Mathematics 4MB3/6MB3 Mathematical Biology

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2019 ASSIGNMENT 3

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This assignment is **due in class** on **Monday 25 February 2019 at 9:30am**.

Analysis of the standard SIR model with vital dynamics

Consider the standard SIR model with vital dynamics,

$$\frac{dS}{dt} = \mu N - \frac{\beta}{N} SI - \mu S \tag{1a}$$

$$\frac{dI}{dt} = \frac{\beta}{N} SI - \gamma I - \mu I \tag{1b}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{1c}$$

where S, I and R denote the numbers of susceptible, infectious and removed individuals, respectively, and $N = S + I + R$ is the total population size. The *per capita* rates of birth and death are the same (both are equal to μ). As usual, β is the transmission rate and γ is the recovery rate.

(a) Since equations (1) represent all changes in the size of each population compartment, the net change in the total population should be the sum of the change in each compartment, i.e. the sum of all equations (1). If the sum of all equations (1) is zero, $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$, the the change in total population size must be zero and the total population size N must be constant.

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = \mu N - \frac{\beta}{N} SI - \mu S + \frac{\beta}{N} SI - \gamma I - \mu I + \gamma I - \mu R \tag{2}$$

$$= \mu N - \mu S - \mu I - \mu R(-\frac{\beta}{N} SI + \frac{\beta}{N} SI)(-\gamma I + \gamma I) \tag{3}$$

$$= \mu(N - (S + I + R)) \tag{4}$$

Since $N = S + I + R$, i.e. the sum of all population compartments is equal to the total population size, 4 evaluates to 0. Thus the sum of population changes in all population compartments is 0 and the total population size remains constant.

Definition 1. *Forward Invariant Set*
Given a dynamical system $\dot{x} = f(x)$, a solution $x(t, x_0)$ with initial condition x_0, a set $\Delta = \{x \in \mathbb{R} \mid \phi(x) = 0\}$ for some positive definite function $\phi(x)$ is forward invariant if $x_0 \in \Delta \implies x(t, x_0) \in \Delta \ \forall \ t \geq 0$.

Since the population size has been shown to be constant and equal to N, the function $\phi(S, I, R) = N - (S + I + R)$ is always equal to zero, given any initial condition (S, I, R) satisfying $0 \leq S, I, R \leq N$ and $S + I + R = N$.

Definition 2. *Biologically Meaningful States*
Define the set $\Delta = \{(S, I, R) \mid 0 \leq S, I, R$ and $\phi(S, I, R) = 0\}$ where $\phi(S, I, R) = N - (S + I + R)$, to be the set of biologically meaningful states for this model.

Once the total population is equal to N, it will remain equal to N in all subsequent time steps due to the population size constancy. If all initial conditions are defined such that they satisfy $\phi(S, I, R) = 0$, then they can only evolve towards other states that satisfy $\phi(S, I, R) = 0$ due to the constant population size. Thus if the set Δ is defined to include all initial conditions x_0 that have a total population equal to N (i.e. all 3-tuples of positive integers $x_0 = (S, I, R)$ such that $\phi(S, I, R) = 0$), then they must necessarily include all possible time steps for solutions to the dynamical system with initial condition x_0, since the total population must remain constant over all time.

(b) Set the following variables:

$$S_p = \frac{S}{N} \tag{5a}$$

$$I_p = \frac{I}{N} \tag{5b}$$

$$R_p = \frac{R}{N} \tag{5c}$$

$$N_p = \frac{N}{N} = 1 \tag{5d}$$

Then substituting equations 5 into equations (1)

$$\begin{aligned}
\frac{dS_p}{dt} &= \mu N_p - \frac{\beta}{N_p} S_p I_p - \mu S_p \\
&= \mu 1 - \frac{\beta}{1} S_p I_p - \mu S_p \\
&= \mu - \beta S_p I_p - \mu S_p \\
&= \mu - \frac{\beta}{N}\frac{SI}{N} - \mu\frac{S}{N} \\
&= \frac{1}{N}(\mu N - \frac{\beta}{N} SI - \mu S) \\
&= \frac{1}{N}\frac{dS}{dt} \qquad (6)
\end{aligned}$$

$$\begin{aligned}
\frac{dI_p}{dt} &= \frac{\beta}{N_p} S_p I_p - \gamma I_p - \mu I_p \\
&= \frac{\beta}{1} S_p I_p - \gamma I_p - \mu I_p \\
&= \frac{\beta}{N}\frac{SI}{N} - \gamma\frac{I}{N} - \mu\frac{I}{N} \\
&= \frac{1}{N}(\frac{\beta}{N} SI - \gamma I - \mu I) \\
&= \frac{1}{N}\frac{dI}{dt} \qquad (7)
\end{aligned}$$

$$\begin{aligned}
\frac{dR_p}{dt} &= \gamma I_p - \mu R_p \\
\frac{dR_p}{dt} &= \gamma\frac{I}{N} - \mu\frac{R}{N} \\
&= \frac{1}{N}(\gamma I - \mu R) \\
&= \frac{1}{N}\frac{dR}{dt} \qquad (8)
\end{aligned}$$

From equations 6,7 and 8 it is clear that the proportional equations are equivalent to the original equations (1) scaled by a constant factor of $\frac{1}{N}$, and thus will retain the same dynamical behaviour.

(c) Using the equations

$$\tau = (\gamma + \mu)t \qquad (9a)$$

$$\mathcal{R}_0 = \frac{\beta}{\gamma + \mu} \qquad (9b)$$

$$\varepsilon = \frac{\mu}{\gamma + \mu} \qquad (9c)$$

First we express dt in terms of τ

$$\begin{aligned}
\tau &= t(\gamma+\mu) \\
d\tau &= dt(\gamma+\mu) \\
\frac{d\tau}{dt} &= (\gamma+\mu) \\
\frac{d\tau}{dt}\frac{d}{d\tau} &= \frac{d}{dt} \\
(\gamma+\mu)\frac{d}{d\tau} &= \frac{d}{dt} \\
\frac{d}{d\tau} &= \frac{1}{(\gamma+\mu)}\frac{d}{dt}
\end{aligned} \tag{10}$$

Next we isolate γ, β, μ,

$$\begin{aligned}
\varepsilon &= \frac{\mu}{\gamma+\mu} \\
\varepsilon(\gamma+\mu) &= \mu \qquad\qquad \gamma+\mu = \frac{\mu}{\varepsilon} \\
\varepsilon\gamma + \varepsilon\mu &= \mu \\
\varepsilon\gamma &= \mu(1-\varepsilon) \\
\gamma &= \frac{\mu}{\varepsilon}(1-\varepsilon) \\
\gamma &= (\gamma+\mu)(1-\varepsilon) \qquad (11)
\end{aligned}$$

From 9 it follows that $\beta = (\gamma+\mu)\mathcal{R}_0$ (12)

From 9 it follows that $\mu = (\gamma+\mu)\varepsilon$ (13)

Next, expressing $\frac{dS}{dt}$ in terms of τ using 10 and substituting equations 11,12 and 13 gives

$$\begin{aligned}
\frac{dS}{d\tau} &= \frac{1}{\gamma+\mu}\frac{dS}{dt} \\
&= \frac{1}{\gamma+\mu}[\mu - \beta SI - \mu S] \\
&= \frac{1}{\gamma+\mu}[\mu(1-S) - \beta SI] \qquad (14) \\
&= \frac{1}{\gamma+\mu}[\varepsilon(\gamma+\mu)(1-S) - (\gamma+\mu)\mathcal{R}_0 SI] \\
&= \frac{1}{\gamma+\mu}(\gamma+\mu)[\varepsilon(1-S) - \mathcal{R}_0 SI] \\
&= \varepsilon(1-S) - \mathcal{R}_0 SI \qquad (15)
\end{aligned}$$

Solving for $\frac{dI}{d\tau}$ using 10, 11, 12 and 13 gives

$$\begin{aligned}
\frac{dI}{d\tau} &= \frac{1}{\gamma+\mu}\frac{dI}{dt} \\
&= \frac{1}{\gamma+\mu}[\beta SI - \gamma I - \mu I] \\
&= \frac{1}{\gamma+\mu}[(\gamma+\mu)\mathcal{R}_0 SI - (\gamma+\mu)(1-\varepsilon)I - (\gamma+\mu)\varepsilon I] \\
&= \frac{1}{\gamma+\mu}(\gamma+\mu)[\mathcal{R}_0 SI - (1-\varepsilon)I - \varepsilon I] \\
&= \mathcal{R}_0 SI - (1-\varepsilon)I - \varepsilon I \\
&= \mathcal{R}_0 SI - (1-2\varepsilon)I
\end{aligned} \tag{16}$$

Finally, solving for $\frac{dR}{d\tau}$ using 10, 11, 12 and 13 gives

$$\begin{aligned}
\frac{dR}{d\tau} &= \frac{1}{\gamma+\mu}\frac{dR}{dt} \\
&= \frac{1}{\gamma+\mu}[\gamma I - \mu R] \\
&= \frac{1}{\gamma+\mu}[(\gamma+\mu)(1-\varepsilon)I - (\gamma+\mu)\varepsilon R] \\
&= \frac{1}{\gamma+\mu}(\gamma+\mu)[(1-\varepsilon)I - \varepsilon R] \\
&= (1-\varepsilon)I - \varepsilon R
\end{aligned}$$

The biological meanings of $\tau, \mathcal{R}_0$ and ε are

- τ is the average proportion of the population infected
- $\mathcal{R}_0$ is the number of secondary infections per infection
- ε is the mortality rate for the infected.

One reason these are good choices for non-dimensionalizing equations because they do not create more complex equations than the originals. These choices also reduce the total number of parameters from 3 (β, μ, γ) to 2 $(\varepsilon, \mathcal{R}_\prime)$. They all also have clear biological interpretations, making it easier to understand the biological relationships represeted by any mathematical reasoning done with them.
In the UK the morality rate from penumonia between 2001-2010 was estimated to be 0.0214% of people[1]. Ebola Virus Diesase is estimated by the WHO to have an average case fatality rate of 50%[2]. The CDC estimates measles to have a mortality rate between 0.1% to 0.2% [3].

(d) From our proportion equations, setting $\frac{dI}{dt} = 0$ we get:

$$
\begin{aligned}
0 &= \beta SI - \gamma I - \mu I \\
0 &= I(\beta S - \gamma - \mu) \\
\beta S &= \gamma + \mu \\
\hat{S} &= \frac{1}{R_0}
\end{aligned}
$$

Adding the proportion equations of $\frac{dS}{dt} = 0$ and $\frac{dI}{dt} = 0$ we also get:

$$
\begin{aligned}
0 &= \mu - \mu S - \gamma I - \mu I \\
1 - S - I &= \frac{\gamma}{\mu} I \\
1 - S &= \frac{\mu + \gamma}{\mu} I \\
1 - S &= \frac{1}{\epsilon} I \\
I &= \epsilon(1 - S) \\
\hat{I} &= \epsilon(1 - \frac{1}{R_0})
\end{aligned}
$$

Therefore $(\hat{S}, \hat{I}) = (\frac{1}{R_0}, \epsilon - \frac{\epsilon}{R_0})$. Both equilibria are biologically relevant as long as $R_0 > 1$, since values of S and I outside of the range $[0, 1]$ are not meaningful as proportions.

(e) Local asymptotic stability can be derived logically from the definition of R_0. When $R_0 < 1$, this means that the number of secondary infections per infection is less than 1. Thus, if the disease has just started, the number of infected will immediately go back to 0 or the disease free equilibrium.
On the other hand if $R_0 > 1$, the disease will spread once it starts. The number of infected (I) can never reach 1 either since ϵ (mortality rate) exists, so there is also an upper limit. Ergo, the equilibrium in between (0,1), or the endemic equilibrium, must be asymptotically stable when $R_0 > 1$.
A more mathematically detailed proof is done in parts f and g, proving global asymptotic stability under these conditions.

(f) Let us start by using the Lyapunov function $L = I$. $L = 0$ when $(S, I) = (1, 0)$. Since $R_0 \leq 1$ we can conclude that $\beta \leq \gamma + \mu$ or $\beta - \gamma - \mu \leq 0$. Calculating $\dot{L}$ we have:

$$
\begin{aligned}
\dot{L} &= \frac{dL}{dI}\frac{dI}{dt} + \frac{dL}{dS}\frac{dS}{dt} \\
&= \beta SI - \gamma I - \mu I + \mu I - \beta SI^2 - \mu SI \\
&= I(\beta S - \gamma - \mu S - \beta SI) \\
&\leq I(\beta S - \gamma S - \mu S - \beta SI) \\
&= I[S(\beta - \gamma - \mu) - \beta SI] \\
&< 0 \forall\ S, I \in (0,1)
\end{aligned}
$$

$L(1,0) = 0$ and $\dot{L} < 0\ \forall S, I \in (0,1)$. Hence, L is negative definite on the interval (0,1). L is therefore a strict Lyapunov function for the DFE on the entire biologically relevant space, which implies that the DFE is globally asymptotically stable.

(g) The EE is $(\hat{S}, \hat{I}) = (\frac{1}{\mathcal{R}_0}, \varepsilon(1-\frac{1}{\mathcal{R}_0})$. Consider the Lyapunov function with $\mathcal{O} = \{(S,I)|0 \leq S, I \leq 1\ and\ S + I = 1\}$

$$
\begin{aligned}
L(S,I) &= S - \frac{1}{\mathcal{R}_0}log(S) + I - \varepsilon(1 - \frac{1}{\mathcal{R}_0})log(I) \\
&= S - \frac{1}{\mathcal{R}_0}log(S) + I - \varepsilon log(I) - (\frac{\varepsilon}{\mathcal{R}_0})log(I) \\
&= S - \frac{1}{\mathcal{R}_0}log(S) + I + \varepsilon log(I)(\frac{1}{\mathcal{R}_0} - 1) \qquad (17)
\end{aligned}
$$

$$
0 \leq S, I \leq 1 \implies log(S), log(I) < 0 \implies
$$

$$
0 < S - \frac{1}{\mathcal{R}_0}log(S) + I + \varepsilon log(I)(\frac{1}{\mathcal{R}_0} - 1) \qquad (18)
$$

Thus 18 shows that 17 is positive on $[0,1]$, the the function is postive definite on $[0,1]$.

$$
\begin{aligned}
L(\hat{S}, \hat{I}) &= \hat{S} - \hat{S}log(\hat{S}) + \hat{I} \qquad (19) \\
&= \hat{S} - \frac{1}{\mathcal{R}_0}log(\frac{1}{\mathcal{R}_0}) + I - \varepsilon(1 - \frac{1}{\mathcal{R}_0})log(I) \qquad (20) \\
& \qquad (21)
\end{aligned}
$$

From Lyapunov's theorem, a function $L(X)$ satisfies $L(X) > L(X_*) \forall\ X \in \mathcal{O} \setminus \{X_*\}$ where $X_* = (\hat{S}, \hat{I})$, and using the same set $\mathcal{O}$ as defined earilier.

$$
L(S,I) > L(\hat{S}, \hat{I})
$$

$$
S - \hat{S}log(S) + I - \hat{I}log(I) > \hat{S} - \hat{S}log(\hat{S}) + \hat{I} - \hat{I}log(\hat{I})
$$

$$
\begin{aligned}
\frac{\partial L}{\partial S} &= 1 - \frac{\hat{S}}{S} \\
\frac{\partial L}{\partial S} &= 1 - \frac{\hat{S}}{S} = 0 \implies S = \hat{S} \\
\frac{\partial L}{\partial I} &= 1 - \frac{\hat{I}}{I} \\
\frac{\partial L}{\partial I} &= 1 - \frac{\hat{I}}{I} = 0 \implies I = \hat{I}
\end{aligned}
$$

The functions $log(S), log(I)$ increase monotonically with respect to $\hat{S}, \hat{I}$. Both partial derivatives $\frac{\partial L}{\partial S}, \frac{\partial L}{\partial I}$ as well, the by **??**, **??** show that $(\hat{S}, \hat{I}$ must be the global minimum of $L(S, I)$ on $[0, 1]$.
Further

$$
\begin{aligned}
\frac{\partial^2 L}{\partial S^2} &= \hat{S} S^{-2} \text{at} \hat{S} = \frac{\hat{S}}{\hat{S}^2} = \frac{1}{\hat{S}} \\
\frac{\partial^2 L}{\partial I^2} &= \hat{I} I^{-2} \text{at} \hat{I} = \frac{\hat{I}}{\hat{I}^2} = \frac{1}{\hat{I}}
\end{aligned}
\tag{22}
$$

are non-negative at the minimum point $(\hat{S}, \hat{I})$, thus $L(S, I) > L(\hat{S}, \hat{I}) \forall\ (S, I) \in \mathcal{O} \setminus \{(\hat{S}, \hat{I})\}$.

From 6, 7

$$
\begin{aligned}
0 &= \beta\hat{S}\hat{I} - \gamma\hat{I} - \mu\hat{I} \implies \beta\hat{S}\hat{I} = \gamma\hat{I} + \mu\hat{I} \\
0 &= \mu - \beta\hat{S}\hat{I} + \mu\hat{S} \implies \beta\hat{S}\hat{I} = \mu - \mu\hat{S} \\
\dot{L}(S,I) &= (1 - \frac{1}{\mathcal{R}_0 S})(\mu - \beta SI - \mu S) + (1 - \frac{\varepsilon(1-\frac{1}{\mathcal{R}_0})}{I})(\beta SI - \gamma I - \mu I) \\
&= \mu - \mu S - \frac{\mu}{\mathcal{R}_0 S} + \frac{\beta I}{\mathcal{R}_0} + \frac{\mu}{\mathcal{R}_0} - \gamma I - \mu I - \beta SI + \gamma\hat{I} + \mu\hat{I} \\
&= \mu(2 - S - \frac{1}{\mathcal{R}_0 S}) + \frac{\beta I}{\mathcal{R}_0} - \frac{\beta S}{\mathcal{R}_0}(\varepsilon\mathcal{R}_0 - \varepsilon) - I(\gamma + \mu) \\
&= \mu(2 - S - \frac{1}{\mathcal{R}_0 S}) + \frac{\beta}{\mathcal{R}_0}(I - S\varepsilon\mathcal{R}_0 + S\varepsilon) - I\frac{\mu}{\varepsilon} \\
&= \mu(2 - S - \frac{1}{\mathcal{R}_0 S}) + \frac{\mu}{\varepsilon}(I - S\varepsilon\mathcal{R}_0 + S\varepsilon) - I\frac{\mu}{\varepsilon} \\
&= \mu(2 - S - \frac{1}{\mathcal{R}_0 S}) + \frac{\mu}{\varepsilon}(I - S\varepsilon\mathcal{R}_0 + S\varepsilon - I) \\
&= \mu(2 - S - \frac{1}{\mathcal{R}_0 S}) + \frac{\mu}{\varepsilon}(-S\varepsilon\mathcal{R}_0 + S\varepsilon) \\
&= \mu(2 - S - \frac{1}{\mathcal{R}_0 S}) + \mu(-S\mathcal{R}_0 + S) \\
&= \mu(2 - S - \frac{1}{\mathcal{R}_0 S} - S\mathcal{R}_0 + S) \\
&= \mu(2 - \frac{\hat{S}}{S} - \frac{S}{\hat{S}}) \\
&= -\mu(\frac{\hat{S}}{S} + \frac{S}{\hat{S}} - 2) \\
&= -\mu\frac{\hat{S}}{S}(1 - \frac{S}{\hat{S}})^2
\end{aligned} \tag{23}
$$

By 23 $\dot{L}(S,I) \leq 0 \forall\ (S,I) \in (0,1)$ and from earlier $\dot{L}(\hat{S},\hat{I}) = 0$. Hence $\dot{L}$ is negative definite on $(0,1)$. Therefore $L(S,I)$ is a strict Lyapunov function for the EE for the biologically relevant states, excluding the DFE, which implies the EE is GAS.

(h) Since the EE is GAS, any oscillations will be damped and approaching the EE. Oscillations will occur if the imaginary parts of the eigenvalues of the Jacobian, evaluated at the EE $(\hat{S},\hat{I}) = (\frac{1}{\mathcal{R}_0}, \varepsilon(1-\frac{1}{\mathcal{R}_0}))$, are non-zero. Since the Jacobian is a 2×2 matrix, the eigenvalues are the roots of the equation $\lambda^2 - T\lambda + D = 0$ where T and D are the trace and determinant of the Jacobian respectively. The roots can be found using the quadratic formula $\frac{-b \pm \sqrt{b^2-4ac}}{2a}$. The imaginary part of the roots will only be non-zero if $\sqrt{b^2-4ac} < 0$, thus proving $\sqrt{b^2-4ac} < 0$ implies damped oscillations approaching the EE.

The Jacobian at the EE is

$$J = \begin{bmatrix} \frac{\partial S}{\partial S} & \frac{\partial S}{\partial I} \\ \frac{\partial I}{\partial S} & \frac{\partial I}{\partial I} \end{bmatrix} \tag{24}$$

$$= \begin{bmatrix} -\beta I - \mu & -\beta S \\ \beta I & \beta S - (\gamma + \mu) \end{bmatrix} \tag{25}$$

$$J(\hat{S}, \hat{I}) = J(\frac{1}{\mathcal{R}_0}, \varepsilon(1 - \frac{1}{\mathcal{R}_0}) \tag{26}$$

$$= \begin{bmatrix} -\beta\varepsilon(1 - \frac{1}{\mathcal{R}_0}) - \mu & -\beta\frac{1}{\mathcal{R}_0} \\ \beta\varepsilon(1 - \frac{1}{\mathcal{R}_0}) & \beta\frac{1}{\mathcal{R}_0} - (\gamma + \mu) \end{bmatrix} \tag{27}$$

Next substitute β, γ, μ using equations 11,12,13

$$= \begin{bmatrix} -(\gamma + \mu)\mathcal{R}_0\varepsilon(1 - \frac{1}{\mathcal{R}_0}) - \varepsilon(\gamma + \mu) & -(\gamma + \mu)\mathcal{R}_0\frac{1}{\mathcal{R}_0} \\ (\gamma + \mu)\mathcal{R}_0\varepsilon(1 - \frac{1}{\mathcal{R}_0}) & (\gamma + \mu)\mathcal{R}_0\frac{1}{\mathcal{R}_0} - (\gamma + \mu) \end{bmatrix} \tag{28}$$

$$= (\gamma + \mu) \begin{bmatrix} -\varepsilon\mathcal{R}_0 & -1 \\ \varepsilon(\mathcal{R}_0 - 1) & 0 \end{bmatrix} \tag{29}$$

Next the trace T, determinant D, and the terms of the quadratic formula a, b, c are

$$T = -\varepsilon\mathcal{R}_0 + 0 \tag{30}$$

$$D = (-\varepsilon\mathcal{R}_0)(0) - (-1)(\varepsilon(\mathcal{R}_0 - 1) \tag{31}$$

$$= \varepsilon(\mathcal{R}_0 - 1) \tag{32}$$

$$0 = \lambda^2 - T\lambda + D \implies a = 1 \quad b = -T \quad c = D \tag{33}$$

$$b = \varepsilon\mathcal{R}_0 \tag{34}$$

$$c = \varepsilon(\mathcal{R}_0 - 1) \tag{35}$$

$$\sqrt{b^2 - 4ac} = \sqrt{(\varepsilon\mathcal{R}_0)^2 - 4(1)(\varepsilon(\mathcal{R}_0 - 1))} \tag{36}$$

$$= \sqrt{\varepsilon^2{\mathcal{R}_0}^2 - 4(\varepsilon(\mathcal{R}_0 + 4\varepsilon} \tag{37}$$

$$= \sqrt{\varepsilon(\varepsilon{\mathcal{R}_0}^2 - 4\mathcal{R}_0 + 4)} \tag{38}$$

Now if we show that the when the inequality

$$\sqrt{\varepsilon(\varepsilon{\mathcal{R}_0}^2 - 4\mathcal{R}_0 + 4)} < 0 \tag{39}$$

holds it implies $\varepsilon < \varepsilon^* = \frac{4\mathcal{R}_0 - 1}{{\mathcal{R}_0}^2}$, then this proves that the approach to EE via damped

oscillations occurs iff $\varepsilon < \varepsilon^*$

$$\sqrt{\varepsilon(\varepsilon{\mathcal{R}_0}^2 - 4\mathcal{R}_0 + 4)} < 0 \tag{40}$$

$$\sqrt{\frac{4\mathcal{R}_0 - 1}{{\mathcal{R}_0}^2}(\frac{4(\mathcal{R}_0 - 1)}{{\mathcal{R}_0}^2}{\mathcal{R}_0}^2 - 4\mathcal{R}_0 + 4)} < 0 \tag{41}$$

$$\sqrt{\frac{4\mathcal{R}_0 - 1}{{\mathcal{R}_0}^2}(4(\mathcal{R}_0 - 1) - 4\mathcal{R}_0 + 4)} < 0 \tag{42}$$

$$\sqrt{\frac{4\mathcal{R}_0 - 1}{{\mathcal{R}_0}^2}(4\mathcal{R}_0 - 4 - 4\mathcal{R}_0 + 4)} < 0 \tag{43}$$

$$\sqrt{\frac{4\mathcal{R}_0 - 1}{{\mathcal{R}_0}^2}(0)} < 0 \tag{44}$$

$$0 < 0 \text{ which is false} \tag{45}$$

Since **??** is 0 when $\varepsilon = \varepsilon^*$, increasing ε will cause $\sqrt{\varepsilon(\varepsilon{\mathcal{R}_0}^2 - 4\mathcal{R}_0 + 4)}$ to become positive and decreasing ε will cause $\sqrt{\varepsilon(\varepsilon{\mathcal{R}_0}^2 - 4\mathcal{R}_0 + 4)}$ to become negative. Thus $\sqrt{\varepsilon(\varepsilon{\mathcal{R}_0}^2 - 4\mathcal{R}_0 + 4)}$ is only negative when $\varepsilon < \varepsilon^*$ and $\sqrt{\varepsilon(\varepsilon{\mathcal{R}_0}^2 - 4\mathcal{R}_0 + 4)} < 0$ implies non-negative imaginary components of the eigenvalue of $J(\hat{S}, \hat{I})$, which in turn implies dampened oscillations when the model is approaching the EE. Thus $\varepsilon < \varepsilon^*$ is a necessary condition for dampened oscillations in the model while approaching the EE.

(i) Assuming $\epsilon < \epsilon^*$, the period of damped oscillations to the EE and the e-folding time of decay of the amplitude of oscilations is determined by analyzing the complex eigenvalue of the Jacobian of the system evaluated at the EE.

The Jacobian of the system is:

$$J(S, I) = \begin{bmatrix} -\beta I - \mu & -\beta S & 0 \\ \beta I & \beta S - (\mu + \gamma) & 0 \\ 0 & \gamma & -\mu \end{bmatrix}$$

To simplify, the above Jacobian can be reduced to the upper left 2×2 matrix (since the system can be reduced to the first two equations) and evaluated at the EE $(\hat{S}, \hat{I})$. The characteristic polynomial is computed by substracting λ on the diagonal and calculating the determinant.
So simplifying $J(\hat{S}, \hat{I})$, the characteristic polynomial is:

$$(-\beta\hat{I} - \mu - \lambda)(\beta\hat{S} - (\mu + \gamma) - \lambda) + \beta^2\hat{S}\hat{I} = 0 \tag{46}$$

The EE is $(\frac{\mu+\gamma}{\beta}, \frac{\mu}{\beta}(\mathcal{R}_0 - 1))$ so the characteristic polynomial at the EE is:

$$
\begin{aligned}
0 &= (-\beta\hat{I} - \mu - \lambda)(\beta\hat{S} - (\mu+\gamma) - \lambda) + \beta^2\hat{S}\hat{I} \\
0 &= (-\mu(\mathcal{R}_0 - 1) - \mu - \lambda)(-\lambda) + (\mu+\gamma)\mu(\mathcal{R}_0 - 1) \\
0 &= \lambda^2 + (\mu\mathcal{R}_0)\lambda + (\mu+\gamma)\mu(\mathcal{R}_0 - 1)
\end{aligned}
$$

Solving for the eigenvalue, λ, using the quadratic equation:

$$
\lambda = -\frac{\mu\mathcal{R}_0}{2} \pm \frac{\sqrt{(\mu\mathcal{R}_0)^2 - 4(\mu+\gamma)\mu(\mathcal{R}_0 - 1)}}{2} \tag{47}
$$

Assuming that$(\mu\mathcal{R}_0)^2$ is relatively small, then this eigenvalue will be complex, $\lambda = -\frac{\mu\mathcal{R}_0}{2} \pm iM$. The period of damped oscillations, T, is $T = 2\pi\frac{1}{M}$ and the e-folding time, $t_e = \frac{1}{re(\lambda)}$, is $t_e = \frac{2}{\mu\mathcal{R}_0}$.

Furthermore if we assume that $(\mu\mathcal{R}_0)^2 \approx 0$, the above can be simplified to:

$$
\lambda \approx -\frac{\mu\mathcal{R}_0}{2} \pm i\sqrt{(\mu+\gamma)\mu(\mathcal{R}_0 - 1)} \tag{48}
$$

So the period of damped oscillations can be approximated as $T \approx \frac{2\pi}{\sqrt{(\mu+\gamma)\mu(\mathcal{R}_0 - 1)}}$.

The period of damped oscillations can observed in the following graph which uses $I(0) = 0.00025, S(0) = 0.1, \beta = 550, \gamma = 365/7, \mu = 1/70$.

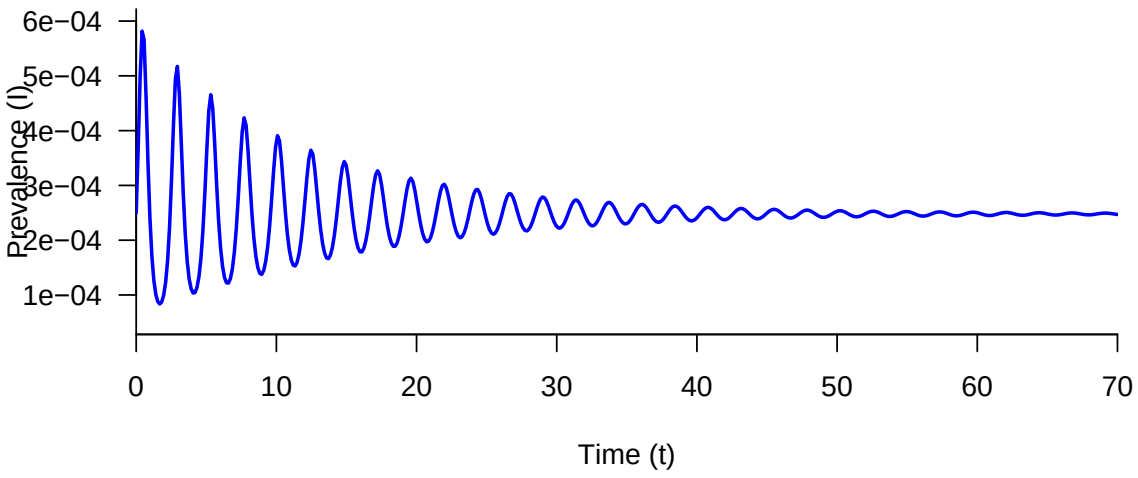
```
SIR.vector.field <- function(t, vars, parms=c(beta=3,gamma=1, mu=0.05)) {
with(as.list(c(parms, vars)), {
dx <- -beta*x*y + mu - mu*x # dS/dt of SIR model
dy <- beta*x*y - gamma*y - mu*y # dI/dt of SIR model
dz <- gamma*y - mu*z #dR/dt of SIR model
vec.fld <- c(dx=dx, dy=dy, dz=dz)
return(list(vec.fld)) # ode() requires a list
})
}
##Plots the solution I(t) of the SIR model
plot.It <- function(ic=c(x=1,y=0,z=0), tmax=1,
times=seq(0,tmax,by=tmax/500),
func, parms, ... ) {
It <- ode(ic, times, func, parms)
lines(times, It[,"y"], col="blue", lwd=2, ... )
}

tmax <- 70 # end time for numerical integration of the ODE
## draws the empty plot:
```

```
plot(0,0,xlim=c(0,70),ylim=c(0.00005,0.0006), xaxs="i",
type="n",bty="L",xlab="Time (t)",ylab="Prevalence (I)",las=1)

## Given initial conditions and parameter values:
I0 <- 0.00025
S0 <- 0.1

{
plot.It(ic=c(x=S0,y=I0,z=0), tmax=tmax,
func=SIR.vector.field,
parms=c(beta=550,
        gamma=365/7, #mean infectious period is 7 days in a year
        mu=1/70 #the average lifespan in the population is 70 years
        )
)
}
```




```
beta <- 550
gamma <- 365/7
mu <- 1/70

R0 <- beta/(gamma+mu)
A <- (gamma+mu)*mu*(R0-1)
epsilon <- mu/(gamma+mu)
period <- 2*pi/Im(sqrt(as.complex((mu*R0)^2-4*A))/2) #equation from previous analysi
efold <- 2/(mu*R0)
```

```
R0
```

```
## [1] 10.54506
```

```
epsilon
```

```
## [1] 0.0002738976
```

```
period
```

```
## [1] 2.356981
```

```
efold
```

```
## [1] 13.27636
```

In the graph, the distance from peak to peak is slightly larger than 2 years, indicating approximately a 2-year cycle of oscillations. This is confirmed with the above calculation where the period is 2.356 years.

(j) As $\mathcal{R}_0$ is increased from 0 to ∞, using the dimensionless forms of the differential equations, it is apparent that one of the bifurcations of $\mathcal{R}_0$ is $\mathcal{R}_0 = 1$ (which is the transcritical bifurcation).

Consider $\frac{dI}{d\tau} = I(\mathcal{R}_0 S - 1)$ when and initially $S \approx 1$ and $I \ll 1$. Then an epidemic can occur if $\frac{dI}{d\tau} > 0$ (meaning that the number of infectious people increases). Hence, for an epidemic (i.e. convergence to the EE):

$$\begin{aligned} I(\mathcal{R}_0 S - 1) &> 0 \\ \mathcal{R}_0 - 1 &> 0 \\ \mathcal{R}_0 &> 1 \end{aligned}$$

The two "bifurcations" that yield biologically relevant changes can be determined by looking at the boundaries of $\mathcal{R}_0$ in terms of ϵ^* threshold of damped oscilation in part (h):

$$\begin{aligned} \epsilon &= \frac{4(\mathcal{R}_0 - 1)}{(\mathcal{R}_0)^2} \\ \epsilon(\mathcal{R}_0)^2 - 4\mathcal{R}_0 + 4 &= 0 \end{aligned}$$

Using the quadratic formula, it follows that there are two possible $\mathcal{R}_0$ values:

$$\mathcal{R}_0 = \frac{4 \pm \sqrt{16 - 16\epsilon}}{2\epsilon}$$

To visualize these results, a value of $\epsilon = \frac{8}{9}$ will be used since it is a biologically reasonable value (and the corresponding "bifurcations" are also biologically valid). Using this value we get $\mathcal{R}_0 = 1.5, 3$.

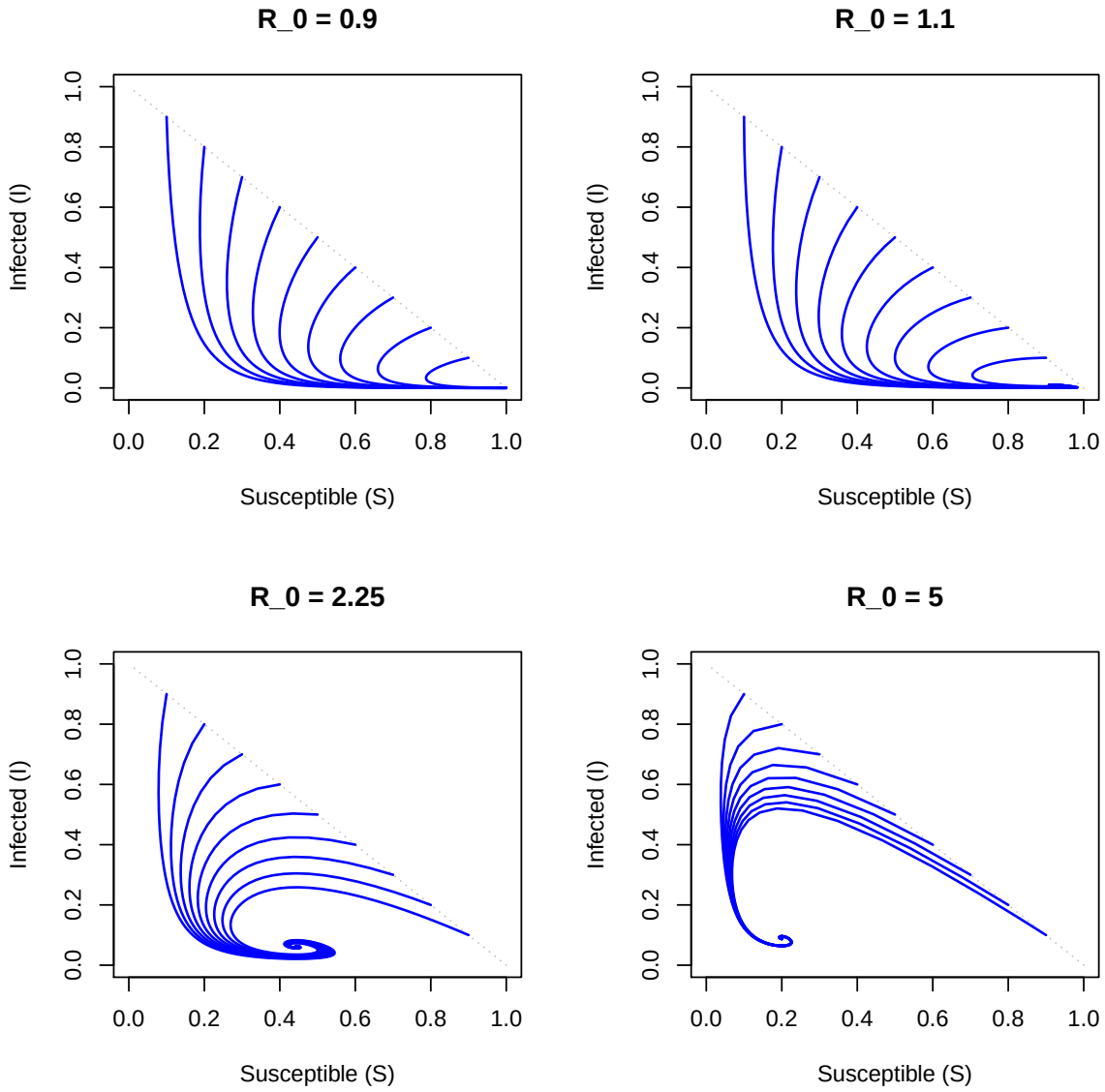
When $0 < \mathcal{R}_0 < 1$, then solutions will converge to the DFE. When $1 < \mathcal{R}_0 < 1.5$, then dynamics will be less oscillatory, meaning that recurrent epidemics will dampen out relatively quickly. This is also similar to the dynamics of the system when $3 < \mathcal{R}_0 < Z$, where Z is large. When $1.5 < \mathcal{R}_0 < 3$, the system will likely show slower damped oscillatory dynamics, where more reccurent epidemics are possible before the system converges to the EE.

```
##Dimensionless form (only parameters are epsilon and \mathcal R_0)##
SIR.vector.field <- function(t, vars, parms=c(epsilon = 8/9, R0 = 5)) {
with(as.list(c(parms, vars)), {
dx <- epsilon*(1-x)-R0*x*y # dS/dt of SIR model
dy <- R0*x*y - y # dI/dt of SIR model
dz <- (1-epsilon)*y - epsilon*z #dR/dt of SIR model
vec.fld <- c(dx=dx, dy=dy, dz=dz)
return(list(vec.fld))
})
}

##S(I) plotting function##
plot.SI <- function(ic=c(x=1,y=0,z=0), tmax=1,
times=seq(0,tmax,by=tmax/500),
func, parms, ... ) {
St <- ode(ic, times, func, parms)
lines(St[,"x"], St[,"y"], col="blue", lwd=1.5, ... )
}

##Various R0 values##
R0vals <- c(0.9, 1.1, 2.25, 5)
#intial conditions
S0 <- seq(0,0.9,by=0.1)[-1]
I0 <- seq(0.9,0, by=-0.1)[-10]
par(mfrow = c(2,2)) #Setting up the subplots
for (i in 1:length(R0vals)) {
  pars <-  c(epsilon = 1/9, R0 = R0vals[i])
  title <- paste("R_0 =", R0vals[i]) #labelling R0 for each plot
```

```
  plot(x=0, y=0, type = "n", xlim = c(0,1), ylim = c(0,1), #empty subplot
       xlab = "Susceptible (S)", ylab= "Infected (I)", main=title)
  lines(x=c(1,0),y=c(0,1),col="grey",lty="dotted")
  for (j in 1:length(S0)) {
    plot.SI(ic=c(x=S0[j],y=I0[j],z=0), tmax=tmax,
            func=SIR.vector.field,
            parms=pars
  )
  }
}
```



(k) There are no diseases that display recurrent epidemics for which the SIR model with vital dynamics is adequate to explain the observed epidemic dynamics. From results in

parts (g) and (h), given that $\mathcal{R}_0 > 1$ (such that an epidemic occurs) the EE is GAS and that for all initial conditions, $I(0) > 0, S(0) > 0$, the system approaches the EE with damped oscillations. Additionally, by observing the Jacobian evaluated at the EE, the complex eigenvalues have negative real part and non-zero imaginary part, implying that the dynamics are always oscilatory. Thus recurrent epidemics with no evidence of damping out (like measles) cannot be explained by the SIR model with vital dynamics.

References

1. Foundation, B. L. *Pneumonia Statistics* https://statistics.blf.org.uk/pneumonia.
2. Organization, W. H. *Ebola Virus Disease* https://statistics.blf.org.uk/pneumonia.
3. Control, C. F. D. & Prevention. *Measles (Rubeola)* https://www.cdc.gov/measles/about/complications.html.

— END OF ASSIGNMENT —

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