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The final size and critical times of an SIVR epidemic model

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Abstract

To understand the impact of vaccination, we consider an SIVR (susceptible–infected–vaccinated–recovered) model that combines impulsive vaccination into the classical SIR model. The final size is firstly defined and estimated, and then the peak value and peak time are considered. Finally, the critical time for a given infected number is studied, and it can be used to define and estimate the stopping time. Our results extend those for the well-understood SIR model.

Mathematics Subject Classification: 35K57; 35R12; 92D25

Keywords: Epidemic model; Peak value; Peak time; Critical time

1 Introduction

Infectious diseases threaten the world in various ways and have a significant impact on human health, economics, social structures, and more [3]. Controlling infectious diseases has always been a global concern.

Vaccination is an effective strategy for minimizing infectious diseases and has been considered in many literatures. The SIR (susceptible–infected–recovered) models and their variants have been extensively explored in [10, 11]. Gao et al. [12] investigated an SIRS epidemic model with seasonal varying contact rate and mixed vaccination strategy. They studied the permanence and extinction of the disease for the SIRS model. The standard SIR epidemic model was extended to a fourth compartment V of vaccinated persons in [21]. The influence of vaccinations on the total cumulative number is calculated by comparing with monitored real time COVID-19 data in different countries. The reduction in the final cumulative fraction of infected persons is given by using the actual pandemic parameters. In [24], Turkyilmazoglu revealed that the vaccine application offers less control over the spread of virus since some portion of vaccinated people is not totally protected/immuned and viable to infection again after a while due to weak/loss immunity offered by the vaccine. See also [15, 22] and the references therein.

As we know, the final size is one of the most concerning indicators for an epidemic. The final size of an epidemic is the total proportion of the population that becomes infected [7, 17]. Knowing the final size is crucial for assessing the severity of epidemics, evaluating the impact of interventions, guiding healthcare planning, and informing public

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health decision-making. To understand the development trend and severity of infectious diseases, researchers have estimated and analyzed the final size by using mathematical models and empirical data [2, 5, 6, 8, 9, 16, 19]. Results tell us that public health measures [2, 19], vaccination campaigns [13, 24], and other interventions [1, 4] all can reduce the final size by limiting the spread of the disease.

Besides the final size, the peak amplitude of an epidemic and the peak time [23] become the main concerns of CDC staff. Understanding the peak value and peak time helps optimize healthcare responses, minimize the burden on healthcare systems, and reduce the overall morbidity and mortality associated with the infectious disease.

The classical SIR model involves the system of ODE [14]

$$\begin{cases} \frac{dS(t)}{dt} = -\beta S(t)I(t), \\ \frac{dI(t)}{dt} = \beta S(t)I(t) - \gamma I(t) \end{cases} \tag{1.1}$$

with the initial conditions

$$S(0) = S_0, I(0) = I_0, S_0 + I_0 = N,$$

where $S(t)$ and $I(t)$ denote the susceptible and infected compartments of a given population in the presence of an infectious disease. The constant N is the size of the population, $R(t) := N - S(t) - I(t)$ is the recovered compartment of the population at time t . The positive parameters β and γ are the infected and recovery rates per unit time, respectively. It is well known that the basic reproduction number is $\mathcal{R}_0 = \frac{\beta}{\gamma}N$.

To introduce vaccination into the SIR model, we first make the following assumptions:

1. Population is partitioned into four classes, the susceptibles $S(t)$, the infectious $I(t)$, the vaccinated $V(t)$, and the recovered $R(t)$ respectively, see the flow chart in Fig. 1. The total population size is N , that is, $S(0) + I(0) := N$.

2. The factor σ ($0 \leq \sigma \leq 1$) is the infection probability of the vaccinated member contacting with the infections, $\sigma = 0$ means that the vaccine is completely effective in preventing infection, and $\sigma = 1$ means that the vaccine has no effect.

3. The vaccinations are implemented at times $t = n\tau$, $n = 1, 2, \dots$, φ ($0 < \varphi < 1$) is pulse vaccination rate, and the interpulse time, i.e., the time between two consecutive pulse vaccinations, is τ .

4. The vaccine wears off at a constant rate θ .



When pulse vaccination is incorporated into SIR model (1.1), the system becomes an SIVR (susceptible–infected–vaccinated–recovered) epidemic model:

$$\left\{ \begin{array}{l} \frac{dS(t)}{dt} = -\beta S(t)I(t) + \theta V(t), \\ \frac{dI(t)}{dt} = \beta S(t)I(t) + \sigma\beta V(t)I(t) - \gamma I(t), \\ \frac{dV(t)}{dt} = -\sigma\beta V(t)I(t) - \theta V(t), \end{array} \right\} t \neq n\tau, n = 1, 2, \dots, \tag{1.2}$$

$$\left\{ \begin{array}{l} S(n\tau^+) = (1 - \varphi)S(n\tau), \\ I(n\tau^+) = I(n\tau), \\ V(n\tau^+) = V(n\tau) + \varphi S(n\tau) \end{array} \right\} t = n\tau, n = 1, 2, \dots,$$

$$S(0) = S_0 > 0, I(0) = I_0 > 0, V(0) = V_0 = 0.$$

We are more interested in the final size, the peak value, the peak time, and the critical times for model (1.2). The paper is structured as follows. The next section deals with the final size, and its estimation is derived. Section 3 is devoted to the peak value and peak time, and four critical times are defined and estimated in Sect. 4. The stopping time is defined in the last section, and its estimates for model (1.1) are presented.

2 The final size

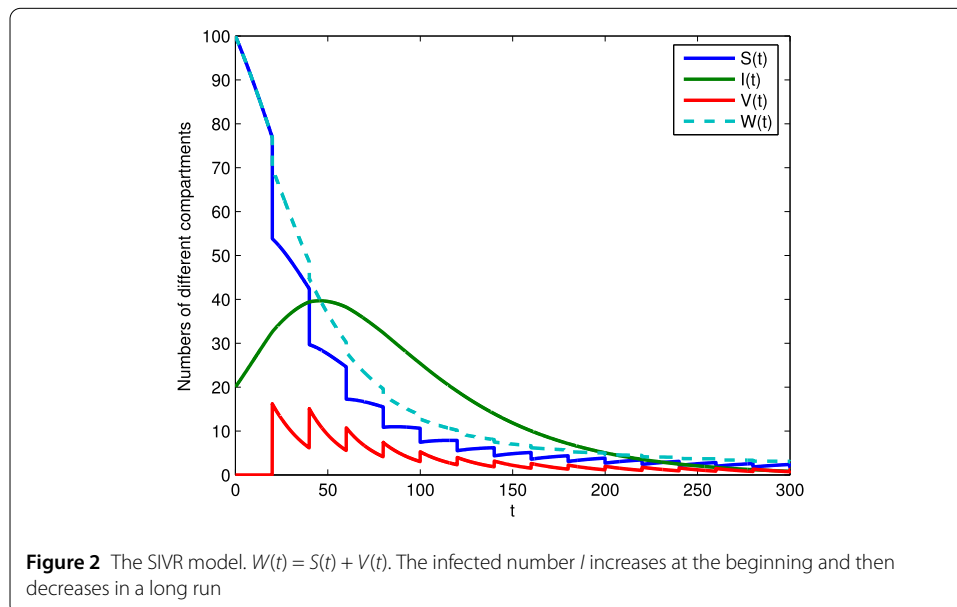
It is easy to see that the solution (S, I, V) to problem (1.2) exists uniquely and is global. Moreover, $S(t) + I(t) + V(t) \leq N$ for $t \geq 0$.

We first claim that

$$\lim_{t \rightarrow \infty} I(t) = 0, \tag{2.1}$$

which means that the disease vanishes eventually, see Fig. 2.

We now prove (2.1) by contradiction. In fact, if $\limsup_{t \rightarrow \infty} I(t) = \varepsilon_0$ for some $\varepsilon_0 > 0$, there exists a sequence $\{t_n\}_{n=1}^{+\infty}$ such that $I(t_n) \geq \frac{\varepsilon_0}{2}$ for any n .



Since S, I are bounded by N , we have $|I'(t)| \leq M$ for some $M \geq 0$ for $t \geq 0$ and $t \neq n\tau$. Therefore, there exists $\delta_0 > 0$ such that

$$|I(t) - I(t_n)| \leq \frac{\varepsilon_0}{4} \text{ for } t \in (t_n - \delta_0, t_n] \text{ or } t \in [t_n, t_n + \delta_0),$$

which means

$$I(t) \geq I(t_n) - |I(t) - I(t_n)| \geq \frac{\varepsilon_0}{2} - \frac{\varepsilon_0}{4} = \frac{\varepsilon_0}{4} \text{ for } t \in (t_n - \delta_0, t_n] \text{ or } t \in [t_n, t_n + \delta_0)$$

and

$$\int_0^\infty I(t)dt \geq \sum_{n=1}^\infty \int_{t_n - \delta_0}^{t_n + \delta_0} I(t)dt \geq \sum_{n=1}^\infty \frac{\varepsilon_0}{4} \delta_0 = \infty. \tag{2.2}$$

On the other hand, since

$$\frac{d}{dt}(S + I + V)(t) = -\gamma I(t), \tag{2.3}$$

integrating from $t = 0$ to $t = +\infty$ yields

$$(S + I + V)(+\infty) - (S + I + V)(0) = -\gamma \int_0^\infty I(t)dt$$

and

$$\int_0^\infty I(t)dt = \frac{-1}{\gamma} [(S + I + V)(\infty) - (S + I + V)(0)] < \infty, \tag{2.4}$$

which leads to a contradiction to (2.2); therefore, $\limsup_{t \rightarrow \infty} I(t) = 0$ and $\lim_{t \rightarrow \infty} I(t) = 0$.

Since $(S + V)' = -\beta S(t)I(t) - \sigma\beta V(t)I(t) \leq 0$ for $t \neq n\tau$ and $(S + V)$ is continuous for $t \geq 0$, the limit of $(S + V)(t)$ as $t \rightarrow \infty$ exists.

As in [17], the final size (Z) of the epidemic is defined as the number of members of the population who are infected over the course of the epidemic. For our model (1.2),

$$Z = N - (S + V)_\infty.$$

Now we estimate Z and define $W(t) = S(t) + V(t)$ for $t \geq 0$. It follows from (1.2) that

$$-\beta W(t)I(t) \leq W'(t) = -\beta S(t)I(t) - \sigma\beta V(t)I(t) \leq -\sigma\beta W(t)I(t), \tag{2.5}$$

and dividing (2.5) by $W(t)$ gives

$$-\beta I(t) \leq W'(t)/W(t) \leq -\sigma\beta I(t). \tag{2.6}$$

Integrating (2.6) from 0 to $+\infty$ yields

$$-\beta \int_0^{+\infty} I(t)dt \leq \ln W_\infty - \ln W_0 \leq -\sigma\beta \int_0^{+\infty} I(t)dt. \tag{2.7}$$

By combining (2.4) and (2.7), we obtain

$$\frac{\beta}{\gamma} [(S + I + V)(\infty) - (S + I + V)(0)] \leq \ln \frac{W_\infty}{W_0} \leq \frac{\sigma\beta}{\gamma} [(S + I + V)(\infty) - (S + I + V)(0)],$$

which means

$$\frac{\sigma\beta}{\gamma} [S_0 + I_0 - (S + V)(\infty)] \leq \ln \frac{W_0}{W_\infty} \leq \frac{\beta}{\gamma} [S_0 + I_0 - (S + V)(\infty)],$$

and equivalently,

$$\frac{\sigma\beta}{\gamma} [N - W_\infty] \leq \ln \frac{W_0}{W_\infty} \leq \frac{\beta}{\gamma} [N - W_\infty].$$

In particular, since $\mathcal{R}_0 = \frac{\beta N}{\gamma}$, we have

$$\sigma \mathcal{R}_0 [1 - \frac{W_\infty}{N}] \leq \ln \frac{W_0}{W_\infty} \leq \mathcal{R}_0 [1 - \frac{W_\infty}{N}].$$

Recalling that $W_0 = S_0$, we have estimates for the final size $Z = N - W_\infty$, where W_∞ satisfies

$$W_* \leq W_\infty \leq W^*,$$

and W_* , W^* are, respectively, the unique positive roots of

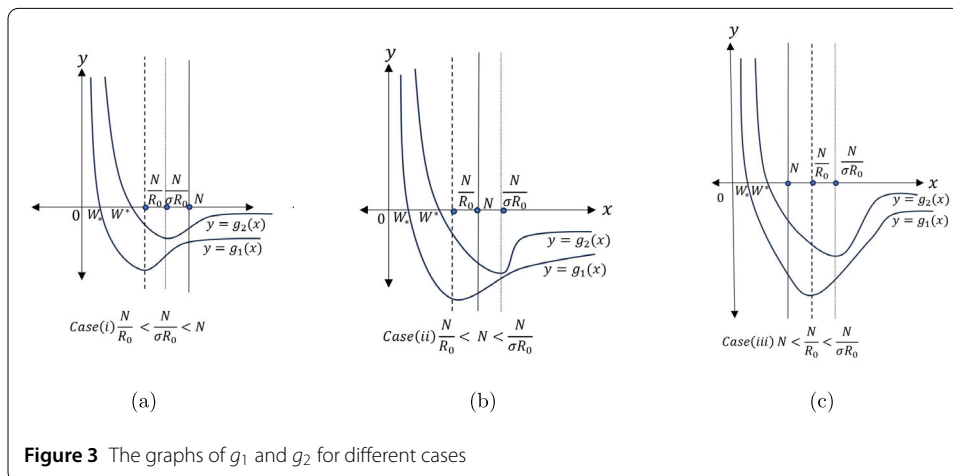
$$g_1(x) := \ln \frac{S_0}{x} - \mathcal{R}_0 [1 - \frac{x}{N}] = 0 \tag{2.8}$$

and

$$g_2(x) := \ln \frac{S_0}{x} - \sigma \mathcal{R}_0 [1 - \frac{x}{N}] = 0. \tag{2.9}$$

In fact, we can see from Fig. 3 that

$$g_1(0^+) > 0, \quad g_1(x) < 0 \text{ for } x \geq N,$$



there exists a unique W_* satisfying $0 < W_* < N$ and

$$g_1(W_*) = 0, g_1(x) < 0 \text{ for } 0 < W_* < x.$$

So we have

$$W_* \leq W_\infty.$$

Similarly,

$$g_2(x) \geq 0 \text{ for } x \leq W_*,$$

there exists unique W^* satisfying $0 < W_* \leq W^* < N$ such that

$$g_2(W^*) = 0, g_2(x) \geq 0 \text{ for } 0 < W_* \leq x \leq W^* \leq N.$$

Therefore

$$W_\infty \leq W^*.$$

Theorem 2.1 *The final size of model (1.2) is $Z = N - W_\infty$, and W_∞ satisfies*

$$W_* \leq W_\infty \leq W^*,$$

where W_* is the unique positive root of $g_1 = 0$ defined in (2.8), and W^* is the unique positive root of $g_2 = 0$ defined in (2.9).

Remark 2.1 If $\sigma = 1$, which means that the vaccine has no effect, we then have $g_1 = g_2$ and $W_* = W_\infty = W^*$, and W_∞ is the unique positive root of $g_1 = 0$, see Sect. 9.2 in [7].

3 The peak value and peak time

Noting that $I(0) > 0$ and $\lim_{t \rightarrow \infty} I(t) = 0$, there exists $t_p \geq 0$ such that $I_m := I(t_p) = \sup_{t \geq 0} I(t)$, we usually call t_p the peak time and $I(t_p)$ is the peak value.

By using equation (1.2) and $W = S + V$, we have

$$\begin{aligned} \frac{d}{dt} [(W + I)(t) - \frac{\gamma}{\beta} \ln(W(t))] &= -\gamma \frac{(1 - \sigma)VI}{W} \leq 0, \\ \frac{d}{dt} [(W + I)(t) - \frac{\gamma}{\sigma\beta} \ln(W(t))] &= \gamma \frac{(1 - \sigma)SI}{\sigma W} \geq 0 \end{aligned}$$

for $t \neq n\tau, n = 1, 2, \dots$, which implies that

$$\frac{\beta}{\gamma} \frac{d}{dt} [(W + I)(t)] \leq \frac{d}{dt} [\ln(W(t))] \leq \frac{\sigma\beta}{\gamma} \frac{d}{dt} [(W + I)(t)]. \tag{3.1}$$

Recalling that W, I are continuous and piecewise differentiable, integrating (3.1) from 0 to t yields

$$\frac{\sigma\beta}{\gamma} [S_0 + I_0 - W(t) - I(t)] \leq \ln \frac{W_0}{W(t)} \leq \frac{\beta}{\gamma} [S_0 + I_0 - W(t) - I(t)] \tag{3.2}$$

for any $t > 0$ and

$$S_0 + I_0 - W(t) - \frac{\gamma}{\sigma\beta} \ln \frac{W_0}{W(t)} \leq I(t) \leq S_0 + I_0 - W(t) - \frac{\gamma}{\beta} \ln \frac{W_0}{W(t)}. \tag{3.3}$$

Usually, the maximum number of infectives is the number of infectives when the derivative of I is zero, but in our model (1.2), $I(t)$ is not differentiable at $t = n\tau, n = 1, 2, \dots$, so we have to consider two cases.

If $t_p \neq n\tau$ for $n = 1, 2, \dots$, we have $I'(t_p) = 0$ and $(S + \sigma V)(t_p) = \frac{\gamma}{\beta}$. Using (3.3) with $t = t_p$ yields

$$S_0 + I_0 - \frac{\gamma}{\sigma\beta} - \frac{\gamma}{\sigma\beta} \ln W_0 + \frac{\gamma}{\sigma\beta} \ln \frac{\gamma}{\beta} \leq I_m \leq S_0 + I_0 - \frac{\gamma}{\beta} - \frac{\gamma}{\beta} \ln W_0 + \frac{\gamma}{\beta} \ln \frac{\gamma}{\sigma\beta} \tag{3.4}$$

since $\frac{\gamma}{\beta} \leq W(t_p) \leq \frac{\gamma}{\sigma\beta}$.

If $t_p = n_0\tau$ for $n_0 = 1, 2, \dots$. In this case, we have $I'(t_p^-) \geq 0$ and $I'(t_p^+) \leq 0$, that is,

$$(S + \sigma V)(t_p) \geq \frac{\gamma}{\beta} \text{ and } (1 - \varphi + \sigma\varphi)S(t_p) + \sigma V(t_p) \leq \frac{\gamma}{\beta},$$

and therefore $\frac{\gamma}{\beta} \leq W(t_p) \leq \frac{\gamma}{\beta} \frac{1}{\min\{(1-\varphi+\sigma\varphi), \sigma\}}$, which together with (3.3) gives

$$\begin{aligned} S_0 + I_0 - \frac{\gamma}{\beta} \frac{1}{\min\{(1-\varphi+\sigma\varphi), \sigma\}} - \frac{\gamma}{\sigma\beta} \ln W_0 + \frac{\gamma}{\sigma\beta} \ln \frac{\gamma}{\beta} &\leq I_m \\ &\leq S_0 + I_0 - \frac{\gamma}{\beta} - \frac{\gamma}{\beta} \ln W_0 + \frac{\gamma}{\beta} \ln \left[\frac{\gamma}{\beta} \frac{1}{\min\{(1-\varphi+\sigma\varphi), \sigma\}} \right]. \end{aligned} \tag{3.5}$$

Combining two cases, we have estimates (3.5) of the peak value since (3.5) holds if (3.4) holds.

We now turn to estimates of the peak time t_p . It follows from (2.6) that

$$-\frac{W'}{\beta WI} \leq 1 \leq -\frac{1}{\sigma} \frac{W'}{\beta WI}, \tag{3.6}$$

which together with (3.3) gives

$$-\frac{W'}{\beta W[S_0+I_0-W(t)-\frac{\gamma}{\beta} \ln W(0)+\frac{\gamma}{\beta} \ln W(t)]} \leq 1 \leq -\frac{1}{\sigma} \frac{W'}{\beta W[S_0+I_0-W(t)-\frac{\gamma}{\sigma\beta} \ln W(0)+\frac{\gamma}{\sigma\beta} \ln W(t)]}, \tag{3.7}$$

and by integrating (3.7) from 0 to t_p , we have

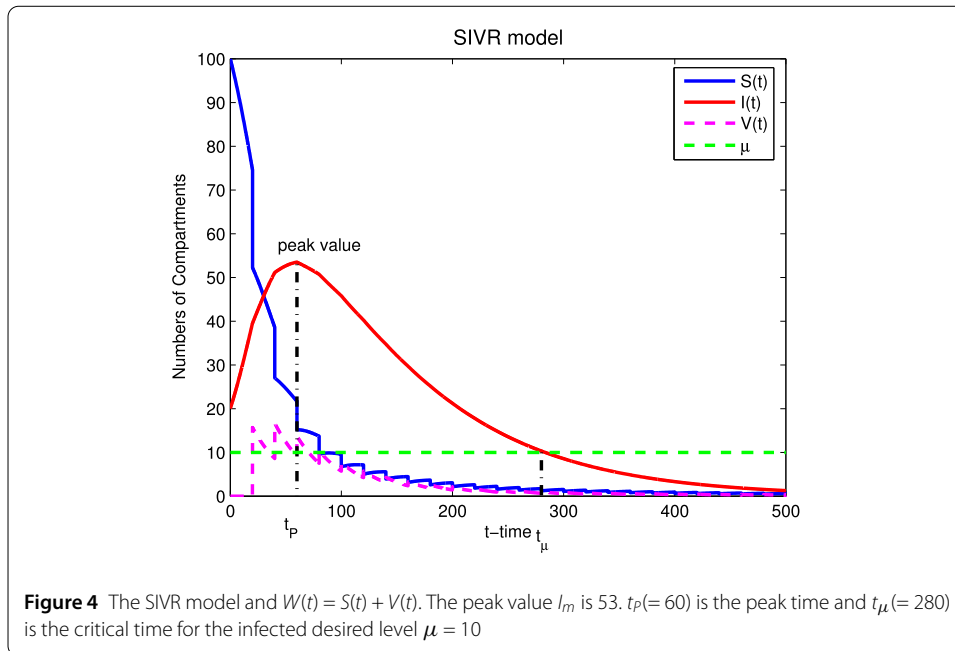
$$\int_{W_0}^{W(t_p)} \frac{dz}{\beta z[z-S_0-I_0+\frac{\gamma}{\beta} \ln W(0)-\frac{\gamma}{\beta} \ln z]} \leq t_p \leq \int_{W_0}^{W(t_p)} \frac{dz}{\sigma\beta z[z-S_0-I_0+\frac{\gamma}{\sigma\beta} \ln W(0)-\frac{\gamma}{\sigma\beta} \ln z]}.$$

Recalling that $\frac{\gamma}{\beta} \leq W(t_p) \leq \frac{\gamma}{\beta} \frac{1}{\min\{(1-\varphi+\sigma\varphi), \sigma\}}$ and $W(0) = S_0$ yields

$$\int_{S_0}^{\frac{\gamma}{\beta}} \frac{dz}{\beta z[z-S_0-I_0+\frac{\gamma}{\beta} \ln S_0-\frac{\gamma}{\beta} \ln z]} \leq t_p \leq \int_{S_0}^{\frac{\gamma}{\beta} \frac{1}{\min\{(1-\varphi+\sigma\varphi), \sigma\}}} \frac{dz}{\sigma\beta z[z-S_0-I_0+\frac{\gamma}{\sigma\beta} \ln S_0-\frac{\gamma}{\sigma\beta} \ln z]}. \tag{3.8}$$

Theorem 3.1 *The peak value I_m of model (1.2) satisfies (3.5), and the peak time t_p satisfies (3.8). Moreover, if $\sigma = 1$, we have*

$$\begin{aligned} I_m &= S_0 + I_0 - \frac{\gamma}{\beta} - \frac{\gamma}{\beta} \ln W_0 + \frac{\gamma}{\beta} \ln \frac{\gamma}{\beta}, \\ t_p &= \int_{S_0}^{\frac{\gamma}{\beta}} \frac{dz}{\beta z[z-S_0-I_0+\frac{\gamma}{\beta} \ln S_0-\frac{\gamma}{\beta} \ln z]}. \end{aligned} \tag{3.9}$$



As an example, we illustrate estimates of the peak time and peak value of the SIVR model in Fig. 4. Assume that there is no initial vaccination, the infection probability σ of the vaccinated member contacting with the infections is small. Let $\beta = 0.0005$, $\theta = 0.03$, $\sigma = 0.002$, $\gamma = 0.01$, $\varphi = 0.3$, and take $S_0 = 100$, $I_0 = 20$. Figure 4 shows that the peak time is $t_p = 60$ and the peak value is $I_m = 53$.

4 The critical times

As in [14], there are two important critical times for the epidemic model. One is the first time (t_μ) the infected population is below a given threshold (μ), and the other is the first time the number of infected individuals begins to decrease, which is in fact the peak time t_p for most models with single wave and can be viewed as the critical time with μ replaced by the peak value I_p .

However, owing to the complexity of the development of infectious diseases, multiple waves of infections are possible. For example, in several countries successive waves of COVID-19 disease have been observed [18, 20]. So we now present the following four critical times.

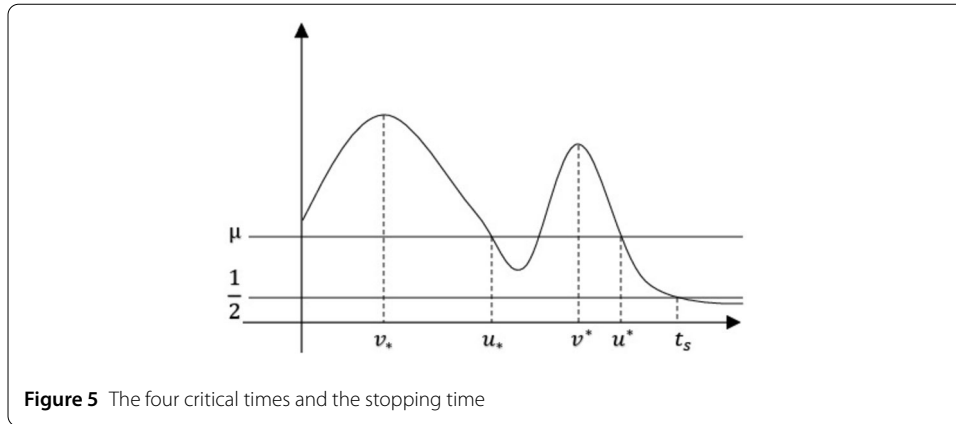
Let (S, I, V) be the solution of (1.2) with $S(0) = x \geq 0$ and $I(0) = y \geq 0$. For a given threshold $\mu > 0$, we denote four critical times as follows, see Fig. 5.

(i) u_* is the first time at which the number of infected individuals is not greater than the given value, that is,

$$u_*(x, y) := \underline{t}_\mu = \inf\{t > 0 : I(t) \leq \mu\};$$

(ii) u^* is the last time at which the number of infected individuals is not less than the given value, that is,

$$u^*(x, y) := \bar{t}_\mu = \sup\{t > 0 : I(t) \geq \mu\};$$



(iii) v_* is the first time from which the number of infected individuals begins to decrease, that is,

$$v_*(x, y) := \inf\{t > 0 : \exists \delta > 0 \text{ such that } I(z) < I(t) \text{ for } z \in (t, t + \delta)\};$$

(iv) v^* is the last time at which the number of infected individuals is not decreasing, that is,

$$v^*(x, y) := \sup\{t > 0 : \exists \delta > 0 \text{ such that } I(z) \leq I(t) \text{ for } z \in (t - \delta, t)\};$$

It is easy to see that $u_*(x, y) = 0$ when $0 \leq y < \mu$, and $v_* = v^*$ for epidemic models with single wave. For our model (1.2), let $\mu = 10$, then the first time \underline{t}_μ at which the number of infected individuals is not greater than μ is 280, see Fig. 4, and the last time \bar{t}_μ at which the number of infected individuals is not less than μ is also 280.

Next we derive some estimates for the critical times.

Theorem 4.1 For each $x \geq 0$ and $y \geq \mu$,

$$\frac{\ln x - \ln \frac{y}{\beta\sigma}}{\beta I_m} \leq u_*(x, y) \leq \frac{x + y}{\gamma \mu}. \tag{4.1}$$

Proof Let $S, I,$ and V be the solution of SIVR model (1.2) with $S(0) = x$ and $I(0) = y$. Since $\frac{d}{dt}(S + I + V)(t) = -\gamma I(t)$,

$$\int_0^t \gamma I(\tau) d\tau + S(t) + I(t) + V(t) = x + y.$$

Choosing $t = u_*(x, y)$ and noting that $I(\tau) \geq \mu$ for $0 \leq \tau \leq u_*(x, y)$ gives

$$u_*(x, y)\gamma\mu \leq \int_0^{u_*(x, y)} \gamma I(\tau) d\tau \leq x + y, \tag{4.2}$$

and we have the right inequality of (4.1).

On the other hand, since $I(t) > \mu = I(u_*)$ for $0 \leq t < u_*$ by the definition of u_* , we have $I'(u_*^-) \leq 0$, which together with the second equation of (1.2) yields

$$(S + \sigma V)(u_*) \leq \frac{\gamma}{\beta},$$

and therefore,

$$(S + V)(u_*) := W(u_*) \leq \left(\frac{S}{\sigma} + V\right)(u_*) \leq \frac{\gamma}{\sigma\beta}. \tag{4.3}$$

It follows from (2.6) that

$$W(u_*) \geq W(0)e^{-\beta \int_0^{u_*} I(\tau) d\tau} \geq xe^{-\beta u_* I_m}, \tag{4.4}$$

which together with (4.3) gives the left inequality of (4.1). □

Theorem 4.2 For each $x \geq \frac{\gamma}{\beta}$ and $y > 0$,

$$\frac{\ln x - \ln\left(\frac{\gamma}{\beta \min\{1-\varphi+\sigma\varphi,\sigma\}}\right)}{\beta I_m} \leq v_*(x, y) \leq \frac{\ln x - \ln\left(\frac{\gamma}{\beta}\right)}{\sigma\beta y}. \tag{4.5}$$

Proof Let (S, I, V) be the solution of SIVR model (1.2) with $S(0) = x$ and $I(0) = y$. Letting $W = S + V$ and integrating equation (2.6) from 0 to t gives

$$W(0)e^{-\beta \int_0^t I(\tau) d\tau} \leq W(t) \leq W(0)e^{-\sigma\beta \int_0^t I(\tau) d\tau} \tag{4.6}$$

for $t \geq 0$.

Since $I(t)$ is continuous and increasing on $t \in [0, v_*(x, y)]$, $y \leq I(t) \leq I_m$ for $t \in [0, v_*(x, y)]$. If $v_* \neq n\tau$ for $n = 1, 2, \dots$, we have $I'(v_*) = 0$ and $(S + \sigma V)(v_*) = \frac{\gamma}{\beta}$. In view of (4.6),

$$\begin{aligned} \frac{\gamma}{\beta} &= (S + \sigma V)(v_*(x, y)) \leq W(v_*(x, y)) \leq xe^{-\sigma\beta \int_0^{v_*} I(\tau) d\tau} \leq xe^{-\sigma\beta y v_*}, \\ \frac{\gamma}{\sigma\beta} &= \left(\frac{S}{\sigma} + V\right)(v_*(x, y)) \geq W(v_*(x, y)) \geq xe^{-\beta \int_0^{v_*} I(\tau) d\tau} \geq xe^{-\beta I_m v_*}. \end{aligned}$$

Taking the natural logarithm and rearranging gives (4.5).

If $v_* = n_0\tau$ for $n_0 = 1, 2, \dots$, we have $I'(v_*^-) \geq 0$ and $I'(v_*^+) \leq 0$, that is,

$$\frac{\gamma}{\beta} \leq (S + \sigma V)(v_*) \leq W(v_*(x, y)) \text{ and } \frac{\gamma}{\beta \min\{1-\varphi+\sigma\varphi,\sigma\}} \geq W(v_*(x, y)).$$

By (4.6),

$$\frac{\gamma}{\beta} \leq W(v_*(x, y)) \leq xe^{-\sigma\beta \int_0^{v_*(x,y)} I(\tau) d\tau} \leq xe^{-\sigma\beta y v_*(x,y)}$$

and

$$\frac{\gamma}{\beta \min\{1-\varphi+\sigma\varphi,\sigma\}} \geq W(v_*(x, y)) \geq xe^{-\beta \int_0^{v_*(x,y)} I(\tau) d\tau} \geq xe^{-\beta v_*(x,y) I_m}.$$

Now we can take the natural logarithm of above two inequations to get (4.5) and complete the proof. \square

5 The stopping time

Usually, we say the epidemic stops if there are no longer infected individuals after a special time t_S , that is, $I(t_S - 1) > 0$ and $I(t) = 0$ for $t \geq t_S$. It is well known that in any actual epidemic situation, the infected number is a nonnegative integer. However, in most epidemic compartment models described by ODEs or PDEs, $I(t)$ is a continuous function of time t . We have the limit $\lim_{t \rightarrow \infty} I(t) = 0$ as proved above, but $I(t) > 0$ for $t > 0$, it is difficult to derive the exact time t_S .

It seems to us that there is no definition for the stopping time. However, the critical time for a given threshold $\mu (> 0)$ provides us a convenient route. Denote

$$t_S := \bar{t}_\mu |_{\mu=0.5} = \sup\{t > 0 : I(t) \geq 0.5\},$$

where (S, I, V) is the solution of (1.2). It is easy to see that $I(t_S - 1) \geq 1$ and $I(t) = 0$ for $t \geq t_S$ if $I(t)$ is a nonnegative integer for any $t \geq 0$.

With the above definition, we have the following estimates of the stopping time for SIR model (1.1) by using the results in [14].

Theorem 5.1 *Let (S, I) be the solution of (1.1) with $S(0) = x > 0$, $I(0) = y > 0.5$. Then we have*

- (i) $\frac{1}{\gamma} \ln\left(\frac{x+y}{\gamma/\beta+0.5}\right) \leq t_S \leq \frac{x+y}{0.5\gamma}$;
- (ii) $t_S \leq \frac{\ln(2y)}{\gamma-\beta x}$ if $x \in [0, \gamma/\beta)$;
- (iii) $\lim_{x+y \rightarrow \infty} \frac{t_S}{\ln(2(x+y))/\gamma} = 1$.

Proof Recalling that SIR model (1.1) admits a single wave, we have $u_*(x, y) = u^*(x, y) := u(x, y)$. It is shown in [14] that

$$\begin{aligned} \frac{1}{\gamma} \ln\left(\frac{x+y}{\gamma/\beta+\mu}\right) &\leq u(x, y) \leq \frac{x+y}{\mu\gamma}, \\ u(x, y) &\leq \frac{\ln(y/\mu)}{\gamma-\beta x} \text{ if } x \in [0, \gamma/\beta), \\ \lim_{x+y \rightarrow \infty} \frac{u(x, y)}{\ln((x+y)/\mu)/\gamma} &= 1. \end{aligned}$$

Replacing μ by 0.5, we have $t_S = u(x, y)$ and complete the proof. \square

Let us consider the example as shown in Fig. 4. Since $\beta = 0.0005$, $\sigma = 0.002$, $\gamma = 0.01$, $x = S_0 = 100$, $y = I_0 = 20$, we have $100 \ln \frac{240}{41} \leq t_S \leq 24000$, which is not satisfactory. However, it is our first attempt to define and estimate the stopping time, and we look forward to future progress.

6 Conclusion and discussion

It is well known that an infectious disease model can be used to understand the current state of the epidemic, to predict pandemic landscape, and to help make decisions. In this

paper, we consider an SIVR epidemic model with impulsive vaccination, which extends the classical SIR model.

For this model, what we are more interested in are the final size, the peak value, the peak time, and the stopping time. The final size is firstly considered. Differently from the classical SIR model, in which the final size can be derived by a formula, we present some estimates of the final size by overcoming the difficulty induced by impulsive vaccination. We also define and estimate the peak value and peak time. Moreover, four critical times for the SIVR model are defined and studied. Our results extend those for the well-understood SIR model.

It seems to us that there is no result for the stopping time, which is very important for any actual epidemic. We try to define the stopping time of the SIVR model by using the critical time for a given threshold $\mu = 0.5$, some rough estimates are also presented. It is worth mentioning that all above definitions and results can be used to investigate similar compartmental models, and the follow-up progress is worth looking forward to.

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Author contributions

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Data availability

The authors confirm that the data supporting the findings of this study are available within the manuscript.

Declarations

Competing interests

The authors declare no competing interests.

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References

1. Bagal, D.K., Rath, A., Barua, A., Patnaik, D.: Estimating the parameters of susceptible-infected-recovered model of COVID-19 cases in India during lockdown periods. *Chaos Solitons Fractals* **140**, 110154 (2020)
2. Barril, C., Bliman, P.-A., Cuadrado, S.: Final size for epidemic models with asymptomatic transmission. *Bull. Math. Biol.* **85**, 52 (2023)
3. Bloom, D.E., Cadarette, D.: Infectious disease threats in the twenty-first century: strengthening the global response. *Front. Immunol.* **10**, 549 (2019)
4. Bradley, J., Ruggieri, A., Spencer, A.H.: Twin Peaks: COVID-19 and the labor market. *Eur. Econ. Rev.* **138**, 103828 (2021)
5. Brauer, F.: Age-of-infection and the final size relation. *Math. Biosci. Eng.* **5**, 681–690 (2008)
6. Brauer, F.: The final size of a serious epidemic. *Bull. Math. Biol.* **81**, 869–877 (2019)
7. Brauer, F., Castillo-Chavez, C.: *Mathematical Models in Population Biology and Epidemiology*. Springer, Berlin (2001)
8. Cadoni, M., Gaeta, G.: Size and timescale of epidemics in the framework. *Physica D* **411**, 132626 (2020)
9. Cui, J., Wu, Y., Guo, S.: Effect of non-homogeneous mixing and asymptomatic individuals on final epidemic size and basic reproduction number in a meta-population model. *Bull. Math. Biol.* **84**, 38 (2022)
10. d'Onofrio, A.: Stability properties of pulse vaccination strategy in SEIR epidemic model. *Math. Biosci.* **179**, 57–72 (2002)
11. Gao, S., Chen, L., Teng, Z.: Pulse vaccination of an SEIR epidemic model with time delay. *Nonlinear Anal., Real World Appl.* **9**, 599–607 (2008)
12. Gao, S., Ouyang, H.: Mixed vaccination strategy in SIRS epidemic model with seasonal variability on infection. *Int. J. Biomath.* **4**, 473–491 (2011)
13. Hui, J., Chen, L.-S.: Impulsive vaccination of SIR epidemic models with nonlinear incidence rates. *Discrete Contin. Dyn. Syst., Ser. B* **4**, 595–605 (2004)
14. Hynd, R., Ikpe, D., Pendleton, T.: Two critical times for the SIR model. *J. Math. Anal. Appl.* **505**, 125507 (2022)

15. Kribs-Zaleta, C., Velasco-Hernandez, J.X.: A simple vaccination model with multiple endemic states. *Math. Biosci.* **164**, 183–201 (2000)
16. Lin, Y., Zang, H.P., Liu, S.Q.: Final size of an n-group SEIR epidemic model with nonlinear incidence rate. *Int. J. Biomath.* (2024). <https://doi.org/10.1142/S1793524524500086>
17. Magal, P., Seydi, O., Webb, G.: Final size of an epidemic for a two-group SIR model. *SIAM J. Appl. Math.* **76**, 2042–2059 (2016)
18. Marijon, E., Karam, N., Jouven, X.: Cardiac arrest occurrence during successive waves of the COVID-19 pandemic: direct and indirect consequences. *Eur. Heart J.* **42**, 1107–1109 (2021)
19. Miller, J.C.: A note on the derivation of epidemic final sizes. *Bull. Math. Biol.* **74**, 2125–2141 (2012)
20. Ruiz-Huerta, C., Canto, M., Ruiz, C., et al.: COVID-19 mortality in patients aged 80 and over residing in nursing homes-six pandemic waves: OCTA-COVID study. *Int. J. Environ. Res. Public Health* **19**, 12019 (2022)
21. Schlickeiser, R., Kröger, M.: Analytical modeling of the temporal evolution of epidemics outbreaks accounting for vaccinations. *Physics* **3**, 386–426 (2021)
22. Stone, L., Shulgin, B., Agur, Z.: Theoretical examination of the pulse vaccination policy in the SIR epidemic model. *Math. Comput. Model.* **31**, 207–215 (2000)
23. Turkyilmazoglu, M.: Explicit formulae for the peak time of an epidemic from the SIR model. *Physica D* **422**, 132902 (2021)
24. Turkyilmazoglu, M.: An extended epidemic model with vaccination: weak-immune SIRVI. *Phys. A* **598**, 127429 (2022)

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