Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
Explicit formulae for the peak time of an epidemic from the SIR model. Which approximant to use?

Martin Kröger a,∗, Mustafa Turkyilmazoglu b,c, Reinhard Schlickeiser d,e

a Polymer Physics, Department of Materials, ETH Zurich, Leopold-Russica-Weg 4, 8093 Zurich, Switzerland
b Department of Mathematics, Hacettepe University, Beytepe, 06532, Ankara, Turkey
c Department of Medical Research, China Medical University Hospital, China Medical University, Taichung, Taiwan
d Institut für Theoretische Physik, Lehrstuhl IV: Weltraum- und Astrophysik, Ruhr-Universität Bochum, 44780 Bochum, Germany
e Institut für Theoretische Physik und Astrophysik, Christian-Albrechts-Universität zu Kiel, Leibnizstr. 15, 24118 Kiel, Germany

A R T I C L E I N F O

Article history:
Received 23 April 2021
Received in revised form 15 June 2021
Accepted 16 June 2021
Available online 24 June 2021
Communicated by V.M. Perez-Garcia

Keywords:
Epidemic
SIR model
Peak thresholds
Peak time
COVID-19

A B S T R A C T

An analytic evaluation of the peak time of a disease allows for the installment of effective epidemic precautions. Recently, an explicit analytic, approximate expression (MT) for the peak time of the fraction of infected persons during an outbreak within the susceptible–infectious–removed (SIR) model had been presented and discussed (Turkyilmazoglu, 2021). There are three existing approximate solutions (SK-I, SK-II, and CG) of the semi-time SIR model in its reduced formulation that allow one to come up with different explicit expressions for the peak time of the infected compartment (Schlickeiser and Kröger, 2021; Carvalho and Gonçalves, 2021). Here we compare the four expressions for any choice of SIR model parameters and find that SK-I, SK-II and CG are more accurate than MT as long as the amount of population to which the SIR model is applied exceeds hundreds by far (countries, ss, cities). For small populations with less than hundreds of individuals (families, small towns), however, the approximant MT outperforms the other approximants. To be able to compare the various approaches, we clarify the equivalence between the four-parametric dimensional SIR equations and their two-dimensional dimensionless analogue. Using Covid-19 data from various countries and sources we identify the relevant regime within the parameter space of the SIR model.

© 2021 The Author(s). Published by Elsevier B.V. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

1. Introduction

The temporal evolution of COVID-19 (or SARS-CoV-2) pandemic waves has been successfully described, discussed, and forecasted by the mathematical susceptible–infectious–removed (SIR) model [1–17] while the model itself had been developed nearly a century ago [18–22]. There are two noticeable quantities that indicate the occurrence of new pandemic waves: the fraction \(i(t)\) of infected persons at time \(t\), and the fraction of newly infected population per day \(\dot{i}(t) = \beta(t)\dot{s}(t)i(t)\), where \(\beta(t)\) denotes the infection rate, and \(\dot{s}(t)\) the fraction of susceptible population. Both indicators \(i(t)\) and \(\dot{i}(t)\) in a pandemic wave first increase with time, undergo a maximum and drop at late times. The two peak times are slightly different. While the peak time in \(\dot{i}(t)\) is the one usually reported in the media on the basis of reported number of newly infected persons, the peak time in \(i(t)\) is the one that determines the peak time of required clinical resources. While an analytic approximant for the measurable peak time in \(\dot{i}\) exists for both the all-time [18,23] and semi-time SIR model [19–21,24], it is the purpose of this communication to clarify how the several existing approximants for the peak time in \(\dot{i}(t)\) compare with each other.

To this end we have collected known approximants for the peak time of the infected compartment in the literature, including the one very recently presented in this journal. We here use “approximant” for an approximate analytic expression whose Taylor expansion about a certain point is not required to exactly coincide with the Taylor expansion of the exact solution about the same point, while such point or points may exist for all approximations to be analyzed. In a first step we are going to explain and prove how the dimensionless and dimensional SIR models are interrelated. The correspondence allows us to compare the existing approximants, as they had been obtained using different notation. We then proceed using a unique language and notation and present all existing approximants without leaving out any single detail in their final expressions. We are not going to repeat all the calculations that lead to these approximants in the several papers we are going to quote, but we are collecting all necessary details in appendices to make this contribution self-contained. The goal of the present study is to find out and clarify, as a service to the readers of Physica D, if the accuracy of the existing
approximants supersedes the one presented to them recently by Turkyilmazoglu [25], or not.

There are various papers [23–33] that aimed at deriving approximate analytic expressions for various quantities that appear in the all-time or semi-time SIR models [23–32,34,35]. And there are several variants [36–43] of the SIR model, including stochastic variants [44–57] or variants that account for vaccination [58–62] or pulse vaccination [63–66]. For the semi-time SIR Heng and Atthaus [26] provided an analytic approximant for the population fraction of susceptible $s(t)$ and infected $i(t)$ persons but only for times prior peak time, and they could not derive an approximant for any of the peak times. Harko et al. [67] were able to express time of the semi-time SIR model in terms of an integral, which can only be evaluated numerically, but did not derive an integral or analytic expressions for peak times. Bidari et al. [27] focused on deriving implicit equations for final sizes of compartments and approximate solutions to such equations, but did not obtain an expression for a peak time. An analytic approximate inverse solution of the semi-time SIR model with special initial condition of initially vanishing population fraction $r(0) = 0$ of recovered/removed persons was presented by Carvalho and Gonçalves [28]. An explicit series solution of SIR and SIS epidemic models was obtained by making use of the homotopy analysis method by Khan et al. [30]. This approach allows one to study convergence properties of the solution, but in practice, it is inefficient to study the solution of the SIR model using an infinite series. Moreover, this approach does not provide an analytic expression for a peak time. Within the same spirit Barlow and Weinstein [33] derived an accurate closed-form infinite series solution of the SIR model that involves a Vandermonde matrix, whose inversion is explicitly known; however, they do not provide a method for estimating peak time.

In [25] the time $t$-dependent SIR model for population fractions $s$ (susceptible), $i$ (infected), and $r$ (removed/recovered) had been written as follows

$$\frac{ds}{dt} = -\beta si, \quad \frac{di}{dt} = \beta si - \gamma i, \quad \frac{dr}{dt} = \gamma i,$$

subject to the general arbitrary (semi-time) initial conditions

$$s(0) = s_0 \in (0, 1), \quad i(0) = i_0 \in (0, 1 - s_0).$$

and where $\beta$ and $\gamma$ are the assumed stationary infection and recovery rates of population fractions. The initial condition for $r$ follows from $r(0) = r_0 = 1 - s_0 - i_0$, because the classical SIR model has only three compartments, and any of the N members of the population belongs to one of the three compartments at any time. Allowing for arbitrary initial conditions and restricting the model to future times $t > 0$ is known as semi-time SIR model [19–21,24]. For the all-time SIR model, $s_0$ and $i_0$ are interrelated [18,23]. Here we consider the semi-time SIR model for which an analytic expression for the peak time $t_{\text{peak}}$ of the infected compartment, defined by

$$\frac{di}{dt} \bigg|_{t=t_{\text{peak}}} = 0$$

had been derived in [25]. It will be reproduced in Eq. (14). In its classical form Eq. (1) with (2) the dimensional SIR model has four parameters, the rates $\beta$ and $\gamma$, and the initial fractions $s_0$ and $i_0$. On the other hand, analytic approximants for the solution of the reduced dimensionless semi-time SIR model are available from [24] and [28]. While the reduced model has only three parameters, it is still equivalent with the original SIR model (the proof of equivalence will be given in the next section). Moreover, one of the three parameters is used to make the time dimensionless, so that one is left with essentially only two parameters $k$ and $\eta$. These parameters appear in the reduced semi-time SIR model [24] as follows

$$\frac{ds}{dr} = -SI, \quad \frac{dt}{dr} = SI - kl, \quad \frac{dR}{dr} = kl,$$

with initial conditions

$$S(0) = 1 - \eta, \quad I(0) = \eta \in (0, 1),$$

Here in general a dimensionless reduced time $\tau$ defined by $\tau \propto \int_0^t \beta(\xi)d\xi$ for an arbitrary (including periodic) time-dependent infection rate $\beta(t)$, but because as in [25] we consider here a stationary infection rate, $\tau$ is simply proportional to time, $\tau = at$ with a constant rate $a$ that is specified in Eq. (7). Moreover, $S = s/(s_0 + i_0)$, $I = i/(s_0 + i_0)$, and $R = 1 - S - I$ are fractions of the initially unrecovered population. This implies $R(0) = 0$ as in [24]. We recall, that the quantities $s, i,$ and $r$ are fractions with respect to the total initial population, including the recovered compartment, and therefore $s \geq S, i \geq I,$ and $r \geq R$.

Yet another version of a reduced semi-time SIR model was investigated in [28]. They introduced $\tilde{\tau} = \tau/a$ to write

$$\frac{dS}{d\tilde{\tau}} = -\tilde{R}_0 S, \quad \frac{dI}{d\tilde{\tau}} = \tilde{R}_0 S - I, \quad \frac{dR}{d\tilde{\tau}} = I,$$

subject to unchanged initial conditions (5). It is important to note here that in the original work Carvalho and Gonçalves [28] formulated their equations in terms of the fractions $s, i$, and $r$, did not allow for non-vanishing $r(0)$, and mentioned $R_0 = \beta/\gamma$, which is a correct assignment but only for this special case of $r(0) = 0$. We are here extending their work to allow for non-vanishing $r(0)$ so that also $R_0$ has to be revised, as shown next. This extension will allow one to compare all available approximants for arbitrary initial conditions $s_0$ and $i_0$.

### 2. Analytical approximants

Starting from the dimensional SIR model with four parameters, the three parameters of the reduced formulation are given by

$$\eta = \frac{i_0}{s_0 + i_0}, \quad a = \beta(s_0 + i_0), \quad k = \frac{\gamma}{a} = \frac{1}{R_0}.$$ (7)

In turn, for given $k$, $\eta$, and $a$, the parameters of the dimensional model are given upon direct inversion of Eqs. (7)

$$i_0 = \frac{s_0}{1 - \eta}, \quad \gamma = ka = \frac{a}{R_0}, \quad \beta = \frac{(1 - \eta)a}{s_0},$$ (8)

just highlighting the fact that, $s_0$ must drop out. Moreover, any characteristic real time $R$ of the dimensional SIR model is related to the corresponding reduced time $\tau = at$ or also $t = \gamma t/a$ as

$$t_{\text{peak}}(\gamma, \eta, s_0, i_0) = \frac{R_{\text{peak}}(\gamma, \eta)}{a} = \frac{R_0 s_{\text{peak}}(R_0, \eta)}{a},$$ (9)

where the dimensionless times $t_{\text{peak}}(\gamma, \eta)$ and $R_{\text{peak}}(R_0, \eta)$ depend on two parameters only: the inverse basic reproduction number $k = 1/R_0$ and the initial fraction of infected population among the non-recovered population, $\eta = I(0)$.

If we wish to test an approximate solution of the SIR model for arbitrary choices of parameters, or if we want to compare the quality of different approximants as we are going to do here, it is hence sufficient to perform the test in the 2-dimensional parameter space built by $k$ and $\eta$. While $\eta \in (0, 1)$ by construction, the $k$ is semipositive in general. However, a peak time in $t(R)$ occurs at positive times $t > 0$ only if the following inequality holds

$$k \leq 1 - \eta.$$ (10)
This inequality follows from [24], as the condition (3) for the peak converts with the help of (4) into
\[ S(\tau_{\text{peak}}) = k \]
within the reduced model, because \( S(0) = 1 - \eta \), and because \( S \) monotonically decreases with increasing \( \tau \) according to Eq. (4).

We have to still prove the equivalence between dimensional and dimensionless forms of the SIR model. To this end it is sufficient to prove Eq. (7), or the equivalent Eq. (8). Inserting \( s = (s_0 + \eta_0)S \) and \( i = (s_0 + \eta_0)i \) as well as Eq. (8) into Eq. (1) gives
\[ \frac{ds}{dt} = (s_0 + \eta_0) \frac{ds}{dt} = (s_0 + \eta_0) \frac{ds}{dt} = -\beta si = -(s_0 + \eta_0) aSI, \]
confirming the equation of change for \( s \) in Eq. (4), as well as
\[ \frac{di}{dt} = (s_0 + \eta_0) \frac{dI}{dt} = \beta si - \gamma i = (s_0 + \eta_0) aSI - k(s_0 + \eta_0) aI, \]
confirming the equation of change for \( i \) in Eq. (4), which is obvious, if we divide both sides of the Eqs. (12) and (13) by \((s_0 + \eta_0)a\). The initial conditions are also equivalent, as \( s_0 = (s_0 + \eta_0)S(0) = (s_0 + \eta_0)(1 - \eta) = s_0 + \eta_0 - \eta_0 = s_0 \) and \( \eta_0 = (s_0 + \eta_0)I(0) = (s_0 + \eta_0)\eta = \eta_0 \) and \( r_0 = 1 - s_0 - i_0 \).

2.1. MT approximant

The MT approximant by Turkyilmazoglu [25] for the peak time of the infected compartment had been formulated using the dimensional SIR formulation (1) with 4 parameters. Using our replacement rule (8), it receives the form of Eq. (9) with the dimensionless peak time (see Appendix A for details)
\[ \tau_{\text{peak}}^\text{MT}(k, \eta) = \frac{1}{2 - 3k} \left[ \ln(A) - \frac{B \left( \coth^{-1}(C) + \tanh^{-1}(D) \right)}{E} \right], \]
where \( k \)- and \( \eta \)-dependent coefficients are given by
\[ A = 4(1 - \eta)^2k - 3 + 2(1 - \eta)^2 - 5(1 - \eta)^2k, \]
\[ B = 2(1 - 2k - \eta), \]
\[ C = (1 - \eta)E, \]
\[ D = k + \eta - 1, \]
\[ E = \sqrt{(1 - k - \eta)^2 + 2k\eta}. \]
Note that the term under the square root \( E \) is positive for all \( \eta \in (0, 1) \) and \( k \in (0, 1) \). For the special case of \( k = 2/3 \), where the denominator of \( \tau_{\text{peak}}^\text{MT} \) vanishes, the expression can still be evaluated using l'Hôpital's rule, i.e., \( \tau_{\text{peak}}^\text{MT}(2/3, \eta) = 3[1 - 9\eta^2 + 4\coth^{-1}[1 - 4/(1 - 3\eta)^2 - 4\tanh^{-1}[1 - 2/(1 + 3\eta)]][2(1 + 3\eta)^2]. \]

2.2. SK approximants SK-I and SK-II

The Schlicker & Kröger (SK) approximants for the peak time of the infected compartment, starting from the reduced SIR model Eqs. (4) had not been explicitly written down in their work [24], where they developed an approximate solution to the whole time-dependency of all SIR quantities, but they can be read off from the provided approximate analytic solution \( S(\tau) \) of the reduced SIR model, using Eq. (11). To be more specific, one can readily solve \( S(\tau_{\text{peak}}) = k = 1 - J_{\text{decay}}(\tau_{\text{peak}}) \) with \( J_{\text{decay}}(\tau) \) from Eq. (71) of [24] for \( \tau_{\text{peak}} \) (for details see Appendix B). In the quoted work, \( J \) denotes the cumulative fraction of infected persons, thus \( J = 1 - S \), and \( J_{\text{decay}} \) applies within the regime of reduced time where the peak time \( \tau_{\text{peak}} \) actually occurs. The resulting time is the reduced peak time (Appendix B)
\[ \tau_{\text{peak}}^K(k, \eta) = \frac{2}{a_j} \tanh^{-1}\left( \frac{a_1}{a_j} \right) - T_{\text{b}}(J_{\text{max}}), \]
with
\[ T_{\text{b}}(x) = \frac{2}{|b_1|} \tanh^{-1}\left( \frac{b_1 + 2b_2(x - J_{\infty})}{|b_1|} \right), \]
in terms of a number of quantities characterizing the solution, that are all expressed in terms of \( k \) and \( \eta \). To be specific, one has [24]
\[ a_0 = \eta(1 - \eta), \]
\[ a_1 = 1 - k - 2\eta, \]
\[ a_2 = J_{\max} - a_0 - a_1(\eta_0 - \eta), \]
\[ a_3 = \sqrt{a_1^2 - 4a_2a_2}, \]
\[ J_{\max} = 1 + kW_0 \left( \frac{(1 - \eta)e^{-1/k}}{k} \right), \]
\[ J_0 = 1 + k \frac{1}{2} W_1 \left( \frac{(2 - (1 - \eta)e^{-1/k}}{ke} \right), \]
\[ J_{\max} = (1 - J_0)(1 - J_0 - k), \]
where \( W_0 \) and \( W_1 \) are the principal and non-principal solutions of Lambert’s equation [23,68]. They are both available like inverse trigonometric functions or elliptic integrals in common software packages (python, Mathematica, matlab, eventually also excel). For the so-called SK-I approximant, the remaining two parameters \( b_1 \) and \( b_2 \) left to be specified are given by (Appendix B)
\[ b_1 = 1 - k - J_{\infty}, \]
\[ b_2 = \frac{a_1(2a_1b_1 - a_2^2 + 4a_2b_2(J_{\infty} - \eta))}{[a_1 + 2a_2(J_{\infty} - \eta)]^2}, \]
while the SK-II approximant is defined by
\[ b_1 = \frac{a_2^2}{a_1 + 2a_2(J_{\infty} - \eta)}, \]
\[ b_2 = \frac{a_2a_2^2}{[a_1 + 2a_2(J_{\infty} - \eta)]^2}. \]
We are not going to interpret all these quantities here, but it may be useful to mention that \( J_{\max} \) is the finally infected population fraction, and \( a_{\max} \) the maximum dimensional rate of newly infected persons \( J_{\max} \) is the maximum reduced rate), that occurs at a time that differs from the reduced peak time \( \tau_{\text{peak}}^k \) in Eq. (16) by the two \( T_{\text{b}} \) terms.

2.3. CG approximant

Carvalho and Gonçalves [28] (CG) obtained, starting from the reduced SIR model (6) with the help of \( w = (1 - r)R_0 \), for the reduced peak time in \( I \) the approximate
\[ \hat{\tau}_{\text{peak}}^C(R_0, \eta) = (F_c - C_1 w_c(w_c = -R_0) + C_1(w_c^2 = -R_0^2) \]
\[ + \ln \left( \frac{|w_c - z_2|}{R_0 - z_1} \right)^{a_1} \frac{|w_c - z_2|^{a_2}}{|R_0 - z_2|^{a_2}} \].
with coefficients given by
\[
z_1 = \frac{(1 - \eta)R_0 - 1}{(1 - \eta)R_0 - 1},
\]
\[
z_2 = S_\infty R_0,
\]
\[
w_c = R_0 - \ln[(1 - \eta)\eta],
\]
\[
A_1 = \left[ (1 - \eta)R_0 \exp\left\{ \frac{-\eta R_0}{(1 - \eta)R_0 - 1} \right\} \right]^{-1},
\]
\[
A_2 = \left[ (1 - \eta)R_0 \exp\left\{ -(1 - S_\infty)R_0 \right\} \right]^{-1},
\]
\[
F_c = \frac{1}{1 - w_c} - \frac{A_1}{A_2} - \frac{w_c - z_1}{w_c - z_2},
\]
\[
C_1 = \frac{A_1}{w_c - z_1^2} + \frac{A_2}{w_c - z_2^2}.
\]
and where \(S_\infty\) is the solution of the nonlinear equation \(S_\infty = (1 - \eta)\exp\left\{ -(1 - S_\infty)R_0 \right\}\). From Schlickeiser and Kröger [24] we know that the nonlinear equation for \(S_\infty\) that remained unsolved in [28] is solved using Lambert’s principal function \(W_0\) [23,68] as follows
\[
S_\infty = 1 - S_\infty = -R_0^{-1}W_0 \left[ -(1 - \eta)R_0 e^{-\eta R_0} \right].
\]
As the reduced times \(\tilde{\tau}\) and \(\tau\) are related by \(\tau = R_0\tilde{\tau}\) according to Eq. (9), with \(R_0 = a/\gamma = k^{-1}\) according to Eq. (7), the reduced peak time for comparison with the remaining approximants is
\[
\tau_{\text{peak}}^{\text{CG}}(k, \eta) = R_0 \tau_{\text{peak}}^{\text{CG}}(R_0, \eta) = k^{-1} \tau_{\text{peak}}^{\text{CG}}(k^{-1}, \eta)
\]
where \(\tau_{\text{peak}}^{\text{CG}}\) is taken from Eq. (21).

2.4 Results and discussion

The exact peak time of the infected compartment calculated from the numerical solution of the SIR equations (4) is shown in Fig. 1a over basically the whole admissible \(k\) (horizontal axis) and \(\eta\) (vertical axis) range. Note that we use a semilogarithmic axis and a coloring scheme that reflects \(\log_{10}(\tau_{\text{peak}})\) to appreciate all details, and that the figure is exactly reproduced if we solve Eqs. (1) or (6) numerically instead. The advantage of (4) or (6) over (1) is that they have no redundant parameters. The corresponding performance of the four approximants CG, SK-I, SK-II, and MT is shown in Figs. 1b–e, while the relative deviation between approximants and exact solution is given by Fig. 1f–j. In each panel, the two variables of the dimensionless SIR model are thus varied, so that every panel shows the behavior of the peak time over the whole domain of SIR model parameters. While (a) shows the exact result (as a reference), (b)–(e) show the peak time for the four approximate expressions presented in this work. The remaining panels (f)–(j) show the same data (b)–(e) in a different fashion. Shown in (f)–(j) is the relative deviation between the approximate expression and the exact result.

While the performance of the MT approximant is rather accurate over the whole \(k-\eta\)-domain, the SK and CG approximants perform better than MT except within the regime of relatively large \(\eta\) close to 1 \(\rightarrow\) 1. This is made more precise in Fig. 2. The color bar for all panels of the first row is shown in (a), the single color bar for the 2nd row is shown in (g). The latter goes from blue (high quality, < 1% deviation from the exact solution) to yellow (low quality, > 5% deviation).

\[
\eta > 1, \quad \eta_c = \min \left( \frac{1}{4}, \frac{1-k}{3} \right).
\]
least in some of the $k$-$\eta$ region. This fact highlights the necessity to use the best available approximant, given by Fig. 1, depending on the $k$-$\eta$ regime that applies to a real situation at hand. Using the combined approximant, the best approximant depending on the $(k, \eta)$ pair value, the relative deviation to the exact result is quantified in Fig. 3.

There are many examples to which the MT approximant had been applied in the original work [25]. We list them in Table 1. Table 2 confirms that the MT approximant is more accurate when $\eta > \eta_c$, while all approximants are good and work very well. We include in the last three rows of the table a case that is not allowed in the semi-time SIR model, the case of $k > 1$, as it has been discussed in [25] as well.

Examples of relevance for the ongoing Covid-19 pandemics in 60 countries are available from [17]. The authors analyze the first and second Covid-19 wave in real time. Rather than adding all additional $(k, \eta)$ pairs from 2021-04-13 to our tables, we have included them all as orange and white circles corresponding to first and second waves to Fig. 2. There is a general trend of a decreasing $k = \gamma/[s_0 + \eta_0]\beta$ for the second pandemic wave, even though the fraction $s_0 + \eta_0 = 1 - r_0$ of the remaining un-recovered population has diminished during the second wave. All crosses reside either in the yellow or white regions.

This means, that for most cases of relevance for the ongoing pandemics the existing SK-II and CG approximants are the most accurate. Still, we had to clarify here the relationship between different notation, dimensional versus dimensionless versions of the SIR equations, to allow for a direct comparison. Here, we clarified the correspondence between equivalent versions. The MT approximant might be a good choice if one does not want to calculate a Lambert value, or if the Lambert function is not available at all within the computational environment.

One should keep in mind that the peak time of the daily reported new cases does not coincide with the peak time of the infected compartment. While the former solves $d(s)/dt = 0$, the latter solves $di/dt = 0$, and the final fraction of infected population is not related to an integral over $i(t)$, but equals $\beta \int_0^\infty s(t)i(t)\,dt$. To be precise, the peak times differ by the two $T_0$ terms in Eq. (16) above. Both terms tend to vanish as $k$ approaches unity. The peak time of the newly infected population fraction is given by $\tau_{\text{daily}} = (2/a_3)\tanh^{-1}(a_1/a_3)$ with $a_1$ and $a_3$ given by Eq. (18), as shown in [24]. This measurable peak time is thus identical for approximants SK-I and SK-II.
Table 1

| Ref. | $N$ | $\beta$ | $\gamma$ | $s_0$ | $\eta$ | $k$ | $\eta_a$ | $a$ | $\eta/\eta_a$ |
|------|-----|--------|---------|-------|-------|-----|----------|----|------------|
| [67] | 45  | 0.45   | 0.02    | 0.4444| 0.3333| 0.057143| 0.42857 | 0.35| 1.7141(*) |
| [70] | 763 | 1.66   | 0.45455 | 0.99476| 0.009318| 0.27418 | 0.003937| 1.6578| 0.016273 |
| [71] | 2.87 $\times 10^6$| 0.91776| 0.70681 | 1 $-$ $\beta_0$| 1.0442 $\times 10^{-6}$| 0.77015 | 1.0442 $\times 10^{-6}$| 0.91776| 1.3629 $\times 10^{-5}$ |
| [75] | 4.6291 | 2.82 | 0.0268 | 0.60919 | 0.0268 | 6.2491 | 0.20573 |
| [75] | 0.5 | 0.3 | 1 $-$ $\beta_0$ | 1.27 $\times 10^{-6}$ | 0.6 | 1.27 $\times 10^{-6}$ | 0.5 | 9.525 $\times 10^{-6}$ |
| [75] | 10 | 1 | 0.05 | 0.1 | 0.05 | 10 | 0.2 |
| [73] | 2 | 1 | 0.9999 | 1 $\times 10^{-5}$ | 0.5005 | 1.0001 $\times 10^{-5}$ | 1.9998 | 6.0011 $\times 10^{-5}$ |
| [74] | 15 000 | 0.13905 | 0.018379 | 1 $-$ $\beta_0$ | 0.00013333 | 0.13218 | 0.00013333 | 0.13905 | 0.00053333 |
| [74] | 15 000 | 0.25695 | 0.014148 | 1 $-$ $\beta_0$ | 0.00013333 | 0.05506 | 0.00013333 | 0.25695 | 0.00053333 |

[25] Tab.1-1 - - 0.3333 0.1111 1 $-$ $\beta_0$ 5 $\times 10^{-10}$ 0.3333 5 $\times 10^{-10}$ 0.3333 2.2500 $\times 10^{-4}$
[25] Tab.1-2 - - 0.2222 0.1111 1 $-$ $\beta_0$ 5 $\times 10^{-6}$ 0.5000 5 $\times 10^{-6}$ 0.5000 3.0000 $\times 10^{-4}$
[25] Tab.1-3 - - 0.3333 0.1667 1 $-$ $\beta_0$ 5 $\times 10^{-6}$ 0.5002 5 $\times 10^{-6}$ 0.5002 3.0009 $\times 10^{-4}$
[25] Tab.1-4 - - 0.1667 0.1111 1 $-$ $\beta_0$ 5 $\times 10^{-6}$ 0.6665 5 $\times 10^{-6}$ 0.6665 4.4973 $\times 10^{-4}$
[25] Tab.1-5 - - 0.3333 0.2222 1 $-$ $\beta_0$ 5 $\times 10^{-6}$ 0.6667 5 $\times 10^{-6}$ 0.6667 4.5000 $\times 10^{-4}$
[25] Tab.1-6 - - 0.1333 0.1111 1 $-$ $\beta_0$ 5 $\times 10^{-6}$ 0.8335 5 $\times 10^{-6}$ 0.8335 9.0068 $\times 10^{-4}$
[25] Tab.1-7 - - 0.3333 0.2778 1 $-$ $\beta_0$ 5 $\times 10^{-6}$ 0.8335 5 $\times 10^{-6}$ 0.8335 9.0081 $\times 10^{-4}$
[25] Tab.1-8 - - 0.3333 0.3222 1 $-$ $\beta_0$ 5 $\times 10^{-6}$ 0.9667 5 $\times 10^{-6}$ 0.9667 4.5041 $\times 10^{-4}$
[25] Tab.1-9 - - 0.1149 0.1111 1 $-$ $\beta_0$ 5 $\times 10^{-6}$ 0.9669 5 $\times 10^{-6}$ 0.9669 4.5355 $\times 10^{-4}$

CRediT authorship contribution statement

**Martin Kröger:** Conceptualization, Methodology, Formal analysis, Writing - original draft. **Mustafa Turkylmezoglu:** Writing - review & editing. **Reinhard Schlickeiser:** Conceptualization, Writing - review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability statement

All data generated or analyzed during this study are included in this published article.

Acknowledgments

We thank the referees for their constructive and helpful comments.

Appendix A. Derivation of $r_{\text{MT peak}}(k, \eta)$

Our Eq. (14) for the reduced peak time $r_{\text{MT peak}}$ arises from the dimensional peak time denoted by $t_{p2}$ in Eq. (7b) of [25]. In this latter work one of us (MT) had already shown that his approximant supersedes alternate approximants such as their Eq. (7a) so that there is no need to compare with those. Using the abbreviation $s_m = \gamma \beta \eta$ he obtained

$$t_{p2} = \frac{1}{A_1} \left( \ln A_2 - A_3 (\text{coth}^{-1}(A_4) - \tanh^{-1}(A_5)) \right)$$

where we here introduce abbreviations for the otherwise rather lengthy original expression as follows

$$A_1 = \beta \left[ 2(l_0 + s_0) - 3s_0 \right]$$
$$A_2 = \frac{2s_0^2(l_0 + s_0) - 5s_0^6S_m + 4s_0^2S_m^2 - s_0^2}{2l_0S_m^2}$$
$$A_3 = 2(s_0 - 2s_m)$$
$$A_4 = \frac{S_0 S_m - S_m^2 + 2l_0S_m^2}{(s_0 - S_m)^2}$$
$$A_5 = \frac{\sqrt{(S_0 - S_m)^2 + 2l_0S_m^2}}{s_0 - S_m}$$
$$A_6 = \sqrt{(S_0 - S_m)^2 + 2l_0S_m^2}$$

(A.2)

So far we have just reproduced the existing expression for $t_{p2}$ that had been obtained for the dimensional SIR model (1). To convert this into the dimensionless counterpart, we have to make use of Eq. (8), i.e., we have to replace $l_0$, $\gamma$, $\beta$, and we have to use Eq. (9), which states $r_{\text{MT peak}}(k, \eta) = a t_{p2}$. As a result, the $s_0$, $r_0$, $a$
should all drop out automatically. Using the transformation rules (8) the quantities in (A.2) become

$$S_m = \gamma \frac{B_s}{\beta},$$

$$A_1 = a(2 - 3k),$$

$$A_2 = 4(1 - \eta)k^2 - k^3 + 2(1 - \eta)^2 - 5(1 - \eta^2)k = A,$$

$$A_3 = \frac{2(1 - 2k - \eta)s_0}{1 - \eta} = \frac{B_s s_0}{1 - \eta},$$

$$A_4 = \frac{(1 - \eta)\sqrt{\eta^2 + (1 - \eta)^2 + (4k - 2)\eta}}{k - \eta} = C,$$

$$A_5 = \frac{1}{k - \eta} = \frac{-\sqrt{\eta^2 + (1 - \eta)^2 + (4k - 2)\eta}}{k - \eta} = \frac{-D}{E},$$

$$A_6 = \frac{s_0\sqrt{\eta^2 + (1 - \eta)^2 + (4k - 2)\eta}}{1 - \eta} = \frac{C s_0}{1 - \eta},$$

where we have re-used the quantities $A-E$ defined by (15) to allow for a direct comparison between (A.1) and (14). The $s_0$ indeed drops out because only the ratio $A_3/A_4$ appears in (A.1), and the remaining sign is taken care of the asymmetry of tanh$^\tau$. The rate $a$ still appearing in $A_3$ drops out in the reduced (dimensionless) peak time because $t_{\text{peak}}^{\text{SK-III}}(k, \eta) = a t_{\text{peak}}$ according to (9). We have thus shown that the reduced time depends only on $k$ and $\eta$, and that (14) is the reduced peak time that corresponds to the dimensional peak time $t_{\text{peak}}$ in [25].

### Appendix B. Derivation of $t_{\text{peak}}^{\text{SK}}(k, \eta)$

This appendix provides details on how to read off Eq. (16) from the results obtained by Schliecker and Kröger [24]. Equation (71) in [24] for the cumulative fraction $J$ of infected persons after the occurrence of a peak in the differential rate of newly infected persons, within the so-called ‘decay’ period for reduced times $\tau \geq \tau_\text{max}$, reads

$$J_{\text{decay}}(\tau) = J_{\text{inf}} = -\frac{b_1}{2b_2} \left[ 1 + \tanh \left( \frac{b_1}{2} (\tau - \tau_\text{max} + T_\text{c}(t_\text{peak})) \right) \right],$$

where $J_{\text{inf}}$ is the cumulative fraction of infected persons, given by Eq. (18), $T_\text{c}(t_\text{peak})$ defined by Eq. (54) of [24] (for the special case of $c = b$, note also that $b_2 = |b_1|$ as stated after Eq. (61) in [24]) and reproduced here in (17). Furthermore $y_\text{t,max}$ is $J_{\text{inf}}$ as mentioned after Eq. (69) of [24], and $\tau$ is a characteristic reduced time given by Eq. (73) in [24], identical with the first term on the right hand side of (16). The coefficients $b_1$ and $b_2$ for the SK-I and SK-II approximants are given by Eqs. (63)- (66) in [24] and reproduced in (19) and (20). Analytic results for the characteristic cumulative fraction $J_0$, the differential rate of infections at peak time $J_{\text{max}}$, and the cumulative fraction $J_0$ and the peak time of $J$ are stated in Eqs. (48), (49), and (52) of [24]. The quantity $J_{\text{decay}}(\tau)$ in (B.1) is the cumulative fraction of infected persons at reduced time $\tau$, and thus $J_{\text{decay}}(\tau) = 1 - S(\tau)$, as $S(\tau)$ denotes the susceptible fraction at reduced time $\tau$. Since we are interested in the peak time of the infected compartment, and because this peak time is delayed with respect to the peak time of
the differential rate of newly infected persons, $J_{\text{new}}$ rather than $J_{\text{case}}$ applies; the latter quantity, valid for $r \leq r_*, $ has been derived in [24] as well. Making use of [11], one has $J_{\text{new}}(t_{\text{peak}}^*) = 1 - k$. To be specific, using [B.1], the equation determining $r_{\text{peak}}^*$ becomes

$$
k = 1 - J_{\text{new}} + \frac{b_1}{2D_2} \left[ 1 + \tanh\left( \frac{b_1}{2} (t_{\text{peak}}^* - \tau + T_0(j_0)) \right) \right].$$

This equation is readily solved for $r_{\text{peak}}^*$, the result is given by Eq. (16).

References

[1] D. Gogoni, P.V. Lakshmi, Susceptible, infectious and recovered (SIR model) predictive model to understand the key factors of COVID-19 transmission, Int. J. Adv. Comput. Sci. Appl. 11 (2020) 296–302.
[2] K.R. Law, K.M. Pearsamasy, B.S. Gill, S. Singh, R.M. Sundram, K. Rajendran, S.C. Dass, Y.L. Lee, P.P. Goh, H. Ibrahim, N.H. Abdullah, Tracking the early depletion transmission dynamics of COVID-19 with a time-varying SIR model, Sci. Rep. 10 (2020) 21721.
[3] S. Ahmet, A. H. Bilge, A. Demirci, A. Peker-Dobie, O. Ergonul, What can we estimate from confirmed and infectious case data using the susceptible-infected-removed (SIR) model? A case study of Covid-19 pandemic, Front. Med. 7 (2020) 556366.
[4] R.A. Neher, R. Drydak, D. Valentin, E.B. Hodcroft, J. Albert, Potential impact of seasonal forcing on a SARS-CoV-2 pandemic, Swiss Med. Wkly. 150 (2020) w20224.
[5] S.G. Babajanyan, K.H. Cheong, Age-structured SIR model and resource management of epidemics—I. Further studies of the problem of endemicity. 1933, Bull. Math. Biol. 53 (1991) 89–118.
[6] X.W. Chen, J. Li, C. Xiao, P.L. Yang, Numerical solution and parameter estimation for uncertain SIR model with application to COVID-19, Fuzzy Optim. Decis. Mak. 20 (2021) 189–208.
[7] X.N. Li, Q.M. Zhang, Time to extinction and stationary distribution of SIR epidemic model with constant vaccination strategy by homotopy perturbation method, Kybernetes 38 (2009) 1566–1575.
[8] M. Cadoni, G. Gaeta, Size and timescale of epidemics in the SIR framework, Physica A 411 (2020) 125626.
[9] A. Chakraborty, S. Sinha, Global threshold dynamics of an infection age-structured SIR epidemic model with diffusion under the Dirichlet boundary condition, J. Differential Equations 269 (8) (2020) 171–187.
[10] N.S. Barlow, S.J. Weinstein, Accurate closed-form solution of the SIR epidemic model, Physica D 408 (2020) 132540.
[11] M. Turkyilmazoglu, Explicit formulae for the peak time of an epidemic SIR model, Physica A 461 (2016) 140–147.
[12] T. Britton, E. Pardoux, F. Ball, C. Larédou, D. Sirl, V.C. Tran, Stochastic Epidemic Models with Inference, in: Lecture Notes in Mathematics, vol. 2255, Springer, Berlin, 2019.
[13] M. Kröger, R. Schlicker, Analytical solution of the SIR-model for the temporal evolution of epidemics. Part A: Time-independent reproduction factor, J. Phys. A 53 (2020) 505601.
[14] R. Schlicker, M. Kröger, Analytical solution of the SIR-model for the temporal evolution of epidemics. Part B: Semi-time case, J. Phys. A 54 (2021) 175601.
[15] M. Turkyilmazoglu, Explicit formulae for the peak time of an epidemic from the SIR model, Physica D 422 (2021) 132902.
[16] K. Heng, C.L. Althaus, The approximately universal shapes of epidemic curves in the susceptible-exposed-infectious-recovered (SEIR) model, Sci. Rep. 10 (2020) 19365.
[17] I. Coifar, A. Mondal, C.G. Antonopoulos, A SIR model assumption for the spread of COVID-19 in different communities, Chaos Solitons Fractals 137 (2020) 109833.
[18] M. Simon, SIR epidemics with stochastic infectious periods, Stochastic Process. Appl. 110 (2009) 297–310.
[19] K.B. Law, K.M. Peariasamy, B.S. Gill, S. Singh, R.M. Sundram, K. Rajendran, S.C. Dass, Y.L. Lee, P.P. Goh, H. Ibrahim, N.H. Abdullah, Tracking the early depletion transmission dynamics of COVID-19 with a time-varying SIR model, Sci. Rep. 10 (2020) 21721.
[20] A.M. Carvalho, S. Goncales, An analytical solution for the Kermack-McKendrick model, Physica A 566 (2021) 125659.
[21] F. Guerrero, F.J. Santonja, R.J. Villanueva, Solving a model for the evolution of smoking habit in Spain with homotopy analysis method, Nonlinear Anal. WMA 14 (1) (2020) 549–558.
[22] H. Khan, R.N. Mohapatra, K. Vajravelu, S.J. Liao, The explicit series solution of SIR and SEIR epidemic models, Appl. Math. Comput. 215 (2) (2009) 653–669.
[23] J.L. Liu, B.Y. Peng, T.L. Zhang, Effect of discretization on dynamical behavior of SEIR and SIR models with non-linear incidence, Appl. Math. Lett. 39 (2015) 66–66.
[24] P. Van Mieghem, Approximate formula and bounds for the time-varying susceptible-infected-susceptible prevalence in networks, Phys. Rev. E 93 (2016).
[25] N.S. Barlow, S.J. Weinstein, Accurate closed-form solution of the SIR epidemic model, Physica D 408 (2020) 132540.
[26] A. Yildirim, Y. Chen, X. P. Zhang, Analytical approximation of a SIR epidemic model with constant vaccination strategy by homotopy perturbation method, Kybernetes 38 (2009) 1566–1575.
[27] M. Cadoni, G. Gaeta, Size and timescale of epidemics in the SIR framework, Physica D 411 (2020) 132626.
[28] A. Chekroun, T. Kuniya, Global threshold dynamics of an infection age-structured SIR epidemic model with diffusion under the Dirichlet boundary condition, J. Differential Equations 269 (8) (2020) 117–148.
[29] C. Imon, H. J. M. Y. Y. M. Z. T. A. N. C. A. D. E. V. I. O. P. R. S. V. T. E. N. S. K. G. A. E. T. A. H. E. T. U. P. E. R. M. A. C. K. 2255, Springer, Berlin, 2019.
[30] A. Simon, SIR epidemics with stochastic infectious periods, Stochastic Process. Appl. 130 (7) (2020) 4252–4276.
[31] M. Khan, Herd behavior and alternative resource to predator, J. Phys. A 52 (42) (2019) 425601.
[32] N. Sene, A. H. B. S. D. A. N. 2019(2019)9275051.
[33] M. Simon, SIR epidemics with stochastic infectious periods, Stochastic Process. Appl. 130 (7) (2020) 4252–4276.
[34] M. Kröger, R. Schlicker, Forecast for the second Covid-19 wave based on the improved SIR model with a constant ratio of recovery to infection rate, R. Soc. Open Sci. (2021) submitted for publication. URL: https://www.complexfluids.ethz.ch/cgi-bin/cgi-bin/covid-19-wavel.
[35] D.G. Kendall, Deterministic and stochastic epidemics in closed populations, in: Proc. Third Bateman Symp. on Math. Statist. and Prob., Vol. 4, Univ. of Calif. Press, Berkeley, United States, 1956, pp. 149–165.
[36] W.O. Kermack, A.G. McKendrick, Contributions to the mathematical theory of epidemics—I. 1927, Bull. Math. Biol. 53 (1991) 33–55.
[37] W.O. Kermack, A.G. McKendrick, Contributions to the mathematical theory of epidemics—II. The problem of endemicity, 1932, Bull. Math. Biol. 53 (1991) 57–87.
[38] W.O. Kermack, A.G. McKendrick, Contributions to the mathematical theory of epidemics—III. Further studies of the problem of endemicity, 1933, Bull. Math. Biol. 53 (1991) 89–118.
[51] C. Nguyen, J.M. Carlson, Optimizing real-time vaccine allocation in a stochastic SIR model, Plos One 11 (2016) 0152950.

[52] F.Y. Wang, X.Y. Wang, S.W. Zhang, C.M. Ding, On pulse vaccine strategy in a periodic stochastic SIR epidemic model, Chaos Solitons Fractals 66 (2014) 127–135.

[53] L. Wang, Z.D. Teng, T.T. Tang, Z.M. Li, Threshold dynamics in stochastic SIRS epidemic models with nonlinear incidence and vaccination, Comput. Math. Methods Med. 2017 (2017) 7294761.

[54] P.J. Witbooi, Stability of a stochastic model of an SIR epidemic with vaccination, Acta Biotheor. 65 (2017) 151–165.

[55] C.Y. Xu, X.Y. Li, The threshold of a stochastic delayed SIRS epidemic model with temporary immunity and vaccination, Chaos Solitons Fractals 111 (2018) 227–234.

[56] Y. Zhang, Y. Li, Q.L. Zhang, A.H. Li, Behavior of a stochastic SIR epidemic model with saturated incidence and vaccination rules, Physica A 501 (2018) 178–187.

[57] X. Zhao, X. He, T. Feng, Z.P. Qiu, A stochastic switched SIRS epidemic model with nonlinear incidence and vaccination: stationary distribution and extinction, Int. J. Biomath. 13 (2020) 2050020.

[58] V. Priesemann, M.M. Brinkmann, S. Ciesek, S. Cuschieri, T. Czypionka, G. Giordano, D. Gurdasani, C. Hanson, N. Hens, E. Iftekhar, M. Kelly-Irving, P. Klimek, M. Kretzschmar, A. Peichl, M. Perc, F. Sannino, F. Schernhammer, A. Schmidt, A. Stainers, E. Szczurek, Calling for pan-European commitment for rapid and sustained reduction in SARS-CoV-2 infections, Lancet 397 (2021) 92–93.

[59] R.M. Colombo, M. Garavello, Optimizing vaccination strategies in an age structured SIR model, Math. Biosci. Eng. 17 (2020) 1074–1089.

[60] R. Schlicker, M. Kröger, Analytical modeling of the temporal evolution of epidemics outbreaks accounting for vaccinations, Physics 3 (2021) 386–426.

[61] S. Mungkasi, Variational iteration and successive approximation methods for a SIR epidemic model with constant vaccination strategy, Appl. Math. Model. 90 (2021) 1–10.

[62] X.Z. Meng, L.S. Chen, The dynamics of a new SIR epidemic model concerning pulse vaccination strategy, Appl. Math. Comput. 197 (2008) 582–597.

[63] A.J. Terry, PULSE vaccination strategies in a metapopulation SIR model, Math. Biosci. Eng. 7 (2010) 455–477.

[64] A. D’Onofrio, Pulse vaccination strategy in the SIR epidemic model: global asymptotic stable eradication in presence of vaccine failures, Math. Comput. Model. 36 (2002) 473–489.

[65] T. Harko, F.S.N. Lobo, M.K. Mak, Exact analytical solutions of the susceptible-infected-recovered (SIR) epidemic model and of the SIR model with equal death and birth rates, Appl. Math. Comput. 236 (2014) 184.

[66] M. Abramowitz, L.A. Stegun, Handbook of Mathematical Functions with Formulas, Graphs, and Mathematical Tables, Dover Publications, New York, 1972.

[67] A.-M. Batiba, B. Batiba, A new method for solving epidemic model, Aust. J. Basic Appl. Sci. 5 (2011) 3122–3126.

[68] T.M. Balkew, The SIR Model When S(T) is a Multi-Exponential Function, East Tennessee State University, Tennessee, USA, 2010.

[69] J. Miller, Mathematical models of SIR disease spread with combined non-sexual and sexual transmission routes, Inf. Dis. Mod. 2 (2017) 35.