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RUHR-UNIVERSITÄT BOCHUM

Covid forecast

Reinhard Schlickeiser
Institut für Theoretische Physik IV: Weltraum- und Astrophysik, Ruhr-Universität Bochum, Germany
Institut für Theoretische Physik und Astrophysik, Christian-Albrechts-Universität, Kiel, Germany

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in collaboration

with Prof. Dr. Martin Kröger, Polymer Physics, Department of Materials, ETH Zurich, Zurich CH-8093, Switzerland

Figure 1: Picture Martin

14 joint publications since 2020

The first publication

"A gaussian model for the time development of the Sars-Cov-2 corona pandemic disease. Predictions for Germany made on 30 March 2020", RS, F. Schlickeiser, Physics 2, 164-170 (2020):
Adopted Gauss distribution for rate of new infections (see Fig. 2)

$$j(t) = I_0 e^{-(\frac{t-E}{\Delta})^2} \tag{1}$$

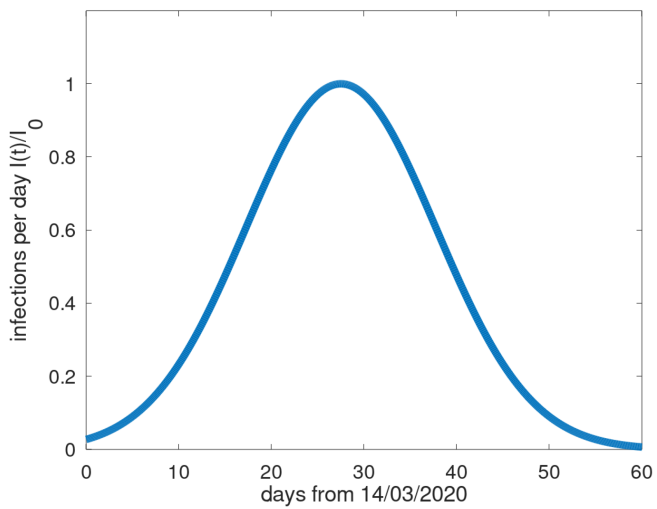

Figure 2: Gaussian model prediction for time evolution of rate of new infections

The first publication (2)

The Gauss distribution (1) implies a time-dependent early doubling time of

$$t_2(t) = \frac{\Delta^2 \ln 2}{2(E-t)} = \frac{2.6}{1-\frac{t}{E}} \text{ days} \qquad (2)$$

with $t_2(0) = 2.6$ days monitored in Germany. The fit of doubling time (2) to monitored data until 28 March 2020 (Fig. 3) yielded $E = 27.5^{+5.4}_{-3.4}$ days with 90-percent confidence. We predicted the peak of the death rate (7 day delay) to occur on 18 April 2020 $^{+5.4}_{-3.4}$ in excellent agreement with the observed peak day of 16 April 2020.

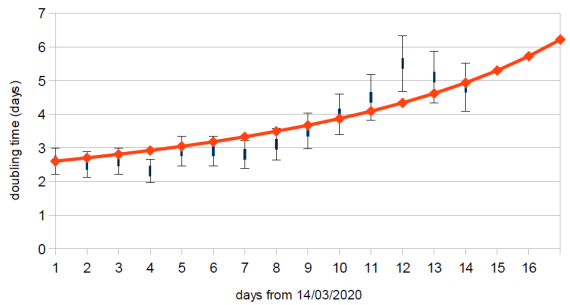

Figure 3: Doubling time Gauss: Fit to 1st Covid-wave in Germany

Follow-up publication

We submitted this work to the medRχiv-server on 30 March; it was posted on 2 April. On NTV at 5 April. On the evening of 2 April I was contacted by Martin Kröger (hereafter referred to as MK). About a week later we submitted
"Covid-19 predictions using a Gauss model, based on data from April 2",
J. Schüttler, RS, F. Schlickeiser, MK, Physics 2, 197-212 (2020)
to the Preprints.org server (submitted 10 April, posted 11 April) and a slightly modified version to the medRχiv- server (posted 18 April)

We again used the Gauss model (1). We did not only fit its shape but also its absolute values to the monitored death rates in 23 countries. We predicted the peak days and the total number of fatalities.

Follow-up publication (2)

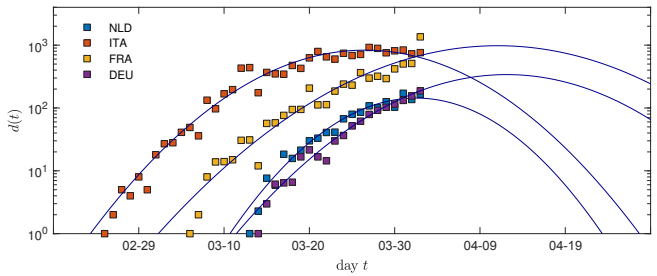

Figure 4: Gauss fit to death rates of first Covid wave

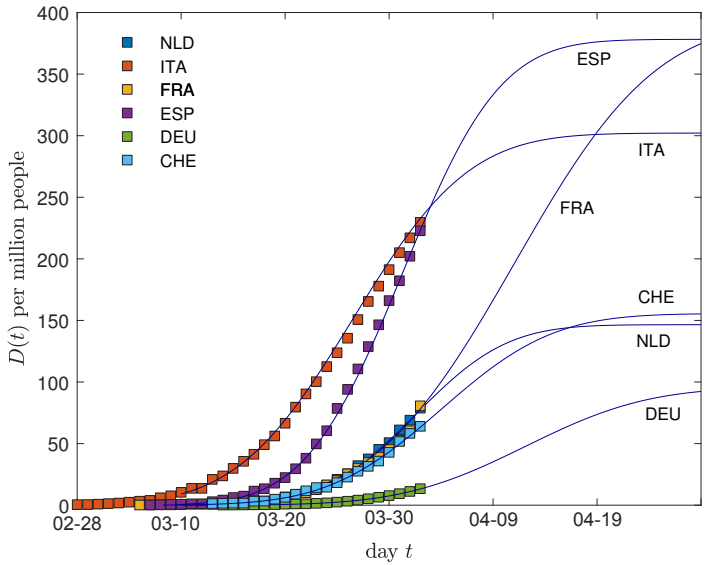

Figure 5: Gauss fit to cumulative number of fatalities of first Covid wave

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SIR/SIRV models of pandemic evolution

Gauss model justified with the central limit theorem of statistics. But it also compares well with the popular SIR pandemics model developed originally by Kermack and McKendrick (1927) and refined by Kendall (1956). The SIR model is the simplest, but still realistic compartment model where persons from a considered population are assigned to the three compartments S (susceptible), I (infectious) and R (recovered/removed). The infection ($a(t)$) and recovery ($\mu(t)$) rates then regulate the transition probability between the compartment fractions. The SIR-model in theoretical epidemic research plays a comparable role as the Schrödinger equation in physics. Later refinements of the SIR-model such as the SEIR, SIRD, SIRS and SIRV have introduced additional compartments. In "Analytical modeling of the temporal evolution of epidemics outbreaks accounting for vaccinations", RS, MK, Physics 3, 386-426 (2021) we extended the SIR-model by introducing a fourth compartment V of vaccinated persons and the vaccination rate $v(t)$ that regulates the relation between S and V (see Fig. 6).

SIR/SIRV models of pandemic evolution (2)

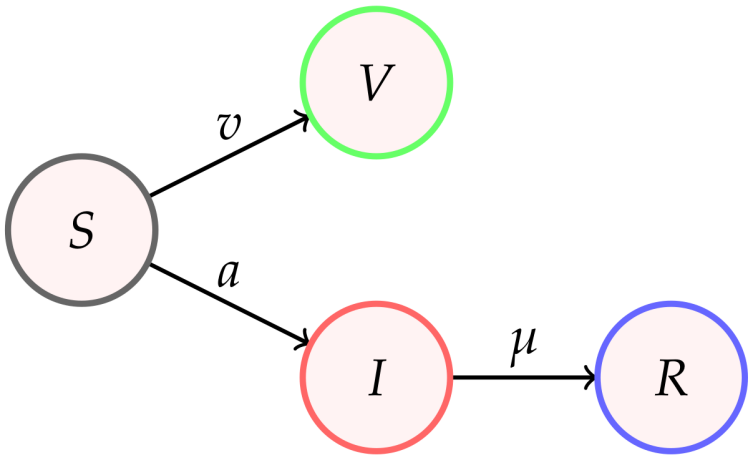

Figure 6: Three time-dependent rates $a(t)$, $\mu(t)$ and $v(t)$ entering the SIRV equations for the four compartments of susceptible, S, infectious, I, recovered, R, and vaccinated, V, population fractions. Upon introducing the reduced time $\tau = \int_{t_0}^{t} dt^{'} a(t^{'})$, the model is characterized by the assumed constant ratios $k = \mu(t)/a(t)$ and $b = v(t)/a(t)$.

The vaccination rate $v(t)$ competes with the infection $(a(t))$ and recovery $(\mu(t))$ rates in determining the time evolution of epidemics. In the SIR-model the transition $S \to V$ does not exist.

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SIR equations

The SIR equations read

$$\frac{dS}{dt} = -a(t)SI, \ \frac{dI}{dt} = a(t)SI - \mu(t)I, \ \frac{dR}{dt} = \mu(t)I \tag{3}$$

and fulfil the sum constraint $S(t) + I(t) + R(t) = 1$ at all times. Note: in sum constraint total population number normalized to $N = 1$, i.e. (S, I, R) refer to relative fractions of population. In the semi-time case ("Analytical solution of the SIR-model for the temporal evolution of epidemics: part B. Semi-time case", RS. MK, J. Phys. A: Math. and Theor. 54, 175601 (2021)) the SIR equations apply after the start of pandemic wave at time t_0 with the initial conditions $I(t_0) = \eta$, $S(t_0) = 1 - \eta$, $R(t_0) = 0$.

Of high interest, also from the medical and public health care points of view, are the rate of new infections $\dot{J}(t) = a(t)S(t)I(t)$ and its corresponding cumulative number $J(t) = \int_{t_0}^{t} d\xi \dot{J}(\xi)$, as the needed hospitalization and death rates are directly proportional to $\dot{J}(t)$.

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Epidemics in a nutshell: public health care

("'Reasonable limiting of 7-day incidence per hundred thousand and herd immunization in Germany and other countries"', RS, MK, Covid 1, 130-136 (2021)) For the earlier $20A.EU1, 20A.EU2, \alpha, \beta, \gamma$ and δ mutants $h = 1$ percent of the infected persons are seriously infected and need access to breathing instruments in hospitals for $m = 1$ months. Every second of these seriously infected persons eventually dies from the virus, so that the mortality rate is $f_{\alpha-\delta} = 0.5 h_{\alpha-\delta} = 5 \cdot 10^{-3}$.

Consequently, the daily death rate $d(t)$, the maximum death rate $d_{\max}$ and the total fatality number D_∞ are given by

$$d(t) = fN\dot{J}(t), \; d_{\max} = fN\dot{J}_{\max}, \; D_\infty = fNJ_\infty, \tag{4}$$

where N denotes the number of persons in a population ($N = 82.7$ million$= 827N_5$ million in Germany), while the peak day of the death rate is $t_{\mathrm{d,max}} = 7 + t(\tau_{j,\max})$.

Epidemics in a nutshell: public health care (2)

The maximum 7-day incidence value per 10^5 persons is given by

$$\mathrm{SDI}_{\max} = 10^5 \int_{t_{\max}-3.5}^{t_{\max}+3.5} dt\, \dot{J}(t) \simeq 7 \cdot 10^5\, \dot{J}_{\max} \tag{5}$$

Including its emergency reserves, Germany in total has about $B = 5 \cdot 10^4 ab = 10^4 a_{20} b$ breathing apparati or intensive treatment (IT) beds, of which, however only $a = 20\mathrm{percent} a_{20} = 0.2 a_{20}$ are available for seriously infected persons (SIPs) with Covid-19. b is a scale factor for IT beds in other countries in units of 50000 (Germany $b = 1$). The majority of these IT beds are used for other emergency patients with strokes, heart attacks and/or cancer in the terminal stage, and a substantial number of IT beds cannot be used because of the lack of sufficiently well-trained nursing personal. The breathing apparati are on average occupied by SIPs for about $30m$ days (m counted in months, $m = 1$ typical). Consequently, every day $B/30m = 333 a_{20} b/m$ breathing apparati are available for new SIPs, or over 7 days $7B/30m = 2333 a_{20} b/m$.

Epidemics in a nutshell: public health care (3)

However, as argued above only $2f = 10^{-2}h$ of the infected persons are seriously infected. Hence without any triage decisions the German health system could have coped with maximum SDI values of

$$\mathrm{SDI}_{\mathrm{maxGermany}} = \frac{2333 a_{20} b}{827 N_5 m \cdot 10^{-2} h} = 282 \frac{a_{20} b}{mh} \tag{6}$$

for the earlier 1st wave and $\alpha - \delta$ mutants. With the relation

$$d_{\max} = 7.14 \cdot 10^{-4} h \frac{N}{N_5} \mathrm{SDI}_{\max} \tag{7}$$

the German maximum value (6) for the $\alpha - \delta$ mutants ($h = 1$) corresponds to $d_{\mathrm{max,Germany}} = 167 a_{20} b/m$ per day.

Epidemics in a nutshell: public health care (4)

Clues: (1) In 2021 the German government imposed strict partial and total lockdowns already for SDI-values exceeding 50! This was far too restrictive and has costed billions of Euros as each German lockdown day has costed about 0.5 billion Euros.
(2) The German hospitals wondered during these mutant waves that their capacities were "'underutilized"' by at least a factor 5.
(3) I wonder why nobody in the government or their experts at the Robert-Koch-Institut were able to do these kind of estimates. However, it is fair to admit that at the beginning of the Covid epidemic the numbers on h, f and m were uncertain.
(4) Even higher values than (6) by a factor of 4 are tolerable by either reducing the duration of intensive care during the period of maximum to $m = 0.5$ and/or making use of the nonuniform spread of the Covid-wave across Germany appearing as in case of omicron

Epidemics in a nutshell: public health care (5)

first in the northern states and considerably later in the southern and eastern states, combined with mutual help in hospital capacities (shamrock method=Kleeblatt-Verfahren).
(5) Do not trust the monitored numbers of new infections by many government agencies (in Germany RKI). They are notoriously smaller than $N\dot{J}(t) = d(t)/f$ from the more reliable reported death rate. In Germany the dark numbers were 8.4 ± 4.0 (95 percent confidence) for the first wave and 4.4 for the omicron wave.
(6) For the omicron mutant (''‘Forecast of omicron wave time evolution''', RS, MK, Covid 2, 216-229 (2022)) $h = 0.1$ is ten times smaller (effect of boosted vaccinations). Therefore the tolerable maximum SDI value (6) for omicron $2820 a_{20} b/m$ and the corresponding maximum death rate (7) for omicron $1670 a_{20} b/m$ per day are also ten times higher.
(7) $\dot{J}(t)$ is the quantity of highest interest!

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Reduced time

In the literature the SIR-equations (3) have been investigated for stationary values of the infection and recovery rates, often numerically. In "Analytical solution of the SIR-model for the temporal evolution of epidemics. Part A: time-independent reproduction factor", MK. RS, J. Phys. A: Mathemat. and Theor. 53 (50), 505601 (2020), 2nd most read with over 11500 downloads, we divided Eqs. (3) by $a(t)$ and introduced the reduced time

$$\tau = \int_{t_0}^{t} d\xi a(\xi) \tag{8}$$

to account for arbitrary but given time-dependent infection rates. This generalization is important to account for non-pharmaceutical interventions taken during a pandemic wave. In terms of the reduced time the SIR-equations (3) read

$$\frac{dS}{d\tau} = -SI, \ \frac{dI}{d\tau} = SI - kI, \ \frac{dR}{d\tau} = kI, \tag{9}$$

KSSIR model

with the ratio $k = \mu(t)/a(t)$ of recovery to infection rate, and the rate of new infections $j(\tau) = S(\tau)I(\tau)$ and $J(\tau) = \int_0^\tau d\xi j(\xi)$. We analytically solved Eqs. (9) by assuming a constant time-independent ratio k, i.e. the temporal dependence of the recovery rate is exactly the same as the temporal dependence of the infection rate (KSSIR-model).

The assumption of a constant ratio k certainly is a restriction as in nature the time dependences of the infection rate $a(t)$ and $\mu(t)$ will be different. There are no obvious natural choices for the real time dependencies of the two rates, and they may differ from mutant to mutant. Initially at the start of the mutant outbreak without any taken non-pharmaceutical interventions (NPIs) both rates have the values $a(t_0) = a_0$ and $\mu(t_0) = \mu_0$. Dedicated medication of infected persons certainly will increase the recovery rate from its initial value, whereas the NPIs (such as social distancing, quarantining and mask obligations) effectively reduce the infection rate from its initial value.

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KSSIR model (2)

Recently in "SIR-Solution for Slowly Time-Dependent Ratio between Recovery and Infection Rates", MK, RS, Physics 4, 504-524 (2022), we derived approximated SIR-solutions for different time dependencies of the infection and recovery rates by using both, the Epstein-Rawer method on wave propagation and the adiabatic approximation from quantum mechanics. The latter assumes that the time-dependent ratio $k(t)$ varies slowly in comparison to the typical time characteristics of the pandemic wave, so that the KSSIR solutions with constant k can be used to insert a-posteriori the slow time dependence ratio $k(\tau)$.
The obtained analytical solutions from the adiabatic approximation agree remarkably well with the exact numerical solutions of the SIR equations. In the worst case the maximum deviation is 68.1 percent but in most cases much less. We are close to a full analytical solution of the SIR equations for different, arbitrary but given time-dependent infection and recovery rates. Elegant introduction of the reduced time (8) has not been discovered before during the 95 years of the SIR investigations.

Exact solution of the KSSIR-model

The SIR-equations (9) with constant k provide

$$I = -\frac{1}{S}\frac{dS}{d\tau},\ R = -k[\ln S - \ln(1-\eta)], \tag{10}$$

so that the sum constraint reads

$$1 = S + I + R = S - \frac{1}{S}\frac{dS}{d\tau} - k[\ln S - \ln(1-\eta)] \tag{11}$$

with the exact solution

$$\tau = \int_{t_0}^{t} a(\xi)d\xi = \int_{1-\eta}^{S} \frac{dx}{x[x - k\ln x - 1 + k\ln(1-\eta)]} \tag{12}$$

Generalizes the Kermack and McKendrick integral for stationary infection rate to arbitrary time dependent infection rate.

Exact solution of the KSSIR-model (2)

As rate of new infection in reduced time is
$j(\tau) = SI = -(dS/d\tau) = (dJ/d\tau)$ one finds for cumulative number $J(\tau) = 1 - S(\tau)$. Substituting $x = 1 - y$ yields for solution (12)

$$\tau = \int_{\eta}^{J} \frac{dy}{(1-y)n(y)}, \quad n(y) = y + k\ln(1-y) - k\ln(1-\eta) \tag{13}$$

Differentiating the solution (13) then yields for the rate of new infections

$$j(\tau) = (1-J)[J + k\ln(1-J) - k\ln(1-\eta)] \tag{14}$$

in terms of $J(\tau)$ implying

$$\frac{dj}{d\tau} = \frac{dJ}{d\tau}\frac{dj}{dJ} = j[1 - k - 2J - k\ln(1-J) + k\ln(1-\eta)] \tag{15}$$

Exact solution of the KSSIR-model (3)

For a pandemic wave to occur the initial slope $(dj/d\tau)_0 > 0$ has to be positive, implying with $J(0) = \eta$ the condition

$$k < 1 - 2\eta \tag{16}$$

The solution (13) indicates that at infinite times $\tau \to \infty$ the final cumulative number is given by $n(J_\infty) = 0$ yielding the transcendental equation

$$J_\infty + k \ln(1 - J_\infty) = k \ln(1 - \eta) \tag{17}$$

with the solution

$$J_\infty = 1 + kW_0(\alpha), \quad \alpha = -(1 - \eta)k^{-1}e^{-\frac{1}{k}} \tag{18}$$

in terms of the principal Lambert function W_0. The Lambert functions solve the equation $z = W(z)e^{W(z)}$.

Exact solution of the KSSIR-model (4)

Eq. (15) indicates that the maximum rate of new infections occurs at J_0 determined by the transcendental equation

$$1 - k - 2J_0 - k\ln(1 - J_0) + k\ln(1 - \eta) = 0 \tag{19}$$

with the solution

$$J_0 = 1 + \frac{k}{2} W_{-1}(\alpha_0), \quad \alpha_0 = 2\alpha/e \tag{20}$$

in terms of the non-principal Lambert function W_{-1} $\rightarrow$ peak reduced time $\tau_{\rm peak} = \int_\eta^{J_0} (dy/(1-y)n(y))$. and $j_{\rm max} = (k^2/4)[(1 + W_{-1}(\alpha_0))^2 - 1]$.

Approximation for early doubling time defined by $\dot{J}_{\rm early}(t + t_2) = 2\dot{J}_{\rm early}(t)$ is $t_2 \simeq \ln 2/a_0(1-k) = \ln 2/(a_0 - \mu_0)$. Note relations $\dot{J}(t) = a(t)j(\tau(t))$, $J(t) = J(\tau(t))$.

Exact solution of the KSSIR-model (5)

Entire dependence in reduced time is determined by only k whereas the dependence on the initial fraction of infected persons $\eta \ll 1$ is very weak. Consequently the entire real time dependence of the pandemic wave is determined by two parameters: the ratio k and the initial value of the infection rate a_0.

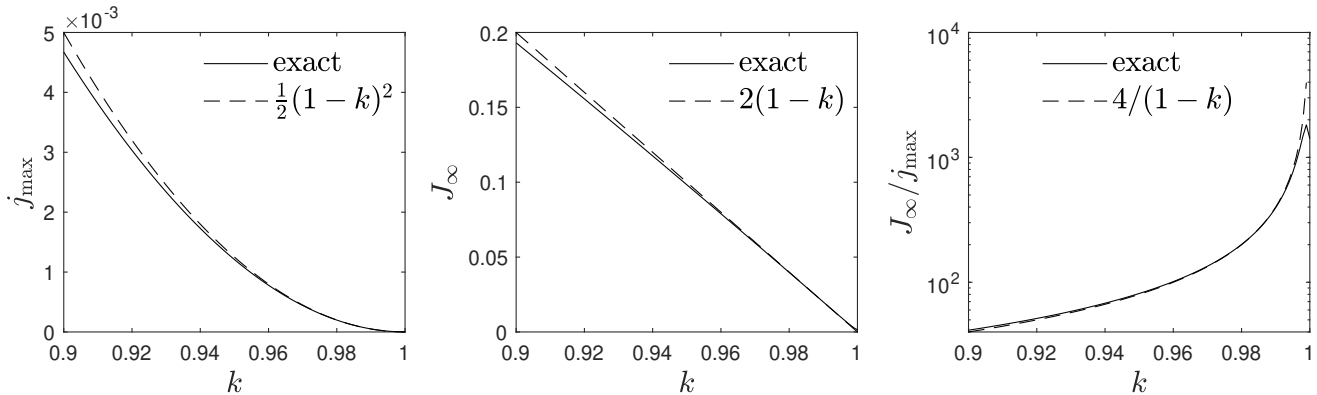

Figure 7: Exact behavior (solid lines) of the peak differential fraction of infected persons $j_{\max}$, the final fraction of infected persons J_∞, and the ratio $J_\infty/j_{\max}$, that characterizes the dimensionless width of the wave, of the SIR-model.

J_∞ and $j_{\max}$ increase strongly with at smaller ratios k.

Constrained 2nd order polynomial approximation

In "Verification of the accuracy of the SIR model in forecasting based on the improved SIR model with a constant ratio of recovery to infection rate by comparing with monitored second wave data", MK, RS, Royal Society Open Science 8, 211379 (2021) we developed the constrained 2nd order polynomial approximation

$$j(J) = \begin{pmatrix} c_0 + c_1(J-\eta) + c_2(J-\eta)^2 \text{ for } J \leq J_0 \\ d_1(J_\infty - J) + d_2(J_\infty - J)^2 \text{ for } J \geq J_0 \end{pmatrix} \tag{21}$$

$c_0 = \eta(1-\eta)$, $c_1 = 1-k-2\eta$ and $d_1 = J_\infty - (1-k)$ are the Taylor expansion coefficients the denominator of $j(J)$ according to Eq. (14). Constrained expansion refers to choosing the second-order expansion coefficients c_2 and d_2 such that the respective expansion evaluated at $J = J_0$ yields the maximum value of the daily case rate, i.e. $j(J0) = j_{\max}$. Thus, a very high agreement between the approximated analytical and the exact numerical pandemic evolution as a function of the reduced time is achieved (see Fig. 8).

Constrained 2nd order polynomial approximation (2)

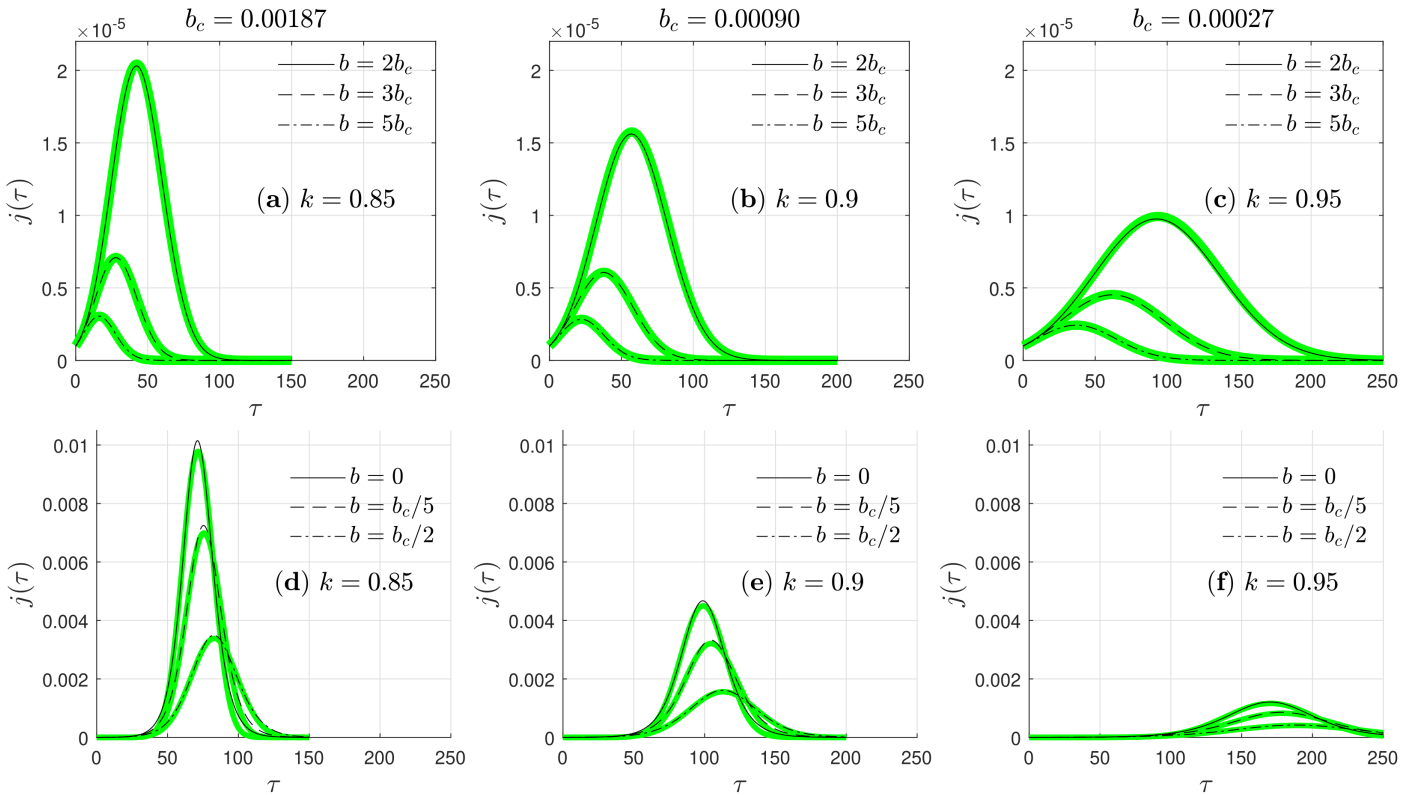

Figure 8: Differential rate $j(\tau)$ of infected population fraction versus reduced time for three different k and various reduced vaccination rates b/b_c . Here, $\eta = 10^{-6}$ is used. Upper panels show the regime $b > b_c$, while lower panels show results for $b < b_c$ including $b = 0$ (SIR model).

Constrained 2nd order polynomial approximation (3)

With the approximation (21) the rate of new infections is

$$\frac{j(\tau)}{j_{\max}} = \begin{cases} \left(\dfrac{\sinh(c_3\tau_m)}{\sinh(c_3\tau)+\sqrt{\frac{j_{\max}}{c_0}}\sinh[c_3(\tau_m-\tau)]} \right)^2 & \text{for } \tau \le \tau_m \\ \dfrac{e^{d_1(\tau-\tau_m)}}{\left(1+\frac{j_{\max}}{d_1(J_\infty-J_0)}\left[e^{d_1(\tau-\tau_m)}-1\right]\right)^2} & \text{for } \tau \ge \tau_m \end{cases} \tag{22}$$

with the dimensionless peak time

$$\tau_m = \frac{1}{c_3}\operatorname{artanh}\frac{2c_3}{c_1+\frac{2c_0}{J_0-\eta}}, \tag{23}$$

and the abbreviation $c_3 = \sqrt{(c_1/2)^2 - c_0 c_2}$. The solution (22) correctly reduces to $j_{\max}$ for $\tau = \tau_m$ and reproduces $j(0) = c_0 = \eta(1-\eta)$ and $\lim_{\tau\to\infty} j(\tau) = 0$.

SIR-forecast 2nd waves

In Figs. 9-11 we display the number of infected persons, estimated from the reported fatality data for four countries (black), assuming a fatality rate of $f = 0.005$, along with predictions resulting from the semi-time SIR model (green). Shown are both the reported data known at the time of original submission, as well as data collected afterwards. The datasets are separated by a red vertical line.

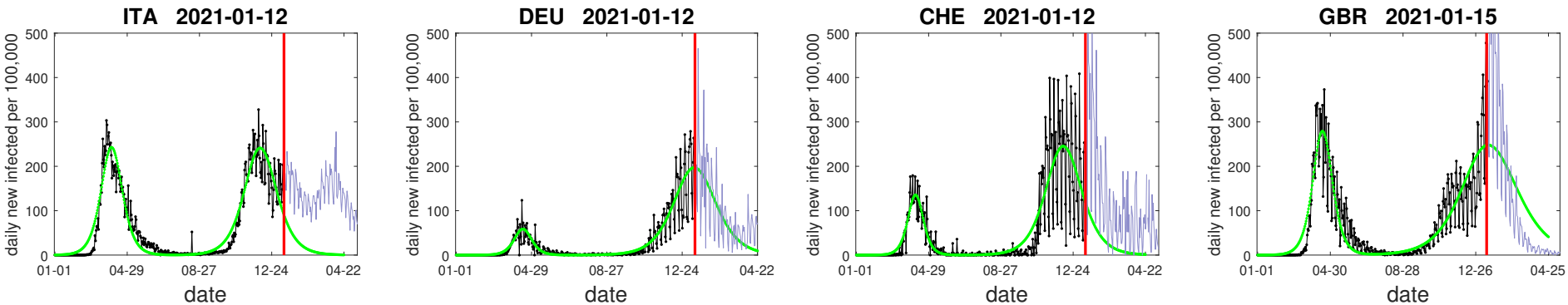

Figure 9: Daily new infected persons per 100,000 inhabitants (black), together with the SIR prediction for the 2nd wave (green).

SIR-forecast 2nd waves

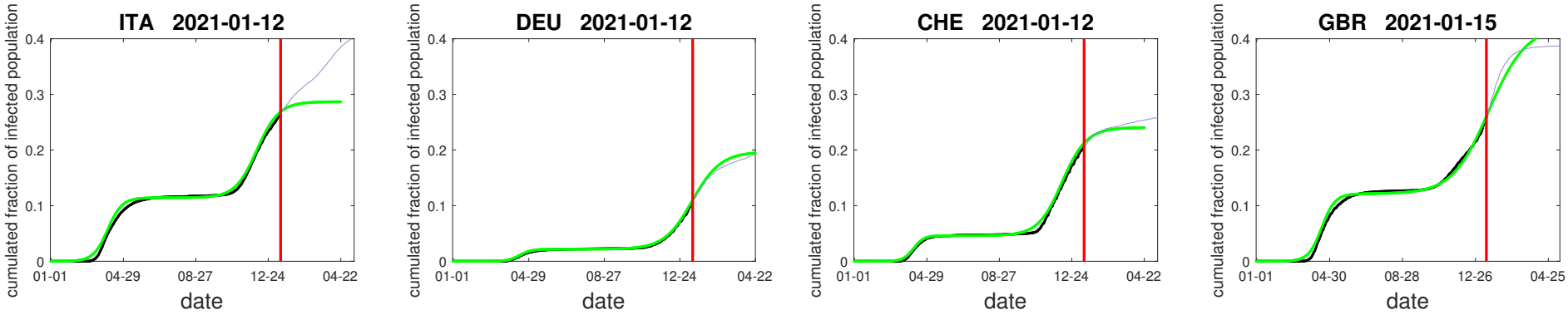

Figure 10: Cumulated fraction of infected persons

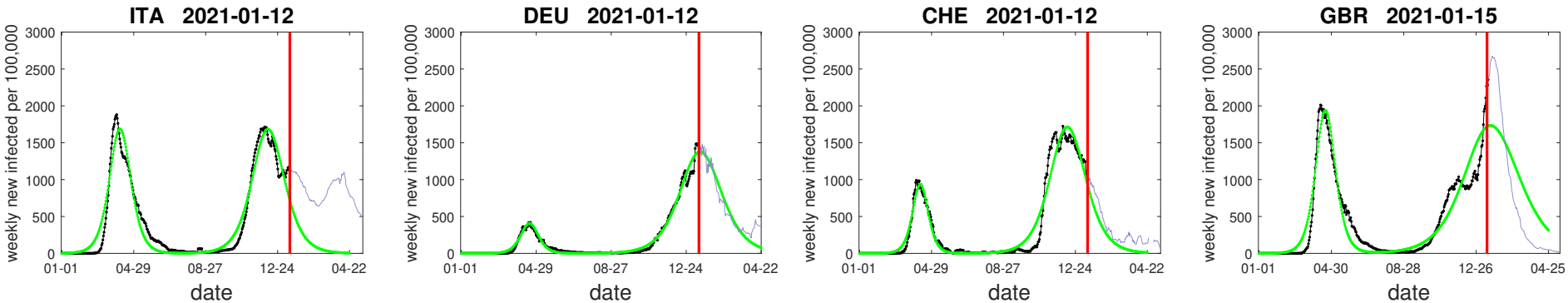

Figure 11: Weekly new infected persons per 100,000 inhabitants.

KSSIRV-model

With reduced time (8) and constant ratio $b = v(t)/a(t)$ of vaccination to infection rate the SIRV-equations read

$$\frac{dS}{d\tau} = -SI - bS,\ \frac{dI}{d\tau} = SI - kI,\ \frac{dR}{d\tau} = kI,\ \frac{dV}{d\tau} = bS \tag{24}$$

with initial conditions $S(0) = 1 - \eta$, $I(0) = \eta$, $R(0) = V(0) = 0$ and generalized sum constraint $S + I + R + V = 1$. For pandemic wave to develop $k < 1 - 2\eta - b$.RS, MK, Physics 3, 386-426 (2021) derived the exact solution for $\alpha = k - b \notin (0, 1)$ in inverse form

$$\tau = \frac{1}{\alpha} \int_{-\frac{E(\psi_1)}{\alpha}}^{-\frac{E(\psi_2)}{\alpha}} \frac{dz}{[\frac{1}{1+e^{-x}} - \frac{k}{\alpha}]z[1 + W_\nu(z)]},$$

$$E(x) = \eta(1 + e^x)e^{-\frac{[1+k(x-\psi_0)]}{\alpha}},\ \ \psi(x) = \ln \frac{S(x)}{I(x)} \tag{25}$$

with place holders W_ν, $\nu = 0, -1$, and ψ_1, ψ_2 for different cases.

KSSIRV-model (2)

$$\text{If } b > b_c(k,\eta) = (32\pi k\eta^2)^{3/5} \exp(W_0[\frac{6(1-k+k\ln k)}{5(32\pi k\eta^2)^{3/5}}]) \qquad (26)$$

(shown in Fig. 12) we have $e^{-x} \ll 1$ and Eq. (25) reduces to

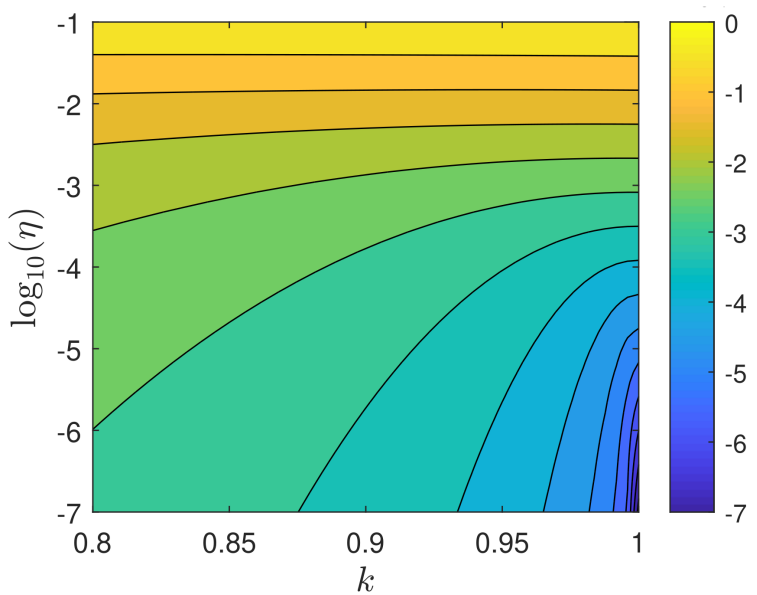

Figure 12: The critical b_c versus k and η. Coloring scheme uses the decadic logarithm of b_c, and the vertical axis is also logarithmic.

KSSIRV-model (3)

$$\tau = \frac{1}{b}\int_{-\frac{E(\psi_2)}{\alpha}}^{-\frac{E(\psi_1)}{\alpha}} \frac{dz}{z[1+W_\nu(z)]} = \frac{1}{b}\ln\frac{W_\nu(-\frac{E(\psi_1)}{\alpha})}{W_\nu(-\frac{E(\psi_2)}{\alpha})} \tag{27}$$

Inverting Eq. (27) yields

$$\psi(\tau) = \ln\frac{S(\tau)}{I(\tau)} = \ln\frac{1-\eta}{\eta} + (k-b)\tau - \frac{1-e^{-b\tau}}{b} \tag{28}$$

providing

$$S(\tau) = \frac{e^{-b\tau}}{1+e^{-\psi(\tau)}},\ I(\tau) = \frac{e^{-b\tau}}{1+e^{\psi(\tau)}},\ R(\tau) = J(\tau) - I(\tau),$$

$$V(\tau) = 1 - S(\tau) - J(\tau),\ j(\tau) = S(\tau)I(\tau) = \frac{e^{-2b\tau}}{4\cosh^2\frac{\psi(\tau}{2}},$$

$$J(\tau) = \eta + \int_0^\tau d\xi j(\xi) \tag{29}$$

KSSIRV-model (4)

For small values $b \leq b_c$ use linear interpolation with known KSSIR-solution

$$j(k, b, \tau) \simeq \frac{b}{b_c} j(k, b_c, \tau) + \frac{b_c - b}{b_c} j_{\mathrm{SIR}}(k) \tag{30}$$

Approximation for $\eta \ll 1$

$$j(\tau, b > b_c) \simeq \eta e^{\frac{1-e^{-b\tau}}{b} - (k+b)\tau} \tag{31}$$

with peak time and maximum value

$$\tau_{\max} = -\frac{\ln(k+b)}{b},\ j_{\max} = \eta e^{1/b} \left(\frac{k+b}{e}\right)^{(k+b)/b} \tag{32}$$

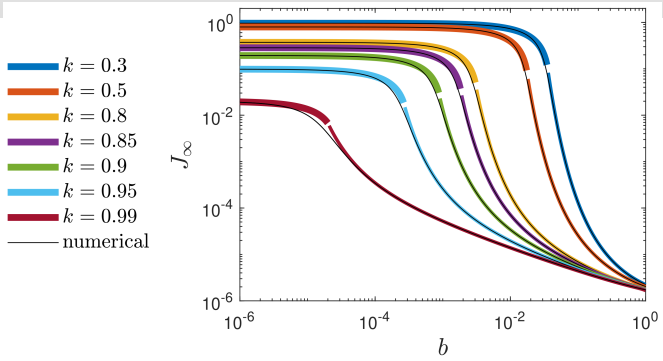

Figure 13: Final fraction of infected persons J_∞ versus reduced vaccination rate b, for various k at $\eta = 10^{-6}$ (double-logarithmic plot). The exact numerical solution (solid black) is compared with the approximants for $b > b_c$ (thin colored), and for $b \leq b_c$ (thick colored).

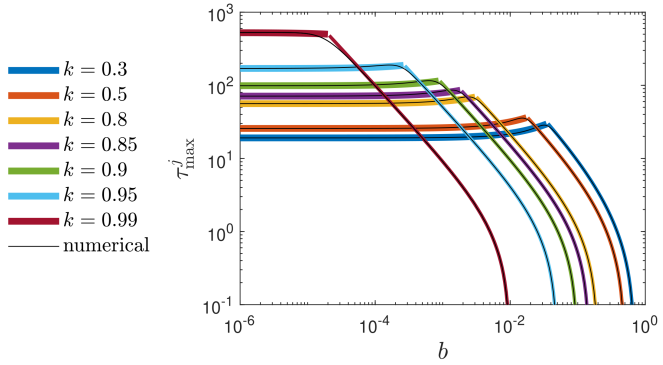

Figure 14: Reduced peak time of the newly infected population fraction.

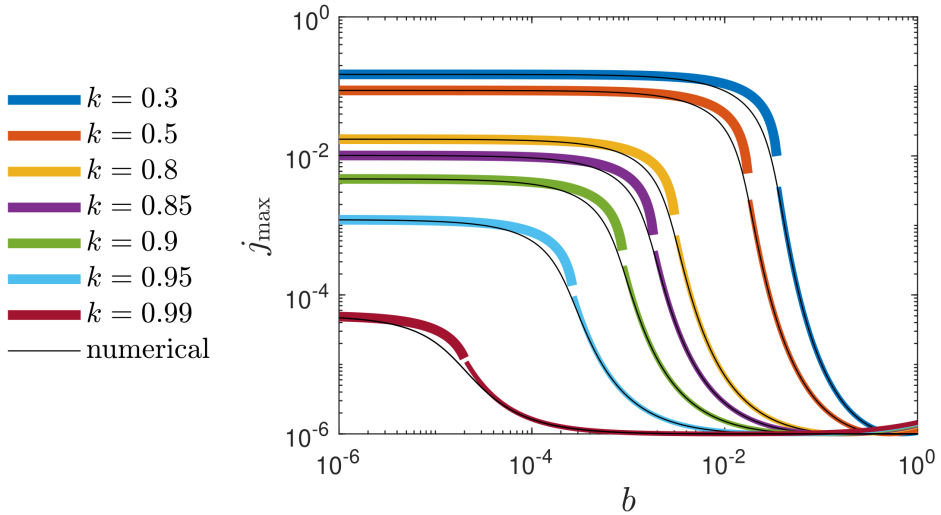

Figure 15: Peak value of the newly infected population fraction.

Forecast omicron waves

In "Forecast of omicron wave time evolution", RS, MK, Covid 2, 216-229 (2022) we forecasted the evolution of the omicron wave on January 13, 2022 for twelve different country with the SIR-model adopting for all countries the early doubling time of $t_{2,\mathrm{omicron}} = 3$ days that has been reported in South Africa, Great Britain and Denmark. At least initially and for short and rapid outbreak evolutions the assumption of a stationary infection rate a_0 is justified. With earlier t_2 then

$$a_0 = \frac{\ln 2}{3(1-k)} = \frac{0.231}{1-k}\ \text{days} \tag{33}$$

in terms of k, so that all quantities of interest are solely determined by the parameter k. Particularly the omicron peak time then is $t_{\mathrm{peak}} = t_0 + 4.328\tau_{\max}(k)(1-k)$.

Forecast omicron waves (2)

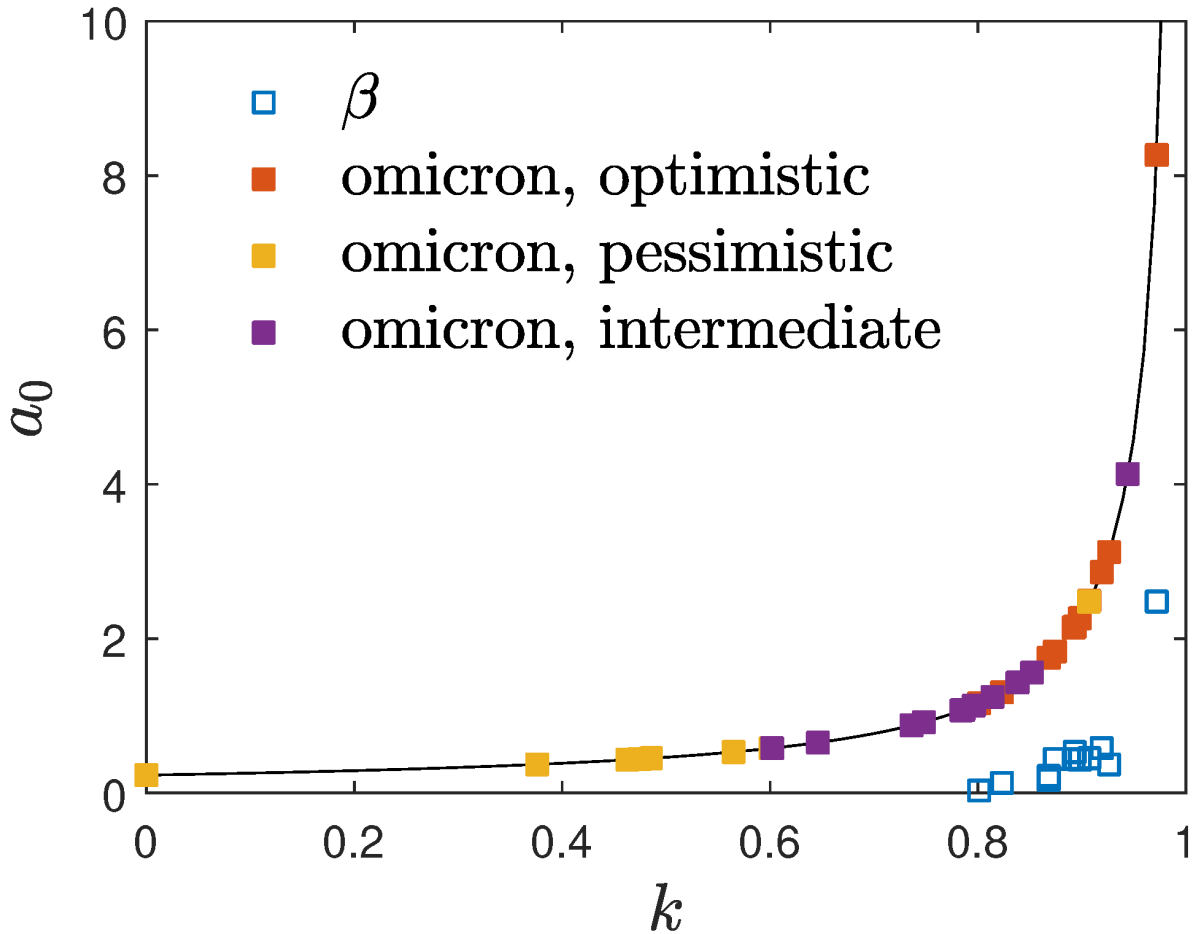

Figure 16: Phase space of SIR omicron waves. The solid black line the location of the 3-day early doubling time. The symbols β represent the values for the earlier β-mutant.

Forecast omicron waves (3)

We assume that in every country just before the start of omicron the earlier determined parameters k and a_0 for the 2nd wave hold (symbols β in Fig. 16). Consider 3 scenarios for the decrease to the 3-day early doubling time for omicron mutant:
(i) optimistic: solely due to an increase in the initial infection rate a_0, whereas k remains the same as for the beta mutant.
(ii) pessimistic: solely due to a decrease in the ratio k, whereas a_0 is the same as for the beta mutant.
(iii) intermediate: half due to an increase in a_0 and half due to decrease in k.
Fig. 17 shows the predictions for the daily rate of new infections as well as the cumulative fraction for the 3 scenarios in 12 countries.

Forecast omicron waves (4)

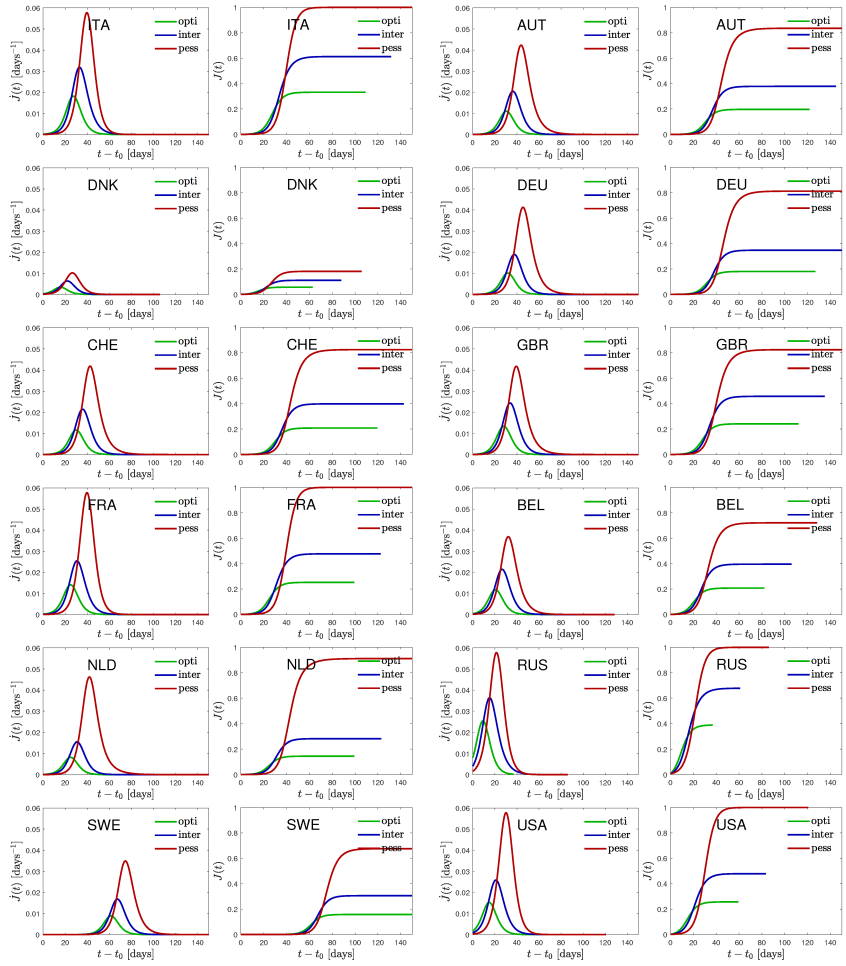

Figure 17: Predicted time dependence of the daily rate of newly infected persons well as the cumulative fraction of infected persons for the 3 scenarios.

Forecast omicron waves (5)

Remarkably good agreement of forecast from 13 January 2022 with later monitored data:

In Germany and Switzerland the monitored data showed that the SDI values attained their maximum values 1594.2 and 2913.8 on 10 February 2022 and 1 February 2022, respectively. These values are in excellent agreement with the predicted days (Germany 1-15 Feb 2022 for the 3 scenarios; Switzerland 31 Jan-13 Feb for the 3 scenarios) and indicate dark numbers of omicron infections greater than 4.4 and 2.8, respectively, from the predicted SDI maxima in the optimistic case of 7090 and 8148, respectively.

RUB

Refinement of SIRV-model

In "'Multi-Hamiltonian structure of the epidemics model accounting for vaccinations and a suitable test for the accuracy of its numerical solvers"', F. Haas, MK, RS, J. Phys. A 55, 225206 (2022), a generalized Hamiltonian formalism for the SIRV epidemic model is derived. The SIRV model admits three possible functionally independent Hamiltonians and hence three associated Poisson structures. The SIRV model is shown to be expressible as an almost Nambu system, except for a scale factor function breaking the divergenceless property. In the autonomous case with time-independent stationary ratios k and b, the SIRV model is shown to be a super-integrable system. This case with its 3 constants of motion allows a rigorous test for the accuracy of numerical schemes that are suited to solve the stiff set of SIRV differential equations.

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Summary and conclusions

- The predicted time dependence of the rate of new infections from the solutions of the SIR- and SIRV epidemic models is close to the earlier used Gaussian distribution function.
- By introducing the reduced time the SIR- and SIRV-model equations can be solved exactly (although in inverse form) for arbitrary time dependencies of the infection rate $a(t)$. The entire SIR-reduced time dependence of a pandemic wave is determined by only one parameter: the (assumed) constant ratio k of the recovery to infection rate.
- The constrained 2nd order polynomial approximation yields very accurate analytical approximations for the rate of new infections $\dot{J}(t)$ which determines the hospitalization and death rates.
- For various mutants the forecasts made agree remarkably well with the later monitored data in different countries.