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Numerical Solution of COVID -19 model of Fractional order showing impact of Immunity Booster

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ABSTRACT
The purpose of this study is to discuss the mathematical model of COVID-19 with the impact of immunity booster (Vitamins and Minerals) to minimize the risk of infection and improve the recovery rate. The immune system is a barrier to dealing with the novel corona virus because with stronger immunity COVID-19 can bring minor symptoms or no symptoms. In the present study, the SEQBAIR model is proposed to analyze the COVID-19 pandemic using the fractional differential equation of various order. The authors have used Atangana Baleanu fractional-order derivative to develop the model and have provided its approximate solution by Lagrange's two-point polynomial. In the presented model, the basic reproduction number is calculated. The local asymptotic stability and endemic equilibria were derived for the fractional-order model. The validation of the model is represented using the real COVID-19 data for India in MATLAB programming.
Keywords: *COVID-19, Basic reproduction number, Immunity booster, Fractional order derivative, MATLAB programming.*

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INTRODUCTION

The first patient of COVID-19 was reported in Wuhan city of China in Dec-2019. This virus soon began to spread all around the world. WHO declared COVID -19 as a pandemic on March 11, 2020[19].222 countries and territories have been affected by corona virus. Worldwide 259M reported cases and 5.1M reported deaths due to corona virus and 234M recovered cases are reported till 24 Nov 2021[1].The corona virus transmitted through human to human (measured with density of population) and airborne viral infectivity [10].Transmission of the virus is mainly through droplets from the nose and mouth of an infected person; once a person inhales the droplets spread by an infected individual (coughs or sneezes) in the air, he will be exposed to the danger of getting infected [5]. People with low immunity like aged ones, people with severe diseases, and children are at high risk of getting infected; hence the best way to minimize the risk of infection is to maintain social distancing and increase intake of some nutrients in diet or supplements of vitamins to boost the immune system [9].An infected person has the symptoms such as fever, breathing difficulty, weakness, cough, loss of taste and smell, and other symptoms (such as gastroenteritis and neurological disease).

Rapidly increase in the number of cases, many countries have imposed lockdown to prevent the spread of corona virus [19].Lockdown has a significant economic damage to the world [3]. To overcome this crisis government decided to remove the lockdown, which further leads to another wave of COVID-19. In this situation, development of immunity level in the human body for resisting the corona virus as an alternative solution before invention of registered medicine[9].Now a days, COVID-19 vaccine is available but vaccination alone is not sufficient to control COVID-19.

The immune system produces antibodies to kill pathogens and protect against viruses. According to WHO, healthy foods, vitamins, minerals and hydration are vital for strong immune system and have a reduced risk of infectious diseases. Along with diet, regular physical exercise also boosts the immune system. The immunity booster plays a vital role in the transmission of COVID-19.

Mathematical modeling is implemented in many fields such as medicine [23], agriculture ([11], [22]), management, and social sciences [18]. Mathematical models are used in epidemiologic research, planning, and evaluation of preventive and control activities, clinical trials, health monitoring, cost-benefit analysis,

and patient diagnosis in the health sector [23].In [19], Panchal and Acharya have given a fractional order SEQAIR mathematical model on impact of quarantine to control the transmission of corona virus.
Bahloul and *et. al* [8], presented fractional order SEIQRDP model for estimating the transmissibility of the COVID-19 by including death and insusceptible class.
Atangana and Baleanu [7], proposed a new fractional derivative operator with non-local and non - singular kernel. Also, new advances and studies for the fractional differential equation have been published from a mathematical modeling point of view in ([3], [5], [7], [9]).
As COVID-19 vaccines are being deployed worldwide, authors formulated model [12] from those pharmaceutical measures such as vaccination and treatment, transmission of COVID-19 can be controlled by taking some other immunity booster[14].
In this paper, Section 2, model formulation is given. In Section 3, the stability analysis of the model is given in terms of basic reproduction number, local asymptotically stable and endemic equilibria. In Section 4, the Atangana Baleanu fractional derivative to develop the SEQBAIR model and provided its numerical solution by Lagrange's two-pointpolynomial method [21]. and In Section 5, the model is validated using real COVID-19 data for India using MATLAB programming and discussed the effect of various values of the parameters graphically. Finally, the conclusion is given in Section 6.

MODEL FORMULATION

In this section, the immunity booster compartment is taken as an extension in the SEQAIR model [19] given by Panchal and Acharya and the SEQBAIR model is developed. Total Population *N(t)* is divided into seven sub classes*. S(t):* Susceptible cases, *E(t):* Exposed cases, *Q(t):* Quarantine, *B(t):* Immunity booster, *A(t):* Asymptomatically infected, *I(t):* Symptomatically infected, *R(t):* Recovered or removed.

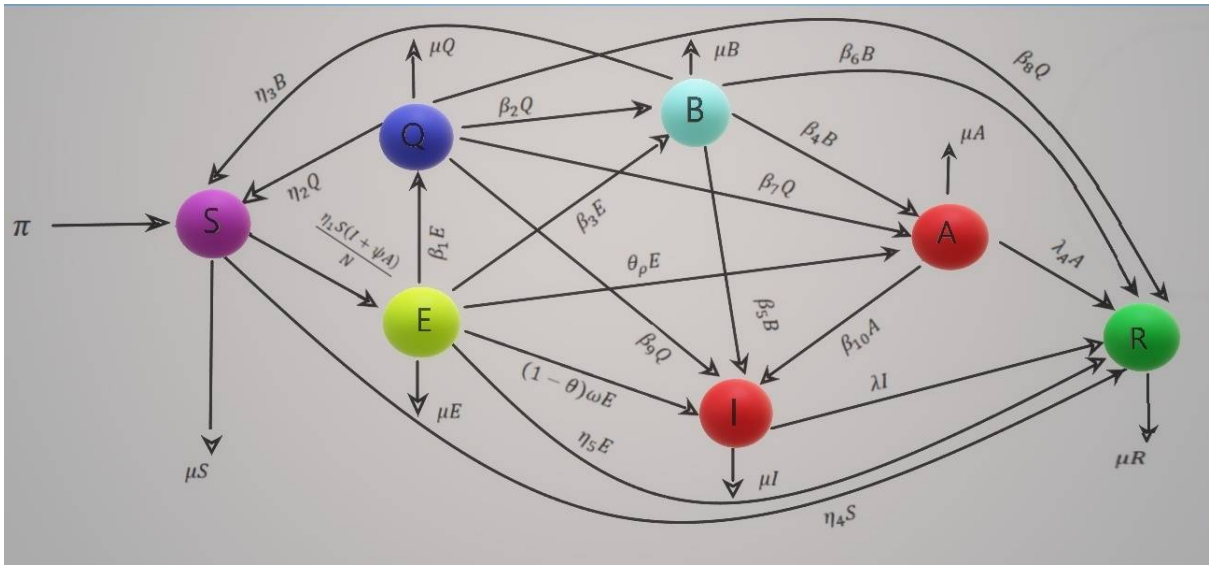

Figure 1: Graphical representation of transmission dynamics of COVID -19.

The dynamical system of the COVID-19 model on impact of immunity booster is given by

$$\left.\begin{aligned}
\frac{dS}{dt} &= \pi + \eta_2 Q + \eta_3 B - \frac{\eta_1 S(I+\psi A)}{N} - \eta_4 S - \mu S \\
\frac{dE}{dt} &= \frac{\eta_1 S(I+\psi A)}{N} - (\beta_1 + \beta_3 + \theta_\rho + \eta_5 + (1-\theta)\omega)E - \mu E \\
\frac{dQ}{dt} &= \beta_1 E - (\eta_2 + \beta_2 + \beta_7 + \beta_9 + \beta_8)Q - \eta_3 B - \mu Q \\
\frac{dB}{dt} &= \beta_3 E + \beta_2 Q - (\beta_4 + \beta_6 + \beta_5)B - \mu B \\
\frac{dA}{dt} &= \beta_7 Q + \beta_4 B + \theta_\rho E - \lambda_A A - \beta_{10} A - \mu A \\
\frac{dI}{dt} &= \beta_9 Q + \beta_5 B + \beta_{10} A + (1-\theta)\omega E - \lambda I - \mu I \\
\frac{dR}{dt} &= \beta_8 Q + \beta_6 B + \lambda_A A + \lambda I + \eta_4 S + \eta_5 E - \mu R
\end{aligned}\right\} \quad (2.1)$$

with initial conditions
$S(0) \geq 0, E(0) \geq 0, Q(0) \geq 0, B(0) \geq 0, A(0) \geq 0, I(0) \geq 0, R(0) \geq 0.$
By adding all seven equations of the model (2.1),The dynamics of the total population is given by

$$\frac{dN}{dt} = \pi - \mu N.$$

The birth and natural death rate of an individual are denoted by π and μ respectively. The susceptible people *S* gets infected through sufficient contacts with the infected people *I* given by the term $\eta_1 SI$, where η_1 denotes the disease transmission coefficient. As discussed earlier, the symptoms of corona virus do not reflect immediately which increases the number of asymptomatically infected people as well as can spread the virus to healthy people and the transmission is given by $\eta_1 \psi SA$, where ψ is the transmissibility multiple of *A* to *I* and ψ=[0,1]. When ψ= 0 then there will be no infection, and when ψ=1, then the infection will be same as *I*. θ represents the proportion of asymptomatic infection. The parameters ω and ρ respectively represent the transmission rate after completing the incubation period and become infected, joining the class *I* and *A*. Before joining infected class,some individual of class *E* joined *Q* due to close contact of infected individual with transmission rate β_1, then*Q* and *E* joined immunity booster class with transmission rate β_2 and $\beta_3$respectively to boosting immunity and Some people of class *B* joined *A*,*I*as well as*S*with rate of transmissionβ_4,$\beta_5$and$\eta_3$respectively. Asymptomatic class can join infected class with rateβ_{10}.A can join directly *R* without joining *I* with rate λ_A .*I* joined *R* with rate λ .*S,E,B,* and *Q*directly join recovered class without getting infected with rate of transmission η_4, η_5 , β_6,and β_8 respectively. Each class remove people die with natural death rate μ.
Detail of rate of transmission given as below.
β_1: The rate of exposed people taken self-quarantines or quarantine due to contact with the infected individual.
η_2: The rate at which quarantine individual transfer to susceptible class.
β_2: The rate at which quarantine individual started to take immunity booster.
η_3: The rate at which quarantine or exposed individual taking immunity booster transfer to susceptible class.
η_4 : The rate at which susceptible individual join recovered class.
η_5 : The rate at which exposed individual join recovered class.
β_3: The rate at which exposed individual started to take immunity booster.
β_4: The rate at which individual taking immunity boostertransfer to asymptotic class.
β_5 : The rate at which individual taking immunity booster transfer to infected class.
β_6 : The rate at which individual taking immunity booster join to recovered class.
β_7 : The rate at which quarantine individual transfer to asymptotic class.
β_9 : The rate at which quarantine individual transfer to infected class.
β_8 : The rate at which quarantine individual join recovered class.
β_{10}: The rate at which asymptotic individual transfer to infected class.
λ_A : The rate at which asymptotic individual join recovered class.
λ: The rate at which infected individual join recovered class.
Let us consider a positive invariant feasible region such that the solution of the system (2.1) is in this feasible region

$$\Omega = \left\{(S,E,Q,B,A,I,R) \in R_+^7 : \ S+E+Q+B+A+I+R = N \leq \frac{\pi}{\mu}\right\}. \qquad \ldots\ldots (2.2)$$

All the parameters of model are non- negative.

1. Stability analysis:

For the stability of result, let us define disease free equilibrium E_0 and the basic reproduction number $\Re_0$[20].
$E_0 = (S_0, 0, 0, 0, 0, 0, 0) = \left(\frac{\pi}{\mu}, 0,0,0,0,0,0\right)$.
To compute the basic reproduction number $\Re_0$ for given system (2.1) computation of matrices *F* and *V* is given by

$$F = \begin{pmatrix} 0 & 0 & 0 & \eta_1\psi & \eta_1 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V=\begin{pmatrix} \beta_1+\beta_3+\theta_\rho+(1-\theta)\omega+\eta_5+\mu & 0 & 0 & 0 & 0 \\ -\beta_1 & \eta_2+\beta_2+\beta_7+\beta_9+\beta_8+\mu & 0 & 0 & 0 \\ -\beta_3 & -\beta_2 & \beta_4+\beta_6+\beta_5+\eta_3+\mu & 0 & 0 \\ -\theta_\rho & -\beta_7 & -\beta_4 & \lambda_A+\beta_{10}+\mu & 0 \\ -(1-\theta)\omega & -\beta_9 & -\beta_5 & -\beta_{10} & \lambda+\mu \end{pmatrix}$$

The basic reproduction number of the system (2.1), is given as

$$\Re_0=\frac{\begin{array}{l}(\eta_1\psi(\lambda+\mu)(\beta_1\beta_2\beta_4+(\beta_1\beta_7+\theta_\rho)(\beta_4+\beta_6+\beta_5+\eta_3+\mu)+\beta_3\beta_4(\eta_2+\beta_2+\beta_7+\beta_9+\beta_8+\mu))+\eta_1(\beta_1\beta_2\beta_4\beta_{10}+(\lambda_A+\beta_{10}+\mu)\\ (\beta_1\beta_2\beta_5+\beta_1\beta_9(\beta_4+\beta_6+\beta_5+\eta_3+\mu)+\beta_3\beta_5(\eta_2+\beta_2+\beta_7+\beta_9+\beta_8+\mu)+(\beta_4+\beta_6+\beta_5+\eta_3+\mu)(\eta_2+\beta_2+\beta_7+\beta_9+\beta_8+\mu)(1-\theta)\omega)\\ +(\eta_2+\beta_2+\beta_7+\beta_9+\beta_8+\mu)(\beta_3\beta_4\beta_{10}+\theta_\rho\beta_{10}(\beta_4+\beta_6+\beta_5+\eta_3+\mu))+\beta_1\beta_7\beta_{10}(\beta_4+\beta_6+\beta_5+\eta_3+\mu)))\end{array}}{(\beta_1+\beta_3+\theta_\rho+(1-\theta)\omega+\eta_5+\mu)(\eta_2+\beta_2+\beta_7+\beta_9+\beta_8+\mu)(\beta_4+\beta_6+\beta_5+\eta_3+\mu)(\lambda_A+\beta_{10}+\mu)(\lambda+\mu)}$$

where spectral radius is $\gamma(FV^{-1})$and using parameter values given in table 1, we obtained$\Re_0$= 1.048154. Next, we will be discussing stability for disease free equilibrium point using concept of eigen values. TheJacobian matrix of system (2.1) is given by

$$J=\begin{pmatrix} -(\eta_4+\mu) & 0 & \eta_2 & \eta_3 & -\eta_1\psi & -\eta_1 & 0 \\ 0 & -(\beta_1+\beta_3+\theta_\rho+(1-\theta)\omega+\eta_5+\mu) & 0 & 0 & \eta_1\psi & \eta_1 & 0 \\ 0 & \beta_1 & -(\beta_2+\beta_7+\eta_2+\beta_9+\beta_8+\mu) & 0 & 0 & 0 & 0 \\ 0 & \beta_3 & \beta_2 & -(\beta_4+\beta_5+\beta_6+\eta_3+\mu) & 0 & 0 & 0 \\ 0 & \theta_\rho & \beta_7 & \beta_4 & -(\lambda_A+\beta_{10}+\mu) & 0 & 0 \\ 0 & (1-\theta)\omega & \beta_9 & \beta_5 & \beta_{10} & -(\lambda+\mu) & 0 \\ \eta_4 & \eta_5 & \beta_8 & \beta_6 & \lambda_A & \lambda & -\mu \end{pmatrix}$$

and the eigen values for above Jacobian matrix about disease free equilibrium point are
-0.0073, -0.2273, 0.0358,-0.6237, -1.8507, -1.8507, -2.2868.

A system is stable if and only if all the system's eigen values have negative real parts, so looking at above eigen values it is clear that the system is unstable because one eigen value has positive real part. Hence, the equilibrium point is not locally asymptotically stable [2].

Endemic equilibrium:

The endemic equilibrium of the model (2.1) is denoted by

$$E_0^*=(S^*,E^*,Q^*,B^*,A^*,I^*,R^*)$$

where,

$$S^*=\frac{\pi}{\lambda^*+\mu}$$

$$E^*=\frac{\lambda^* S^*}{\beta_1+\beta_3+\theta_\rho+\eta_5+(1-\theta)\omega}$$

$$Q^*=\frac{\beta_1 E}{\eta_2+\beta_2+\beta_7+\beta_9+\beta_8}$$

$$A^*=\frac{\beta_7 Q+\beta_4 B+\theta_\rho E}{\lambda_A+\beta_{10}+\mu}$$

$$B^*=\frac{\beta_3 E+\beta_2 Q}{\beta_4+\beta_6+\beta_5}$$

$$I^*=\frac{\beta_9 Q+\beta_5 B+\beta_{10} A+(1-\theta)\omega E}{\lambda+\mu}$$

$$R^*=\frac{\beta_8 Q+\beta_6 B+\lambda_A A+\lambda I+\eta_4 S+\eta_5 E}{\mu}$$

and

$$\lambda^*=\frac{\eta_1(\psi A^*+I^*)}{S^*+E^*+Q^*+B^*+A^*+I^*+R^*}$$

which satisfies the equation $P(\lambda^*)=m_1(\lambda^*)^2+m_2\lambda^*=0$, m_1 and m_2 are given by

$$m_1=(\beta_1+\beta_3+\theta_\rho+\eta_5+(1-\theta)\omega)(\eta_2+\beta_2+\beta_7+\beta_9+\beta_8)(\lambda_A+\beta_{10}+\mu)(\beta_4+\beta_6+\beta_5)(\lambda+\mu)$$

$m_2 = (\beta_1 + \beta_3 + \theta_\rho + \eta_5 + (1-\theta)\omega)(\eta_2 + \beta_2 + \beta_7 + \beta_9 + \beta_8)(\lambda_A + \beta_{10} + \mu)(\beta_4 + \beta_6 + \beta_5)(\lambda + \mu)$
$(1 - \Re_0)$

Obviously, $m_1 \geq 0$ and $m_2 \geq 0$ whenever $\Re_0 < 1$, so that $\lambda^* = \frac{-m_2}{m_1} \leq 0$ when $\Re_0 < 1$, the endemic equilibrium does not exists.

Fractional -order Model

Generalization of this model by applying Atangana-Baleanu fractional derivative in Caputo sense and obtain the Model [13].

$^{ABC}_{0}D_t^{\alpha} S(t) = \pi + \eta_2 Q(t) + \eta_3 B(t) - \frac{\eta_1 S(t)(I(t)+\psi A(t))}{N} - \eta_4 S(t) - \mu S(t)$
$^{ABC}_{0}D_t^{\alpha} E(t) = \frac{\eta_1 S(t)(I(t)+\psi A(t))}{N} - (\beta_1 + \beta_3 + \theta_\rho + \eta_5 + (1-\theta)\omega)E(t) - \mu E(t)$
$^{ABC}_{0}D_t^{\alpha} Q(t) = \beta_1 E(t) - (\eta_2 + \beta_2 + \beta_7 + \beta_9 + \beta_8)Q(t) - \eta_3 B(t) - \mu Q(t)$
$^{ABC}_{0}D_t^{\alpha} B(t) = \beta_3 E(t) + \beta_2 Q(t) - (\beta_4 + \beta_6 + \beta_5)B(t) - \mu B(t)$
$^{ABC}_{0}D_t^{\alpha} A(t) = \beta_7 Q(t) + \beta_4 B(t) + \theta_\rho E(t) - \lambda_A A(t) - \beta_{10} A(t) - \mu A(t)$
$^{ABC}_{0}D_t^{\alpha} I(t) = \beta_9 Q(t) + \beta_5 B(t) + \beta_{10} A(t) + (1-\theta)\omega E(t) - \lambda I(t) - \mu I(t)$
$^{ABC}_{0}D_t^{\alpha} R(t) = \beta_8 Q(t) + \beta_6 B(t) + \lambda_A A(t) + \lambda I(t) + \eta_4 S(t) + \eta_5 E(t) - \mu R(t)$

Definition of fractional derivative and integral:

Let the function be *g(t)* and $0 \leq \alpha \leq 1$ then representation of Atangana Balenau derivative is given by

$^{ABC}_{a}D_t^{\alpha} g(t) = \frac{C(\alpha)}{1-\alpha}\int_a^t g(k)E_\alpha$

$C(\alpha)$ is normalization function.

Integral is given by

$^{ABC}_{a}I_t^{\alpha} g(t) = \frac{1-\alpha}{C(\alpha)} g(t) + \frac{\alpha}{C(\alpha)\Gamma\alpha}\int_0^t g(y)(t-y)^{\alpha-1}dy$

Solution of (SEQBAIR) model is given by

$S(t) - S(0) = \frac{1-\alpha}{C(\alpha)}\{\pi + \eta_2 Q(t) + \eta_3 B(t) - \frac{\eta_1 S(t)(I(t)+\psi A(t))}{N} - \eta_4 S(t) - \mu S(t)\}$
$+ \frac{\alpha}{C(\alpha)\Gamma\alpha}\int_0^t (t-k)^{\alpha-1}\{\pi + \eta_2 Q(k) + \eta_3 B(k) - \frac{\eta_1 S(k)(I(k)+\psi A(k))}{N} - \eta_4 S(k) - \mu S(k)\}dk$

$E(t) - E(0) = \frac{1-\alpha}{C(\alpha)}\left\{\frac{\eta_1 S(t)(I(t)+\psi A(t))}{N} - (\beta_1 + \beta_3 + \theta_\rho + \eta_5 + (1-\theta)\omega)E(t) - \mu E(t)\right\} + \frac{\alpha}{C(\alpha)\Gamma\alpha}\int_0^t (t-k)^{\alpha-1}\left\{\frac{\eta_1 S(k)(I(k)+\psi A(k))}{N} - (\beta_1 + \beta_3 + \theta_\rho + \eta_5 + (1-\theta)\omega)E(k) - \mu E(k)\right\}dk$

$Q(t) - Q(0) = \frac{1-\alpha}{C(\alpha)}\{\beta_1 E(t) - (\eta_2 + \beta_2 + \beta_7 + \beta_9 + \beta_8)Q(t) - \eta_3 B(t) - \mu Q(t)\}$
$+ \frac{\alpha}{C(\alpha)\Gamma\alpha}\int_0^t (t-k)^{\alpha-1}\{\beta_1 E(k) - (\eta_2 + \beta_2 + \beta_7 + \beta_9 + \beta_8)Q(k) - \eta_3 B(k) - \mu Q(k)\}dk$

$B(t) - B(0) = \frac{1-\alpha}{C(\alpha)}\{\beta_3 E(t) + \beta_2 Q(t) - (\beta_4 + \beta_6 + \beta_5)B(t) - \mu B(t)\}$
$+ \frac{\alpha}{C(\alpha)\Gamma\alpha}\int_0^t (t-k)^{\alpha-1}\{\beta_3 E(k) + \beta_2 Q(k) - (\beta_4 B + \beta_6 B + \beta_5)B(k) - \mu B(k)\}dk$

$A(t) - A(0) = \frac{1-\alpha}{C(\alpha)}\{\beta_7 Q(t) + \beta_4 B(t) + \theta_\rho E(t) - \lambda_A A(t) - \beta_{10} A(t) - \mu A(t)\}$
$+ \frac{\alpha}{C(\alpha)\Gamma\alpha}\int_0^t (t-k)^{\alpha-1}\{\beta_7 Q(k) + \beta_4 B(k) + \theta_\rho E(k) - \lambda_A A(k) - \beta_{10} A(k) - \mu A(k)\}dk$

$I(t) - I(0) = \frac{1-\alpha}{C(\alpha)}\{\beta_9 Q(t) + \beta_5 B(t) + \beta_{10} A(t) + (1-\theta)\omega E(t) - \lambda I(t) - \mu I(t)\}$
$+ \frac{\alpha}{C(\alpha)\Gamma\alpha}\int_0^t (t-k)^{\alpha-1}\{\beta_9 Q(k) + \beta_5 B(k) + \beta_{10} A(k) + (1-\theta)\omega E(k) - \lambda I(k) - \mu I(k)\}dk$

$R(t) - R(0) = \frac{1-\alpha}{C(\alpha)}\{\beta_8 Q(t) + \beta_6 B(t) + \lambda_A A(t) + \lambda I(t) + \eta_4 S(t) + \eta_5 E(t) - \mu R(t)\}$
$+ \frac{\alpha}{C(\alpha)\Gamma\alpha}\int_0^t (t-k)^{\alpha-1}\{\beta_8 Q(k) + \beta_6 B(k) + \lambda_A A(k) + \lambda I(k) + \eta_4 S(k) + \eta_5 E(k) - \mu R(k)\}dk$

Using $t = t_{n+1}$, $n = 0,1,2\ldots\ldots$ in above equation leads to the system below:

$$\left.\begin{aligned}
S(t_{n+1})-\ S\ (0) &= \tfrac{1-\alpha}{C(\alpha)}\{H\ (t_n\ ,S)\} + \tfrac{\alpha}{C(\alpha)\Gamma\alpha}\textstyle\sum_{k=0}^{n}\int_{t_k}^{t_{k+1}} H(k,S)(t_{n+1}-k)^{\alpha-1})\ dk\\
E(t_{n+1})-\ E\ (0) &= \tfrac{1-\alpha}{C(\alpha)}\{H\ (t_n\ ,E)\} + \tfrac{\alpha}{C(\alpha)\Gamma\alpha}\textstyle\sum_{k=0}^{n}\int_{t_k}^{t_{k+1}} H(k,E)(t_{n+1}-k)^{\alpha-1})\ dk\\
Q(t_{n+1})-\ Q\ (0) &= \tfrac{1-\alpha}{C(\alpha)}\{H\ (t_n\ ,Q)\} + \tfrac{\alpha}{C(\alpha)\Gamma\alpha}\textstyle\sum_{k=0}^{n}\int_{t_k}^{t_{k+1}} H(k,Q)(t_{n+1}-k)^{\alpha-1})\ dk\\
B(t_{n+1})-B\ (0) &= \tfrac{1-\alpha}{C(\alpha)}\{H\ (t_n\ ,B)\} + \tfrac{\alpha}{C(\alpha)\Gamma\alpha}\textstyle\sum_{k=0}^{n}\int_{t_k}^{t_{k+1}} H(k,B)(t_{n+1}-k)^{\alpha-1})\ dk\\
A(t_{n+1})-\ A\ (0) &= \tfrac{1-\alpha}{C(\alpha)}\{H\ (t_n\ ,A)\} + \tfrac{\alpha}{C(\alpha)\Gamma\alpha}\textstyle\sum_{k=0}^{n}\int_{t_k}^{t_{k+1}} H(k,A)(t_{n+1}-k)^{\alpha-1})\ dk\\
I(t_{n+1})-\ I\ (0) &= \tfrac{1-\alpha}{C(\alpha)}\{H\ (t_n\ ,I)\} + \tfrac{\alpha}{C(\alpha)\Gamma\alpha}\textstyle\sum_{k=0}^{n}\int_{t_k}^{t_{k+1}} H(k,I)(t_{n+1}-k)^{\alpha-1})\ dk\\
R(t_{n+1})-\ R\ (0) &= \tfrac{1-\alpha}{C(\alpha)}\{H\ (t_n\ ,R)\} + \tfrac{\alpha}{C(\alpha)\Gamma\alpha}\textstyle\sum_{k=0}^{n}\int_{t_k}^{t_{k+1}} H(k,R)(t_{n+1}-k)^{\alpha-1})\ dk
\end{aligned}\right\} (4.1)$$

where

$H(t,S) = \pi + \eta_2 Q(t) + \eta_3 B(t) - \frac{\eta_1 S(t)(I(t)+\psi A(t))}{N} - \eta_4 S(t) - \mu S(t)$

$H(t, E) = \frac{\eta_1 S(t)(I(t)+\psi A(t))}{N} - (\beta_1 + \beta_3 + \theta_\rho + \eta_5 + (1-\theta)\omega)E(t) - \mu E(t)$

$H(t, Q) = \beta_1 E(t) - (\eta_2 + \beta_2 + \beta_7 + \beta_9 + \beta_8)Q(t) - \eta_3 B(t) - \mu Q(t)$

$H(t, B) = \beta_3 E(t) + \beta_2 Q(t) - (\beta_4 + \beta_6 + \beta_5)B(t) - \mu B(t)$

$H(t, A) = \beta_7 Q(t) + \beta_4 B(t) + \theta_\rho E(t) - \lambda_A A(t) - \beta_{10} A(t) - \mu A(t)$

$H(t, I) = \beta_9 Q(t) + \beta_5 B(t) + \beta_{10} A(t) + (1-\theta)\omega E(t) - \lambda I(t) - \mu I(t)$

$H(t, R) = \beta_8 Q(t) + \beta_6 B(t) + \lambda_A A(t) + \lambda I(t) + \eta_4 S(t) + \eta_5 E(t) - \mu R(t)$

Using two step Lagrange's polynomial for the simplification of integral (4.1),the following numerical scheme is obtained for coronavirus model.

$$S(t_{n+1}) = S(t_0) + \tfrac{1-\alpha}{C(\alpha)}\ H(t_n,S) + \tfrac{\alpha}{C(\alpha)}\textstyle\sum_{k=0}^{n} \frac{h^\alpha H(t_k\ ,S)}{\Gamma\alpha+2}\big((n+1-k)^\alpha(n-k+2+\alpha)$$
$$-\big(n-k)^\alpha(n-k+2+2\alpha)\big) - \frac{h^\alpha H(t_{k-1},S)}{\Gamma\alpha+2}(n+1-k)^{\alpha+1} - (n-k)^\alpha(n-k+1+\alpha)$$

$$E(t_{n+1}) = E(t_0) + \tfrac{1-\alpha}{C(\alpha)}\ H(t_n,E) + \tfrac{\alpha}{C(\alpha)}\textstyle\sum_{k=0}^{n} \frac{h^\alpha H(t_k\ ,E)}{\Gamma\alpha+2}\big((n+1-k)^\alpha(n-k+2+\alpha)$$
$$-\big(n-k)^\alpha(n-k+2+2\alpha)\big) - \frac{h^\alpha H(t_{k-1},E)}{\Gamma\alpha+2}(n+1-k)^{\alpha+1} - (n-k)^\alpha(n-k+1+\alpha)$$

$$Q(t_{n+1}) = Q(t_0) + \tfrac{1-\alpha}{C(\alpha)}\ H(t_n,Q) + \tfrac{\alpha}{C(\alpha)}\textstyle\sum_{k=0}^{n} \frac{h^\alpha H(t_k\ ,Q)}{\Gamma\alpha+2}\big((n+1-k)^\alpha(n-k+2+\alpha)$$
$$-\big(n-k)^\alpha(n-k+2+2\alpha)\big) - \frac{h^\alpha H(t_{k-1},Q)}{\Gamma\alpha+2}(n+1-k)^{\alpha+1} - (n-k)^\alpha(n-k+1+\alpha)$$

$$B(t_{n+1}) = B(t_0) + \tfrac{1-\alpha}{C(\alpha)}\ H(t_n,B) + \tfrac{\alpha}{C(\alpha)}\textstyle\sum_{k=0}^{n} \frac{h^\alpha H(t_k\ ,B)}{\Gamma\alpha+2}\big((n+1-k)^\alpha(n-k+2+\alpha)$$
$$-\big(n-k)^\alpha(n-k+2+2\alpha)\big) - \frac{h^\alpha H(t_{k-1},B)}{\Gamma\alpha+2}(n+1-k)^{\alpha+1} - (n-k)^\alpha(n-k+1+\alpha)$$

$$A(t_{n+1}) = A(t_0) + \tfrac{1-\alpha}{C(\alpha)}\ H(t_n,A) + \tfrac{\alpha}{C(\alpha)}\textstyle\sum_{k=0}^{n} \frac{h^\alpha H(t_k\ ,A)}{\Gamma\alpha+2}\big((n+1-k)^\alpha(n-k+2+\alpha)$$
$$-\big(n-k)^\alpha(n-k+2+2\alpha)\big) - \frac{h^\alpha H(t_{k-1},A)}{\Gamma\alpha+2}(n+1-k)^{\alpha+1} - (n-k)^\alpha(n-k+1+\alpha)$$

$$I(t_{n+1}) = I(t_0) + \tfrac{1-\alpha}{C(\alpha)}\ H(t_n,I) + \tfrac{\alpha}{C(\alpha)}\textstyle\sum_{k=0}^{n} \frac{h^\alpha H(t_k\ ,I)}{\Gamma\alpha+2}\big((n+1-k)^\alpha(n-k+2+\alpha)$$
$$-\big(n-k)^\alpha(n-k+2+2\alpha)\big) - \frac{h^\alpha H(t_{k-1},I)}{\Gamma\alpha+2}(n+1-k)^{\alpha+1} - (n-k)^\alpha(n-k+1+\alpha)$$

$$R(t_{n+1}) = R(t_0) + \tfrac{1-\alpha}{C(\alpha)}\ H(t_n,R) + \tfrac{\alpha}{C(\alpha)}\textstyle\sum_{k=0}^{n} \frac{h^\alpha H(t_k\ ,R)}{\Gamma\alpha+2}\big((n+1-k)^\alpha(n-k+2+\alpha)$$
$$-\big(n-k)^\alpha(n-k+2+2\alpha)\big) - \frac{h^\alpha H(t_{k-1},R)}{\Gamma\alpha+2}(n+1-k)^{\alpha+1} - (n-k)^\alpha(n-k+1+\alpha)$$

Table 1: Parameters used in model (2.1)

Parameters	Description	Value
π	Birth Rate.	0.017
μ	Natural mortality rate.	0.00734
θ	Proportion of Asymptomatic infection.	0.55
ω	Rate at which exposed individual becomes infected.	0.7606
ρ	Rate at which exposed individual becomes Asymptomatic infected.	0.55
η_1	Contact rate.	0.75
η_2	Rate at which Quarantine individual transfer to susceptible class.	0.42
η_3	rate at which individual taking immunity booster transfer to susceptible class.	0.25
η_4	Rate at which susceptible individual join recovered class.	0.22
η_5	Rate at which exposed individual join recovered class.	0.333
β_1	the rate of quarantine individual due to contact with the infected individual.	0.50
β_2	Rate at which quarantine individual started to take immunity booster (like medicine).	0.40
β_3	Rate at which exposed individual started to take immunity booster (like medicine).	0.452
β_4	Rate at which individual taking immunity booster transfer to asymptotic class.	0.510
β_5	Rate at which individual taking immunity booster transfer to infected class.	0.55
β_6	Rate at which individual taking immunity booster join to recovered class.	0.4
β_7	Rate at which quarantine individual transfer to asymptotic class.	0.4
β_8	Rate at which quarantine individual join recovered class.	0.375
β_9	Rate at which quarantine individual transfer to infected class.	0.45
β_{10}	Rate at which asymptotic individual transfer to infected class.	0.5312
λ_A	Rate at which asymptotic individual join recovered class.	0.2672
λ	Rate at which infected individual join recovered class.	0.465

Graphical representation of model

Graphical presentation of SEQBAIR model is given using MATLAB with various fractional order. For the graphical representation, the number of individuals is taken on *Y*-axis and time is consider on *X*-axis.

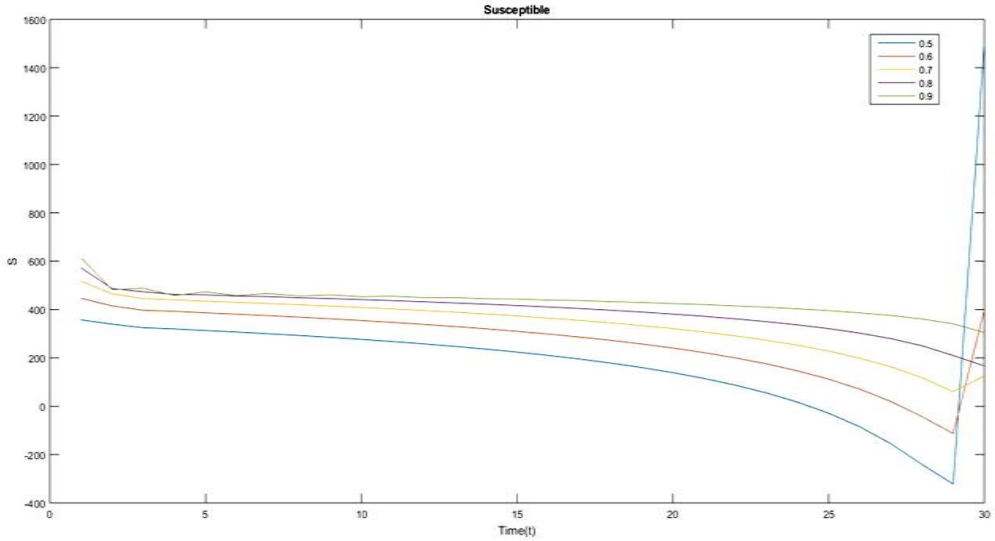

Figure 2:Number of Susceptible(S) individual vs.Time(t)

In Figure 2, reduction in η_1 due to self-quarantine decreases the number of susceptible individuals. And if η_1 increase due to mass gathering then number of susceptible individual increases. The number of susceptible individual will decreases with the increase in η_3.

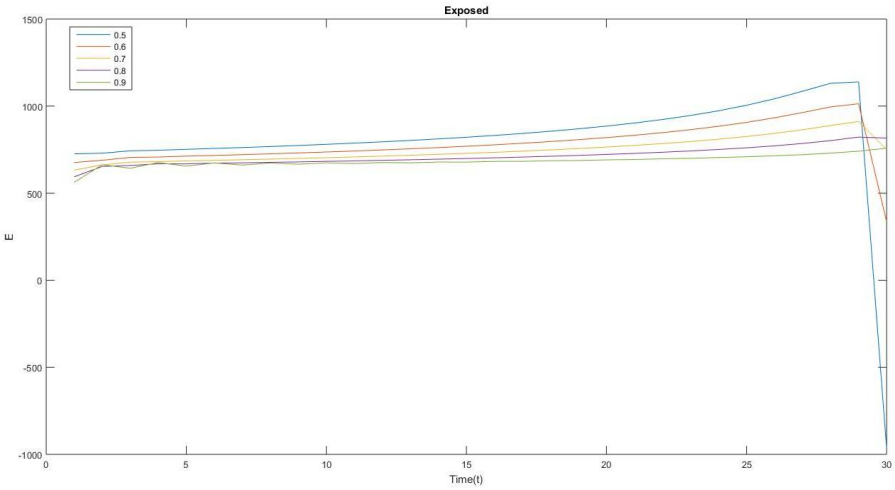

Figure 3: Number of Exposed individual (E) vs. Time(t)

Figure3 shows gradual increment in exposed individual with time due to increased η_1(rate of contact) and then decrement due to β_1(rate of self-quarantine).

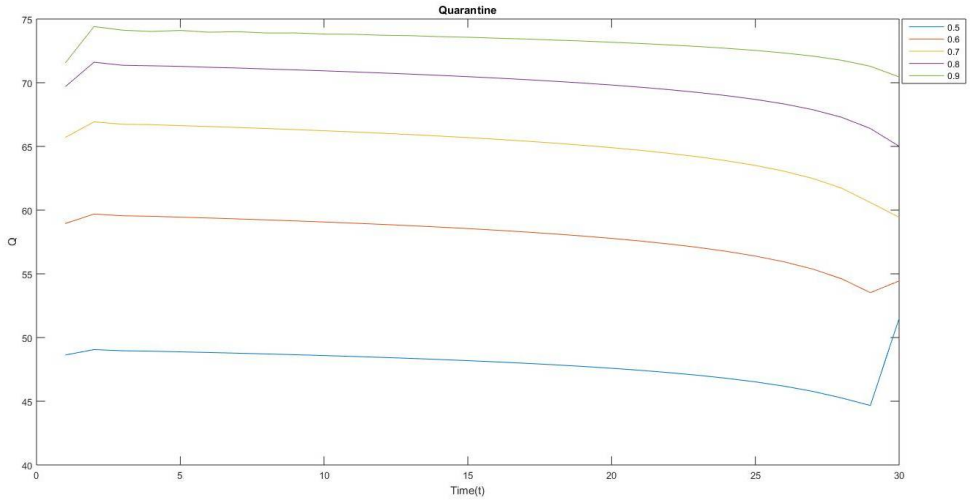

Figure 4:Number of Quarantine individual (Q) vs.Time(t)

Figure 4 represents the number of quarantine individual is affected due to rate of contact (η_1). With increase in η_1 the number of quarantine people will reduce.

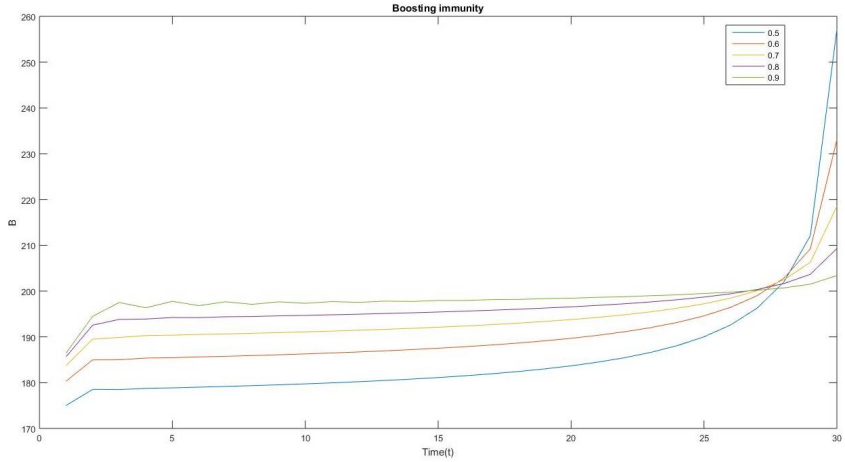

Figure 5: Number of individuals taking Immunity Booster (B)vs. Time (t)

Immune people will increase with increasing (β_3) rate of taking immunity booster (vaccination or other source to boosting immunity).

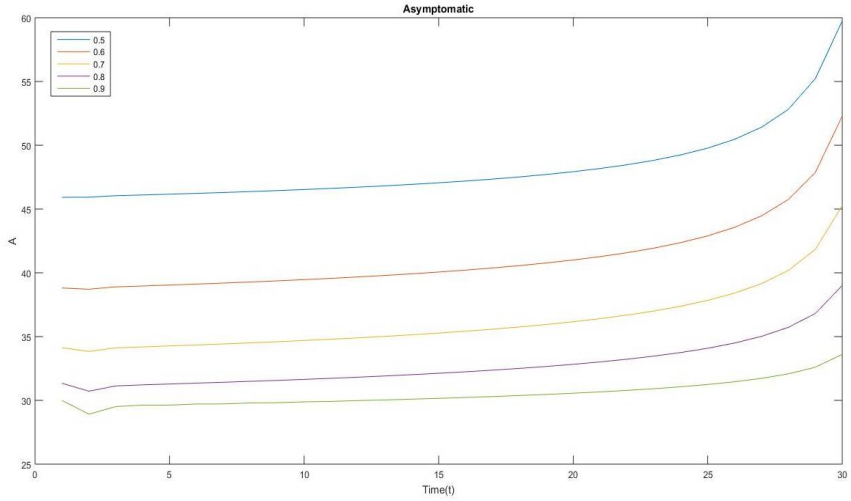

Figure 6: Number of Asymptomatic individual(A) vs.Time(t)

Increment in the number of asymptomatic people is affected by$\rho,\beta_3,\beta_4,\beta_7$.With increasing $\rho,\beta_3,\beta_4,\beta_7$ will increase asymptomatic individual.

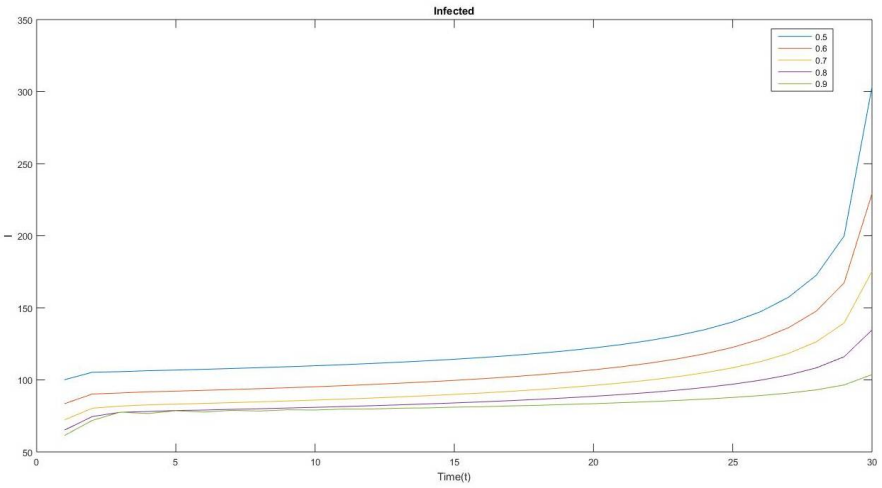

Figure 7: Number of Infected individual (I) vs. Time (t)

Symptomatic individual will increase with decreasing $\beta_3$due to weakened immune system.
Symptomatic individual will increase with increasing β_5, β_9, and β_{10}.

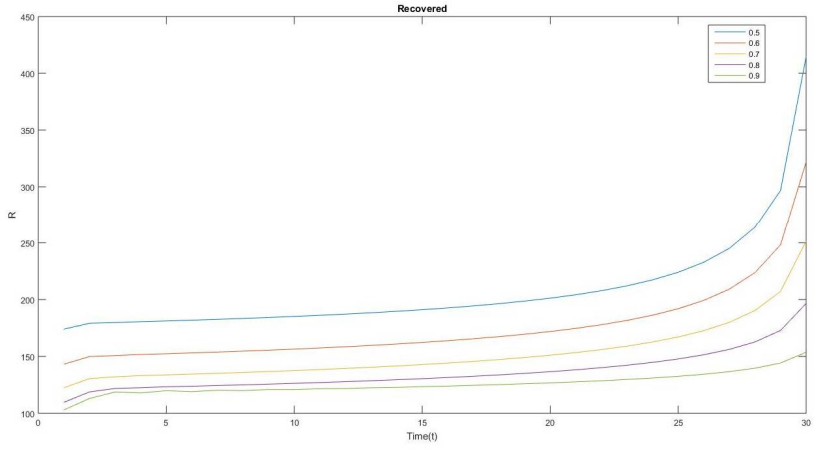

Figure 8: Number of Recovered Individual(R)vs. Time (t)

The number of recovered individuals will increase with increasing λ_A and λ.R will increase also with increasing individual have strong immunity.

CONCLUSION

In this research, the authors have developed a mathematical model for transmission and control of novel corona virus disease from human to human and exhibited the impact of consuming immunity boosters. The studies conclude that with the help of immunity boosters like medicines, the risk of symptomatic infection from corona virus can be reduced. The authors performed a mathematical analysis using fractional differential equations and presented the results graphically using MATLAB, which may help minimize the infection and maximize rate of recovery. The data used in the MATLAB programming is based on disease spread in an institute of India. The basic reproduction rate $\Re_0$ is obtained for the model. In presented model, most affecting parameter of $\Re_0$ is rate of contact (η_1) when it reduces, the basic reproduction number ($\Re_0$) will be decreased. It is observed that when $\Re_0 < 1$ the disease-free equilibrium is locally asymptotically stable otherwise unstable. The numerical solution of the system of fractional differential equation (2.2) indicates that the spread of the infection of corona virus is declining with time due to a large number of infected individuals getting recovered.

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