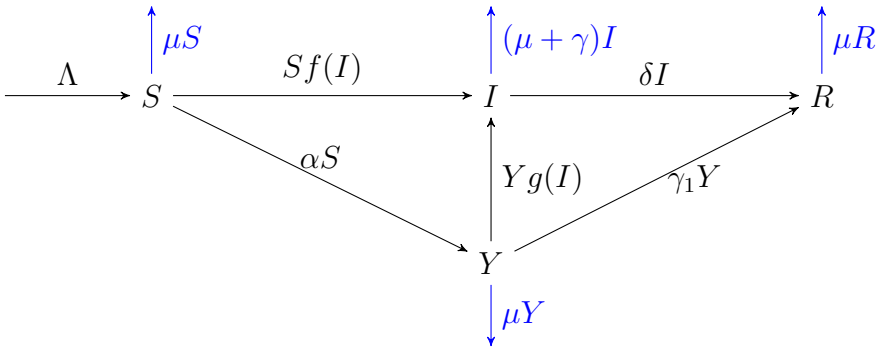

FIGURE 3. The Disease Transfer Diagram of the $SIYR$ Model

When the immigration arrives at rate W; ti distributed in compartments according to the fractions p, q, u, and r, where p, q, u, and r are the fraction of immigrants that enter the relevent groups with assumptions (H3) $p, u, r \in [0, 1]$ and $q \in (0, 1]$ with $q+p+u+r = 1$. In fact, the $SIYR$ disease model with immigration is a special case of the $SIYR$ model without immigration with $p < 1$. Also, (H4) $\mu, \Lambda, \alpha, \gamma, \delta, W > 0$ and , $\gamma_1 \geq 0$,

The disease model becomes:

$$\begin{aligned}
\frac{dS}{dt} &= pW + \Lambda - Sf(I) - (\alpha + \mu)S \\
\frac{dI}{dt} &= qW + Sf(I) + Yg(I) - (\gamma + \mu + \delta)I \\
\frac{dY}{dt} &= uW + \alpha S - Yg(I) - (\mu + \gamma_1)Y \\
\frac{dR}{dt} &= rW + \gamma_1 Y + \delta I - \mu R
\end{aligned} \tag{4}$$

The disease transfer diagram becomes as Figure 4 shows

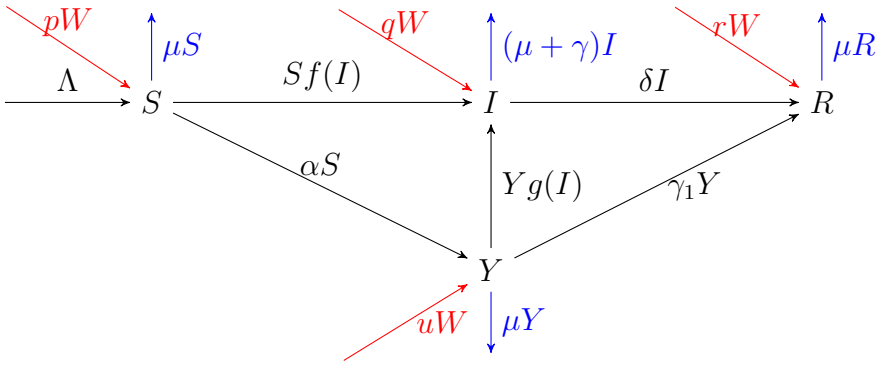

FIGURE 4. The Disease Transfer Diagram of the $SIYR$ Model with Immigration

Functions f and g satisfy the assumption that follows:

$$h(0) = 0, \quad h(I) \geq 0, \quad h^{'}(I) \geq 0, \quad h^{''}(I) \leq 0 \tag{5}$$

for $I > 0$.

Assumption (5) in the infectious disease-transmission shows when there is no infection (i.e. $I = 0$) then the forces of infection equal to zero, whereas at $I > 0$, which means there are infected individuals then the change of forces of infection becomes positive due to the movement of the infected through the disease compartments or zero if there is no movement. However, the second derivative of incidence functions is negative or equal to zero due to the change of the rate change of incidence functions is decreasing as the infected individuals increasing or zero if there is no change appear on the rate change of incidence functions.

The infectious diseases are transmitted as shown by the incidence functions. The $Sf(I), Yg(I)$ are nonlinear incidence function (i.e. forces of infection) for susceptible, vaccination classes instead of using the linear incidence function in the previous model [10]. In addition, the nonlinear incidence function addresses the change of the rate that individuals leave the susceptible class due to becoming infected with the disease. The nonlinear incidence function includes the Holling types by note that the third type does not satisfy the condition $h''(I) \leq 0$.

These functional types have positive first derivative which means it increasing functions of I, but the second derivative sign as shown in Figure 5. Incidence function type **I** is βSI which called mass action incidence function. This function has a linear increase in the first derivative and the second derivative is zero. Type **II** incidence function is $\frac{\beta SI}{1+mI}$ where m is a ratio of characteristic time. In fact, this type appropriate when the $f(I), g(I)$ have a maximum value. In this case, the forces of infection is concave function which means the second derivative is always negative. The third typ is a higher order of the second type $\frac{\beta SI^k}{1+mI^k}$ for $k > 1$. Type **III** shows that the second derivative becomes positive and then change to be negative as shown in Figure 5, and this type of Holling does not satisfies assumption $h''(I) \leq 0$ [4]. Those types can apply to more complex disease models.

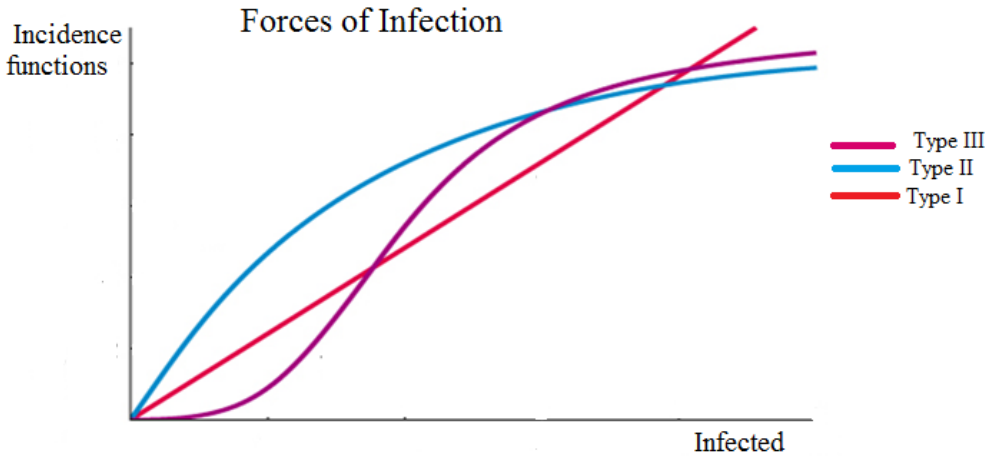

FIGURE 5. forces of infection Types

TABLE 2. Parameters and Variables of the SIYR Models

symbols	Meaning
S	Susceptible individuals
I	Infected individuals
Y	Vaccinated individuals
R	Recovered individuals
Λ	The rate that individuals enter the susceptible class
W	Total immigration rate
$f(I)$	Incidence function for susceptible class
$g(I)$	Yg(I) vaccination class
μ	Per capita death rate of susceptible class
α	Per capita rate of vaccination rate from S to Y
μ	Per capita death rate for non-disease reasons
μ	Per capita death rate of recovered class
γ	Per capita death rate due to disease
γ_1	Per capita rate of recovered class
δ	Per capita rate of movement individuals from I to R
p	Fraction of immigration that enter the susceptible class
q	Fraction of immigration that enter the infected class
u	Fraction of immigration that enter the vaccination class
r	Fraction of immigration that enter the recovered class

3.3. **The Staged Progression Disease Model.** The stage progression model was studied first in [13] for a model of HIV transmission. This sexual disease has many stages of infections. However, the study of stability of the model shows the disease free equilibrium becomes a globally asymptotically stable for $\mathcal{R}_0 < 1$, and is unstable when $\mathcal{R}_0 > 1$. Whereas, for $\mathcal{R}_0 > 1$ the endemic equilibrium is globally asymptotically stable.

One of the special cases of stage progression model is the SEI model that has two satges of infection. In this staged progression disease model, the susceptible individuals become infected according to the incidence function $S\sum_{i=1}^{k}\beta_i I_i$. This model is used to understand the behavior of diseases that may have more than one infection stage. Therefore, the disease model has multiple infection classes from 1 to k. In class I_i, an individual spends an average time $\frac{1}{\gamma_i}$ before progressing to the next stage of infection. However, they also face death rate $\mu_i I_i$ for all $i = 1, 2, ..., k$. Also, the death rate for S is dS. For biological reason, we assume that $\mu_1, ..., \mu_k \geq d > 0$

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - dS \\
\frac{dI_1}{dt} &= (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - (\gamma_1 + \mu_1)I_1 \\
\frac{dI_2}{dt} &= \gamma_1 I_1 - (\gamma_2 + \mu_2)I_2 \\
&\vdots \\
\frac{dI_k}{dt} &= \gamma_{k-1} I_{k-1} - \mu_k I_k
\end{aligned} \tag{6}$$

The disease model transfer diagram as follows:

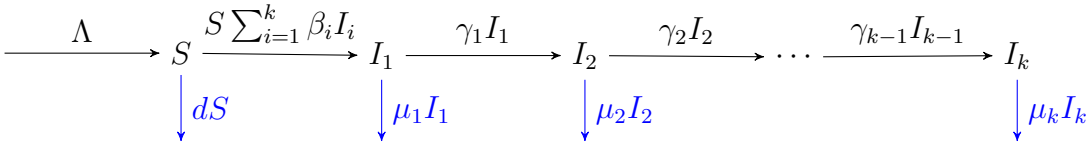

FIGURE 6. The Disease Transfer Diagram of the Staged Progression Disease Model.

When the immigration arrive at rate W separated into the disease classes according to the fractions $q_1, ..., q_k \in [0, 1)$, which implies that $q_1 + ... + q_k > 0$.

The corresponding system of the differential equations is

$$\begin{aligned}
\frac{dS}{dt} &= pW + \Lambda - (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - dS \\
\frac{dI_1}{dt} &= q_1 W + (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - (\gamma_1 + \mu_1)I_1 \\
\frac{dI_2}{dt} &= q_2 W + \gamma_1 I_1 - (\gamma_2 + \mu_2)I_2 \\
&\vdots \\
\frac{dI_k}{dt} &= q_k W + \gamma_{k-1} I_{k-1} - \mu_k I_k
\end{aligned} \tag{7}$$

The stage progression model whithout immigration is a special case of stage progression model with immigration with $p = 1$. All of the variables and the parameters of the staged progression disease model are define in Table 3.

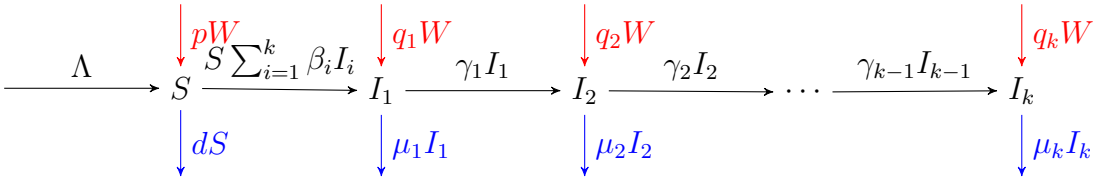

FIGURE 7. The Disease Transfer Diagram of the Staged Progression Disease Model with Immigration

TABLE 3. Parameters and Variables of The Stage Progression Disease Model

symbols	Meaning
S	Susceptible individuals
I_i	Individuals in infection stage i
W	Total immigration rate
p	Fraction of immigration that entert susceptible class
$q_i, i = 1, 2, ..., k$	Fraction fo immigration that enter infected class
Λ	The rate that individuals enter the susceptible class
β_i	Mass action incidence cofficient for infection class i.
dS	Per capita death rate of susceptible individuals
μ_i	Per capita death rate of individuals in infection class i for i=1, 2, . . .,k.
γ_i	Per capita rate of movement individuals from I_i to I_{i+1} for i=1, 2, . . .,k-1

4. Background Information

This chapter introduces some basic terminology and results that are important to understanding the aim of this paper.

4.1. **The Next Generation Matrix.**

Definition 4.1. *[17, Definition 2]. Consider the differential equation*

$$x'(t) = f(x(t)). \tag{8}$$

Let D be an open subset of $\mathbb{R}^n$*, let* $f \in C^1(D)$*, and let* Φ_t*: D* $\to$*D be the flow of the differential equation (8) defined for all* $t \in \mathbb{R}$*. Then a set* $H \subset D$ *is called invariant with respect to the flow* ϕ_t *if* $\phi_t(H) \subseteq H$ *for all* $t \in \mathbb{R}$ *and H is called positively (negatively) invariant with respect to the flow* ϕ_t *if* $\phi_t(H) \subseteq H$*for all* $t > 0$ $(t < 0)$*.*

Theorem 4.2. *[8, Proposition 2.1]. Suppose* $\frac{dx_j}{dt} = f_j(x_1, x_2, \cdots, x_n)$ *for j=1,2,3,..,n and that solutions are unique. Suppose that* $x_j = 0$ *implies* $f_j(x_1, x_2, \cdots, x_n) \geq 0$ *for* $x_1, x_2, \cdots, x_n \geq 0$*. Then* $\mathbb{R}^n_{\geq 0}$ *is positively invariant.*

Theorem 4.3. *[17, Theorem 2.2]. Let D be an open subset of* $\mathbb{R}^n$ *containing* x_0 *and assume that* $f \in C^1(D \to \mathbb{R})$*. Then there exists an* $a > 0$ *such that the initial value problem* $\dot{x} = f(x)$ *where* $x(0) = x_0$ *has a unique solution x(t) on the enterval [-a, a].*

Definition 4.4. *Next Generation Matrix [19]. Consider a differential equation*

$$\dot{x}(t) = f(x(t)) \tag{9}$$

where $f : \mathbb{R}^n \to \mathbb{R}^n$ *is differentiable. We assume that the variables are organized so that* $x_1, ..., x_m$ *are infected classes (including exposed and infectious, for example) and* $x_{m+1}, ..., x_n$ *are non-infected classes (including susceptible and recovered, for example). We define* X_{DF} *to be the disease-free space. That is,* $X_{DF} = \{x \in \mathbb{R}^n_{\geq 0} : x_i = 0 \text{ for } i = 1, ..., m\}$*. We rewrite Equation (9) as* $\dot{x}(t) = \mathcal{F}(x(t)) - \mathcal{V}(x(t))$*, where* $\mathcal{F}$ *consists of the terms that represent new infections that enter the infected classes and V includes all of the other terms, with* $\mathcal{V} = \mathcal{V}_i^- - \mathcal{V}^+$*. The vector functions* $\mathcal{F}, \mathcal{V}^-, \mathcal{V}^+$*must satisfy the follows assumptions:*
(H1) If $x \in \mathbb{R}^n_{\geq 0}$*, then* $\mathcal{F}(x), \mathcal{V}^-(x), \mathcal{V}^+(x) \in \mathbb{R}^n_{\geq 0}$*.*
(H2) If $x_i = 0$*, then* $\mathcal{V}_i^- = 0$ for $i = 1, ..., n$*.*

(H3) $\mathcal{F}_i = 0$ for $i > m$.

(H4) If $x \in X_{DF}$, *then* $\mathcal{F}_i = \mathcal{V}_i^+ = \mathcal{V}_i^- = 0$ for $i = 1, \ldots, m$.

(H5) Let $\bar{X}$ *be an equilibrium in* X_{DF}. *If* $\mathcal{F}$ *is replaced with the zero vector, then* $\bar{X}$ *is locally asymptotically stable.*

Now we begin calculating. First we construct $m \times m$ *matrices* F *and* V. *They are similar to the Jacobian matrices evaluated at* $\bar{X}$, *but are* $m \times m$ *instead of* $n \times n$. *Let*

$$F = \begin{bmatrix} \frac{\partial \mathcal{F}_1}{\partial x_1}(\bar{X}) & \cdots & \frac{\partial \mathcal{F}_1}{\partial x_m}(\bar{X}) \\ \vdots & \ddots & \vdots \\ \frac{\partial \mathcal{F}_m}{\partial x_1}(\bar{X}) & \cdots & \frac{\partial \mathcal{F}_m}{\partial x_m}(\bar{X}) \end{bmatrix} \tag{10}$$

and

$$V = \begin{bmatrix} \frac{\partial \mathcal{V}_1}{\partial x_1}(\bar{X}) & \cdots & \frac{\partial \mathcal{V}_1}{\partial x_m}(\bar{X}) \\ \vdots & \ddots & \vdots \\ \frac{\partial \mathcal{V}_m}{\partial x_1}(\bar{X}) & \cdots & \frac{\partial \mathcal{V}_m}{\partial x_m}(\bar{X}) \end{bmatrix}. \tag{11}$$

The product FV^{-1} *is called the next generation matrix. Let* $\lambda_1, \ldots, \lambda_m \in \mathbb{C}$ *be the eigenvalues of* FV^{-1}. *Then the basic reproduction number* $\mathcal{R}_0$ *is defined as* $\mathcal{R}_0 = \max |\lambda_i|, i = 1, ..., m$. *This is also called the spectral radius of the matrix and denoted by* ρ, *so that*

$$\mathcal{R}_0 = \rho(FV^{-1}).$$

Definition 4.5. *The basic reproduction number* $\mathcal{R}_0$ *is defined as the spectral radius of the next generation matrix*

$$\mathcal{R}_0 = \rho(FV^{-1}).$$

An important concept in understanding the spread of an infectious disease is the basic reproduction number $\mathcal{R}_0$, which is defined in Definition 4.5. The aim of using $\mathcal{R}_0$ is to determine if the disease can invade the population or not. To calculate $\mathcal{R}_0$, we study the system of differential equations at the disease-free steady state. After that, we look to the $\mathcal{R}_0$ quantity. If $\mathcal{R}_0 < 1$ then a low level of disease will die out. If $\mathcal{R}_0 > 1$, then the disease

can invade and survive [9].

Definition 4.6. *An equilibrium of disease model for which the infected individuals* $x_1 = ... = x_n = 0$ *is called a disease-free equilibrium (DFE) [6].*

4.2. **Equilibria and Local Stability.**

Theorem 4.7. *[19, Theorem 2]. For models without immigration, if* $\mathcal{R}_0 < 1$*, disease-free equilibrium is locally asymptotically stable, and if* $\mathcal{R}_0 > 1$*, then disease-free equilibrium is unstable.*

Consider the system of ordinary differential equations given in (8.1) where $x = (x_1, \cdots, x_n)^T$ and $f = (f_1, \cdots, f_n)^T$. The local stability of an equilibrium is studied by using the Jacobian matrix

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial x_1} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \vdots & \ddots & \vdots \\ \frac{\partial f_n}{\partial x_1} & \cdots & \frac{\partial f_n}{\partial x_n} \end{bmatrix}. \tag{12}$$

If all eigenvalues of J evaluated at X^* have negative real parts, then X^* is locally asymptotically stable. In contrast, if one or more eigenvalues have positive real parts then X^* is unstable.

When n=3, we can use the second compound matrix. Consider the 3×3 matrix:

$$M = \begin{bmatrix} A & B & C \\ D & E & F \\ G & H & I \end{bmatrix}. \tag{13}$$

Definition 4.8. *[12]. The second compound of M, denoted by* $M^{[2]}$*,is defined as:*

$$M^{[2]} = \begin{bmatrix} A+E & F & -C \\ H & A+I & B \\ -G & D & E+I \end{bmatrix}. \tag{14}$$

Theorem 4.9. *[16, Lemma 3]. Let M be a 3×3 real matrix. All eigenvalues of M have negative real parts if and only if trace(M),det(M),and* $det(M^{[2]}) < 0$*..*

4.3. **M-matrix.** Many disease models present matrices that have a certain sign pattern. One significant form is the M-matrix, which has nonnegative diagonal entries and nonpositive off-diagonals. M-matrices are important for many biological systems including disease models. Therefore, we introduce some properties of M-matrices, that are used later in the paper.

Let A be an $n \times n$ matrix given by

$$A = \begin{bmatrix} a_{11} & -a_{12} & -a_{13} & \cdots & -a_{1n} \\ -a_{21} & a_{22} & -a_{23} & \cdots & -a_{2n} \\ -a_{31} & -a_{32} & a_{33} & \cdots & -a_{3n} \\ \vdots & \vdots & \cdots & \ddots & \\ -a_{n1} & -a_{n2} & -a_{n3} & \cdots & a_{nn} \end{bmatrix}. \tag{15}$$

where the a_{ij} are nonnegative. Note that A can be expressed in the form $A = sI - B$, $s \in \mathbb{R}_{>0}$, and $B \geq 0$, so the matrix B is a non-negative matrix [1].

Definition 4.10. *The spectral abscissa of matrix K is $s(K)$ the maximum real part of all eigenvalues of matrix K [19].*

Definition 4.11. *The spectral radius of a square matrix K is defines as*

$$\rho(K) = max \mid \lambda \mid \tag{16}$$

for $\lambda \in$ spectrum(K)

This definition means that the spectral radius of a matrix measures how far the furthest one is from the origin. If the K is the next generation matrix then, $\rho(K)$ means the long-term average per generation multiplication number [6].

Theorem 4.12. *[6, Theorem 7.3]. Let $B \geq 0$. Then the spectral radius $\rho(B)$ is the dominant eigenvalue of B. That is, $|\lambda| \leq \rho(B)$ for all other eigenvalues λ of B.*

Definition 4.13. *A matrix A is called an M-matrix if there exist $s \in \mathbb{R}$ and $B \geq 0$ such that $s \geq \rho(B)$ and $A = sI - B$ [1].*

Definition 4.14. *A square matrix $A = [a_{ij}]$ has the Z sign pattern if $a_{ij} \leq 0$ for all $i \neq j$,and we say that A is a Z-matrix. Z is the set of all matrices that have the Z sign pattern [1].*

As a result, M-matrices are a sub-class of the Z- matrices [1].

Definition 4.15. *Irreducible Matrices : Let the (i,j) entry of the $n \times n$ matrix D be denoted by d_{ij}. Let $S = \{1, 2, \cdots, n\}$. Suppose there exist disjoint non-empty sets I and J such that:*
1. S is the union of I and J.
2. $d_{ij} = 0$ whenever $i \in I$ and $j \in J$.
Then D is said to be reducible. D is said to be irreducible if no such sets I and J exist.

Suppose A is reducible, with index sets I and J. Then, in the directed graph representation of A, it is impossible to get from any of the vertices in set I to any of the vertices in set J.

If I= {1, 2, ..., k} and J= {k+1, ..., n}, then the matrix A has a block of 0's filling the top right portion of the matrix. This block of 0's will have k rows and n-k columns. If I and J are different, then the basis of $\mathbb{R}^n$ can be re-ordered to put A into this form [5].

Theorem 4.16. *Let A be an irreducible Z-matrix. Then each of the following conditions is equivalent to the statement "A is a nonsingular M-matrix"*
(i) $A^{-1} \geq 0$
(ii)$Ax > 0$ for some $x \geq 0$

Theorem 4.17. *[7, Theorem 5.1.1]. Let P be a Z-matrix. Then the following properties are equivalent:*
(i)P is a non-singular and $P^{-1} \geq 0$.
(ii) The real part of any eigenvalue of P is positive.
(iii) There exists a vector $x \geq 0$ such that $Px > 0$.

Theorem 4.18. *[7, Theorem 5.2.10]. If $(V - F)$ is irreducible M-matrix, then the following statements are equivalent:*
(i) $(V - F)^{-1} > 0$.
(ii) There exists a vector $x > 0$ such that $(V - F)x > 0$.

Lemma 4.19. *[19, Lemma 1]. If the x_0 is the DFE of equation $\dot{x}_i = f(x_i) = \mathcal{F}_i(x) - \mathcal{V}_i(x)$, for all $i = 1, 2, \cdots, n$ and $f_i(x)$ satisfies the conditions* ***(H1)*** *to* ***(H6)*** *in Definition 4.4, then the derivatives $D\mathcal{F}(x_0)$ and $D\mathcal{V}(x_0)$ are partitioned as*

$$D\mathcal{F}(x_0) = \begin{bmatrix} F & 0 \\ 0 & 0 \end{bmatrix}, D\mathcal{V}(x_0) = \begin{bmatrix} V & 0 \\ J_3 & J_4 \end{bmatrix}, \tag{17}$$

where F and V are $n \times n$ matrices defined by

$$F = \left[\frac{\partial \mathcal{F}_i(x_0)}{\partial x_j}\right], V = \left[\frac{\partial \mathcal{V}_i(x_0)}{\partial x_j}\right], \tag{18}$$

with $1 \leq i$, and $j \leq n$.

Further, $F \geq 0$, V is a non-singular M-matrix, and all eignvalues of J_4 have positive real part.

Lemma 4.20. *[19, Lemma 6]. Let H is a non-singular M-matrix, and suppose $K \geq 0$. Then*

(i) $(H - K)$ is an M-matrix if and only if $I - KH^{-1}$ is an M-matrix.

(ii) $(H - K)$ is a non-singular M-matrix if and only if $I - KH^{-1}$ is a non-singular M-matrix.

(iii) $(H - K)$ is a singular M-matrix if and only if $I - KH^{-1}$ is a singular M-matrix.

4.4. **General Disease Model without Immigration.** The general disease model without immigration given by the differential equation

$$\dot{x}(t) = f(x(t)) \tag{19}$$

where $x = (x_1, x_2, ..., x_k)$ with $x_i \geq 0$ for all $i = 1, 2, ..., k$. In fact, there is a clear distinction in x_i, where the x_i for $i = 1, 2, ..., n$ describes the infected individuals and, whereas, $x_{n+1}, x_{n+2}, ..., x_k$ are uninfected individual. At the disease-free equilibrium (DFE) state, all infected variables are 0, and uninfected variables are greater than or equal to zero. The disease-free space is $X_{DF} = \{x \in \mathbb{R}^k_{\geq 0} : x_i = 0 \text{ for } i = 1, 2, ..., n\}$. In fact, the x_{DFE} is the disease-free equilibrium point.

To analyze the disease model, we differentiate between the terms that represent new infectious individual and all other terms. Therefore, we present $\mathcal{F}_i$ that includes all new infected individuals entering the i^{th} class. Whereas, $\mathcal{V}_i$ includes all other movement in and out of the i^{th} class. This includes $\mathcal{V}^-{}_i$ which addresses the death rate caused by disease or natural reasons death, and per capita rate of movement form class i to other classes. Also, $\mathcal{V}^+{}_i$ includes movement into class i from the other classes. Thus, $\mathcal{V}_i = \mathcal{V}_i^- - \mathcal{V}_i^+$. Thus, we could write the disease model in the form: $\dot{x}_i = f_i(x) = \mathcal{F}_i - \mathcal{V}_i$, for $i = 1, 2, ..., k$.

We consider the disease model under certain assumptions. Since $\mathcal{F}_i$, $\mathcal{V}^+$, and $\mathcal{V}^-$ describe the movement of individuals in the disease model, the first assumption states :
(A1) If $x_i \geq 0$, then $\mathcal{F}_i$, $\mathcal{V}_i^-$, and $\mathcal{V}_i^+ \geq 0$ for all $i = 1, 2, ..., k$.
However, if $x_i = 0$ for some i, then there can be no transfer out of x_i.
(A2) If $x_i = 0$, then $\mathcal{V}_i^- = 0$ for all $i = 1, 2, ..., k$.
(A3) $\mathcal{F}_i = 0$ for all $i = n + 1, n + 2, ..., k$.
This means there are no new infections that appear in the uninfected groups.

The conditions $(A_1), (A_2)$ can be used to show the positive invariance, of $\mathbb{R}^k_{\geq 0}$ In order to prove the invariance of disease-free space, we state the assumption:
(A4) If $x_i \in X_{DF}$ then $\mathcal{F}_i = 0$ and $\mathcal{V}^+{}_i = 0$ for all $i = 1, 2, , n$.

While the functions $\mathcal{F}_i$, $\mathcal{V}^+{}_i$ and $\mathcal{V}^-{}_i$ are continuously differentiable in each variable, we assume that:

(A5) If $\mathcal{F}$ is set of zero then all the eigenvalues of $Df(x_{DFE})$have negative real parts which means that the disease model at DFE is locally stable.

5. SEI Disease Model with No Immigration

In this section, we study the stability of the SEI disease model without immigration in two cases, depending on whether $\mathcal{R}_0 < 1$ or $\mathcal{R}_0 > 1$.

$$\begin{aligned} \frac{dS}{dt} &= \Lambda - \beta SI - \mu_1 S \\ \frac{dE}{dt} &= \beta SI - (\alpha + \mu_2)E \\ \frac{dI}{dt} &= \alpha E - \mu_3 I \end{aligned} \tag{20}$$

with $\Lambda, \beta, \mu_1, \mu_2, \mu_3, \alpha > 0$. The initial condition is $X_0 = (S(0), E(0), I(0)) \in \mathbb{R}^3_{\geq 0}$.

5.1. **Equilibria.** In order to ensure the existence of a unique solution to the SEI model with a given initial condition, we apply Theorem 4.3 to the SEI model (20). Letting $D = \mathbb{R}^3$, there exists an $a > 0$ such that the IVP has a unique solution $x(t)$ for t $\in [-a, a]$.

To study the disease-free equilibrium (DFE) we set $E = I = 0$. Then we get the equilibrium $(S_0, 0, 0) = (\frac{\Lambda}{\mu_1}, 0, 0)$. However, this model may have an endemic equilibrium point (EEP) with $E \neq 0, I \neq 0$. In order to find the EEP, we let $\frac{dI}{dt} = 0$. Then the third equation in (20) will be $E^* = \frac{\mu_3}{\alpha} I^*$. By substituting this into $\frac{dE}{dt} = 0$, we get $S^* = \dfrac{(\alpha + \mu_2)\mu_3}{\alpha\beta}$. Then we substitute S^* into $\frac{dS}{dt} = 0$, so $I^* = \dfrac{\Lambda - \mu_1 S^*}{\beta S^*}$. After that the EEP is $(S^*, E^*, I^*) = (\dfrac{(\alpha + \mu_2)\mu_3}{\alpha\beta}, \dfrac{\mu_3}{\alpha}\dfrac{\mu_1}{\beta}(\dfrac{\Lambda\alpha\beta}{\mu_1\mu_3(\alpha + \mu_2)} - 1), \dfrac{\mu_1}{\beta}(\dfrac{\Lambda\alpha\beta}{\mu_1\mu_3(\alpha + \mu_2)} - 1))$.

The basic reproduction number will be found by using the next generation matrix. We now change the order of the variables to (E, I, S) to agree with the method described in Section 4.1. Let

$$\mathcal{F} = \begin{bmatrix} \beta SI \\ 0 \\ * \end{bmatrix} \tag{21}$$

and

$$\mathcal{V} = \begin{bmatrix} (\alpha + \mu_2)E \\ -\alpha E + \mu_3 I \\ * \end{bmatrix}. \tag{22}$$

Then,

$$F = \begin{bmatrix} 0 & \beta\dfrac{\Lambda}{\mu_1} \\ 0 & 0 \end{bmatrix} \tag{23}$$

$$V = \begin{bmatrix} (\alpha + \mu_2) & 0 \\ -\alpha & \mu_3 \end{bmatrix}, \tag{24}$$

and,

$$V^{-1} = \begin{bmatrix} \dfrac{1}{(\alpha + \mu_2)} & 0 \\ \dfrac{\alpha}{(\alpha + \mu_2)\mu_3} & \dfrac{1}{\mu_3} \end{bmatrix}. \tag{25}$$

Thus,

$$FV^{-1} = \begin{bmatrix} \dfrac{\beta\Lambda\alpha}{(\alpha + \mu_2)\mu_3\mu_1} & \dfrac{\beta\Lambda}{\mu_3\mu_1} \\ 0 & 0 \end{bmatrix}. \tag{26}$$

The eigenvalues of FV^{-1} are $\lambda_1 = \dfrac{\beta\Lambda\alpha}{(\alpha + \mu_2)\mu_3\mu_1}$ and $\lambda_2 = 0$. Then, by using Definition 4.4,

$$\mathcal{R}_0 = \frac{\beta\Lambda\alpha}{(\alpha + \mu_2)\mu_3\mu_1}.$$

Note that, we may now write $\beta I^* = \mu_1(\mathcal{R}_0 - 1)$. This will be useful when studying the stability of the EEP.

5.2. **The Stability of the Disease Model.** Theorem 4.9 can be applied to model (20) in two cases: when $\mathcal{R}_0 < 1$, and $\mathcal{R}_0 > 1$. When $\mathcal{R}_0 < 1$ we have one DFE point, that is $(S_0, 0, 0)$. Conversely, at $\mathcal{R}_0 > 1$ we have two points, the DFE and the endemic equilibrium (S^*, E^*, I^*).

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial E} & \frac{\partial f_1}{\partial I} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial E} & \frac{\partial f_2}{\partial I} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial E} & \frac{\partial f_3}{\partial I} \end{bmatrix} = \begin{bmatrix} -(\beta I + \mu_1) & 0 & -\beta S \\ \beta I & -\alpha - \mu_2 & \beta S \\ 0 & \alpha & -\mu_3 \end{bmatrix} \tag{27}$$

Case 1: $\mathcal{R}_0 < 1$. Then, at the DFE we have

$$J = \begin{bmatrix} -\mu_1 & 0 & -\beta\frac{\Lambda}{\mu_1} \\ 0 & -\alpha - \mu_2 & \beta\frac{\Lambda}{\mu_1} \\ 0 & \alpha & -\mu_3 \end{bmatrix} \tag{28}$$

and

$$J^{[2]} = \begin{bmatrix} -(\mu_1 + \alpha + \mu_2) & \beta\frac{\Lambda}{\mu_1} & \beta\frac{\Lambda}{\mu_1} \\ \alpha & -\mu_1 - \mu_3 & 0 \\ 0 & 0 & -(\alpha + \mu_2 + \mu_3) \end{bmatrix} \tag{29}$$

Trace J=$-(\alpha + \mu_1 + \mu_2 + \mu_3) < 0$, and

$$\begin{aligned} \det J &= -\mu_1 \left[\mu_3(\alpha + \mu_2) - \alpha\beta\frac{\Lambda}{\mu_1} \right] \\ &= -\mu_1\mu_3(\alpha + \mu_2)\left[1 - \mathcal{R}_0\right] < 0, \end{aligned}$$

since $\mathcal{R}_0 < 1$.

$$\begin{aligned}
\det J^{[2]} &= -(\alpha+\mu_2+\mu_3)\left[(\mu_1+\mu_3)(\mu_1+\alpha+\mu_2)-\alpha\beta\frac{\Lambda}{\mu_1}\right] \\
&= -(\alpha+\mu_2+\mu_3)\mu_3(\alpha+\mu_2)\left[\frac{(\mu_1+\mu_3)(\mu_1+\alpha+\mu_2)}{\mu_3(\alpha+\mu_2)}-\frac{\alpha\beta\Lambda}{(\alpha+\mu_2)\mu_3\mu_1}\right] \\
&= -(\alpha+\mu_2+\mu_3)\mu_3(\alpha+\mu_2)\left[\frac{(\mu_1+\mu_3)(\mu_1+\alpha+\mu_2)}{\mu_3(\alpha+\mu_2)}-\mathcal{R}_0\right]
\end{aligned}$$

Since $\dfrac{(\mu_1+\mu_3)(\mu_1+\alpha+\mu_2)}{\mu_3(\alpha+\mu_2)}$ is large than one and $\mathcal{R}_0 < 1$, the term $\left[\dfrac{(\mu_1+\mu_3)(\mu_1+\alpha+\mu_2)}{\mu_3(\alpha+\mu_2)}-\mathcal{R}_0\right]$ is positive, thus, $\det J^{[2]} < 0$. Then by Theorem 4.9, the DFE is locally asymptotically stable.

Case 2: $\mathcal{R}_0 > 1$. At the DFE , we have

$$\det J(S_0,0,0) = -\mu_1\left[\mu_3(\alpha+\mu_2)-\alpha\beta\frac{\Lambda}{\mu_1}\right] = -\mu_1\mu_3(\alpha+\mu_2)[1-\mathcal{R}_0].$$

For $\mathcal{R}_0 > 1$, this is negative. Thus, Theorem(4.9) implies the DFE is unstable.

The endemic equilibrium point is (S^*, E^*, I^*), using $\beta I^* = \mu_1(\mathcal{R}_0 - 1)$, and $\beta S^* = \dfrac{\mu_3(\alpha+\mu_2)}{\alpha}$, we have

$$J = \begin{bmatrix} -\mu_1\mathcal{R}_0 & 0 & -\dfrac{(\alpha+\mu_2)\mu_3}{\alpha} \\ \mu_1(\mathcal{R}_0-1) & -\alpha-\mu_2 & \dfrac{(\alpha+\mu_2)\mu_3}{\alpha} \\ 0 & \alpha & -\mu_3 \end{bmatrix}. \tag{30}$$

Then

$$\text{Trace } J = -\left[\mu_1\mathcal{R}_0 + \alpha + \mu_2 + \mu_3\right] < 0,$$

$$\begin{aligned}
\det J =& -\frac{\mu_3(\alpha+\mu_2)}{\alpha}(\mu_1\alpha(\mathcal{R}_0-1)) - \frac{\mu_3(\alpha+\mu_2)}{\alpha}(-\alpha\mu_1\mathcal{R}_0) - \mu_3(\mu_1\mathcal{R}_0(\alpha+\mu_2)) \\
=& -(\alpha+\mu_2)\mu_3\mu_1(\mathcal{R}_0-1) + (\alpha+\mu_2)\mu_3\mu_1\mathcal{R}_0 - (\alpha+\mu_2)\mu_3\mu_1\mathcal{R}_0 \\
=& -(\alpha+\mu_2)\mu_3\mu_1(\mathcal{R}_0-1) \\
<& 0,
\end{aligned}$$

since $\mathcal{R}_0 > 1$.

$$J^{[2]} = \begin{bmatrix} -\mu_1\mathcal{R}_0 - (\alpha+\mu_2) & \frac{\mu_3(\alpha+\mu_2)}{\alpha} & \frac{\mu_3(\alpha+\mu_2)}{\alpha} \\ \alpha & -\mu_1\mathcal{R}_0 - \mu_3 & 0 \\ 0 & \mu_1(\mathcal{R}_0-1) & -(\alpha+\mu_2+\mu_3). \end{bmatrix} \tag{31}$$

$$\det J^{[2]} = -(\alpha+\mu_2+\mu_3)\left[(\mu_1\mathcal{R}_0+\alpha+\mu_2)(\mu_1\mathcal{R}_0+\mu_3) - \mu_3(\alpha+\mu_2)\right] + \mu_3(\alpha+\mu_2)[\mu_1(\mathcal{R}_0-1)]$$

$$= -(\alpha+\mu_2+\mu_3)\mu_3(\alpha+\mu_2)\left[\frac{(\mu_1\mathcal{R}_0+\alpha+\mu_2)(\mu_1\mathcal{R}_0+\mu_3)}{\mu_3(\alpha+\mu_2)} - 1 + \frac{\mu_1(\mathcal{R}_0-1)}{\alpha+\mu_2+\mu_3}\right]$$

$$= -(\alpha+\mu_2+\mu_3)\mu_3(\alpha+\mu_2)\left[\frac{(\mu_1\mathcal{R}_0)^2 + (\mu_3+\alpha+\mu_2)\mu_1\mathcal{R}_0}{\mu_3(\alpha+\mu_2)} + 1 - 1 + \frac{\mu_1(\mathcal{R}_0-1)}{\alpha+\mu_2+\mu_3}\right]$$

$$= -(\alpha+\mu_2+\mu_3)\mu_3(\alpha+\mu_2)\left[\frac{(\mu_1\mathcal{R}_0)^2 + (\mu_3+\alpha+\mu_2)\mu_1\mathcal{R}_0}{\mu_3(\alpha+\mu_2)} + \frac{\mu_1(\mathcal{R}_0-1)}{\alpha+\mu_2+\mu_3}\right]$$

$$< 0,$$

since $\mathcal{R}_0 > 1$, ans so

$$\det J^{[2]} < 0.$$

Therefore, by Theorem 4.9, the equilibrium (S^*, E^*, I^*) is LAS.

We now have the following result.

Theorem 5.1. *If $\mathcal{R}_0 < 1$, then the only equilibrium is the DFE and it is LAS. If $\mathcal{R}_0 > 1$, then there are two equilibria, the DFE which is unstable and an EEP which is LAS.*

6. SEI Model with Immigration

In this chapter, we study the SEI model as the immigration rate W increases from 0. In particular, we focus on how the infected variables of the disease-free equilibrium change with respect to W. After that, we look at the sign of these derivatives as a function of the sign of $\mathcal{R}_0 - 1$.

The SEI model with immigration [18]:

$$\begin{aligned} \frac{dS}{dt} &= pW + \Lambda - \beta SI - \mu_1 S \\ \frac{dE}{dt} &= qW + \beta SI - (\alpha + \mu_2)E \\ \frac{dI}{dt} &= rW + \alpha E - \mu_3 I \end{aligned} \tag{32}$$

where $p, qr \geq 0$, $p + q + r = 1$, and $q + r > 0$. $\Lambda, \beta, \mu_1, \mu_2, \mu_3 > 0$.
This model can be written in the form

$$\begin{bmatrix} \frac{dS}{dt} \\ \\ \frac{dE}{dt} \\ \\ \frac{dI}{dt} \end{bmatrix} = W \begin{bmatrix} p \\ \\ q \\ \\ r \end{bmatrix} + \begin{bmatrix} \Lambda - (\beta I + \mu_1)S \\ \\ \beta SI - (\alpha + \mu_2)E \\ \\ \alpha E - \mu_3 I \end{bmatrix}. \tag{33}$$

The equilibrium equations with respect to W are as follows:

$$\begin{aligned} 0 &= pW + \Lambda - \beta S(W)I(W) - \mu_1 S(W) \\ 0 &= qW + \beta S(W)I(W) - (\alpha + \mu_2)E(W) \\ 0 &= rW + \alpha E(W) - \mu_3 I(W) \end{aligned} \tag{34}$$

We differentiate the equilibrium equations with respect to W in order to study how the equilibrium value of E and I depend on W.

$$
\begin{aligned}
0 &= p - \beta \frac{\partial S}{\partial W} I(W) - \beta S(W) \frac{\partial I}{\partial W} - \mu_1 \frac{\partial S}{\partial W} \\
0 &= q + \beta \frac{\partial S}{\partial W} I(W) + \beta S(W) \frac{\partial I}{\partial W} - (\alpha + \mu_2) \frac{\partial E}{\partial W} \\
0 &= r + \alpha \frac{\partial E}{\partial W} - \mu_3 \frac{\partial I}{\partial W}
\end{aligned} \tag{35}
$$

6.1. **Equilibria.** At W=0 , E=0, I=0 we have the DFE

$$
\begin{bmatrix} S \\ E \\ I \end{bmatrix} = \begin{bmatrix} \frac{\Lambda}{\mu_1} \\ 0 \\ 0 \end{bmatrix}. \tag{36}
$$

Filling this into equation (35) gives

$$
\begin{aligned}
0 &= p - \beta \frac{\Lambda}{\mu_1} \frac{\partial I}{\partial W} - \mu_1 \frac{\partial S}{\partial W} \\
0 &= q + \beta \frac{\Lambda}{\mu_1} \frac{\partial I}{\partial W} - (\alpha + \mu_2) \frac{\partial E}{\partial W} \\
0 &= r + \alpha \frac{\partial E}{\partial W} - \mu_3 \frac{\partial I}{\partial W}.
\end{aligned}
$$

Rearranging, we obtain

$$
\begin{aligned}
p &= \beta \frac{\Lambda}{\mu_1} \frac{\partial I}{\partial W} + \mu_1 \frac{\partial S}{\partial W} \\
q &= -\beta \frac{\Lambda}{\mu_1} \frac{\partial I}{\partial W} + (\alpha + \mu_2) \frac{\partial E}{\partial W} \\
r &= -\alpha \frac{\partial E}{\partial W} + \mu_3 \frac{\partial I}{\partial W}.
\end{aligned}
$$

Writing the equations in matrix form, we have

$$\begin{bmatrix} \mu_1 & 0 & \beta\frac{\Lambda}{\mu_1} \\ 0 & \alpha+\mu_2 & -\beta\frac{\Lambda}{\mu_1} \\ 0 & -\alpha & \mu_3 \end{bmatrix} \begin{bmatrix} \frac{\partial S}{\partial W} \\ \frac{\partial E}{\partial W} \\ \frac{\partial I}{\partial W} \end{bmatrix} = \begin{bmatrix} p \\ q \\ r \end{bmatrix}. \tag{37}$$

Let

$$A = \begin{bmatrix} \mu_1 & 0 & \beta\frac{\Lambda}{\mu_1} \\ 0 & \alpha+\mu_2 & -\beta\frac{\Lambda}{\mu_1} \\ 0 & -\alpha & \mu_3 \end{bmatrix}. \tag{38}$$

We now use A^{-1} to rearrange Equation (37), as

$$\begin{bmatrix} \frac{\partial S}{\partial W} \\ \frac{\partial E}{\partial W} \\ \frac{\partial I}{\partial W} \end{bmatrix} = A^{-1} \begin{bmatrix} p \\ q \\ r \end{bmatrix}$$

$$\begin{bmatrix} \frac{\partial S}{\partial W} \\ \frac{\partial E}{\partial W} \\ \frac{\partial I}{\partial W} \end{bmatrix} = \begin{bmatrix} \frac{1}{\mu_1} & -\beta\frac{\Lambda}{\mu_1^2}\frac{\alpha}{\mu_3(\mu_2+\alpha)(1-\mathcal{R}_0)} & \beta\frac{\Lambda}{\mu_1^2}\frac{1}{\mu_3(\mu_2+\alpha)(1-\mathcal{R}_0)} \\ 0 & \frac{1}{(\alpha+\mu_2)(1-\mathcal{R}_0)} & \beta\frac{\Lambda}{\mu_1}\frac{1}{\mu_3(\mu_2+\alpha)(1-\mathcal{R}_0)} \\ 0 & \frac{\alpha}{\mu_3(\mu_2+\alpha)(1-\mathcal{R}_0)} & \frac{1}{\mu_3(1-\mathcal{R}_0)} \end{bmatrix} \begin{bmatrix} p \\ q \\ r \end{bmatrix}.$$

Thus,

$$\begin{aligned} \frac{\partial E}{\partial W} &= \frac{1}{(\mu_2+\alpha)(1-\mathcal{R}_0)}\left[q + r\beta\frac{\Lambda}{\mu_1}\frac{1}{\mu_3}\right] \\ \frac{\partial I}{\partial W} &= \frac{1}{\mu_3(1-\mathcal{R}_0)}\left[\frac{q\alpha}{\mu_2+\alpha} + r\right] \end{aligned}$$

It is now clear that the signs of $\frac{\partial E}{\partial W}$ and $\frac{\partial I}{\partial W}$ change depending on the sign of $\mathcal{R}_0 - 1$.

Theorem 6.1. *If $\mathcal{R}_0 < 1$, then the infected variables at the DFE become positive as W increases from 0, whereas for $\mathcal{R}_0 > 1$ they become negative as W increases from 0.*

Corollary 6.2. *If $\mathcal{R}_0 < 1$, there exists $\bar{W} > 0$ such that for $W \in (0, \bar{W})$ an endemic equilibrium exists. Note that $\bar{W} \in (0, \infty]$.*

7. The Disease Model with Vaccination and Immigration

In Chapter 6, we deal with the $SIYR$ disease model with immigration (4), which comes from [10]. We use the same mathematical steps that we used in Chapter 5. However, the $SIYR$ disease model with immigration in Section 3.2 satisfies the assumptions given in (5), and it satisfies (H1) (H2) (H3) (H4) in Section 3.2. Then the model is as follows:

$$\begin{aligned}
\frac{dS}{dt} &= pW + \Lambda - Sf(I) - (\alpha + \mu)S \\
\frac{dI}{dt} &= qW + Sf(I) + Yg(I) - (\gamma + \mu + \delta)I \\
\frac{dY}{dt} &= uW + \alpha S - Yg(I) - (\mu + \gamma_1)Y \\
\frac{dR}{dt} &= rW + \gamma_1 Y + \delta I - \mu R
\end{aligned} \tag{39}$$

Since the recovered class doesn't appear in the first three equations, we can ignore it. Henceforth, we reduce the system to:

$$\begin{aligned}
\frac{dS}{dt} &= pW + \Lambda - Sf(I) - (\alpha + \mu)S \\
\frac{dI}{dt} &= qW + Sf(I) + Yg(I) - (\gamma + \mu + \delta)I. \\
\frac{dY}{dt} &= uW + \alpha S - Yg(I) - (\mu + \gamma_1)Y
\end{aligned}$$

The equilibrium equations with respect to W are as follows:

$$\begin{aligned}
0 &= pW + \Lambda - S(W)f(I(W)) - (\alpha + \mu)S(W) \\
0 &= qW + S(W)f(I(W)) + Y(W)g(I(W)) - (\gamma + \mu + \delta)I(W). \\
0 &= uW + \alpha S(W) - Y(W)g(I(W)) - (\mu + \gamma_1)Y(W)
\end{aligned}$$

We differentiate the equilibrium equations with regards to W, getting

$$\begin{aligned}
0 &= p - \frac{\partial S}{\partial W} f(I(W)) - S(W)\frac{\partial f}{\partial I}\frac{dI}{dW} - (\alpha + \mu)\frac{\partial S}{\partial W} \\
0 &= q + \frac{\partial S}{\partial W} f(I(W)) + S(W)\frac{\partial f}{\partial I}\frac{dI}{dW} + \frac{\partial Y}{\partial W}\, g(I(W)) + Y(W)\frac{\partial g}{\partial I}\frac{dI}{dW} \\
&\qquad - (\gamma + \mu + \delta)\frac{\partial I}{\partial W} \\
0 &= u + \alpha\frac{\partial S}{\partial W} - \frac{\partial Y}{\partial W}\, g(I(W)) - Y(W)\frac{\partial g}{\partial I}\frac{dI}{dW} - (\mu + \gamma_1)\frac{\partial Y}{\partial W}
\end{aligned} \tag{40}$$

7.1. **Equilibria.** The disease-free equilibrium point when $W = 0$, $I = 0$ is:

$$\begin{bmatrix} S^* \\ \\ I \\ \\ Y^* \end{bmatrix} = \begin{bmatrix} \dfrac{\Lambda}{\mu+\alpha} \\ \\ 0 \\ \\ \dfrac{\Lambda\alpha}{(\mu+\alpha)\mu+\gamma_1} \end{bmatrix}. \tag{41}$$

Thus, recalling that $f(0) = g(0) = 0$, at $W = 0$ and $I = 0$, the second line of Equation (40) becomes

$$\begin{aligned} q &= -S^*\frac{\partial f}{\partial I}(0)\frac{dI}{dW} - Y^*\frac{\partial g}{\partial I}(0)\frac{dI}{dW} + (\gamma+\mu+\delta)\frac{\partial I}{\partial W} \\ &= \left[(\gamma+\mu+\delta) - \left(S^*\frac{\partial f}{\partial I}(0) + Y^*\frac{\partial g}{\partial I}(0)\right)\right]\frac{dI}{dW}. \end{aligned} \tag{42}$$

Let $\beta_1 = \dfrac{\partial f}{\partial I}(0)$ and $\beta_2 = \dfrac{\partial g}{\partial I}(0)$. Then Equation (42) can be rearranged to get

$$\begin{aligned} \frac{dI}{dW} &= \frac{q}{(\gamma+\mu+\delta) - (S^*\beta_1 + Y^*\beta_2)} \\ &= \frac{q}{(\gamma+\mu+\delta) - \left(\dfrac{\Lambda}{\mu+\alpha}\beta_1 + \dfrac{\Lambda\alpha}{(\mu+\alpha)\mu+\gamma_1}\beta_2\right)} \end{aligned} \tag{43}$$

Now we find $\mathcal{R}_0$ by using the next generation matrix.

By changing the order of the variables to (I, Y, S) in order to apply Definition 4.4 described in Section 4.1. Let

$$\mathcal{F} = \begin{bmatrix} Sf(I) + Yg(I) \\ * \\ * \end{bmatrix}.$$

and

$$\mathcal{V} = \begin{bmatrix} (\gamma+\mu+\delta)I \\ * \\ * \end{bmatrix},$$

where $*$ represents information that we don't need. Then,

$$F = \left[\; S\frac{\partial f}{\partial I} + Y\frac{\partial g}{\partial I} \; \right]_{DFE} = \left[\; \left(\frac{\Lambda}{\mu+\alpha}\right)\beta_1 + \left(\frac{\Lambda\alpha}{(\mu+\alpha)\mu+\gamma_1}\right)\beta_2 \; \right]$$

and

$$V = \; \gamma + \mu + \delta.$$

Then

$$\mathcal{R}_0 = \rho(FV^{-1}) = \left[\frac{\left(\frac{\Lambda}{\mu+\alpha}\right)\beta_1 + \left(\frac{\Lambda\alpha}{(\mu+\alpha)\mu+\gamma_1}\right)\beta_2}{(\gamma+\mu+\delta)} \right],$$

Thus, Equation(43) can be written as

$$\frac{dI}{dW} = \frac{q}{(\gamma+\mu+\delta)(1-\mathcal{R}_0)} \tag{44}$$

The sign of $\dfrac{\partial I}{\partial W}$ is the same as the sign of $1-\mathcal{R}_0$.

Theorem 7.1. *If $\mathcal{R}_0 < 1$ then at the DFE, I becomes positive as W increases from 0, whereas for $\mathcal{R}_0 > 1$, I becomes negative as W increases from 0.*

Corollary 7.2. *If $\mathcal{R}_0 < 1$, there exists $\bar{W} > 0$ such that for $W \in (0, \bar{W})$ an endemic equilibrium exists. Note that $\bar{W} \in (0, \infty]$.*

8. The Disease Model with Stage Progression

We consider the model with staged progression as follows:

$$\begin{aligned}
\frac{dS}{dt} &= \Lambda - (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - dS + pW \\
\frac{dI_1}{dt} &= (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - (\gamma_1 + \mu_1)I_1 + q_1 W \\
\frac{dI_2}{dt} &= \gamma_1 I_1 - (\gamma_2 + \mu_2)I_2 + q_2 W \\
&\vdots \\
\frac{dI_k}{dt} &= \gamma_{k-1} I_{k-1} - \mu_k I_k + q_k W
\end{aligned}$$

We assume that

- $\mu_1, ..., \mu_k \geq d > 0$, and $\Lambda, \gamma_1, ..., \gamma_k > 0$
- $\beta_1, ..., \beta_k$ with $\beta_1 + ... + \beta_k > 0$, $W > 0$
- $q_1, ..., q_k \in [0, 1)$, $p = 1 - q_1, ..., q_k \in [0, 1)$ which implies that $q_1 + ... + q_k > 0$

8.1. **Equilibria.** By using the same mathematical process that we used to prove the existence of a unique solution of SEI, and $SIYR$, we get a unique solution for the stage progression mode. For $W = 0$, there is a DFE that is $(S_0, 0, 0, 0, ..., 0) = (\frac{\Lambda}{d}, 0, 0, 0, ..., 0)$. Now we use the next generation matrix to find $\mathcal{R}_0$. Note that the $\dot{x}_i = f_i(x) = \mathcal{F}_i(x(t)) - \mathcal{V}_i(x(t))$, $i = 1, 2, ..., n$ where $\mathcal{V}_i = \mathcal{V}_i^- - \mathcal{V}_i^+$ satisfies the conditions (A_1) to (A_5) in [19]. We now change the order of the variables to $(I_1, I_2 \ldots, S)$ to agree with the method described in Section 4.1.

$$\mathcal{F} = \begin{bmatrix} (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S \\ 0 \\ 0 \\ \vdots \\ 0 \\ \Lambda - (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - dS \end{bmatrix} \in \mathbb{R}^{k+1}_{>0} \tag{45}$$

and

$$\mathcal{V} = \begin{bmatrix} (\gamma_1+\mu_1)I_1 \\ (\gamma_2+\mu_2)I_2 - \gamma_1 I_1 \\ \vdots \\ \mu_k I_k - \gamma_{k-1} I_{k-1} \\ 0 \end{bmatrix} \in \mathbb{R}^{k+1}_{>0}. \tag{46}$$

Then,

$$F = \begin{bmatrix} S_0\beta_1 & S_0\beta_2 & \cdots & S_0\beta_k \\ 0 & 0 & \cdots & 0 \\ \vdots & \vdots & \cdots & \vdots \\ 0 & 0 & \cdots & 0 \end{bmatrix} = \begin{bmatrix} \frac{\Lambda}{d}\beta_1 & \frac{\Lambda}{d}\beta_2 & \cdots & \frac{\Lambda}{d}\beta_k \\ 0 & 0 & \cdots & 0 \\ \vdots & \vdots & \cdots & \vdots \\ 0 & 0 & \cdots & 0 \end{bmatrix}_{k\times k} \tag{47}$$

and

$$V = \begin{bmatrix} \gamma_1+\mu_1 & 0 & 0 & 0 & \cdots & 0 & 0 \\ -\gamma_1 & \gamma_2+\mu_2 & 0 & 0 & \cdots & 0 & 0 \\ 0 & -\gamma_2 & \gamma_3+\mu_3 & 0 & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \cdots & \gamma_{k-1}+\mu_{k-1} & \vdots \\ 0 & 0 & 0 & 0 & \cdots & -\gamma_{k-1} & \mu_k \end{bmatrix}_{k\times k} \tag{48}$$

and V^{-1} is the upper triangular matrix

$$V^{-1} = \begin{bmatrix} \frac{1}{\gamma_1+\mu_1} & 0 & 0 & \cdots & 0 \\ \frac{\gamma_1}{(\gamma_1+\mu_1)(\gamma_2+\mu_2)} & \frac{1}{\gamma_2+\mu_2} & 0 & \cdots & 0 \\ \frac{\gamma_1\gamma_2}{(\gamma_1+\mu_1)(\gamma_2+\mu_2)(\gamma_3+\mu_3)} & \frac{\gamma_1}{(\gamma_1+\mu_1)(\gamma_2+\mu_2)} & \frac{1}{\gamma_3+\mu_3} & \cdots & 0 \\ \vdots & \vdots & \vdots & \vdots & \\ \frac{\gamma_1\gamma_2\gamma_3\cdots\gamma_{k-1}}{(\gamma_1+\mu_1)(\gamma_2+\mu_2)(\gamma_3+\mu_3)(\gamma_4+\mu_4)\cdots(\mu_k)} & \frac{\gamma_2\gamma_3\cdots\gamma_{k-1}}{(\gamma_2+\mu_2)(\gamma_3+\mu_3)(\gamma_4+\mu_4)\cdots(\mu_k)} & \frac{\gamma_3\cdots\gamma_{k-1}}{(\gamma_3+\mu_3)(\gamma_4+\mu_4)\cdots(\mu_k)} & \cdots & \frac{1}{(\mu_k)} \end{bmatrix}$$

Similar to the calculation of $\mathcal{R}_0$ for the SEI model in Section 5.1, we find that the only non-zero entries of (FV^{-1}) are the first row. Thus all but one of the eigenvalues are 0, and the remaining eigenvalue is given by the $(1,1)$ entry. This eignvalue will be $\mathcal{R}_0$, and so

$$\begin{aligned}\mathcal{R}_0 =& \frac{S_0\beta_1}{(\gamma_1+\mu_1)} + \frac{S_0\beta_2\gamma_1}{(\gamma_1+\mu_1)(\gamma_2+\mu_2)} + \frac{S_0\beta_3\gamma_1\gamma_2}{(\gamma_1+\mu_1)(\gamma_2+\mu_2)(\gamma_3+\mu_3)} \\ &+ \frac{S_0\beta_4\gamma_1\gamma_2\gamma_3}{(\gamma_1+\mu_1)(\gamma_2+\mu_2)(\gamma_3+\mu_3)(\gamma_4+\mu_4)} + ... + \frac{S_0\beta_k\gamma_1...\gamma_{k-1}}{(\gamma_1+\mu_1)(\gamma_2+\mu_2)....(\mu_k)}\end{aligned}$$

The equilibrium equations are in matrix form as follows:

$$\begin{bmatrix} 0 \\ 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix} = W \begin{bmatrix} p \\ q_1 \\ q_2 \\ \vdots \\ q_k \end{bmatrix} + \begin{bmatrix} \Lambda - (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - dS \\ (\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k)S - (\gamma_1+\mu_1)I_1 \\ \gamma_1 I_1 - (\gamma_2+\mu_2)I_2 \\ \vdots \\ \gamma_{k-1}I_{k-1} - \mu_k I_k \end{bmatrix} \tag{49}$$

The next step is to differentiate the equations (55) with respect to W.

$$\begin{aligned}
0 &= p - d\frac{\partial S}{\partial W} - \left[\frac{\partial S}{\partial W}(\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k) + S\left(\beta_1\frac{\partial I_1}{dW} + \beta_2\frac{\partial I_2}{dW} + ... + \beta_k\frac{\partial I_k}{dW}\right)\right] \\
0 &= q_1 + \left[\frac{\partial S}{\partial w}(\beta_1 I_1 + \beta_2 I_2 + \beta_3 I_3 + ... + \beta_k I_k) + S\left(\beta_1\frac{\partial I_1}{dW} + \beta_2\frac{\partial I_2}{dW} + ... + \beta_k\frac{\partial I_k}{dW}\right)\right] \\
&- (\gamma_1+\mu_1)\frac{\partial I_1}{\partial W} \\
0 &= q_2 + \gamma_1\frac{\partial I_1}{\partial W} - (\gamma_2+\mu_2)\frac{\partial I_2}{\partial W} \\
&\vdots \\
0 &= q_k + \gamma_{k-1}\frac{\partial I_{k-1}}{\partial W} - \mu_{k-1}\frac{\partial I_k}{\partial W}.
\end{aligned}$$

Rearranging and evaluating at the DFE with $W = 0$, we have

$$
\begin{aligned}
p &= d\frac{\partial S}{\partial W} + S_0\left(\beta_1\frac{\partial I_1}{dW} + \beta_2\frac{\partial I_2}{dW} + ... + \beta_k\frac{\partial I_k}{dW}\right)\\
q_1 &= -S_0\left(\beta_1\frac{\partial I_1}{dW} + \beta_2\frac{\partial I_2}{dW} + ... + \beta_k\frac{\partial I_k}{dW}\right) + (\gamma_1+\mu_1)\frac{\partial I_1}{\partial W}\\
q_2 &= -\gamma_1\frac{\partial I_1}{\partial W} + (\gamma_2+\mu_2)\frac{\partial I_2}{\partial W}\\
&\vdots\\
q_k &= -\gamma_{k-1}\frac{\partial I_{k-1}}{\partial W} + \mu_{k-1}\frac{\partial I_k}{\partial W}.
\end{aligned}
\tag{50}
$$

Let

$$
A = \begin{bmatrix}
d & S_0\beta_1 & S_0\beta_2 & S_0\beta_3 & \cdots & S_0\beta_k\\
0 & (\gamma_1+\mu_1) - S_0\beta_1 & -S_0\beta_2 & -S_0\beta_3 & \cdots & -S_0\beta_k\\
0 & -\gamma_1 & (\gamma_2+\mu_2) & \cdots & 0 & 0\\
\vdots & \vdots & \vdots & \vdots & \vdots & 0\\
0 & 0 & 0 & \cdots & -\gamma_{k-1} & \mu_k
\end{bmatrix}. \tag{51}
$$

Note that the bottom right $k \times k$ block of A is equal to $V - F$. Putting Equation (50) in to matrix form, we have

$$
A\begin{bmatrix}
\frac{\partial S}{\partial W}\\
\frac{\partial I_1}{\partial W}\\
\vdots\\
\frac{\partial I_k}{\partial W}
\end{bmatrix} = \begin{bmatrix}
p\\
q_1\\
\vdots\\
q_k
\end{bmatrix}. \tag{52}
$$

Our goal is to see the sign of $\frac{\partial I_j}{\partial W}$, for $j = 1, 2, 3, ...k$. The inverse of A is

$$
A^{-1} = \begin{bmatrix}
\frac{1}{d} & \vec{U}\\
0 & \\
\vdots & (V-F)^{-1}\\
0 &
\end{bmatrix},
$$

where $\vec{U} = -\frac{S_0}{d}[\beta_1, ..., \beta_k](V-F)^{-1}$. Then,

$$\begin{bmatrix} \frac{\partial S}{\partial W} \\ \\ \frac{\partial I_1}{\partial W} \\ \\ \vdots \\ \frac{\partial I_k}{\partial W} \end{bmatrix} = A^{-1} \begin{bmatrix} p \\ \\ q_1 \\ \\ \vdots \\ q_k \end{bmatrix} = \begin{bmatrix} \frac{1}{d} & \vec{U} \\ 0 & \\ \vdots & (V-F)^{-1} \\ 0 & \end{bmatrix} \begin{bmatrix} p \\ \\ q_1 \\ \\ \vdots \\ q_k \end{bmatrix}. \tag{53}$$

Due to the zeros in the first column of A^{-1}, the bottom k rows of (53) can be written as

$$\begin{bmatrix} \frac{\partial I_1}{\partial W} \\ \\ \frac{\partial I_2}{\partial W} \\ \\ \vdots \\ \frac{\partial I_k}{\partial W} \end{bmatrix} = (V-F)^{-1} q_i,$$

where

$$q_i = \begin{bmatrix} p \\ \\ q_1 \\ \\ \vdots \\ q_k \end{bmatrix}.$$

Here we consider two cases : $\mathcal{R}_0 < 1$ and $\mathcal{R}_0 > 1$

Theorem 8.1. *If $\mathcal{R}_0 < 1$, then the DFE moves to $\mathbb{R}^{k+1}_{>0}$ as W increases from 0:*

$$\begin{bmatrix} \dfrac{\partial I_1}{\partial W} \\ \dfrac{\partial I_2}{\partial W} \\ \vdots \\ \dfrac{\partial I_k}{\partial W} \end{bmatrix}_{W=0} = (V-F)^{-1}q > 0.$$

Theorem 8.2. *If $\mathcal{R}_0 > 1$, then the DFE moves away from $\mathbb{R}^{k+1}_{\geq 0}$ as W increases from 0:*

$$\begin{bmatrix} \dfrac{\partial I_1}{\partial W} \\ \dfrac{\partial I_2}{\partial W} \\ \vdots \\ \dfrac{\partial I_k}{\partial W} \end{bmatrix}_{W=0} \notin \mathbb{R}^{k+1}_{\geq 0}.$$

.

The proofs of Theorems 8.1 and 8.2 are omitted because these theorems special cases of Theorems 9.2, in Chapter 8.

Corollary 8.3. *If $\mathcal{R}_0 < 1$, there exists $\bar{W} > 0$ such that for $W \in (0, \bar{W})$ an endemic equilibrium exists. Note that $\bar{W} \in (0, \infty]$.*

9. General Disease Model with Immigration

Consider a disease model with immigration given by the differential equation

$$\dot{x} = f(x(t)) + Wq \tag{54}$$

where W is the immigration rate and $q = [q_1, q_2, \cdots, q_k]^T$ gives the fractions of immigrants that enter the different classes. Moreover, q_i includes the infected immigration individuals that are $q_1, q_2, ..., q_n$, and q_j the uninfected immigration individuals $q_{n+1}..., q_k$.

If one or more of $q_1, q_2, \cdots, q_n$ is non-zero for $W > 0$, then there is no DFE and there is an endemic equilibria for all $\mathcal{R}_0$. To do this, we focus on the signs of the derivatives of the infected variables (at equilibrium) with respect to W.

An equilibrium $\bar{x}$ is now a function at W. We are interested in the curve of equilibria that gives the DFE when $W = 0$. That is, $\bar{x}_1(0) = \bar{x}_2(0) = \cdots = \bar{x}_n(0) = 0$.

Figure [8] shows the location of the equilibrium of the SEI model without immigration class in the yellow line. However, when the immigration rate W increases above zero in the SEI model, the sign of the derivative of the equilibrium values of the infected variables E, I with respect to W changes as $\mathcal{R}_0$ becomes positive when $\mathcal{R}_0 < 1$. Otherwise it becomes negative, as showes in Figure[9]. Thus, the DFE becomes an endemic for $\mathcal{R}_0$ less than one and vanishes for $\mathcal{R}_0$ above one as Figure (10) showes.

To generalize this phenomenon, we work with a more general disease model (19). At this point we add an additional assumption:

(A6) The matrix $(V - F)$ is irreducible.

Condition **(A6)** is used to prove that the DFE moves to $\mathbb{R}^k_{>0}$, when $\mathcal{R}_0 < 1$, whereas, when $\mathcal{R}_0 > 1$ the DFE moves away from $\mathbb{R}^k_{\geq 0}$.

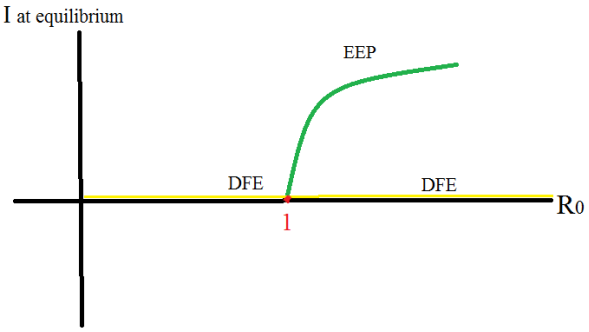

FIGURE 8. Equilibria for the SEI model without immigration.

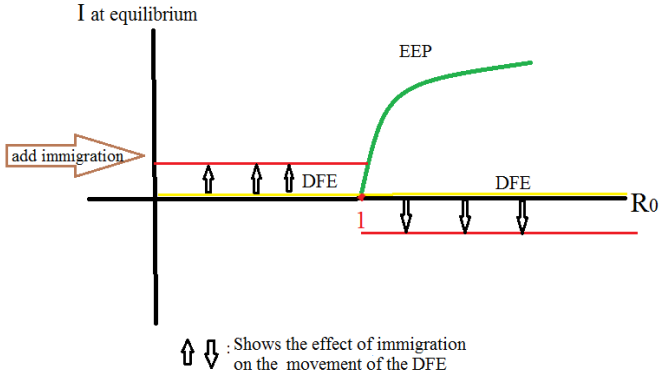

FIGURE 9. Movement of the disease-free equilibrium for the SEI model with immigration as W increases from 0.

(A7) The matrix $(V - F)$ is invertible for $\mathcal{R}_0 \neq 1$, so the inverse of $(V - F)$ exists.

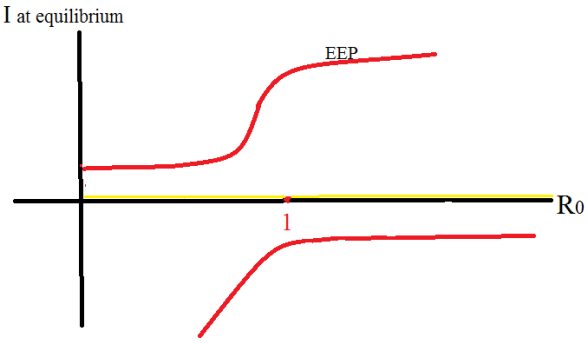

FIGURE 10. Equilibria for the SEI model with immigration for $W \neq 0$.

Combined with **(A1)** $-$ **(A5)**, **(A7)** implies the Jacobian matrix at $\frac{\partial f}{\partial x}|_{W=0|_{DFE}}$ is non-singular for $\mathcal{R}_0 \neq 1$.

In the first part of this thesis, we have shown that the sign of the derivative of the equilibrium values of the infected variables with respect to W for the SEI model depends on $\mathcal{R}_0$. Then, we studied the $SIYR$ disease model with vaccination including immigration and the stage progression model, getting the same result.

We now deal with a general disease model by using the properties of the M-matrices and assumptions **(A1)** to **(A7)**. We show that the phenomenon continues. To do this, we need to consider the two cases $\mathcal{R}_0 < 1$, and $\mathcal{R}_0 > 1$.

The general disease model equation is follows:

$$\dot{x} = f(x(t)) + Wq$$

The equilibrium equation is

$$\vec{0} = f(\bar{x}) + Wq \tag{55}$$

The next step is, by using the Implicit Function Theorem where the equilibrium equation at DFE, $W = 0$, and by assumption **(A7)** then, for $\mathcal{R}_0 \neq 1$, there exists a curve of equilibria $x(W)$ such that $x(0)$ gives the DFE.

Thus, we differentiate the equilibrium equation (55) with respect to W.

$$\vec{0} = \left[\frac{\partial f}{\partial x}(x(W))\right]\left[\frac{\partial x}{\partial W}\right] + q. \tag{56}$$

The $\vec{0}$, q , and $\dfrac{\partial x}{\partial W}$ are $k \times 1$ and $\dfrac{\partial f}{\partial x}(x(W))$ is $k \times k$.

Evaluate Equation (56) at $W = 0$ and DFE.

$$\vec{0} = \left[\frac{\partial f}{\partial x}(DFE)\right]_{W=0}\left[\frac{\partial x}{\partial W}\right]_{W=0} + q. \tag{57}$$

Previously, we have been written the disease model in form that $\dot{x} = f(x) = \mathcal{F}_i(x) - \mathcal{V}_i(x)$, for $i = 1, 2, ..., k$, with $Y = [x_1, x_2, ..., x_n]$ infected variables and $Z = [x_{n+1}, x_{n+2}, ..., x_k]$ uninfected variables.

Then the Jacobian matrix at the DFE with $W = 0$ is

$$J = \begin{bmatrix} F & 0 \\ 0 & 0 \end{bmatrix} - \begin{bmatrix} V & 0 \\ J_3 & J_4 \end{bmatrix}, \tag{58}$$

where F and V are $n \times n$. Substituting the block Jacobian matrix into (57), we have

$$\vec{0} = \begin{bmatrix} F - V & 0 \\ -J_3 & -J_4 \end{bmatrix}\begin{bmatrix} \dfrac{\partial Y}{\partial W} \\ \dfrac{\partial Z}{\partial W} \end{bmatrix} + \begin{bmatrix} Q \\ Q_0 \end{bmatrix}, \tag{59}$$

where

$$\frac{\partial Y}{\partial W} = \begin{bmatrix} \dfrac{\partial x_1}{\partial W} \\ \dfrac{\partial x_2}{\partial W} \\ \vdots \\ \dfrac{\partial x_n}{\partial W} \end{bmatrix}_{W=0} (DFE), \qquad \frac{\partial Z}{\partial W} = \begin{bmatrix} \dfrac{\partial x_{n+1}}{\partial W} \\ \dfrac{\partial x_{n+2}}{\partial W} \\ \vdots \\ \dfrac{\partial x_k}{\partial W} \end{bmatrix}_{W=0} (DFE),$$

and

$$Q = \begin{bmatrix} q_1 \\ q_2 \\ \vdots \\ q_n \end{bmatrix}, \qquad Q_0 = \begin{bmatrix} q_{n+1} \\ q_{n+2} \\ \vdots \\ q_k \end{bmatrix}$$

The first row of (59) gives us

$$\vec{0} = (F - V)\frac{\partial Y}{\partial W} + Q.$$

$$(V - F)\frac{\partial Y}{\partial W} = Q.$$

$$\frac{\partial Y}{\partial W} = (V - F)^{-1}Q.$$

Now, we want to determine the signs of the enteries of $(V - F)^{-1}Q$, to learn how the DFE moves when W is increased from 0.

We have shown:

Proposition 9.1.
- *If $(V - F)^{-1}Q \in \mathbb{R}^n_{>0}$, then the DFE move to $\mathbb{R}^k_{>0}$ as W increases from 0.*
- *If $(V - F)^{-1}Q \notin \mathbb{R}^n_{\geq 0}$, then the DFE move away from $\mathbb{R}^n_{>0}$ as W increases from 0.*

Theorem 9.2. *If $\mathcal{R}_0 < 1$, then the DFE moves to $\mathbb{R}^k_{>0}$ as W increases from 0.*

Proof. From Lemma 4.19 we have V is a non-singular M-matrix, and $F \geq 0$. Also, by assumption, we assum that $q \in \mathbb{R}^k_{\geq 0}$, with $Q \neq \vec{0}$. And $(V - F)$ is irreducible.

Since we know that V is a non-singular M-matrix, and by using Theorem 4.16, we have that $V^{-1} \geq 0$, and it follows that $FV^{-1} \geq 0$. By Theorem 4.12 we have that $\rho(FV^{-1})$ is the dominant eigenvalue of FV^{-1}. $\mathcal{R}_0$ has been defined as the spectral radius of the next

generation matrix (i.e. $\mathcal{R}_0 = \rho(FV^{-1})$), in Definition 4.11. In our case, we have $\mathcal{R}_0 < 1$, so this requires $\rho(FV^{-1}) < 1$.

If Ω is an eigenvalue of (FV^{-1}), then $-1 < Re(\Omega) < 1$. Let $\lambda = -\Omega$. Then λ is an eigenvalue of $-(FV^{-1})$. Moreover, for any eigenvalue λ of $-(FV^{-1})$, we have $-1 < Re(\lambda) < 1$.

From linear algebra we knew that if we have a matrix C with an eigenvalue Λ, and identity matrix I, then $\bar{\Lambda} = \Lambda + 1$ is an the eigenvalue of $I + C$.

Applying this knowledge with $C = -(FV^{-1})$, and for any eigenvalue λ of $-(FV^{-1})$, it follows that if $\bar{\lambda}$ is an eigenvalue of $(I - FV^{-1})$, then $0 < Re(\lambda) < 2$. From $0 < Re(\lambda) < 2$, we know that $(I - FV^{-1})$ is non-singular.

By using Definition 4.13 of an M-matrix, with $B = FV^{-1} \geq 0$ and $s = 1 > \mathcal{R}_0 = \rho(FV^{-1})$, we know that $I - FV^{-1}$ is an M-matrix, which we have already shown is non-singular. By using Lemma 4.20 part (i), with $H = V$ and $K = F$ we see that $(V - F)$ is also a non-singular M-matrix.

Since $(V - F)$ is an irreducible M-matrix, it follows from Theorem 4.18, that $(V - F)^{-1} > 0$, that is, each entry of $(V - F)^{-1}$ is strictly positive.

Since $Q \in \mathbb{R}^n_{\geq 0}$, with $Q \neq 0$, we can now say that $(V - F)^{-1}Q \in \mathbb{R}^n_{>0}$. Thus, the theorem follows from Proposition 9.1.

□

Proposition 9.3. *If A is an M-matrix, then each eigenvalue of A has non-negative real part.*

Proof. Suppose A is an M-matrix 4.13, then there exist matrix B with $B \geq 0$ and $s \geq \rho(B)$ such that $A = sI - B$. The eigenvalue of B are $\lambda_1, \lambda_2. \cdots, \lambda_n$. then $|\lambda_j| \leq \rho(B)$ for all $j = 1, 2, \cdots, n$. Then $-\rho(B) \leq Re(\lambda_j) \leq \rho(B)$. Then

$$Re(\lambda_j) \leq \rho(B),$$

since $s \geq \rho(B)$

$$0 \leq s - \rho(B) \leq s + Re(-\lambda_j) \leq s + \rho(B).$$

Note that the eigenvalue of A is $\bar{\lambda}_j = s - \lambda_j$ for $j = 1, 2, \cdots, n$. It follows that

$$Re(\bar{\lambda}_j) = Re(s - \lambda_j) = s - Re(\lambda_j) \geq s - \rho(B) \geq 0$$

□

Proposition 9.4. *Suppose V is a non-singular M-matrix, $F \geq 0$, and $\rho(FV^{-1}) > 1$. Then $V - F$ is not an M-matrix.*

Proof. Theorem 4.16 implies $V^{-1} \geq 0$. Thus $FV^{-1} \geq 0$. Let $r = \rho(FV^{-1}) > 1$. Then, Theorem 4.12 implies r is an eigenvalue of FV^{-1}. Thus, $1 - r < 0$ is an eigenvalue of $I - FV^{-1}$, and so Proposition 9.3 implies $I - FV^{-1}$ is not an M-matrix. Therefore, by Lemma 4.20, $V - F$ is not an M-matrix.

□

Theorem 9.5. *If $\mathcal{R}_0 > 1$, then the DFE moves away from $\mathbb{R}^n_{\geq 0}$ as W increases from 0.*

Proof. By Proposition 9.4, $V - F$ is not an M-matrix. However, $V - F$ is irreducible Z-matrix. So, Theorem 4.16 implies the following

$$\text{if } \vec{u} \in \mathbb{R}^n_{\geq 0}, \text{ then } (V - F)\vec{u} \notin \mathbb{R}^n_{>0}. \tag{60}$$

Suppose $\dfrac{\partial Y}{\partial W}$ is in the interior of $\mathbb{R}^n_{\geq 0}$ i.e. $\dfrac{\partial Y}{\partial W} \in \mathbb{R}^n_{>0}$. We have $(V - F)\dfrac{\partial Y}{\partial W} = Q \in \mathbb{R}^n_{\geq 0}$. In order to not contradict (60), we must have Q lying on the boundary of $\mathbb{R}^n_{\geq 0}$. Let $N \subseteq \mathbb{R}^n_{>0}$ be a neighborhood of $\dfrac{\partial Y}{\partial W}$. Then by continuity there exist $\vec{u}_1 \in N \subseteq \mathbb{R}^n_{>0}$ such that

$(V-F)\vec{u}_1 \in \mathbb{R}^n_{>0}$, but now this contradicts (60). Thus, we can not have $\dfrac{\partial Y}{\partial W} \in \mathbb{R}^n_{>0}$.

Now suppose $\dfrac{\partial Y}{\partial W}$ is in the boundary of $\mathbb{R}^n_{\geq 0}$. Since $(V-F)\dfrac{\partial Y}{\partial W} = Q \neq \vec{0}$, we know that $\dfrac{\partial Y}{\partial W} \neq \vec{0}$. Without the loss of generality

$$\frac{\partial Y}{\partial W} = \begin{bmatrix} g_1 \\ g_2 \\ \vdots \\ g_p \\ 0 \\ \vdots \\ 0 \end{bmatrix} \in \mathbb{R}^n_{\geq 0},$$

with $1 \leq p < n$, and $g_1, g_2, \cdots, g_p > 0$.

Rewrite $(V-F)$ as

$$(V-F) = \begin{bmatrix} A & B \\ C & D \end{bmatrix},$$

where A is $p \times p$ and D is $(n-p) \times (n-p)$. Then by using the Definition 4.14 of a

Z-matrix, we have B,C ≤ 0 , but not equal to zero since $(V - F)$ is irreducible. Also, let

$$G = \begin{bmatrix} g_1 \\ g_2 \\ \vdots \\ g_p \end{bmatrix} \in \mathbb{R}^p_{>0}.$$

Then

$$Q = (V - F)\frac{\partial Y}{\partial W} = \begin{bmatrix} A & B \\ C & D \end{bmatrix} \begin{bmatrix} G \\ \vec{0} \end{bmatrix} = \begin{bmatrix} AG \\ CG \end{bmatrix}$$

Note that $C \leq 0$, but $C \neq 0$, and $G > 0$, so CG has at least one negative entry. This contradicts the fact that $Q \in \mathbb{R}^n_{\geq 0}$, thus, we cannot have $\frac{\partial Y}{\partial W} \in \mathbb{R}^n_{\geq 0}$. Therefore, $\frac{\partial Y}{\partial W} \notin \mathbb{R}^n_{\geq 0}$. Thus, as W increases from 0, the DFE move away from $\mathbb{R}^n_{\geq 0}$.

□

Corollary 9.6. *If $\mathcal{R}_0 < 1$, there exists $\bar{W} > 0$ such that for $W \in (0, \bar{W})$ an endemic equilibrium exists. Note that $\bar{W} \in (0, \infty]$.*

10. The Disease Model with Age-of-Infection

10.1. **Introduction.** In the ODE disease models, we have seen that all members of a population sub-group (susceptible, exposed, infectious, vaccinated, or recovered) are assumed to be interchangeable. Adding more structure to simple disease models helps to achieve an understanding of complex disease systems. An example of this structure is the Stage Progression disease model that has multiple classes of infection which addresses more complicated diseases. One of the significant structures is age-of-infection; this characteristic in modeling of infectious disease is important in a different respect. For many diseases, parameters such as the level of infectiousness are a function of how long an individual has had the disease, that is, the individual's age-of-infection.

Consider the disease transmission model that depending on the age of infection studies in [15], where the age of the infection$a$ is $a \geq 0$. In fact, different age of infections allows to different interpretations of the transmission of the disease. In [15] , the paper analysed the stability of the age of infection model. It shows that the disease-free equilibrium is globally asymptotically stable for $\mathcal{R}_0 < 1$. Furthermore, when $\mathcal{R}_0 > 1$ the model has an endemic equilibrium, which is locally asymptotically stable.

However, including immigration of infected individuals affects the DFE in disease models, as we have seen in previous chapters. Adding an age characteristic to an immigration disease model is a great tool for extending the phenomenon described in Chapter 8. Therefore, the disease model in this chapter is different from earlier models. Indeed, the age-of-infection model has a partial differential equation [3], [11].

Addressing age structure in the study of disease models can lead to important information that helps to develop the public health in general.

In this chapter, we study the age-of-infection disease model, and its equilibria. After that, we study the impact of immigration on the DFE of the age-of-infection model.

10.2. **The Model of Age-of-Infection.** Consider the following SI disease model with age-of-infection.

$$\frac{dS}{dt} = \Lambda - \mu S - \int_{a=0}^{\infty} \beta(a)S(t)i(t,a)da$$

$$\frac{\partial i}{\partial t} + \frac{\partial i}{\partial a} = -(\mu + d(a))i(t,a) \tag{61}$$

$$i(t,0) = \int_{a=0}^{\infty} \beta(a)S(t)i(t,a)da$$

In this model $S(t) \in \mathbb{R}_{\geq 0}$, and $i(t,.) \in C^1(\mathbb{R}_{\geq 0}, \mathbb{R}_{\geq 0})$ with $\int_{a=0}^{\infty} i(t,a)da < \infty$ for each t. The state space is

$$X = \mathbb{R}_{\geq 0} \times \left\{ y \in C^1(\mathbb{R}_{\geq 0}, \mathbb{R}_{\geq 0}) | \int_{a=0}^{\infty} y(t,a)da < \infty \right\}$$

$a \in [0, \infty)$ shows how long the infected individuals have been infected, and $i(t,a)$ gives the density of individuals that have been infected for duration a at time t. Compared with an ODE version of the model, we have replaced I by i since $I = \int_0^{\infty} i(t,a)da$ gives the total number of infected individuals at time t.

10.3. **Equilibria.** The equilibria of Equation (61), are the solutions that do not depend on t. If $\bar{X} = (\bar{S}, \bar{i}(.))$ is an equilibrium, then $\bar{X}$ is a constant solution, with $S(t) = \bar{S}$ for all t, and $i(t,a) = \bar{i}(a)$ for all t. In order to determine the DFE and the endemic equilibrium point (EEP), we solve the following equations:

$$0 = \Lambda - \mu\bar{S} - \int_{a=0}^{\infty} \beta(a)\bar{S}\bar{i}(a)da$$

$$\frac{\partial \bar{i}}{\partial a} = -(\mu + d(a))\bar{i}(a) \tag{62}$$

$$\bar{i}(0) = \int_{a=0}^{\infty} \beta(a)\bar{S}\bar{i}(a)da$$

Combining the first and the third equations, we get

$$\bar{i}(0) = \Lambda - \mu\bar{S} \tag{63}$$

We want to find the value of $\bar{i}(a)$ in terms of $\bar{i}(0)$, so we solve the second equation, which is a homogeneous linear equation, using the intergrating factor:

$$u(a) \;=\; e^{-\int_0^a(\mu+d(\tau))d\tau}. \tag{64}$$

We find

$$\bar{i}(a) \;=\; \bar{i}(0)e^{-\int_0^a(\mu+d(\tau))d\tau}.$$

Then we substitute $\bar{i}(0)$ given in (63), to have

$$\bar{i}(a) \;=\; (\Lambda - \mu\bar{S})e^{-\int_0^a(\mu+d(\tau))d\tau}.$$

Filling $\bar{i}(0)$ and $\bar{i}(a)$ into the third equation of (62), we get

$$\Lambda - \mu\bar{S} = \bar{S}\int_{a=0}^{\infty}\beta(a)(\Lambda - \mu\bar{S})e^{-\int_0^a(\mu+d(\tau))d\tau}da \tag{65}$$

Then, we have two cases:
Case 1: If $\Lambda - \mu\bar{S} = 0$,then $\bar{S} = \frac{\Lambda}{\mu}$. This gives the DFE as $(\bar{S}, \bar{i}(a)) = \left(\frac{\Lambda}{\mu}, 0\right)$.
Case 2: If $\Lambda - \mu\bar{S} \neq 0$, then equation (65) becomes $1 = \bar{S}\int_{a=0}^{\infty}\beta(a)e^{-\int_0^a(\mu+d(\tau))d\tau}da$.
Therefore $\bar{S} = \dfrac{1}{\int_{a=0}^{\infty}\beta(a)e^{-\int_0^a(\mu+d(\tau))d\tau}da}$.

Let

$$\mathcal{R}_0 = \frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)e^{-\int_0^a(\mu+d(\tau))d\tau}da. \tag{66}$$

Then, the EEP is $(\bar{S}, \bar{i}(a)) = \left(\frac{\Lambda}{\mu}.\frac{1}{\mathcal{R}_0}, \frac{\Lambda(\mathcal{R}_0-1)}{\mathcal{R}_0}e^{-\int_0^a(\mu+d(\tau))d\tau}\right)$

10.4. **The Disease Model of Age Structure with Immigration.** If we add immigration to Equation (61), we get

$$\begin{aligned} \frac{dS}{dt} &= \Lambda + qW - \mu S - \int_{a=0}^{\infty} \beta(a)S(t)i(t,a)da \\ \frac{\partial i}{\partial t} + \frac{\partial i}{\partial a} &= q(a)W - (\mu + d(a))i(t,a)) \\ i(t,0) &= rW + \int_{a=0}^{\infty} \beta(a)S(t)i(t,a)da, \end{aligned}$$

where W is the total immigration rate, $q(a) \geq 0$ is the rate of immigration with infection of age a with $r = q(0)$, and $q \geq 0$ is the immigration rate of susceptibles with the assumption that

$$q + \int_0^{\infty} q(a)da = 1.$$

10.5. **Equilibria.** At an equilibrium $\bar{X}$ we have

$$0 = \Lambda + qW - \mu\bar{S} - \int_{a=0}^{\infty} \beta(a)\bar{S}\bar{i}(a)da \tag{67}$$

$$\frac{\partial \bar{i}}{\partial a} = q(a)W - (\mu + d(a))\bar{i}(a)) \tag{68}$$

$$\bar{i}(0) = rW + \int_{a=0}^{\infty} \beta(a)\bar{S}\bar{i}(a)da \tag{69}$$

Solving equation (68), which is a non-homogeneous linear equation, we obtain

$$\bar{i}(a) = \bar{i}(0)e^{-\int_0^a (\mu + d(\tau))d\tau} + \frac{\Gamma(a,W)}{u(a)},$$

where $u(a)$ is the integrating factor in (64), and $\Gamma(a,W) = \int_{\tau=0}^{a} q(\tau)Wu(\tau)d\tau$. Combining (67) and (69), we get

$$\bar{i}(0) = \Lambda - \mu\bar{S} + qW + rW$$

Therefore,

$$\bar{i}(a) = (\Lambda - \mu\bar{S} + qW + rW)e^{-\int_0^a(\mu+d(\tau))d\tau} + \frac{\Gamma(a,W)}{u(a)}.$$

By substituting $\bar{i}(a)$ and $\bar{i}(0)$ in Equation (69), we get

$$\Lambda - \mu\bar{S} + qW + rW = rW + \bar{S}\int_{a=0}^{\infty}\beta(a)\left[(\Lambda - \mu\bar{S} + qW + rW)e^{-\int_0^a(\mu+d(\tau))d\tau} + \frac{\Gamma(a,W)}{u(a)}\right]da$$

As a result,

$$\begin{aligned}\Lambda - \mu\bar{S} + qW + rW = rW + \bar{S}(\Lambda - \mu\bar{S} + qW + rW)\int_{a=0}^{\infty}\beta(a)e^{-\int_0^a(\mu+d(\tau))d\tau}da \\ + \bar{S}\int_{a=0}^{\infty}\beta(a)\frac{\Gamma(a,W)}{u(a)}da\end{aligned} \tag{70}$$

Let

$$A = \int_{a=0}^{\infty}\beta(a)e^{-\int_0^a(\mu+d(\tau))d\tau}da,$$

and

$$B = \int_{a=0}^{\infty}\beta(a)\frac{\Gamma(a,W)}{u(a)}da.$$

Substituting A and B in equation (70), we get a quadratic in $\bar{S}$. Then $\bar{S}$ is a solution of (70) if and only if it is a zero of $f(\bar{S})$, where

$$f(\bar{S}) = -(\Lambda + qW) + ((\Lambda + qW + rW)A + B + \mu)\bar{S} - \mu A\bar{S}^2.$$

To ensure $\bar{S} \geq 0$, and $\bar{i}(0) \geq 0$, we must have $0 \leq \bar{S} \leq \dfrac{\Lambda + qW + rW}{\mu}$. Evaluating the function f at 0 and $\dfrac{\Lambda + qW + rW}{\mu}$ gives

$$f(0) = -\Lambda - qW < 0,$$

and

$$\begin{aligned} f\left(\frac{\Lambda + qW + rW}{\mu}\right) &= -(\Lambda + qW) + ((\Lambda + qW + rW)A + B + \mu)\left(\frac{\Lambda + qW + rW}{\mu}\right) \\ &- \left(\frac{(\Lambda + qW + rW)^2}{\mu}\right)A \\ &= -(\Lambda + qW) + (B + \mu)\frac{\Lambda + qW + rW}{\mu} \\ &= B\frac{\Lambda + qW + rW}{\mu} + rW \\ &> 0 \end{aligned}$$

By the Intermediate Value Theorem, there exists $\bar{S}$ with $0 < \bar{S} < \dfrac{\Lambda + qW + rW}{\mu}$ such that $f(\bar{S}) = 0$. Since f is quadratic in $\bar{S}$, f has a unique zero in that interval. Thus, the system has a unique equilibrium when $W > 0$, with

$$\bar{i}(0) = \Lambda - \mu\bar{S} + qW + rW,$$

and

$$\bar{i}(a) = (\Lambda - \mu\bar{S} + qW + rW)e^{-\int_0^a (\mu + d(\tau))d\tau} + \frac{\Gamma(a, W)}{u(a)} > 0.$$

10.6. **The Impact of Immigration in the Disease Model of Age Structure.** If we differentiate the Equations (67, 68, 69) with respect to W at the DFE $(\bar{S}, \bar{i}(a)) = \left(\frac{\Lambda}{\mu}, 0\right)$, with $W = 0$ we get,

$$\begin{aligned} 0 &= q - \mu\frac{\partial \bar{S}}{\partial W} - \frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)\frac{\partial \bar{i}(a,0)}{\partial W}da \\ \frac{\partial^2 \bar{i}(a,0)}{\partial W \partial a} &= q(a) - (\mu + d(a))\frac{\partial \bar{i}(a,0)}{\partial W} \\ \frac{\partial \bar{i}(0,0)}{\partial W} &= r + \frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)\frac{\partial \bar{i}(a,0)}{\partial W}da. \end{aligned}$$

Rearranged, we have

$$q = \mu\frac{\partial \bar{S}}{\partial W} + \frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)\frac{\partial \bar{i}(a,0)}{\partial W}da \tag{71}$$

$$q(a) = (\mu + d(a))\frac{\partial \bar{i}(a,0)}{\partial W} + \frac{\partial^2 \bar{i}(a,0)}{\partial W \partial a} \tag{72}$$

$$r = \frac{\partial \bar{i}(0,0)}{\partial W} - \frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)\frac{\partial \bar{i}(a,0)}{\partial W}da \tag{73}$$

Solve (72), by letting $Y(a) = \frac{\partial \bar{i}(a,0)}{\partial W}|_{W=0}$, then $Y(0) = \frac{\partial \bar{i}(0,0)}{\partial W}|_{DFE}$. Then equation (72) becomes a non-homogeneous equation for Y with the solution

$$Y(a) = Y(0)e^{-\int_0^a(\mu+d(\tau))d\tau} + \int_0^a e^{-\int_\sigma^a(\mu+d\tau)d\tau}q(\sigma)d\sigma.$$

$$Y(a) = \frac{\partial \bar{i}(0,0)}{\partial W}|_{DFE}\ e^{-\int_0^a(\mu+d(\tau))d\tau} + \int_0^a e^{-\int_\sigma^a(\mu+d\tau)d\tau}q(\sigma)d\sigma.$$

Let $Z(a) = \int_0^a e^{-\int_\sigma^a(\mu+d(\tau))d\tau}q(\sigma)d\sigma$. Then

$$Y(a) = \frac{\partial \bar{i}(a,0)}{\partial W} = \frac{\partial \bar{i}(0,0)}{\partial W}e^{-\int_0^a(\mu+d(\tau))d\tau} + Z(a). \tag{74}$$

Therefore, from (74) we can substitute $\frac{\partial \bar{i}(a,0)}{\partial W}$ into equations (71) and (73) to get the following

$$\begin{aligned} q&= \mu\frac{\partial \bar{S}}{\partial W}+\frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)\left(\frac{\partial \bar{i}(0,0)}{\partial W}e^{-\int_0^a(\mu+d(\tau))d\tau}+Z(a)\right)da \\ r&= \frac{\partial \bar{i}(0,0)}{\partial W}-\frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)\left(\frac{\partial \bar{i}(0,0)}{\partial W}e^{-\int_0^a(\mu+d(\tau))d\tau}+Z(a)\right)da \end{aligned} \tag{75}$$

Using $\mathcal{R}_0$ that given in (66) to simplify (75), we get

$$\begin{aligned} q&= \mu\frac{\partial \bar{S}}{\partial W}+\mathcal{R}_0\frac{\partial \bar{i}(0,0)}{\partial W}+\frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)Z(a)da \\ r&= \frac{\partial \bar{i}(0,0)}{\partial W}-\mathcal{R}_0\frac{\partial \bar{i}(0,0)}{\partial W}-\frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)Z(a))da \end{aligned} \tag{76}$$

Let

$$Z^*=\frac{\Lambda}{\mu}\int_{a=0}^{\infty}\beta(a)Z(a)da$$

Then the equation (76) becomes

$$\begin{aligned} q-Z^*&= \mu\frac{\partial \bar{S}}{\partial W}+\mathcal{R}_0\frac{\partial \bar{i}(0,0)}{\partial W} \\ r+Z^*&= \frac{\partial \bar{i}(0,0)}{\partial W}-\mathcal{R}_0\frac{\partial \bar{i}(0,0)}{\partial W}. \end{aligned} \tag{77}$$

The second line of (77) gives

$$\frac{\partial \bar{i}(0,0)}{\partial W}=\frac{r+Z^*}{1-\mathcal{R}_0}$$

Here we have two cases.

Theorem 10.1. *If $\mathcal{R}_0 < 1$, then the DFE moves to the interior of X as W increases from 0.*

Theorem 10.2. *If $\mathcal{R}_0 > 1$, then the DFE moves away from X as W increases from 0.*

Corollary 10.3. *If $\mathcal{R}_0 < 1$, there exists $\bar{W} > 0$ such that for $W \in (0, \bar{W})$ an endemic equilibrium exists. Note that $\bar{W} \in (0, \infty]$.*

11. Conclusion

11.1. **Mathematical Discussion.** We have studied the stability of the SEI disease model. In fact, there exists a unique solution for the SEI model without immigration. We proved the dynamic stability of the disease models by using the basic reproduction number $\mathcal{R}_0$. In the case of an absence of the infected individual in the disease model, we found that the disease free-equilibrium is locally asymptotically stable when $\mathcal{R}_0 < 1$ whereas, at $\mathcal{R}_0 > 1$ the DFE becomes unstable. However, when the infected individuals are introduced to the disease model $I > 0$, we have found that there are two equilibria to the SEI model. For $\mathcal{R}_0 > 1$, an endemic equilibrium exists and is locally asymptotically stable.

In the general disease model with immigration, we studied the model to determine the existence of endemic equilibrium by studying the behaviour of the disease-free equilibrium when the immigration individuals enter the model. Therefore, we have studied the sign of the derivative of the infected variables at disease-free equilibria with respect to immigration $W_{|_0}$ as a function of the basic reproduction number $\mathcal{R}_0$. We found that for $\mathcal{R}_0 < 1$, the sign becomes positive which means the disease equilibrium moves to the interior of the positive cone as immigration increases from zero, so the DFE approach to endemic equilibrium is $W > 0$. In fact, the DFE does not exist for the general class of disease transmission models as $W > 0$. However, when $\mathcal{R}_0 > 1$, we have a negative sign at DFE which means the DFE equilibrium vanishes.

Movement of the DFE towards an endemic equilibrium is a phenomenon that comes into existence of an endemic point for general disease transmission. Indeed, the forward bifurcation of the DFE in Figure (10) illustrates this phenomenon of the existence of an endemic equilibrium that the DFE approaches. This also applies to backward bifurcation. Since this phenomenon occurs in general disease models involving ordinary differential equations, we are studying the age of infection model that has partial differential equations. We have achieved some results, thus, the phenomenon occurs in the age of infection disease model with immigration.

11.2. **Biological Discussion.** Biologically, the population that has been exposed to infectious disease then spreads this disease among the population due to contact with the susceptible individuals. When the population is free from the infected individuals, the introduction of a single infected in the population with an average that one single infected can infect fewer individuals which means the disease can not invade the population. Thus, the population becomes stable at this level because the disease dies out. In contrast, if there is a higher chance for the susceptible to be infected by single infected individuals which means single infected individual can able to be infected many susceptible individuals, then the disease has transmitted through the population. The immigration occurs when one or more individuals enter the population from the outside. Since some of them may be infected with infectious disease, this situation puts the health of the community at risk.

If there is an infected immigration entering the population through any sources such as airports or from different destinations, then the disease is transmitted among individuals and then the number of infected increases. In this case, the disease-free state becomes endemic as the infected immigration increases. Then, the disease-free state vanishes. Therefore, the population in a state that is free of disease becomes a population that has an endemic or an epidemic disease. Indeed, changing the situation of the population occurs even if there is a different age or level of infection. This situation flares up in a lot of countries around the word. Thus, controlling disease becomes an important issue that needs to be considered by health organizations in order to maintain the health of a society.

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