A Study of Borderline Application on Mathematical Modelling of Leprosy Transmission in Nigeria

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ABSTRACT

Leprosy, one of the neglected tropical illnesses, is a chronic, painful, crippling, and disfiguring disorder that is most prevalent in the context of extreme poverty, particularly among the rural poor and certain disadvantaged urban groups. Peripheral nerves are largely impacted by leprosy. This study's main goal is to use a deterministic mathematical model based on ordinary differential equations and numerical simulations to model the leprosy transmission in Nigeria.

The model divided the population concerned into six compartments namely susceptible (S(t)), exposed (E(t)), multibacillary leprosy (MB), paucibacillary leprosy (PB), recovered rate (R(t)) due to treatment and borderline infection (BI) which was newly introduced and were formulated and analyzed with numerical simulations. The outcome of the numerical simulations indicates that while the addition of an exposed population, or the E(t) compartment, appears to slow the outbreak but does not appear to reduce the number of people ultimately infected by the disease. Also, the borderline, PB and MB slowly increase before flattening out. The vulnerability level off after reaching a peak and then level off. The recovered rate increases over 100 years before levelling off, which is consistent with real-world circumstances. In conclusion, we can show that the simulation roughly matches the real-life situation of the symptoms. Consequently, the susceptible and exposed population should receive vaccination intervention that is properly administered in the meantime and to stop the disease from spreading further in Nigeria, the resurgence of the disease needs to be addressed.

(Keywords: mathematical model, simulation, susceptible, exposed, multibacillary leprosy, paucibacillary leprosy, recovery rate, borderline)

INTRODUCTION

Leprosy, one of the neglected tropical diseases, is a chronic, incapacitating, disfiguring condition that is most common in areas of extreme poverty, particularly among underprivileged populations in some disadvantaged urban areas. The chronic infectious disease leprosy, sometimes referred to as Hansen's disease after the scientist identified *Mycobacterium leprae* in 1873, mainly affects the skin, peripheral nerves, upper respiratory system, and eyes.

The main leprosy symptom is disfiguring skin lumps, pimples, or sores that last for several weeks or months. The sores on the skin are pale in color. Muscle weakness and a loss of feeling in the arms and legs are two symptoms of nerve injury. The light-yellow patches depict body sections where few patients reported experiencing pain; the orange and light-red areas depict regions where pain episodes occurred on average frequently (Haroun, *et al*., 2019).

The patients also filled out the nine-item Brief Pain Inventory (BPI) short form, which assesses pain intensity and interference (Haroun, Vollert, and Lockwood, 2019). It normally takes 3 to 5 years after contact with the leprosy-causing germs for symptoms to appear. Some may take twenty years to begin exhibiting symptoms. The incubation period is the time frame between contact with the pathogens and the appearance of symptoms. Because leprosy takes so long to manifest, doctors have a tough time determining how and when a patient caught the illness. Leprosy may be treated.

Over 14 million leprosy patients have received a cure in the past 20 years. Leprosy is one of the infectious diseases in Nigeria as well as other developing countries which cannot be underrated due to its hideous deformities to the

afflicted if undetected with time or adhering to self-medication at various homes which can contribute to a high transmission rate of the disease.

A member of a fixed population mix homogeneously can become infected and infectious (Kermack and McKendrick, 1927). The dynamics of leprosy transmission among specific individuals in a population are explored in the majority. The epidemiology, the management, the impact of various parameters and situations, interactions with various opportunistic infections, and other aspects of leprosy have all been modelled. Sadly, only a small number of research efforts have focused on some particular parts of the epidemic in Nigeria.

The fact that only a little research has been done in the field of leprosy's epidemiology modelling, even though it is one of the infectious illnesses in Nigeria, serves as the inspiration for this work. This research aims for specific mathematical models that can aid in our comprehension and control of disease transmission and the effects of vaccination in Nigeria. This assessment can therefore be performed using a deterministic mathematical model, having in mind some studies which have boycotted some biological features and transmission patterns of leprosy diseases in Nigeria that are not included in the basic model will be strategized out in the future model.

Epidemiologists, health policymakers, and healthcare professionals will all be able to explain the rise and fall in the number of patients seeking medical attention using this future model. The sole objective of this study is to employ a deterministic mathematical model to study the transmission of leprosy in Nigeria. The second objective is to establish the reproduction numbers (R_0), for the models and determine the stability and disease-free equilibrium states of the diseases. Another objective was to examine the compliance and adequacy of treatment on SEIR and SEIRD transmission models for leprosy disease in Nigeria which will contribute immensely to the existing body of knowledge.

LITERATURE REVIEW

Leprosy outbreaks have had a tremendous impact on the human population. Despite decades of study, the widespread availability of a vaccine, and a highly visible WHO effort to promote a coordinated global leprosy eradication plan, leprosy still exists in several underdeveloped nations. Included is Nigeria. Leprosy eradication as a public health concern was a commitment made by the World Health Organization (WHO) and its member nations by the year 2000.

Elimination was defined as a prevalence of less than 1 case per 10,000 individuals. Leprosy is currently under control in the majority of countries, but multiple studies show that the disease is becoming more common globally as a result of the continent's recovery (Mushayabasa, *et al*., 2012). The obligate intracellular parasite *Mycobacterium leprae*, which is closely related to the bacterium Mycobacterium tuberculosis and causes the infectious disease known as leprosy, also referred to as Hansen's disease is the cause of this chronic, progressive condition.

Leprosy tends to recur more frequently in Africa (Nyamogoba, Mbuthia, and Mulambalah, 2019). Nigeria was one of seven African nations that reported more than 1,000 new cases annually in 2006. In 2003, Nigeria had less than one leprosy case per 10,000 residents. Since then, though, it has fought against prejudice against those who have the disease and its evident symptoms as well as the impairment it brings about. Many people struggle to ask for help because they worry about being stigmatized.

Graham, *et al*. (2018) employed the Quantitative Modeling of the Leprosy method. Leprosy transmission dynamics are non-linear, which means that each person's exposure to *M. leprae* in the past influences the incidence of leprosy today. Consequently, mathematical modelling is a potent and useful tool for capturing non-linear transmission dynamics and determining the intervention's long-term effects (Medley, Blok and Crump, 2018).

According to Shatanawi, *et al*. (2020), many mathematical models have been explored using a variety of methodologies, and these models show instances of randomness. To comprehend the phenomenon of leprosy transmission better, Souza and Luna (2019) claim that geographical data modelling and the integration of several mathematical models might be applied.

Around three million people worldwide suffer from leprosy-related disabilities, according to Britton and Lockwood (2004). If the illness is not

controlled, it is predicted that this figure will rise to one million in the coming decades (Meima, *et al.*, 2008).

METHODOLOGY

Several efforts have been made by researchers in modelling disease epidemiology abound in the deterministic formulation and methods of solution. In this section, more effort will be made to improve on these models with the primary aim to modify and adopt Chiyaka Hybrid model for the analysis of leprosy transmission.

Model Assumption

Kermack and McKendrick (1927) gave some assumptions a good deterministic compartment model should satisfy:

1) Population must be fixed
2) The only way a person can leave the susceptible group is to become infected.
3) The only way a person can leave the infected group is to recover from the disease.
4) Once a person has recovered, the person received immunity
5) Age, sex, social status, and race do not affect the probability of being infected.
6) There is no inherited immunity
7) The member of the population mix homogeneously (have the same interactions with one another to the same degree.

Following the supposition above and after studying the aforementioned deterministic compartment models, the discovery of *Leprae* in 1874 refuted the hereditary theory of leprosy. However, the argument over how *M. leprae* is transmitted is still being debated today. Skin-to-skin contact and airborne transmission, with the release of bacilli from the nasal mucosa of infectious individuals and entry of bacilli through the respiratory system, are the two most popular explanations for leprosy transmission.

The probe will first consider the unresolved issue of who and how much is facilitating transmission. The idea that patients are the only sources of infection will also be challenged. Furthermore, the length of the research periods for disease transmission is inadequate, which is problematic given that leprosy transmission changes in populations only occur gradually due to the disease's lengthy and variable incubation period.

Modified Chiyaka Hybrid SEIR and SEI Leprosy Model

Following from the Chiyaka et al. (2013) hybrid deterministic SEIR model for paucibacillary leprosy (PB) and SEI model form multibacillary leprosy (MB) when no treatment and control measures are put in place. The new model proposed in this thesis will incorporate the borderline infection (BI) which involve symptoms of PB and MB infection. The model will divide the population concerned into the following six compartments in Table 1.

Table 1: The Six Compartment of Modified Chiyaka Hybrid SEIR and SEI Leprosy Model.

S(t): susceptible individuals who are yet to come into contact with the infection.
E(t): individuals who have been infected by leprosy but not yet infectious nor showing any symptoms,
P(t): infectious class of individuals whose infection has progressed to paucibacillary leprosy,
M(t): infectious class of individuals whose infection has progressed to multibacillary leprosy,
B(t): infectious class of individuals whose infection has progressed to borderline leprosy and
R(t): non-infectious group of people who have successfully recovered from the disease and are immune to re-infections.

Individuals move from one class to the other as their status with the disease evolves. Let *N(t)* be the total number of people in the population at any time *t*, then:

$M/N, P/N$ and B/N

represent the probability that a randomly selected individual has multibacillary, paucibacillary and borderline leprosy, respectively. Let the probability of infecting a susceptible during interaction be β_M, β_P and β_B for MB, PB and BI cases, respectively. The probability of a susceptible being infected by an MB and a PB case is:

$\frac{\beta_M M}{N}, \frac{\beta_P P}{N}$ and $\frac{\beta_B B}{N}$

correspondingly. The force of infection for the disease can be expressed as:

$$S\left(\frac{\beta_M M}{N} + \frac{\beta_P P}{N} + \frac{\beta_B B}{N}\right)$$

Infection is transmitted to the susceptible persons through successful contacts with either a paucibacillary or multibacillary or borderline patient.

Class *E(t)* is increased by graduands from the susceptible class and decreases by natural death, progression of the infections to either PB or MB or BI leprosy and by subsequent recoveries by some of its members.

For patients who move to class *M(t)*or *B(t)*, they either die naturally or due to leprosy related complications or eventually succumb to the wasting effects of the disease itself. Once an individual has progressed to *P(t)* compartment he/she eventually recovers and moves to class *R(t)* where he/she is immune to reinfections and is non-infectious.

Assumptions of the Model:

i. The population is homogenous, and each individual is equally likely to interact with the other.

ii. Transmission follows the mass action principle; if *I(t) i*s the number of infectious individuals and *S(t)* and *N(t)* have their usual meaning, then the standard incidence per unit time is of the form:

$$\frac{\beta_i SI}{N}, for\ i = M, P, B$$

iii. Transmission is only through interactions between the susceptible person and either a PB or MB or BI individual.

iv. Patients who recover from the disease become immune to re-infections and are no longer infectious.

v. No individual is naturally or artificially immune to the disease, immunity is only acquired through recovery from infection.

vi. Paucibacillary is not fatal, it is self-limiting and all its cases eventually recover.

vii. Multibacillary and borderline are relentlessly progressive and is fatal.

viii. MB and BI patients are not isolated thus continue to be infectious until they pass away.

ix. There is no migration, new recruits enter the population through birth and the population decreases by natural or disease induced mortality.

The population transfer among the six compartments is schematically depicted in the transfer diagram in Figure 1.

Model Equations for Modified Chiyaka Hybrid SEIR and SEI Leprosy Model without Treatment

The evolution of the number of individuals in each compartment is described by the following system of ordinary differential equations:

Table 2: Parameters for Modified Chiyaka Hybrid SEIR and SEI Leprosy Model Without Treatment.

β_M: the probability of an MB case infecting a susceptible during interaction.
β_P: the probability of a PB case infecting a susceptible during interaction.
β_B: the probability of aBI case infecting a susceptible during interaction.
α_M: the rate of progression from *E(t)* to multibacillary leprosy.
α_P: the rate of progression from *E(t)* to paucibacillary leprosy.
α_B: the rate of progression from *E(t)* to borderline leprosy.
δ_E: the recovery rate for the asymptomatic patients in *E(t)*.
δ_P: the recovery rate for the PB patients.
μ: the natural death rate,
η_M: disease induced mortality rate for MB patients,
η_B: disease induced mortality rate for BI patients, and
Λ: birth rate.

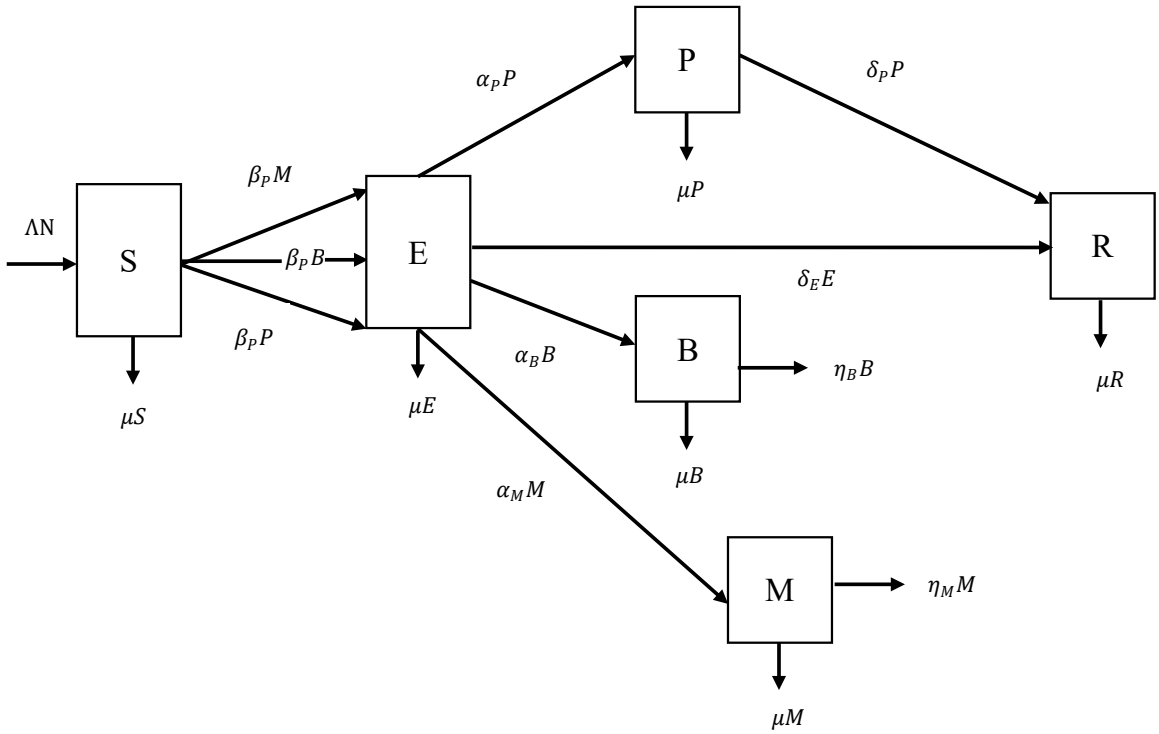

Figure 1: Modified Chiyaka Hybrid SEIR and SEI Leprosy Model without Treatment.

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Lambda N - \frac{\beta_P SP}{N} - \frac{\beta_B SB}{N} - \frac{\beta_M SM}{N} - \mu S \\
\frac{dE}{dt} &= \frac{\beta_P SP}{N} + \frac{\beta_B SB}{N} + \frac{\beta_M SM}{N} - (\alpha_M + \alpha_P + \alpha_B + \delta_E + \mu)E, \\
\frac{dM}{dt} &= \alpha_M E - (\eta_M + \mu)M, \\
\frac{dB}{dt} &= \alpha_B E - (\eta_B + \mu)B, \\
\frac{dP}{dt} &= \alpha_P E - (\delta_P + \mu)P, \\
\frac{dR}{dt} &= \delta_E E + \delta_P P - \mu R.
\end{aligned}\right\} \quad \textbf{(1)}$$

Initial conditions of system (1) are $S(0) = S_0, E(0) = E_0, M(0) = M_0, P(0) = P_0,\ B(0) = B_0,$ $R(0) = R_0$ and $N(0) = N_0$, where $S_0, E_0, M_0, P_0, B_0, R_0$ and N_0 are all greater than zero and $N(t) = S(t) + E(t) + P(t) + B(t) + M(t) + R(t)$

Table 3: Parameters for Modified Chiyaka Hybrid SEIR, SEI and SEIRD Leprosy Model With Treatment.

β_M: the probability of an MB case infecting a susceptible during interaction.
β_P: the probability of a PB case infecting a susceptible during interaction.
β_B: the probability of aBI case infecting a susceptible during interaction.
α_M: the rate of progression from *E(t)* to multibacillary leprosy.
α_P: the rate of progression from *E(t)* to paucibacillary leprosy.
α_B: the rate of progression from *E(t)* to borderline leprosy.
δ_E: the recovery rate for the asymptomatic patients in *E(t)*.
δ_M: the recovery rate for the MB patients.
δ_B: the recovery rate for the BI patients.
δ_P: the recovery rate for the PB patients.
μ: the natural death rate,
η_M: disease induced mortality rate for MB patients,
η_B: disease induced mortality rate for BI patients, and
Λ: birth rate.

The population transfer among the six compartments is schematically depicted in the transfer diagram in Figure 2).

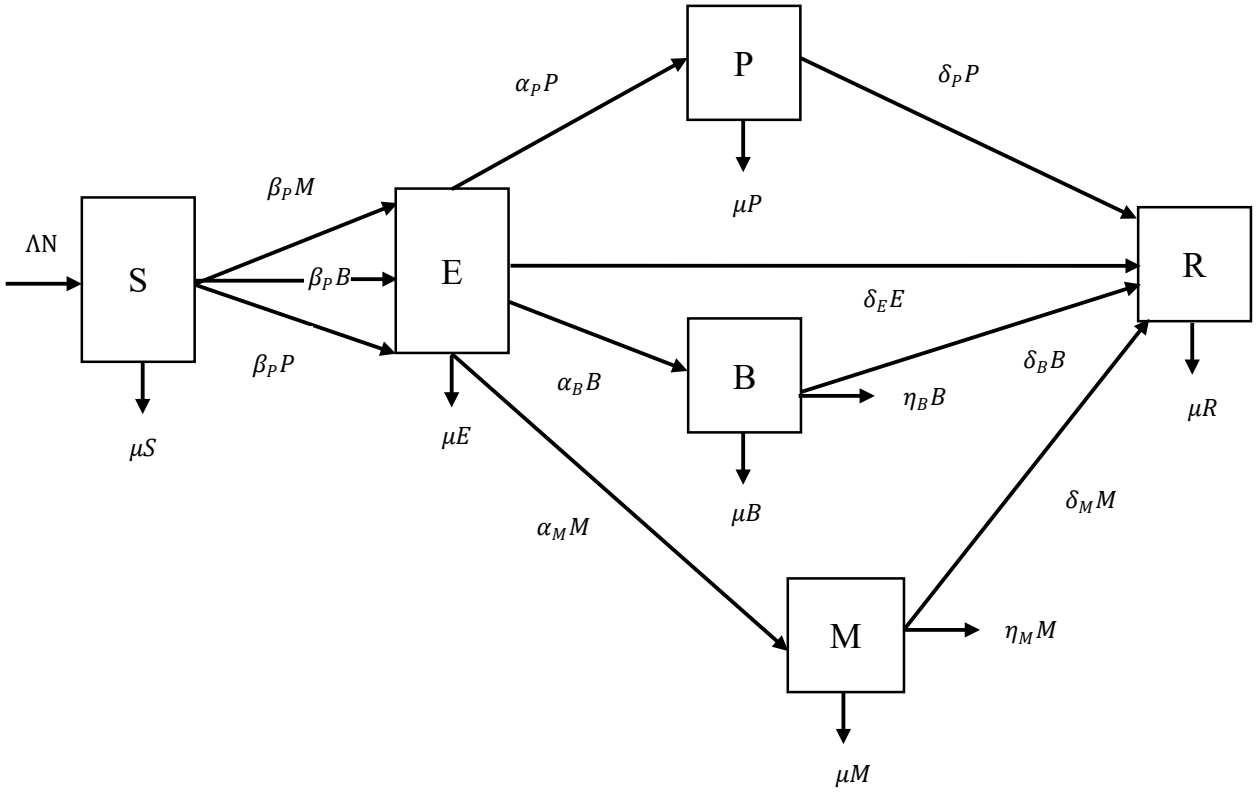

Figure 2: Modified Chiyaka Hybrid SEIR and SEI Leprosy Model with Treatment.

Model Equations for Modified Chiyaka hybrid SEIR and SEI Leprosy Model with Treatment

The evolution of the number of individuals in each compartment is described by the following system of ordinary differential equations:

$$\left.\begin{aligned}
\frac{dS}{dt} &= \Lambda N - \frac{\beta_P SP}{N} - \frac{\beta_B SB}{N} - \frac{\beta_M SM}{N} - \mu S \\
\frac{dE}{dt} &= \frac{\beta_P SP}{N} + \frac{\beta_B SB}{N} + \frac{\beta_M SM}{N} - (\alpha_M + \alpha_P + \alpha_B + \delta_E + \mu)E, \\
\frac{dM}{dt} &= \alpha_M E - (\delta_M + \eta_M + \mu)M, \\
\frac{dB}{dt} &= \alpha_B E - (\delta_B + \eta_B + \mu)B, \\
\frac{dP}{dt} &= \alpha_P E - (\delta_P + \mu)P, \\
\frac{dR}{dt} &= \delta_E E + \delta_M M + \delta_B B + \delta_P P - \mu R.
\end{aligned}\right\} \quad \textbf{(2)}$$

Initial conditions of system (1) are $S(0) = S_0, E(0) = E_0, M(0) = M_0, P(0) = P_0$, $B(0) = B_0$, $R(0) = R_0$ and $N(0) = N_0$, where S_0, E_0, M_0, P_0, R_0 and N_0 are all greater than zero and $N(t) = S(t) + E(t) + P(t) + B(t) + M(t) + R(t)$

Basic Reproduction Number

The basic reproduction number, R_0, is defined as the average number of secondary infections produced by one primary infection in a wholly susceptible population during his/her entire life as infectious. If $R_0 < 1$, then on average an infected individual produces less than one new infected individual over the course of its infectious period, and the infection cannot grow.

Conversely, if $R_0 > 1$, then each infected individual produces, on average, more than one new infection, and the disease can invade the population. In this study, R_0 refers to the average number of secondary *M. leprae* infections produced by a typical multibacillary or a paucibacillary or borderline patient in a totally susceptible population during his/her course of infectiousness. To calculate R_0, we follow the method outlined by (Wartmough, 2008).

Mathematically, Reproduction number can be expressed below as:

$$R_0 = \frac{1}{\alpha_M + \alpha_P + \alpha_B + \delta_E + \mu}\left(\frac{\beta_M \alpha_M}{\eta_M + \mu} + \frac{\beta_P \alpha_P}{\delta_P + \mu} + \frac{\beta_B \alpha_B}{\eta_B + \mu}\right),$$

RESULTS AND DISCUSSION

Table 4: Model Parameters Values used in Simulation.

Description	Parameter symbol	Parameters estimate
The probability of an MB case infecting a susceptible during interaction	β_M	0.08/year
The probability of a PB case infecting a susceptible during interaction.	β_P	0.02/year
The probability of a BI case infecting a susceptible during interaction	β_B	0.04/year
The rate of progression from E(t) to multibacillary leprosy	α_M	0.25/year
The rate of progression from *E(t)* to paucibacillary leprosy	α_P	0.03/year
The rate of progression from *E(t)* to borderline leprosy	α_B	0.06/year
The recovery rate for the asymptomatic patients in *E(t)*	δ_E	0.14/year
The recovery rate for the PB patients	δ_P	0.05/year
The natural death rate	μ	0.01/year
Disease induced mortality rate for MB patients	η_M	0.12/year
Disease induced mortality rate for BI patients	η_B	0.83/year

The above parameters were estimated so as to determine the reproduction number (Ro) for stability and disease-free equilibrium states of the leprosy diseases.

$$R_0 = \frac{1}{\alpha_M + \alpha_P + \alpha_B + \delta_E + \mu}\left(\frac{\beta_M \alpha_M}{\eta_M + \mu} + \frac{\beta_P \alpha_P}{\delta_P + \mu} + \frac{\beta_B \alpha_B}{\eta_B + \mu}\right),$$

Ro = 0.34 which is less than 1 and this satisfy the condition of disease-free equilibrium state.

Simulation Results

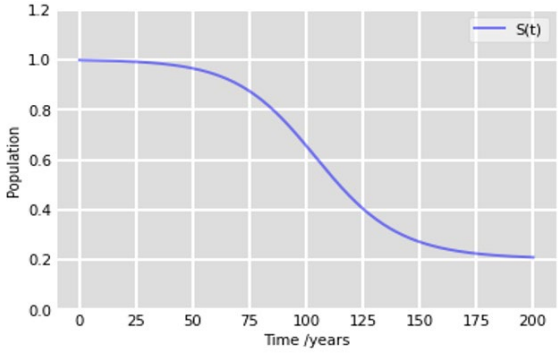

Figure 3: Susceptible population over time.

Figure 3 shows the simulation of the susceptible population (in 1000) that decline from the peak to close to 200 population over 200 years.

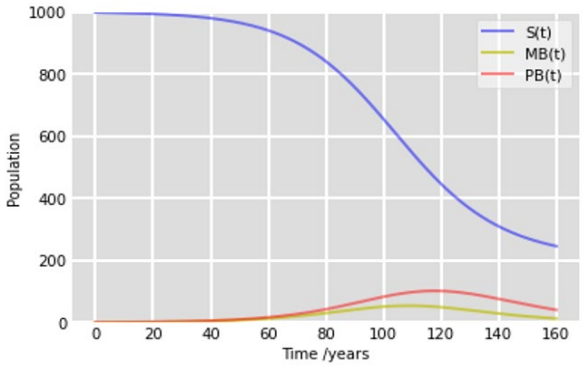

Figure 4: Susceptible, Multibacillary and Paucibacillary.

Figure 4 shows that susceptible decline from the peak to close to 200 population over 160 years while paucibacillary and multibacillary increases slowly over the period under review.

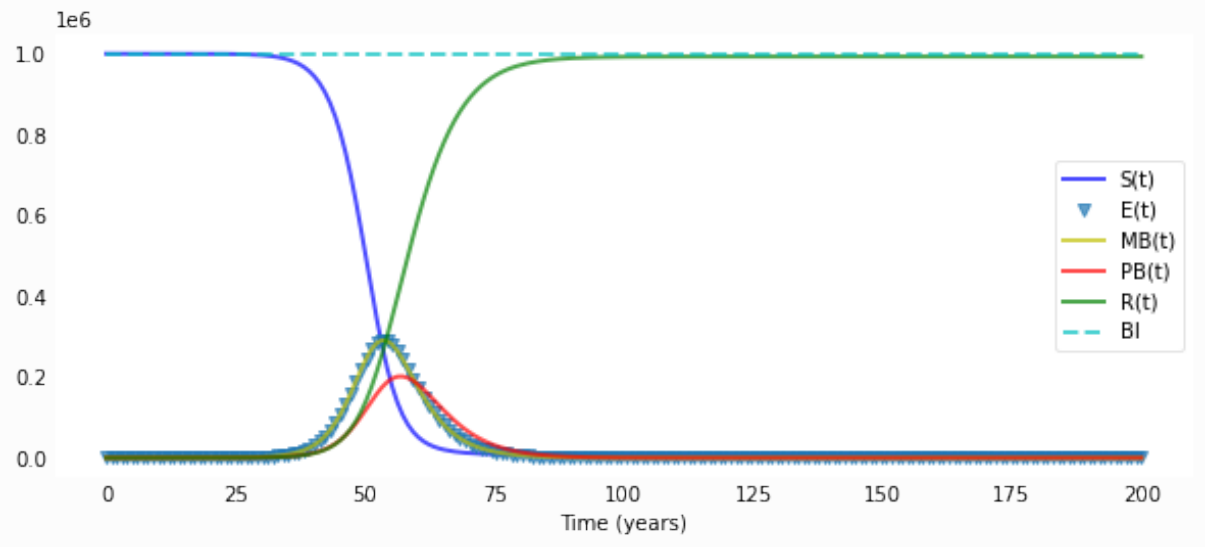

Figure 5: Susceptible, Exposed, Paucibacillary, Multibacillary, Borderline and Recovered.

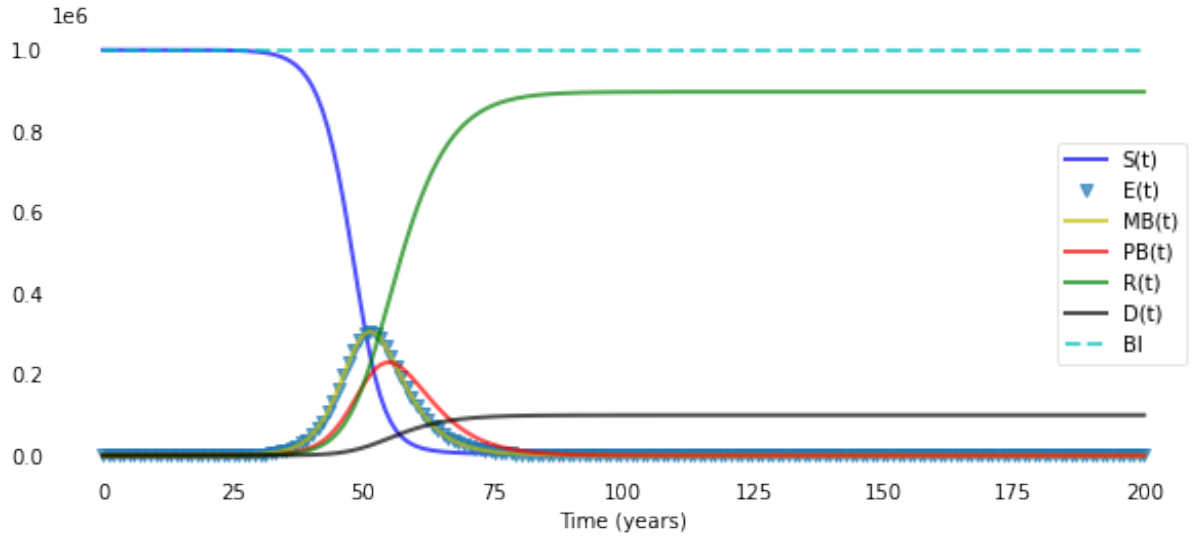

Figure 6: Susceptible, Exposed, Paucibacillary, Multibacillary, Borderline, Recovered and Death.

Figure 5 shows introduction of the new model which includes Borderline which is the combination of paucibacillary and multibacillary infection.Although the epidemic is slowed by the addition of an exposed population compartment, it doesn't seem to have any effect on how many people end up with the illness. The borderline drops slowly and flattens out over time while PB and MB increases slowly before flattening out. The susceptible decline from the peak and then flatten out. The recovered rate agrees with real life situation as it increases over 100years before flattening out.

Real Life Data Results

According to Chiyaka et al (2013), SEIR model was proposed with respect to paucibacillary leprosy (PB), multibacillary leprosy (MB) and SEI model and this research as therefore gone a step further to specify SEIRD model with respect to Borderline leprosy as improvement to SEIR model using simulation approach to estimate parameters of the SEI, SEIR and SEIRD models for the three leprosy diseases accordingly with the aid of Python 3 software programming.

However, real life data was collected on the three leprosy diseases via world health organization publications (https://www.who.int) and was also estimated accordingly.

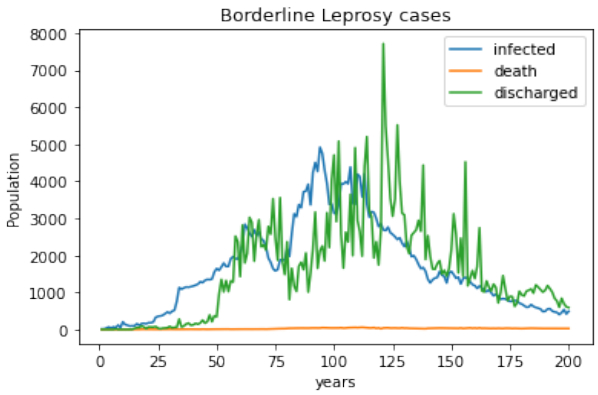

Figure 7: Borderline Leprosy.

Figure 7 shows that the borderline cases graphical estimation shows that the mortality/death rate is zero level while infected rate and discharge rate increases haphazardly.

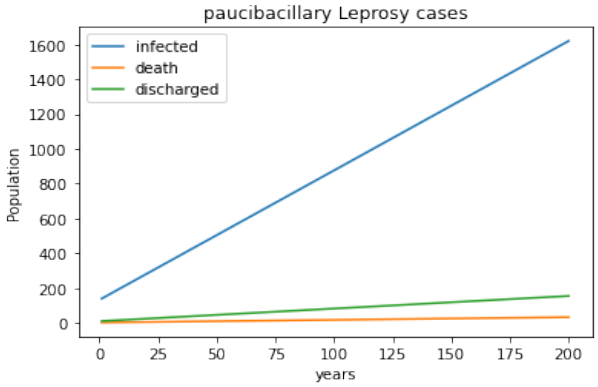

Figure 8: Paucibacillary Leprosy.

Figure 8 shows that the paucibacillary leprosy cases reveal that infected rate rises strongly and sharply at a constant rate during the period of 200 years under review while discharge cases increase at a slow rate and dead case is at zero level which means mortality rate is insignificant.

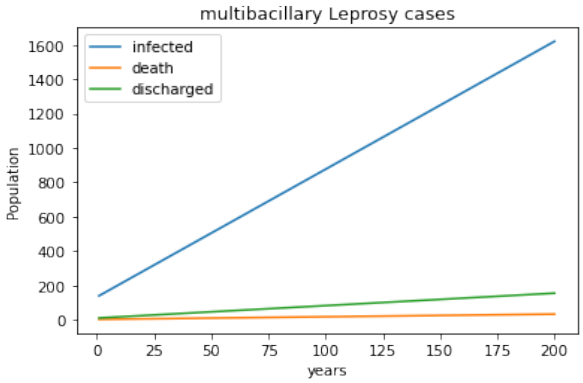

Figure 9: Multibacillary Leprosy.

Figure 9 shows that the infected rate rises strongly and sharply at a constant rate during the period of 200 years under review while discharge cases increase at a slow rate and dead case is at zero level which means mortality rate is insignificant.

DISCUSSION OF FINDINGS

Python 3 programming was utilized to compute numerical simulations of the three models PB, MB, and BI. In this simulation, parameter values were estimated based on the findings of various sub-Saharan African literature and surveys.

Where relevant data was lacking, statistics from Indian studies, which were the most extensive available, were used. Due to the lack of a test to identify sub-clinical infections, the progression rates to clinical infections were estimated using the average incubation times of 5 and 10 years for PB, MB, and BI.

A population of about 200 million people was taken for granted throughout this exercise. The (worst case) prevalence rate of 10 per 1000 people in Sub-Saharan African regions where the disease is still endemic served as the basis for the initial conditions of the infectious classes.

A study done in Ethiopia found that 6% of the general population harbors the disease. This observation led to the initial value for latent infections. First, simulations for the fundamental model to depict the behavior of leprosy in a fictitious population. We then present simulations of the model after treatment.

In addition, numerical values of the parameters are computed (see Table 4). Figure 5 depicts the introduction of the new model, which includes Borderline, which is the combination of paucibacillary and multibacillary infection.

Figure 4 depicts the decline of the susceptible population from its peak to close to 200 over 160 years, while paucibacillary and multibacillary infections increased slowly over the same period.

Although the introduction of an exposed population compartment appears to impede disease transmission, it does not appear to lower the overall infection rate. Consequently, according to Figure 6, the borderline is constant and levels off over time, whereas PB and MB rise gradually before levelling off. The vulnerable decrease from their peak and then level off. The recovered rate agrees with the real-life situations as it increases over 100 years before flattening out.

CONCLUSION

Borderline infection (BI) was newly introduced as it was not captured by the existing model according to Chiyaka, *et al*. (2013) and was also analyzed with numerical simulation. The reproduction number (Ro) estimated for the model was 0.34. The model parameter values used in the simulation were also computed to determine the reproduction number (Ro) which indicates that Ro<1 and this suggests that we have a disease-free equilibrium state of the leprosy disease.

The numerical simulations result shows that the addition of an exposed population, the E(t) compartment slows the outbreak, but doesn't appear to reduce the number of people ultimately infected by the disease while the borderline drops slowly and flattens out over time while PB and MB increase slowly before flattening out.

The susceptible decline from the peak and then flatten out. The recovered rate agrees with real-life situations as it increases over 100years before flattening out. According to Chiyaka, *et al*. (2013), the SEIR model was proposed concerning paucibacillary leprosy (PB), multibacillary leprosy (MB) and SEI model and this research has therefore gone a step further to specify the SEIRD model concerning Borderline leprosy as an improvement to the SEIR model using simulation approach to estimate parameters of the SEI, SEIR and SEIRD models for the three leprosy diseases.

The SEIR and SEIRD transmission model for leprosy in Nigeria were adequately developed. Comparing with the real-life data we can see that the borderline shows high volatility in its cases which indicate how chronic it is and the simulation shows it flattens out over time due to the severity. Meanwhile, the death is kept very low for all the three diseases which shows the same for the simulation.

We can therefore depict that the simulation approximately agrees with the real-life situation of the symptoms. Although leprosy is currently well controlled in most countries, numerous studies indicate that the overall global incidence of leprosy is rising as a result of the resurgence of the disease in Africa. Meanwhile, vaccination intervention should be adequately applied to the susceptible and exposed population. The resurgence of the disease should be addressed to prevent further transmission of the disease in Nigeria.

RECOMMENDATIONS

The newly specify SEIRD model concerning Borderline leprosy as an improvement to the SEIR model using a simulation approach to estimate parameters of the SEI, SEIR and SEIRD models should be adopted by policymakers and epidemiologists to study the trend in the transmission of leprosy. The government through the Centre for Disease Control should discourage the stigmatization of people infected with leprosy and make adequate provision for an isolation Centre in the same way they did for COVID-19 pandemic to aid the recovery process. The causes of the resurgence of leprosy should be addressed adequately with an effective vaccination treatment to mitigate the spread in Africa including Nigeria or even eradicate the disease completely.

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