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Research Article

MATHEMATICS

Numerical and Qualitative Study of SICQR Epidemic Model

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ABSTRACT

In this article, the nonlinear SICQR model explains the dynamics of transmission of infectious diseases in a community. This model has five epidemiological compartments: susceptible S, infective I, individuals with strong immunity C, quarantined Q and recovered R. The desired model owns different equilibrium cases as an endemic equilibrium and a disease free equilibrium. This model describes the importance of strong immunity for community members to control the spread of COVID-19. The shifted Chebyshev spectral collocation (SCSC) technique is utilized to find the numerical solutions the desired model. The obtained results clarify the influence of strengthening the immunity of community members on controlling the spread of the disease.

Introduction

Infectious diseases are transmitted from person to person, insects, animals, food, and water spread a few. These include influenza, COVID-19, Hepatitis, and measles **(Anderson and May, 1979; HethCote, 2000; Tyrrell and Bynoe, 1966).** The most common infectious disease in this period is COVID-19. The coronavirus that affects the respiratory system is a lung infection **(Anderson and May, 1998).** It becomes a great danger in society and the cause of many deaths, especially among the elderly, people with weak immunity, and people with chronic diseases. On March 11, 2020, the eradication of COVID-19 has become one of the world's most critical issues and challenges. Mathematical modeling of infectious diseases is essential for a deeper understanding of the disease's spread patterns and an assessment of control measures **(Bailey, 1975).** The two scientists, Kermack and McKendrick (1927), developed the first model to simulate infectious disease transmission. That is the starting point for inspiring many researchers **(Kermack and McKendrick, 1927).** Also, some studies are interested in the mathematical modeling of infectious diseases **(Hethcote and Driessche, 1989; Moghadas and Gumel, 2003; Shereen et al., 2020).** In this respect, the SIR model has described many epidemiological disorders **(Khader and Babatin, 2014; Makinde, 2007; Yano1 et al.,2016; Paul et al., 2022; Brauer and Castillo-Chavez, 2001; Das and Pal, 2018; Alshammari and Khan, 2021; Ibrahim et al., 2023; Blackwood, 2018; Shereen and Khan, 2020).**

Numerous arithmetic systems have been suggested across literature to designate the epidemiological environment of infectious diseases in human beings **(Diekmann et al., 1990; Diekmann et al., 2009; Martcheva, 2015; Boyce and Diprima, 2012; Brauer, 2001; Glendinning, 1994; Derrick and Grossman, 1976; Arrowsmith, 1983; Ahmed et al., 2021; Kim et al., 2008; Canfell et al., 2012).** Their research methods depend on modeling contact between individuals infected (or who have been infected) with diverse viral straining. To reach this goal, multiple SIR (sensitivity - infection - recoveries) models using specific parameters of cross immunity **(Canfell et al., 2012; Van de Velde et al., 2010).** Analysis and study of these models showed that multiple strains of infectious diseases can persevere in human beings and that their pervasiveness can display self-sustaining changeability over time.

The main objective of this article is to discuss the qualitative analysis and stability of the SICQR model, which is one of many modifications of the standard SIR model. People with strong immunity are less susceptible than susceptible individuals.

from one person to another. Immunity boosters include pharmaceutical interventions, such as using drugs to treat and Strong immunity helps individuals recover quickly from the disease and reduce the chance of infection immunize susceptible people. It has been proven that strong immunity is one of the best ways to avoid the spread of infectious diseases.

The structure of the following paper: In Section 2 and 3 we introduce SICQR system, the qualitative analysis and stability of the SICQR model are described. Section 4, SCSC method is used to solve the desired model. Finally, we conclude the paper and give a discussion in Section 5.

The Mathematical Model

The model divides births into two groups: with and without passive immunity. Antibodies that in infants transmitted to them from the mother starting from the last months of pregnancy are called temporary passive immunity and protect them from viruses. The model could be written as

$$\frac{dS}{dt} = -\beta IS - [\alpha + \mu]S + [1-\theta]\Lambda$$

$$\frac{dI}{dt} = \beta I[S + \sigma C] - [\mu + \delta + b]I$$

$$\frac{dC}{dt} = -\beta I\sigma C + \alpha S - \mu C \qquad (1)$$

$$\frac{dQ}{dt} = \delta I - (\mu + \gamma)Q$$

$$\frac{dR}{dt} = \gamma Q - \mu R + \theta\,\Lambda$$

Where $(1-\theta)\boldsymbol{\Lambda}$ are infants without passive immunity, and $\boldsymbol{\theta\Lambda}$ are infants who have passive immunity where

$0 \leq \theta \leq 1$

$S(t), I(t), C(t), Q(t)$ and $R(t)$ are measured by the derivatives $\frac{dS}{dt}, \frac{dQ}{dt}, \frac{dC}{dt}, \frac{dI}{dt}$ and $\frac{dR}{dt}$ also,

$$N = S + I + C + Q + R, \qquad (2)$$

while its derivative is given by

$$\frac{dN}{dt} = \Lambda - \mu N - b\,I \qquad (3)$$

We have parameters β, μ, Λ, γ, δ, θ, α and σ are positive. Table (1) explains the meaning of the parameters.

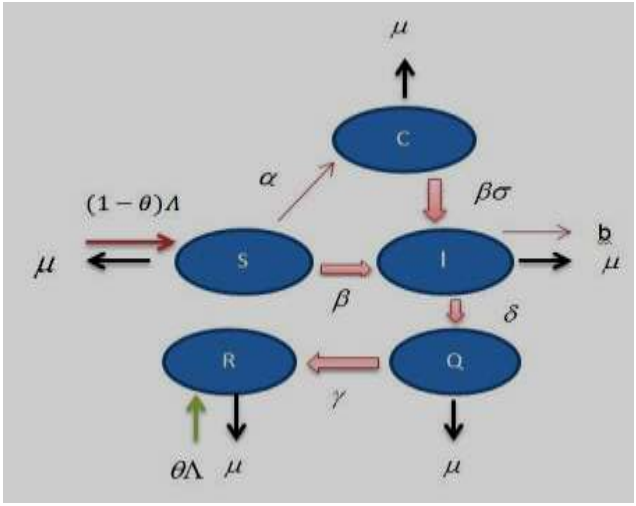

Fig. (1): S I C Q R Model flow chart

Qualitative Analysis and Stability

The model was evaluated qualitatively in region Φ. A qualitative analysis indicates that two equilibrium states exist in the intended model: equilibrium diseases free $E_0 = (S_0, I_0, C_0, Q_0, R_0) = (\frac{[1-\theta]\Lambda}{[\alpha+\mu]}, 0, \frac{\alpha[1-\theta]\Lambda}{\mu(\alpha+\mu)}, 0, \frac{\theta\Lambda}{\mu})$

Which no disease is present (I=0) and endemic case E^* at which is in the presence of disease, they are calculated by putting the system's right side equal zero. The two equilibrium cases and R_0 are calculated.

$$E^* = (S^*, Q^*, I^*, C^*, R^*)$$

which means that $I \neq 0$ an algebraic system which can be solved with

$$N^* = S^* + I^* + C^* + Q^* + R^*, \quad (4)$$

Table (1): The meaning of the symbols

symbols	Meaning
β	contact rate
μ	death by natural causes
Λ	birth ratio
γ	recovery rate
δ	isolation rate for infected individuals
θ	the proportion of births with passive immune
α	Strong immunity rate for susceptible
σ	the rate of infection reduction by treatment
b	the mortality rate from the disease

We obtain

$$I^* = \frac{\Lambda - \mu N^*}{b},$$
$$S^* = \frac{[1-\theta]\Lambda}{\beta I^* + \alpha + \mu},$$
$$C^* = \frac{\alpha S^*}{\beta I^* \sigma + \mu}, \quad (5)$$
$$R^* = \frac{\theta\Lambda + \gamma Q^*}{\mu},$$
$$Q^* = \frac{\delta I^*}{\gamma + \mu}$$

Proposition 1:

The quantities $S(t)$, $I(t)$, $C(t)$, $Q(t)$, and $R(t)$ are positive, and

$$\Phi = (S, I, C, Q, R) \in R^5, 0 \leq N \leq \frac{\Lambda}{\mu}$$

is bounded

Proof

Since

$$\frac{dS}{dt} \geq -\beta IS - [\alpha + \mu]S,$$
$$\frac{dI}{dt} \geq -[\mu + \delta + b]I,$$
$$\frac{dQ}{dt} \geq -(\mu + \gamma)Q, \quad (6)$$
$$\frac{dC}{dt} \geq -(\beta I\sigma + \mu)C,$$
$$\frac{dR}{dt} \geq -\mu R$$

The result of integrating the two sides of (6) over the interval [0, t] becomes

$$S(0)\, e^{-\int_0^t \beta I(a)da - (\mu+\alpha)t} \leq S(t),$$
$$I(0)e^{-[\mu+\delta+b]t} \leq I(t),$$
$$C(0)\, e^{-\mu t - \int_0^t \beta\sigma I(a)da} \leq C(t),$$
$$Q(0)\, e^{-[\mu+\gamma]t} \leq Q(t),$$
$$R(0)e^{-\mu t} \leq R(t). \quad (7)$$

Clearly S, I, C, Q and R are positive functions.

.

$$\frac{dN}{dt} = -\mu N - bI + \Lambda \leq -\mu N + \Lambda,$$

$$N(t) \leq -\left(\frac{\Lambda}{\mu} - N(0)\right)e^{-\mu t} + \frac{\Lambda}{\mu}.$$

(8)

Now,

Clearly, the feasible region $\Phi = (S, I, C, Q, R) \in R^5, 0 \leq N \leq \frac{\Lambda}{\mu}$ is bounded and positivity region.

We know that R_0 indicates how fast the coronavirus spreads; it refers to the anticipated total number of cases in a population that are directly caused by infected case. R_0 is the greatest absolute eigenvalue of the matrix FG^{-1} **(Diekmann et al., 2009).** Both of the matrices G and F are known as

$$F = \begin{pmatrix} \beta(S_0 + \sigma C_0) & 0 \\ 0 & 0 \end{pmatrix}, \quad (9)$$

$$G = \begin{pmatrix} \mu + \delta + b & 0 \\ -\delta & \gamma + \mu \end{pmatrix}, \quad (10)$$

$$G^{-1} = \frac{1}{(\gamma+\mu)(\mu+\delta+b)}\begin{pmatrix} \gamma + \mu & 0 \\ \delta & \delta + \mu + b \end{pmatrix}, \quad (11)$$

$$FG^{-1} = \begin{pmatrix} \frac{\beta(S_0+\sigma C_0)}{\delta+\mu+b} & 0 \\ 0 & 0 \end{pmatrix}. \quad (12)$$

This gives,

$$R_0 = \frac{\beta(S_0+\sigma C_0)}{\delta+\mu+b} = \frac{\beta\Lambda[1-\theta](\mu+\alpha\sigma)}{\mu(\alpha+\mu)(\mu+\delta+b)} \quad (13)$$

The Jacobin matrix **(Boyce and Diprima, 2012; Brauer and Castillo-Chavez, 2001; Arrowsmith and Place, 1983)** at any point is

$$\begin{pmatrix} -\beta I - (\alpha+\mu) & -\beta S & 0 & 0 & 0 \\ \beta I & \beta(S+\sigma C) - (\mu+\delta+b) & \beta\sigma I & 0 & 0 \\ \alpha & -\beta\sigma C & -\mu - \beta\sigma I & 0 & 0 \\ 0 & \delta & 0 & -\mu-\gamma & 0 \\ 0 & 0 & 0 & \gamma & -\mu \end{pmatrix}.$$

Theorem 1

The disease- free equilibrium when $R_0 < 1$ *is local stable unlike when* $R_0 > 1$ is unstable.

Proof:

When $E_0 = \left(\frac{[1-\theta]\Lambda}{[\alpha+\mu]}, 0, \frac{\alpha[1-\theta]\Lambda}{\mu(\alpha+\mu)}, 0, \frac{\theta\Lambda}{\mu}\right)$

the Jacobian matrix is

$$\begin{pmatrix} -(\alpha+\mu) & -\beta S_0 & 0 & 0 & 0 \\ 0 & \beta(S_0+\sigma C_0) - (\mu+\delta+b) & 0 & 0 & 0 \\ \alpha & -\beta\sigma C_0 & -\mu & 0 & 0 \\ 0 & \delta & 0 & -\mu-\gamma & 0 \\ 0 & 0 & 0 & \gamma & -\mu \end{pmatrix}$$

This matrix's eigenvalues are $-(\alpha+\mu), -\mu, -\mu, -(\mu+\gamma)$ and $(\mu+\delta+b)(R_0-1)$. The first four eigenvalues are negative and the fifth value will also be negative when $R_0 < 1$

Clearly, E_0 becomes asymptotic local stable when $R_0 < 1$ and when $R_0 > 1$ becomes unstable.

Theorem 2

The endemic state E^* for $R_0 > 1$ is local asymptotical stable.

Proof:

Since

$$\begin{pmatrix} -\beta I^* - (\alpha+\mu) & -\beta S^* & 0 & 0 & 0 \\ \beta I^* & \beta(S^*+\sigma C^*) - (\mu+\delta+b) & \beta\sigma I^* & 0 & 0 \\ \alpha & -\beta\sigma C^* & -\beta\sigma I^* - \mu & 0 & 0 \\ 0 & \delta & 0 & -\mu-\gamma & 0 \\ 0 & 0 & 0 & \gamma & -\mu \end{pmatrix}$$

the eigenvalues are $(-\mu-\lambda),(-\gamma\ -\mu-\lambda)$ and $\lambda^3 + b\lambda^2 + c\lambda + d = 0$ where $b = \beta\ I^*\ +\alpha+\ 2\mu+\beta\sigma\ I^*\ >\ 0$, $c = \beta^2\sigma^2 I^* C^* + (\beta I^* + \alpha + \mu)(\beta\sigma I^* + \mu) + \beta^2 I^* S^* > 0$, $d = \beta^2 S^* I^*\ (\beta I^*\sigma + \mu) + \beta I^*\sigma\alpha + (\beta I^* + \alpha + \mu)(\beta^2\sigma^2 I^* C^*) > 0$.

There are two negative eigenvalues $\lambda_1 = -\mu$, $\lambda_2 = -\gamma - \mu$, and other eigenvalues satisfy the equation $\lambda^3 + b\,\lambda^2 + c\,\lambda + d = 0$ by the Routh Stability Criterion **(Derrick and Grossman, 1976; Arrowsmith 1983)**, E^* is local asymptotical stable.

Theorem 3

The disease-free equilibrium point E_0 of the proposed model for $R_0 < 1$ is global asymptotical stable and unstable otherwise.

Proof:

a Liapounov function defined as

$V = I$,

$$\frac{dV}{dt} = \frac{dI}{dt} = \beta I[S + \sigma C] - [\mu + \delta + b]I \leq (\beta[S_0 + \sigma C_0] - [\mu + \delta + b])I \quad , (14)$$

it follows that,

$$\frac{dV}{dt} \leq I[\mu + \delta + b](R_0 - 1). \quad (15)$$

It is obvious that $\frac{dV}{dt} < 0$ in case $R_0 < 1$ and $\frac{dV}{dt} > 0$ in case $R_0 > 1$, in addition, $\frac{dV}{dt} = 0$ if and only if I=0. Therefore, by LaSalle's extension to Lyapunov's principle (**Derrick and Grossman, 1976; Arrowsmith, 1983**). E_0 is globally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$.

Theorem 4

When $R_0 > 1$ and $U < 0$ the endemic state $E^* = (S^*, Q^*, I^*, C^*, R^*)$ is globally asymptotically stable.

Proof:

Let Lyapunov function as

$$V = (S - S^* - S^* ln\frac{S}{S^*}) + (Q - Q^* - Q^* ln\frac{Q}{Q^*}) + (C - C^* - C^* ln\frac{C}{C^*}) + \left(I - I^* - I^* ln\frac{I}{I^*}\right), \quad (16)$$

$$\frac{dV}{dt} = (1 - \frac{S^*}{S})\frac{ds}{dt} + (1 - \frac{Q^*}{Q})\frac{dQ}{dt} + \left(1 - \frac{C^*}{C}\right)\frac{dC}{dt} + \left(1 - \frac{I^*}{I}\right)\frac{dI}{dt}, \quad (17)$$

at steady state

$$[1 - \theta]\Lambda = \beta I^* S^* + [\alpha + \mu]S^*,$$

$$[\mu + \delta + b] = \beta[S^* + \sigma C^*] \quad , \quad (18)$$

$$\frac{\delta I^*}{Q^*} = (\mu + \gamma),$$

gives

$$\frac{dV}{dt} = \frac{-(\alpha+\mu)}{S}(S - S^*)^2 - \frac{\beta I^*}{S}(S - S^*)^2 + \delta\left(I + I^* - \frac{I^* Q}{Q^*} - \frac{I Q^*}{Q}\right) + + \left(\alpha S - \frac{\alpha S C^*}{C}\right) + (\beta\sigma I^*[C^* - C] + \mu(C^* - C)) \quad , \quad (19)$$

It is obvious that $\frac{dV}{dt} = 0$ when

$S = S^*$, $C = C^*$, $Q = Q^*$, $I = I^*$.

Clearly, $\frac{dV}{dt} < 0$ if $U < 0$ where,

$$U = \delta\left(I + I^* - \frac{I^*Q}{Q^*} - \frac{I\,Q^*}{Q}\right) + \left(\alpha S - \frac{\alpha S C^*}{C}\right) + \left(\beta\sigma I^*[C^* - C] + \mu(C^* - C)\right) \quad (20)$$

By LaSalle principle of invariance **(Glendinning, 1994; Derrick, 1976)**. E^* is globally asymptotically stable in Φ if $U < 0$.

Numerical Solution Using SCSC Method

To clarify the SCSC technique, first, We offer the recurrence formula that can be used to determine the polynomials of Chebyshev **(Khader and Sweilam, 2013; Snyder, 1966)** which determined on the range [-1, 1] as

$T_{m+1}(y) = 2yT_m(y) - T_{m-1}(y)$,

$T_0(y) = 1$, $T_1(y) = y$, $m = 1,2,...$ (21)

It is understood that $T_m(-1) = (-1)^m$, $T_m(1) = 1$. The Chebyshev polynomials $T_m(y)$ of degree m have the following analytic form:

$$T_m(y) = \sum_{s=0}^{[m/2]} (-1)^s 2^{m-2s-1} \frac{m(m-s-1)!}{(s)!(m-2s)!} y^{m-2s} \quad (22)$$

where $[m/2]$ represents the integer component of $m/2$. When orthogonally exists,

$$\int_{-1}^{1} \frac{T_s(Y)T_j(Y)}{\sqrt{1-y^2}} dy = \begin{cases} \pi, & for\ s = j = 0; \\ \frac{\pi}{2}, & for\ s = j \neq 0; \\ 0, & for\ s \neq j. \end{cases} \quad (23)$$

By changing the variable $y = 2xL - 1$, we define shifted Chebyshev polynomials, which can be used on the interval [0, L]. Because of this, there is a description of the shifted Chebyshev polynomials as

$$T_m^*(X) = T_m\left(\frac{2x}{L} - 1\right) = T_{2m}\left(\sqrt{\frac{x}{L}}\right). \quad (24)$$

$T_m^*(x)$ of degree m has the following analytic form

$$T_m^*(x) = m\sum_{k=0}^{m} (-1)^{m-k} \frac{(m+k-1)!2^{2k}}{(m-k)!(2k)!L^k} x^k, \quad m=2,3,\ldots$$

Where, $T_m^*(1), T_m^*(0) = (-1)^m$

These polynomials' orthogonally condition is

$$\int_0^n T_k^*(x) w(x) T_j^*(x) dx = \delta_{jk} h_k, \quad (25)$$

the weight function as

$w(x) = \frac{1}{\sqrt{Lx - x^2}}$, $b_k = \frac{h_k}{2}\pi$, with

$h_0 = 2$, $h_k = 1$, $k \geqslant 1$. The square integrabel function defined in [0, n], $Z(x)$ can be represented as shifted Chebyshev polynomials.

$$Z(x) = \sum_{m=0}^{\infty} c_m T_m^*(x), \quad (26)$$

where the coefficients c_m are defined as follows

$$c_m = \frac{1}{b_m} \int_0^n w(x) Z(x) T_m^*(x) dx, \quad m = 0, 1, \ldots \quad (27)$$

to find the model's numerical solution. We first provide a convergence analysis of the suggested formula.

***Theorem 5* (Snyder, 1966)**

The sum of the absolute values of all the disregarded coefficients serves as a boundary for the inaccuracy in approximating X(t) by the sum of its first m terms. If $X_z(t) = \sum_{k=0}^{z} c_k T_k(t)$, (28)

$E_T(z) = |X(t) - X_z(t)| \leq \sum_{k=z+1}^{\infty} |c_k|$,

$t \in [-1, 1]$.

To solve the model using the SCSC method. The main steps of the procedure solution can be summarized as follows

Step (1): we first approximation $S(t), I(t), R(t), Q(t)$ and *C(t)* by using *N* terms of $S_m(t)$, $I_m(t)$, $C_m(t)$, $Q_m(t)$ and $R_m(t)$.

$$S_m(t) = \sum_{m=0}^{h} a_m T_m^*(t),$$

$$I_m(t) = \sum_{m=0}^{h} b_m T_m^*(t),$$

$$C_m(t) = \sum_{m=0}^{h} f_m T_m^*(t), \qquad (29)$$

$$Q_m(t) = \sum_{m=0}^{h} d_m T_m^*(t),$$

$$R_m(t) = \sum_{m=0}^{h} e_m T_m^*(t),$$

Where, a_m, b_m, f_m, d_m and e_m are constants to be determined. By applying this approximation to the ***SICQR*** model we obtain

$$\sum_{m=0}^{h} a_m T_m'^*(t) = -\beta \sum_{m=0}^{h} b_m T_m^*(t) \sum_{m=0}^{h} a_m T_m^*(t) - [\alpha + \mu] \sum_{m=0}^{h} a_m T_m^*(t) + [1-\theta]\Lambda,$$

$$\sum_{m=0}^{h} b_m T_m'^*(t) = \beta \sum_{m=0}^{h} b_m T_m^*(t) \left[\sum_{m=0}^{h} a_m T_m^*(t) + \sigma \sum_{m=0}^{h} f_m T_m^*(t) \right] - [\mu + \delta + b] \sum_{m=0}^{h} b_m T_m^*(t),$$

$$\sum_{m=0}^{h} f_m T_m'^*(t) = -\beta\sigma \sum_{m=0}^{h} b_m T_m^*(t) \sum_{m=0}^{h} f_m T_m^*(t) + \alpha \sum_{m=0}^{h} a_m T_m^*(t) - \mu \sum_{m=0}^{h} f_m T_m^*(t),$$

$$\sum_{m=0}^{h} d_m T_m'^*(t) = \delta \sum_{m=0}^{h} b_m T_m^*(t) - (\gamma + \mu) \sum_{m=0}^{h} d_m T_m^*(t),$$

$$\sum_{m=0}^{h} e_m T_m'^*(t) = \gamma \sum_{m=0}^{h} d_m T_m^*(t) - \mu \sum_{m=0}^{h} e_m T_m^*(t) + \theta \Lambda$$

, (30)

For m=0,1,..., 5, the initial conditions give equations as follows

$\sum_{m=0}^{h} (-1)^m a_m = S_0$, $\sum_{m=0}^{h} (-1)^m b_m = I_0$,

$\sum_{m=0}^{h} (-1)^m f_m = C_0$,

$\sum_{m=0}^{h} (-1)^m d_m = Q_0, \sum_{m=0}^{h} (-1)^m e_m = R_0$,

(31)

Step (2): Collocate Eq.(30) at the 5*h* points. For a suitable collocation points, use the of the SCSC roots T_h^*.

Step (3): An algebraic system is represented by the equations derived in step 2 and the initial conditions with 5(h+1) of unknowns.

The numerical solutions obtained by the SCSC method show the spread of the virus among the general public. Mathematic 11 was used to create all of the codes. The parameter values used are

μ = 0.04, θ = 0.3, Λ = 0.1, σ = 0.15,

δ = 0.09, γ = 0.1, β = 4.2,

α = 0, 0.5, 0.9, 1.5, b=0.002 ,

$S(0)$ = 0.5, $I(0)$ = 0.2, $C(0)$ = 0, $Q(0)$ = 0, $R(0)$ = 0.3.

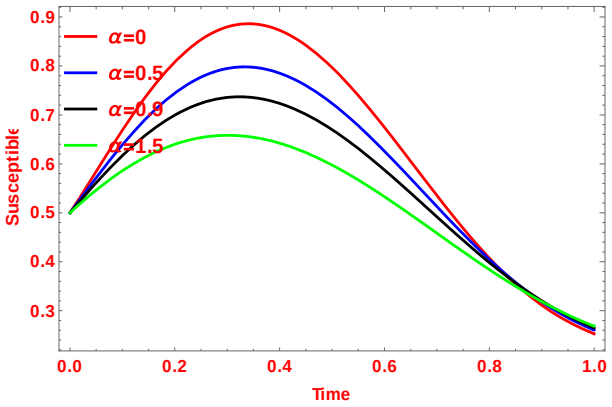

Fig. (2): The impact of changing α on susceptible

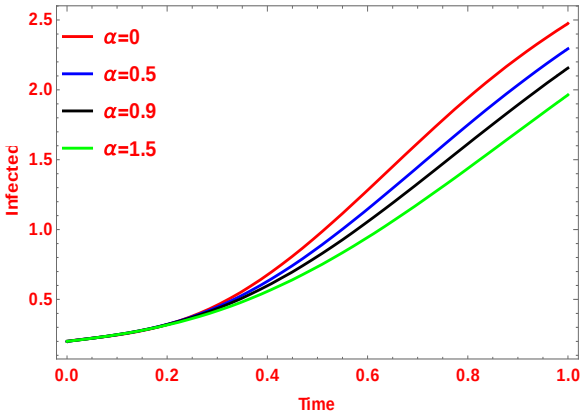

Fig. (3): The influence of various α values on infected

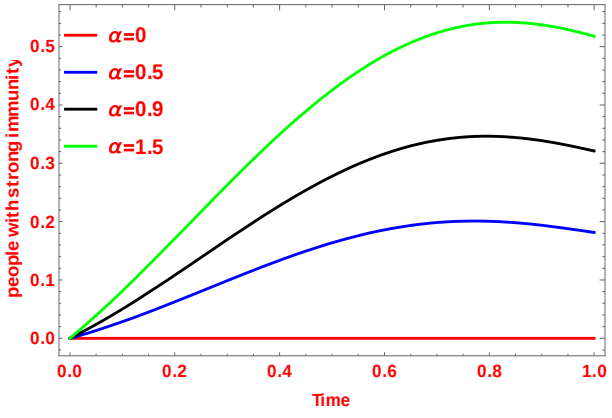

Fig. (4): The influence of various α values on people with strong immunity

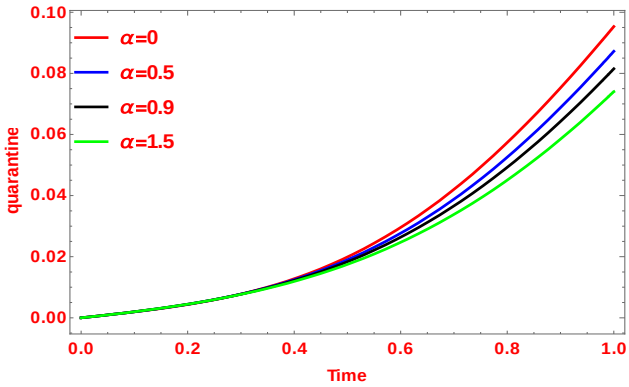

Fig. (5): The influence of various α values on quarantines

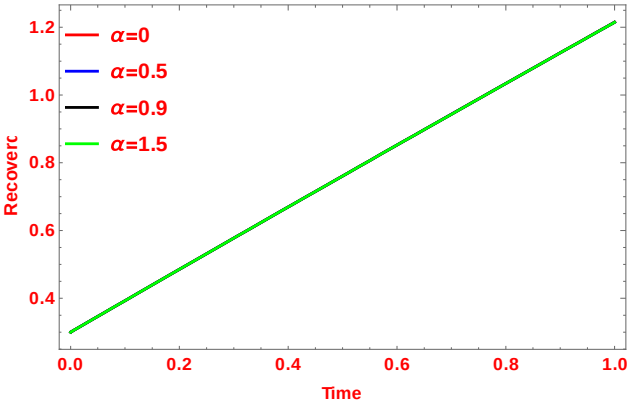

Fig. (6): The influence of various α values on recovered

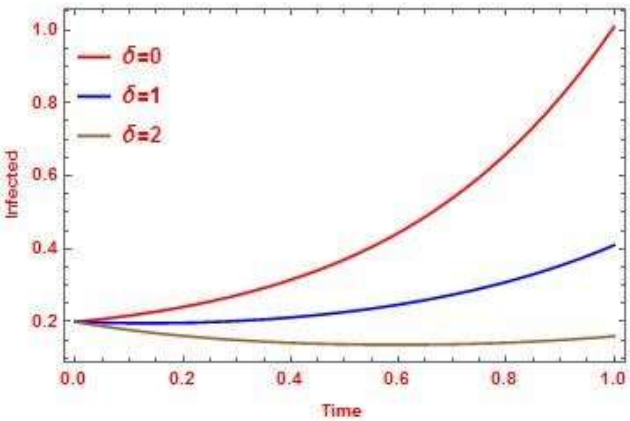

Fig. (7): The impact of isolation rate on the infected people

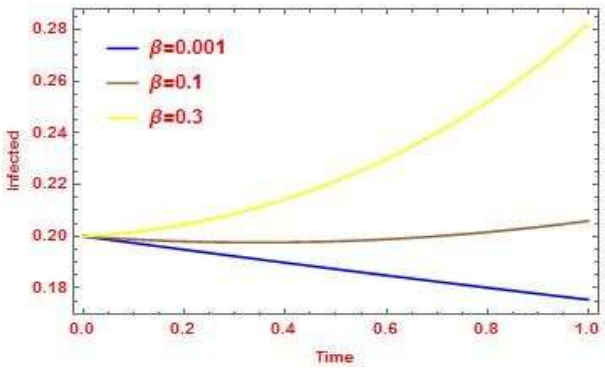

Fig. (8): Contact rate's effect on the infected people

Figure (2) represents the relationship between susceptible individuals when α values change over time. We notice that the number of susceptible people gets smaller with time. When $\alpha = 0$ the number of susceptible individuals was as large as possible. When α = 0.5, the number of susceptible individuals decreased as indicated by the blue curve. By increasing the value of α from 0 to 1.5, as shown by the green curve the number of susceptible individuals decreases until it becomes a small number. Figures 2 to 6 show the importance of strong immunity and its importance in controlling the spread of disease. One can see from figures 3, 4, 5, and 6 that by increasing the value of α the number of infected and quarantine decreases with time, but the number of recoveries is unaffected. These figures show the importance of strong immunity and its importance in controlling the spread of disease. Strong immunity helps individuals resist and recover from disease and reduces the chance of transmission of the disease from one person to another. In infectious diseases, the number of susceptible people plays a significant role in the disease's transmission and development into an epidemic. It is necessary to use medication or vaccination to strengthen susceptible people's immunity.

Initially, when α = 0 (no treatment) became $R_0 = 55.6 > 1$, the illness was clearly spreading quickly and becoming an epidemic gradually. The value of R_0 declines as α is increased and the number of infected and susceptible persons decreases.

Conclusions and Remarks

Studying infectious diseases, especially COVID-19, is crucial for understanding their transmission, developing effective treatments, and implementing preventive measures. This knowledge helps in controlling outbreaks, protecting public health, and advancing medical science to be better prepared for future challenges. A class of SIR modeling with vital behavior and a bounding community has been introduced in this paper. The SICQR model has been offered as a mathematical model for infectious diseases such as (COVID-19). According to qualitative analysis, the SICQR model has two equilibrium cases: equilibrium diseases free E_0 and

equilibrium endemic E^*. The stability revealed that E_0 was local and global asymptotically stable whenever R_0 <1. Unlike E^* it was global and local asymptotically stable whenever R_0 >1. The SICQR model has been resolved using the SCSC method. This method has the ability to transform the system under study into an algebraic system of equations, which is easy to solve by using any iterative methods. Graphical illustrations of the outcomes are given. The numerical analysis with various values for the parameter α was estimated to explain the importance of strong immunity in disease control. The mathematic software was used for computing mathematical simulations.

References

Ahmed, I., Modu, G. U., Yusuf, A., Kumam, P., and Yusuf, I. (2021). A mathematical model of coronavirus disease (COVID-19) containing asymptomatic and symptomatic classes. *Results Phys*., 21: 103776.

Alshammari, F. S., and Khan, M. A. (2021). Dynamic behaviors of a modified SIR model with nonlinear incidence and recovery rates. Alexandria Engineering Journal. 60(3): 2997-3005.

Anderson, R. M., and May, R. M. (1998). Infectious Diseases of Humans: Dynamics and Central oxford.

Arrowsmith, D. K. (1983). Place C.M. Ordinary differential equations, series 2. Chapman and Hall. 26: 287-288.

Bailey, N. T. J. (1975). The Mathematical Theory of Infectious Disease Griffin. London.

Blackwood, J. C., and Childs, L. M. (2018). An introduction to compartmental modeling for the budding infectious disease modeler. *Let. Biomath.*, 5(1): 195-221.

Boyce, W. E., and Diprima, R. C. (2012). Elementary Differential equations and Boundary Value problems. 10th ed. Wiley PLUS .

Brauer, F., and Castillo-Chavez, C. (2001). Mathematical models in population biology and epidemiology. *Springer-Verlag*., 40:xxiv+-416.

Canfell, K., Chesson, H., Kulasingam, S. L., Berkhof, J., Diaz, M., and Kim J.J. (2012). Modeling preventative strategies against human papillomavirus-related disease in developed countries Vaccine. 30 (suppl. 5): F157-F167.

Das, A., Pal, M. (2018). A mathematical study of an imprecise SIR epidemic model with treatment control. *Appl. Math Comput*., 56: 477-500.

Derrick, W. R., Grossman, S. I. (1976). Elementary Differential Equations With Applications. Addison-Wesley Series in Mathematics.

Diekmann, O., Heesterbeek, J. A. P., and Metz, J. A. J. (1990). On the definition and the computation of the basic reproduction ratio *R*0 in models for infectious diseases in heterogeneous populations. *J. Math. Biol.*, 28(4): 365–382.

Diekmann, O., Heesterbeek, J. A. P., and Roberts, M. G. (2009). The construction of next-generation matrices for compartmental epidemic models. J R Soc Interface,7(47):873-885.

Glendinning, P. (1994). Stability, Instability and Chaos An Introduction to the Theory of Nonlinear Differential Equations. Cambridge Texts in Applied Mathematics.

Hethcote, H. W., Lewis, M. A., and Driessche, V. D. (1989). An epidemiological model with a delay and a nonlinear incidence rate. *J. Math. Biol.*, 27(1): 49-64.

HethCote, H. W. (2000). The Mathematics of Infectious diseases. *Soc. Indus. App. Math.*, 42: 599-653.

Ibrahim, Y. F., Abd El-Bar, S. E., Khader, M. .M., and Adel, M. (2023). Studying and Simulating the Fractional COVID-19 Model Using an Efficient Spectral Collocation Approach. Fractal and Fractional. 7(4): 307.

Kermack, W. O., and McKendrick, A. G. (1927). A contribution to the mathematical theory of epidemics. Proc Royal Society of London. Series A, Containing Papersofa *Math. Phys. Character.*, 115(772): 700-721.

Khader, M. M., Sweilam, N. H. (2013). On the approximate solutions for system of fractional integro-differential equations using Chebyshev pseudo-spectral method. *Appl. Math. Model.*, 37(24): 9819–9828.

Khader, M. M., Babatin, M. M. (2014). Numerical treatment for solving fractional SIRC model and influenza *A. Comp. Appl. Math.*, 33: 543–556.

Kim, J. J., Brisson, M., Edmunds, W. J., and Goldie, S. J. (2008). Modeling cervical cancer prevention in developed countries Vaccine. 26 (suppl 10): K76-K86.

Kim, J. J. (2012). Modeling preventative strategies against human papillomavirus-related disease indeveloped countries Vaccine. 30 (suppl 05): F157-F167.

May, R. M.; Anderson, R. M. (1979). Population biology of infectious diseases. Part II. *Nature*, 280: 455-461.

Makinde, O. D. (2007). Adomian decomposition approach to a SIR epidemic model with constant vaccination strategy. *Appl. Math. Comput.* 184(2): 84.

Martcheva, M. (2015). An Introduction to Mathematical Epidemiology. Springer, New York.2-848.

Moghadas, S. M., and Gumel, A. B. (2003). A mathematical study of a model for childhood diseases with non-permanent immunity. *J. comput. Appl. Math.*, 153: 347-363.

Paul, S., Animesh, M., Supriya, M., and Banamali, R. (2022). Dynamics of SIQR epidemic model with fractional order derivative. *Partial Differ. Equ. Appl. Math.*, 5(6): 1-12.

Shereen, M. A., and Khan, S., Kazmi A., Bashir, N., Siddique, R. (2020). COVID-19 Infection: origin, transmission, and characteristics of human corona viruses. *J. Adv. Res.*,16 (24): 91-98.

Snyder, M. A. (1966). Chebyshev Methods in Numerical Approximation. Prentice-Hall, Inc.: Englewood Cliffs, NJ, USA.

Tyrrell, D. A., and Bynoe, M. L. (1998). Cultivation of viruses from a high proportion of patients with colds. *Lancet*, (8): 76-83.

دراسة عددية ونوعية لنموذج الوباء S I C Q R

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يتناول البحث الحالى شرح لنموذج SICQR غير الخطي ديناميكيات انتقال الأمراض المعدية في المجتمع. يحتوي هذا النموذج على خمس أقسام وبائية: الفئه المعرضه والفئه المصابه والأفراد ذوي المناعة القوية و الفئه المعزوله فى الحجر الصحي والمتعافين. و يمتلك النموذج المقترح حالات توازن مختلفة كتوازن متوطن وتوازن خالي من الأمراض. يصف هذا النموذج أهمية المناعة القوية لأفراد المجتمع للسيطرة على انتشار وباء كوفيد-١٩. تم استخدام تقنية (SCSC) للنموذج المقترح لإيجاد الحلول العددية للنموذج المطلوب. وأوضحت نتائج البحث وجود تأثير ايجابى لتقوية مناعة أفراد المجتمع فى السيطرة على انتشار المرض.