

# The behaviour of an epidemiological model

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**Abstract.** In this work we study the next system:

$$\begin{cases} S' &= A - \beta(1 + \nu I)SI \\ E' &= \beta(1 + \nu I)SI - \alpha E \\ I' &= \alpha E - \gamma I \\ R' &= \gamma I \end{cases}$$

which is a SEIR model, where first of all the probability of disease transmission depend linear of the number of infectious.

We also consider and study the behaviour of the system if the probability of disease transmission depend of two degree polinom of the number of infectious.

## 1 Introduction

The SIR model is one of the simplest compartmental models, and many models are derivatives of this basic form [1]. The model consists of three compartments:

**S:** The number of susceptible individuals. When a susceptible and an infectious individual come into "infectious contact", the susceptible individual contracts the disease and transitions to the infectious compartment.

**I:** The number of infectious individuals. These are individuals who have been infected and are capable of infecting susceptible individuals.

**R** for the number of removed (and immune) or deceased individuals. These are individuals who have been infected and have either recovered from the disease and entered the removed compartment, or died. It is assumed that the number of deaths is negligible with respect to the total population. This compartment may also be called "recovered" or "resistant".

This model is reasonably predictive for infectious diseases that are transmitted from human to human, and where recovery confers lasting resistance, such as measles, mumps and rubella [2].

Spatial SIR model simulation. Each cell can infect its eight immediate neighbors.

These variables (S, I, and R) represent the number of people in each compartment at a particular time. To represent that the number of susceptible, infectious and removed individuals may vary over time (even if the total population size remains constant), we make the precise numbers a function of t (time): S(t), I(t) and R(t). For a specific disease in a specific population, these functions may be worked out in order to predict possible outbreaks and bring them under control.

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## 2 The SEIR model

For many important infections, there is a significant latency period during which individuals have been infected but are not yet infectious themselves. During this period the individual is in compartment E (for exposed).

Such a simple model represents well a generic behavior of epidemics and a related advantage consists in a small number of parameters to be identified [3]. This is an important outcome in the case of a virus attack with a limited amount of data available. The basic reproduction ratio is the classical epidemiological measure associated with the reproductive power of the disease. For the SEIR model, it is:

$$\tilde{R}_0 = \frac{\alpha\beta A}{\mu(\mu + \gamma)(\mu + \alpha)} \tag{1}$$

It gives the average number of secondary cases of infection generated by an infectious individual. Therefore, it is used to estimate the growth of the virus outbreak. When  $\tilde{R}_0 < 1$ , the disease dies out; when  $\tilde{R}_0 > 1$ , an epidemic occurs. In terms of parameter  $\beta$ , when  $\beta < \tilde{\beta}_0$ , with  $\tilde{\beta}_0 = \frac{\mu(\mu+\gamma)(\mu+\alpha)}{A\alpha}$ , the disease disappears, and when  $\beta > \tilde{\beta}_0$  the disease starts an epidemic.

In this work we consider the next system:

$$\begin{cases} S' &= A - \beta(1 + \nu I)SI \\ E' &= \beta(1 + \nu I)SI - \alpha E \\ I' &= \alpha E - \gamma I \end{cases}$$

that means the probability of disease transmission depend linear of the number of infectious.

$S(t)$  denoting the number of susceptible individuals,

$E(t)$  the number of exposed individuals (were the individuals are infected but not infectious),

$I(t)$  the number of infectious individuals

$R(t)$  the number of recovered individuals

The parameters are defined as:

$A$  per-capita birth rate,

$\alpha$  rate of progression from exposed to infectious (the reciprocal is the incubation period),

$\beta$  probability of disease transmission per contact times the number of contacts per unit time,

$\gamma$  recovery rate of infectious individuals (the reciprocal is the infectious period)

$\mu$  per-capita natural death rate.

We will find the equilibrium points and will study their stability.

Also we will study the next system:

$$\begin{cases} S' &= A - \beta(1 + \nu^2 I)SI \\ E' &= \beta(1 + \nu^2 I)SI - \alpha E \\ I' &= \alpha E - \gamma I \end{cases}$$

that means the probability of disease transmission depend of two degree polynomial of the number of infectious.

### 3 Stability analysis of equilibrium points

In the following we consider the next system:

$$\begin{cases} S' &= A - \beta(1 + \nu I)SI \\ E' &= \beta(1 + \nu I)SI - \alpha E \\ I' &= \alpha E - \gamma I \end{cases}$$

that means the probability of disease transmission depend linear of the number of infectious.

To find the equilibrium points we solve the system:

$$\begin{cases} A - \beta(1 + \nu I)SI - \mu S &= 0 \\ \beta(1 + \nu I)SI - \alpha E - \mu E &= 0 \\ \alpha E - \gamma I &= 0 \end{cases}$$

with  $\nu$  positive.

We obtain a single equilibrium point  $E\left(\frac{\gamma^2}{\beta(\gamma+\nu A)}, \frac{A}{\alpha}, \frac{A}{\gamma}\right)$ .

The jacobian matrix is:

$$J = \begin{pmatrix} -\beta(1 + \nu I)I & 0 & -\beta S - 2\beta\nu SI \\ \beta(1 + \nu I)I & -\alpha & \beta S + 2\beta\nu SI \\ 0 & \alpha & -\gamma \end{pmatrix}$$

The jacobian matrix at  $E$  is:

$$J(E) = \begin{pmatrix} -\frac{\beta(\gamma+\nu A)A}{\gamma^2} & 0 & -\frac{\gamma(\gamma+2\nu A)}{\gamma+\nu A} \\ \frac{\beta(\gamma+\nu A)A}{\gamma^2} & -\alpha & \frac{\gamma(\gamma+2\nu A)}{\gamma+\nu A} \\ 0 & \alpha & -\gamma \end{pmatrix}$$

The characteristic polynomial associate with the jacobian matrix above is:

$$P(\lambda) = \lambda^3 + a_2\lambda^2 + a_1\lambda + a_0$$

where

$$a_2 = \frac{A^2\beta\nu + A\beta\gamma + \alpha\gamma^2}{\gamma^2}$$

$$a_1 = \frac{A(A^2\alpha\beta\nu^2 + A^2\beta\gamma\nu^2 + 2A\alpha\beta\gamma\nu + 2A\alpha\beta\gamma^2\nu - \alpha\gamma^3\nu + \alpha\beta\gamma^2 + \beta\gamma^3)}{\gamma^2(A\nu + \gamma)}$$

$$a_0 = \frac{(A\nu + \gamma)\beta A\alpha}{\gamma}$$

If we consider the next system:

$$\begin{cases} S' &= A - \beta(1 + \nu^2 I)SI \\ E' &= \beta(1 + \nu^2 I)SI - \alpha E \\ I' &= \alpha E - \gamma I \end{cases}$$

that means the probability of disease transmission depend of two degree polinom of the number of infectious.

To find the equilibrium points we solve the system:

$$\begin{cases} A - \beta(1 + v^2I)SI & = 0 \\ \beta(1 + v^2I)SI - \alpha E & = 0 \\ \alpha E - \gamma I & = 0 \end{cases}$$

We obtain a single equilibrium point  $E_1 \left( \frac{\gamma^2}{\beta(\gamma+v^2A)}, \frac{A}{\alpha}, \frac{A}{\gamma} \right)$ .

The jacobian matrix is:

$$J = \begin{pmatrix} -\beta(1 + v^2I)I & 0 & -\beta S - 2\beta v^2SI \\ \beta(1 + v^2I)I & -\alpha & \beta S + 2\beta v^2SI \\ 0 & \alpha & -\gamma \end{pmatrix}$$

The jacobian matrix at  $E_1$  is:

$$J(E_1) = \begin{pmatrix} -\frac{\beta(\gamma+v^2A)A}{\gamma^2} & 0 & -\frac{\gamma(\gamma+2v^2A)}{\gamma+vA} \\ \frac{\beta(\gamma+v^2A)A}{\gamma^2} & -\alpha & \frac{\gamma(\gamma+2v^2A)}{\gamma+vA} \\ 0 & \alpha & -\gamma \end{pmatrix}$$

The characteristic polynomial associate with the jacobian matrix above is:

$$P(\lambda) = \lambda^3 + b_2\lambda^2 + b_1\lambda + b_0$$

where

$$b_2 = \frac{A^2\beta v^2 + A\beta\gamma + \alpha\gamma^2 + \gamma^3}{\gamma^2}$$

$$b_1 = \frac{A(A^2\alpha\beta v^3 + A^2\beta\gamma v^3 + A\alpha\beta\gamma v^2 + A\beta\gamma^2 v^2 + \gamma^3\alpha v(2 - v) + A\alpha\beta\gamma v + \alpha\beta\gamma^2 + \beta\gamma^3)}{\gamma^2(Av + \gamma)}$$

$$b_0 = \frac{(Av^2 + \gamma)\beta A\alpha}{\gamma}$$

**Proposition 3.1** Assume  $v < \min\left(\frac{\beta}{\alpha}, \frac{\beta}{\gamma}\right)$ . Then the endemic equilibrium  $E$  is locally asymptotically stable.

*Proof.* The result become from Routh-Hurwitz conditions [4]:

$$a_0 > 0,$$

$$a_1 = \frac{A(A^2\alpha\beta v^2 + A^2\beta\gamma v^2 + 2A\alpha\beta\gamma v + 2A\alpha\beta\gamma^2 v + \gamma^3(\beta - \alpha v) + \alpha\beta\gamma^2 + \beta\gamma^3)}{\gamma^2(Av + \gamma)} > 0,$$

$$\text{because } v < \min\left(\frac{\beta}{\alpha}, \frac{\beta}{\gamma}\right) < \frac{\beta}{\alpha}$$

$$a_2 > 0,$$

$$a_1 a_2 - a_0 = \frac{A}{\gamma^4(Av + \gamma)} (C_4 A^4 + C_3 A^3 + C_2 A^2 + C_1 A + C_0) > 0, \text{ where}$$

$$C_4 = \beta^2 v^3 (\alpha + \gamma) > 0$$

$$C_3 = 3\beta^2 v^2 \gamma (\alpha + \gamma) > 0$$

$$C_2 = \beta\gamma^2 v^2 (\alpha^2 + \gamma^2) + 3\beta^2 \gamma^2 v (\alpha + \gamma) > 0$$

$$C_1 = 2\gamma^3 \beta v (\alpha^2 + \gamma^2) + \beta\gamma^3 (\gamma v \alpha + \beta \alpha + \beta \gamma) > 0$$

$$C_0 = \gamma^4 \alpha^2 (\beta - \gamma v) + \gamma^5 \alpha (\beta - \gamma v) + \beta\gamma^6 > 0$$

$$\text{because } v < \min\left(\frac{\beta}{\alpha}, \frac{\beta}{\gamma}\right) < \frac{\beta}{\gamma}.$$

□

If we consider the next system:

$$\begin{cases} S' &= A - \beta(1 + v^2I)SI \\ E' &= \beta(1 + v^2I)SI - \alpha E \\ I' &= \alpha E - \gamma I \end{cases}$$

that means the probability of disease transmission depend of two degree polinom of the number of infectious.

To find the equilibrium points we solve the system:

$$\begin{cases} A - \beta(1 + v^2I)SI &= 0 \\ \beta(1 + v^2I)SI - \alpha E &= 0 \\ \alpha E - \gamma I &= 0 \end{cases}$$

We obtain a single equilibrium point  $E_1 \left( \frac{\gamma^2}{\beta(\gamma + v^2A)}, \frac{A}{\alpha}, \frac{A}{\gamma} \right)$ .

The jacobian matrix is:

$$J = \begin{pmatrix} -\beta(1 + v^2I)I & 0 & -\beta S - 2\beta v^2SI \\ \beta(1 + v^2I)I & -\alpha & \beta S + 2\beta v^2SI \\ 0 & \alpha & -\gamma \end{pmatrix}$$

The jacobian matrix at  $E_1$  is:

$$J(E_1) = \begin{pmatrix} -\frac{\beta(\gamma + v^2A)A}{\gamma^2} & 0 & -\frac{\gamma(\gamma + 2v^2A)}{\gamma + vA} \\ \frac{\beta(\gamma + v^2A)A}{\gamma^2} & -\alpha & \frac{\gamma(\gamma + 2v^2A)}{\gamma + vA} \\ 0 & \alpha & -\gamma \end{pmatrix}$$

The characteristic polinomial associate with the jacobian matrix above is:

$$P(\lambda) = \lambda^3 + b_2\lambda^2 + b_1\lambda + b_0$$

where

$$b_2 = \frac{A^2\beta v^2 + A\beta\gamma + \alpha\gamma^2 + \gamma^3}{\gamma^2}$$

$$b_1 = \frac{A(A^2\alpha\beta v^3 + A^2\beta\gamma v^3 + A\alpha\beta\gamma v^2 + A\beta\gamma^2 v^2 + \gamma^3\alpha v(2 - v) + A\alpha\beta\gamma v + \alpha\beta\gamma^2 + \beta\gamma^3)}{\gamma^2(Av + \gamma)}$$

$$b_0 = \frac{(Av^2 + \gamma)\beta A\alpha}{\gamma}$$

**Proposition 3.2** Assume  $v < \frac{1}{2}$ . Then the endemic equilibrium  $E_1$  is locally asymptotically stable.

*Proof.* The result become from Routh-Hurwitz conditions:

$$b_1b_2 - b_0 = \frac{A}{\gamma^4(Av + \gamma)} (D_4A^4 + D_3A^3 + D_2A^2 + D_1A + D_0) > 0, \text{ where}$$

$$D_4 = \beta^2v^5(\alpha + \gamma) > 0$$

$$D_3 = \beta^2v^3(v + 2)\gamma(\alpha + \gamma) > 0$$

$$D_2 = \gamma^2v(2v + 1)\beta^2(\alpha + \gamma) + 2\gamma^3v^3\beta\alpha(1 - v) + \gamma^4v^3\beta > 0$$

$$\begin{aligned} D_1 &= \gamma^3 \beta \nu \alpha^2 (\nu + 1) + \beta^2 \gamma^3 \alpha + \gamma^4 \nu (2 - \nu) \alpha \beta + \gamma^4 \beta^2 + \gamma^5 \nu \beta (\nu + 1) > 0 \\ D_0 &= \gamma^4 \beta + \gamma^5 \nu \alpha^2 (1 - 2\nu) + (\beta \gamma^5 + \gamma^6 \nu (1 - 2\nu)) \alpha + \beta \gamma^6 > 0 \\ &\text{because } \nu < \frac{1}{2}. \end{aligned}$$

□

## 4 Conclusions

We considered in this paper a SEIR model in which the disease transmission depends on a polynomial depends on the number of infectious individuals, in the first case of the first degree, in the second case of a polynomial of the second degree.

In both cases the endemic equilibrium point proved asymptotically stable in some situations.

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## References

- [1] W. Yang, D. Zhang, L. Peng, C. Zhuge, and L. Hong, Rational evaluation of various epidemic models based on the COVID-19 data of China, preprint, arXiv:2003.05666v1, 2020.
- [2] M.J. Keeling, and P. Rohani, *Modeling infectious diseases in humans and animals*, Princeton University Press, 2008.
- [3] Z. Wang, C. T. Bauch, S. Bhattacharyya, A. Onofrio, P. Manfredi, M. Perc, N. Perra, M. Salathe, and D. Zhao, Statistical physics of vaccination, *Physics Reports* **664**, 1–113 (2016).
- [4] M. Martcheva, *An Introduction to Mathematical Epidemiology*, Texts in Applied Mathematics **61**, Springer, New York 2015.