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PREDICTING THE TRANSMISSION DYNAMICS OF TUBERCULOSIS VIA CAPUTO FRACTIONAL ORDER MODEL WITH NEURAL NETWORK

LINUS MANU SAMSON, ESHI PRIEBE DOVI, SAMUEL SHIKAA, RICHARD TAPARKI

Abstract. This study presents the development of a hybrid Fractional Order Differential Equation (FODE) and Artificial Neural Network (ANN) model designed to predict the dynamics of Tuberculosis (TB) in Nigeria. The analysis utilized data sourced from the World Health Organization (WHO) TB Database and the Nigeria category, spanning the years 2010 to 2020. The Caputo derivative was used to formulate the fractional tuberculosis model which was enhanced with an ANN framework. The derived FODEs were discretized using the Grünwald-Letnikov method for parameter estimation and numerical simulation of the TB data in MATLAB, employing varying memory values for the fractional-order model parameter $0 < \alpha \leq 1$. To enhance predictive accuracy, we integrate an Artificial Neural Network (ANN) with the FDE model, leveraging machine learning techniques for parameter estimation and forecasting. The ANN is trained using real-world TB data, employing the sigmoid function to represent time-dependent transmission rates. Our results demonstrate that the fractional-order model provides a more flexible and accurate representation of TB dynamics compared to classical integer-order models. The proposed hybrid approach effectively captures disease trends, making it a valuable tool for epidemiological analysis and public health decision-making.

1. Introduction

Tuberculosis (TB) has long posed a significant threat to global health. According to the World Health Organization (WHO) in 2020, there were an estimated 10 million new cases of active TB worldwide, translating to approximately 130 cases per 100,000 people. TB affects individuals across all countries and age groups. In 2019, the distribution of cases indicated that 56% were adult males, 32% were adult females, and 12% were children. The disease remains a major health concern,

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particularly in Low- and Middle-Income Countries (LMICs). Nigeria, for example, ranks 6th among the 30 countries with the highest TB burden globally and hold the top spot in Africa (GHE, 2020). In 2017, Nigeria was one of the top three countries responsible for 80% of the global gap between TB incidence and reported cases [1]. Additionally, Nigeria is classified as one of the 14 high-burden countries for TB, TB/HIV co-infections, and multi-drugresistant TB. In 2018, it was reported that around 30,000 children in Nigeria develop TB annually, and an alarming 18 people succumb to the disease every hour equating to 436 daily deaths (Centre for Disease Control and Prevention, 2019). This alarming situation underscores the urgent need for effective strategies to curb the spread of TB, a highly contagious airborne disease, and to protect lives.

TB is an airborne infectious disease caused by the bacterium Mycobacterium tuberculosis (MTB). TB is categorized into two types based on the area it affects. When the bacteria target the lungs and nearby regions, it is referred to as Pulmonary Tuberculosis (PTB). If the bacteria spread to other parts of the body, it is classified as Extra-Pulmonary Tuberculosis (EPTB). There are also two primary conditions of TB that are significant contributors to TB-related deaths worldwide, making them critical global health concerns: Active Tuberculosis (ATB) and Latent Tuberculosis (LTB). Active TB occurs when the bacteria are active and multiplying within the body. Individuals with active TB may exhibit symptoms such as a persistent cough lasting over three weeks, weight loss, night sweats, weakness, fever, chills, coughing up blood, increased mucus production, chest pain, and loss of appetite. They can spread the bacteria to others through the air when they talk, cough, laugh, or sneeze [2]. While TB primarily affects the lungs, it can occasionally impact other parts of the body, including the brain, spine, and kidneys [3]. Active TB is diagnosed through various methods, such as a skin test, blood test, chest X-ray, positive sputum smear culture, or a combination of these. In contrast, latent TB remains dormant in the body, does not cause symptoms, and cannot be transmitted to others. It is typically identified when an individual tests positive via a skin test or blood test [3]. Risk factors contributing to the development of TB include a weakened immune system caused by conditions such as HIV/AIDS, diabetes, and cancer. Additional factors include smoking, overcrowded living conditions, prisons, substance abuse, alcoholism, end-stage renal disease, and malnutrition, particularly among healthcare workers [4]. TB is an infectious disease that can be treated and cured using antibiotics. Prevention measures include administering BCG vaccines to infants and healthcare workers, covering the mouth when coughing or sneezing, and proper handling of sputum by laboratory personnel [5, 6].

The use of fractional derivatives in epidemiological modeling has gained significance due to their ability to account for the memory effects naturally present in many biological systems. Fractional derivative models provide a realistic representation of phenomena associated with the problem being studied [7]. These derivatives and integrals effectively capture the memory and hereditary characteristics inherent in various materials and processes[8]. As a result, non-integer models exhibit memory effects, and many operators possess cross-over properties that improve predictive accuracy.

Caputo and Fabrizio [9] introduced a new definition of fractional derivatives without a singular kernel, which has proven effective. Many researchers have adopted

this approach and further explored the concept of fractional derivatives and their application to hysteresis phenomena, particularly in 2017 [10, 11]. Fractional-order models effectively account for the memory effects associated with diseases. They are also widely recognized for their suitability in data fitting, offering flexibility through a range of fractional-order parameter options. In recent years, numerous studies have focused on fractional differential equation models for tuberculosis (TB). Fatmawati et al.[7] introduced a new fractional-order mathematical model for TB transmission dynamics, categorizing the population into two groups: children and adults. Their research utilized a novel fractional order to examine the dynamics of TB transmission within these age groups. They proposed an innovative numerical method to solve the fractional-order equations and employed two fractional operators, Caputo and Atangana-Baleanu, with graphical comparisons of their results provided. Saima et al. [12] introduced a novel mathematical framework using generalized fractional-order derivatives to analyze a TB model with treatment. Their study employed a generalized Caputo fractional derivative to investigate the nonlinear dynamics of the TB model, using Nigeria as a case study.

Saif Ullah et al. [13] developed a fractional model to study the dynamics of tuberculosis (TB) infection using the Caputo-Fabrizio derivative. Their research analyzed TB dynamics using confirmed cases reported by the National Tuberculosis Program in Khyber Pakhtunkhwa, Pakistan, between 2002 and 2017 to estimate the model's biological parameters. They applied the Adams-Bashforth technique to derive an iterative solution for the model. The study found that the fractional TB model in the Caputo-Fabrizio sense provided valuable insights into the model's complexity and offered reliable information for both integer and non-integer cases. A valuable approach in studying the epidemiology of TB is the application of Artificial Intelligence (AI) methods for evaluating TB transmission and diagnosis. The use of computer technologies has become increasingly significant in TB diagnostic procedures. In this context, Artificial Neural Networks (ANNs) are computational models designed to mimic the human brain. They comprise interconnected nodes (neurons) that process information, leveraging their self-learning capabilities to produce more accurate and reliable results. Syeda Meraj et al. [14] reviewed the application of artificial intelligence in diagnosing TB.

The research was motivated by the rising number of TB infections in Nigeria, which ranks 6th among the countries with the highest TB burden globally and 1st in Africa. Despite significant efforts by the Federal Government of Nigeria, the National Tuberculosis and Leprosy Control Program (NTBLCP), the Ministry of Health, and the WHO to combat the disease, TB remains a pressing public health challenge. To date, no mathematical model incorporating hybrid fractional differential equations and ANN methods has been proposed to simulate and predict the spread of TB in Nigeria. This study aims to fill that gap by formulating a hybrid fractional differential equation model combined with ANN techniques to forecast the transmission dynamics of TB in the country. ANN establishes patterns for precise calculations at each node in the architecture, driven by the sigmoid function. On the other hand, FODE incorporate memory effects associated with diseases, making them well-suited for data fitting and prediction, with the flexibility to select various fractional order parameters, α. Combining FODE with ANN creates an effective tool for data fitting and prediction. ANN performs accurate calculations of input data at each node, while FODE predicts the output data generated by the ANN

framework. This integration forms the foundation for using the hybrid FODE/ANN model to predict TB transmission in Nigeria.

2. Material and Methods

2.1. **Methodology of Fractional Differential Equation Models.** The model is an SEIRS epidemic type introduced by infecting one individual. The model describes the transmission dynamics of a population that is susceptible to infection by Mycobacterium tuberculosis. This model on the spread of TB transmission consists of four compartments according to the disease related to the individual, namely; Susceptible $S(t)$, Exposed $E(t)$, Infected I(t), and Recovered R(t) at any given time, t. The model explains the transmission dynamics of a population susceptible to infection by Mycobacterium tuberculosis. In this framework, individuals in the latent stage are not infectious, while those in the infected compartment have active TB bacteria and can transmit the disease. Individuals in the recovered compartment have undergone treatment, recovered from TB , and acquired temporary immunity. However, they eventually return to the susceptible compartment and can be reinfected [15]. The population has two parameters, the birth rate b and the death rate μ; and the model disease has five compartments, the transmission rate β, the progression rate to infection ε the recovery rate γ, the disease death rate δ and the acquired immunity temporary rate θ. The population size at time t, is $N(t) = S(t) + E(t) + I(t) + R(t)$ (when n is important an n -index is added). The populates then initiate at $Z(0) = S(0), E(0), I(0), R(0) = (n - 1, 1, 0, 0)$.
Considering the description, assumptions variables, and parameters, the system dynamics of TB transmission is shown in Figure 1:

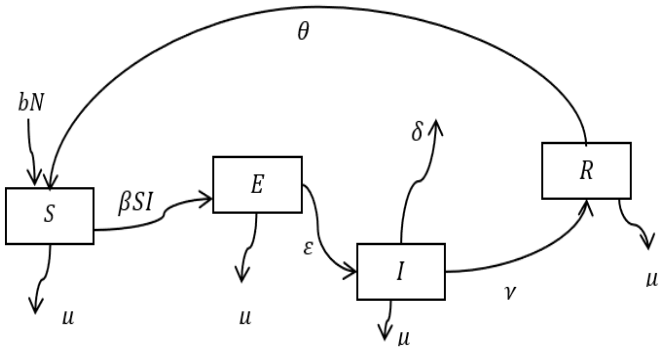

Figure 1. Schematic representation of tuberculosis transmission.

The deterministic SEIRS model is given by the following system of ordinary differential equations:

$$\frac{dS(t)}{dt} = bN - \beta S(t)I(t) - \mu S(t) + \theta R(t) \tag{1}$$

$$\frac{dE(t)}{dt} = \beta S(t)I(t) - (\varepsilon + \mu)E(t), \tag{2}$$

$$\frac{dI(t)}{dt} = \varepsilon E(t) - (\gamma + \mu + \delta)I(t), \tag{3}$$

$$\frac{dR(t)}{dt} = \gamma(t) - (\mu + \theta)R(t), \tag{4}$$

$S(0) > 0; E(0) > 0; I(0) > 0; R(0) \geq 0.$

We derive our model equations using fractional differential equations, as they offer an effective method for predicting and describing memory characteristics, a fundamental feature of biological systems [16]. The fractional-order model for TB transmission, expressed in the Caputo sense, is presented in equation 5-8:

$${}^{c}D_t^{\alpha} S = b - \beta S(t)I(t) - \mu S(t) + \theta R(t), \tag{5}$$

$${}^{c}D_t^{\alpha} E = \beta S(t)I(t) - (\varepsilon + \mu)E(t), \tag{6}$$

$${}^{c}D_t^{\alpha} I = \varepsilon E(t) - (\gamma + \mu + \delta)I(t) \tag{7}$$

,

$${}^{c}D_t^{\alpha} R = \gamma I(t) - (\theta + \mu)R(t), \tag{8}$$

where ${}^{c}D_t^{\alpha}$ is the left Caputo derivative of order $\alpha \in [0, 1]$, α represents the fractional order and $0 < \alpha \leq 1$.

The initial values for the model variables in the fractional order model are given by:

$$S(0) = S_0, E(0) = E_0, I(0) = I_0, R(0) = R_0 \tag{9}$$

2.2. **Grünwald-Letnikov Method.** We use the Grünwald-Letnikov Method according to Dorcak [17] for our numerical simulation in Matlab. The relation for the numerical approximation of $\alpha - tk$ derivative at the point $kh, (k = 1, 2, 3, \ldots)$ has the following form:

$$(K - Lm/h)D_{tk}^{\alpha} f(t) \approx h^{\alpha} \sum_{j}^{k} (-1)^j f\left(t_{k-1}\right) = h^{\alpha} \sum_{j=v}^{k} C_{-j}^{\alpha} f\left(t_{k-j}\right), \tag{10}$$

where Lm is the memory length, $tk = kh$, where h the time is a step of calculation and $Cj(j = 1, 2, 3, \ldots)$ are binomial coefficients. For their calculation, we can use for instance the following expression:

$$C_0^{\alpha} = 1, C_j^{\alpha} = \left(1 - \frac{1 + \alpha}{j}\right) C_{j-1}^{\alpha}. \tag{11}$$

A general numerical solution of a non-linear fractional differential equation in the form

$$ {}_aD_t^{\alpha} y(t) = f(y(t)) \tag{12}$$

This is expressed using the relations 11 and 12 as follow:

$$ y\left(t_k\right) = f\left(y\left(t_k\right), t_k\right) h^{\alpha} - \sum C_j^{\alpha} f\left(t_{k-j}\right), \tag{13}$$

The proposed numerical simulation on the set of four non-linear FODEs used for describing the mathematical model for predicting TB in 5 - 8 with fractional order α has a solution of the form:

$$\begin{aligned}
S\left(t_k\right) &= \left[b - \beta S\left(t_{k-1}\right)\right)\left(t_{k-1}\right) - \mu\left(t_{k-1}\right) + \theta R\left(t_{k-1}\right) h^{\alpha} - \sum_{j=v}^{k} C_j^{\alpha} S\left(t_{k-j}\right) \\
E\left(t_k\right) &= \left[\beta S\left(t_k\right) I\left(t_{k-1}\right) - (\varepsilon + \mu) E\left(t_{k-1}\right)\right] h^{\alpha} - \sum_{j=v}^{k} C_j^{\alpha} E\left(t_{k-j}\right) \\
I\left(t_k\right) &= \left[\eta E\left(t_{k-1}\right) - (\delta + m + \sigma) I\left(t_{k-1}\right)\right] h^{\alpha} - \sum_{j=v}^{k} C_j^{\alpha} I\left(t_{k-j}\right) \\
R\left(t_k\right) &= \left[\gamma\left(t_k\right) - (\mu + \theta) R\left(t_{k-1}\right)\right] h^{\alpha} - \sum_{j=v}^{k} C_j^{\alpha} R\left(t_{k-j}\right)
\end{aligned} \tag{14}$$

2.3. **Fitting Data on FODE Model.** In this study, a numerical solution for the model is obtained by fitting TB data to the FODE model to validate the accuracy of the data. The Grünwald-Letnikov method is applied to derive explicit solutions for the non-linear fractional order differential equation. Initially, the system of equations for the TB model is discretized, as shown in equation (14), and a MATLAB code is developed to simulate the system. The time horizon for the simulation spans 11 years. For parameter estimation, the first curve fit function in MATLAB is utilized, employing the Levenberg-Marquardt algorithm. Additionally, the sigmoid function is used to calculate the transmission rate $\beta(t)$, considering the time dependency of the transmission parameters.

2.4. **Description of Artificial Neural Network (ANN).** An Artificial Neural Network (ANN) is a highly interconnected network of multiple processing units, referred to as neurons, structured in a manner that mimics the human brain. The fundamental objective of neural networks is to transform input data into meaningful outputs. These computational models operate in parallel, utilizing numerous simple units, and are particularly effective in tasks such as pattern recognition [18].

A standard ANN model comprises three distinct layers with interconnected nodes that facilitate signal transmission between them: the input layer, hidden layer, and output layer. Neurons within the network are linked and interact with one another. Each node receives input data, processes it through basic computations, and transmits the output to the subsequent neuron. This output, known as the activation or node value, is determined by assigned weights for each connection. The ANN framework is systematically structured into the following three layers:

- Layer 1 (Input layer): this is the first layer that receives the input values or data.
- Layer 2 (Hidden layer): this is the second layer where the computations are carried out to give the required output. Weights are being adjusted at each node to the desired output. This is also where learning or training is carried out at this stage. This is the determinant of the output. It is made up of a set of neurons between inputs and output layers. The layers can be single or multiple depending on the desired model output.
- Layer 3 (Output layer): The output layer typically consists of multiple neurons corresponding to the predicted compartments of the model. In this case, the output includes Susceptible (S), Exposed (E), Infected (I), and Recovered (R) individuals. Each output neuron provides a value ranging between 0 and 1, representing the proportion of the population in each compartment. The number of output neurons depends on the training of the model to capture the required epidemiological dynamics.

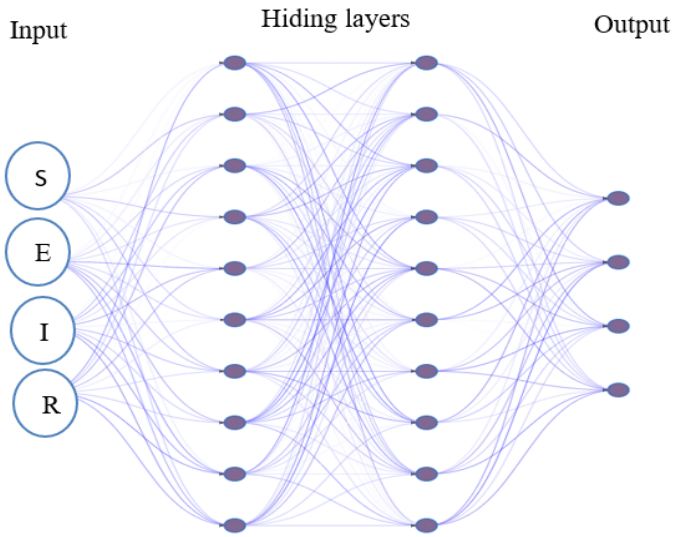

FIGURE 2. Artificial Neural Network Scheme for SEIR TB model.

2.5. **Artificial Neural Network Model Analysis.** For the NN model analysis, we utilized an ANN, specifically a simple feed-forward neural network, to predict TB cases for a given year. The model comprises three layers: an input layer, two hidden layers with multiple nodes, and an output layer. The input layer consists of four nodes, corresponding to the four input variables Susceptible (S), Exposed (E), Infected (I), and Recovered (R) from the SEIR TB model. The data used for simulation includes either yearly confirmed infection cases or cumulative infection cases. Since these plots exhibit non-linear trends, they can be effectively represented using an exponential function, such as the sigmoid function, which is expressed as follows: Sigmoid function $= \frac{1}{1+e^{-a(t-c)}}$

Here, a represents the power gain (exponent), which can be either positive or negative, while c denotes the time constant. The sigmoid function remains positive regardless of the signs of these parameters, ensuring its suitability for representing physical components such as the variables in this model. At each time c, when a significant change occurs in the reported data, the sigmoid function adjusts its magnitude to determine new parameter values. In other words, the newly proposed rate function is composed of multiple branches of sigmoid functions, each characterized by a distinct gain and time constant. The final rate function is obtained by summing these branch functions, as expressed below:

Rate Function $(1) = \sum_{i=1}^{n} \frac{g(i)}{1+e^{-a(t-c(i))}}$
where g is the gain of the branch $-i$. The following rate function is the latter concept with a generalized infection or recovery rate function used for tracking the problem. The higher the number of branches (n) the smoother and better the correlation between the reported and the
simulated plots. The generalized rate is given by:

$$R(t) = \begin{cases} \sum\limits_{i=1}^{n} \left| \frac{g(i)}{1+e^{-a(t-0)}} - \frac{g(i+1)}{1+e^{-a(t-c(1))}} \right|, & \text{for } i = 1 \\ \sum\limits_{i=2}^{n-1} \left(\frac{g(i)}{1+e^{-a(t-c(i))}} - \frac{g(i+1)}{1+e^{-a(t-c(i+))}} \right), & \text{for } i \neq \{1, n\} \\ \sum\limits_{i=1}^{n} \frac{g(i)}{1+e^{-a(t-c(i))}}, & \text{for } i = n \end{cases} \tag{15}$$

The time parameter c is represented by a vector whose length is the number of sigmoid branches i.e. the number of iterations of the rate functions. The summed sigmoid function can further be generalized by subtracting the previous sigmoid function from the one under consideration. Parameters with other options can be estimated using the following equation:
Rate function $(3) = \sum((1) + (2) + (3))e^{-pt} + q$
where p and q are the parameters that need to be estimated.
To determine the initial parameter values, we utilize the confirmed infection ratio and normalize it within the range of 0 to 1. This normalized value is then applied to the gain parameters of the sigmoid branches, denoted as g . Considering the time parameter c from serial number 2 in equation 15, a statistical approach is employed to automatically identify the optimal parameter values for the best curve fit. Due to its simplicity and broad applicability, this statistical method is regarded as the standard approach for the program.

3. Result and discussion

3.1. **Data Presentations.** These data were obtained from TB reports by the WHO, Nigeria TB Data Base 2021. The data sourced was from 2010 to 2020 for Exposed, Infected, and Recovered individuals over the period as shown in Table 1. The parameters used for the model plots and their estimated values are presented in Table 2;

Year	Exposed	Infected	Recovered
2010	347000	84121	70340
2011	357000	86778	72562
2012	366000	92818	77613
2013	376000	94825	79080
2014	386000	86464	74824
2015	397000	87211	73071
2016	407000	97279	83626
2017	418000	102387	87643
2018	429000	103921	90075
2019	440000	117320	103029
2020	452000	135784	121785

TABLE 1. Nigeria TB Data from 2010-2020

Parameter	Value
A	0.2500
P	7.5365
Q	0.0000
Λ	0.0752
Γ	0.0299
$\alpha 1$	0.9490
$\alpha 2$	1.0000
$\alpha 3$	1.0000
$\alpha 4$	0.9012
B	0.9325
M	0.1524
C	0.9000
Θ	0.3917
Δ	0.0292
B	0.9164
R2	0.9968

TABLE 2. Model parameters and estimated values

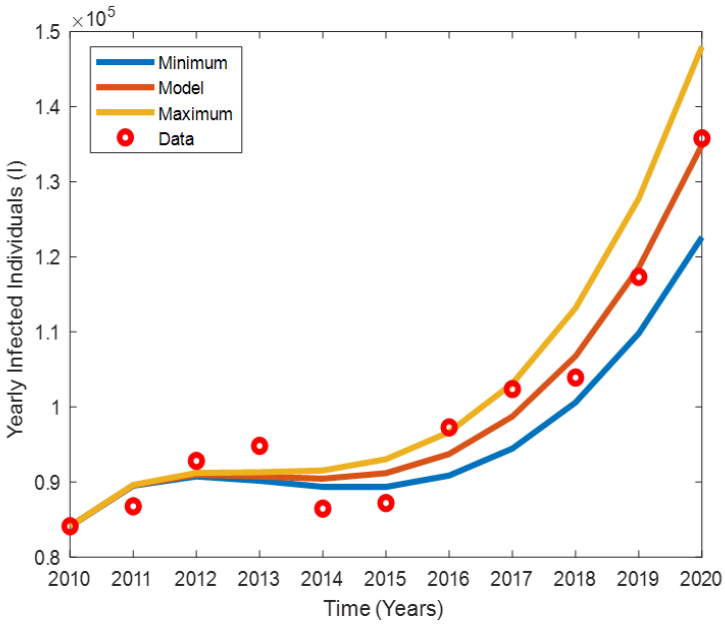

FIGURE 3. Plot of yearly infected individuals.

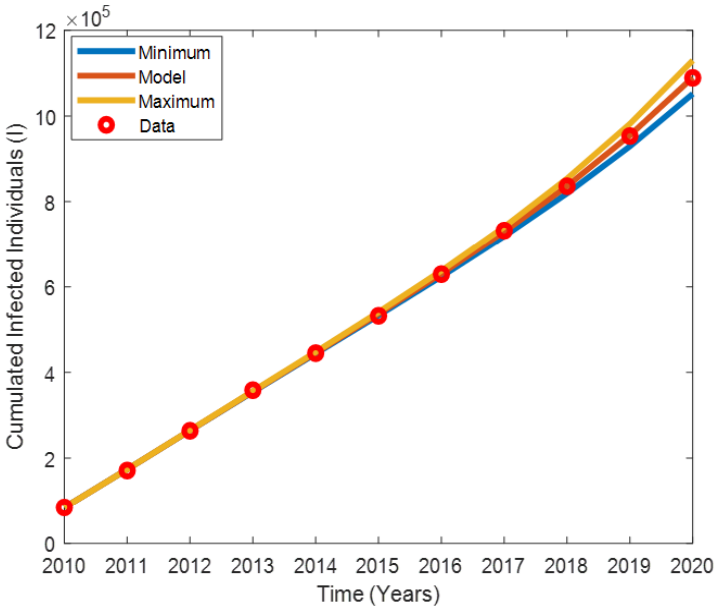

FIGURE 4. Plot of cumulative infected individuals.

Examining the plots of yearly infected TB individuals in Figure 3 and cumulative infected TB individuals in Figure 4, it is evident that the orange line, representing the model data, aligns more closely with the reported data in Figure 4 than in Figure 3. This suggests that the transmission rate β of TB is estimated more accurately when using cumulative yearly TB infection data rather than yearly infection data alone. Consequently, the orange line signifies the model data that closely matches all reported TB data points within a 15% confidence interval. A 15% confidence interval indicates that the transmission rate predictor β provides a more precise and reliable fit between the reported TB data and the model data. As a result, the accuracy and stability of the model coefficients improve when using cumulative TB case data. Therefore, forecasting the transmission rate of TB cases in Nigeria is more effective when cumulative infection data is incorporated into the model rather than relying solely on yearly infection data. Additionally, it is important to note that a higher confidence interval reduces prediction accuracy, whereas a lower confidence interval enhances the precision of the predictions.

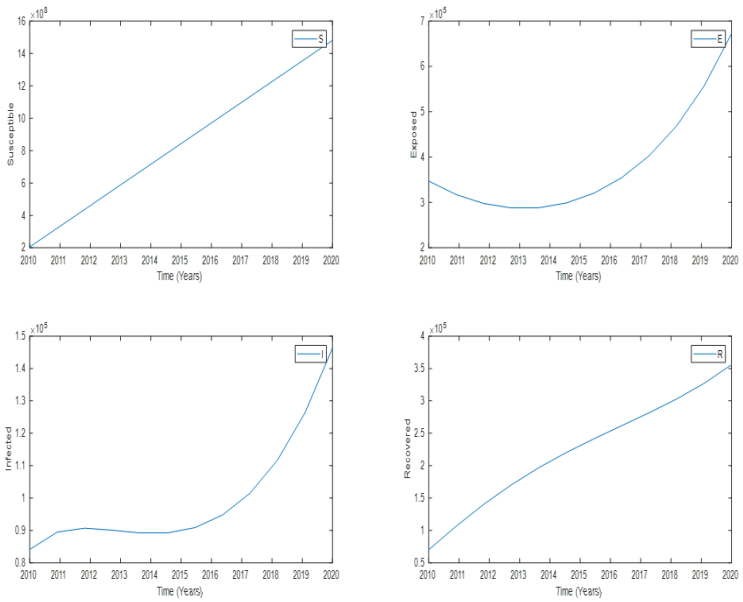

FIGURE 5. Plots of the FODE model.

Figure 5 presents the FODE model plots for TB data in Nigeria, illustrating the trends of susceptible, exposed, infected, and recovered individuals from 2010 to 2020. The results indicate a proportional increase in recovered cases alongside infected cases over the years. This trend suggests that with enhanced intervention strategies, there is potential for significant reduction or even eradication of TB in Nigeria.

3.2. **Fitting Data on Hybrid FODE/ANN Models.** In this section, we integrate TB data into a hybrid FODE and ANN model by combining the outputs of both models to create a unified FODE/ANN framework. The results are then compared to identify the most accurate approach for predicting TB cases in Nigeria. The SEIR model is trained within the ANN using the estimated parameters from the FODE model. Figures 5 and 6 illustrate the predictive performance and validation accuracy of the FODE and ANN models, respectively. Figure 5 presents the FODE model's predictions of the number of infected individuals from 2010 to 2020, comparing the model's elevated predictions with recorded data. This comparison highlights the model's capability to capture the trend of TB transmission over time. Meanwhile, Figure 6 demonstrates the ANN model's validation performance, showing that the best Mean Squared Error (MSE) achieved is 1.196×10^{-14} at epoch 63. This exceptionally low MSE indicates the ANN model's high predictive accuracy, reinforcing its reliability in forecasting TB dynamics.

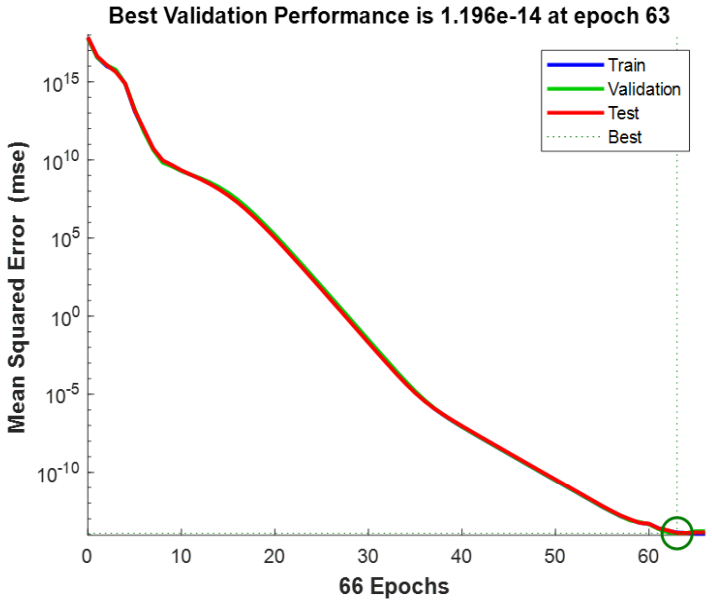

FIGURE 6. Validation performance of the ANN model

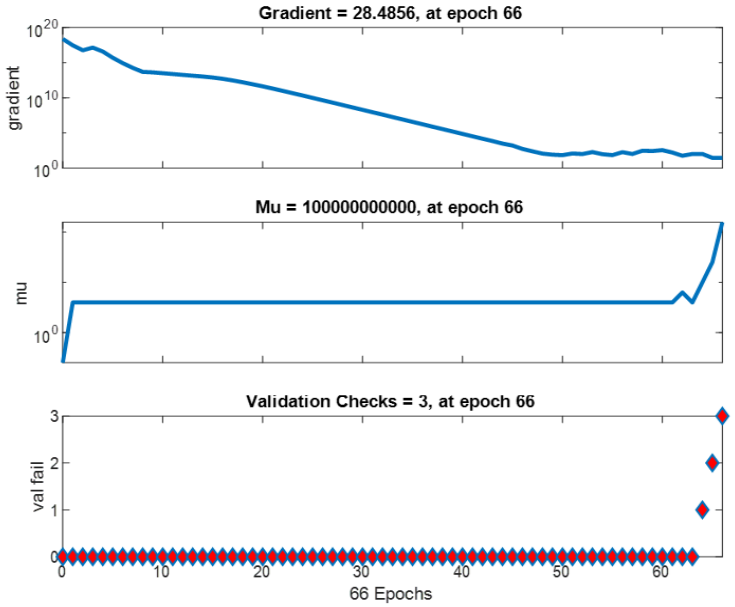

FIGURE 7. Training stage of the ANN model

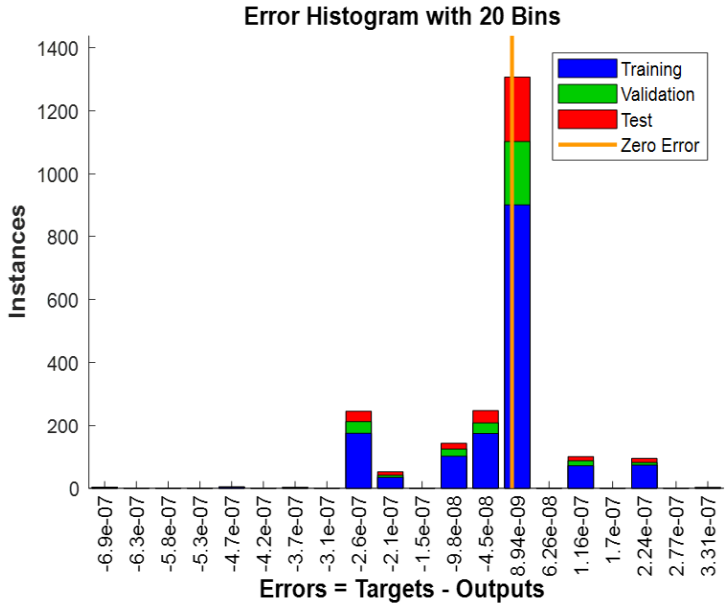

FIGURE 8. Error histogram of the ANN model

Figures 7–10 provide a comprehensive analysis of the training and performance of the Hybrid ANN and FODE model. Figure 7 highlights the training progress of the ANN model, showing key parameters such as the gradient (28.4856) and Mu value (10^{10}) at epoch 66, along with three validation checks, indicating model stability. Figure 8 presents the error histogram with 20 bins, illustrating the distribution of errors across training, validation, and test datasets, which helps assess biases and anomalies. Figure 9 showcases the regression analysis, visually demonstrating the alignment between the model's predictions and actual data, thereby validating its accuracy. Finally, Figure 10 displays the hybrid ANN and FODE model's predictive performance, emphasizing the advantage of integrating ANN with FODE to enhance the model's reliability and precision.

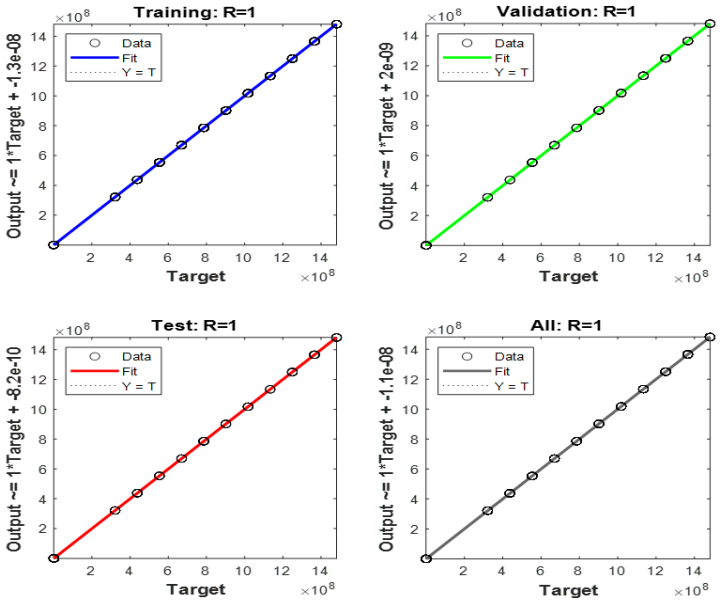

FIGURE 9. Regression of the data and ANN model prediction

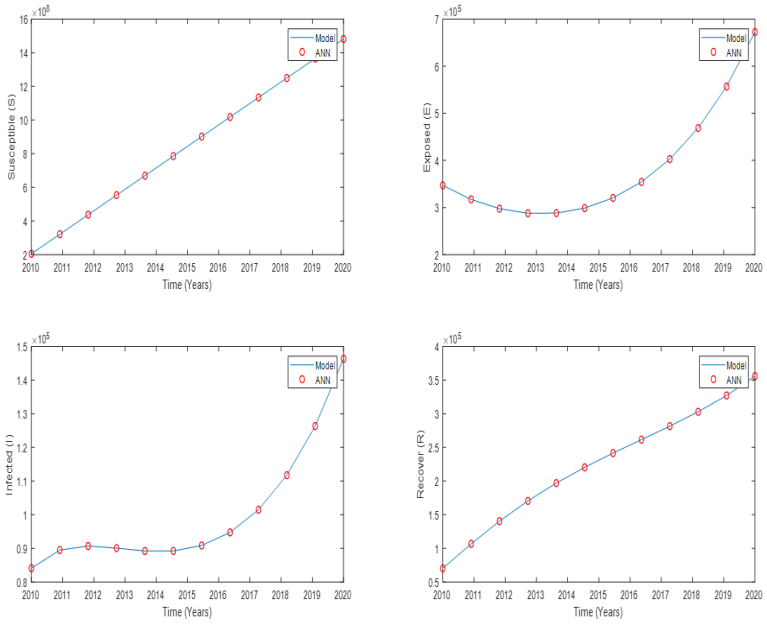

FIGURE 10. Plot of the Hybrid ANN and the FODE model

4. Conclusion

In this study, we developed and analyzed a fractional-order SEIRS model to investigate the transmission dynamics of tuberculosis (TB). The model incorporates the memory effect inherent in fractional differential equations, which provides a more realistic representation of TB progression compared to classical integer-order models. The deterministic SEIRS model was extended to its fractional counterpart using the Caputo derivative, which effectively captures the long-term dependencies in disease transmission and recovery processes. The numerical simulation was performed using the Grunwald-Letnikov method, allowing us to approximate the solutions of the fractional-order system. Our findings demonstrate that the fractional-order approach offers improved flexibility in modeling the spread of TB by accounting for past states of the system, thereby enhancing predictive accuracy. The estimated parameters obtained through curve fitting with real-world TB data confirm the validity of the fractional model in capturing epidemiological trends. Additionally, we integrated an Artificial Neural Network (ANN) framework to refine model predictions and provide a data-driven approach to forecasting TB cases. The ANN model, structured as a feed-forward network with multiple hidden layers, effectively mapped the complex non-linear relationships within the SEIRS compartments. By using sigmoid functions, the ANN was able to adjust transmission rate parameters dynamically, improving the model's capability to predict infection trends over time. Our results indicate that the combination of fractional differential equations and artificial intelligence techniques enhances the understanding of TB transmission dynamics. This hybrid modeling approach not only offers a robust theoretical foundation but also serves as a valuable tool for public health planning and intervention strategies. Future work may focus on incorporating additional factors such as vaccination strategies, drug resistance, and spatial effects to further refine the model's applicability to real-world scenarios.

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