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Numerical assessment of the spread dynamics of the new coronavirus infection SARS-CoV-2 using multicompartmental models with distributed parameters

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Численная оценка динамики распространения новой коронавирусной инфекции SARS-CoV-2 с использованием многокомпонентных моделей с распределенными параметрами

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Abstract. We propose multicompartmental models of infectious diseases dynamics for numerical study of the spread parameters of the new coronavirus infection SARS-CoV-2, which take into account the delay effects associated with the presence of the latent period of the infection, as well as the possibility of an asymptomatic course of the disease. The dynamics of the spread of COVID-19 in the Russian Federation was investigated, using these models with distributed parameters that formalize the interactions of the models' compartments. The paper provides numerical estimates of the spread dynamics of the new coronavirus infection in various age groups of the population. We also investigate possible consequences of the mask regime and quarantine measures. We obtain an explicit estimate allowing to assess the necessary scope of these measures for the epidemy extinction.

Keywords: compartmental models of epidemics, distributed parameters, numerical solution, COVID-19 modelling

Mathematics Subject Classification: 65Z05, 92D30

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Аннотация. В работе предлагаются многокомпонентные модели динамики инфекционных заболеваний для численного исследования параметров распространения новой коронавирусной инфекции SARS-CoV-2, учитывающие в том числе эффекты запаздывания, связанные с наличием латентного периода инфекции, а также возможность бессимптомного течения заболевания. На основании данных моделей исследуется динамика распространения COVID-19 в РФ с использованием распределенных констант, формализующих взаимодействия компонент в рамках моделей. В работе получены численные оценки динамики распространения новой коронавирусной инфекции в различных возрастных группах населения. Также исследуется влияние «масочного режима» и карантинных мероприятий. В последнем случае получается выражение, позволяющее оценить необходимый масштаб данных мер для затухания эпидемии.

Ключевые слова: компонентные модели эпидемических заболеваний, распределенные параметры, численное решение, моделирование эпидемии COVID-19

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Introduction

Since the seminal work of Kermack and McKendrick [1] compartmental models has been widely used in mathematical epidemiology studies (see e. g. the reviews [2, 3]). After the outbreak of the new coronavirus infection SARS-CoV-2 a new wave of interest to this modelling framework has arisen in the epidemics modelling community [4–17]. The results obtained using this framework depend crucially on the choice of the input parameters in the system of modeling equations, which characterize the fundamental interrelations between the model compartments (i.e. disease transmission rate, recovery and mortality rates, etc.). A review of the vast literature on the characteristics reveals significant variance in the values of the aforementioned fundamental parameters. For example, the transmission rate estimates vary in the interval from 0.08 to 0.37 (see [18–21]), and the latent period duration varies from 2 to 11 days (see [18, 19, 22]). In the present research we are aiming to capture the uncertainty in the parameters' values determination by collecting and interpreting the results of a series simulations based on compartmental models with randomly generated parameters that obey certain distributions. The interpretation of the numerical results obtained is probabilistic. Namely, we assess confidence intervals for the parameter values of interest.

We first focus on a relatively simple 7-compartmental model that takes into account the delay effects connected to the latent period of infection and the possibility of asymptomatic progression of the disease. Then we switch to a modification of this model that involves subdivisions of the initially suggested basic compartments. This allows to capture e. g. the effects connected to effects of using face masks, the effects of isolation and quarantine, and the age factors of the epidemic parameters.

The paper is organized as follows. In Section 2 the main modelling frameworks are introduced and described. Numerical results obtained using these models are presented in Section 3. Section 4 provides a summary of the main results. Verification of fundamental properties of the

mathematical models used in the paper and technical calculations related to the assessment of the basic reproduction numbers are given in Appendix A and Appendix B, respectively.

1. Main results

The basic modelling framework of this research reads as follows:

$$\begin{aligned}
&\dot{S}(t) = -\beta\tfrac{I(t)S(t)}{N} - r_{I_a}\beta\tfrac{I_a(t)S(t)}{N} - r_E\beta\tfrac{E(t)S(t)}{N},\\
&\dot{E}_a(t) = \beta\tfrac{I(t)S(t)}{N} - \lambda_1 E_a(t),\\
&\dot{E}(t) = r_E\beta\tfrac{E_2(t)S(t)}{N} + \lambda_a(1-p_a)E_a(t) - \lambda E(t),\\
&\dot{I}_a(t) = r_{I_a}\beta\tfrac{I_a(t)S(t)}{N} + \lambda_a p_a E_a(t) - \gamma I_a(t),\\
&\dot{I}(t) = \gamma I_a(t) + \lambda_2 E(t) - \gamma I(t),\\
&\dot{R}(t) = \gamma(I + I_a),\\
&N = S(t) + E_a(t) + E(t) + I_a(t) + I(t) + R(t).
\end{aligned} \tag{1.1}$$

Here S are susceptible, E_a are exposed, infected, but not infectious, E are pre-symptomatic infected, I_a are infectious asymptomatic, I are symptomatic infected, R are recovered (and/or deceased), $\beta > 0$ and $\gamma > 0$ are the disease transmission and recovery rates, respectively, $0 < r_{I_a} \leq 1$, $0 < r_E \leq 1$ are the transmission modifiers for the interaction between the respective categories of the population, $\lambda_a > 0$, $\lambda > 0$, — are the transition rates for the respective categories of the population, p_a is the probability of asymptomatic infection.

Fundamental mathematical properties of the modelling framework (1.1) such as positive invariance of the solutions corresponding to non-negative initial conditions and the well-posedness of (1.1) are verified in Appendix A.

In our modelling we use normally distributed parameters with the following 3σ-intervals based on a review of the literature on the main characteristics of the disease.

Table 1

Parameters' distributions for the model (1.1)

Parameter	Meaning	3σ-Interval	References
β	Transmission rate	[0.08, 0.37]	[18–21], [23]
r_{I_a}	Infectiousness of asympt.	[0.5, 0.9]	[18, 24–26]
r_E	Infectiousness of pre-sympt.	[0.5, 0.85]	[18, 24, 25, 27, 28]
$1/\lambda_a$	Exposed period	[2, 6]	[18, 19, 22–24, 30]
$1/\lambda$	Pre-symptomatic period	[2, 5]	[18, 19, 24, 27–29]
p_a	Probab. of asympt. infection	[0.3, 0.65]	[24–26, 29]
$1/\gamma$	Infectious period	[4, 12]	[19, 23, 31–33]

Figure 1 demonstrates the dynamics of the new coronavirus disease in the Russian Federation.

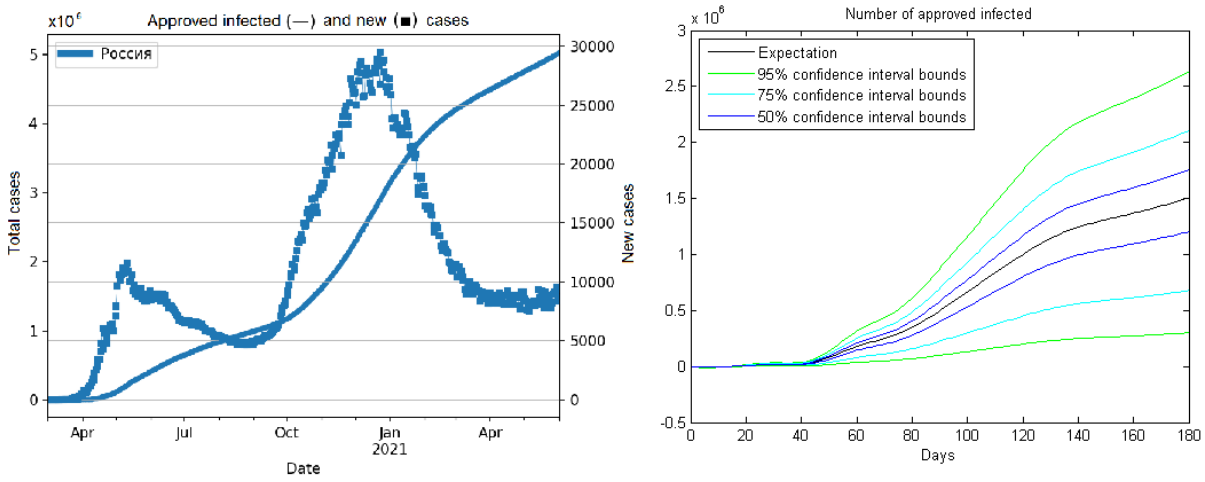

Figure 1. The initial stage of COVID-19 spread in the Russian Federation: according to Johns Hopkins Institute data (left) and according to the simulations based on the framework (1.1).

Figure 2 demonstrates the prognoses on the number of infected in the Russian Federation obtained by polynomial extrapolation of statistical data for the previous three months (left) and obtained by simulations based on the model (1.1) and the parameters with the characteristics presented in Table 1 (right).

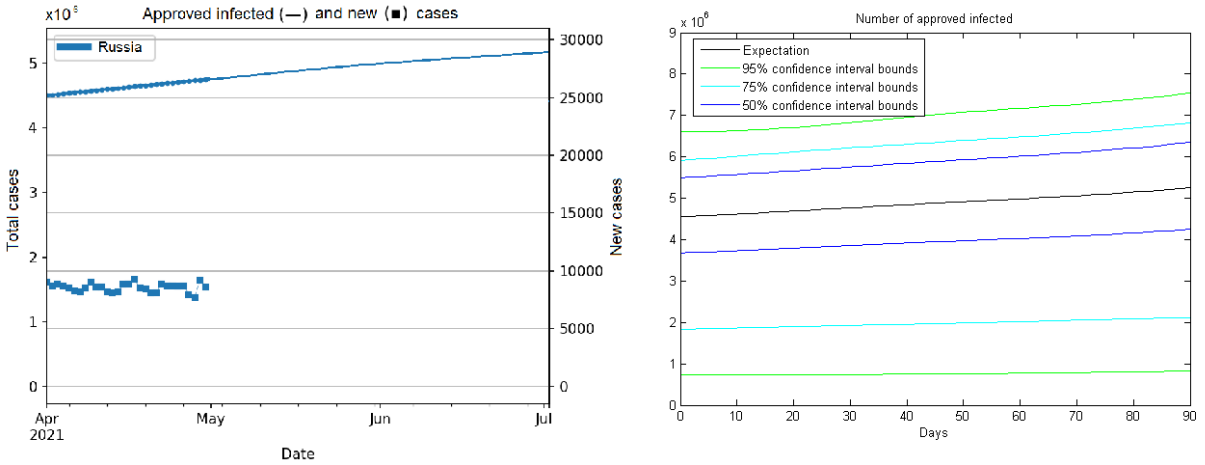

Figure 2. The prognoses on the number of infected in the Russian Federation obtained by polynomial extrapolation (indicated by thin line) of statistical data (indicated by bold line) for the preceding three months (left) and obtained by epy simulations based on the framework (1.1).

The assessment of the basic reproduction number R_0 of COVID-19 based on the model (1.1) and the parameters from Table 1 gives the following results. The expectation of R_0 equals to 2.13. The bounds of 50%, 75%, and 95% confidence intervals for R_0 are [2.02, 2.16], [1.89, 2.28], and [1.71, 2.46], respectively. The value $R_0 = \max\{\frac{r_E\beta}{\lambda}, \frac{r_{I_a}\beta}{\gamma+\beta}\}$ is obtained using the new generation matrix method [34] (The calculation of R_0 is presented in Apendix B).

In order to study more issues connected to the spread of the new coronavirus disease, we introduce the following generalization of the model (1.1).

$$
\begin{aligned}
\dot{S}_1(t) &= -\beta_{11}\frac{I_1(t)S_1(t)}{N} - r_{I_a}\beta_{11}\frac{I_{a1}(t)S_1(t)}{N} - r_E\beta_{11}\frac{E_1(t)S_1(t)}{N} \\
&\quad -\beta_{12}\frac{I_2(t)S_1(t)}{N} - r_{I_a}\beta_{12}\frac{I_{a2}(t)S_1(t)}{N} - r_E\beta_{12}\frac{E_2(t)S_1(t)}{N}, \\
\dot{S}_2(t) &= -\beta_{22}\frac{I_2(t)S_2(t)}{N} - r_{I_a}\beta_{22}\frac{I_{a2}(t)S_2(t)}{N} - r_E\beta_{22}\frac{E_2(t)S_2(t)}{N} \\
&\quad -\beta_{21}\frac{I_1(t)S_2(t)}{N} - r_{I_a}\beta_{21}\frac{I_{a1}(t)S_2(t)}{N} - r_E\beta_{21}\frac{E_1(t)S_2(t)}{N}, \\
\dot{E}_{a1}(t) &= \beta_{11}\frac{I_1(t)S_1(t)}{N} + \beta_{12}\frac{I_2(t)S_1(t)}{N} - \lambda_a E_{a1}(t), \\
\dot{E}_1(t) &= r_E\beta_{11}\frac{E_1(t)S_1(t)}{N} + r_E\beta_{12}\frac{E_2(t)S_1(t)}{N} + \lambda_a(1-p_a)E_{a1}(t) - \lambda E_1(t), \\
\dot{E}_{a2}(t) &= \beta_{22}\frac{I_2(t)S_2(t)}{N} + \beta_{21}\frac{I_1(t)S_2(t)}{N} - \lambda_a E_{a2}(t), \\
\dot{E}_2(t) &= r_E\beta_{22}\frac{E_2(t)S_2(t)}{N} + r_E\beta_{21}\frac{E_1(t)S_2(t)}{N} + \lambda_a(1-p_a)E_{a2}(t) - \lambda E_2(t), \\
\dot{I}_{a1}(t) &= r_{I_a}\beta_{11}\frac{I_{a1}(t)S_1(t)}{N} + r_{I_a}\beta_{12}\frac{I_{a2}(t)S_1(t)}{N} + \lambda_a p_a E_{a1}(t) - \gamma_1 I_{a1}(t), \\
\dot{I}_{a2}(t) &= r_{I_a}\beta_{22}\frac{I_{a2}(t)S_2(t)}{N} + r_{I_a}\beta_{21}\frac{I_{a1}(t)S_2(t)}{N} + \lambda_a p_a E_{a2}(t) - \gamma_2 I_{a2}(t), \\
\dot{I}_1(t) &= \gamma_1 I_{a1}(t) + \lambda E_1(t) - \gamma_1 I_1(t), \\
\dot{I}_2(t) &= \gamma_2 I_{a2}(t) + \lambda E_2(t) - \gamma_2 I_2(t), \\
\dot{R}(t) &= \gamma_1(I_1(t) + I_{a1}(t)) + \gamma_2(I_2(t) + I_{a2}(t)), \\
N &= S_1(t)+E_{a1}(t)+E_1(t)+I_{a1}(t)+I_1(t)+S_2(t)+E_{a2}(t)+E_2(t)+I_{a2}(t)+I_2(t)+R(t).
\end{aligned}
\tag{1.2}
$$

Here the numbered compartments stand for subdivisions of the respective compartments of (1.1) separated with respect to certain properties that we address to below.

The first issue that we capture using the framework (1.2) is the difference of the new coronavirus disease parameters for different age groups. We divide the whole population into the subgroups of individuals aged below (indexed by "1") and above 65 years (indexed by "2"). In this setting we make the following assumptions on the parameters involved in (1.2): $\beta_{11} = \beta$, the values β_{12}, $\beta_{21} = \beta_{22}$, γ_1, and γ_2 are normally distributed with the 3σ-intervals $[0.08,\ 0.37]$, $[0.1,\ 0.46]$, $[0.07,\ 0.19]$, and $[0.11,\ 0.28]$, respectively. The transmission rates here are estimated based on the statistical data [19,23], the values of γ_1 and γ_2 are estimated based on the recovery and mortality rates in the respective age categories [35–38]. The ratio $S_1(0)/S_2(0)$ is taken to be equal to $17/3$. The values of the rest parameters are chosen according to Table 1.

Figure 3 demonstrates the dynamics of the new coronavirus disease in the aforementioned age categories of the population.

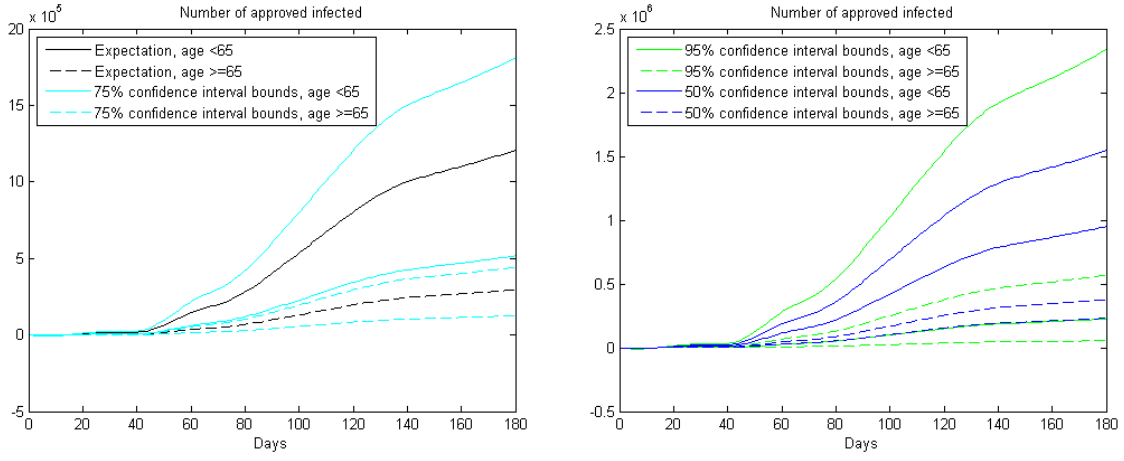

Figure 3. The initial stage of COVID-19 spread in the age categories of below (solid lines) and above (dashed lines) 65 years old according to the simulations based on the framework (1.2).

The second effect we model using the framework (1.2) are the consequences of face masks use by a subcategory of the whole population. We make a simplifying assumption of strict separation of the groups of individuals who do not use face masks (indexed by "1") and who always wear face masks during the contacts with others (indexed by "2"). Here we make the following assumptions on the parameters in (1.2): $\beta_{11} = \beta$, $\gamma_1 = \gamma_2 = \gamma$, the values of β_{12}, β_{21}, and β_{22} has normal distributions with the 3σ-intervals [0.07, 0.32], [0.05, 0.25], and [0.04, 0.17], respectively (based on the statistical data [39–44]). The values of the rest parameters are the same as in the first modelling setting (see Table 1). Below we demonstrate the result of the face masks regime implementation starting from the 90th day from the disease outbreak with the ratio $S_1(90)/S_2(90) = 2/3$ (see Figure 4).

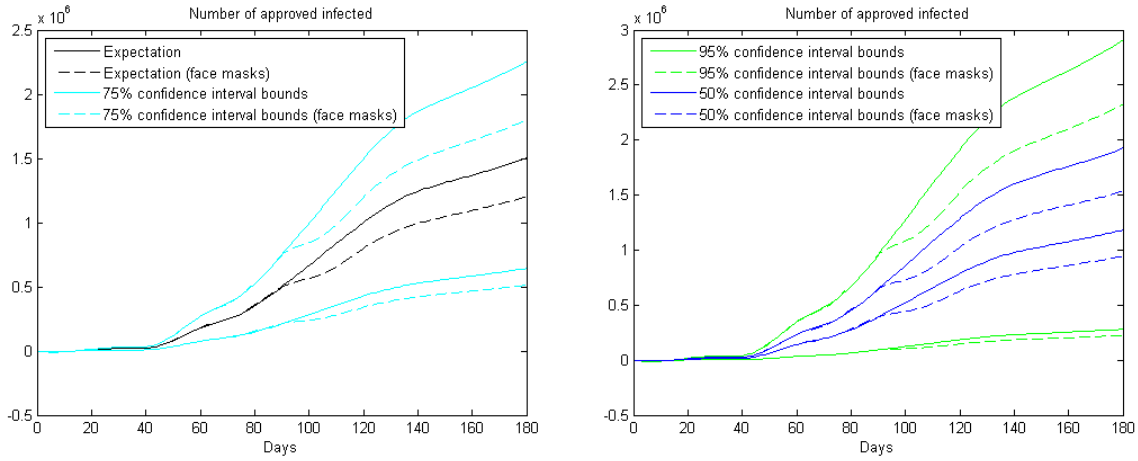

Figure 4. The results of the face masks regime implementation (dashed lines) at the 90th day from the outbreak of COVID-19 in the Russian Federation according to the simulations based on the framework (1.2).

The assessment of the basic reproduction number R_0 corresponding to the face masks regime gives the following results. The expectation of R_0 equals to 1.71. The bounds of 50%, 75%, and 95% confidence intervals for R_0 are [1.61, 1.79], [1.51, 1.83], and [1.37, 2.09], respectively.

Generally, the basic reproduction number value in the framework (1.2) can be found as

$$R_0 = \max\{\frac{N\beta_{22}r_{E_2} - S_1(0)\beta_{22}r_{E_2}}{N\lambda}; \frac{S_1(0)\beta_{11}r_{E_1}}{N\lambda}; \frac{N\beta_{22}r_{I_2} - S_1(0)\beta_{22}r_{I_2}}{N\gamma_2}; \frac{S_1(0)\beta_{11}r_{I_{a_1}}}{N\gamma_1}\}$$

by the same procedure as was implemented in the case of (1.1).

The third case we consider using the framework (1.2) concerns lockdown measures. We divide the population into the subgroups of non-isolated (indexed by "1") and isolated (indexed by "2") individuals. Here we make the following assumptions on the parameters involved in (1.2): $\beta_{11} = \beta$, $\beta_{12} = \beta_{21} = \beta/15$ (see [45, 46]), $\beta_{22} = 0$, $\gamma_1 = \gamma_2 = \gamma$ (see Table 1).

Figure 5 demonstrates the result of the implementation of the lockdown regime with the ratio $S_1(90)/S_2(90) = 2$ starting from the 90th day since the disease outbreak (see Figure 2).

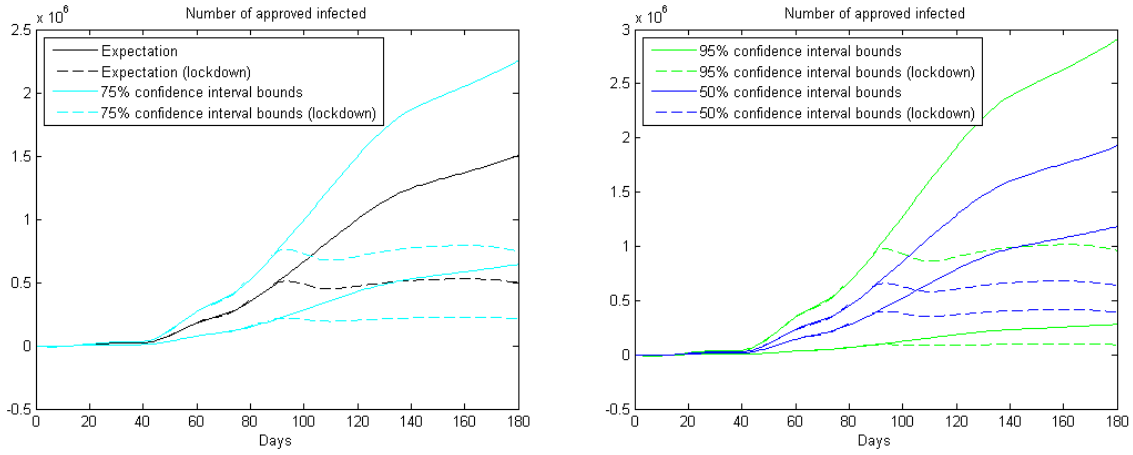

Figure 5. The results of the lockdown regime implementation (dashed lines) at the 90th day from the outbreak of COVID-19 in the Russian Federation according to the simulations based on the framework (1.2).

The assessment of the basic reproduction number R_0 corresponding to the lockdown regime gives the following results. The expectation of R_0 equals to 0.96. The bounds of 50%, 75%, and 95% confidence intervals for R_0 in this case are [0.92, 1.01], [0.88, 1.06], and [0.83, 1.1], respectively.

2. Conclusions

In this paper we investigated numerically the spread dynamics parameters of the new coronavirus disease in the Russian Federation. We employed the multi-compartmental epidemic models (1.1) and (1.2), which parameters were distributed according to the statistical data. We assessed the following additional features in our modelling based on the framework (1.2): the dynamics of the disease in different age groups and the effects of the face masks and the lockdown regimes on the COVID-19 spread. Interestingly, the obtained expression for the basic reproduction number in (1.2) can be used for direct assessment of the scope of the face masks or the lockdown measures required for the epidemy extinction.

Appendix A

Let us verify here the well-posedness property of (1.1). We first note that the vector-function $f : \mathbb{R}^6 \to \mathbb{R}^6$ that corresponds to the right-hand side of the differential equaations of the system (1.1) obviously satisfies Caratheodori conditions, i.e. $f(\cdot)$ is continuous and for any $k > 0$, there exists some constant L_k such that $|f(X)| \le L_k$ for any $X \in \mathbb{R}^6$, $|X| \le k$. In addition, the structure of the system (1.1) and the a-priori boundedness of its solutions imply the validity of Lipschitz condition for the right-hand side of (1.1) with some positive constant. Let us now denote $g(X, u_0) = f(X)$, where $u_0 = (\beta, r_{I_a}, r_E, \lambda_a, \lambda, p_a, \gamma)$. It is straightforward to check that $g(X_i(\cdot), u_i) \to g(X_0(\cdot), u_0)$ in measure for any $u_i \to u_0$ and any continuous functions X_0, X_i $(i = 1, 2, \dots)$ such that $X_i(\cdot) \to X_0(\cdot)$ in measure. Applying Corollary 3 from [47], due to a-priori boundedness of solutions to (1.1), we obtain the well-posedness of (1.1) on any closed interval $[0, T]$ of time for any initial condition $X^0 = (S(0), E_a(0), E(0), I_a(0), I(0), R(0))$.

The proof of well-posedness of (1.2) is analogous.

In order to verify the positive invariance property, we address Lemma 2.1 in [48]. This statement guarantees the property needed provided that the gradient of the vector field generated by (1.1) estimated at any point of the boundary of the set $[0,\infty)^6$ is not oriented outside of this set. Obviously, the latter property takes place for the models (1.1) and (1.2).

Appendix B

We first assess the basic reproduction number for the model (1.1). Let us denote by $\mathfrak{F}$ the growth rate of infected individuals and by $\mathfrak{V}$ – the transition rate of infected to other compartments. The disease-free equilibrium is $x_0 = (S(0), 0, 0, 0, 0, 0)$. New infected arise in the compartments E_a, E, I_a, so we have

$$\mathfrak{F} = \begin{pmatrix} \beta\frac{I(t)S(t)}{N(t)} \\ r_E\beta\frac{E(t)S(t)}{N(t)} \\ r_{I_a}\beta\frac{I_a(t)S(t)}{N(t)} \\ 0 \\ 0 \\ 0 \end{pmatrix}, \mathfrak{V} = \begin{pmatrix} \lambda_a E_a(t) \\ -\lambda_a(1-p_a)E_a(t) + \lambda E(t) \\ -\lambda_a p_a E_a(t) + \gamma I_a(t) \\ -\gamma I_a(t) - \lambda E(t) + \gamma I(t) \\ \beta\frac{I(t)S(t)}{N(t)} + r_{I_a}\beta\frac{I_a(t)S(t)}{N(t)} + r_E\beta\frac{E(t)S(t)}{N(t)} \\ -\gamma(I + I_a) \end{pmatrix}.$$

Let us approximate $S(0)$ by N. Let us find the matrices $F = [\frac{\partial \mathfrak{F}_i}{\partial x_j}(x_0)]$, $V = [\frac{\partial \mathfrak{V}_i}{\partial x_j}(x_0)]$, where $1 \le i, j \le 4$.

We get

$$F = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & r_E\beta & 0 & 0 \\ 0 & 0 & r_{I_a}\beta & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, V = \begin{pmatrix} \lambda_a & 0 & 0 & 0 \\ -\lambda_a(1-p_a) & \lambda & 0 & 0 \\ -\lambda_a p_a & 0 & \gamma & 0 \\ 0 & -\lambda & -\gamma & \gamma \end{pmatrix}.$$

The basic reproduction number R_0 can be found as $R_o = \rho(FV^{-1})$, where $\rho(FV^{-1})$ is the spectral radius of the matrix FV^{-1}.

$$FV^{-1} = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & r_E\beta & 0 & 0 \\ 0 & 0 & r_{I_a}\beta & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \cdot \begin{pmatrix} \frac{1}{\lambda_a} & 0 & 0 & 0 \\ \frac{p_a-1}{\lambda} & \frac{1}{\lambda} & 0 & 0 \\ \frac{-p_a\beta-\beta+\gamma p_a}{\gamma(\gamma+\beta)} & 0 & \frac{1}{\gamma+\beta} & 0 \\ \frac{2p_a-1}{\gamma+\beta} & \frac{1}{\gamma+\beta} & \frac{1}{\gamma+\beta} & \frac{1}{\gamma+\beta} \end{pmatrix} =$$

$$= \begin{pmatrix} 0 & 0 & 0 & 0 \\ \frac{r_E\beta(p_a-1)}{\lambda} & \frac{r_E\beta}{\lambda} & 0 & 0 \\ \frac{r_{I_a}\beta(-p_a\beta-\beta+\gamma p_a)}{\gamma(\gamma+\beta)} & 0 & \frac{r_{I_a}\beta}{\gamma+\beta} & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

Next, we find the eigenvalues of FV^{-1}:

$$\begin{vmatrix} -\widetilde{\lambda} & 0 & 0 & 0 \\ \frac{r_E\beta(p_a-1)}{\lambda} & \frac{r_E\beta}{\lambda} - \widetilde{\lambda} & 0 & 0 \\ \frac{r_{I_a}\beta(-p_a\beta-\beta+\gamma p_a)}{\gamma(\gamma+\beta)} & 0 & \frac{r_{I_a}\beta}{\gamma+\beta} - \widetilde{\lambda} & 0 \\ 0 & 0 & 0 & -\widetilde{\lambda} \end{vmatrix} = 0,$$

$$-\widetilde{\lambda}\cdot(\frac{r_E\beta}{\lambda}-\widetilde{\lambda})\cdot(\frac{r_{I_a}\beta}{\gamma+\beta}-\widetilde{\lambda})\cdot(-\widetilde{\lambda})=0,$$

$$\begin{cases}\widetilde{\lambda}_{1,2}=0;\\ \widetilde{\lambda}_3=\dfrac{r_E\beta}{\lambda};\\ \widetilde{\lambda}_4=\dfrac{r_{I_a}\beta}{\gamma+\beta}.\end{cases}$$

We therefore have

$$R_0=\max\{\frac{r_E\beta}{\lambda},\frac{r_{I_a}\beta}{\gamma+\beta}\}.$$

Proceeding in the same manner, we obtain the following expression for the basic reproduction number in (1.2):

$$R_0=\{\frac{N\beta_{22}r_{E_2}-S_1(0)\beta_{22}r_{E_2}}{N\lambda};\frac{S_1(0)\beta_{11}r_{E_1}}{N\lambda};\frac{N\beta_{22}r_{I_2}-S_1(0)\beta_{22}r_{I_2}}{N\gamma_2};\frac{S_1(0)\beta_{11}r_{I_{a_1}}}{N\gamma_1}\}.$$

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