# COVID-19 MODELLING WITH SQUARE ROOT SUSCEPTIBLE-INFECTED INTERACTION

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We propose a COVID-19 mathematical model related to functional shape with square root susceptible-infected interaction. Using the Hurwitz criterion and then a graph theoretical-method for the construction of a Lyapunov function, we discuss both local and global stability. The analytical solution of the system is obtained in a special case. A non-standard finite difference scheme is then developed with the aim to obtain a proper discrete-time version of the model. Simulations show a good agreement between the proposed discretization and the results given by standard numerical methods.

Key words: COVID model, square-root function, numerical solution, stability analysis non-standard finite difference scheme

## Introduction

Modelling Infectious disease using mathematical models proved its role in providing information on the methods and efficiency of public health measures. The development and investigation of such models can offer assistance and serve as an instrument for the characterization of the transmission, thus, allow to provide methods of control, prevent, predict infections, ensuring population well-being [1]. For this reason, numerous mathematical models have been considered for prediction purposes, *e.g.* [2-6], and references therein.

As researches mention, the Coronaviruses are transmitted for animals to human such as pigs, cats, and bats. Most part of Coronavirus diseases cause mild upper-respiratory tract ailments. Few of these infections cause a deadly infection. Examples include the SARS coronavirus (SARS-COV) and, from December 2019, COVID-19, which showed up in Wuhan, China [7, 8]. The WHO declared the outbreak of COVID-19 a public health emergency of a pandemic in mid 2020 and, since then, different mathematical and numerical modelsare used for predicting COVID-19 outbreak, which includes all categories of researchers including drug specialists, chemists, and mathematicians, *e.g.* [9-19], and references there in. Stochastic differential

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equation models have also received attention [20, 21], as well as delayed and fractional models [22]. Here we discuss, for the first time, a functional square-root form for the susceptible and infected classes.

### Formulation of the COVID-19 model with square root interaction

Square-root dynamics have shown to be useful in the context of a giving up smoking model [23]. Here, according to the nature of COVID-19, we propose to consider the interaction of susceptible and infected people in the light of a square-root term:

$$\frac{d\mathcal{S}(t)}{dt} = \lambda - \beta \sqrt{\mathcal{I}(t)\mathcal{S}(t)} - \mu \mathcal{S}(t) + \xi \mathcal{R}(t)$$

$$\frac{d\mathcal{I}(t)}{dt} = \beta \sqrt{\mathcal{I}(t)\mathcal{S}(t)} - (\gamma + d + \mu)\mathcal{I}(t)$$

$$\frac{d\mathcal{R}(t)}{dt} = \gamma \mathcal{I}(t) - (\mu + \xi)\mathcal{R}(t)$$
(1)

where S(t) is the susceptible individuals, I(t) – the infected class, and  $\mathcal{R}(t)$  – the recovered people from the effect of coronavirus. Parameters used are:  $\mu$  – stands for the natural death rate,  $\gamma$  – the recovery rate for the infected class,  $\beta$  – the transmission coefficient of susceptible population infected class, d – the disease death rate occurred in the infected class due to COVID-19,  $\xi$  – the rate for a recovered person quit R-class to S-class, and  $\lambda$  – the recruitment rate.

Our main focus is for a proper discrete-time model formulation of system (1): see section *Numerical scheme*. Note that our system of ODE's (1) satisfies the law:

$$\frac{d\mathcal{N}(t)}{dt} = -(\mu+d)\mathcal{N}(t) + \lambda \tag{2}$$

with  $\mathcal{N}(t)$  is the total population with information, hence,

$$\mathcal{N}(t) = \mathcal{S}(t) + \mathcal{I}(t) + \mathcal{R}(t)$$

which yields the exact solution in the form:

$$\mathcal{N}(t) = \frac{\lambda}{\mu+d} + \left(\mathcal{N}_0 - \frac{\lambda}{\mu+d}\right) e^{-(\mu+d)t}$$
(3)

with

$$\mathcal{N}_0 = \mathcal{S}(0) + \mathcal{I}(0) + \mathcal{R}(0)$$

We conclude that  $\mathcal{N}(t)$  is a decreasing function:

$$\lim_{t \to \infty} \mathcal{N}(t) = \frac{\lambda}{\mu + d} \tag{4}$$

Also, if we have:

$$\mathcal{S}(0) \ge 0, \ \mathcal{I}(0) \ge 0, \ \mathcal{R}(0) \ge 0 \tag{5}$$

then  $S(t) \ge 0$ ,  $I(t) \ge 0$ , and  $\mathcal{R}(t) \ge 0$  for all time t > 0. Thus, the solution fulfills the positivity property.

## Dynamics of the model

Our system (1) has the unique positive equilibrium point  $\mathcal{E}^* = (\mathcal{S}^*, \mathcal{I}^*, \mathcal{R}^*)$  with:

S324

$$S^{*} = \frac{\lambda(\mu + \xi)(\gamma + d + \mu)}{\beta^{2}(\mu + \xi) + \mu(\mu + \xi)(\mu + d + \gamma) + \gamma\beta^{2}}$$
$$\mathcal{I}^{*} = \frac{\beta^{2}}{(\gamma + d + \mu)^{2}}S^{*}$$
$$\mathcal{R}^{*} = \frac{\gamma}{\mu + \xi}\frac{\beta^{2}}{(\gamma + d + \mu)^{2}}S^{*}$$
(6)

The positivity of  $S^*$ ,  $\mathcal{I}^*$ , and  $\mathcal{R}^*$  can be deduce from the fact that all parameters are positive.

Local stability

The Jacobian matrix of our model (1):

$$\mathcal{J}(\mathcal{X}(t)) = \begin{pmatrix} -\frac{\beta I}{2\sqrt{IS}} - \mu & -\frac{\beta}{2}\sqrt{\frac{S}{I}} & \xi \\ \frac{\beta}{2}\sqrt{\frac{I}{S}} & \frac{\beta}{2}\sqrt{\frac{S}{I}} - m_1 & 0 \\ 0 & \gamma & -m_2 \end{pmatrix}$$

where  $m_1 = \gamma + d + \mu$  and  $m_2 = \mu + \xi$ . At  $\mathcal{E}^*$  the Jacobian gets the form

$$\mathcal{J}(\mathcal{E}^*) = \begin{pmatrix} \frac{-\beta^2 - 2\mu m_1}{2m_1} & -\frac{m_1}{2} & \xi \\ \frac{\beta^2}{2m_1} & \frac{-m_1}{2} & 0 \\ 0 & \gamma & -m_2 \end{pmatrix}$$

Solving this for eigen values  $(\lambda_1, \lambda_2, \lambda_3)$ , leads to the characteristic equation:

$$\lambda^3 + a\lambda^2 + b\lambda + c = 0 \tag{7}$$

where

$$a = \frac{\beta^2 + 2\mu m_1 + m_1^2 + 2m_1 m_2}{2m_1}$$
$$b = \frac{\beta^2 + \mu m_1}{2}$$
$$c = \frac{m_2 \beta^2 + \mu m_1}{2} - \frac{\beta^2 \gamma \xi}{2m_1}$$

By applying the Hurwitz criterion, we have a > 0, b > 0, c > 0, and bc > 0 if:

$$\frac{\beta^2 \gamma \xi}{m_1 (m_2 \beta^2 + \mu m_1)} < 1 \tag{8}$$

Hence, the system of eq. (1) is locally asymptotically stable at  $\mathcal{E}^*$ .

Theorem 1. If eq. (8) holds, then model (1) is locally asymptotically stable at  $\mathcal{E}^* = (\mathcal{S}^*, \mathcal{I}^*, \mathcal{R}^*)$  eq. (6).

Global stability analysis from a graph-theoretical approach

Next, we show global stability of  $\mathcal{E}^*$ .

For general definitions on a directed graph (digraph) denoted  $\mathcal{G}$  we refer [24] or [25]. A sub-digraph of  $\mathcal{G}$  is denoted  $\mathcal{H}$ . The  $w(\mathcal{H})$  represents the weight of a sub-digraph  $\mathcal{H}$ .

A tree is a sub-digraph  $\mathcal{T}$  of  $\mathcal{G}$  that is a single associated component and in which the in-degree of one vertex, the root, is zero, but each of the remaining vertices have in-degree 1. A path  $\mathcal{P}$  is a sub-digraph with particular vertices named  $i_1, i_2, \dots, i_m$  so that its arcs are of the form  $(i_k, i_{k+1}), k = 1, 2, \dots, m - 1$ . A cycle  $\mathcal{C}$  is the sub-digraph gotten from such a path  $\mathcal{P}$  by including the arc  $(i_m, i_j)$ . In case m = 1, the cycle comprising of a single vertex  $i_1$  and a single arc  $(i_1, i_1)$  is called a loop. A unicyclic chart is a sub-digraph  $\mathcal{Q}$  consisting of a collection of disjoint established trees whose roots are the vertices of a co-ordinated cycle.

A weighted digraph ( $\mathcal{G}$ ,  $\mathcal{A}$ ) is strongly connected if and only if the weight matrix is irreducible [25], with  $\mathcal{A} = [a_{ii}]$  is  $n \times n$  weight matrix.

Now, we apply the general results [12, 25] to show the global asymptotic stability of (29), *e.g.* [24, 25] and references therein.

*Theorem 2.* The  $\mathcal{E}^* = (\mathcal{S}^*, \mathcal{I}^*, \mathcal{R}^*)$  is globally asymptotically stable *Proof.* Let

$$\mathcal{L}_{1} := \mathcal{S} - \mathcal{S}^{*} - \mathcal{S}^{*} \ln \frac{\mathcal{S}}{\mathcal{S}^{*}}$$
$$\mathcal{L}_{2} := \mathcal{I} - \mathcal{I}^{*} - \mathcal{I}^{*} \ln \frac{\mathcal{I}}{\mathcal{I}^{*}}$$
$$\mathcal{L}_{3} := \mathcal{R} - \mathcal{R}^{*} - \mathcal{R}^{*} \ln \frac{\mathcal{R}}{\mathcal{R}^{*}}$$

Differentiating, we have:

Gul, N., et al.: Covid-19 Modelling with Square Root Susceptible-Infected ... THERMAL SCIENCE: Year 2023, Vol. 27, Special Issue 1, pp. S323-S332

Here,

$$a_{12} = a_{21} = \beta \sqrt{\mathcal{I}^* \mathcal{S}^*}, \ a_{13} = \xi \mathcal{R}^*, \ a_{32} = \gamma I^*$$

From fig. 1,  $(\mathcal{G}, \mathcal{A})$  contains three vertices, also, we have:

$$\mathcal{G}_{12} + \mathcal{G}_{21} = 0$$
 and  $\mathcal{G}_{21} + \mathcal{G}_{32} + \mathcal{G}_{13} = 0$ 

Theorem 3.5. [26] Implies  $d_j$ ,  $1 \le j \le 3$ , verifying  $\mathcal{L} = \sum_{j=1}^{3} d_j \mathcal{L}_j$  is a Lyapunov function for (1). The relations between the  $d'_j$  is can be derived using *Theorems 3.3 and 3.4* of [26] as  $d_1 = d_2$  and

$$d_3 = \frac{\xi R^*}{\gamma I^*} d_1$$

hence

$$\mathcal{L} = d_1 \mathcal{L}_1 + d_2 \mathcal{L}_2 + d_3 \mathcal{L}_3$$



#### Exact solution in a special case

We now obtain the explicit solution system (1) in the case when no new entry to the susceptible population, in the form of birth, migration, relapse, *etc.*, exists, meaning that the susceptible population does not replicate, *i.e.*,  $\lambda + \zeta \mathcal{R}(t) = 0$ :

$$\frac{dS(t)}{dt} = -\beta \sqrt{\mathcal{I}(t)S(t)} - \mu S(t)$$

$$\frac{d\mathcal{I}(t)}{dt} = \beta \sqrt{\mathcal{I}(t)S(t)} - (\gamma + d + \mu)\mathcal{I}(t)$$

$$\frac{d\mathcal{R}(t)}{dt} = \gamma \mathcal{I}(t) - (\mu + \xi)\mathcal{R}(t)$$
(9)

We can compute the exact solution of system (9) and keep generality in mind, it is enough to solve first two equations of system (9):

$$\frac{d\mathcal{S}(t)}{dt} = -\beta \sqrt{\mathcal{I}(t)\mathcal{S}(t)} - \mu \mathcal{S}(t)$$

$$\frac{d\mathcal{I}(t)}{dt} = \beta \sqrt{\mathcal{I}(t)\mathcal{S}(t)} - (\gamma + d + \mu)\mathcal{I}(t)$$
(10)

Let us do the following change of variables:

$$m(t) = \sqrt{S(t)}, \ n(t) = \sqrt{\mathcal{I}(t)}$$

In the new variables, we get a 1<sup>st</sup> order linear ODE system:

$$\frac{dm(t)}{dt} = -\left(\frac{\beta}{2}\right)n(t) - \frac{\mu}{2}m(t)$$

$$\frac{dn(t)}{dt} = \left(\frac{\beta}{2}\right)m(t) - \frac{(d+\mu+\gamma)}{2}n(t)$$
(11)

The exact solution of (11) can be determined with the help of standard methods. By eliminating the variable n(t), we have the 2<sup>nd</sup> order linear ODE:



$$\frac{d^2m(t)}{dt^2} + \left(\frac{d+2\mu+\gamma}{2}\right)\frac{dm(t)}{dt} + \left(\frac{\mu(d+\mu+\gamma)+\beta^2}{4}\right)m(t) = 0$$
(12)

This is a linear and damped consonant oscillator equation with solution:

$$m(t) = K_1 \varepsilon^{u^+ t} + K_2 \varepsilon^{u^- t}$$

where

$$u^{\pm} = \frac{-(d+2\mu+\gamma) \pm \sqrt{(d+2\mu+\gamma)^2 - 4(\mu(d+\mu+\gamma) + \beta^2)}}{4}$$

and constants  $K_1$  and  $K_2$  are determined from given initial conditions.

## Numerical scheme

Here, we apply the results by Mickens [27-30]. Let:

$$y'_{k} = f(t, y_{1}, y_{2}, ..., y_{m}), \ k = 1, 2, ..., m$$

with  $f[t, y_k(t)]$  is the non-linear term. Using Mickens' finite difference method, we get:

$$y_1' = \frac{y_{1,k+1} - y_{1,k}}{\phi_k(h)}$$
(13)

$$y_2' = \frac{y_{2,k+1} - y_{2,k}}{\phi_k(h)} \tag{14}$$

$$y'_{m} = \frac{y_{m,k+1} - y_{m,k}}{\phi_{k}(h)}$$
(15)

where  $\phi_k$  is a function of the step size  $h = \Delta t$ . The  $\phi_k$  satisfy:

$$\phi_k(h) = h + o(h^2) \text{ for } h \to 0 \tag{16}$$

As example, the functions h, sin(h),  $sinh(h)e^{h} - 1$ , and  $(1-e^{-\lambda h})/\lambda$  satisfy eq. (16). For example, we consider:

$$y^2 \approx y_k y_{k+1} \tag{17}$$

$$y^{3} \approx \left(\frac{y_{k+1} + y_{k-1}}{2}\right) y_{k}^{2}$$
 (18)

with  $t_n = nh$ , h = T/N, for  $n = 0, 1, ..., N \in \mathbb{N}$ . Letting:

$$t \to t_k = (\Delta t)k, \ \left(\mathcal{S}(t), \mathcal{I}(t), \mathcal{R}(t)\right) \to \left(\mathcal{S}_k, \mathcal{I}_k, \mathcal{R}_k\right)$$

with  $\Delta t = h$  is the step-size.

The non-standard finite difference scheme for (1) keeps the positivity, and fixed points a the original modeland fulfills a similar law (2) with:

$$\mathcal{N}_k := \mathcal{S}_k + \mathcal{I}_k + \mathcal{R}_k$$

S328

Then we get:

$$\frac{\mathcal{S}_{k+1} - \mathcal{S}_{k}}{\phi} = \lambda - \beta \sqrt{\mathcal{I}_{k} \mathcal{S}_{k+1}} - \mu \mathcal{S}_{k+1} + \xi \mathcal{R}_{k}$$

$$\frac{\mathcal{I}_{k+1} - \mathcal{I}_{k}}{\phi} = \beta \sqrt{\mathcal{I}_{k} \mathcal{S}_{k+1}} - (\gamma + d + \mu) \mathcal{I}_{k+1}$$

$$\frac{\mathcal{R}_{k+1} - \mathcal{R}_{k}}{\phi} = \gamma \mathcal{I}_{k+1} - (\mu + \xi) \mathcal{R}_{k+1}$$
(19)

with

$$\phi = \phi(h, \mathcal{G}) = \frac{e^{\mathcal{G}h} - 1}{\mathcal{G}}$$

and  $\vartheta = \mu + d$ . It easy to check that eq. (19) has fixed-points

$$\mathcal{S}^* = \overline{\mathcal{S}}, \ \mathcal{I}^* = \overline{\mathcal{I}}, \ \mathcal{R}^* = \overline{\mathcal{R}}$$

with  $(\mathcal{S}^*, \mathcal{I}^*, \mathcal{R}^*)$  is defined in eq. (6). Using the transformation:

$$s_{k+1} = \sqrt{\mathcal{S}_{k+1}} \tag{20}$$

leads to

$$(1+\phi\mu)s_{k+1}^2 + \left(\phi\beta\sqrt{\mathcal{I}_k}\right)s_{k+1} - \left(\mathcal{S}_k + \phi\lambda + \phi\xi\mathcal{R}_k\right) = 0$$

To find the value of  $Sk_{+1}$ , we solve the aforementioned quadratic equation:

$$s_{k+1} = \frac{-\beta\phi\sqrt{\mathcal{I}_k} + \sqrt{\beta^2\phi^2\mathcal{I}_k + 4(1+\phi\mu)(\mathcal{S}_k + \lambda\phi + \phi\xi\mathcal{R}_k)}}{2(1+\phi\mu)}$$
(21)

Similarly, we obtain:

$$\mathcal{I}_{k+1} = \frac{\phi \beta \sqrt{\mathcal{I}_k} s_{k+1} + \mathcal{I}_k}{1 + \phi(\gamma + \mu + d)}$$
(22)

$$\mathcal{R}_{k+1} = \frac{\phi \gamma \mathcal{I}_{k+1} + \mathcal{R}_k}{1 + \phi(\mu + \xi)}$$
(23)

for the discrete system (19).

## Numerical simulations

Numerically, we showed that the non-standard finite difference (NSFD) scheme (19) yields accurate results when compared the obtained graphs to the Runge-Kutta RK technique and ODE45 graphs, see fig. 2.

## Conclusion

Most theoretical work on epidemiology, mathematical biology, and the dynamics of interacting species in a biological community, has been based on systems of differential equations, with the state variables representing the individual species/populations. The original justification for the susceptible-infected interaction functional form was its similarity to the law of mass action in chemistry. However, such functional form has properties that are difficult to



justify biologically, and many other forms have been discussed in the literature to address the problem [31, 32]. Moreover, all susceptible-infected interaction functionals considered in the COVID-19 literature do not admit a closed-form solution for the system time trajectories. Here, by replacing first-order terms with square root terms and second-order terms with first-order terms, we proposed a model that appears to be more biologically reasonable. Furthermore, because the resulting model is a simple transform of a linear model, the system time trajectories are available in closed form. The current paper is related to the functional shape, which is in the frame of square-root of susceptible and infected individuals. We formulated the model, we discussed the local stability using the Hurwitz criterion and the global stability using a graph theoretic-method for the construction of a Lyapunov function. Then, the explicit analytical solution of the model was obtained in a special case. The NSFD scheme was utilized to propose a proper discrete-time model. Numerical simulations are presented, showing a good agreement between the discrete-time model and those obtained by the Runge-Kutta fourth (RK4) order strategy and the MATLAB routine ODE45 applied to the continuous model.

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Gul, N., et al.: Covid-19 Modelling with Square Root Susceptible-Infected ... THERMAL SCIENCE: Year 2023, Vol. 27, Special Issue 1, pp. S323-S332

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