

GLOBAL JOURNAL OF SCIENCE FRONTIER RESEARCH: F MATHEMATICS AND DECISION SCIENCES Volume 20 Issue 8 Version 1.0 Year 2020 Type : Double Blind Peer Reviewed International Research Journal Publisher: Global Journals Online ISSN: 2249-4626 & Print ISSN: 0975-5896

First Consistent Determination of the Basic Reproduction Number for the First Covid-19 Wave in 71 Countries from the SIR-Epidemics Model with a Constant Ratio of Recovery to Infection Rate

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GJSFR-F Classification: MSC 2010: 30C15

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Notes

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R. Schlickeiser ^a & M. Kröger ^o

Abstract- The box-shaped serial interval distribution and the analytical solution of the Susceptible Infectious-Recovered (SIR)-epidemics model with a constant time-independent ratio of the recovery (μ_0) to infection rate (a_0) are used to calculate the effective reproduction factor and the basic reproduction number R_0 . The latter depends on the positively valued net infection number $x = 13.5(a_0 - \mu_0)$ as $R_0(x) = x(1 - e^{-x})^{-1}$ which for all values of x is greater unity. This dependence differs from the simple relation $R_0 = a_0/\mu_0$. With the earlier determination of the values of k and a_0 of the Covid-19 pandemic waves in 71 countries the net infection rates and the basic reproduction numbers for these countries are calculated.

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I. INTRODUCTION

The effective reproduction factor R(t) and the basic reproduction number R_0 are key quantities to measure the dynamical evolution of epidemics. If the number of daily new cases c(t) (deaths or infections) is known, either from monitoring or from Susceptible-Infectious- Recovered (SIR)-modelling, the effective reproduction factor is defined by^{1,2}

$$R(t) = \frac{c(t)}{\int_0^\infty ds \, W(s)c(t-s)},\tag{1}$$

where W(t) is the properly normalized serial interval distribution³ and time t taken in units of days. This serial interval distribution describes the probability for the time lag between a person's infection and the subsequent transmission of the virus to a second person. As different choices of the serial interval distribution W(t) are used in the literature this leads to differences in the calculated associated effective reproduction

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factors $\mathbf{R}(t)$. Most frequently,² for the serial interval distribution W(t) either, the gamma distribution

$$W(t) = \frac{b^3}{2}s^2e^{-bt}, \qquad b = 4/9,$$
(2)

with the mean value $\langle t \rangle = 3/b = 27/4 = 6.75$ days, or the box-shaped distribution

$$W_{\text{box}}(t) = \frac{\Theta(0, t, t_b)}{t_b}, \qquad t_b = 2 \langle t \rangle = 13.5, \tag{3}$$

with the two-sided Heaviside function $\Theta(x, A; B) = 1$ for $A \leq x \leq B$ and $\Theta(x) = 0$ otherwise, are chosen. The box-shaped serial distribution (3) readily yields for the effective reproduction factor (1) that

$$R_{\text{box}}(t) = \frac{c(t)t_b}{\int_0^{t_b} ds \, c(t-s)} = \frac{c(t)t_b}{\int_{t-t_b}^t dx \, c(x)}$$
(4)

for any given number of daily new cases c(t).

In earlier work² we calculated the effective reproduction factor by adopting a Gaussian distribution of daily cases both for the gamma (Eq. (2)) and box-shaped (Eq. (3)) serial distributions, respectively. Fig. 5 of ref.² indicates that the two effective reproduction factors are very similar. Here we use the analytical approximations⁴ for the daily cases resulting from the SIR-modelling of epidemics to calculate the corresponding effective reproduction factors with the simpler box-shaped serial distribution (4). The SIR model decribes the time evolution of infectious diseases in human populations. The SIR system is the simplest and most fundamental of the compartmental models and its variations (for a recent review see ref.⁵).

The calculated effective reproduction factors R(t) are then used to infer the basic reproduction number R_0 which has been defined^{6,7} as the average number of secondary infections produced when one infected individual is introduced into a host population where everyone is susceptible. As such $R_0 = R(t_0)$ is identical to the value of the effective reproduction factor $R(t_0)$ at the starting time of the outbreak.² If a specific mathematical model for the time evolution of the pandemic outbreak such as e.g. the SIR-model is used, this model should then obey the initial condition that one infected individual occurs at time t_0 . We are particularly interested in the relation of the SIRbasic reproduction number R_0 with the ratio $k = \mu_0/a_0$ of the initial recovery (μ_0) and infection (a_0) rates entering the SIR-model rate equations.

The inverse of this ratio k is often referred to as the inverse microscopic SIRbasic reproduction number.⁵ However, the recent application⁸ of analytical approximations of the solution of the SIR-model to the monitored death and infection rates in many countries provided values of k > 0.9 close to unity for the majority of countries investigated corresponding to microsciopic SIR-basic reproduction numbers $R_0 = 1/k < 1.11$ only slightly greater than unity. These values are significantly smaller than the estimates of $R_0 \in [2.4, 5.6]$ in the mainstream literature on Covid-19 based on the monitored effective reproduction factors.^{5,9} It is the purpose of the present manuscript to resolve this discrepancy by calculating the relation between the SIR-basic reproduction number and the value of the ratio k. It is shown that this relationship is different from the simple microscopic $kR_0 = 1$ relationship. Notes

II. ANALYTICAL APPROXIMATIONS OF THE SIR-MODEL

We start by reviewing our main earlier results ^{4,8} on the analytical solution of the SIR-epidemics model. Here ratio the considered population of $N \gg 1$ persons is assigned to the three compartments s (susceptible), i (infectious) or r (recovered/removed). Persons from the population may progress with time between these compartments with given infection (a(t)) and recovery rates $(\mu(t))$ which in general vary with time due to non-pharmaceutical interventions taken during the pandemic evolution.

It is convenient to introduce with I(t) = i(t)/N, S(t) = s(t)/N and R(t) = r(t)/Nthe infected, susceptible and recovered/removed fractions of persons involved in the infection at time t, with the sum requirement I(t) + S(t) + R(t) = 1. In terms of the reduced time $\tau(t) = \int_0^t d\xi a(\xi)$, accounting for arbitrary but given time-dependent infection rates, and the medically interesting daily rate of new infections

$$\dot{J}(t) = a(t)j(\tau) = \dot{\tau}j(\tau) = \dot{\tau}\frac{dJ}{d\tau},$$
(5)

where the dot denotes a derivative with respect to t, the SIR-model equations can be written as

$$\frac{dI}{d\tau} = j - KI, \quad \frac{dS}{d\tau} = -j, \quad \frac{dR}{d\tau} = KI,$$
(6)

with $K(t) = \mu(t)/a(t)$ and the dimensionless $j(\tau)$.

For the special and important case of a time independent ratio K(t) = k = const., new analytical results of the SIR-model (6) have been recently derived.⁴ For a growing epidemics with time the constant ratio k < 1 has to be smaller than unity corresponding to the initial infection rate a_0 at time t = 0 being larger than the initial recovery rate μ_0 , both in units of days⁻¹. The new analytical solutions assume that the SIR equations are valid for all times $t \in [-\infty, \infty]$, and that the time $t = \tau = t_0 = 0$ refers to the 'observing time' when the existence of a pandemic wave in the society is realized and the monitoring of newly infected persons J(t) is started. As only initial condition the fraction of initially (at the observing time) infected persons $S(0) = e^{-\varepsilon}$ is adopted which corresponds to

$$I(0) = 1 - k\varepsilon - e^{-\varepsilon} \simeq (1 - k)\varepsilon,$$

$$J(0) = 1 - e^{-\varepsilon} \simeq \varepsilon,$$
(7)

where the two last approximations hold for small values $\varepsilon \ll 1$, for the initial fraction of infected persons I(0) and the initial cumulative fraction J(0), respectively. In order to meet the above demanded initial condition, that one infected individual is introduced at time $t_0 = 0$ into a host population where everyone is susceptible, demands that $\varepsilon = 1/N$, where N denotes the total number of the host population.

The exact solution for the cumulative number of infected persons $J(\tau)$ as a function of the reduced time is given by^{4,8}

$$\tau = \int_{1-e^{-\varepsilon}}^{J} \frac{dy}{(1-y)f(y)}, \quad f(y) = y + k\ln(1-y)$$
(8)

Taking the derivative of the exact solution (8) with respect to τ provides the exact relationship

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$$j(\tau) = \frac{dJ}{d\tau} = (1 - J)[J + k\ln(1 - J)]$$
(9)

between the daily rate $j(\tau)$ and its corresponding cumulative number $J(\tau)$. Moreover, with $J(\tau)$ known one obtains

$$S(\tau) = 1 - J(\tau),$$

$$I(\tau) = J(\tau) + k \ln[1 - J(\tau)],$$

$$R(\tau) = -k \ln[1 - J(\tau)].$$
(10) Notes

III. SIR Box-Shaped Effective Reproduction Factor

Identifying in Eq. (4) $c(t) = \dot{J}(t)$ we readily obtain

$$R_{\text{box}}(t) = \frac{\dot{J}(t)t_b}{\int_{t-t_b}^t dx \, \dot{J}(x)} = \frac{\dot{J}(t)t_b}{J(t) - J(t-t_b)} \tag{11}$$

Using the invariance of $J(t) = J(\tau)$ and Eq. (5) then provides

$$R_{\text{box}}(t) = \frac{a(t)t_b j(\tau)}{J(\tau) - J(\tau - \tau_b)}$$

= $\frac{a(t)t_b [1 - J(\tau)] \{J(\tau) + k \ln[1 - J(\tau)]\}}{J(\tau) - J(\tau - \tau_b)},$ (12)

where we inserted the exact Eq. (9) in the last step. According to Eq. (12) the SIR boxshaped effective reproduction factor is directly related to the time-dependent infection rate a(t) and the cumulative number of new infections depending on the reduced time $\tau = \int_0^t d\xi \, a(\xi)$. For given time-dependencies of the infection rate a(t) we can immediately calculate the reduced time. Then for any value of k the cumulative numbers $J(\tau)$ are calculated according to Eq. (8), and as a consequence the SIR boxshaped effective reproduction factor is obtained.

We proceed with two important special limits.

a) Slowly varying infection rate

For slowly varying infection rates a(t) we Taylor expand the cumulative number $J(t-t_b)$ on the right hand side of Eq. (11) as

$$J(t-t_b) \simeq J(t) - t_b \left. \frac{dJ}{dt} \right|_t = J(t) - t_b \dot{J}(t)$$
(13)

With this approximation the SIR box-shaped effective reproduction factor (11) reduces to $R_{\text{box}}(t) \simeq 1$, correctly agreeing with the limit for stationary case distributions.

b) Infinite time

According to the solution (8) the time $\tau = \infty$ corresponds to the cumulative number $J_{\infty}(k)$ given by the solution of the transcendental equation

$$J_{\infty} + k\ln(1 - J_{\infty}) = 0 \tag{14}$$

Consequently, according to the relation (9) the daily rate $j(\infty) = 0$ vanishes at the infinite time implying with Eq. (12) that the effective reproduction factor vanishes at infinite time $R_{\text{box}}(\infty) = 0$.

IV. BASIC REPRODUCTION NUMBER

In order to calculate $J(-\tau_b)$ we use its asymptotic behavior for early times by integrating Eq. (68) of ref.⁴, i.e.

 N_{otes}

$$J(\tau) \simeq J(0)e^{(1-k)\tau} \tag{15}$$

With $J(0) = 1 - e^{-\varepsilon}$ fom Eq. (7) this implies

$$J(0) - J(-\tau_b) \simeq J(0)[1 - e^{-(1-k)\tau_b}]$$

= $[1 - e^{-\varepsilon}][1 - e^{-(1-k)\tau_b}]$ (16)

With the initial infection rate $a_0 = a(t = 0)$ we then calculate from Eq. (12)

 $R_0 = R_{\rm box}(0)$

$$= \frac{a_0 t_b [1 - J(0)] \{J(0) + k \ln[1 - J(0)]\}}{J(0) - J(-\tau_b)}$$
$$= \frac{a_0 t_b [1 - k\varepsilon - e^{-\varepsilon}]}{[e^{\varepsilon} - 1] [1 - e^{-(1 - k)\tau_b}]}$$
$$\simeq \frac{a_0 t_b (1 - k)}{1 - e^{-(1 - k)\tau_b}},$$
(17)

Here, the last approximation assumes small values of $\varepsilon \ll 1$. Note that in this limit the resulting basic reproduction number is independent from the value of ε .

At early negative times no nonpharmaceutical interventions have been taken so that $a(t) \simeq a_0$ is constant and the reduced time $\tau_b \simeq a_0 t_b$. The SIR-basic reproduction number (17) then becomes

$$R_0(x) \simeq \frac{x}{1 - e^{-x}} \simeq \begin{cases} 1 + \frac{x}{2} & \text{for } x \ll 1\\ x & \text{for } x \gg 1 \end{cases}$$
(18)

in terms of the dimensionless quantity

$$x = a_0 t_b (1 - k) = 13.5 a_0 (1 - k) = 13.5 (a_0 - \mu_0),$$
(19)

to which we refer as net injection number.



Notes

Fig. 1: SIR basic reproduction number (17) and its asymptotics as a function of the net infection number $x = a_0 t_b (1-k)$.

In Fig. 1 we plot the SIR-basic reproduction number $R_0(x)$ as a function of x. For small values of $x \ll 1$ we note that $R_0(x \ll 1)$ is only slightly larger than unity, whereas for large values of $x \gg 1$ there is the direct proportionality $R_0(x) \propto x$.

In principle, for values of k close to unity as obtained for most countries,⁸ large values of $x \gg 1$ are possible provided the infection rate is large enough $a_0 \gg 1/13.5$ days⁻¹. The discrepancy noted in the introduction is therefore resolved even for values of k close to unity.

Values of k > 0.9 obviously correspond to net infection numbers smaller than $x < 1.3a_0$ which still can be much larger than unity provided the initial infection rate is significantly greater than $a_0 > 1/1.3 = 0.77$ days⁻¹. For k = 0.9 reported values of $R_0 \in [2.4, 5.6]$ are possible for initial infection rates greater than $a_0 = [1.8, 4.3]$ days⁻¹. Likewise, for k = 0.95 even larger initial infection rates $a_0 \in [3.5, 8.6]$ days⁻¹ are needed.

In our earlier modeling⁸ of the Covid-19 pandemic wave in 71 countries we determined not only the value of k but also the value of the initial infection rate a_0 (see Table 2 and 3 in ref.⁸). It is therefore straightforward to calculate the resulting net infection rates x and the basic reproduction numbers $R_0(x)$ for these 71 countries. The results are summarized in Table 1 and indicate large differences in the values of the basic reproduction numbers.

V. Summary and Conclusions

The box-shaped serial interval distribution and the analytical solution of the SIR-epidemics model with a constant time-independent ratio of the recovery (μ_0) to infection rate (a_0) are used to calculate the effective reproduction factor and the basic reproduction number R_0 . The latter depends on the positively valued net infection number $x = 13.5(a_0 - \mu_0)$ as $R_0(x) = x(1 - e^{-x})^{-1}$ which for all values of x is greater unity. This dependence differs from the simple relation $R_0 = a_0/\mu_0$. With the more general dependence of $R_0(x)$ values of basic reproduction numbers significantly greater than unity can occur even for values of k close to unity provided the initial infection rate is large enough. As we have determined the values of k and a_0 in our earlier modeling of the Covid-19 pandemic waves in 71 countries we have calculated here the resulting net infection rates and the basic reproduction numbers for these countries.

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Table 1: x and R_0 for all those countries (alpha-3 country code) for which k and a_0 have been determined in Ref.⁸

country	k	a_0	x	R_0	country	k	a_0	x	R_0	country	k	a_0	x	R_0
AFG	0.995	68.9	4.7	4.7	ALB	0.988	24.4	4.0	4.0	AND	0.931	7.6	7.1	7.1
ARG	0.987	21.8	3.8	3.9	ARM	0.897	1.1	1.5	2.0	AUT	0.992	149.8	16.2	16.2
BEL	0.911	6.1	7.3	7.3	BFA	0.999	1754.5	23.7	23.7	BGR	0.974	10.1	3.5	3.7
BLR	0.975	40.9	13.8	13.8	BOL	0.968	7.9	3.4	3.5	BRA	0.919	12.1	13.2	13.2
CAF	0.999	123.9	1.7	2.1	CHE	0.976	22.0	7.1	7.1	CHL	0.910	2.0	2.4	2.7
CHN	0.999	1544.6	20.9	20.9	COL	0.899	4.0	5.5	5.5	CUB	0.999	631.5	8.5	8.5
CZE	0.997	235.1	9.5	9.5	DEU	0.989	57.7	8.6	8.6	DNK	0.989	52.6	7.8	7.8
DOM	0.747	2.6	8.9	8.9	DZA	0.977	18.4	5.7	5.7	ECU	0.935	15.5	13.6	13.6
EGY	0.994	52.5	4.3	4.3	ESP	0.937	12.4	10.5	10.5	ETH	0.999	215	2.9	3.1
FRA	0.954	10.0	6.2	6.2	GAB	0.997	64.6	2.6	2.8	GBR	0.925	8.9	9.0	9.0
GHA	0.999	464.9	6.3	6.3	GRC	0.998	191.9	5.2	5.2	GTM	0.985	9.7	2.0	2.3
HND	0.978	26.0	7.7	7.7	HRV	0.996	72.3	3.9	4.0	IND	0.997	189.9	7.7	7.7
IRL	0.962	21.2	10.9	10.9	IRN	0.819	3.1	7.6	7.6	ITA	0.940	10.2	8.3	8.3
KOR	0.999	989.6	13.4	13.4	KWT	0.986	21.8	4.1	4.2	LBN	0.999	95.5	1.3	1.8
LUX	0.981	29.5	7.6	7.6	MAR	0.999	628.8	8.5	8.5	MDA	0.973	25.9	9.4	9.4
MEX	0.954	16.2	10.1	10.1	MKD	0.927	5.4	5.3	5.3	MRT	0.996	66.4	3.6	3.7
MYS	0.999	2064.2	27.9	27.9	NGA	0.999	405.4	5.5	5.5	NLD	0.963	15.4	7.7	7.7
NPL	0.999	953.4	12.9	12.9	PAK	0.997	101.1	4.1	4.2	PAN	0.848	3.5	7.2	7.2
PER	0.703	3.2	12.8	12.8	PHL	0.996	142.4	7.7	7.7	POL	0.993	63.1	6.0	6.0
PRT	0.982	86.4	21	21.0	ROU	0.909	13.8	17	17.0	RUS	0.984	60.7	13.1	13.1
SEN	0.998	79.9	2.2	2.4	SMR	0.867	2.9	5.2	5.2	SOM	0.999	591.7	8.0	8.0
SRB	0.931	10.1	9.4	9.4	SWE	0.935	10.1	8.9	8.9	TCD	0.999	1387.0	18.7	18.7
THA	0.999	3463.0	46.8	46.8	TUN	0.999	659.7	8.9	8.9	TUR	0.990	144.0	19.4	19.4
USA	0.938	10.2	8.5	8.5	\mathbf{ZAF}	0.968	6.5	2.8	3.0					

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