Numerical modelling of disease propagation

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Math project I. presentation

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Aim of the project -

- To get familiar with the different aspects and techniques of epidemiological modeling.
- compartmental deterministic models
- Use these methods to compare the "basic" SEIR and "SEIRV" models.
- How an additional compartment - a new transmission rate - changes the basics of the model.

For the latter my main sources were:

Martcheva, Maia. An introduction to mathematical epidemiology. Vol. 61. New York: Springer, 2015.

Capasso, Vincenzo. Mathematical structures of epidemic systems. Vol. 88. Berlin: Springer, 1993.

2020, Yang and Wang proposed the following compartmental model[1]:

$$\begin{aligned}
\frac{\mathrm{d}S}{\mathrm{d}t} &= \Lambda - \beta_E SE - \beta_I SI - \beta_V SV - \mu S \\
\frac{\mathrm{d}E}{\mathrm{d}t} &= \beta_E SE + \beta_I SI + \beta_V SV - (\alpha + \mu)E \\
\frac{\mathrm{d}I}{\mathrm{d}t} &= \alpha E - (w + \gamma + \mu)I \\
\frac{\mathrm{d}R}{\mathrm{d}t} &= \gamma I - \mu R \\
\frac{\mathrm{d}V}{\mathrm{d}t} &= \xi_1 E + \xi_2 I - \sigma V
\end{aligned} \tag{1}$$

Parameters

Λ	Population influx	ξ_1	Rate of the exposed individuals contributing the virus to the environment
μ	Natural death rate		
w	Disease induced death rate	ξ_2	Rate of the infected individuals contributing the virus to the environment
$1/\alpha$	Mean incubation period		
γ	Recovery rate	σ	Rate of (natural and artificial) removal of the virus from the environment
β_I	Transmission rate by infected individual		
β_E	Transmission rate by exposed individual		
β_V	Transmission rate by the environmental reservoir		

- Reasons for the new compartment

Disease-free equilibrium (DFE)

- no infections in the population (derivatives and disease compartments zero)
- $\mathscr{E}_0 = (S_0, E_0, I_0, R_0, V_0) = (\frac{\Lambda}{\mu}, 0, 0, 0, 0)$

Endemic equilibrium (for the ususal SEIR $\beta_V = 0$

$$\hat{E} = \frac{\lambda}{\alpha + \mu} - \frac{\mu}{\beta_E + \frac{\alpha}{w_1}\beta_I + c\beta_V}$$

$$\hat{I} = \frac{\Lambda\alpha}{w_1(\alpha + \mu)} - \frac{\alpha\mu}{w_1(\beta_E + \frac{\alpha}{w_1}\beta_I + c\beta_V)}$$

$$\hat{R} = \frac{\gamma\alpha\Lambda}{\mu w_1(\alpha + \mu)} - \frac{\gamma\alpha}{w_1(\beta_E + \frac{\alpha}{w_1}\beta_I + c\beta_V)}$$

$$\hat{V} = \frac{c}{\alpha + \mu} - \frac{c\mu}{\beta_E + \frac{\alpha}{w_1}\beta_I + c\beta_v}$$

$$\hat{S} = \frac{\mu}{\beta_E + \frac{\alpha}{w_1}\beta_I + c\beta_V}$$

where $c = \frac{w_1\xi_1 + \xi_2\alpha}{\sigma w_1}$.

The *basic reproduction number* - $\mathcal{R}_0$ - I.

- Important measure of potential disease spread
- Number of secondary infections produced by an infected individual in a completely susceptible population
- can be computed by the *next generation approach*[2]
- $$\begin{aligned} x_i' &= \mathcal{F}_i(x,y) - \mathcal{V}_i(x,y) \quad i = 1,2,3 \\ y_j' &= g_j(x,y) \quad j = 1,2 \end{aligned} \tag{2}$$

  where $(x_1, x_2, x_3) = (E, I, V)$, $(y_1, y_2) = (S, R)$
- $$\mathcal{F} = \begin{pmatrix} \beta_E SE + \beta_I SI + \beta_V SV \\ 0 \\ 0 \end{pmatrix} \quad , \quad \mathcal{V} = \begin{pmatrix} (\alpha + \mu)E \\ -\alpha E + (w + \gamma + \mu)I \\ -\xi_1 E - \xi_2 I + \sigma V \end{pmatrix}$$

The *basic reproduction number* - $\mathcal{R}_0$ - II.

- Linearizing the system at the DFE $(0, y_0) = (E_0, I_0, V_0, S_0, R_0) = (0, 0, 0, \frac{\Lambda}{\mu}, 0)$
- Jacobi matrices $F = \mathbf{J}\mathcal{F}(X_0)$ and $V = \mathbf{J}\mathcal{V}(X_0)$
- for every pair (i, j):

$$\frac{\partial \mathcal{F}_i(0, y_0)}{\partial y_j} = \frac{\partial \mathcal{V}_i(0, y_0)}{\partial y_j} = 0.$$

- Disease compartments x decouples from y variables $\rightarrow$

$$x' = (F - V)x \tag{3}$$

- for $F = 0$(no secondary infections): $x' = -Vx_0, \quad x(0) = x_0$

The *basic reproduction number* - $\mathcal{R}_0$ - III.

Expected number of secondary infections produced by the index case:

$$F \int_0^\infty e^{-Vt} x_0 \, dt = F V^{-1} x_0 \tag{4}$$

- The *next generation matrix* is defined as:
- $$K = FV^{-1} = \begin{pmatrix} \frac{\beta_E S_0}{\alpha+\mu} + \frac{\beta_I S_0 \alpha}{(\alpha+\mu)(w+\gamma+\mu)} + \frac{\beta_V S_0(\alpha\xi_2 + (w+\gamma+\mu)\xi_1)}{(\alpha+\mu)(w+\gamma+\mu)\sigma} & \frac{\beta_I S_0}{w+\gamma+\mu} + \frac{\beta_V S_0 \xi_2}{(w+\gamma+\mu)\sigma} & \frac{\beta_V S_0}{\sigma} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$
- $$\rho(K) = \mathcal{R}_0 = \frac{\beta_E S_0}{\alpha+\mu} + \frac{\beta_I S_0 \alpha}{(\alpha+\mu)(w+\gamma+\mu)} + \left(\frac{\beta_V S_0 \xi_1}{(\alpha+\mu)\sigma} + \frac{\beta_V S_0 \alpha \xi_2}{(\alpha+\mu)(w+\gamma+\mu)\sigma} \right) =: \mathcal{R}_1 + \mathcal{R}_2 + \mathcal{R}_3$$
- nicely interpretable as the number of secondary infections from an initially exposed individual
- Usual SEIR model: $\beta_V = 0$
- both systems exhibit forward bifurcation

Positive invariance

- We would except that the solutions are biologically reliable
- One aspect of this: $\Omega = \mathbb{R}^5_+$ is positively invariant
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\begin{aligned}
&\text{if} \quad S(\bar{t}) = 0, \text{ then } \frac{\mathrm{d}S(\bar{t})}{\mathrm{d}t} = \Lambda \geq 0 \\
&\text{if} \quad E(\bar{t}) = 0, \text{ then } \frac{\mathrm{d}E(\bar{t})}{\mathrm{d}t} = \beta_I S(\bar{t}) I(\bar{t}) + \beta_V S(\bar{t}) V(\bar{t}) \geq 0 \\
&\text{if} \quad I(\bar{t}) = 0, \text{ then } \frac{\mathrm{d}I(\bar{t})}{\mathrm{d}t} = \alpha E(\bar{t}) \geq 0 \\
&\text{if} \quad R(\bar{t}) = 0, \text{ then } \frac{\mathrm{d}R(\bar{t})}{\mathrm{d}t} = \gamma I(\bar{t}) \geq 0 \\
&\text{if} \quad V(\bar{t}) = 0, \text{ then } \frac{\mathrm{d}V(\bar{t})}{\mathrm{d}t} = \xi_1 E(\bar{t}) + \xi_2 I(\bar{t}) \geq 0
\end{aligned}
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Discussion, future directions

- Check other models with the additional dynamics of the environmental reservoir (e.g. Lagrangian and Eulerian movement models).
- further study the parameters $\beta_V, \xi_1, \xi_2, \sigma$ from the aspect of control.
- numerical modeling aspect of these models (i.e. which properties of the model are inherited after discretization)
- for example positive invariance, stability

References I

[1]–Yang, Chayu, and Jin Wang. "A mathematical model for the novel coronavirus epidemic in Wuhan, China." Mathematical biosciences and engineering: MBE 17.3 (2020): 2708.
[2]–Van den Driessche, P., and James Watmough. "Further notes on the basic reproduction number." Mathematical epidemiology. Springer, Berlin, Heidelberg, 2008. 159-178.