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The daily computed weighted averaging basic reproduction number $R^n_{0,k,\omega}$ for MERS-CoV in South Korea

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HIGHLIGHTS

- We propose the daily basic reproduction number for MERS-CoV in South Korea.
- We use an SIR model with piecewise constant contact and removed rates.
- We apply the explicit Euler's method for the solution of the SIR model.
- We use nonlinear least-square fitting procedure for finding the best parameters.

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ABSTRACT

In this paper, we propose the daily computed weighted averaging basic reproduction number $R^n_{0,k,\omega}$ for Middle East respiratory syndrome coronavirus (MERS-CoV) outbreak in South Korea, May to July 2015. We use an SIR model with piecewise constant parameters β (contact rate) and γ (removed rate). We use the explicit Euler's method for the solution of the SIR model and a nonlinear least-square fitting procedure for finding the best parameters. In $R^n_{0,k,\omega}$, the parameters n, k, and w denote days from a reference date, the number of days in averaging, and a weighting factor, respectively. We perform a series of numerical experiments and compare the results with the real-world data. In particular, using the predicted reproduction number based on the previous two consecutive reproduction numbers, we can predict the future behavior of the reproduction number.

1. Introduction

Middle East respiratory syndrome coronavirus (MERS-CoV), first identified in Saudi Arabia in June 2012, is a viral respiratory disease caused by a novel coronavirus [1]. South Korea experienced the largest outbreak of MERS-CoV infections outside the Arabian peninsula [2]. There have been 186 confirmed infective cases in South Korea within two months after the first infective person who returned from a trip to the Arabian peninsula was diagnosed on 11 May, 2015, and 38 people died and more than 16,000 people were quarantined due to the spread of the disease. Fig. 1 represents the epidemic curve of MERS-CoV, South Korea, 20 May–17 July 2015 [3,4].

In order to implement appropriate surveillance and control measures, it is very important to predict the future trend of the epidemic. Therefore, it is the purpose of the present paper to show daily computed reproduction numbers for epidemics, in particular, MERS-CoV, so that we can predict the future behavior of the reproduction number day-by-day.

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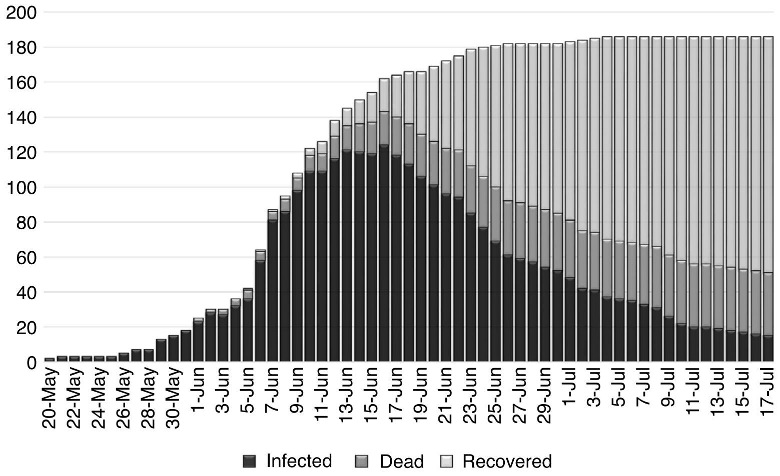

Fig. 1. Epidemic curve of MERS-CoV, South Korea, 20 May–17 July 2015.

In the mathematical modeling of the spread of an epidemic disease, it is crucial to estimate the parameters (e.g., contact rate and recovery rate in an SIR model), but it is difficult to do so due to the lack of data available for the estimation. In case of the MERS-CoV spread in South Korea, there are almost complete daily data of the spread of the disease, and we choose the MERS-CoV spread case in South Korea as an epidemic model to verify the validity and accuracy of the method proposed in this paper. To the authors' knowledge, there have been no previous works that present computational methods for estimation of the values of the epidemic parameters based on actual daily epidemic data.

The rest of the paper is organized as follows. In Section 2, we describe the mathematical model. In Section 3, we provide a numerical algorithm for the estimation of the parameters. We perform several numerical experiments in Section 4. In Section 5, we provide a summary and present our conclusions.

2. The mathematical model

In this paper, we consider the SIR model that was introduced in 1927 by A.G. McKendrick and W.O. Kermack [5]. The model is simple and has been widely used so far, for instance, in multigroup epidemic modeling [6], online social network dynamics [7], the model adopting the delay term [8], stochastic model [6,9,10], vaccination strategy [11,12]. In this model, the population is divided into susceptible $S(t)$, infected $I(t)$, and removed $R(t)$ individuals at time t. The governing ordinary differential equations for the SIR model are as follows:

$$\frac{\mathrm{d}S(t)}{\mathrm{d}t} = -\beta S(t)I(t), \tag{1}$$

$$\frac{\mathrm{d}I(t)}{\mathrm{d}t} = \beta S(t)I(t) - \gamma I(t), \tag{2}$$

$$\frac{\mathrm{d}R(t)}{\mathrm{d}t} = \gamma I(t) \tag{3}$$

with initial condition $S(0) = S^0, I(0) = I^0$, and $R(0) = R^0$. Here, the parameters β and γ denote the contact (susceptibility to disease) and removed (either dead or recovered) rates from disease, respectively [13]. We assume that a removed individual can never be infected again. Let N be the constant total population size. Therefore, it is sufficient to solve only two Eqs. (1) and (2), i.e., $R(t) = N - S(t) - I(t)$. By assuming that β and γ are time-dependent parameters, we generalize Eqs. (1)–(3) as follows:

$$\frac{\mathrm{d}S(t)}{\mathrm{d}t} = -\beta(t)S(t)I(t), \tag{4}$$

$$\frac{\mathrm{d}I(t)}{\mathrm{d}t} = \beta(t)S(t)I(t) - \gamma(t)I(t), \tag{5}$$

$$\frac{\mathrm{d}R(t)}{\mathrm{d}t} = \gamma(t)I(t). \tag{6}$$

For example, the transmission of the vector-borne diseases such as Dengue fever and Malaria has strong seasonal patterns and thus the parameters are estimated as the time-dependent functions [14,15]. Another example is a seasonal SIR model for the spread of the whooping cough in which the contact rate β is given as a time-dependent periodic function which accounts seasonal changes [16].