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A “$SE(QF)(IH)R$” Approach to the Introducing New “Pandemic Threshold” and “Pandemic Estimator” Parameters for an Infectious Disease

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Abstract. Using the concept of SIR... systems, we construct the “$SE(QF)(IH)R$” system which simulates patterns of the pandemic by an infectious disease. This system helps us to introduce new “Pandemic Threshold” and “Pandemic Estimator” parameters. We see that these newly defined parameters forecast patterns of the pandemic by the disease. We also show that the “$SE(QF)(IH)R$” system contains two subsystems such that local bifurcations of these subsystems cause local bifurcations of the “$SE(QF)(IH)R$” system. This especially occurs when the “Pandemic Estimator” is greater than the “Pandemic Threshold”. Finally we use the results for influenza. We see that the model can predict probably forthcoming waves of the pandemic and their strength which are depended on the values of the “Pandemic Threshold” and the “Pandemic Estimator” parameters.

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1. Introduction

By the middle years of the last century, the effectiveness of improved antivirals and antibiotics together with the global vaccination programs supported by the world health organization (WHO) created a confidence that the infectious diseases would be soon eliminated. But the infectious diseases have continued to be the major reasons of suffering and mortality and they are still receiving a major part of health budget throughout the globe. Even in 2010 again, WHO warned of a substantial risk of the pandemic by influenza A throughout the globe, including the developed countries.

Today, it is probably well known that the genetical mutation of viruses and the acquisitive immunity of many bacteries against antibiotics are always providing a risk of pandemic by the viral (or bacterial) infections. Moreover, some infectious diseases can adapt and evolve, so that new infectious diseases have emerged and some existing diseases have reemerged [16, 21]; and today we have an exciting account of emergence and detections of new diseases [11]

These facts led scientists to the fact that the infectious diseases will remain in the top of the list of diseases which threat human societies in the next century. This is enough convincing that any development or improvement in the methods which enable us to predict and analyze patterns of the pandemic by an infectious disease, are of the great importance.

In this regard, the mathematical models have become an advanced tool for simulating and analyzing patterns of the pandemic by an infectious diseases. These models formulate assumptions, variables, and parameters such that they can give a mathematical measurement for various aspects of the disease. Furthermore, they provide this opportunity to define, expand and apply conceptual results such as basic reproduction numbers, contact numbers, transmission risk, replacement numbers and many other parameters and variables. This provides the possibility for scientists to build theories, assess quantitative conjectures, answer specific questions, determine sensitivities to changes in parametric values and estimate key parameters from data (see the references specially [3, 11, 18, 19]).

The first mathematical modeling was probably formulated and solved by Daniel Bernoulli in 1760 in order to evaluate the effectiveness of variolation of healthy people with the smallpox virus, but, deterministic epidemiology modeling seems to have been started in the 20th century, so that a tremendous variety of models has now been formulated, analyzed mathematically, and applied to infectious diseases. The most recent epidemiological models are based upon systems of ordinary differential equations (ODEs) dividing the community into several subcommunities , as the variables of the ODEs, indicate susceptible individuals (S), infected individuals (I), recovered individuals (R) and so forth. These systems describe the dynamics of different classes of subpopulations in the model. In this way, acronyms for epidemiological models are often based on the flow patterns between the compartment such as MSEIR, MSEIRS, SEIR, SEIRS, SIR, SIRS, SEI, SI and other similar models. All these and most of the current models are extensions of the SIR model introduced by Kermack and McKendrick in 1927 (see [14, 18]).

In this paper, we impose several substantial assumptions on the SIR system and construct a new model which we name $SE(QF)(IH)R$. The model, as its name indicates, contains seven subcommunities: susceptible individuals, individuals who are exposed to the infection, quarantined individuals, infected individuals who are not quarantined and they are in the latency period, infectious individuals, infected individuals who get hospitality and finally, recovered individuals. Section 2 is devoted to introducing and analyzing the basic properties of the $SE(QF)(IH)R$ system. First, we describe concepts and assumptions of the model and indicate rules by which the subcommunities effect on each other. In order to avoid unnecessary discussions, the mathematical formalizations and biological passibility of the solutions are done in an appendix section at the end of the paper. In the appendix section it will be seen that the $SE(QF)(IH)R$ system has four invariant subspaces, each of them has a biological interpretation. Also we see that the system is biologically passable, that is, any solution with nonnegative initial conditions remains bounded, nonnegative and definable for all positive values of the time variable $t \geq 0$. This is done by defining the nonnegative area of $\mathbb{R}^7$ as the "suitable cone" and introducing the concept of the "suitable solution".

In Section 3, we rescale the parameters and the variables in order to bring the $SE(QF)$ $(IH)R$ system into a dimensionless system. We see that the $SE(QF)(IH)R$ system is decomposed into two subsystems $SQHR$ and EIF perturbing each other through nonlinear terms. This helps us to proceed further analysis in Section 3.

In Section 4, local bifurcations of the dimensionless $SE(QF)(IH)R$ system which is decomposed precisely into two subsystems $SQHR$ and EIF are studied. We see that local bifurcations of the EIF system may cause local bifurcations for the $SE(QF)(IH)R$ system. Indeed, we consider the portion of the quarantined exposed individuals, say a; the average number of contacts between the individuals in the subcommunities, say $\bar{n}$ and the infection transmission risk, say p; as the major parameters and define a new parameter $\theta = (1-a)\,\bar{n}\,p$. Then, we reduce the bifurcation problem of the EIF system into a polynomial equation of the form

$$U(f) = f(\alpha_4 f^4 + \alpha_3 f^3 + \alpha_2 f^2 + \alpha_1 f^1 + \alpha_0) = 0,$$

where f stands for the dimensionless amount of the individuals in the F subcommunity and α_i, $i = 1, 2, 3, 4$, are with respect to the θ and other parameters of the system. It will be seen that there exists a critical value θ_0 such that for $\theta > \theta_0$ a branch of the equilibrium points of $U(f)$ emerges from $f = 0$. This causes in consequence a unique branch of the local singularities for the $SE(QF)(IH)R$ system. This specially occurs when the free singularity of the system has a one dimensional unstable manifold absorbed by this local singularities. This leads us to define two new parameters "Pandemic Threshold" and "Pandemic Estimator" determining the behavior of the system. That is, if the "Pandemic Estimator" is lesser than the "Pandemic Threshold" then the free singularity is a hyperbolic sink. This biologically means that the community eventually gets healing. But if the "Pandemic Estimator" is greater than the "Pandemic Threshold" then the free singularity is a hyperbolic saddle which means biologically that the community will not get healing generally.

Finally in Section 5, as a standard test, we apply the system for simulating patterns of the pandemic by influenza. We will compute the parameters for the disease and discuss about the various values of the parameters and the behavior of the system with respect to them. The results are in adaption with the numerical plots. Also we can see that the model can predict the existence of second and third waves of the pandemic occurring suddenly within forth coming days after the first and second damp of the pandemic. This is in adaption with the experimental observations. Also the strength of this waves is in direct relation with the "Pandemic Estimator" parameter.

We note that, due to the complexity and length of the mathematical computations in some of the formulas in Section 4, we leave long computations whose validity is confirmed through using mathematical softwares, so we present just the results.

2. Introducing the $SE(QF)(IH)R$ system

2.1. Assumptions and conditions

This simulation is based on a few assumptions which we explain here. We assume that there exists an infectious disease with a latency duration in a supposed community. Thus, some of the individuals may be at risk of infection through near contacts with infective individuals. We assume that the community has a health system quarantining and providing hospitality for infected individuals. Indeed, the health system distinguishes some of the individuals who are infected or exposed to the infection and keeps the infected individuals in the hospitality and quarantines the exposed individuals. After the latency period, that part of the quarantined individuals who are infected will be kept in the hospitality and the rest of them remain susceptible. Also some of the hospitaled individuals will get full recovery and they will remain immune to the infection for a while. On the other hand, we assume that there exist individuals exposed to the infection but they are not distinguished and quarantined by the health system. Naturally a part of these individuals are infected. They are not infective in the latency period, but after that, they are infective and may disperse the disease through near contacts with the susceptible individuals. Naturally, we assume that some of these infective individuals will get the hospitality after the latency period [1], but probably, rest of them will be never observed so they remain infectious. Also a portion of these individuals will get full recovery and they will remain immune to the disease for a while. Obviously, if the individuals from the recovered subgroups contact with the infective individuals they will not get infection; hence the exposed individuals from this subgroup return to this subgroup totally. Finally we assume that the recovered individuals will lose their immunity after a while and they will be susceptible again. These assumptions yield that, at any time, our community consists of at least six coexisting subcommunities:

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[1] However, this portion is still infectious in the time between the end of the latency period and getting the hospitality.

1. The susceptible individuals who have not any specific immunity against the disease. We denote this subcommunity by S.
2. The quarantined individuals containing a portion of individuals exposed to infection. The health system isolates them from the community for a while and keeps them in the quarantine. We denote this subcommunity by Q.
3. The non-quarantined infected individuals who are not isolated from the community and they are in the latency period. We denote this subcommunity by F.
4. The infective individuals containing that portion of the non-quarantined individuals who are infected but they are unknown (or hidden) to the health system, so they have not been quarantined and so they can contact to the other individuals in the community and disperse the disease. We denote this subcommunity by I.
5. The hospitaled individuals containing of those individuals who are infected and now they get the hospitality. We denote this subcommunity by H.
6. The recovered subcommunity consisting of former infected individuals who currently have full recovery and they possess immunity against the disease for a certain time. We denote this subcommunity by R.

Finally, in order to simplify description of the above system, we have to consider the exposed individuals as a complete subcommunity; so the 7-th subcommunity of the system is introduced as below

7. The exposed individuals, consisting of those individuals who were exposed to the infection. We denote this subcommunity by E.

Naturally, we assume that the individuals in the subcommunities Q and H have no contact with the other individuals so, only individuals in the subcommunities S, F, I and R may be in contact with infective individuals. Thus we consider $\mathfrak{A} = \{S, E, Q, F, I, H, R\}$ as the set of the subcommunities of the community and $\mathfrak{B} = \{S, F, I, R\}$ as the set of the active subcommunities. The Figure 1 shows the model of interactions between these subcommunities.

The above assumptions lead us to the $SE(QF)(IH)R$ system simulating patterns of the pandemic in the community. The simulation is done by a system of parametric ordinary differential equations. Here, we leave definitions, concepts and mathematical computations of these parameters and equations for the appendix section at the end of this paper and introduce the $SE(QF)(IH)R$ system as below.

$$\begin{aligned}
\dot{S} &= b-\nu_0 S+b^R R-\bar{n}S\frac{I}{\sum_{X\in\mathfrak{B}} X}+(1-p)\left((1-a)b^E\,E\frac{S}{\sum_{X\in\mathfrak{B}} X}+b^Q Q\frac{S}{S+F}\right)\\
&:= \mathfrak{L}_S(S,E,Q,F,I,H,R),\\
\dot{E} &= -(\nu_0+b^E)E+\bar{n}I\\
&:= \mathfrak{L}_E(S,E,Q,F,I,H,R),
\end{aligned}$$

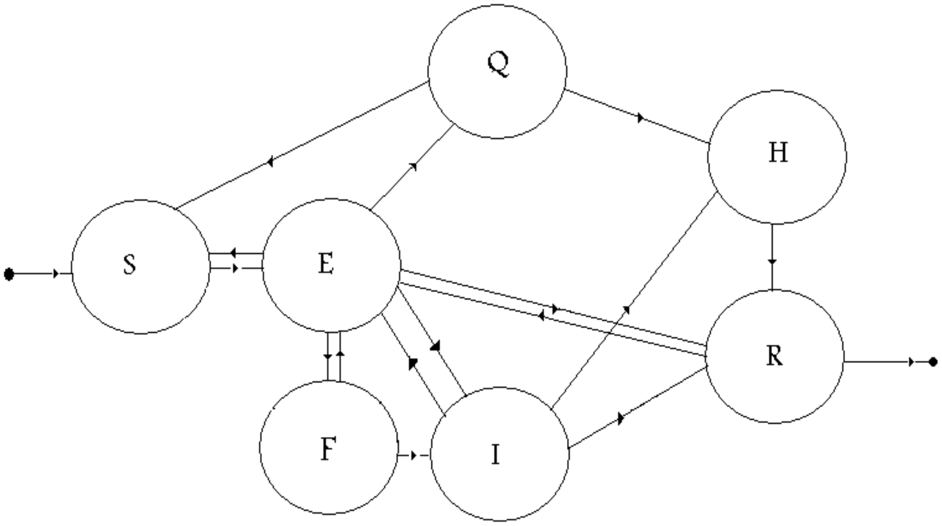

Fig. 1 The system of interactions between the subcommunities.

$$
\begin{aligned}
\dot{Q} &= -(\nu_0 + b^Q)Q + ab^E\, E \frac{S+F}{\sum_{X\in\mathfrak{B}} X} \\
&:= \mathfrak{L}_Q(S,E,Q,F,I,H,R), \\
\dot{F} &= -(\nu_0 + b^F)F - \bar{n}F \frac{I}{\sum_{X\in\mathfrak{B}} X} + (1-a)b^E\, E \frac{F+pS}{\sum_{X\in\mathfrak{B}} X} \\
&:= \mathfrak{L}_F(S,E,Q,F,I,H,R), \\
\dot{I} &= -(\nu_0 + \nu_1 + b^I)I + b^F F - \bar{n}I \frac{I}{\sum_{X\in\mathfrak{B}} X} + (1-a)b^E\, E \frac{I}{\sum_{X\in\mathfrak{B}} X} \\
&:= \mathfrak{L}_I(S,E,Q,F,I,H,R), \\
\dot{H} &= -(\nu_0 + \nu_2 + b^H)H + a^{(IH)} I + ab^E\, E \frac{I}{\sum_{X\in\mathfrak{B}} X} + b^Q Q \frac{F+pS}{F+S} \\
&:= \mathfrak{L}_H(S,E,Q,F,I,H,R), \\
\dot{R} &= -(\nu_0 + b^R)R + b^H H + a^{(IR)} I - \bar{n}R \frac{I}{\sum_{X\in\mathfrak{B}} X} + b^E E \frac{R}{\sum_{X\in\mathfrak{B}} X} \\
&:= \mathfrak{L}_R(S,E,Q,F,I,H,R),
\end{aligned}
\tag{1}
$$

where all parameters are nonnegative real numbers and $a^{(IR)} + a^{(IH)} = b^I$. The trajectories of the model are in the space of variables $(S,E,Q,F,I,H,R) \in \mathbb{R}^7$ and the parameters $b, b^X,\ (X \in \mathfrak{A}), a^{(IR)},\ a^{(IH)}, \nu_i,\ (i = 0,1,2), \bar{n}, p$ and a build the space of parameters which is linearly isomorphic to $\mathbb{R}^{14}$. From the appendix 1, each of the above parameters has a biological interpretation as below:

b: natural birth rate of the community.

ν_0: natural mortality of the community.

ν_1: mortality of individuals in I subcommunity due to the infection.

ν_2: mortality of individuals in H subcommunity due to the infection.

$b^X,\ X \in \mathfrak{A}$: number of individuals who leave X subcommunity to other subcommunities at per unit of time.

$a^{(IH)}$: number of individuals who leave I subcommunity to H subcommunity.

$a^{(IR)}$: number of individuals who leave I subcommunity to R subcommunity.

a: portion of individuals who are exposed to the infection and they are quarantined.

p: infection transmission risk which shows the probability that infection transfer from an infectious individual to a susceptible individual by a near contact.

$\bar{n}$: average number of contacts between individuals in active subcommunities $\mathfrak{B}$.

The total size of the community is given by $N(t) = \sum_{X\in\mathfrak{A}} X(t)$ and holds the conservative equation

$$\dot{N} = b - \nu_0 N - \nu_1 H - \nu_2 I. \tag{2}$$

This guaranties that the total size of the community, and in consequence the size of the subcommunities, remain bounded. It is easy to see that the subspaces

$$\begin{aligned}
\mathfrak{N}_1 &= \mathbb{R} \times \{(0,0,0,0,0,0)\},\\
\mathfrak{N}_2 &= \mathbb{R} \times \{(0,0,0,0,0\} \times \mathbb{R},\\
\mathfrak{N}_3 &= \mathbb{R} \times \{(0,0,0,0\} \times \mathbb{R}^2,\\
\mathfrak{N}_4 &= \mathbb{R} \times \{0\} \times \mathbb{R} \times \{(0,0)\} \times \mathbb{R}^2,\\
\mathfrak{N}_5 &= \mathbb{R}^7
\end{aligned}$$

are invariant.

The free singularity of (1) is $\zeta_1 = (b/\nu_0, 0, 0, 0, 0, 0, 0)$ and other steady states of the system (local singularities), if any exists, are isolated and they have nonzero components in the E, F or I subcommunity (see the appendix section).

Since all variables in (1) stand for the number of the individuals in the corresponding subcommunities , so negative initial conditions or values for them is biologically meaningless; so just the nonnegative values of the parameters and variables are biologically acceptable. Also, we are naturally interested in situations for which the infectious disease and the susceptible individuals exist simultaneously. Thus, we have to consider the solutions of (1) whose components have nonnegative initial values and remain nonnegative for $t \geq 0$.

Definition 2.1. A solution $\gamma(t) = (S(t), E(t), Q(t), F(t), I(t), H(t), R(t))$ of (1) with $S(0) > 0$ and $E(0)$, $Q(0)$, $F(0)$, $I(0)$, $H(0)$, $R(0) \geq 0$ is called a suitable solution. Also the cone $\Gamma = \{(S, E, Q, F, I, H, R) \,:\, S > 0,\ E,\, Q,\, F,\, I,\, H,\, R \geq 0\} \subset \mathbb{R}^7$ is called the suitable cone.

Throughout this paper we assume that $\gamma(t)$ is a suitable solution and for any $X \in \mathfrak{A}$, $X(t)$ is a component of $\gamma(t)$. It can be checked that any suitable solution is defined for $t \in [0\,,\, +\infty]$ and remains bounded in the suitable cone Γ. (see the appendix section).

3. Dimensionless system

Now, we change the parameters and variables of the $SE(QF)(IH)R$ system to obtain a dimensionless system. Then we apart this dimensionless system into two simple subsystems which are coupled to each other. These new systems will help us to investigate local bifurcations of the $SE(QF)(IH)R$ system.

Proposition 6.4 states that all components of the suitable solutions remain nonzero and bounded in the suitable cone Γ for all $t \geq 0$. This enables us to define the dimensionless parameter τ as below:

$$\tau = \int_0^t \frac{N_0^2 \nu_0}{(S(t) + F(t)) \sum_{X \in \mathfrak{B}} X(t)} \, dt, \quad t \geq 0,$$

where N_0 stands for the initial population of the community. Now, we can re-scale the system by considering the dimensionless variables $x(\tau) = X(t)/N_0$ for all $X \in \mathfrak{A}$. This changes the $S(EQ)(IHR$ system (1) to the following dimensionless polynomial system

$$\dot{x} = \frac{d}{d\tau} x = \frac{1}{\nu_0 N_0} (s+f)(\sum_{X \in \mathfrak{B}} x) \mathfrak{L}_X(N_0 s, N_0 e, N_0 q, N_0 f, N_0 i, N_0 h, N_0 r), \quad X \in \mathfrak{A}.$$

It is easy to check that we can write the dimensionless system by

$$\dot{x} = (s+f)(\sum_{X \in \mathfrak{B}} x) \mathfrak{L}_X(s, e, q, f, i, h, r), \quad X \in \mathfrak{A},$$

where the parameter b in (1) is rescaled by $b/(N_0 \nu_0)$ and the rest of the parameters, except p and a, are rescaled by their division to ν_0; however we still use the same notifications as (1). Specially for the dimensionless system we have $\nu_0 = 1$; thus the space of the parameters is linearly isomorphic to $\mathbb{R}^{13}$; but just the nonnegative values are biologically acceptable. Finally, we can transfer the free singularity ζ_1 to the origin by replacing $s + b$ by s and obtain

$$\begin{aligned}\dot{x} &= (s+f+b)\Big(\sum_{X\in\mathfrak{B}} x+b\Big)\mathfrak{L}_X(s+b,e,q,f,i,h,r)\\ &:= \mathfrak{M}_x(s,e,q,f,i,h,r), \quad X\in\mathfrak{A}. \end{aligned} \tag{3}$$

It is easy to check that the subspaces $\mathfrak{N}_i$, $i=1,2,3,4$ and the suitable cone Γ^+ are still invariant for (3). Thus, specially, we consider (3) as two distinct parts: variables which are in $\mathfrak{N}_4$ and variables which are in $\mathfrak{N}_5-\mathfrak{N}_4$. In this regard, let $X=(s,q,h,r)\in\mathfrak{N}_4$ and $Y=(e,f,i)\in\mathfrak{N}_5-\mathfrak{N}_4$ and define

$$\begin{aligned}
&A=\partial(\mathfrak{M}_s,\mathfrak{M}_q,\mathfrak{M}_h,\mathfrak{M}_r)/\partial X|_{(X,Y)=(0,0)},\\
&F_1(X)=(\mathfrak{M}_s,\mathfrak{M}_q,\mathfrak{M}_h,\mathfrak{M}_r)|_{(X,\,0)}-AX,\\
&\widetilde{H}_1(X,Y)=(\mathfrak{M}_s,\mathfrak{M}_q,\mathfrak{M}_h,\mathfrak{M}_r)|_{(X,Y)}-(AX+F_1(X))\,,\\
&C=\partial\widetilde{H}_1/\partial Y|_{(0,0)},\\
&F_2(Y)=\widetilde{H}_1(0,Y)-CY,\\
&H_1(X,Y)=\widetilde{H}_1(X,Y)-\widetilde{H}_1(0,Y),\\
&B=\partial(\mathfrak{M}_e,\mathfrak{M}_f,\mathfrak{M}_i)/\partial Y|_{(X,Y)=(0,0)}\,,\\
&G(Y)=(\mathfrak{M}_e,\mathfrak{M}_f,\mathfrak{M}_i)|_{(0\,,Y)}-BY,\\
&H_2(X,Y)=(\mathfrak{M}_e,\mathfrak{M}_f,\mathfrak{M}_i)|_{(X,Y)}-(BY+G(Y)))\,.
\end{aligned}$$

Then we can rewrite (3) as below

$$\begin{aligned}
\dot{X}&=AX+F_1(X)+\widetilde{H}_1(X,Y)\\
&=AX+F_1(X)+CY+F_2(Y)+H_1(X,Y),\\
\dot{Y}&=BY+G(Y)+H_2(X,Y)
\end{aligned} \tag{4}$$

with $F_1(0)=0$, $F_2(0)=0$, $G(0)=0$, $DF_1(0)=0$, $DF_2(0)=0$, $DG(0)=0$, $\widetilde{H}_1(X,0)=0$, $H_2(0,Y)=H_2(X,0)=0$, $D_X\widetilde{H}_1(X,0)=0$, $D_YH_1(0,Y)=0$, $D_XH_1(X,0)=0$, $D_YH_2(0,Y)=0$, $D_XH_2(X,0)=0$. This helps us to consider this newly obtained system as two distinct dimensionless systems $\dot{X}=AX+F(X)$ and $\dot{Y}=BY+G(Y)$ which are coupled to each other through $\widetilde{H}_1(X,Y)$ and $H_2(X,Y)$. In the next section, we will see that the local bifurcations of $\dot{Y}=BY+G(Y)$ which passes through the steady state $Y=0$ may cause the same bifurcations for the dimensionless system (4) passing through the free singularity $\zeta_1=(X,Y)=0$.

4. Local bifurcations of the free singularity

In this section we investigate the local bifurcations of (4) passing through the free singularity $\zeta_1=(X,Y)=(0,0)$. This specially helps us to find the local bifurcations of the $SE(QF)(IH)R$ system.

We begin by determining the type of the free singularity ζ_1 depending on values of the parameters. This is done by indicating the eigenvalues of the corresponding linear part. We note that the existence of complex eigenvalues implies that some solutions of the system has spiral virtue [9, 15, 20]. This is biologically important because the spiral orbits means existence of an oscillation in the number of the individuals in the subcommunities. This can be biologically interpreted as incoming waves of the infection during the time. In order to improve notations, we define the new parameter

$$0 \leq \theta = \bar{n}\, p\, (1-a)$$

and determine the type of ζ_1 and the corresponding bifurcations with respect to θ. Note that the linear part of the coupled system (4) is given by

$$K = \begin{pmatrix} A & \frac{\partial \widetilde{H}_1}{\partial Y} \\ o & B \end{pmatrix}.$$

For a matrix G let Spect.(G) stand for the set of all eigenvalues of G and assume that $\lambda \in$ Spect.(A) with the eigenvector x. It is easy to see that $\lambda \in$ Spect.(K) with the eigenvector $(x, 0)$; that is Spect.$(A) \subset$ Spect.(K). Now let $\lambda \in$ Spect.$(B) -$ Spect.(A) with the corresponding eigenvector y, then $\lambda \in$ Spect.(K) with the corresponding eigenvector (x, y), where $x = -(A+I)^{-1} \frac{\partial \widetilde{H}_1}{\partial Y} y$. Thus

$$\text{Spect.}(A) \cup \text{Spect.}(B) \subset \text{Spect.}(K).$$

On the other hand, if $\lambda \in$ Spect.$(K) -$ Spect.(B) with the eigenvector (x, y) then we have

$$Ax + \frac{\partial \widetilde{H}_1}{\partial Y} y = \lambda x, \qquad By = \lambda y.$$

This means that $y = 0$ and $\lambda \in$ Spect.(A) with the corresponding eigenvector x. This implies that

$$\text{Spect.}(K) \subset \text{Spect.}(A) \cup \text{Spect.}(B).$$

Thus we have proven the following lemma

Lemma 4.1. *We have always* Spect.$(K) =$ Spect.$(A) \cup$ Spect.(B).

This lemma provides situation for which the eigenvalues of the linear part of (4) at ζ_1 is given by the eigenvalues of A together with the eigenvalues of B. Now let consider the subsystem $\dot{Y} = BY + G(Y)$. This system has the origin as a steady state point and the corresponding eigenvalues are obtained by solving the characteristic equation $\lambda^3 + u\lambda^2 + v\lambda + w = 0$, with

$$\begin{aligned} u &= b^2(b^E + b^F + b^I + \nu_1 + 3), \\ v &= b^4\left((b^E+1)(b^F+1) + (b^E+1)(b^I+\nu_1+1) + (b^F+1)(b^I+\nu_1+1)\right), \\ w &= b^6\left((b^E+1)(b^F+1)(b^I+\nu_1+1) - \theta\, b^E\, b^F\right) = -(b^2\,\alpha_0)/(\theta\, b^E). \end{aligned}$$

The parameters $u,\ v$ are nonnegative real numbers and we can choose the parameter θ such that w varies independently on u and v. Thus, $0 \neq \lambda_0$ is an eigenvalue for B if and only if

$$0 \leq \theta = \frac{\lambda_0^3 + \lambda_0^2\, u + \lambda_0\, v + b^6 (b^E + 1)(b^F + 1)(b^I + \nu_1 + 1)}{b^6\, b^E\, b^F}.$$

In this case, two other eigenvalues of B are given by

$$\lambda_{1,2} = \frac{-1}{2}(u^* \pm \sqrt{u^{*2} - 4v^*}),$$

where

$$v^* = -w/\lambda_0 > 0, \quad u^* = u + \lambda_0.$$

Thus if $u^{*2} < 4v^*$ then B has two complex eigenvalues. This last inequality holds if and only if $v > (u - \lambda_0)^2/4 - \lambda_0^2$.[2] We summarize the results in the following theorem.

Theorem 4.2. *Let* λ_0 *be a real number. Then,* λ_0 *is an eigenvalue for the linear part of* (4) *at* ζ_1 *if and only if*

$$0 \leq \theta = \frac{\lambda_0^3 + \lambda_0^2\, u + \lambda_0\, v + b^6 (b^E + 1)(b^F + 1)(b^I + \nu_1 + 1)}{b^6\, b^E\, b^F}.$$

Furthermore, let

$$\theta_0 = \frac{(b^E + 1)(b^F + 1)(b^I + \nu_1 + 1)}{b^E\, b^F}.$$

Then, we have:

(a) ζ_1 *is a hyperbolic sink if and only if* $\theta < \theta_0$. *In this case,* ζ_1 *has a pair of complex eigenvalues if and only if* $v > (u - \lambda_0)^2/4 - \lambda_0^2$. *Moreover,* ζ_1 *is a stable node if* $v \leq (u - \lambda_0)^2/4 - \lambda_0^2$*;*

(b) ζ_1 *is a hyperbolic saddle if and only if* $\theta \geq \theta_0$. *In this case,* ζ_1 *has a one dimensional unstable manifold corresponding to a real positive eigenvalue. Also* ζ_1 *has a pair of complex eigenvalues if and only if* $v > (u-\lambda_0)^2/4-\lambda_0^2$*;*

(c) *If* $\theta = \theta_0$ *then* ζ_1 *has one zero eigenvalue and so it is a non hyperbolic steady state.*

Remark 4.3. As we know that the hyperbolic singularities do not pass through local bifurcations, so we expect that any local bifurcation for (4) at ζ_1 must occur for the case (c) above, i.e., $\theta = \theta_0$.

We end this section by investigating local bifurcations of (4) passing through ζ_1. It can be checked directly that, for positive values of the parameters, (4) does not pass through a Hopf bifurcation at ζ_1. Thus we investigate the local bifurcations at ζ_1. As we mentioned before, (4) depends on 13 parameters; but

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[2] It can be checked that for $u = -\lambda_0 > 0$, we find $\theta_0 < 0$ which is not acceptable.

here, the parameters $\bar{n}$, p, $(1-a)$ are the main parameters for studying the local bifurcations in (4). Also b^E, $a^{(IH)}$ are considered as the incidental parameters. This is mostly because of the nature of $\bar{n}$, p, $(1-a)$ making them parameters which are controlled by the health system. Also, by their biological interpretation, b^E, $a^{(IH)}$ depend on the cultural/commercial situation of the community. The rest of the parameters b, b^Q, $\ldots$, b^R and ν_1, ν_2 usually depend on the nature of the disease.

The system $\dot{X} = AX + F(X)$ is the restricted system (29) and the steady state $X = 0$ is a hyperbolic sink with the corresponding eigenvalues

$$\lambda_1 = -b^2, \quad \lambda_2 = -b^2(b^Q + 1), \quad \lambda_3 = -b^2(b^R + 1), \quad \lambda_4 = -b^2(b^H + \nu_2 + 1).$$

Thus, for $\|Y\|$ sufficiently small, $\dot{X} = AX + F(X) + \widetilde{H}_1(X, Y)$ has a unique steady state $X(Y)$ of type of hyperbolic sink which is close to ζ_1. This means that, for $\|Y\|$ sufficiently small, the first equation in (4) has no local bifurcation at the origin. Proposition 6 states that any branch of the singularities which is caused by a local bifurcation through ζ_1 bifurcates into $\mathfrak{N}_5 - \mathfrak{N}_4$ and all of its components are nonzero.

Now, let $V \subseteq \mathbb{R}^{13}$ be a linear subspace of the parameters of the system (4) and $Y(\Lambda)$, $\Lambda \in V$, be a C^1 family of the steady states of the subsystem $\dot{Y} = BY + G(Y)$ such that $\lim_{\Lambda\to\Lambda_0} Y(\Lambda) = 0$. Easy application of the implicit function theorem shows that for any Λ with $0 < \|\Lambda - \Lambda_0\|$ sufficiently small, there exists a C^1 family of steady states $X(\Lambda)$ for the subsystem $\dot{X} = AX + F_1(X) + \widetilde{H}_1(X, Y(\Lambda))$ such that $X(\Lambda)$ is a hyperbolic sink and $\lim_{\Lambda\to\Lambda_0} X(\Lambda) = 0$. In this case $\zeta(\Lambda) = (X(\Lambda), Y(\Lambda))$ is a steady state for (4) if and only if $H_2(X(\Lambda), Y(\Lambda)) = 0$. This convinces us to look for the relation between the local bifurcations of the third dimensional subsystem

$$\dot{Y} = BY + G(Y), \quad Y = (e, f, i) \in \mathbb{R}^3 \tag{5}$$

with the local bifurcations of the full system (4).

For this purpose, we can solve the first and second equations in (5) with respect to the variables e and i respectively and find that $Y = (e, f, i)$ is a steady state for (5) if and only if

$$e = \frac{\bar{n}}{1 + b^E} i, \quad i = \frac{(f + b)(1 + b^E)(1 + b^F) f}{f(\bar{n} + a\,\bar{n}\,b^E + (1 + b^E)(1 + b^F)) - \theta\, b\, b^E}. \tag{6}$$

Then we can replace the values of e and i from (6) in the third equation of (5) and find that f is an equilibrium point of the equation

$$\begin{aligned} 0 = U(f) &= f\left(\alpha_4 f^4 + \alpha_3 f^3 + \alpha_2 f^2 + \alpha_1 f^1 + \alpha_0\right) \\ &= \alpha_4\, f\left(f^4 + \frac{\alpha_3}{\alpha_4} f^3 + \frac{\alpha_2}{\alpha_4} f^2 + \frac{\alpha_1}{\alpha_4} f^1 + \frac{\alpha_0}{\alpha_4}\right) \end{aligned} \tag{7}$$

with

$$\begin{aligned}
\alpha_4 &= \bar{n}(1+ab^E)(\bar{n}(1+ab^E)b^F + (1+b^E)(1+b^F)(b^I+\nu_1)) > 0,\\
\alpha_3 &= \bar{n}b((-1+a)pb^E(1+b^I+\nu_1+b^F(2+2\bar{n}+b^F+b^I+\nu_1)\\
&\quad +b^E(1+b^I+\nu_1+b^F(2+2a\bar{n}+b^F+b^I+\nu_1)))\\
&\quad +(1+ab^E)(-(1+b^E){b^F}^2+3(1+b^E)(b^I+\nu_1)\\
&\quad +b^F(2\bar{n}(1+ab^E)+(1+b^E)(-1+3b^I+3\nu_1)))),\\
\alpha_2 &= \bar{n}b^2((-1+a)^2\bar{n}p^2{b^E}^2b^F+(1+ab^E)(-2(1+b^E){b^F}^2+3(1+b^E)(b^I+\nu_1)\\
&\quad +b^F(\bar{n}+a\bar{n}b^E+(1+b^E)(-2+3b^I+3\nu_1)))+(-1+a)pb^E(3(1+b^I+\nu_1)\\
&\quad +b^F(5+4\bar{n}+2b^F+3b^I+3\nu_1)+b^E(3(1+b^I+nu_1)\\
&\quad +b^F(5+4a\bar{n}+2b^F+3b^E+3\nu_1)))),\\
\alpha_1 &= \bar{n}b^3(2(-1+a)^2\bar{n}p^2{b^E}^2b^F-(1+b^E)(1+ab^E)(1+b^F)(b^F-b^I-\nu_1)\\
&\quad +(-1+a)pb^E(3(1+b^I+\nu_1)+b^F(4+2\bar{n}+b^F+3b^I+3\nu_1)\\
&\quad +b^E(3(1+b^I+\nu_1)+b^F(4+2a\bar{n}+b^F+3b^I+3\nu_1)))),\\
\alpha_0 &= b^4b^E\theta\big(b^Eb^F\theta-(1+b^E)(1+b^F)(1+b^I+\nu_1)\big)
\end{aligned}$$

By (6), these steady states are in the suitable cone Γ^+ if and only if

$$0 \le f < \frac{(1-a)p\theta b b^E}{\theta(1+ab^E)+(1-a)p(1+b^E)(1+b^F)}. \tag{8}$$

On the other hand, easy application of the implicit function theorem shows that for $\theta \ge \theta_0 = (1+b^E)(1+b^F)(1+b^I+\nu_1)/b^Eb^F$, a unique branch of the positive equilibrium points of $U(f)$, say $f(\theta)$, emerges from the equilibrium $f=0$ and satisfies the inequality (8). Thus we have proven the following lemma.

Lemma 4.4. *Any positive branch of the equilibrium bifurcations for the equation* (7) *passing through* $f=0$ *and satisfying* (8)*, causes the same bifurcation in the steady states of the subsystem* (5) *passing through* $Y=0$*, especially for* $\theta > \theta_0$ *there exists a unique branch of the steady states of the subsystem* (5) *emerging from* $Y=0$ *into the suitable cone* Γ^+.

Now, suppose that $V \subseteq \mathbb{R}^{13}$ be a linear subspace of the parameters and

$$V^+ = \{\Lambda \in V : \text{all parameters in (4) involved with } \Lambda \text{ having positive value}\}.$$

Also assume that $f(\Lambda)$, $\Lambda \in V^+$, is a branch of the equilibrium points for (7) caused by a equilibrium bifurcation passing through $f=0$. Thus $Y(\Lambda) = (e, f(\Lambda), i)$ is a branch of the steady states of (5) which passes through $Y=0$, where e and i are given by (6). We can expand $Y(\Lambda)$ with respect to f and obtain

$$\begin{aligned}
Y(\Lambda) &= \frac{f}{pb^E(1-a)}\left(1+b^F, 1, \frac{(1+b^E+b^F+b^E\,b^F)}{\bar{n}}\right)+o(f^2)\\
&:= \frac{f}{pb^E(1-a)}\left(Y_0+o(f)\right).
\end{aligned}$$

Then we can use the implicit function theorem and find that the corresponding steady state $X(\Lambda)$ for the subsystem $\dot{X} = AX + F_1(X) + \widetilde{H}_1(X, Y(\Lambda))$ has the form

$$\begin{aligned} X(\Lambda) &= \frac{f}{pb^E(1-a)} \left(-A^{-1}CY_0 + o(f)\right) \\ &:= \frac{f}{pb^E(1-a)} \left(X_0 + o(f)\right). \end{aligned}$$

Now we concern on the equation $H_2(X(\Lambda), Y(\Lambda)) = 0$. First let $H_{2j}(X,Y),\ j = 1,2,3$ be the j-th component of H_2. Also assume that

$$H_{22}(X,Y) = P_2(X,Y) + P_3(X,Y) + P_4(X,Y),$$

$$H_{23}(X,Y) = Q_2(X,Y) + Q_3(X,Y) + Q_4(X,Y),$$

where $P_j(X,Y),\ Q_j(X,Y),\ j = 1,2,3$ are respectively polynomials consisting of terms of the degree j. It can be checked that for e and i given by (6), $H_{21}(X,Y) = 0$, thus specially the first component of $H_2(X, Y(\Lambda))$ is permanently zero for all X. We can replace $X(\Lambda)$ and $Y(\Lambda)$ in the two rest components and obtain

$$\begin{aligned} H_{22}(X(\Lambda), Y(\Lambda)) &= \Big(\frac{f}{p\, b^E(1-a)}\Big)^2 P_2(Y_1, Y_0) + o(f^3) \\ &= \Big(\frac{f}{pb^E(1-a)}\Big)^2 \left\{P_2(Y_1, Y_0) + o(f)\right\}, \\ H_{23}(X(\Lambda), Y(\Lambda)) &= \Big(\frac{f}{pb^E(1-a)}\Big)^2 Q_2(Y_1, Y_0) + o(f^3) \\ &= \Big(\frac{f}{pb^E(1-a)}\Big)^2 \left\{Q_2(Y_1, Y_0) + o(f)\right\}. \end{aligned}$$

Thus, the equation $H_2(X(\Lambda), Y(\Lambda)) = 0$ is restricted to the equations

$$P_2(X_0, Y_0) + o(f) = 0, \quad Q_2(X_0, Y_0) + o(f) = 0.$$

If there exists a nonnegative set of the parameters $\Lambda_0 \in \mathbb{R}^{13}$ for which

$$P_2(X_0, Y_0) = 0, \quad Q_2(X_0, Y_0) = 0 \tag{9}$$

and

$$\det \frac{\partial(P_2(X_0, Y_0), Q_2(X_0, Y_0))}{\partial(\mu_1, \mu_2)} \neq 0, \quad \mu_1, \mu_2 \text{ are two components of } \Lambda_0, \tag{10}$$

then by the implicit function theorem we can find a solution for $H_2(X,Y) = 0$. Specially, we find by a long mathematical computation that one solution for (9) satisfying (10) exists when $a = b^I = 0$ and $\theta = \theta_0 = (1 + b^E)(1 + b^F)(1 + \nu_1)/(b^E b^F)$. Thus we have the following theorem.

Theorem 4.5. *Suppose that $V \subseteq \mathbb{R}^{13}$ is a linear subspace of the parameters such that for $\Lambda = \Lambda_0 \in V^+$ a local bifurcation occurs for the equilibrium points of* (7) *at $f = 0$ such that* (8), (9) *and* (10) *hold. Then, for $\Lambda = \Lambda_0$, the same local bifurcation occurs for* (4) *at the free equilibrium ζ_1. Specially, for $\theta > \theta_0 = (1 + b^E)(1 + b^F)(1 + \nu_1)/(b^E b^F)$ there exists a unique branch of the local singularities emerging from the free singularity ζ_1.*

Remark 4.6. Theorem 4.5 indicates how the local bifurcations of the subsystem (5) cause the local bifurcations for (4); but there is always a direct way to find the other steady states of the system. For this, let Y_0 be a steady state of (5) and X_0 be such that (X_0, Y_0) is a steady state for

$$\dot{X} = AX + F_1(X) + \widetilde{H}_1(X, Y_0).$$

In this case, if the equation $H_2(X_0, Y_0) = 0$ can be solved with respect to the parameters then (X_0, Y_0) is a steady state for (4).

Remark 4.7. We note that the hyperbolic steady states are isolated, hence if the local bifurcation in Theorem 4.5 occurs then $\theta = \theta_0$. Furthermore, if $\theta > \theta_0$ then ζ_1 has a one dimensional unstable manifold [9, 20]. On the other hand we have

$$\frac{d}{d\tau} n = b - n - \nu_1 i - \nu_2 h$$

which shows that $n(\tau) = s(\tau) + e(\tau) + q(\tau) + f(\tau) + i(\tau) + h(\tau) + r(\tau)$ is a decreasing function, so it is not a wandering curve. This implies that if variables of (4) are on the unstable manifold of ζ_1, then $n(\tau)$ is absorbed by another steady state situation. Thus there exists another steady state point[3] for (4) absorbing the unstable manifold of ζ_1. In this case, only the solutions on the stable manifold of ζ_1 are absorbed by ζ_1. But this is a 6 dimensional immersed submanifold of $\mathfrak{N}_5$ which is a subset with zero measure. Thus we expect that the solutions of the system are generically absorbed by the local singularities in Theorem 4.5.[4].

Finally we re-scale back the parameters by dividing them to ν_0 and find θ and θ_0 with respect to the dimensional parameters as below

$$\theta_0 = \frac{(b^E + \nu_0)(b^F + \nu_0)(b^I + \nu_1 + \nu_0)}{\nu_0\, b^E\, b^F}, \quad \theta = \frac{\bar{n}}{\nu_0} p\,(1 - a).$$

Thus the inequalities $\theta < \theta_0$ and $\theta > \theta_0$ in Theorem 4.2 are redefined respectively by

$$\Theta = \bar{n}p(1 - a) < \Theta_0 = \frac{(b^E + \nu_0)(b^F + \nu_0)(b^I + \nu_1 + \nu_0)}{b^E b^F} \quad \text{and} \tag{11}$$

$$\Theta = \bar{n}p(1 - a) > \Theta_0 = \frac{(b^E + \nu_0)(b^F + \nu_0)(b^I + \nu_1 + \nu_0)}{b^E b^F}. \tag{12}$$

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[3] This steady state is caused by a local bifurcation from ζ_1.

[4] This will be seen in graphs of the solutions in the next section.

We note that $\Theta_0 = \nu_0\theta_0$ and $\Theta = \nu_0\theta$ are with dimension "Day^{-1}". The results of Theorems 4.2 and 4.5 convince us to name these parameters preciously in the following definition.

Definition 4.8. The parameters Θ_0 and Θ in (11) are called respectively "*Pandemic Threshold*" and "*Pandemic Estimator*". If the "Pandemic Estimator" is lesser than the "Pandemic Threshold" then all individuals get healing, else there remain some individuals infected.

5. Application, influenza

For who are interested in the study of infectious diseases, the influenza is of great importance. Since the influenza virus continues always evolving, so there exists a menace of the pandemic by the mutant influenza virus and it is still an important problem for the public health systems, and today again, the World Health Organization (WHO) has warned of a substantial risk of pandemic of influenza A throughout the globe. The typical SIR... approach to this problem is the modeling of the interactions between individuals who are (or have been) infected by one or different viral strains (see the references, specially [1, 3, 4, 11]). For example in [10], the authors showed that the simultaneous circulation of several antigenic variants of the same pathogen can give rise to complex dynamics. This may occur when a genetic mutation for influenza A causes simultaneous existence of two or more various strains. In [17], the authors considered an epidemiological model consisting of a linear chain of three co-circulating influenza A strains that provide hosts exposed to a given strain with partial immune cross-protection against other strains. They could find a sub-model that exhibits sustained oscillations. Since genetic mutation for influenza A is occurred usually ones within per several years, so the models which simulate mid time patterns, consider the pandemic by a single strain. Such simulations have been done for example in [5, 12, 22], where a SIR or SIRC model develops a simple ordinary differential equation for studying patterns of the infection in a certain mid-time interval. For an especial case, in [2], a SIRC model is considered to simulate the epidemiological consequences of the drift mechanism for the influenza A viruses. One year later, in [13], a mathematical model is proposed to interpret the spread of avian influenza from the bird world to the human world. The authors gave their results on the spread of avian influenza and mutant avian influenza and measures to control the spread of avian influenza. Since the complete immunity is usually lost within a more than several weeks, so the short time patterns are usually simulated by simple SIR models (see for example [1, 3, 4, 6]).

In this section we apply the $SE(QF)(IH)R$ system to simulate patterns of the pandemic by influenza for an assumed community. In fact, the parameters ν_0 and N_0 are considered for a community with 7×10^6 population and almost 70 years hope of life[5]. Thus, the birth rate parameter b and the natural mortality are given respectively by (see [3])

$$b = \frac{\text{population}}{(\text{hope of life}) \times 365} = \frac{70 \times 10^6}{70 \times 365} \approx 2740 \text{ with dimension } \left\{ \frac{\text{individuals}}{\text{per day}} \right\},$$

and

$$\nu_0 = \frac{\text{birth rate}}{\text{population}} = \frac{2740}{70 \times 10^6} \approx 0.00004 \ \text{ with dimension } \ \left\{ \frac{1}{\text{per day}} \right\}.$$

The other parameters of the system are mostly calibrated by the medical observations (see [3, 6, 22]) and mathematical formula (19) in the appendix section. The Table 1 shows these parameters and their approximated values.

Table 1 Numerical values of some parameters

Parameter	b^Q	b^F	b^H	b^R	ν_1	ν_2
Number of days individuals expend in subcommunities	3–5	2–5	4–7	30–365	–	–
Dimensional value	0.333–0.2	0.485–0.2	0.2437–0.1372	0.0333–0.0027	0.02	0.01

We also assume that the maximum time that an individual is continuously exposed to the infection is at most one hour; so we have $b^E \geq 24$. Also, we assume that almost all individuals in the I subcommunity get hospitality within at most half of a day after end of the latency period when the clinical evidence appears. This implies that $b^I \geq 2$ and $a^{(IH)} = b^I$.

If we use the average values for the dimensional parameters in the Table 1 and $b^I = 2$ then we find the "Pandemic Threshold" as below

$$\Theta_0 = 2.02027 + \frac{7.88 \times 10^{-5}}{b^E} \geq 2.02027.$$

Thus, from Theorem 4.2, Definition 4.8 and Remark 4.7, if $\Theta = \bar{n}\, p\, (1-a)$ is greater than Θ_0 then ζ_1 is a hyperbolic saddle and some solutions absorbed by another steady state point. This biologically means that in a pandemic by the influenza, the number of the individuals in subcommunities go generally far from the steady state ζ_1. Also, Theorem 4.2 implies that if Θ is sufficiently large then we have eventually $v > (u-\lambda_0)^2/4 - \lambda_0^2$ so ζ_1 has a pair of complex eigenvalues. This biologically means that we must expect an oscillation in the solutions of the system which are absorbed by another steady state point. Consequently, if $\Theta < \Theta_0$ then ζ_1 is a hyperbolic sink, so all individuals get healing.

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[5] These values are near to those ones in the Iranian community, but they can be easily replaced by appropriate values for simulating other communities.

We end this section with plotting some curves obtained from the dimensional system to show the effects of the increase of the "Pandemic Estimator" on the behavior of the system. All solutions are plotted for a period of one year (365 days), mean values of the parameters in Table 1 and the initial conditions $F(0)/N_0 = 10^{-6}$ and $S(0)/N_0 = 1 - F(0)$. This simulates patterns of the pandemic in one year when initially all individuals in the community are susceptible except almost 0.00001% of the community which are infected but they are not detected to be quarantined. Let define

$$\mu(t) = \big(S(t) + aE(t) + Q(t) + H(t) + R(t)\big)/N_0,$$
$$\eta(t) = \big((1-a)E(t) + F(t) + I(t)\big)/N_0.$$

Thus $\mu(t) + \eta(t) = N(t)/N_0$ and $\mu(t)$ and $\eta(t)$ stand respectively for portion of the individuals in the noninfectious and the infectious subcommunities. The Figure 2 shows the graphs of $\mu(t)$ and $\eta(t)$ for $p = 0.25$, $a = 0.4$ and $\bar{n} \in \{20, 23, 25, 28, 31, 34\}$. Thus in all solutions $\Theta = \bar{n} \times 0.25 \times 0.6 \geq 3.45 > \Theta_0$. As we expect, increasing the values of Θ, as $\bar{n}$ increases, causes and resonates an oscillation in the graphs. Also the graphs are absorbed by another steady state situation. Also it can be seen that in the infection by influenza, the first wave of the pandemic comes within the first 100 days. After that, we may expect the second wave within 200 days after the first wave. The length of the waves is damped but their strength is resonated by increasing the values of Θ. This is an adaption with experimental observations.

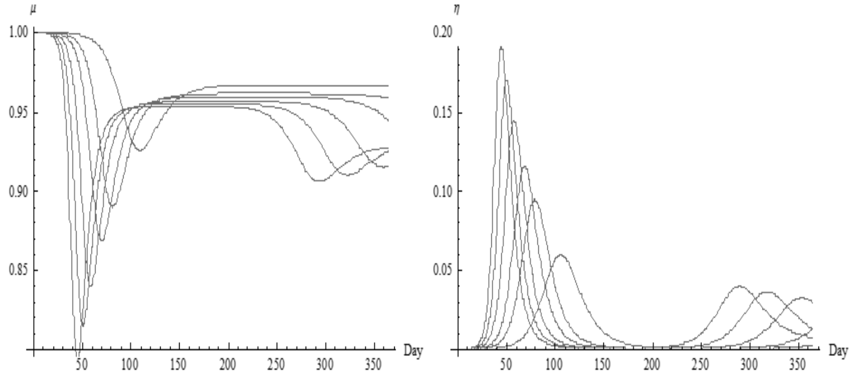

Fig. 2 Graphs of $\mu(t)$ and $\eta(t)$ for $p = 0.25$, $a = 0.4$ and $\bar{n} \in \{20, 23, 25, 28, 31, 34\}$

Similarly, the Figure 3 shows the graphs of $\mu(t)$ and $\eta(t)$ for $p \in \{0.25, 0.35, 0.45, 0.55, 0.65, 0.75\}$, $a = 0.4$ and $\bar{n} = 20$. Thus in all solutions $\Theta = 20 \times p \times 0.6 \geq 3 > \Theta_0$. As we expect, increasing the values of Θ, as p increases, causes and resonates an oscillation in the graphs. As we expect, the length of the waves is damped but their strength is resonated by increasing the values of Θ.

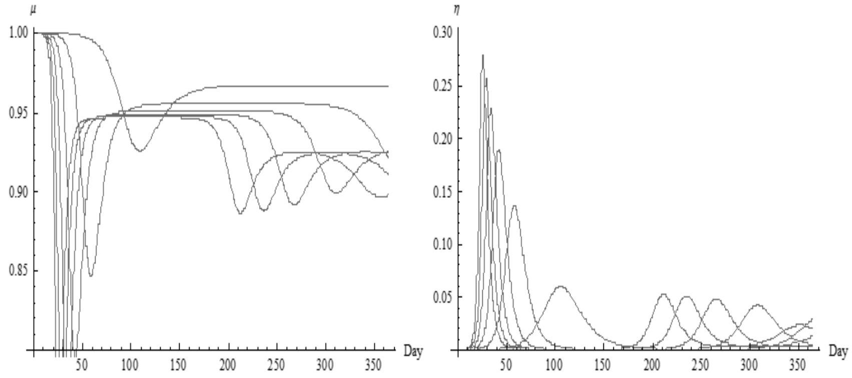

Fig. 3 Graphs of $\mu(t)$ and $\eta(t)$ for $p \in \{0.25, 0.35, 0.45, 0.55, 0.65, 0.75\}$, $a = 0.4$ and $\bar{n} = 20$

The Figure 4 shows the graphs of $\mu(t)$ and $\eta(t)$ for $p = 0.25, a \in \{0, 0.2, 0.4, 0.6, 0.8, 1\}$ and $\bar{n} = 20$. Thus, for $a = 1, 0.8, 0.6$ we have $\Theta < \Theta_0$, hence ζ_1 is a sink and we expect all graphs are absorbed by ζ_1. Also for $a = 0, 0.2, 0.4$ we have $\Theta > \Theta_0$, so ζ_1 is a saddle and we expect that the graphs are absorbed by another steady state. These can be completely seen in the figure. Also, as we expect, increasing the values of Θ, as a decreases, causes and resonates an oscillation in the graphs.

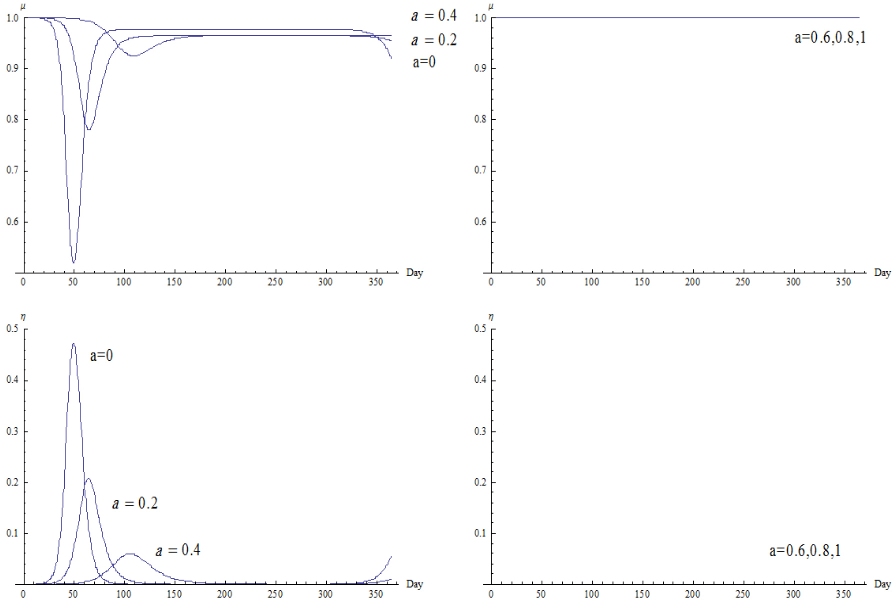

Fig. 4 Graphs of $\mu(t)$ and $\eta(t)$ for $p = 0.25, a \in \{0, 0.2, 0.4, 0.6, 0.8, 1\}$ and $\bar{n} = 20$

6. Appendix

In this section we introduce the mathematical definitions, concepts, computations of the parameters and equations for the $SE(QF)(IH)R$ system (1). We follow paths in the Figure 1 and determine the number of individuals moving between subcommunities at per unit of time.

Let for $X \in \mathfrak{A}$ and $t \in \mathbb{R}$, $X(t)$ denotes the number of the individuals which are in the subcommunity X at time t. Then the total size of the community, at time t, is given by

$$N(t) = \sum_{X \in \mathfrak{A}} X(t). \tag{13}$$

Also the change in the size of the subcommunity $X \in \mathfrak{A}$ during the time between t and $t + \Delta t$ is given by $X(t + \Delta t) - X(t)$ which equals the difference between the number of the individuals who, mean while, entered into X and who left X. Let $\Delta X^i(t)$ and $\Delta X^o(t)$ denote respectively the number of the individuals who enter X and who leave X at per unit time. Thus for Δt small enough we have $X(t+\Delta t) - X(t) = \Delta t \left(\Delta X^i(t) - \Delta X^o(t)\right)$, or respectively,

$$\frac{dX}{dt}(t) = \Delta X^i(t) - \Delta X^o(t). \tag{14}$$

Thus, in our effort for simulating the interactions between the subcommunities by the system of the ordinary differential equations, the goal is to find $\Delta X^i(t)$ and $\Delta X^o(t)$ for all $X \in \mathfrak{A}$. The simplest equation is obtained for N; indeed, let b stand for the average birth rate of the community and ν_0, ν_1 and ν_2 stand respectively for the rate of the natural mortality and the mortality of the infective and hospitaled subcommunities due to the infection. Then we have

$$\frac{dN}{dt}(t) = b - \nu_0 N(t) - \nu_1 I(t) - \nu_2 H(t).$$

This yields that our system of ordinary differential equations has to satisfy the following equation which is known as the conservative equation.

$$\sum_{X \in \mathfrak{A}} (\Delta X^i(t) - \Delta X^o(t)) = \frac{d}{dt} \sum_{X \in \mathfrak{A}} X = b - \nu_0 \sum_{X \in \mathfrak{A}} X - \nu_1 I(t) - \nu_2 H(t). \tag{15}$$

Now we begin to determine equations of the system. First, for all $X \in \mathfrak{A}$, let us divide $\Delta X^i(t)$ and $\Delta X^o(t)$ into linear and nonlinear parts, that is

$$\Delta X^i(t) = \sum_{(X \neq) Y \in \mathfrak{A}} a^{(YX)} Y(t) + \{\text{nonlinear terms}\}, \tag{16}$$

$$\Delta X^o(t) = -(\mu + b^X) X(t) + \{\text{nonlinear terms}\} \tag{17}$$

with $a^{(YX)}, b^X, \mu$ being nonnegative real numbers. In equation (16), $a^{(YX)}$ stands for the portion of the individuals in the subcommunity Y who are entering into the subcommunity X at per unit of time. Similarly, in the equation (17), b^X stands for the number of the individuals who are leaving the subcommunity X for other subcommunities and μ stands for the rate of the mortality in this subcommunity [6]. Thus, the conservative equation (15) implies that

$$\sum_{(X\neq)Y\in\mathfrak{A}} a^{(XY)} = b^X. \tag{18}$$

If there exists an integer number $n \in \mathbb{N}$ which shows the average number of the days that an individuals expends in the subcommunity X (here, such n exists except for the subcommunities S and I), then the coefficient b^X is usually calibrated with the inverse of n, i.e., $b^X \approx 1/n$ (see for example [3, 7, 8] and etc.; but here, we give another estimation which we believe that it is more exact). Let μ stand for the mortality of the individuals in this subcommunity and X^j, $(1 \leq j \leq n)$, shows the number of individuals who are expending their j-th day in this subcommunity. Thus $X(t) = \sum_j X^j$ and the number of the individuals who are leaving this subcommunity for other subcommunities is $(1-\mu)X^n$. Now if we take the mortality in account, we see that X^{j+1} is well calibrated by $(1-\mu)X^j$. Thus, $X^n \approx (1-\mu)^{n-1}X^1$ and we have

$$\begin{aligned}(1-\mu)X^n = b^X X(t) &= b^X \sum_{j=1}^{n} X^j \\ &\approx b^X \left(\frac{1-(1-\mu)^n}{\mu}\right) X^1 \\ &\approx b^X \left(\frac{1-(1-\mu)^n}{\mu(1-\mu)^{(n-1)}}\right) X^n.\end{aligned}$$

This gives a well estimation for b^X as below

$$b^X = b^X(n,\mu) = \frac{\mu(1-\mu)^n}{1-(1-\mu)^n}. \tag{19}$$

This together with the equation (18) explain the structure of the linear part for the system. Now we turn out the nonlinear parts of the system. We begin with computing the number of exposed individuals at per unit of time. If $\bar{n}$ stands for the average number of contacts of individuals in active subcommunities at per unit of time[7], then, the number of exposed individuals at per unit of time is obtained by the total number of contacts of these individuals multiplying by the probability that a contact occurs with an infective individual, i.e.,

$$\bar{n} \sum_{X\in\mathfrak{B}} X(t) \times \frac{I(t)}{\sum_{X\in\mathfrak{B}} X(t)} = \bar{n} I(t).$$

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[6] It can include the natural mortality and mortality due to the infection.

[7] Naturally, we assume that a quarantined or hospitaled individual has no contact with other individuals.

Thus, regarding to the conservative equation (15) and the Figure 1, we have

$$\Delta E^i(t) = \bar{n}I(t). \tag{20}$$

Similarly, for each $Y \in \mathfrak{B}$, the number of individuals in Y who are exposed to the infection is calibrated by

$$\bar{n}Y(t)\frac{I(t)}{\sum_{X\in\mathfrak{B}} X(t)}. \tag{21}$$

Now, let consider the exposed subcommunity E at time t. By our assumptions, the members of the exposed subcommunity consist of the former members of the active subcommunities; furthermore the number of the individuals who leave this subcommunity at per unit of time is calibrated by $b^E\,E(t)$. Naturally, a part of exposed individuals are from recovered subcommunity, so the number of exposed individuals who leave the subcommunity for the recovered subcommunity at per unit of time is calibrated by $b^E\,E(t)$ multiplying by this probability that an individual is from recovered subcommunity, i.e.,

$$b^E\,E(t)\frac{R(t)}{\sum_{X\in\mathfrak{B}} X(t)}. \tag{22}$$

Now, let a portion, say $a\%$, of the exposed individuals be observed by the health system. This means that the number of the exposed individuals who are not being observed at per unit of time is $(1-a)\,b^E\,E(t)$. Those individuals who are infective or in the latency period, leave E for the subcommunities I and F respectively. The numbers of these individuals are calibrated respectively by

$$(1-a)b^E E(t)\frac{I(t)}{\sum_{X\in\mathfrak{B}} X(t)}, \quad (1-a)b^E E(t)\frac{F(t)}{\sum_{X\in\mathfrak{B}} X(t)}. \tag{23}$$

Now let consider the non-quarantined susceptible exposed individuals. These individuals leave the subcommunity E for the subcommunities S or F. The number of these individuals at per unit of time are calibrated by

$$(1-a)b^E E(t)\frac{S(t)}{\sum_{X\in\mathfrak{B}} X(t)}. \tag{24}$$

This number multiplying by the probability that an individual has an effective contact (i.e., the contact causes infection) indicates the number of these individuals who leave E for F. Thus the number of the non-quarantined susceptible exposed individuals leaving the subcommunity E for the subcommunities S and F are calibrated respectively by

$$(1-p)(1-a)b^E E(t)\frac{S(t)}{\sum_{X\in\mathfrak{B}} X(t)}, \quad p(1-a)b^E E(t)\frac{S(t)}{\sum_{X\in\mathfrak{B}} X(t)}, \tag{25}$$

where p denoting the probability of the effective contact is known as the risk of infection [3, 13, 2].

Now let consider the portion of the exposed subcommunity which is observed by the health system. It is motivated to accept that the health system distinguishes the infective individuals and gets them in hospitality. Therefore the number of the observed exposed individuals which are infective and get hospitality at per unit of time is calibrated by

$$ab^E E(t)\frac{I(t)}{\sum_{X\in\mathfrak{B}} X(t)}. \tag{26}$$

The rest of these individuals get in quarantine, the number of these individuals at per unit of time is calibrated by

$$ab^E E(t)\frac{S(t)+F(t)}{\sum_{X\in\mathfrak{B}} X(t)}. \tag{27}$$

Now let consider the quarantined subcommunity. By our assumptions, the members of this subcommunity are the former members of the subcommunities S and F. By Figure 1, the individuals leave this subcommunity for the subcommunities S and H. The number of the individuals leaving this subcommunity for S and H are calibrated respectively by

$$(1-p)b^Q Q(t)\frac{S(t)}{S(t)+F(t)}, \quad pb^Q Q(t)\frac{F(t)}{S(t)+F(t)}. \tag{28}$$

This completes the nonlinear part of our system. Thus, regarding to the equations (16)–(28) and the conservative equation (15) and the Figure 1, we are convinced to introduce our $SE(QF)(IH)R$ system as below.

$$\begin{aligned}
\dot{S} &= b - \nu_0 S + b^R R - \bar{n} S\frac{I}{\sum_{X\in\mathfrak{B}} X} + (1-p)\left((1-a)b^E E\frac{S}{\sum_{X\in\mathfrak{B}} X} + b^Q Q\frac{S}{S+F}\right),\\
\dot{E} &= -(\nu_0 + b^E)E + \bar{n} I,\\
\dot{Q} &= -(\nu_0 + b^Q)Q + ab^E\, E\frac{S+F}{\sum_{X\in\mathfrak{B}} X},\\
\dot{F} &= -(\nu_0 + b^F)F - \bar{n} F\frac{I}{\sum_{X\in\mathfrak{B}} X} + (1-a)b^E\, E\frac{F+pS}{\sum_{X\in\mathfrak{B}} X},\\
\dot{I} &= -(\nu_0 + \nu_1 + b^I)I + b^F F - \bar{n} I\frac{I}{\sum_{X\in\mathfrak{B}} X} + (1-a)b^E\, E\frac{I}{\sum_{X\in\mathfrak{B}} X},\\
\dot{H} &= -(\nu_0 + \nu_2 + b^H)H + a^{(IH)} I + ab^E\, E\frac{I}{\sum_{X\in\mathfrak{B}} X} + b^Q Q\frac{F+pS}{F+S},\\
\dot{R} &= -(\nu_0 + b^R)R + b^H H + a^{(IR)} I - \bar{n} R\frac{I}{\sum_{X\in\mathfrak{B}} X} + b^E E\frac{R}{\sum_{X\in\mathfrak{B}} X}.
\end{aligned}$$

In the rest of this section, we prove some essential properties of the model which show that the model is biologically passable.

The invariant subspaces $\mathfrak{N}_i$, $i = 1, 2, \dots, 5$, are ordered as $\mathfrak{N}_1 \subset \mathfrak{N}_2 \subset \mathfrak{N}_3 \subset \mathfrak{N}_4 \subset \mathfrak{N}_5$. Thus any trajectory intersecting $\mathfrak{N}_i$, $i = 1, \dots, 5$, is contained completely in it. Thus any trajectory intersecting $\mathfrak{N}_i - \mathfrak{N}_{i-1}$ is contained completely in $\mathfrak{N}_i - \mathfrak{N}_{i-1}$. Each of the subspaces $\mathfrak{N}_i$, $i = 1, \dots, 5$ has a biological interpretation. For example, $\mathfrak{N}_1$ indicates the situation in which there is no disease in the community so all individuals are susceptible; $\mathfrak{N}_2$ indicates the situation in which the disease has been damped so all individuals are susceptible or recovered; $\mathfrak{N}_3$ indicates the situation in which the disease is under complete control so all individuals are susceptible, hospitaled or recovered; $\mathfrak{N}_4$ indicates the situation in which the disease is under control so there is no infected or exposed individual in the community; and finally $\mathfrak{N}_5$ indicates the situation in which the disease is dispersed in the community.

6.1. Suitable solutions. Through the next lemmas and propositions we show that a suitable solution is defined for all $t > 0$ and its components are bounded and nonnegative. This means that the suitable solutions are biologically passable.

Lemma 6.1. *Let $\gamma(t)$ be a suitable solution. Then there exists $\delta > 0$ such that, for $t \in (0, \delta)$, $S(t) > 0$ and all components of $\gamma(t)$ are nonnegative.*

Proof. For simplification let $X(0) = x_0$ for each $X \in \mathfrak{A}$. Since $s_0 > 0$ so there exists $\delta_S > 0$ such that $S(t) > 0$ for all $t \in (0\,, \delta_S)$. Now, let consider two cases.

Case one: $\gamma(t) \subset \mathfrak{N}_4$. In this case $E(t) = F(t) = I(t) \equiv 0$ and the system (1) is restricted to

$$\begin{cases} \dot{S} = b - \nu_0 S + b^R R + (1-p) b^Q Q, \\ \dot{Q} = -(\nu_0 + b^Q) Q, \\ \dot{H} = -(\nu_0 + \nu_2 + b^H) H + p b^Q Q, \\ \dot{R} = -(\nu_0 + b^R) R + b^H H, \end{cases} \tag{29}$$

From the second equation above we find $Q(t) = q_0 \exp(-(\nu_0 + b^Q)t) \geq 0$. Now, consider the third equation above. If $q_0 = 0$ then

$$H(t) = h_0 \exp(-(\nu_0 + \nu_2 + b^H)t) \geq 0.$$

Let $q_0 > 0$. If $h_0 > 0$ then for all $0 < t$ sufficiently small we have $H(t) > 0$ and if $h_0 = 0$ then $\dot{H}(0) = b^Q q_0 > 0$. This shows that there exists $\delta_H > 0$ such that $H(t) > 0$ for $t \in (0\,, \delta_H)$. A similar way shows that there exists $\delta_R > 0$ such that $R(t) > 0$ for $t \in (0\,, \delta_R)$. Now the proof is completed by putting $\delta = \min(\delta_S, \delta_H, \delta_R)$.

Case two: $\gamma(t) \subset \mathfrak{N}_5 - \mathfrak{N}_4$. In this case i_0, f_0 and e_0 are not simultaneously zero. We have to prove the lemma for each of the components of $\gamma(t)$ one by one. In fact we prove it for $E(t)$ and $F(t)$ to indicate the method of the proof. The proof for other components is quite similar.

We begin with the second equation of (1). If $e_0 > 0$ then for all $0 < t$ sufficiently small we have $E(t) > 0$, and if $e_0 = 0$ then $\dot{E}(0) = i_0$. Thus if $i_0 > 0$ then for all $0 < t$ sufficiently small we have $\dot{E}(t)$, $E(t) > 0$ and if $i_0 = 0$, then $\ddot{E}(0) = \bar{n} b^F f_0 > 0$. These all show that there exists $\delta_E > 0$ such that $E(t) > 0$ for $t \in (0, \delta_E)$.

Now consider the subcommunity F. If $f_0 > 0$ then for all $0 < t$ sufficiently small we have $F(t) > 0$, and if $f_0 = 0$ then $\dot{F}(0) = p(1-a)b^E e_0\,(s_0/(s_0 + i_0 + r_0))$. Thus if $e_0 > 0$ then for all $0 < t$ sufficiently small we have $\dot{F}(t)$, $F(t) > 0$ and if $e_0 = 0$, then $\ddot{F}(0) = \bar{n} p(1-a) b^E i_0\,(s_0/(s_0 + i_0 + r_0)) > 0$. These all show that there exists $\delta_E > 0$ such that $E(t) > 0$ for $t \in (0\,,\,\delta_E)$.

A similar method as above proves the existence of $\delta_X > 0$, for each $X \in \mathfrak{A}$, such that $X(t) > 0$ for $t \in (0, \delta_X)$. Then the proof is completed by putting $0 < \delta = \min\{\delta_X : X \in \mathfrak{A}\}$. ■

Lemma 6.2. *The suitable cone is positively invariant for the suitable solutions. Indeed, let $[0, \alpha)$ be the positive maximal interval of existence for a suitable solution $\gamma(t)$, then for all $t \in [0, \alpha)$, $S(t) > 0$ and all components of $\gamma(t)$ are nonnegative.*

Proof. We prove the lemma for $\gamma(t) \subset \mathfrak{N}_5 - \mathfrak{N}_4$, the other cases $\gamma(t) \subset \mathfrak{N}_{i+1} - \mathfrak{N}_i$, $i = 1, 2, 3$, are easier and similar. Since $\gamma(t) \subset \mathfrak{N}_5 - \mathfrak{N}_4$ so $E(t)$, $F(t)$ and $I(t)$ are not simultaneously zero; also, from the proof of the Case two of Lemma 6.1, we know that there exists $\delta > 0$ such that $S(t)$, $E(t)$, $F(t)$, $I(t) > 0$, and all components of $\gamma(t)$ are nonnegative for $t \in [0, \delta)$. Let $\delta \leq \alpha$ be the maximal real number having this property, it is sufficient to show that $\delta = \alpha$. Suppose that $\delta < \alpha$, we show that $S(\delta) > 0$ and the other components of $\gamma(t)$ are positive for all $\delta < t$ sufficiently close to δ. If $S(\delta) = 0$ then $\dot{S}(\delta) = b + b^R R(\delta) > 0$. This means that $S(t)$ is increasing for t sufficiently close to δ, Thus $S(\delta) > 0$. If $E(\delta) > 0$ then $E(t) > 0$ for all $\delta < t$ sufficiently close to δ, and if $E(\delta) = 0$ then $\dot{E}(\delta) = \bar{n} I(\delta)$. Thus if $I(\delta) > 0$ then $\dot{E}(\delta),\ E(\delta) > 0$ for all $\delta < t$ sufficiently close to δ, but if $I(\delta) = 0$ then $\ddot{E}(\delta) = b^F F(\delta) > 0$. These all show that $E(t) > 0$ for all $\delta < t$ sufficiently close to δ. A similar way shows that all components of $\gamma(t)$ are nonnegative for $\delta < t$ sufficiently close to δ. This proves that $\delta = \alpha$ and completes the proof. ■

Lemma 6.3. *Let $\gamma(t)$ be a suitable solution, then $\gamma(t)$ is bounded and defined for all $t > 0$.*

Proof. Let $[0, \alpha)$ be the positive maximal interval of the existence for a suitable solution $\gamma(t)$. It is sufficient to show that $\alpha = +\infty$. Suppose that $\alpha < +\infty$ and let $N(t)$ be the size of the community defined in the appendix section and satisfying the conservative equation $\dot{N} = b - \nu_0 N - \nu_1 I - \nu_2 H$. From Lemma 6.2, we know that $N(t) > 0$ for all $t \in [0, \alpha)$. If $\lim_{t \to \alpha} N(t) = 0$, then $\lim_{t \to \alpha} \dot{N}(t) = b > 0$ which is a contradiction. Thus $\gamma(t)$ can not converge to the borders of the suitable cone Γ; and hence, $\lim_{t \to \alpha} N(t) = +\infty$, [9, 20]. On the other hand, from Lemma 6.2 we know that $I(t),\ H(t) \geq 0$, hence $\dot{N} < b - \nu_0 N$. This shows that $N(t)$

does not diverge to $+\infty$. This shows that $N(t)$ and therefore all components of $\gamma(t)$ are bounded and defined for all $t \geq 0$ [9, 20]. ■

We summarize the above lemmas in the following proposition.

Proposition 6.4. *All suitable solutions of* (1) *are defined on the interval* $t \geq 0$. *Furthermore, they are positively bounded and contained in the suitable cone* Γ.

6.2. Steady states and invariant sets. Let $\zeta = (s, e, q, f, i, h, r) \in \Gamma$ be a steady state point of (1). From the first equation in (1) it follows that $s \neq 0$. On the other hand, it is easy to see that $\zeta_1 = (b/\nu_0, 0, 0, 0, 0, 0, 0)$ is the only steady state point of (1) contained in $\mathfrak{N}_4 \cap \Gamma$. In all systems emerging from SIR systems, ζ_1 is usually known as "free singularity" or "free equilibrium"; other steady states are usually known as "local singularity" or "local equilibrium" (see [3, 18]). Thus the "local singularities" belong to $(\mathfrak{N}_5 - \mathfrak{N}_4) \cap \Gamma$. This means that the components e, i and f are not simultaneously zero. Indeed, by using the method of the proofs of Lemmas 6.2 and 6.3, it then follows that all components of ζ are nonzero. Thus we have the following proposition.

Proposition 6.5. *The free singularity* ζ_1 *is the only steady state contained in* $\mathfrak{N}_1 \cap \Gamma$. *Other singularities, if any exists, are contained in* $(\mathfrak{N}_5 - \mathfrak{N}_4) \cap \Gamma$, *so they have nonzero components.*

The "free singularity" is biologically important. It is mostly because ζ_1 is the only steady state point that the solutions may converge to it in the case of the healing. Also, as we will see in the next section, ζ_1 may pass through a local bifurcation. Other steady states in $(\mathfrak{N}_5 - \mathfrak{N}_4) \cap \Gamma$, however, do not have the same motivation and they are too complicated to be analyzed in a general case. Finding a local singularity $\zeta \in (\mathfrak{N}_5 - \mathfrak{N}_4) \cap \Gamma$ needs a long computation which we ignore here; but, an easier process can be done by solving the system of equations

$$\mathfrak{L}_i(S, E, Q, F, I, H, R) = 0, \quad i = 1, 2, \ldots, 7$$

with respect to b and b^X, $(X \in \mathfrak{A})$. Thus we find the solutions $b^X = b^X(s, e, q, f, i, h, r)$, $(X \in \mathfrak{A})$ which are passable for certain positive values of $s, \ldots, r$. It can be seen through a direct computation that

$$\det\left(\frac{\partial(\mathfrak{L}_1, \mathfrak{L}_3, \mathfrak{L}_3, \mathfrak{L}_4, \mathfrak{L}_5, \mathfrak{L}_6, \mathfrak{L}_7)}{\partial(b, b^E, b^Q, b^F, b^I, b^H, b^R)}\right) = seqfihr \neq 0.$$

Thus, by the implicit function theorem, we have the following proposition.

Proposition 6.6. *Any local singularity* $\zeta \in (\mathfrak{N}_5 - \mathfrak{N}_4) \cap \Gamma$ *is isolated and depends continuously on the parameters of* (1).

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