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A Discrete Model of TB Dynamics in Khyber Pakhtunkhwa-Pakistan

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Abstract: The present paper investigates the theoretical analysis of the tuberculosis (TB) model in the discrete-time case. The model is parameterized by the TB infection cases in the Pakistani province of Khyber Pakhtunkhwa between 2002 and 2017. The model is parameterized and the basic reproduction number is obtained and it is found $\mathcal{R}_0 = 1.5853$. The stability analysis for the model is presented and it is shown that the discrete-time tuberculosis model is stable at the disease-free equilibrium whenever $\mathcal{R}_0 < 1$ and further we establish the results for the endemic equilibria and prove that the model is globally asymptotically stable if $\mathcal{R}_0 > 1$. A discrete fractional model in the sense of Caputo derivative is presented. The numerical results of the model with various parameters and their effect on the model are presented. A comparison of discrete-time method with continuous-time model is presented graphically. A discrete fractional approach is compared with the existing method in literature and some reasonable results are achieved. Finally, a summary of results and conclusion are presented.

Keywords: Discrete TB model; real data; equilibria; Lyapunov; stability; Caputo derivative

1 Introduction

Mathematical models associated to the infectious diseases are gaining much attention day by day due to their applications in disease control and their prevention. The epidemic models are not only formulated in PDEs or ODEs types but also in discrete type. The discrete epidemic models are more useful than continuous-time models [1,2]. The reason is that the data obtained from experiments. Many researchers try to formulate mathematical models with possible best fit to the real data. Discrete-time models are useful for such problems. There are many practical phenomena occurring in the field of engineering and sciences where the data is of the discrete form. To make a reasonable fit to the data, one can obtain the reasonable set of parameters values that can predict the dynamics of real world problem in an effective way. It is to be noted that the continuous-time models have their own importance and it cannot be ignored due to the reason that it is user friendly and computationally efficient.

Various mathematical models in literature were constructed to study the dynamics of infectious diseases in discrete sense. In [1], a discrete mathematical model on SARS disease has been constructed to investigate its dynamics. Using the Euler Backward discretization, an epidemic model of an SIR type is investigated by choosing the nonlinear incidence rate [3]. Further, it is mentioned that by using a suitable monotone property, then one can obtain the asymptotical global results associated to equilibria characterized by the basic reproduction number $\mathcal{R}_0$. An SI model is studied in [4] with nonlinear incidence rate and where it has been observed that the model for a specific rate of the disease, the discrete model attains a unique point of endemic equilibrium. A discrete mathematical model about the West Nile virus has been studied in [5] based on [6]. An SIR model of discrete type has been studied in [7] and also presented the bifurcation analysis. The authors in [8] considered initially a continuous-time epidemic model with immigration of infective and then used a nonstandard discretization technique to obtain the discrete-time model. Most recently, a discrete model with a general incidence rate is studied in [2] for the schistosomiasis disease. A malaria mathematicl model in discrete sense has been analyzed in [9]. A comparison among discrete and continuous-time model for Hepatitis B is studied in [10]. It is shown that dynamics of a viral infection can be described well through discrete time models rather than continuous-time models.

The above mathematical models were proposed on different infectious disease models and a little attention was made to describe the epidemic model with real data of infectious diseases. Therefore, we proposed a continuous-time model of TB and use the Euler backward method for the discritization and then using the real data of TB infective cases of the province Khyber Pakhtunkhwa, Pakistan, since 2002-2017. Tuberculosis (TB) is one the major health problem and causing many infections both mortality and morbidity in Pakistan. Pakistan has been ranked in 5th position in the world due higher number of TB cases. It is evident that half of million new cases emerge to the population due to TB and approximately 15 thousands death in children and more than 70,000 deaths in Pakistani population occur per year. Pakistan has been ranked in position fourth in the world due multi drug resistant tuberculosis (MDR-TB) [11–13] of high prevalence. In Khyber Pakhtunkhwa, a province of Pakistan, TB is considered the major health problem like the other infectious diseases and producing deaths and infected cases every year. The source National TB control Program of Khyber Pakhtunkhwa [12] shows that about 462920 cases of TB infected have been registered and treated since 2002 till 2017. We will use the TB cases registered in Khyber Pakhtunkhwa hospitals since 2002-2017 available in [12] to parameterize the TB model and will discuss the parameters effects on the model.

In case of continuous-time models the associated mathematical model can be best described through the threshold quality known as basic reproduction number that can identify the disease spread or control, if the threshold is less than unity then the disease can be eradicated easily while for the case when it greater than 1 then the disease will remain in the population and there may occur epidemic or outbreak. However, in the case of discrete-time epidemic models it has a complex dynamical behavior which includes chaos phenomena, Hopf bifurcation and flip bifurcation [14,15]. The models discussed above are obtained from the continuous-time models with appropriate discretization scheme.

The application of the fractional calculus related to science and engineering cannot be ignored. The ordinary derivative cannot capture well the dynamics of a practical problem. Because the models formulated with fractional calculus provide many information such as the heredity and the memory effects. The information at each instant of the fractional order can only be possible in fractional model. There are many papers related to fractional Caputo operator are available in literature for the continuous time models see for example [16,17] and the reference therein but a very little attention has been made to fractional discrete modeling for the epidemiological models such as given in literature [18,19]. The importance of the discrete time-models whether it is obtained from a classical or a fractional model give more dynamics such as the bifurcation analysis and other much more properties etc.

Due to the importance of discrete-time models and their application to epidemiological models, we construct a discrete time mathematical model and apply the real data of Tuberculosis cases of KP, Pakistan and explore their dynamics. Further, the main important goal of this work is to explore different disctrization such as euler discritization as a integer case and the Caputo derivative discritization for non-integer case. We compare the solution of discrete model versus integer model and then the iterative procedure with the available fractional technique. We briefly discussed the literature on the TB model above. The rest of the work is partitioned is as follows: The discrete model formulation and the parameters description is shown in Section 2. Section 3 describes the mathematical results associated to model for the case of disease free case. Section is given in order to show the dynamics of the discrete model in the case of endemic equilibrium. Section 5 briefly explored the dynamics of a fractional discrete TB model and their iterative procedure for their solution. Section 6, describes the parameters estimations, the sensitivity analysis and the numerical results of the model. A brief conclusion has been given that summarize the work in Section 7.

2 Model Framework

In the present section, we provide a TB model in the continuous-time given in [20] by the following equations:

$$\begin{aligned}
\frac{dS}{dt} &= \Pi - \frac{\beta SI}{M} - \mu S,\\
\frac{dE}{dt} &= \frac{(1-q)\beta SI}{M} - (\kappa+\mu)E,\\
\frac{dI}{dt} &= \frac{q\beta SI}{M} + \kappa E - (\gamma+\mu+\delta)I,\\
\frac{dR}{dt} &= \gamma I - \mu R,
\end{aligned} \tag{1}$$

with appropriate nonnegative initial conditions given by

$$S_0 = S_0 \geq 0, E_0 = E_0 \geq 0, I_0 = I_0 \geq 0, R_0 = R_0 \geq 0. \tag{2}$$

The variables in the model Eq. (1) are defined as: S, E, I and R respectively show the population of susceptible, latent, infected and recovered at any time t, where M is the total size of the population. The population of susceptible is recruited through the birth rate shown by π, μ represents the natural mortality in each class while the infection rate is given by κ. The parameter γ and δ respectively, show the rate of recovery from infection and the death due to TB. The parameter q measure the fraction of fast developing infectious cases and β is the effective contact rate. Since the discrete model formulate the human dynamics so, all the parameters and the variables in Eq. (1) are nonnegative. The Euler backward difference scheme that discritize system Eq. (1) with step size $h = 1$, leads to the following set of equations:

$$\begin{aligned}
S(n+1) - S(n) &= \Pi - \frac{\beta S(n+1)I(n+1)}{M(n+1)} - \mu S(n+1),\\
E(n+1) - E(n) &= \frac{(1-q)\beta S(n+1)I(n+1)}{M(n+1)} - (\kappa+\mu)E(n+1),\\
I(n+1) - I(n) &= \frac{q\beta S(n+1)I(n+1)}{M(n+1)} + \kappa E(n+1) - (\gamma+\mu+\delta)I(n+1),\\
R(n+1) - R(n) &= \gamma I(n+1) - \mu R(n+1),
\end{aligned} \tag{3}$$

with the specified initial conditions

$$S_0 = S_0 \geq 0, E_0 = E_0 \geq 0, I_0 = I_0 \geq 0, R_0 = R_0 \geq 0, \tag{4}$$

where the parameters have been defined briefly above. The feasible region for the discrete TB model Eq. (1) is

$$\Gamma = \left\{ (S(n), E(n), I(n), R(n)) \in \mathbb{R}_+^4 : M(n) \leq \frac{\Pi}{\mu} \right\},$$

which is positively invariant. The brief literature with model construction is discussed in detailed in the current section. The remaining sections of the paper is organized by following this: The stability results for the disease free case is in investigated in Section 2 while in Section 3, we show the existence and the stability results for the endemic case. Numerical simulations for the model are obtained to illustrate the previous results by using the real data estimated or fitted for the TB infection cases is presented in Section 4. A detail discussion on the results investigated in the previous sections are summarized in Section 5.

3 Stability Analysis of Disease-Free Equilibrium (DFE)

3.1 DFE Equilibrium and Their Analysis

The discrete TB model Eq. (3) has the DFE, E_0 and is given by

$$E_0 = (S^*,\ E^*,\ I^*,\ R^*) = (\Pi/\mu,\ 0,\ 0,\ 0). \tag{5}$$

The *basic reproduction number* [21,22] of the discrete tuberculosis model Eq. (3) will be calculated using the method described in [23,24]. The method is used to obtain the necessary matrices that are useful for the obtaining of the threshold parameter called the basic reproduction number of the model Eq. (3), are obtained as follows:

$$F = \begin{pmatrix} 0 & (1-q)\beta \\ 0 & q\beta \end{pmatrix},$$

and

$$V = \begin{pmatrix} k_1 & 0 \\ -\kappa & k_2 \end{pmatrix}.$$

The *basic reproduction number*, for the discrete tuberculosis model Eq. (3), shown by $\mathcal{R}_0 = \rho(FV^{-1})$, and is finally obtained is as follows:

$$\mathcal{R}_0 = \frac{\beta[\kappa(1-q) + qk_1]}{k_1 k_2},$$

where $k_1 = (\kappa + \mu)$ and $k_2 = (\delta + \mu + \gamma)$.

In the following we established the result based on the Theorem 2 in [24].

Lemma 3.1 If $\mathcal{R}_0 < 1$ then the model given by Eq. (3), is locally-asymptotically stable (LAS) at the disease free case.

3.2 Global Stability Analysis of DFE

We have the following result on the global stability of the DFE.

Theorem 3.1 If $\mathcal{R}_0 < 1$, then the model given by Eq. (3) is globally-asymptotically stable (GAS) in Γ at the disease free case.

Proof. To show that the discrete model given by Eq. (3) is stable globally asymptotically, the following Lyapunov function is defined:

$$\mathcal{V}(n) = \left(\frac{\kappa}{k_1}\right)E(n) + I(n),$$

calculating the backward difference of $\mathcal{V}$ gives,

$$\begin{aligned}\Delta\mathcal{V} &= \mathcal{V}(n+1) - \mathcal{V}(n)\\ &= \left(\frac{\kappa}{k_1}\right)[E(n+1) - E(n)] + [I(n+1) - I(n)]\\ &= \left(\frac{\kappa}{k_1}\right)\left(\frac{(1-q)\beta S(n+1)I(n+1)}{M(n+1)} - k_1E(n+1)\right)\\ &\quad + \left(\frac{q\beta S(n+1)I(n+1)}{M(n+1)} + \kappa E(n+1) - k_2I(n+1)\right),\end{aligned}$$

since $\dfrac{S(n+1)}{M(n+1)} \leq 1$ in Γ it follows that

$$\begin{aligned}\Delta\mathcal{V} &\leq \left(\frac{\kappa}{k_1}\right)[(1-q)\beta I(n+1) - k_1E(n+1)]\\ &\quad + [q\beta S(n+1)I(n+1) + \kappa E(n+1) - k_2I(n+1)]\\ &= k_2(\mathcal{R}_0 - 1)(I(n+1)).\end{aligned}$$

Thus, $\Delta\mathcal{V} \leq 0$ for $\mathcal{R}_0 \leq 1$ and $\Delta\mathcal{V} = 0$ if and only if $E(n+1) = I(n+1) = 0$. Thus,$(E, I) \to (0, 0)$ as $t \to \infty$. Using $E = I = 0$ in the first and the last equations of Eq. (3) shows that $S \to \Pi/\mu$, and $R \to 0$ as $t \to \infty$. This shows that the DFE (E_0) is the maximal invariable set in $\{(S(n),E(n),I(n),R(n)): V(n) = 0\}$. It follows from Theorem 6.3 in [25] that to each equation associated to model Eq. (3), with the given initial conditions in Γ, approaches E_0 as $t \to \infty$.

4 Analysis of the Endemic Equilibria

4.1 Existence of Endemic Equilibrium Point (EEP)

Let $E_1 = (S^{**}, E^{**}, I^{**}, R^{**})$ represent any endemic equilibrium point for the model Eq. (3). We claim the following result.

Lemma 4.1 For the model Eq. (3) there exists a unique endemic equilibrium, say E_1, if $\mathcal{R}_0 > 1$.

Proof. At a steady-state the solution of the equation associated to the system Eq. (3), lead to

$$\begin{aligned}S^{**} &= \frac{\Pi}{\lambda^{**} + \mu},\\ E^{**} &= \frac{(1-q)\lambda^{**}S^{**}}{k_1},\\ I^{**} &= \frac{k_1q + \kappa(1-q)\lambda^{**}S^{**}}{k_1k_2},\\ R^{**} &= \frac{\gamma(k_1q + \kappa(1-q))\lambda^{**}S^{**}}{k_1k_2\mu}.\end{aligned} \tag{6}$$

It should be noted that at a steady-state, we can express $\lambda(n)$, as

$$\lambda^{**} = \frac{\beta(I^{**})}{S^{**} + E^{**} + I^{**}R^{**}}. \tag{7}$$

Substituting the expressions in Eq. (6) into Eq. (7) and simplifying to obtain

$$1 + c\lambda^{**} = \mathcal{R}_0, \tag{8}$$

where,

$$c = \frac{\mu k_2(1-q) + \mu(k_1 q + \kappa(1-q)) + \gamma(k_1 q + \kappa(1-q))}{k_1 k_2 \mu}.$$

Solving Eq. (4.1) for λ^{**} gives, $\lambda^{**} = \dfrac{\mathcal{R}_0 - 1}{c} > 0$ if and only if $\mathcal{R}_0 > 1$. Plugging the value of λ^{**} in to the Eq. (6) shows the components of E_1 are positive whenever $\mathcal{R}_0 > 1$.

4.2 Stability Analysis of Endemic Equilibrium

We establish the global asymptotic stability of the unique equilibrium point for the special case ($\delta = 0$) when the disease mortality death is considered negligible. Define, $\Gamma_0 = \{(S,E,I,R) \in \Gamma: E = I = R = 0\}$. We claim the following result.

Theorem 4.1 The unique endemic equilibrium of the model Eq. (3) with $\delta = 0$ is GAS in $\Gamma \backslash \Gamma_0$ if $\mathcal{R}_0|_{\delta=0} > 1$.

Proof. Let the system Eq. (3) when $\delta = 0$. Further, consider the following non-linear Lyapunov function

$$\mathcal{F}(n) = \frac{1}{2}[S(n) - S^{**} + E(n) - E^{**} + I(n) - I^{**} + R(n) - R^{**}]^2.$$

Computing the backward difference of $\mathcal{F}$ gives,

$$\begin{aligned}
\Delta\mathcal{F} &= \mathcal{F}(n+1) - \mathcal{F}(n) \\
&= \frac{1}{2}[M(n+1) - M^{**}]^2 - \frac{1}{2}[M(n) - M^{**}]^2 \\
&= \frac{1}{2}[M(n+1) - 2M^{**} + M(n)][M(n+1) - M(n)] \\
&= \frac{1}{2}[2M(n+1) - 2M^{**} - M(n+1) + M(n)][M(n+1) - M(n)] \\
&= -\frac{1}{2}[M(n+1) - M(n)]^2 + [M(n+1) - M^{**}][M(n+1) - M(n)] \\
&\leq [M(n+1) - M^{**}][M(n+1) - M(n)]
\end{aligned}$$

Summing the equations of the system Eq. (3) with $\delta = 0$ gives $M(n+1) - M(n) = \pi - \mu\, M(n+1)$ and using the fact that at steady state $\pi = \mu\, M^{**}$, hence,

$$\begin{aligned}
\Delta\mathcal{F} &\leq [M(n+1) - M^{**}][\Pi - \mu M(n+1)] \\
&= [M(n+1) - M^{**}][\mu M^{**} - \mu M(n+1)] \\
&= -\mu[M^{**} - M(n+1)]^2 \leq 0.
\end{aligned}$$

So, $\mathcal{F}$ represent a Lyapunov function on $\Gamma \backslash \Gamma_0$. Therefore, it follows from the published results given in [25], that to each solution of the equation associated to the system Eq. (3), with $\delta = 0$, approaches the EE of the model Eq. (3) as $t \to \infty$ for $\mathcal{R}_0|_{\delta=0} > 1$.

5 A Fractional Model

Before start the analysis for a fractional TB model we first write the definition of Caputo derivative and their fractional integral.

Definition 5.1 A fractional integral having order $\theta \in \mathbb{R}^+$ associated to some function $g(t)$, $t>0$, can be defined as

$$I^{\theta}g(t) = \int_0^t \frac{(t-\psi)^{\theta-1}}{\Gamma(\theta)} g(\psi)d\psi,$$

while the fractional derivative of order θ, where $n-1<\theta<n$ of some function $g(t)$, $t>0$, is defined by

$$D^{\theta}g(t) = I^{n-\theta}D^n g(t), \theta > 0,$$

where the nth derivative of $g(t)$ is shown by $g^{(n)}$, $n=|\theta|$ represent the value of θ rounded to the close integer, I^{θ} is the θth order Riemann-Liouville integer operator and $\Gamma(.)$ is an Euler Gamma function. D^{θ} shows the θth order Caputo operator.

The system that describes the dynamics of TB Eq. (1) can be represented in Caputo derivative in the following form:

$$\begin{aligned} D_t^{\theta}S(t) &= \Pi - \frac{\beta SI}{M} - \mu S, \\ D_t^{\theta}E(t) &= \frac{(1-q)\beta SI}{M} - (\kappa+\mu)E, \\ D_t^{\theta}I(t) &= \frac{q\beta SI}{M} + \kappa E - (\gamma+\mu+\delta)I, \\ D_t^{\theta}R(t) &= \gamma I - \mu R, \end{aligned} \tag{9}$$

where D_t^{θ} describes the Caputo derivative, $t>0$ and the fractional order is shown by θ that satisfies $0<\theta\leq 1$.

The system that describes the dynamics of TB Eq. (9) is now discretized by using the time derivative of Eq. (9) with the procedure $D^{\theta}y(t) = g(y(t))$, where $\theta \in (0, 1)$, $t>0$ and assume that $S(0) = S_0$, $E(0) = E_0$, $I(0) = I_0$ and $R(0) = R_0$ is the given initial conditions. The discritization of the fractional TB model is as follows:

$$\begin{aligned} D_t^{\theta}S(t) &= \Pi - \frac{\beta S\left(\left[\frac{t}{y}\right]y\right)I\left(\left[\frac{t}{y}\right]y\right)}{M\left(\left[\frac{t}{y}\right]y\right)} - \mu S\left(\left[\frac{t}{y}\right]y\right), \\ D_t^{\theta}E(t) &= \frac{(1-q)\beta S\left(\left[\frac{t}{y}\right]y\right)I\left(\left[\frac{t}{y}\right]y\right)}{M\left(\left[\frac{t}{y}\right]y\right)} - (\kappa+\mu)E\left(\left[\frac{t}{y}\right]y\right), \\ D_t^{\theta}I(t) &= \frac{q\beta S\left(\left[\frac{t}{y}\right]y\right)I\left(\left[\frac{t}{y}\right]y\right)}{M\left(\left[\frac{t}{y}\right]y\right)} + \kappa E\left(\left[\frac{t}{y}\right]y\right) - (\gamma+\mu+\delta)I\left(\left[\frac{t}{y}\right]y\right), \\ D_t^{\theta}R(t) &= \gamma I\left(\left[\frac{t}{y}\right]y\right) - \mu R\left(\left[\frac{t}{y}\right]y\right). \end{aligned} \tag{10}$$

Let first $t \in [0, h)$, $t/h \in [0, 1)$. Then

$$
\begin{aligned}
D_t^\theta S(t) &= \Pi - \frac{\beta S_0 I_0}{M_0} - \mu S_0, \\
D_t^\theta E(t) &= \frac{(1-q)\beta S_0 I_0}{M_0} - (\kappa+\mu)E_0, \\
D_t^\theta I(t) &= \frac{q\beta S_0 I_0}{M_0} + \kappa E_0 - (\gamma+\mu+\delta)I_0, \\
D_t^\theta R(t) &= \gamma I_0 - \mu R_0,
\end{aligned} \tag{11}
$$

and the solution to Eq. (11) reduces to

$$
\begin{aligned}
S_1(t) &= S_0 + J^\theta[\Pi - \frac{\beta S_0 I_0}{M_0} - \mu S_0] \\
&= S_0 + \frac{t^\theta}{\Gamma(1+\theta)}[\Pi - \frac{\beta S_0 I_0}{M_0} - \mu S_0], \\
E_1(t) &= E_0 + J^\theta[\frac{(1-q)\beta S_0 I_0}{M_0} - (\kappa+\mu)E_0] \\
&= E_0 + \frac{t^\theta}{\Gamma(1+\theta)}[\frac{(1-q)\beta S_0 I_0}{M_0} - (\kappa+\mu)E_0], \\
I_1(t) &= I_0 + J^\theta[\frac{q\beta S_0 I_0}{M_0} + \kappa E_0 - (\gamma+\mu+\delta)I_0] \\
&= I_0 + \frac{t^\theta}{\Gamma(1+\theta)}[\frac{q\beta S_0 I_0}{M_0} + \kappa E_0 - (\gamma+\mu+\delta)I_0], \\
R_1(t) &= R_0 + J^\theta[\gamma I_0 - \mu R_0] \\
&= R_0 + \frac{t^\theta}{\Gamma(1+\theta)}[\gamma I_0 - \mu R_0].
\end{aligned} \tag{12}
$$

For $t \in [h, 2h)$, $t/h \in [1, 2)$. So, we have the following

$$
\begin{aligned}
D_t^\theta S(t) &= \Pi - \frac{\beta S_1 I_1}{M_1} - \mu S_1, \\
D_t^\theta E(t) &= \frac{(1-q)\beta S_1 I_1}{M_1} - (\kappa+\mu)E_1, \\
D_t^\theta I(t) &= \frac{q\beta S_1 I_1}{M_1} + \kappa E_1 - (\gamma+\mu+\delta)I_1, \\
D_t^\theta R(t) &= \gamma I_1 - \mu R_1,
\end{aligned} \tag{13}
$$

which have the solution given by

$$
\begin{aligned}
S_2(t) &= S_1(y) + \frac{(t-h)^\theta}{\Gamma(1+\theta)}[\Pi - \frac{\beta S_1(y) I_1(y)}{M_1(y)} - \mu S_1(y)], \\
E_2(t) &= E_1(y) + \frac{(t-h)^\theta}{\Gamma(1+\theta)}[\frac{(1-q)\beta S_1(y) I_1(y)}{M_1(y)} - (\kappa+\mu)E_1(y)], \\
I_2(t) &= I_1(y) + \frac{(t-h)^\theta}{\Gamma(1+\theta)}[\frac{q\beta S_1(y) I_1(y)}{M_1(y)} + \kappa E_1(y) - (\gamma+\mu+\delta)I_1(y)], \\
R_2(t) &= R_1(y) + \frac{(t-h)^\theta}{\Gamma(1+\theta)}[\gamma I_1(y) - \mu R_1(y)].
\end{aligned} \tag{14}
$$

We repeat this process n-times and obtain the following:

$$\begin{aligned}
S_{(n+1)}(t) &= S_n(ny) + \frac{(t-nh)^{\theta}}{\Gamma(1+\theta)}[\Pi - \frac{\beta S_n(ny) I_n(ny)}{M_n(ny)} - \mu S_n(ny)],\\
E_{(n+1)}(t) &= E_n(ny) + \frac{(t-nh)^{\theta}}{\Gamma(1+\theta)}[\frac{(1-q)\beta S_n(ny) I_n(ny)}{M_n(ny)} - (\kappa+\mu)E_n(ny)],\\
I_{(n+1)}(t) &= I_n(ny) + \frac{(t-nh)^{\theta}}{\Gamma(1+\theta)}[\frac{q\beta S_n(ny) I_n(ny)}{M_n(ny)} + \kappa E_n(ny) - (\gamma+\mu+\delta)I_n(ny)],\\
R_{(n+1)}(t) &= R_n(ny) + \frac{(t-nh)^{\theta}}{\Gamma(1+\theta)}[\gamma I_n(ny) - \mu R_n(ny)],
\end{aligned} \tag{15}$$

where $t \in [nh, (n+1)h)$, $t/h \in [1, 2)$. When $t \to (n+1)h$, then the system given by (15) reduced to the form

$$\begin{aligned}
S_{(n+1)}(t) &= S_n + \frac{(h)^{\theta}}{\Gamma(1+\theta)}[\Pi - \frac{\beta S_n I_n}{M_n} - \mu S_n],\\
E_{(n+1)}(t) &= E_n + \frac{(h)^{\theta}}{\Gamma(1+\theta)}[\frac{(1-q)\beta S_n I_n}{M_n} - (\kappa+\mu)E_n,\\
I_{(n+1)}(t) &= I_n + \frac{(h)^{\theta}}{\Gamma(1+\theta)}[\frac{q\beta S_n I_n}{M_n} + \kappa E_n - (\gamma+\mu+\delta)I_n],\\
R_{(n+1)}(t) &= R_n + \frac{(h)^{\theta}}{\Gamma(1+\theta)}[\gamma I_n - \mu R_n],
\end{aligned} \tag{16}$$

Consider $\theta \to 1$ in system Eq. (16), we obtain the Euler discretization of an SEIR TB model.

6 Numerical Results

6.1 Data Fitting

It is obvious that the data come from the experiments is of discrete nature and the discrete model are much suitable for such data which comes from epidemics. So, in this subsection, we estimate the parameters for the discrete TB model Eq. (3), based on the available TB data from national TB control program Pakistan [26,13]. In order to parameterize the discrete TB model Eq. (3), some key parameters and their values are taken from the literature (see Tab. 1), while the rest of the parameters are fitted or estimated based on the Khyber Pakhtunkhwa Health Department (TB control Program) data (see Fig. 1). We estimate the parameter, μ, as $\mu = 1/67.7$ *per* year, where 67.7 years represent the average lifespan a Pakistani individual [13]. We estimate the parameter, π, as follows, since the total population of Khyber

Table 1: Numerical values for the parameters of the discrete TB model (3).

Parameter	Baseline value	Reference
π	450862.20088626	Estimated
β	0.482783	Fitted
γ	0.247758	Fitted
μ	1/67.7	[13]
δ	0.009872	Fitted
κ	0.11148	Fitted
q	0.098	Fitted

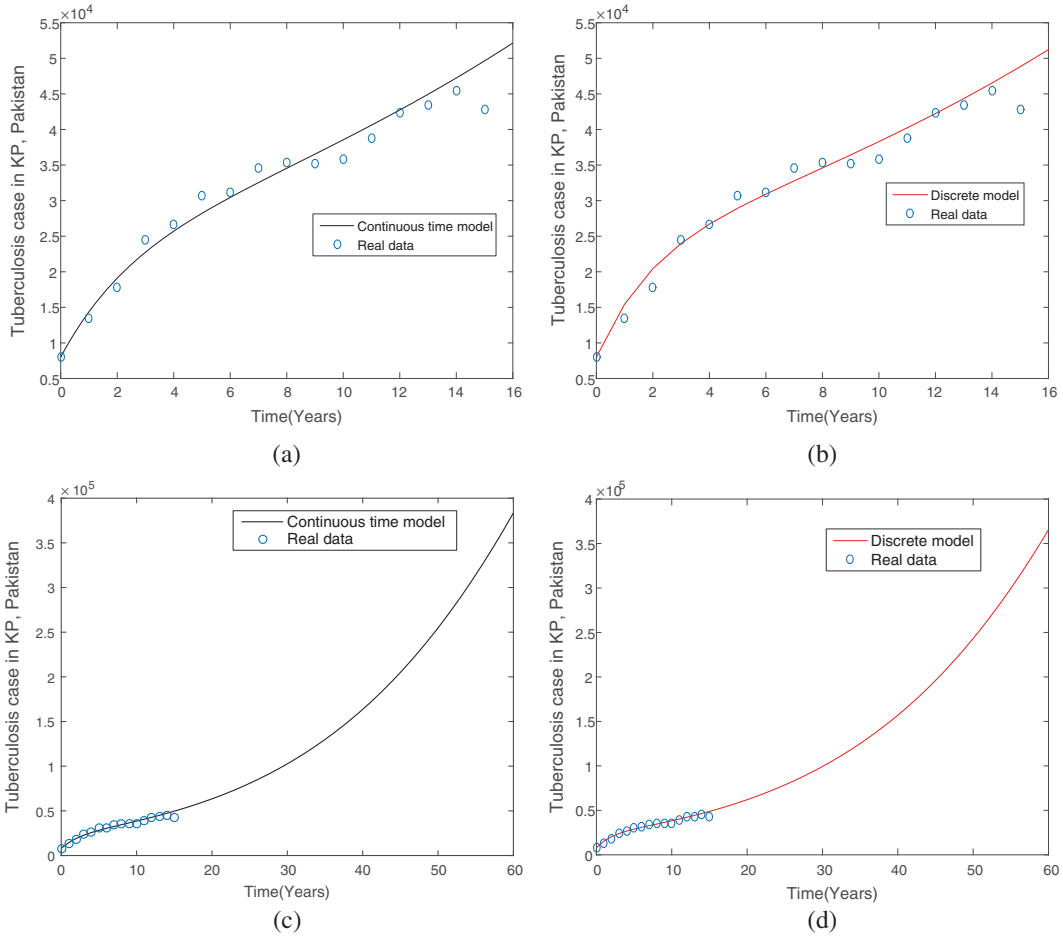

Figure 1: Comparison of discrete and continuous-time models for the real data

Pakhtunkhwa province as at 2017 was 30,523,371 [12], we assumed that π/μ, that represents the total human population in the disease absence, is 30,523,371, so that $\pi = 450{,}862.20088626$ *per* year. Using the estimated and the fitted parameters the value of the basic reproduction number $\mathcal{R}_0$ for the period 2002-2017 TB cases in Khyber Pakhtunkhwa Pakistan is $\mathcal{R}_0 \approx 1.5853$.

The numerical results are obtained by using the parameters estimated and fitted from the Tab. 1 and considered the initial conditions for the model. In Fig. 1, the tuberculosis infection cases of Khyber Pakhtunkhwa, Pakistan is shown in subgraph 1(a) in comparison with Runge-Kutta order four scheme. Figs. 1c and 1d is the comparison of incidences cases of TB with continuous and discrete model respectively for long time behavior. Fig. 2 and their subgraphs show the behavior of different compartments when the basic reproduction number greater $\mathcal{R}_0 = 1.5853 > 1$. Fig. 2 demonstrates that the endemic equilibrium is locally asymptotically stable when the basic reduction number greater than 1. The subplots in Fig. 2 represent the behavior of susceptible, exposed, infected and recovered individuals. We plotted the model behavior for the long time as 60 years which shows that data accurately fit to the model and it is an alarming for the health department of Khyber Pakhtunkhwa, Pakistan which is continuously increasing for both the continuous and discrete time models, see Figs. 1c and 1d. Fig. 3 and their subgraphs show the population of susceptible, exposed, infected and recovered individuals when $\mathcal{R}_0 = 0.6002 < 1$, that demonstrate that the disease free equilibrium is locally asymptotically stable. The population of susceptible individuals decreases when $\mathcal{R}_0 = 1.5853 > 1$ and the population of exposed,

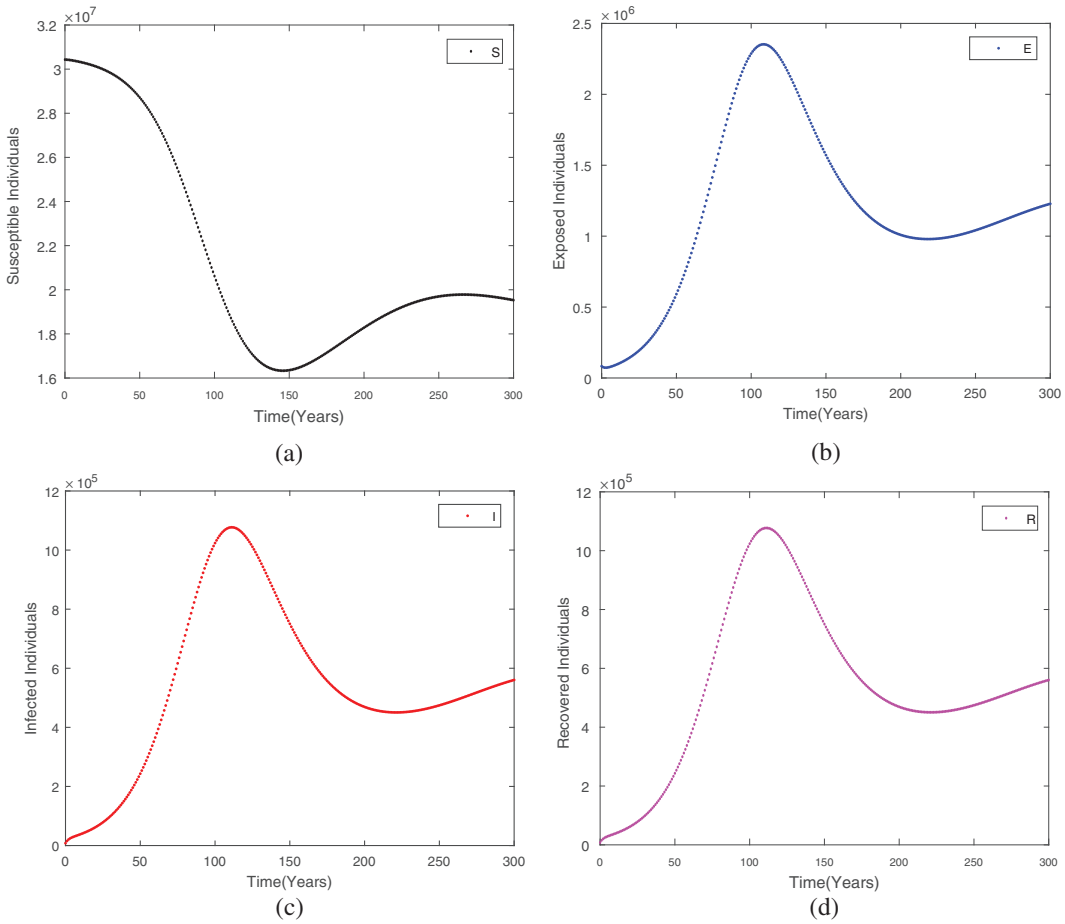

Figure 2: Simulations of the model variables when $\mathcal{R}_0 = 1.5853 > 1$

infected and recovered increases in the presence of infection. When $\mathcal{R}_0 = 0.6002 < 1$, we obtain graphical result for total number of infected compartments depicted in Fig. 4a by choosing different initial conditions $\mathcal{R}_0 = 1.5853 > 1$ and when $\mathcal{R}_0 = 0.6002 < 1$ see Fig. 4b for different initial conditions.

Fig. 5a shows the total number of infected individuals when $\mathcal{R}_0 = 1.5853 > 1$ by choosing different values of the parameter γ. We can see in Fig. 5a that by increasing the parameter γ the total number of infected individuals decreases, which shows that the parameter γ has an effective role in the decrease of infection. Fig. 5b is the joint plot of the total number of infected versus susceptible individuals. Red bold line shows the populations of total number of infected compartments while the black bold line is the population of susceptible individuals. Fig. 6 shows the cumulative number of infective cases for different values of the parameter q. The graphical results for the discrete fractional Caputo is presented in Figs. 7–9. In a comparison of the real data versus the discrete fractional approach (DFA) is presented while in Fig. 7b a comparison with real data by using different values of the fractional order θ is shown. The result provided in Fig. 7 is reasonable to the discrete case and the Runge-Kutta order scheme presented for the integer case. Further, some numerical results are shown in Figs. 8 and 9 for different fractional order θ with the existing numerical approach of fractional differential equations and having some reasonable results.

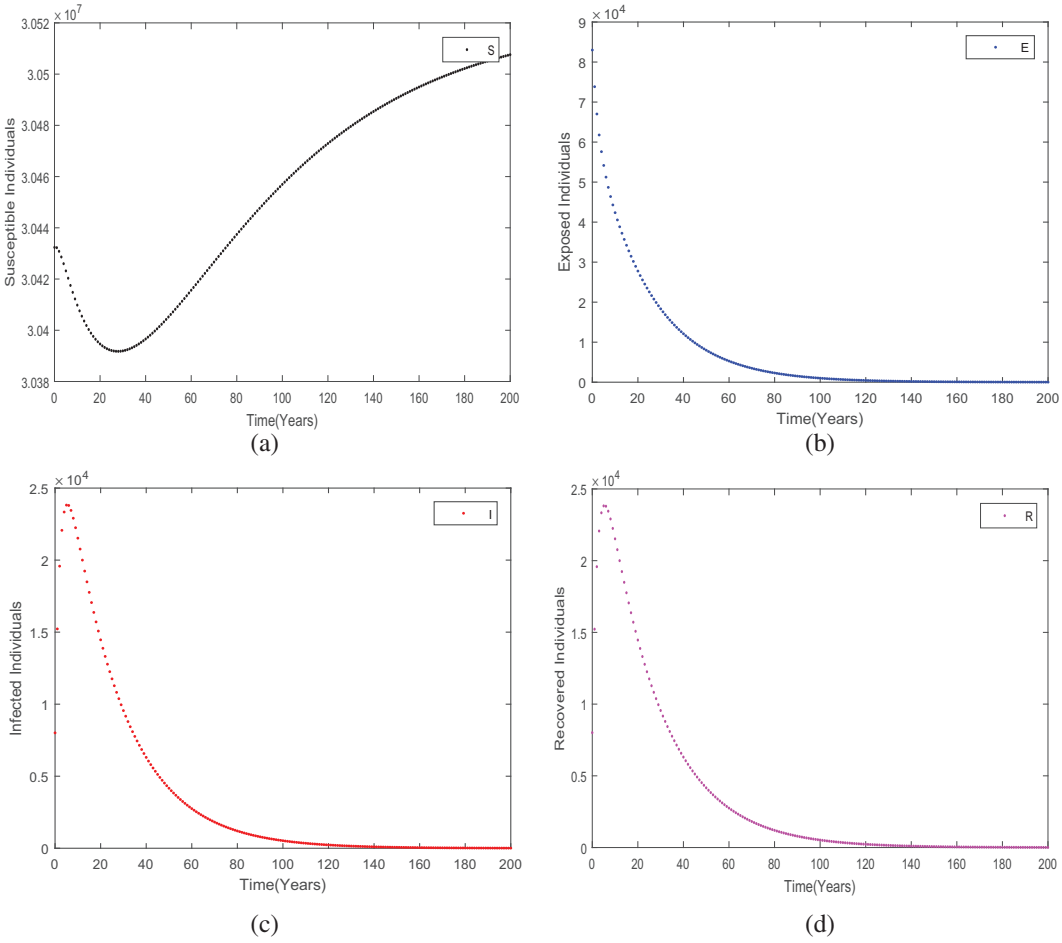

Figure 3: Simulations of the model variables when $\mathcal{R}_0 = 0.6002 < 1$

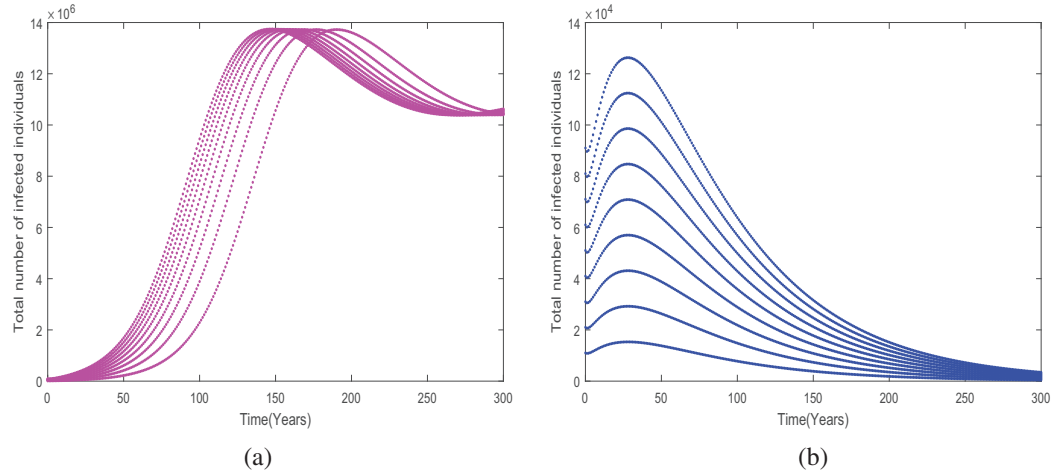

Figure 4: (a) Total number of infected individuals when $\mathcal{R}_0 = 1.5853 > 1$, (b) Total number of infected individuals when $\mathcal{R}_0 = 0.6002 < 1$. and $\beta = 0.182783$

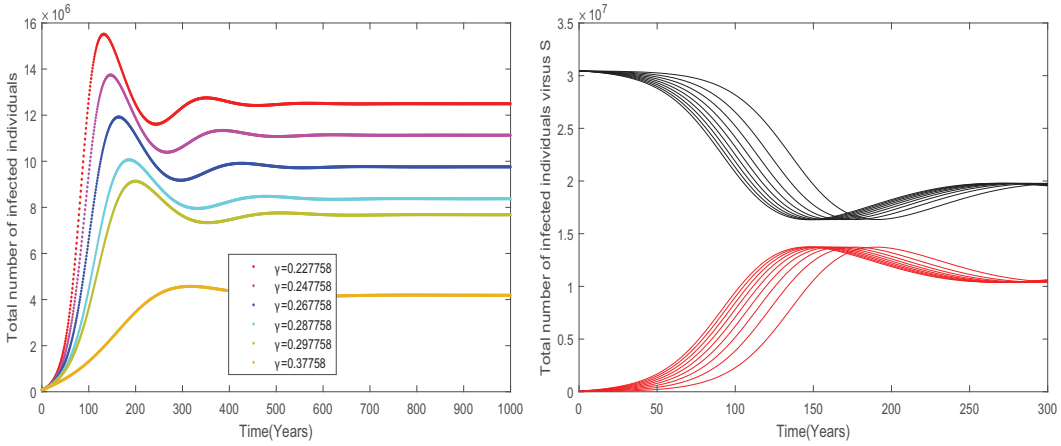

Figure 5: (a) Total number of infected individuals when $\mathcal{R}_0 = 1.5853 > 1$ and $\beta = 0.482783$ with various values of γ, (b) Total number of infected individuals when $\mathcal{R}_0 = 1.5853 > 1$ and $\beta = 0.482783$, comparison of infected compartments versus non-infected compartments for various initial conditions

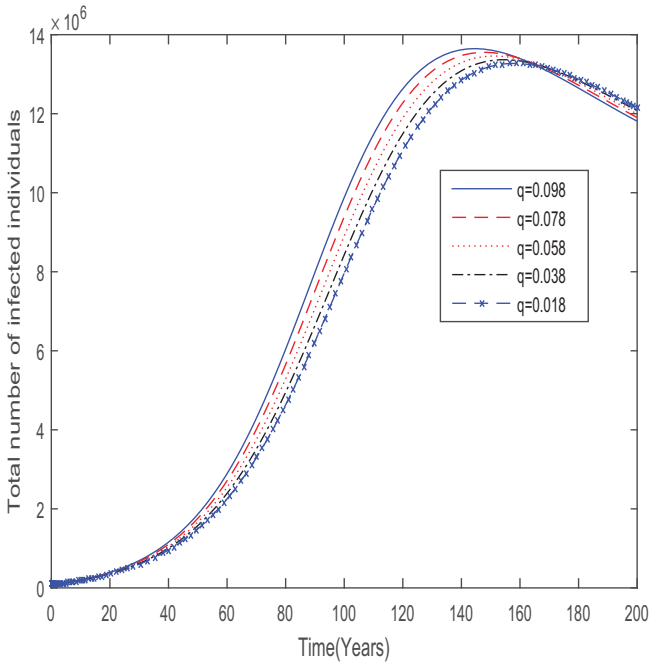

Figure 6: The cumulative number of cases with the value of q

6.2 Sensitivity Analysis of $\mathcal{R}_0$

The present section determines the sensitivity analysis of the of the basic reproduction number $\mathcal{R}_0$ versus model parameters. In order to do this, initially, we obtain the partial derivatives of the basic reproduction number versus the model parameters β, κ, q, μ, δ and γ. The following definition is used to obtain the corresponding partial derivatives:

Definition 6.1 The normalized sensitivity index of $\mathcal{R}_0$ depending on the differentiability on a parameter Φ is defined as follows:

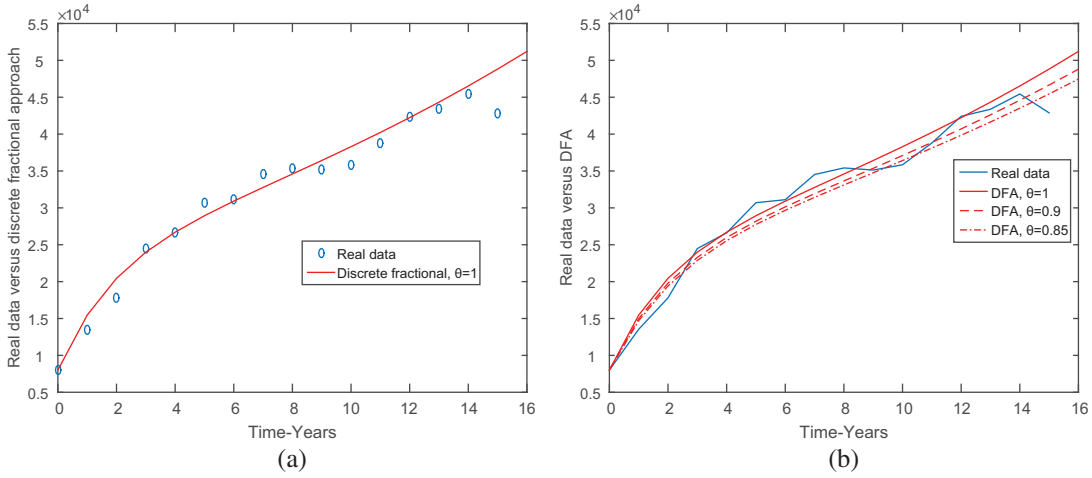

Figure 7: Data *vs.* discrete fractional, (a), $\theta = 1$ *vs.* DFA (b) DFA(discrete fractional approach), $\theta = 1$, 0.9, 0.85 *vs.* real data

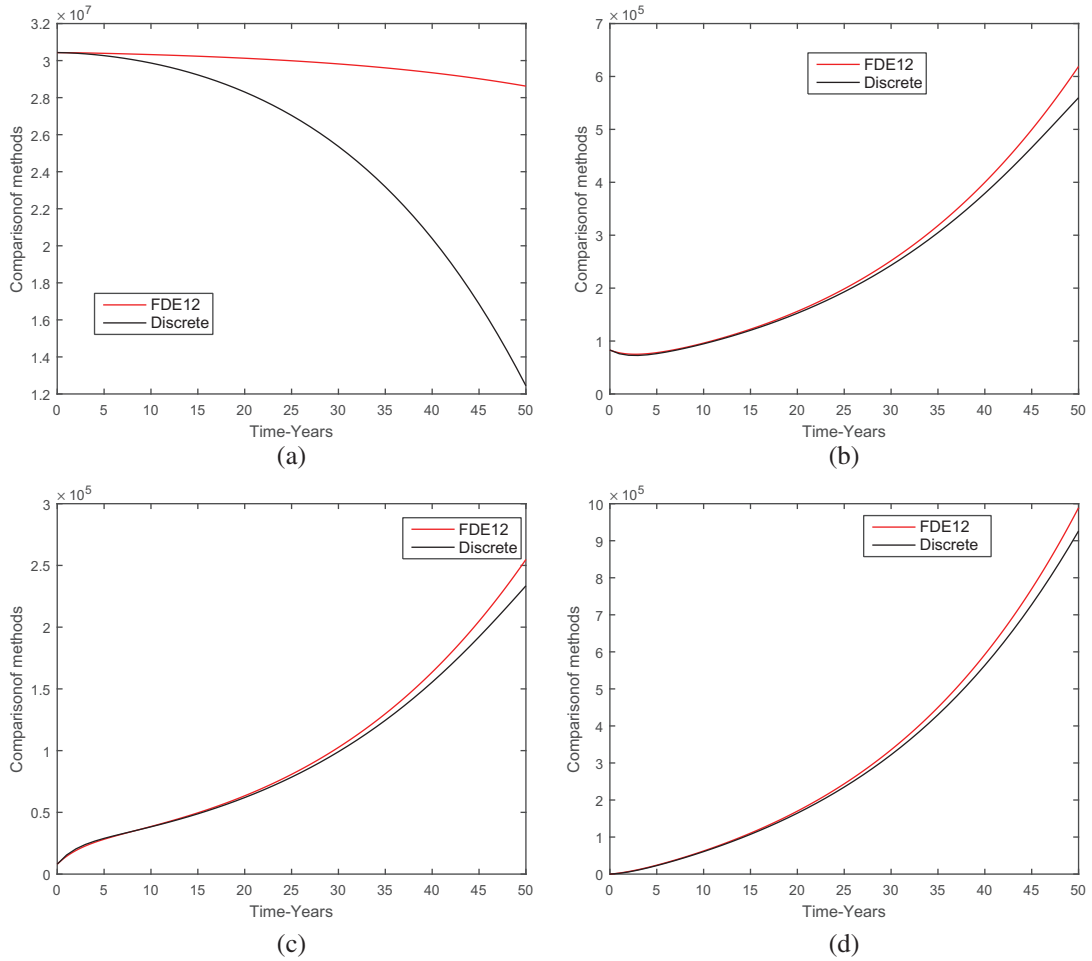

Figure 8: Comparison of FDE12 and the discrete fractional system (16) for $\theta = 1$, when $\mathcal{R}_0 = 1.5853 > 1$

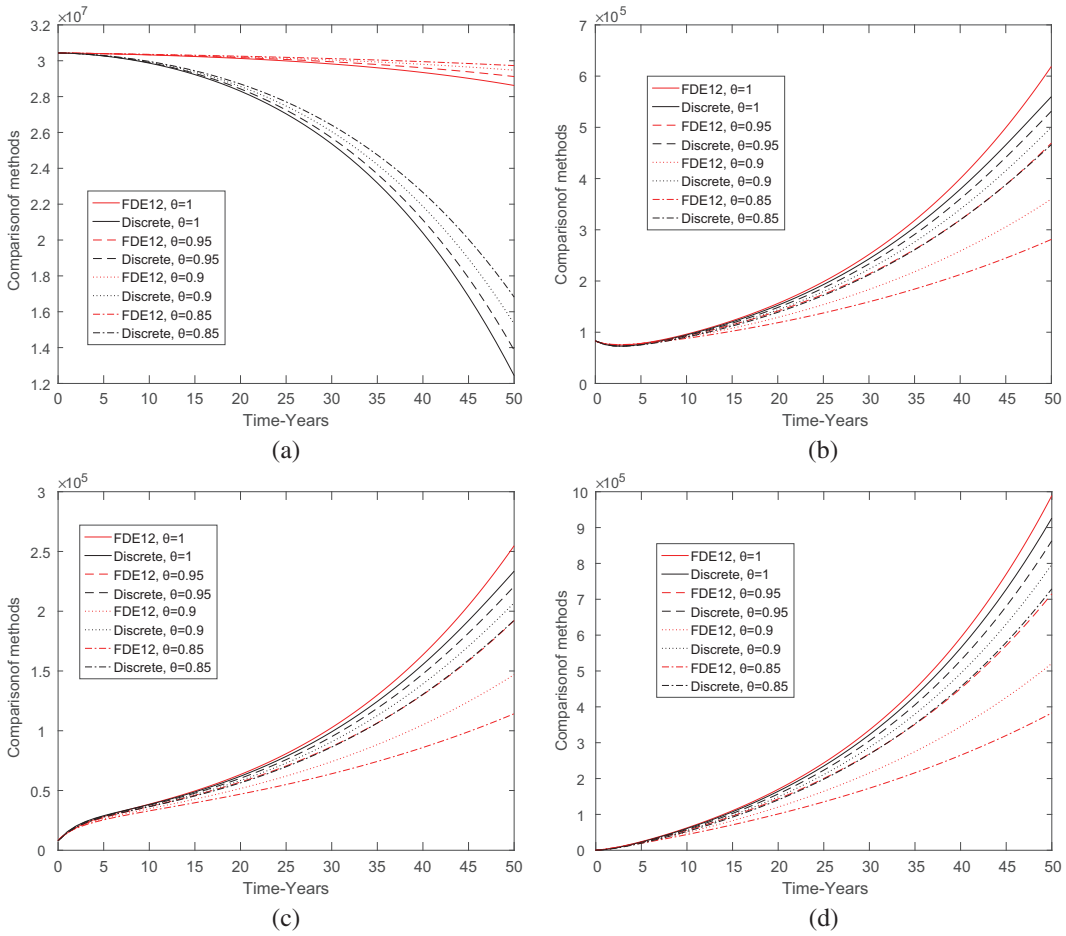

Figure 9: Comparison of FDE12 and the discrete fractional system (16) for $\theta = 1, 0.95. 0.9. 0.85$, when $\mathcal{R}_0 = 1.5853 > 1$

$$S_{\Phi}^{\mathcal{R}_0} = \frac{\Phi}{\mathcal{R}_0}\frac{\partial \mathcal{R}_0}{\partial \Phi}.$$

Using the definition above, we have the following partial derivatives.

$$\frac{\beta}{\mathcal{R}_0}\frac{\partial \mathcal{R}_0}{\partial \beta} = 1 > 0,$$

$$\frac{\kappa}{\mathcal{R}_0}\frac{\partial \mathcal{R}_0}{\partial \kappa} = \frac{\kappa\mu(1-q)}{(\kappa+\mu)(\kappa+\mu q)} = 0.104179,$$

$$\frac{q}{\mathcal{R}_0}\frac{\partial \mathcal{R}_0}{\partial q} = \frac{\mu q}{q(\kappa+\mu)+\kappa(1-q)} = 0.0128185,$$

$$\frac{\mu}{\mathcal{R}_0}\frac{\partial \mathcal{R}_0}{\partial \mu} = -\frac{\mu(\kappa^2+2\kappa\mu+\gamma(\kappa-\kappa q)+\delta(\kappa-\kappa q)+\mu^2 q)}{(\kappa+\mu)(\gamma+\delta+\mu)(\kappa+\mu q)} = -0.158404,$$

$$\frac{\delta}{\mathcal{R}_0}\frac{\partial \mathcal{R}_0}{\partial \mu} = -\frac{\delta}{\gamma+\delta+\mu} = -0.0362407,$$

$$\frac{\gamma}{\mathcal{R}_0}\frac{\partial \mathcal{R}_0}{\partial \gamma} = -\frac{\gamma}{\gamma+\delta+\mu} = -0.909534,$$

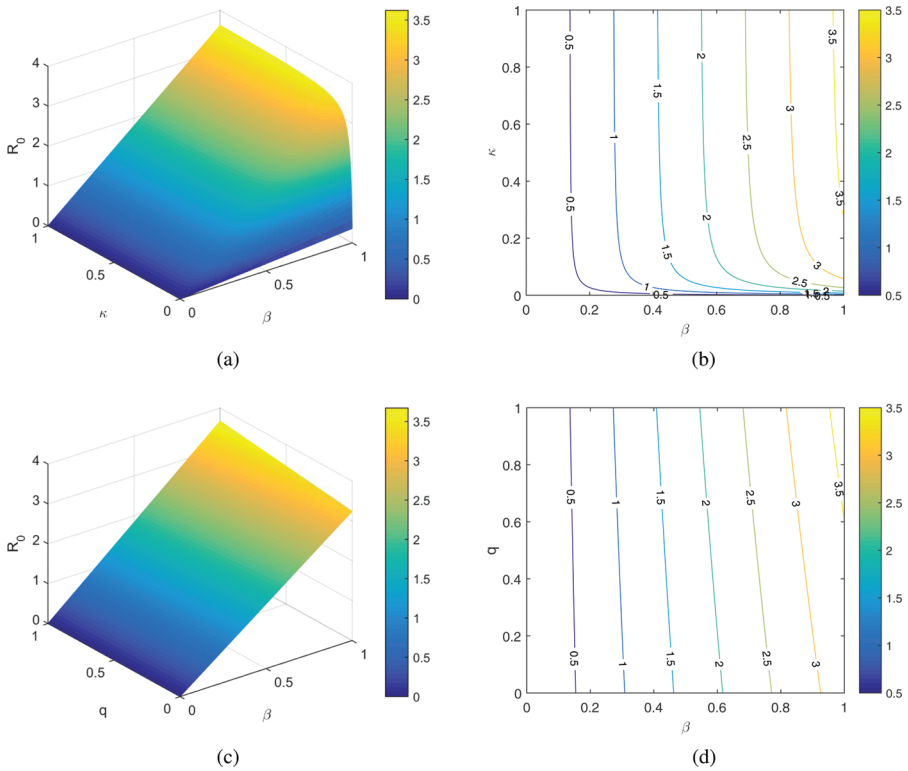

Figure 10: Plot of the model parameters *vs.* $\mathcal{R}_0$, (a) β, κ *vs.* $\mathcal{R}_0$, (b) contour plot of β and κ, (c) β and q *vs.* $\mathcal{R}_0$, (d) contour plot of β and q

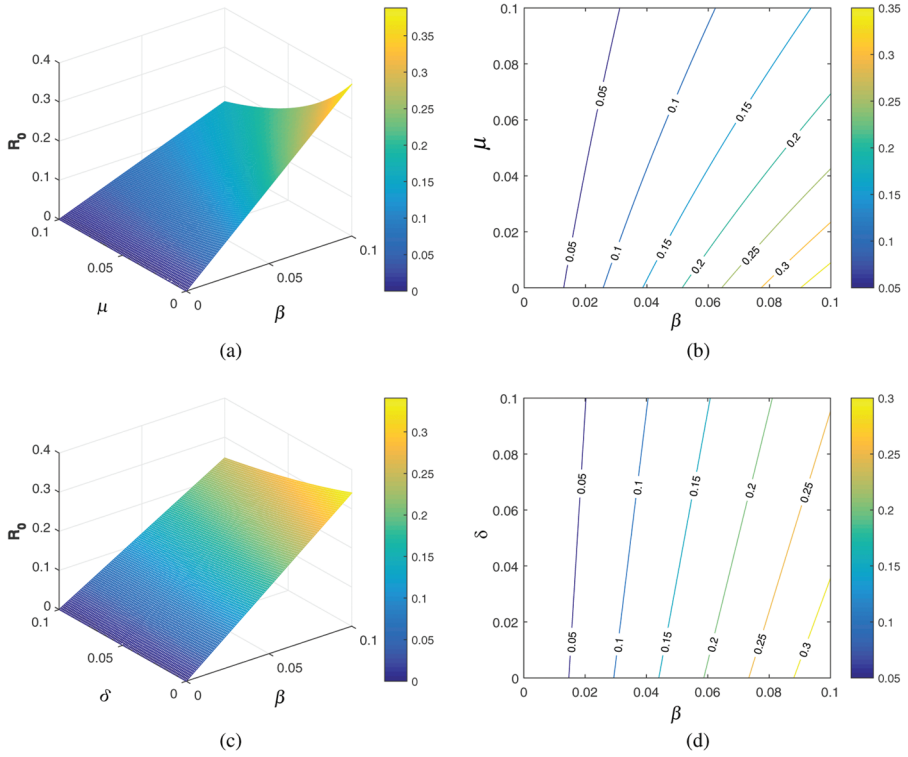

Figure 11: Plot of the model parameters *vs.* $\mathcal{R}_0$, (a) β, μ *vs.* $\mathcal{R}_0$, (b) contour plot of β and μ, (c) β and μ *vs.* $\mathcal{R}_0$, (d) contour plot of β and μ

In these partial derivatives $\frac{\partial \mathcal{R}_0}{\partial \beta} > 0$, $\frac{\partial \mathcal{R}_0}{\partial \kappa} > 0$, $\frac{\partial \mathcal{R}_0}{\partial q} > 0$, which shows a positive effect on the basic reproduction number, decrease the value of these parameter cause decrease the basic reproduction will have decrease the infection in the community. The others parameters that shown above have the negative sign indicate that increasing the values of these parameter can decrease the value of the basic reproduction number. Some of plots related to the sensitivity analysis are shown in Figs. 10–12. The parameters that have positive effects on the basic reproduction number such as β, κ and q and those have negative effect on the basic reproduction number respectively should be decreases and increased.

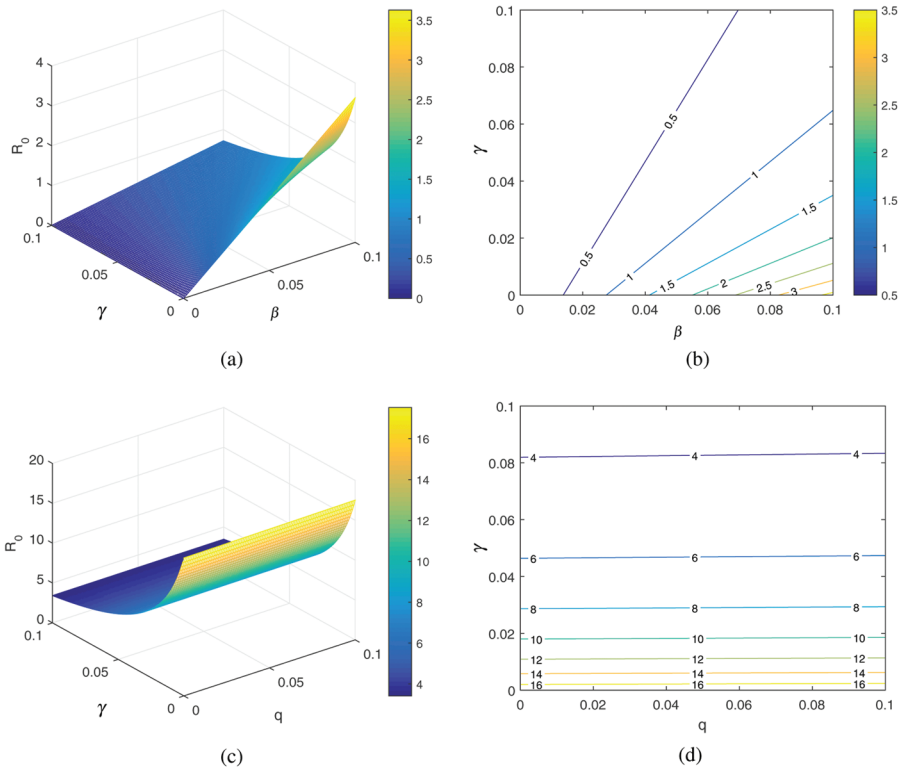

Figure 12: Plot of the model parameters *vs.* $\mathcal{R}_0$, (a) β, γ *vs.* $\mathcal{R}_0$, (b) contour plot of β and γ, (c) q and γ *vs.* $\mathcal{R}_0$, (d) contour plot of q and γ

7 Conclusion

The present work was proposed to analyze the dynamics of a discrete TB model. The discrete model is formulated on the basis of the continuous-time model by Euler backward method with step size $h = 1$. The basic model analysis and their properties are obtained and discussed. The model is found to be stable both locally and globally when the basic reproduction number less than unity. Further, the endemic equilibrium of the model is obtained and discussed and it is proven that the model is globally asymptotically stable at the endemic equilibrium when $\mathcal{R}_0 > 1$. Moreover, we used the real data of TB incidence cases of the province Khyber Pakhtunkhwa, Pakistan and parameterized the parameters of the discrete tuberculosis model and estimated the basic reproduction number $\mathcal{R}_0 = 1.5853$. The TB cases versus model fitting provided a good fit and is reasonable to predict the disease future status. The sensitivity analysis of the model parameters versus basic reproduction number is obtained and discussed the important parameters that can reduce the infection in community. The model with long term behavior with real data is plotted and one can see that the data gives a good fit by using the time upto 60 years. The long term behavior of the data with the model fitting shows that the disease will persists in the population for the long term. Therefore it

is an alarming for the public health department of Khyber Pakhtunkhwa. Further, we use different parameters to analyze the effect of model parameters on model. A discrete fractional approach is used in the sense of Caputo derivative for the numerical solution of the fractional TB model. The discretize approach is compared with the existing method in literature and obtained some reasonable results. A comparison of the real data of TB versus discrete fractional approach is compared with real data and found some reasonable results.

We observed that the discrete time model versus data fitting gives reasonable fitting as the integer model does but for the integer model we only study the model dynamics for an integer case while for a fractional model we can obtain many results associated to the model when the fractional order varies. It is well known that many properties of the model in the sense of discrete-time model such as bifurcation analysis and other properties can be explored well. The TB is an active disease and producing many cases in Pakistan and also in Khyber Pakhtunkhwa. Therefore, it is necessary that government should take positive steps in urgent basis to reduce the disease burden on the population of Khyber Pkahtunkhwa. Proper treatment and other health facility should be provided to the people of Pakhtunkhwa and also make awareness in the individuals by electronic media, Facebook, newspapers etc.

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