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# Mathematical Modelling of Tuberculosis with Case Detection, Quarantine and Treatment as Control Strategies.

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***Abstract***
*Tuberculosis (TB) is a chronic disease caused mainly by Mycobacterium and spread from one person to another principally by airborne transmission. This paper is set to develop a mathematical model of TB with case detection, quarantine and treatment as control strategies. This model consists of six ordinary differential equations. The basic properties of the model in terms of existence and uniqueness, positivity and boundedness of the solution were established. The disease - free equilibrium point was obtained and it has shown that it is locally asymptotically stable (LAS). The infective reproduction number ($R_0$) of the model was computed by the next generation matrix method, and the analysis of $R_0$ showed that combination of the three control strategies (case detection, quarantine and treatment) should be used simultaneously and continuously in order to reduce the endemicity of the infection of the disease (TB).*
***Keywords****: Tuberculosis, Reproduction Number, Quarantine, Case Detection, Mycobacterium.*

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## I. Introduction

TB is a bacterial disease spread from one person to another principally by airborne transmission. The causal agent is mycobacterium TB (the tubercle bacillus). TB can affect any organ in the body. Pulmonary TB is the most frequent site of involvement; while Extra-pulmonary TB is less frequent. It is only pulmonary TB that is infectious. TB is a concern world-wide; because it affects both humans and animals, and cause significant impact of financial losses and loss of human lives and animal stock every year (Athithan, 2015).

According to World Health Organization's (WHO's) estimations, more than 1.9 million deaths occur due to TB in 1997. More than 1 million in South-East Asia, fewer than 42,000 in industrialized countries. TB is the cause of an estimated 2.8% of deaths in the world in all age groups and 26% of avoidable deaths in developing countries (Nadia, 2003).

According to Nadia (2003), TB kills more young people and adults than any other infectious disease, and that 95% of individuals with TB live in poorest countries because of the poor health coverage of the population, and that only a proportion of these patients are detected and treated.

The eradication of the disease is not easy because of several factors which are hindering the success of control strategies, for instance, financing of vaccine, diagnostic process, insurgency, Public Health Campaign, immigration, nutritional problem, to mention a few. Mathematical modelling plays a vital role in understanding and formulation of TB control strategies, which can be used in establishing interim goals for intervention programs.

Study of the spread of TB disease have been conducted by several researchers (Augusto, 2009; Fenz et al, 2000; K. Hattaf, 2009; Tewa, 2012). Also, Athithan (2013) and Andest (2022, 2023) studied the effects of case detection, Public Health Campaign and treatment, considering the case detection and treatment as constants (fixed) parameters, however, it varies with time.

At this juncture, it is paramount to define the strategies;

**Quarantine:**

Refers to the separation of persons who, while not ill, have been exposed to an infectious agent and thereafter may become infectious. Quarantine may be used when a person has been exposed to a highly dangerous and infectious diseases and include a range of disease control strategies that may be used individually or in combination. Quarantine includes short-term voluntary home confinement; restrictions on travel by those who may have been exposed; and out of a geographic area. Quarantine also include other measures to control the spread of disease, such as restriction on the assembly of groups of people (e.g. school events); suspension of public

gathering and closure of mass transit system or broad restrictions on travel by air, rail or water may be used (CDC; 2014).

**Case Detection:**

Case detection is the investigation of infectious disease through either laboratory means or Direct Observation Therapy Strategy (DOTS). Christopher & Martien (2008) conducted case over 11 years between 1994 and 2005, a total of 26.5 million TB patients were diagnosed and reported under DOTS. That in 2005, DOTS programs worldwide reported 4.8 million new and relapsed cases, among which 2.3 million were smear-positive. The smear-positive case detection was 60% (90% uncertainty limits, 52-69%) of the 3.9 million new cases estimate. The estimate of case detection was below the 70% target. The estimated case detection rate increased almost linearly from 11% globally in 1995 to 28% in 2000. They concluded that case detection has since accelerated from 2003 to 2004.

**Sanitarium**:

This is a medical facility for long term illness management. It is a hospital where people who have had a serious illness like TB go so that health care workers can take care of them to recuperate. The efficiency of sanitarium treatment depends on early detection and reference of patients. Sanitarium can also be used as an educational center where TB patients receive both didactic and practical instructions.

In view of the above mentioned models by other researchers, this paper is set to develop a new version of mathematical model on the dynamics of TB with case detection, quarantine and treatment as control strategies, and to achieve the following; the disease - free equilibrium point of the model, positivity of the model parameters and invariant region, reproduction number, and local stability of the model.

## II. Materials and Method

### 2.1 Assumptions

The model is based on the following assumptions;

i) The recruitment rate is constant.
ii) Population is homogeneously mixed.
iii) All exposed individuals suspected of TB are quarantined.
iv) Screening is done at exposed level.
v) Quarantined individuals that tested positive go for treatment.
vi) Natural death occurs across the compartment.

### 2.2 Variables and Parameters

| Variables | Definitions |
|---|---|
| $S(t)$ | The population of Susceptible individuals at time t. |
| $E(t)$ | The population of Exposed individuals at time t. |
| $I(t)$ | The population of Infected individuals at time t. |
| $Q(t)$ | The population of Quarantined individuals at time t. |
| $T(t)$ | The population of Treated individuals at time t. |
| $R(t)$ | The Population of Recovered Individuals at time t. |

Table 2.1: Variables of the Model and their Definitions.

| Parameters | Definitions |
|---|---|
| $\wedge$ | Recruitment rate. |
| $\mu$ | Natural death rate. |
| $\theta_1$ | Per capita TB transmission rate. |
| $\alpha$ | The rate at which the infected go for treatment. |
| $\tau$ | The rate at which the individuals are diagonized. |
| $p$ | The rate of progression from exposed to infected. |
| $\gamma$ | The proportion of exposed individuals that are quarantined. |
| $1-\gamma$ | Proportion of exposed not quarantined. |
| $\omega$ | Proportion of quarantined individuals that are infected go for treatment. |
| $1-\omega$ | Proportion of quarantined not infected |
| $r_1$ | Rate of recovery. |
| | Rate at which recovered individuals became susceptible. |
| | TB – induced death for individuals that are infected. |
| | TB-induced death for individuals on treatment. |

| |
|---|
| $\beta$ |
| $d_1$ |
| $d_2$ |

Table 2.2: Model Parameters and their Definitions.

**2.3 Model Description**

The population is divided into six (6) compartments based on epidemiological status of the individuals. The compartments are; the population of Susceptible individuals, $S(t)$, the population of Exposed individuals, $E(t)$ , the population of Infected individuals, $I(t)$ , the population of Quarantined individuals, $Q(t)$ , the population of Treated individuals, $T(t)$ , and the population of Recovered individuals, $R(t)$ . It is referred to a compartmental-based model as $SEQITR$ model, where total population is given by;

$$N(t) = S(t) + E(t) + Q(t) + I(t) + T(t) + R(t).$$

The recruitment into the susceptible population is by birth or immigration, given by $\wedge$ and reduces by natural death, hence governed by the equation;

$$\frac{dS}{dt} = \wedge + \beta R + \tau(1-\omega)Q - \alpha_1 SI - \mu S.$$

The proportion of exposed individuals is generated by susceptible individuals at the rate $\alpha_1 SI$ , and decreases due to progression into infected class at the rate $p(1-\gamma)E$ , and those suspected at the rate $\gamma E$ and natural death $\mu E,$ hence the equation;

$$\frac{dE}{dt} = \alpha_1 SI - p(1-\gamma)E - \gamma E - \mu E.$$

The proportion of quarantined individuals increase by suspected exposed individuals at the rate $\gamma E$ and reduces/decreases by those found positive and went for treatment at the rate $\tau\omega Q$ , and those tested negative at the rate $\tau(1-\omega)Q$ , hence the equation;

$$\frac{dQ}{dt} = \gamma E - \tau(1-\omega)Q - \tau\omega Q - \mu Q.$$

The proportion of infected individuals increases by those exposed individuals that progress to infected class at the rate $p(1-\gamma)E$ and reduces by those infected individuals that go for treatment at the rate $\alpha I$ and by natural and TB-induced death $(\mu + d_1)I$ , hence the equation;

$$\frac{dI}{dt} = p(1-\gamma)E - \alpha I - (\mu + d_1)I.$$

The treated class increases by those infected individuals, tested positive at the rate $\alpha I$ , $\tau\omega Q$ respectively and decreases by those who recover at the rate $r_1 T$ and natural death or by TB at the rate $(\mu + d_2)T$ . Hence, the equation;

$$\frac{dT}{dt} = \alpha I + \tau\omega Q - r_1 T - (\mu + d_2)T.$$

Finally, the proportion of recovered individuals increase by those that responded positively to treatment at the rate $r_1 T$ and decreases by those that become susceptible again, at the rate $\beta R$ and by death $\mu R$ . Hence, the equation;

$$\frac{dR}{dt} = r_1 T - \beta R - \mu R.$$

**Flow Diagram of the Model;**

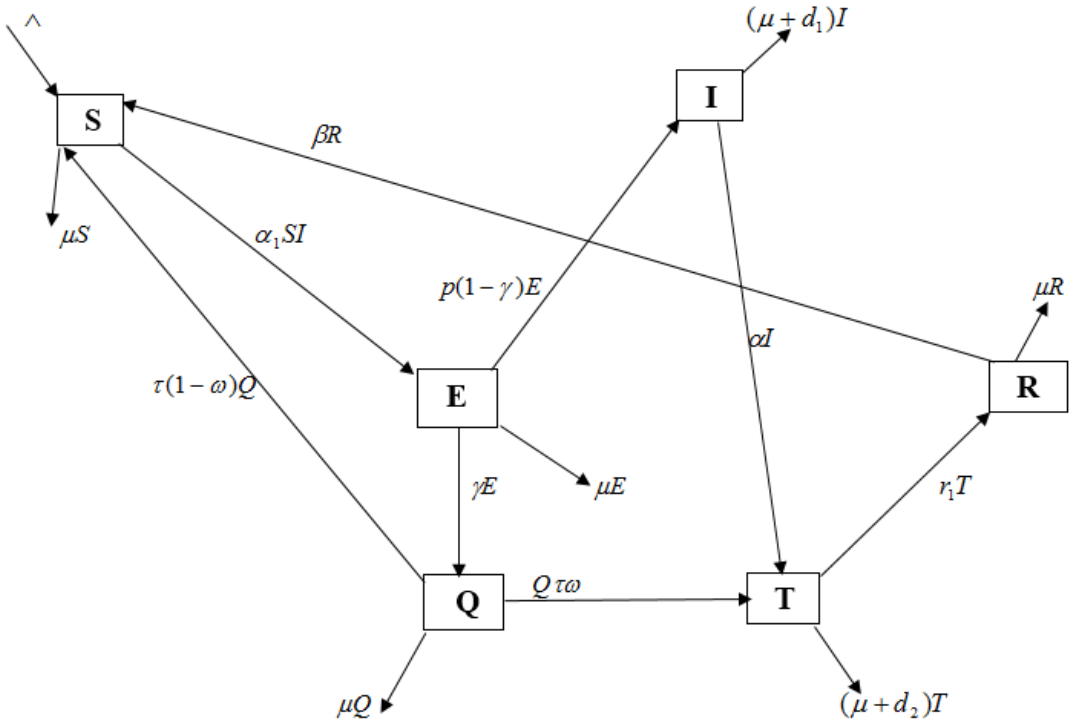


Figure 2.1: The Schematic Flow Diagram of SEQITR Model.

### 2.4 Model Equations

Based on the assumptions, description and the schematic flow diagram of the model in figure 2.1, the following set of first order ordinary differential equations for the model (SEQITR) were obtained;

$$\begin{aligned}
\frac{dS}{dt} &= \wedge + \beta R + \tau(1-\omega)Q - \alpha_1 SI - \mu S.\\
\frac{dE}{dt} &= \alpha_1 SI - p(1-\gamma)E - \gamma E - \mu E.\\
\frac{dQ}{dt} &= \gamma E - \tau(1-\omega)Q - \tau\omega Q - \mu Q.\\
\frac{dI}{dt} &= p(1-\gamma)E - \alpha I - (\mu + d_1)I.\\
\frac{dT}{dt} &= \alpha I + \tau\omega Q - r_1 T - (\mu + d_2)T.\\
\frac{dR}{dt} &= r_1 T - \beta R - \mu R.
\end{aligned} \tag{2.1}$$

$$N(t) = S(t) + E(t) + Q(T) + I(t) + T(t) + R(t).$$

Subject to the following initial condition;

$$S(0) > 0, E(0) \geq 0, Q(0) \geq 0, I(0) \geq 0, T(0) \geq 0, R(0) \geq 0.$$

### 2.5 Model Analysis

In this section, we prove the boundedness solutions of the model equations, established equilibrium points and analyze the model for stability.

Methods of model analysis include;

i) Cauchy-Lipchitz condition for existence and uniqueness.
ii) Separation of variables and of integrating factor for positivity and boundedness.
iii) Next generation matrix for computing the basic reproduction number.
iv) Equilibrium points of the model by setting the right hand side of the equations to zero and then solve for the associated state variables in the absence of infection.
v) Local stability is established using the method of negativity of eigenvalues.

## III. Results and Discussions

### 3.1 Existence and Uniqueness

**Theorem 3.1:**

Suppose that the function $f(t, y_{1,} y_{2,}, ..., y_n)$ in the model equations given satisfies Lipchitz condition in the region $D = \{(t, y) : 0 \leq | t - t_0 | \leq a, 0 \leq | y - y_0 | \leq b\}$, for some $a > 0, b > 0, ab \in D,$ then there exists a constant number $\delta_1 > 0,$ such that a unique continuous vector solution $y(t)$ of the model equations exists in the interval $| t - t_0 | < \delta_1$ exists.

**Proof:**

Let;

$$
\begin{aligned}
f_1(t, y_1) &= \frac{dS}{dt} = \wedge + \beta R + \tau(1-\omega)Q - \alpha_1 SI - \mu S. \\
f_2(t, y_2) &= \frac{dE}{dt} = \alpha_1 SI - p(1-\gamma)E - \gamma E - \mu E. \\
f_3(t, y_3) &= \frac{dQ}{dt} = \gamma E - \tau(1-\omega)Q - \tau\omega Q - \mu Q. \\
f_4(t, y_4) &= \frac{dI}{dt} = p(1-\gamma)E - \alpha I - (\mu + d_1)I. \\
f_5(t, y_5) &= \frac{dT}{dt} = \alpha I + \tau\omega Q - r_1 T - (\mu + d_2)T. \\
f_6(t, y_6) &= \frac{dR}{dt} = r_1 T - \beta R - \mu R.
\end{aligned}
\tag{3.1}
$$

For equation (3.1) to satisfy Lipchitz condition, it is sufficient to show that;

$\frac{\partial f_i}{\partial y_j}, (i, j = 1,2,...,6)$ are continuous and bounded in the region D.

From the first equation of the system (3.1)

$$
\frac{\partial f_1}{\partial S} = -\mu < \infty, \frac{\partial f_1}{\partial E} = 0 < \infty, \frac{\partial f_1}{\partial Q} = \tau(1-\omega) < \infty, \frac{\partial f_1}{\partial I} = 0 < \infty,
$$

$$
\frac{\partial f_1}{\partial T} = 0 < \infty, \frac{\partial f_1}{\partial R} = \beta < \infty.
$$

From the second equation of (3.1);

$$
\frac{\partial f_2}{\partial S} = 0 < \infty, \frac{\partial f_2}{\partial E} = -(p(1-\gamma) - \gamma - \mu) < \infty, \frac{\partial f_2}{\partial Q} = 0 < \infty,
$$

$$
\frac{\partial f_2}{\partial I} = 0 < \infty, \frac{\partial f_2}{\partial T} = 0 < \infty, \frac{\partial f_2}{\partial R} = 0 < \infty.
$$

From the third equation of (3.1);

$$\frac{\partial f_3}{\partial S} = 0 < \infty, \frac{\partial f_3}{\partial E} = \gamma < \infty, \frac{\partial f_3}{\partial Q} = -\tau(1-\omega) - \tau\omega - \mu < \infty,$$
$$\frac{\partial f_3}{\partial I} = 0 < \infty, \frac{\partial f_3}{\partial T} = 0 < \infty, \frac{\partial f_3}{\partial R} = 0 < \infty.$$

From the fourth equation of (3.1);

$$\frac{\partial f_4}{\partial S} = 0 < \infty, \frac{\partial f_4}{\partial E} = p(1-\gamma) < \infty, \frac{\partial f_4}{\partial Q} = 0 < \infty,$$
$$\frac{\partial f_4}{\partial I} = -\alpha - (\mu + d_1) < \infty, \frac{\partial f_4}{\partial T} = 0 < \infty, \frac{\partial f_4}{\partial R} = 0 < \infty.$$

From the fifth equation of (3.1);

$$\frac{\partial f_5}{\partial S} = 0 < \infty, \frac{\partial f_5}{\partial E} = 0 < \infty, \frac{\partial f_5}{\partial Q} = \tau\omega < \infty,$$
$$\frac{\partial f_5}{\partial I} = \alpha < \infty, \frac{\partial f_5}{\partial T} = -(r_1 + \mu + d_2) < \infty, \frac{\partial f_5}{\partial R} = 0 < \infty.$$

Finally, from the sixth equation of (3.1);

$$\frac{\partial f_6}{\partial S} = 0 < \infty, \frac{\partial f_6}{\partial E} = 0 < \infty, \frac{\partial f_6}{\partial Q} = 0 < \infty,$$
$$\frac{\partial f_6}{\partial I} = 0 < \infty, \frac{\partial f_6}{\partial T} = r_1 < \infty, \frac{\partial f_6}{\partial R} = -\beta - \mu < \infty.$$

Observe that all the partial derivatives of the functions are continuous and bounded in the interval $0 < D < \infty$, thus, the functions satisfy Lipchitz condition and hence, there exists a unique solution of the model equations in the region D.

**3.2 Positivity of the Model Solution**

**Theorem 3.2:**

For non-negative initial conditions for the model equation given by system (2.1), the solutions (S,E,Q,I,T,R) of the model equations are all non-negative for all time $t \geq 0.$

**Proof:**

Let $t^*$ be the maximum time for the epidemics. This implies that;

$t^* = Sup\{t^* > 0 : (S, E, Q, I, T, R) > 0\}$, thus, $t^* \geq 0.$

From the first equation of system (2.1), we have;

$$\frac{dS}{dt} = \wedge + \beta R + \tau(1-\omega)Q - \alpha_1 SI - \mu S \geq -(\alpha_1 I + \mu)S.$$
$$\frac{dS}{S} \geq -(\alpha_1 I + \mu)dt$$

Integrating from $t = 0$ to $t = t^*$, We have;

$$\int_0^{t^*} \frac{dS}{S} \geq -\int_0^{t^*} (\alpha_1 I + \mu)dt \qquad 3.2$$
$$\ln S \geq -(\mu)t^* - \int_0^{t^*} \alpha_1 I$$

Taking exponential of both sides of 3.2, we have;

$S(t^*) \geq S(0)\exp(-(\mu))t^* - \int_0^{t^*} \alpha_1 I \geq 0,$ hence, $S(t^*) \geq 0.$

This implies $S(t) \geq 0$ for all $t > 0.$

From the second equation of system (2.1);

$$\frac{\mathrm{dE}}{\mathrm{dt}} = \alpha_1 SI - p(1-\gamma)E - \gamma E - \mu E.$$

$$\frac{\mathrm{dE}}{\mathrm{dt}} \geq -(p(1-\gamma) + \gamma + \mu)E \qquad 3.3$$

Integrating (3.3),

$$\int_0^{t^*} \frac{\mathrm{dE}}{\mathrm{E}} \geq -\int_0^{t^*} (p(1-\gamma) + \gamma + \mu)dt$$

$$\ln E \geq -(p(1-\gamma) + \gamma + \mu)t^* \qquad 3.4$$

Take exponential of (3.4)

$E(t^*) \geq E(0)\exp(-(p(1-\gamma) + \gamma + \mu)t^*) \geq 0.$

Hence, $E(t) \geq 0$ for all $t > 0.$

From the third equation of system (2.1);

$$\frac{dQ}{dt} = \gamma E - \tau(1-\omega)Q - \tau\omega Q - \mu Q.$$

$$\frac{dQ}{dt} \geq -[\tau(1-\omega) + \tau\omega + \mu]Q. \qquad 3.5$$

Integrating (3.5);

$$\int_0^{t^*} \frac{dQ}{Q} \geq -\int_0^{t^*} (\tau(1-\omega) + \tau\omega + \mu)dt.$$

$$\ln Q \geq -(\tau(1-\omega) + \tau\omega + \mu)t^* \qquad 3.6$$

Taking exponential of equation (3.6);

$Q(t^*) \geq Q(0)\exp(-(\tau(1-\omega) + \tau\omega + \mu)t^*) \geq 0.$

Hence, $Q(t) > 0$ for all $t > 0.$

From the fourth equation of system (2.1);

$$\frac{dI}{dt} = p(1-\gamma)E - \alpha_1 I - (\mu + d_1)I \geq -(\alpha_1 + \mu + d_1).$$

$$\frac{dI}{I} \geq -(\alpha_1 + \mu + d_1)dt. \qquad 3.7$$

Integrating (3.7);

$$\int_0^{t^*} \frac{dI}{I} \geq -\int_0^{t^*} (\alpha_1 + \mu + d_1)dt.$$

$$\ln I \geq -(\alpha_1 + \mu + d_1)t^* \qquad 3.8$$

Taking the exponential of (3.8);

$I(t) \geq I(0)\exp(-(\alpha_1 + \mu + d_1)t^*) \geq 0$.

Hence, $I(t) \geq 0$ for all $t > 0$.

From the fifth equation of system (2.1);

$$\frac{dT}{dt} = \alpha I + \tau\omega Q - r_1 T - (\mu + d_2)T \geq -(\mu + d_1)T.$$

$$\frac{dT}{T} \geq -(r_1 + \mu + d_2)dt. \qquad 3.9$$

Integrating equation (3.9);

$$\int_0^{t^*} \frac{dT}{T} \geq -\int_0^{t^*} (r_1 + \mu + d_2)dt.$$

$$\ln T \geq -(r_1 + \mu + d_2)t^*. \qquad 3.10$$

Taking exponential of (3.10);

$T(t) \geq T(0)\exp(-(r_1 + \mu + d_2)t^*) \geq 0.$

Hence, $T(t) \geq 0$ for all $t > 0$.

From the sixth equation of system (2.1);

$$\frac{dR}{dt} = r_1 T - \beta R - \mu R \geq -(\beta + \mu - r_1)R.$$

$$\frac{dR}{R} \geq -(\beta + \mu)dt \qquad 3.11$$

Integrating (3.11);

$$\int_0^{t^*} \frac{dR}{R} \geq -\int_0^{t^*} (\beta + \mu)dt$$

$$\ln R \geq -(\beta + \mu)t^* \qquad 3.12$$

Taking the exponential of (3.12);

$R(t) \geq R(0)\exp(-(\beta + \mu)t^*) \geq 0.$

Hence, $R(t) \geq 0$ for all $t > 0$.

### 3.3 Disease Free Equilibrium (DFE)

The disease free equilibrium(DFE) points are steady state solutions that depicts the absence of the disease in the population. This implies that at the TB-free equilibrium point, by setting the right hand sides of equation (2.1) to zero, i.e

$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dQ}{dt} = \frac{dI}{dt} = \frac{dT}{dt} = \frac{dR}{dt} = 0$, and then set all parameters and state variables related to TB to zero, i.e $E = I = Q = T = 0.$

Therefore, we have;

$$\frac{dS}{dt} = \wedge + \beta R + \tau(1-\omega)Q - \alpha_1 SI - \mu S$$

When $E = I = Q = T = 0,$ we have;

$$\frac{dS}{dt} = \wedge - \mu S$$

$$\frac{dS}{dt} + \mu S = \wedge$$

By method of integrating factor;

$$N(t) = \frac{\wedge}{\mu}\left(1 - e^{-\mu t}\right)$$

$$\lim_{t\to\infty} N(t) = \frac{\wedge}{\mu}.$$

**3.4 Endemic Equilibrium Points(EEP);**

Endemic Equilibrium Points(EEP) are obtained by solving for the state variables. Therefore, the EEP are as follows;

From the first equation of system (2.1);

$$\wedge + \beta R^* + \tau(1-\omega)Q^* - S^*(\alpha_1 I^* + \mu) = 0.$$

$$S^* = \frac{\wedge + \beta R^* + \tau(1-\omega)Q^*}{\alpha_1 I^* + \mu} \qquad 3.13$$

From the second equation of system (2.1);

$$\alpha_1 S^* I^* - p(1-\gamma)E^* - \gamma E^* - \mu E^* = 0.$$

$$E^* = \frac{\alpha_1 S^* I^*}{p(1-\gamma) + \gamma + \mu}. \qquad 3.14$$

From the third equation of System (2.1);

$$\gamma E^* - \tau(1-\omega)Q^* - \tau\omega Q^* - \mu Q^* = 0.$$

$$Q^* = \frac{\gamma E^*}{\tau + \mu}. \qquad 3.15$$

From the fourth equation of system (2.1);

$$p(1-\gamma)E^* - \alpha_1 I^* - (\mu + d_1)I^* = 0.$$

$$I^* = \frac{p(1-\gamma)E^*}{\alpha_1 + \mu + d_2}. \qquad 3.16$$

From the fifth equation of system (2.1);

$$\alpha I^* + \tau\omega Q^* - r_1 T^* - (\mu + d_2)T^* = 0.$$

$$T^* = \frac{\alpha I^* + \tau\omega Q^*}{r_1 + \mu + d_2}. \qquad 3.17$$

Lastly, we have;

$$r_1 T^* - \beta R^* - \mu R^* = 0.$$

$$R^* = \frac{r_1 T^*}{\beta + \mu}. \qquad 3.18$$

Thus, the endemic equilibrium point of the model is given by

$X_1 = (S^*, E^*, Q^*, I^*, T^*, R^*).$

Where $S^*, E^*, Q^*, I^*, T^*, R^*$ are defined in equations 3.13 – 3.18 respectively.

**3.5 Invariant Region**

**Theorem 2.7.**

The solution of the model given by system (2.1) is bounded in the closed set

$$\theta = \left\{ (S, E, Q, I, T, R) \in R_+^6 : N(t) \le \frac{\wedge}{\mu} \right\}.$$

Moreover, the set $\theta$ is positively invariant and attracting with respect to model equations given by system (2.1).

**Proof:**

Given that;

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dQ}{dt} + \frac{dI}{dt} + \frac{dT}{dt} + \frac{dR}{dt}.$$

Adding the model equations of the system (2.1) we have;

$$\frac{dN}{dt} = \wedge - \mu(S + E + Q + I + T + R) - (d_1 + d_2).$$

In the absence of TB-induced death, $d_1 = d_2 = 0.$

$$\Rightarrow \frac{dN}{dt} = \wedge - \mu N$$

$$\Rightarrow \frac{dN}{dt} \le \wedge - \mu N \ .$$

$$\Rightarrow \frac{dN}{dt} + \mu N \le \wedge.$$

Applying the method of integrating factor, we have;

$$N(t) \le N(0)e^{-\mu t} + \frac{\wedge}{\mu}\left(1 - e^{-\mu t}\right)$$

$$\lim_{t \to \infty} SupN(t) \le \frac{\wedge}{\mu}.$$

**3.6 Reproduction Number ( $R_0$ )**

The basic reproduction number is defined as the average number of secondary cases of infections generated by a typical infected person in an otherwise disease free population. The basic reproduction number **( $R_0$ )** of the system (2.1) is computed using the next generation matrix method. Here, $F_i$ denotes the rates of appearance of new infections and $V_i$ represents the transfer of infection into and out of any compartment respectively.

There are four infective classes, i.e $E, Q, I, T$, hence the $F_i$ and $V_i$ are given as;

$$F_i = \begin{bmatrix} \alpha_1 SI \\ 0 \\ 0 \\ 0 \end{bmatrix}, \qquad \text{and} \qquad V_i = \begin{bmatrix} p(1-\gamma)E + \gamma E + \mu E \\ -\gamma E + \tau(1-\omega)Q + \tau\omega Q + \mu Q \\ -p(1-\gamma)E + \alpha I + (\mu + d_1)I \\ -\alpha I - \tau\omega Q + r_1 T + (\mu + d_2)T \end{bmatrix}.$$

$$F = \frac{\partial f_i(x_0)}{\partial x_j} = \begin{bmatrix} 0 & 0 & \frac{\alpha_1 \wedge}{\mu} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \qquad V = \frac{\partial v_i(x_0)}{\partial x_j} = \begin{bmatrix} p(1-\gamma)+\gamma+\mu & 0 & 0 & 0 \\ -\gamma & \tau+\mu & 0 & 0 \\ -p(1-\gamma) & 0 & \alpha+\mu+d_1 & 0 \\ 0 & -\tau\omega & 0 & r_1+\mu+d_2 \end{bmatrix}$$

$$V^{-1} = \begin{bmatrix} \frac{1}{p(1-\gamma)+\gamma+\mu} & 0 & 0 & 0 \\ \frac{\gamma}{(p(1-\gamma)+\gamma+\mu)(\tau+\mu)} & \frac{1}{\tau+\mu} & 0 & 0 \\ \frac{p(1-\gamma)}{(p(1-\gamma)+\gamma+\mu)(\alpha+\mu+d_1)} & 0 & \frac{1}{\alpha+\mu+d_1} & 0 \\ \frac{\tau\omega\gamma}{(\tau+\mu)(P(1-\gamma)+\gamma+\mu)(r_1+\mu+d_2)} & \frac{\tau\omega}{(\tau+\mu)(r_1+\mu+d_2)} & 0 & \frac{1}{r_1+\mu+d_2} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} 0 & 0 & \frac{\alpha_1\xi}{\mu} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{p(1-\gamma)+\gamma+\mu} & 0 & 0 & 0 \\ \frac{\gamma}{(p(1-\gamma)+\gamma+\mu)(\tau+\mu)} & \frac{1}{\tau+\mu} & 0 & 0 \\ \frac{p(1-\gamma)}{(p(1-\gamma)+\gamma+\mu)(\alpha+\mu+d_1)} & 0 & \frac{1}{\alpha+\mu+d_1} & 0 \\ \frac{\tau\omega\gamma}{(\tau+\mu)(p(1-\gamma)+\gamma+\mu)(r_1+\mu+d_2)} & \frac{\tau\omega}{(\tau+\mu)(r_1+\mu+d_2)} & 0 & \frac{1}{r_1+\mu+d_2} \end{bmatrix}$$

Where $\xi = \wedge$.

$$FV^{-1} = \begin{bmatrix} \frac{\alpha\xi p(1-\gamma)}{\mu(p(1-\gamma)+\gamma+\mu)(\alpha+\mu+d_1)} & 0 & \frac{\alpha\xi}{\alpha+\mu+d_1} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$FV^{-1} - \lambda I = \begin{bmatrix} \frac{\alpha\xi p(1-\gamma)}{\mu(p(1-\gamma)+\gamma+\mu)(\alpha+\mu+d_1)} & 0 & \frac{\alpha\xi}{\alpha+\mu+d_1} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} - \lambda \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

$$FV^{-1} - \lambda I = \begin{bmatrix} \frac{\alpha\xi p(1-\gamma)}{\mu(p(1-\gamma)+\gamma+\mu)(\alpha+\mu+d_1)} - \lambda & 0 & \frac{\alpha\xi}{\alpha+\mu+d_1} & 0 \\ 0 & -\lambda & 0 & 0 \\ 0 & 0 & -\lambda & 0 \\ 0 & 0 & 0 & -\lambda \end{bmatrix}$$

Now the determinant is given as;

$$\left|FV^{-1}-\lambda I\right|=-\left(\frac{\alpha\xi p(1-\gamma)}{\mu(p(1-\gamma)+\gamma+\mu)(\alpha+\mu+d_1)}-\lambda\right)\lambda^3$$

The characteristics polynomial is given as;

$$-\left(\frac{\alpha\xi p(1-\gamma)}{\mu(p(1-\gamma)+\gamma+\mu)(\alpha+\mu+d_1)}-\lambda\right)\lambda^3=0,$$

From where we obtain the following eigenvalues by substituting back $\xi=\wedge$;

$$\left[\lambda_1=\frac{\alpha\wedge p(1-\gamma)}{\mu(p(1-\gamma)\alpha+p(1-\gamma)\mu+p(1-\gamma)d_1+\gamma\alpha+\gamma\mu+\gamma d_1+\mu\alpha+\mu^2+\mu d_1)},\lambda_2=0,\lambda_3=0,\lambda_4=0\right].$$

Clearly, $\lambda_1$ is the dominant eigenvalue and thus, it is the effective reproduction number.

Therefore; $R_{SQT}=\lambda_1=\dfrac{\alpha\wedge p(1-\gamma)}{\mu(p(1-\gamma)\alpha+p(1-\gamma)\mu+p(1-\gamma)d_1+\gamma\alpha+\gamma\mu+\gamma d_1+\mu\alpha+\mu^2+\mu d_1)}.$

When there is no screening, that is $\gamma=0,$ the reproduction number with quarantine and treatment only is given by;

$$R_{QT}=\frac{\alpha\wedge p}{\mu(p(\alpha+\mu+d_1)+\mu(\alpha+\mu+d_1))}$$

$R_{QT}>R_{SQT}$ and it implies that $R_{ST}>R_{SQT}$.

$R_{QT}>R_{SQT}$ , we conclude that endemicity of the infection of the disease (TB) is reduced more when combination of case detection, quarantine and treatment are used simultaneously.

**3. 7 Local Stability**

**Theorem:**

The Tuberculosis free equilibrium of system (2.1) is locally asymptotically stable if $R_0<1$ and is unstable ( $R_0>1$) if and only if Jacobian $J(x_0)$ have negative eigenvalues.

**Proof:**

The Jacobian of the system (2.1) at disease free equilibrium point is given by

$$J(x_0)=\begin{bmatrix}-\mu & 0 & \tau(1-\omega) & 0 & 0 & 0\\ 0 & -[p(1-\gamma)+\gamma+\mu] & 0 & 0 & 0 & 0\\ 0 & \gamma & -(\tau+\mu) & 0 & 0 & 0\\ 0 & p(1-\gamma) & 0 & -(\alpha+\mu+d_1) & 0 & 0\\ 0 & 0 & \tau\omega & \alpha & -(r_1+\mu+d_2) & 0\\ 0 & 0 & 0 & 0 & r_1 & -(\beta+\mu)\end{bmatrix};$$

Let $a=[p(1-\gamma)+\gamma+\mu],b=(\tau+\mu),c=(\alpha+\mu+d_1),d=(r_1+\mu+d_2),e=(\beta+\mu).$

Let the eigenvalues be $\lambda_i$, for $i=1,2,...,6.$

$$J(x_0)=\begin{bmatrix}-\mu & 0 & \tau(1-\omega) & 0 & 0 & 0\\ 0 & -a & 0 & 0 & 0 & 0\\ 0 & \gamma & -b & 0 & 0 & 0\\ 0 & p(1-\gamma) & 0 & -c & 0 & 0\\ 0 & 0 & \tau\omega & \alpha & -d & 0\\ 0 & 0 & 0 & 0 & r_1 & -e\end{bmatrix}$$

Column six is less than zero, therefore, we have $\lambda_1=-e=-(\beta+\mu).$

Deleting the sixth row and column, we have;

$$J(x_0)=\begin{bmatrix} -\mu & 0 & \tau(1-\omega) & 0 & 0 \\ 0 & -a & 0 & 0 & 0 \\ 0 & \gamma & -b & 0 & 0 \\ 0 & p(1-\gamma) & 0 & -c & 0 \\ 0 & 0 & \tau\omega & \alpha & -d \end{bmatrix}$$

Column five is less than zero, implies $\lambda_2 = -d = -(r_1 + \mu + d_2).$

Therefore, deleting fifth row and column we have;

$$J(x_0)=\begin{bmatrix} -\mu & 0 & \tau(1-\omega) & 0 \\ 0 & -a & 0 & 0 \\ 0 & \gamma & -b & 0 \\ 0 & p(1-\gamma) & 0 & -c \end{bmatrix}.$$

Column four is less than zero, implies $\lambda_3 = -c = -(\alpha + \mu + d_1).$

Therefore, deleting the fourth row and column, we have;

$$J(x_0)=\begin{bmatrix} -\mu & 0 & \tau(1-\omega) \\ 0 & -a & 0 \\ 0 & -\gamma & -b \end{bmatrix}.$$

Column one is less than zero, therefore $\lambda_4 = -\mu.$

Deleting the first row and column, we have;

$$J(x_0)=\begin{bmatrix} -a & 0 \\ \gamma & -b \end{bmatrix}$$

Deleting first row and column, $\lambda_5 = -a = -(p(1-\gamma) + \gamma + \mu).$

Leaving us with a single element $[-b]$, which implies $\lambda_6 = -b = -(\tau + \mu).$

Observe that ; $\lambda_1 = -(\beta + \mu)$, $\lambda_2 = -(r_1 + \mu + d_2)$, $\lambda_3 = -(\alpha + \mu + d_1)$, $\lambda_4 = -\mu,$ $\lambda_5 = -(p(1-\gamma) + \gamma + \mu)$ and $\lambda_6 = -(\tau + \mu).$

Since all the eigenvalues are negative, it implies that the disease free equilibrium point is locally asymptotically stable (LAS). Hence the proof.

## IV. Conclusion:

A mathematical model for the transmission of TB with three control strategies was developed. The existence, positivity, invariant region, and boundedness of the solution were investigated and all shown that the model is epidemiologically well-posed. The basic reproduction number was determined and analyzed. The disease-free equilibrium was obtained and proved to be locally asymptotically stable (LAS). It was established that the combination of the three strategies yields better result and effective way of controlling the spread of TB in an environment.

## V. Recommendations:

i). Further extension of the model is suggested for future researchers.
ii). Patients on treatment should complete the treatments as expected as it is very important for their recovery.
iii). Government to expand screening facilities and improve screening equipments.
iv). The three (3) control strategies are to be used simultaneously and continuously.

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