A Discrete Epidemic Model Which Incorporated Dead- Infective Population

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Keywords: Ebola, Epidemic models, Properties.

Abstract. This paper proposes a new discrete epidemic model based on a continuous-time one. The model has six populations and three controls. In particular, it incorporates the lying corpses as infective ones and the asymptomatic infectious population so that it has a total of three infectious populations: asymptomatic/symptomatic infective and infective lying corpses.

Introduction

Epidemic models are an interesting mathematical tool to study the infection propagation [1-4]. They contain several interacting populations which describe the disease spread, the individuals being subject to transitions from a stage to another one through time as the disease evolves. This paper proposes and investigates a new epidemic model of discrete nature which is based on a continuous-time one proposed and studied in [1]. The model extends the SEIR (susceptible-exposed-infectious- recovered or immune) one with two more populations, i.e. the asymptomatic infectious (A) and the infected dead bodies (D). Therefore, it is referred to as an SEIADR epidemic model. It is well-known that infective corpses are relevant in some disease transmissions as, for instance, Ebola. It can have three feedback controls, [5], namely, susceptible vaccination, treatment on the symptomatic infectious and dead-infective culling.

Discrete SEIADR Epidemic Model and Equilibrium Points

The SEIADR ( acronym: susceptible (S)-exposed (E)-symptomatic infectious (I)- asymptomatic infectious (A), dead-infectious (D) and recovered or immune (R)) discrete epidemic model is got from its continuous-time counterpart proposed and developed in [1] by using the discretization Euler method \( x(t + h) \approx x(t) + h \Delta x(t) \), where \( h \) is the sampling period, to yield:

\[
\begin{align*}
S_{n+1} &= S_n + h(b_1 - (b_2 + \beta I_n + \beta_A A_n + \beta_D D_n) S_n + \eta R_n - V_n) \\
E_{n+1} &= E_n + h(-b_2 + (\gamma + \delta) E_n + (\beta I_n + \beta_A A_n + \beta_D D_n) S_n) \\
I_{n+1} &= I_n + h(\gamma I_n + \eta P E_n - \xi_n) \\
A_{n+1} &= A_n + h(-\mu A_n + \gamma(1 - p) E_n) \\
D_{n+1} &= D_n + h(-\mu(1 - p) D_n + b_2 (I_n + A_n) + \alpha I_n) \\
R_{n+1} &= R_n + h(-b_2 + \eta) R_n + \tau (I_n + A_n) + \xi_n + V_n) \\
V_n &= V_n + k_v \xi_n S_n \\
\xi_n &= k_{\xi_n} I_n 
\end{align*}
\]

for \( n \geq 0 \) under non-zero initial conditions, \( b_1 \) is the recruiting rate, \( b_2 \) is the natural death rate, \( 1/\eta \) is the average duration of the immunity period, \( \gamma \) is the percentage of exposed population to asymptomatic infectious, \( \alpha \) is the infectious mortality rate, \( \tau \) is the response rate to the whole infective population, \( p \) is the fraction of exposed population with symptoms, \( 1/\mu \) is the average post-mortem infective period and \( 1 - p \) is the fraction of exposed population which becomes asymptomatic infectious. The disease transmission rates of the various infectious subpopulations are
are $\beta$, $\beta_A = \beta_1 \beta$, $\beta_D = \beta_0 \beta$. $V_n$ and $\xi_n$ are the vaccination and treatment controls on the susceptible and symptomatic infectious respectively. The first one has a constant term plus a feedback control with a proportional gain on the susceptible and the second one is a linear feedback on the symptomatic infectious. The parameter $\rho_D$ is a culling gain which takes into account the withdrawal rate of dead-infective population lying on the ground by the sanitary cleaning brigades and taking place at sampling instants. It is assumed here the usual case that the illness is spreading in third-world countries with scarce meanings to deal with the disease. In summary, note that three controls are eventually involved, namely, vaccination, treatment and lying corpses retirement, the last one being an impulsive or culling action. The superscript “+” in the dead population stands to the right of the corresponding sampling instant when the corpses withdrawal takes place. We get the more compacted epidemic model description:

\[
\begin{align*}
S_{n+1} &= S_n + h(b_1 + (b_2 + \beta I_n + \beta_A A_n + \beta_D D_n + k_v n) S_n + \eta R_n - v_n) \\
E_{n+1} &= E_n + h((-b_2 + \gamma) E_n + (I_n + \beta_A A_n + \beta_D D_n) S_n) \\
I_{n+1} &= I_n + h((-b_2 + \alpha + \tau + k_\xi n) I_n + \gamma p E_n) \\
A_{n+1} &= A_n + h((-b_2 + \tau) A_n + \gamma(1-p) E_n) \\
D_{n+1}^+ &= (1-\rho_D) D_n + h(-\mu(1-\rho_D) D_n + b_2 I_n + A_n) + \alpha I_n \\
R_{n+1} &= R_n + h((-b_2 + \eta) R_n + \tau(I_n + A_n) + k_\xi I_n + v_n + k_v S_n)
\end{align*}
\]

Note that the total and alive populations are, respectively, given by:

\[
N_{n+1}^T = N_n^T + b_2(S_n + E_n + R_n) - ((1-\rho)\mu + \rho_D) D_n
\]

\[
N_{n+1}^V = N_n^V + b_2(S_n + E_n + I_n + A_n + R_n) - \alpha I_n
\]

There are two equilibrium points, the so-called disease-free equilibrium point with all the infectious populations being null (the populations in the model being subscripted with “df”) and the endemic one for which the disease is permanent (the populations in the model being subscripted by “end”).

**Theorem 1.** The discrete SEIADR model has two equilibrium points, namely, the disease-free one and the endemic one with subpopulations subscripted with “end” as follows:

\[
(S_{df}^*, E_{df}^*, I_{df}^*, A_{df}^*, D_{df}^*, R_{df}^*) = \left( \frac{b_1 b_2 + \eta b_1 - b_2 v_0}{b_2(b_2 + k_v + \eta)}, 0, 0, 0, 0, \frac{b_1 k_V + b_2 v_0}{b_2(b_2 + k_v + \eta)} \right)
\]

\[
S_{end}^* = \frac{p b c d e_1}{\gamma p (\beta_A + \beta_A (1-p) c e_1 + \beta_D ((b_2 + \alpha) p d + b_2 (1-p) c))}
\]

\[
I_{end}^* = \frac{b_2 S_{end}^* - b_1 (b_2 + 2\eta) + b_2 (b_2 S_{end}^* + 2(v_0 + k_v S_{end}^*) - b_1)}{(b_2 + 2\eta)(k_\xi + \tau (1 + AA) - B S_{end}^* - b_2(B S_{end}^* + k_\xi + \tau(1 + AA)))}
\]

\[
E_{end}^* = \frac{c}{\gamma p} I_{end}^*
\]

\[
A_{end}^* = \frac{(1-p)(b_2 + \alpha + \tau + k_\xi)e}{pd} I_{end}^*
\]

\[
D_{end}^* = \frac{b_2 + \alpha}{pd} I_{end}^*
\]

\[
R_{end}^* = \frac{b_2 S_{end}^* + 2(v_0 + k_v S_{end}^*) - b_1 + (B S_{end}^* + \tau + k_\xi + \tau AA) I_{end}^*}{(b_2 + 2\tau)}
\]
equivalently rewritten as,

\[
S_{\text{end}}^* = \frac{(b_2 + \gamma)E_{\text{end}}^*}{\beta I_{\text{end}}^* + \beta_A A_{\text{end}}^* + \beta_D D_{\text{end}}^*} = \frac{(b_2 + \gamma)EEI_{\text{end}}^*}{\beta(1 + \beta_A AA + \beta_D DD)I_{\text{end}}^*} = \frac{(b_2 + \gamma)EE}{\beta(1 + \beta_A AA + \beta_D DD)}
\]

\[
P_{\text{end}}^* = \frac{b_2 S_{\text{end}}^* + 2(v_0 + k_v S_{\text{end}}^*) - b_1 + (B B S_{\text{end}}^* + \tau + k_\xi + \tau AA)I_{\text{end}}^*}{b_2 + 2\eta}
\]

\[
I_{\text{end}}^* = \frac{(b_2 S_{\text{end}}^* - b_1)(b_2 + 2\eta) + b_2(b_2 S_{\text{end}}^* + 2(v_0 + k_v S_{\text{end}}^*) - b_1)}{(b_2 + 2\eta)(\tau + k_\xi + \tau AA - BS_{\text{end}}^*) - b_2(B S_{\text{end}}^* + \tau + k_\xi + \tau AA)}
\]

\[
S_{\text{end}}^* < (1 + \frac{k_v}{b_2 + \eta})S_{\text{df}}^*
\]

\[
EE = \frac{c}{\gamma p}
\]

\[
AA = \frac{(1 - p)c}{pd}
\]

\[
DD = \frac{(b_2 + \alpha)pd + b_2(1 - p)c}{pde_1}
\]

\[
BB = \beta(1 + \tilde{\beta}_A AA + \tilde{\beta}_D DD)
\]

The proof of Theorem 1 is organized just by equalizing the values of each state variable at consecutive sampling instants to the value at the equilibrium point found. The following auxiliary constraints are found relating the other infectious populations to the symptomatic infectious one:

\[
E_{\text{end}}^* = \frac{(b_2 + \alpha + \tau + k_\xi)}{\gamma p} I_{\text{end}}^* = \frac{c}{\gamma p} I_{\text{end}}^*
\]

\[
A_{\text{end}}^* = \frac{\gamma (1 - p)E_{\text{end}}^*}{(b_2 + \tau)} = \frac{(1 - p)c}{pd} I_{\text{end}}^*
\]

\[
D_{\text{end}}^* = \frac{(b_2 + \alpha)pd + b_2(1 - p)c}{pde_1} I_{\text{end}}^*
\]

The local stability analysis about the equilibrium points is characterized through the allocation of the eigenvalues of the respective Jacobian matrices. The Jacobian matrix about any equilibrium point is:

\[
J = \begin{pmatrix}
1-h(b_2+\beta I^*+\beta_A A^*+\beta_D D^*+K_v^*) & 0 & -h\beta S^* & -h\beta_A S^* & -h\beta_D S^* & h\eta \\
h(\beta I^*+\beta_A A^*+\beta_D D^*) & 1-h(b_2+\gamma) & h\beta S^* & h\beta_A S^* & h\beta_D S^* & 0 \\
0 & h\gamma p & 1-h(b_2+\alpha+\tau+K_v^*) & 0 & 0 & 0 \\
0 & h\gamma(1-p) & 0 & 1-h(b_2+\tau) & 0 & 0 \\
0 & 0 & h(b_2+\alpha) & h(b_2+\alpha) & (1-p_D)(1-h_\mu) & 0 \\
hK_v^* & 0 & h(\tau+K_v^*) & h\tau & 0 & 1-h(b_2+\eta)
\end{pmatrix}
\]

(9)
The Jacobian matrix is strictly column diagonal dominant with positive diagonal entries if the subsequent constraints hold:

\[
\begin{align*}
    h(\beta I^* + \beta_A A^* + \beta_D D^* + k_v) &< 1 - h(b_2 + \beta I^* + \beta_A A^* + \beta_D D^* + k_v) \\
    h\gamma &< 1 - h(b_2 + \gamma) \\
    2h\beta S^* + h(b_2 + \alpha + \tau + k_\xi) &< 1 - h(b_2 + \alpha + \tau + k_\xi) \\
    2h\beta_A S^* + h(b_2 + \tau) &< 1 - h(b_2 + \tau) \\
    2\beta_D S^* &< 1 - \rho - h\mu + h\mu\rho \\
    h\eta &< 1 - h(b_2 + \eta)
\end{align*}
\]

Recombining appropriately the above constraints, one gets that \(J = (a_y)\) is a convergent matrix if any eigenvalue \(\lambda\) satisfies the constraint \(|\lambda - a_y| < \sum_{(a_i)_y} |a_y| < 1\). This is guaranteed for the disease-free equilibrium point if the coefficient transmission rate of the infectious is small enough satisfying:

\[
\beta < \frac{b_{cde_1}}{S^*_{de}(\gamma p d e_1 + \tilde{\beta} A \gamma (1 - p) c e_1 + \tilde{\beta}_D h(b_2 \gamma c(1 - p) + (\alpha + b_2) \gamma p d))}
\]

\[
\begin{align*}
\alpha &= \beta I^* + \beta_A A^* + \beta_D D^* \\
b &= (b_2 + \gamma) \\
c &= (b_2 + \alpha + \tau + k_\xi) \\
d &= (b_2 + \tau) \\
e &= (1 - \rho_D)(1 - h\mu) \\
e_1 &= (\frac{\rho_D}{h\mu} + \mu(1 - \rho_D)) \\
f &= (b_2 + \eta)
\end{align*}
\]

(11)

\section*{Numerical Example}

The following model parameterization is used for testing with \(h = 1\):

\[
\begin{align*}
b_1 &= 1/(70 \cdot 365) = b_2 \\
\beta &= 0.16 \\
\beta_A &= 0.05 \\
\beta_D &= 0.5 \\
\gamma &= 1/15.8 \\
\rho &= 0.1 \\
\mu &= 1/20 \\
\eta &= 1/1000
\end{align*}
\]

(13)

The solution in the control-free and under some culling controls of the infective corpses are displayed on Figures 1 and 2, respectively.
Figure 1. Trajectories in the absence of controls.

Figures 2. Trajectories under constant and culling controls.

Acknowledgements
This research was supported by Grant DPI2015-64766-R (MINECO/FEDER, EU) and by UPV/EHU via Grant PGC 17/33.

References

