Dynamics of the SEIR Model with Limited Hospital Treatment

Ivan Kirev

Imperial College London

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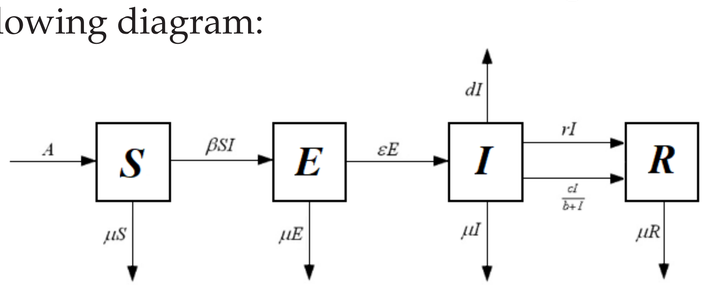
Introduction

Here we consider an SEIR type disease with limited hospital treatment. The total population is divided into four groups: susceptible $S(t)$, exposed $E(t)$ (infected but not infectious), infected $I(t)$ (may be asymptomatic), and recovered $R(t)$ (lifelong immunity assumed).

The Model

We construct our model according to the following diagram:



where A is the birth rate, μ is the natural death rate, β is the infection rate, ε is the rate of progression from E to I, r is the recovery rate and d is the fatality rate.

In many cases, the number of patients that require treatment exceeds the capacity of the local healthcare system. Therefore, we have also included the recovery rate with hospital treatment $\frac{cI}{b+I}$ [1].
The governing differential equations for the model are:

$$\begin{aligned}
\frac{dS}{dt} &= A - \mu S - \beta SI \\
\frac{dE}{dt} &= \beta SI - (\mu + \varepsilon)E \\
\frac{dI}{dt} &= \varepsilon E - (\mu + r + d)I - \frac{cI}{b+I} \\
\frac{dR}{dt} &= rI - \mu R + \frac{cI}{b+I}
\end{aligned} \tag{1}$$

Here c is the maximum recovery per unit of time and b measures how fast there is a saturation.

Since the R compartment appears only in the last equation, we can consider the first three equations of (1) as our system.

The R_0 Parameter

The Basic reproduction number, R_0, represents the number of people who got infected by a typical infective individual. We will calculate it using the method described in [2].
If we let $x = (E, I, S)^T$, we have

$$\frac{dx}{dt} = \mathcal{F}(x) - \mathcal{V}(x), \text{ where}$$

$$\mathcal{F}(x) = \begin{bmatrix} \beta SI \\ 0 \\ 0 \end{bmatrix},$$

$$\mathcal{V}(x) = \begin{bmatrix} (\mu+\varepsilon)E \\ -\varepsilon E + (\mu + r + d)I - \frac{cI}{b+I} \\ -A + \beta SI + \mu S \end{bmatrix}$$

R_0 is the spectral radius of the matrix FV^{-1}, where we can find that

$$F = \begin{bmatrix} 0 & \frac{bA}{\mu} \\ 0 & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \mu+\varepsilon & 0 \\ -\varepsilon & \mu + r + d + \frac{c}{b} \end{bmatrix}.$$

Therefore, we can conclude that:

$$R_0 = \frac{\beta \varepsilon A b}{\mu(\mu+\varepsilon)(\mu b + rb + db + c)}.$$

Equilibria

We always have the **disease-free equilibrium** $X_0 = (\frac{A}{\mu}, 0, 0)$. The **endemic equilibrium** can be deduced from the system to be $X^* = (S^*, E^*, I^*)$, where

$$S^* = \frac{A}{\beta I^* + \mu}, E^* = \frac{\beta A I^*}{\mu^2 + \mu\varepsilon + (\mu\beta + \mu\varepsilon)I^*},$$

and I^* is the positive solution to the equation $a_1 {I^*}^2 + a_2 I^* + a_3 = 0$, where

$$\begin{aligned}
a_1 &= \beta(\mu+\varepsilon)(\mu + r + d), \\
a_2 &= (\mu+\varepsilon)(\mu^2 + \mu\beta b + \mu d + \mu r + c\beta + db\beta \\
&\quad + rb\beta) - \varepsilon\beta A, \\
a_3 &= \mu(\mu+\varepsilon)(\mu b + rb + db + c)(R_0 - 1),
\end{aligned}$$

and R_0^* is the solution for R_0 of $a_2^2 - 4a_1a_3 = 0$.
Analysing the quadratic we see that there are:
1. **No endemic equilibria** when:
$-R_0 \leq 1, a_2 > 0$
$-R_0 < R_0^* < 1, a_2 < 0$
2. **An unique endemic equilibrium** when:
$-R_0 > 1, a_2 > 0$
$-R_0^* = R_0 < 1, a_2 < 0$
$-R_0 = 1, a_2 < 0$
3. **Two endemic equilibria** when:
$-R_0^* < R_0 < 1, a_2 < 0.$

Stability of Equilibria

Figures 1, 2 and 3 represent the phase portraits of the model in three different scenarios:

- **Figure 1.**
Here we have no endemic equilibria (plot is made for $R_0 < 1, a_2 > 0$). From the figure we can see that the disease-free equilibrium is **globally asymptotically stable**.
- **Figure 2.**
Here we have one endemic equilibrium (plot is made when $R_0 > 1$). From the figure we can see that the endemic equilibrium is **globally asymptotically stable**, while the disease-free equilibrium is **unstable**.
- **Figure 3.**
Here we have two endemic equilibria ($R_0^* < R_0 < 1, a_2 < 0$). From the figure we can see that the first endemic equilibrium and the disease-free one are **globally asymptotically stable**, while the second endemic equilibrium is **unstable**.

The deductions here are made by analysing the graphs of specific numerical simulations. For an analytical proof see [3].

Plots

Figure 1.

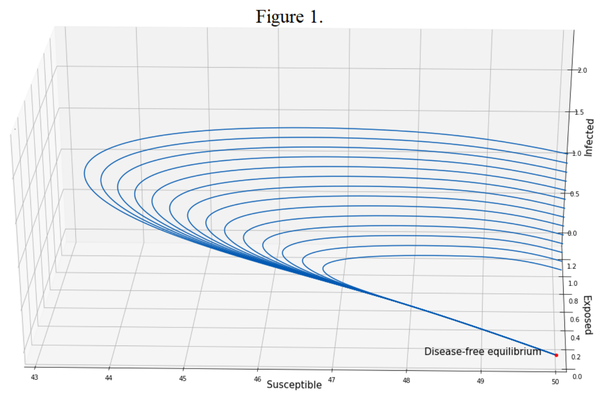


Figure 2.

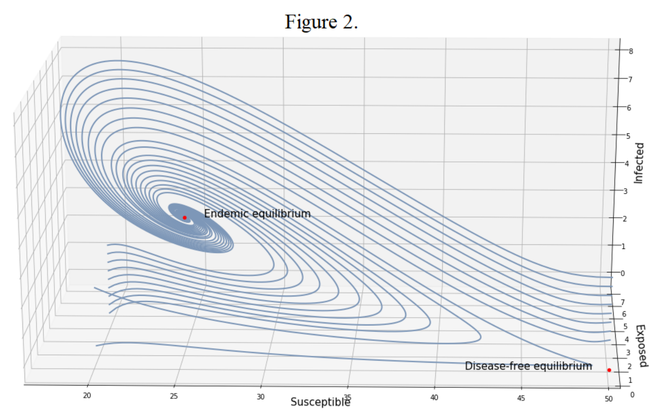


Figure 3.

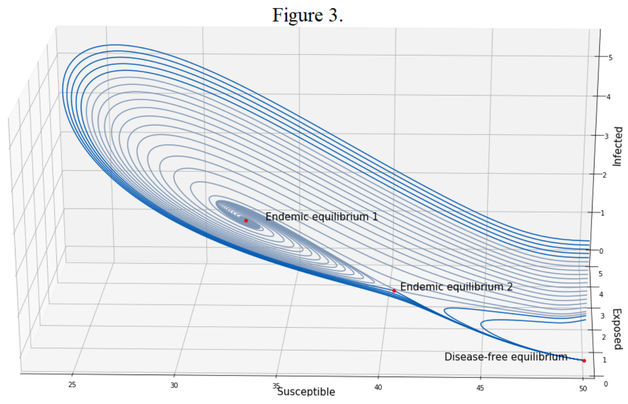
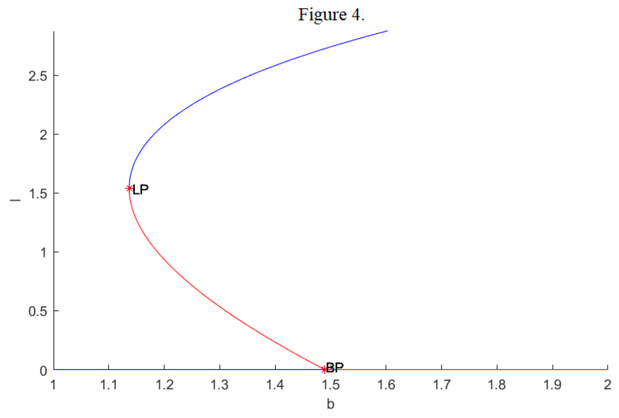


Figure 4.



Bifurcation Analysis

Figure 4 represents the bifurcation diagram for the parameter b. There are two threshold values for b - a Limit Point and a Branch Point, so we can consider the following three cases:

- When $\mathbf{b < LP}$ we only have one **stable disease-free equilibrium**. In this case the disease *dies out* in time.
- When $\mathbf{LP < b < BP}$ we have one **stable** and one **unstable endemic equilibria** and also one **stable disease-free equilibrium**. In this case the disease either *dies our or converges* to an endemic equilibrium (as in Figure 3).
- When $\mathbf{b > BP}$ there is one **stable endemic equilibrium** and an **unstable disease-free** one. In this case the disease *doesn't die out* in time.

Conclusion

This paper considers an SEIR model with limited hospital treatment. We deduce that there can be either (1) no endemic equilibrium - disease dies out, (2) one stable endemic equilibrium and one unstable disease-free equilibrium or (3) two endemic equilibria - one stable and one unstable. In order for the disease to die out, we can reduce R_0 below $R_0^* < 1$. This can be done by reducing the b parameter or, in other words, by improving medical conditions.

References

[1] Jingán Cui, Xiaoxia Mu, and Hui Wan. "Saturation recovery leads to multiple endemic equilibria and backward bifurcation". In: *Journal of Theoretical Biology* 254.2 (2008), pp. 275–283.

[2] P van den Driessche and J Watmough. "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission". In: (2002), 29–48.

[3] Xueyong Zhou and Jingan Cui. "Analysis of stability and bifurcation for an SEIR epidemic model with saturated recovery rate". In: (2011).