### Dynamics of a Tuberculosis Model with Vaccination and Dual Treatments: a Mathematical model Analysis

<sup>a</sup>ShimelisBekeleZerefe, <sup>b</sup>TemesgenTibebuMekonnen

<sup>a</sup>Department of Mathematics, Addis Ababa Science and Technology University, Addis Ababa, Ethiopia, <sup>b</sup>Department of Mathematics, DebreBerhan University, DebreBerhan, Ethiopia

**Abstract:** This article considers nonlinear dynamical system to study the dynamics of tuberculosis through vaccination and dual treatments. By dual treatments we studychemoprophylaxis and therapeuticstreatments of latent and active tuberculosis respectively. The total population is divided in to ten compartments. We found the dynamical system has disease free equilibrium point and endemic equilibrium point. We also found that the basic reproduction number of the considered dynamical system is

 $R_{0} = \begin{cases} \frac{c\omega\left((1-\psi)\zeta+\theta\right)\alpha\varepsilon(1-p)\delta\gamma}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)} + \frac{c\omega\sigma\psi\zeta\alpha\ \varepsilon(1-p)\delta\gamma}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)} + \\ \frac{c\omega\left((1-\psi)\zeta+\theta\right)\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)} + \frac{c\omega\sigma\psi\zeta\alpha\ (1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)} + \end{cases}. This depends on thirteen parameters.$ 

We proved that the disease free equilibrium point is locally stable if  $R_0 < 1$  and the endemic equilibrium point is locally stable if  $R_0 > 1$ . we also proved that the global stability of both equilibriums using Liapunov functions. Using standard data collected from different sources we found the numerical value of the basic reproduction number is  $R_0 = 0.7 < 1$  which shows that the tuberculosis disease not spreads in the community. We have done also sensitivity analysis to identify the most influential parameter that affects the basic reproduction number and we found rate of vaccine waning $\theta$  is the most influential parameter to change the basic reproduction number. To support the analytical findings we have done the numerical simulation of the dynamical system.

Key words: Nonlinear dynamical system, Vaccination, Dual treatments, Stability Analysis, Sensitivity Analysis

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#### I. Introduction

Tuberculosis is an air borne and highly infectious disease caused by infection with the bacteria mycobacterium tuberculosis <sup>[7]</sup>. Tuberculosis patients are divided into active tuberculosis and latent (passive) tuberculosis where active tuberculosis can transmit disease. According to the World Health Organization, one-third of the world's population is infected, either latently or actively with tuberculosis <sup>[4, 5]</sup>. The disease is most commonly transmitted from a person suffering from infectious (active) tuberculosis to other persons by infected droplets created when the person with active tuberculosis coughs, sneeze, sing or speak. The infectious bacilli are inhaled as droplets from the atmosphere. In the lung the bacteria are phagocytosed by alveolar macrophages and induce a localized pro inflammatory response that leads to the recruitment of mononuclear cells from neighboring blood vessels <sup>[6, 10]</sup>.

Data from a variety of sources suggest that the life time risk of developing clinically evident tuberculosis after being infected is approximately 10%, with 90% likelihood of the infection remaining latent. Individuals who have a latent tuberculosis infection are neither clinically ill nor capable of transmitting tuberculosis. At greater ages, the immunity of persons who have been previously infected may wane, and they may be then at risk of developing active tuberculosis as a consequence of either exogenous reinfection (i.e., acquiring a new infection from another infectious individual) or endogenous reactivation of latent bacilli (i.e., re-activation of a pre-existing dormant infection)<sup>[5, 7, 8, 10]</sup>.

The general symptoms of tuberculosis disease include feelings of sickness or weakness, weight loss, fever, and night sweats. The symptoms of tuberculosis disease of the lungs also include coughing, chest pain, and the coughing up of blood <sup>[7, 10]</sup>. Diagnosis relies on radiology (commonly chest X- ray), a tuberculin skin test, blood tests, as well as microscopic examination and microbiological culture of bodily fluids (such as sputum) <sup>[1, 7]</sup>.

Tuberculosis affects all countries and all age groups, but overall the best estimates for 2017 were that 90% of cases were adults (aged  $\geq$ 15 years), 64% were male, 9% were people living with HIV (72% of them in Africa) and two thirds were in eight countries: India (27%), China (9%), Indonesia (8%), the Philippines (6%), Pakistan (5%), Nigeria (4%), Bangladesh (4%) and South Africa (3%). Only 6% of cases were in the WHO European Region and the WHO Region of the Americas, each of which had 3% of cases <sup>[12]</sup>.

WHO report, Ethiopia is one of the 30 high burden tuberculosis countries in the world which together account for 87% of the global tuberculosis cases, with an estimated incidence of tuberculosis172,000 individuals in 2017. This number ranks Ethiopia 10<sup>th</sup> globally and 4<sup>th</sup> in Africa in terms of absolute tuberculosis-burden after Nigeria, South Africa and the Democratic Republic of Congo of estimated incidence tuberculosis 418,000, 322,000 and 262,000 individuals respectively in 2017 <sup>[12]</sup>. Tuberculosis kills an estimated 32,000 Ethiopians every year (more than 80 people per day) <sup>[11, 13]</sup>.

Epidemiology is the science of public health. It studies the distribution and determinants of disease status or events in populations, with the aim of controlling public health problems. The study of epidemiology ranges from cluster investigation at the individual level to building mathematical models to simulate disease dynamics at the population level<sup>[4]</sup>.

Mathematical models are important tools in analyzing the spread and control of infectious diseases. This started as far back as 1760 when Daniel Bernoulli developed a model for smallpox <sup>[2]</sup>. Many mathematical models have been developed for many infectious diseases including tuberculosis. Several researchers have continuously researched on how to reduce tuberculosis infection using mathematical models by incorporating control measures such as Bacilli Calmette-Guérin(BCG) vaccination, education, screening and treatment <sup>[2, 9]</sup>.

Long-term effects of tuberculosis can be examined using epidemiological models. Epidemiological models consist of compartments which represent sets of individuals grouped by disease status. The links between compartments represent transitions from one state of disease to another state. The future of an epidemic can be estimated by finding the basic reproductive number of the model<sup>[6]</sup>

#### **II.** The Mathematical Model

In this work we extend the basic SEIR Mathematical model done by ImaneAbduelkheir<sup>[7]</sup>under the title of Optimal Control Strategy of a Tuberculosis Epidemic Model with Drug Resistant tuberculosisandwe introduce a deterministic tuberculosis model. The total population N(t) is divided in to eight disjoint classes depending on the epidemiological status of individuals: Susceptible S(t), who have never exposed to the Mycobacterium tuberculosis; Vaccinated V(t), individuals who are vaccinated against mycobacterium tuberculosis; we assumed that persons with latent tuberculosis infection are considered at high risk of developing active tuberculosis during the first 2 years of infection, during which approximately 5% of those persons develop active tuberculosis and the likelihood of developing active disease after infection decreases with the age of the infection. Thus, we divide them in to two stages depending on the duration of time they spent after primary infection: An early stage with high risk of developing active tuberculosis  $H_r(t)$  (in the first two years after primary infection) and Later(Long) stage with low risk of developing active disease  $L_r(t)$  (More than two years after primary infection but not transformed to active tuberculosis), individuals who screened and treating at early latent stage tuberculosis T(t), Infectious individuals with tuberculosis I(t)that are not yet in treatment, treating infectious $I_T(t)$  and Recovered individuals R(t).

#### 2.1 Model Assumptions

We assumed that individuals are recruited into the population by a constant rate  $\Lambda$  with the proportions  $\psi$  of which are vaccinated to protect them against tuberculosis infection and the remaining proportion are susceptible. All susceptible individuals are equally likely to be infected by infectious individuals in case of contact. Furthermore, the vaccine has a waning effect over time (after a time  $\frac{1}{\theta}$  vaccinated individuals become susceptible). Susceptible population increases due to the coming in of new births not vaccinated against the infection and those who were vaccinated but lose their immunity. When some susceptible individuals come into contact with infectious individuals, they get infected and progress to latently infected classes at a force of infection rate  $\lambda$  where  $\lambda = c\omega \left(\frac{1}{N}\right)$  and  $\omega$  is the probability that an individual is infected by one infectious individual, and *c* is the percapita contact rate.

The proportion p of class  $H_r$  have got a chance of screened and treatment while the remaining proportion (1-p) of the high risk latently tuberculosis infected individuals may not have opportunity for treatment. The proportion  $\varepsilon$  and  $(1-\varepsilon)$  of individuals of the early latent/exposed individuals for tuberculosis who do not get chance for screened will go to  $L_r$  and I respectively at the rate  $\alpha$ . Thus, the proportion  $p,\varepsilon(1-p$ and  $1-\varepsilon 1-p$  of individuals in the class Hr is transferred to classes T, Lr and I respectively at a rate  $\alpha$ . Individual leaves class  $L_r$  at the rate  $\gamma$  in which, the proportion  $\delta$  goes to class I and; the remaining proportion $(1-\delta)$  recovers naturally and enter to recovered class R. The proportion q of individuals in class I goes for treatment in  $I_T$  and the remaining proportion(1-q) enters to class R at the rate  $\rho$ . Individuals leave the screened class  $S_T$  and treating class  $I_T$  at the rates $\phi$ , and  $\varphi$  respectively, and go to recovered class, where  $\phi > \varphi$ .

Individuals in the recovered class are temporarily recovered. Soon they revert back to the latently infected classes  $H_r$  after been re-infected by tuberculosis at the rate  $\kappa\lambda$ , where  $\kappa$  is the reduction in susceptibility

due to prior endogenous infection of tuberculosis. We assume that each class conforms to natural death at the rate  $\mu$  while infectious individuals in *I* are die due to tuberculosis diseases at the rate *d*.

Population is closed which means the increase or decrease of population is only caused by birth and death, while the increase and reduction caused by other factors is ignored. That is, there are no immigrants and emigrants. The only way of entry into the population is through new – born babies and the only way of exit is through death from natural causes or death from tuberculosis-related causes. Death caused by factors other than tuberculosis infection is considered a natural death.Population is homogeneous.All newborns are previously uninfected by tuberculosis and therefore join either the vaccinated compartment or the susceptible compartment depending on whether they are vaccinated or not. The immunity conferred on individuals by vaccination expires after some time at a given rate. Infected individuals are divided into two groups: latent infected and active infected. The individual active infected can transmit tuberculosis disease.Latently Infected individuals are divided into two sub groups: early latent infected. All susceptible individuals are equally likely to be infected by infectious individuals in case of contact. Individuals in each compartment have equal natural death rate. Individuals on recovered classes will return to be individuals on infected classes.

Based on the above assumptions we do have the following flow chart:



Figure-1: Flow chart of dynamical system of tuberculosis

With the above assumptions and relations between different compartments the dynamics of tuberculosis model can be ruled by the following nonlinear ordinary differential equations.

$\frac{dv}{dt} = \psi \Lambda - (\sigma \lambda + \theta + \mu) V$		(1)
$\frac{ds}{dt} = (1 - \psi)\Lambda + \theta V - (\lambda + \mu)S$	(2)	
$\frac{dH_r}{dt} = \lambda(S + \sigma V + \kappa R) - (\alpha + \mu)H_r$		(3)
$\frac{dL_r}{dt} = \alpha \varepsilon (1-p)H_r - (\gamma + \mu)L_r$	(4)	
$\frac{dT}{dt} = \alpha p H_r - (\phi + \mu) T$	(5)	
$\frac{dI}{dt} = \delta \gamma L_r + \alpha (1 - \varepsilon)(1 - p)H_r - (\rho + \mu + d)I$	(6)	
$\frac{dI_T}{dt} = q\rho I - (\varphi + \mu)I_T$	(7)	
$\frac{dR}{dt} = \phi T + (1 - q)\rho I + (1 - \delta)\gamma L_r - (\kappa \lambda + \mu)R$	(8)	
With the total population at a given time t is		

 $N(t) = S(t) + V(t) + H_r(t) + L_r(t) + I(t) + T(t) + R(t).$ 

Table-1: Symbols and	their descriptions for sta	ate variables and	parameters in the model
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Symbols	Description
S(t)	Susceptible individuals who are at risk of being infected by tuberculosis at time t.
V(t)	Vaccinated individuals against tuberculosis at time <i>t</i> .
$H_r(t)$	Early latently(High risk) infected individuals at time <i>t</i> .
$L_r(t)$	Long latently(Low risk) infected individuals at time t.
T(t)	Screened and treating individuals at time <i>t</i> .
l(t)	Individuals who are infectious at time t.
R	Individuals Recovered against tuberculosis at time t.
Λ	Recruitment of the population

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$\psi$	Proportions new born vaccinated
μ	Natural death rate
σ	The rate of inefficacy of vaccine
θ	The rate of vaccine waning
φ	The rate of chemoprophylaxis treatment of early latent tuberculosis
λ	Force of infection
ω	Probability of acquiring tuberculosis infections one infectious individual
С	Number of effective contacts susceptible individuals makes with infectious individuals per year.
α	The rate of progression of individuals from early latently infected
d	Death rate due to the disease
p	Proportion of early latently infected individuals who go for treatment.
γ	Progression rate from Long latently infected tuberculosis to active tuberculosis.
δ	The portion of $L_r$ enter in to $I$ .
ε	Proportion of individuals who do not get chance for screened at $H_r$ and will go to $L_r$ class.
ρ	The rate at which individuals leave infectious class.
q	Proportion of infectious individuals who go for treatment.
φ	The rate of therapeutic treatment of active tuberculosis individuals in $I_T$
κ	Acquired immunity due to previous treatment.

#### 2.2 Positivity of Solutions

**Theorem-1:** Let the initial value for the model is  $V(0) > 0, S(0) > 0, H_r(0) > 0, L_r(0) > 0$ ,  $I(0) > 0, T(0) > 0, I_T(0) > 0$  and R(0) > 0. Then, the solutions  $V(t), S(t), H_r(t), L_r(t), I(t), T(t), I_T(t)$  and R(t) of the dynamical system (1) – (8) will be remain positive for all time t > 0. **Proof** 

Let  $\bar{t} = \sup\{t > 0: S(t) > 0, E(t) > 0, I(t) > 0, R(t) > 0\} \in [0, t]$  and by considering the eight ordinary differential equations and after taking some steps on finding their solution we do have

i.  $\frac{dV}{dt} = \psi \Lambda - (\sigma \lambda + \theta + \mu) V$  whose solution is

$$V(\bar{t}) = V(0)M_V + M_V \int_0^t \psi \Lambda exp\left\{\mu t + \theta t + \int_0^w (\lambda(v))dv\right\} dw > 0$$

Since  $M_V = exp - \left\{\mu \bar{t} + \theta \bar{t} + \int_0^{\bar{t}} \lambda(v) dv\right\} > 0$ ii  $\frac{ds}{ds} = (1 - v)\Lambda + \theta V - (\lambda + v)$  Swhose solution i

$$\frac{1}{dt} = (1 - \psi)\Lambda + \theta V - (\lambda + \mu)S \text{ whose solution is}$$

$$S(\bar{t}) = S(0)M_S + M_S \int_0^{\bar{t}} ((1 - \psi)\Lambda + \theta V(t))exp\left\{\mu\bar{t} + \int_0^w (\lambda(v))dv\right\}dw > 0$$

Since  $M_S = exp - \left\{\mu \bar{t} + \int_0^{\bar{t}} \lambda(v) dv\right\} > 0$ 

 $\frac{dH_r}{dt} = \lambda(S + \sigma V + \kappa R) - (\alpha + \mu)H_r$  whose solution is iii.  $H_r(\bar{t}) = H_r(0)M_H + M_H \int_0^{\bar{t}} \lambda(t)(S(t) + \sigma V(t) + \kappa R(t))exp[\alpha \bar{t} + \mu \bar{t}]dw > 0, \text{ Since } M_H = exp - M_H = 0$  $\left[\alpha \bar{t} + \mu \bar{t}\right] > 0$  $\frac{dL_r}{dt} = \alpha \varepsilon (1-p)H_r - (\gamma + \mu)L_r$  Whose solution is iv.  $L_r(\bar{t}) = L_r(0)M_L + M_L \int_0^{\bar{t}} \alpha \varepsilon (1-p)H_r exp[\gamma \bar{t} + \mu \bar{t}]dw > 0$ since  $M_L = exp - [\alpha \bar{t} + \mu \bar{t}] > 0$  $\frac{dT}{dt} = \alpha p H_r + q \rho I - (\phi + \mu) T$  whose solution is v.  $T(\bar{t}) = T(0)M_T + M_T \int_0^{\bar{t}} \alpha p H_r exp[\phi \bar{t} + \mu \bar{t}] dt > 0 \text{ since } M_T = exp - [\phi \bar{t} + \mu \bar{t}] > 0$  $\frac{dI}{dt} = \delta \gamma L_r + \alpha (1 - \varepsilon)(1 - p)H_r - (\rho + \mu + d)I$  whose solution is vi.  $I(\bar{t}) = I(0)M_I + M_I \int_0^{\bar{t}} [\delta\gamma L_r + \alpha(1-\varepsilon)(1-p)H_r] exp[\rho\bar{t} + d\bar{t} + \mu\bar{t}]dt > 0$  since  $M_H = exp - [\rho\bar{t} + d\bar{t} + \mu\bar{t}] > 0$  $\frac{dI_T}{dt} = q\rho I - (\varphi + \mu)I_T$  whose solution is vii.  $I_T(\bar{t}) = I_T(0)M_{IT} + M_{IT}\int_0^{\bar{t}} q\rho Iexp[\varphi\bar{t} + \mu\bar{t}]dt > 0 \text{since}M_{IT} = exp - [\varphi\bar{t} + \mu\bar{t}] > 0$ viii.  $\frac{dR}{dt} = \varphi T + (1 - q)\rho I + \varphi I_T + (1 - \delta)\gamma L_r - (\kappa\lambda + \mu)R \text{ whose solution is}$  $R(\bar{t}) = R(0)M_R + M_R \int_0^t [T + (1 - q)\rho I + \varphi I_T + (1 - \delta)\gamma L_r] exp\left[\mu \bar{t} + \int_0^t \lambda(v) dv\right] dw > 0$ 

Since  $M_R = exp - \left\{\mu \bar{t} + \int_0^{\bar{t}} \lambda(v) dv\right\} > 0$ 

#### 2.3 Roundedness of Solutions

**Theorem-2:** The closed set  $\Omega = \{(V, S, H_r, L_r, T, I, I_T, R) \in \mathcal{R}^8_+ : N \leq \frac{\Lambda}{n}\}$  is positively invariant and attracts all positive solutions of the dynamical system (1) - (8).

#### Proof.

Consider the biologically feasible region,  $\Omega$  and observe that the rate of change of the total population obtained Consider the biologically feasible region,  $\Omega$  and observe that the rate of change of the total population obtained by adding all the equations of the model (1)-(8) is given by  $\frac{dN}{dt} = \Lambda - \mu N - dI \le \Lambda - \mu N$ . It follows that  $\frac{dN}{dt} < 0$  whenever  $N > \frac{\Lambda}{\mu}$ . Furthermore, since  $\frac{dN}{dt} \le \Lambda - \mu N$ ; Now using a standard comparison theorem we do have  $\int \frac{dN}{\Lambda - \mu N} \le \int dt$ . Integrating both sides gives  $\Lambda - \mu N \ge Ae^{-\mu t}$ , where  $A = e^{-c\mu}$  it is a constant. By using initial condition N(0) we do have  $\Lambda - \mu N(0) \ge A$ or  $N(0) \le \frac{\Lambda}{\mu} - \frac{\Lambda}{\mu} \le \frac{\Lambda}{\mu}$  and  $N(t) \le N(0)e^{-\mu t} + \frac{\Lambda}{\mu}(1 - e^{-\mu t})$ . Thus  $\lim_{t \to \infty} N(t) \le N(0)e^{-\mu t} + \frac{\Lambda}{\mu}(1 - e^{-\mu t})$  $\Rightarrow \lim_{t \to \infty} N(t) \le N(0)e^{-\mu t} - \frac{\Lambda}{\mu}e^{-\mu t} + \frac{\Lambda}{\mu} \le \frac{\Lambda}{\mu}$  since  $(0) \le \frac{\Lambda}{\mu}$ . Hence as  $t \to \infty$  the population size  $N(t) \to \frac{\Lambda}{\mu}$ which implies that  $0 \le N(t) \le \frac{\Lambda}{\mu}$ . Therefore, all feasible solutions of the dynamical system (1) - (8) with initial conditions in  $\Omega = \{(V, S, H_r, L_r, T, I, I_T, R) \in \mathcal{R}^8_+ : N \leq \frac{\Lambda}{u}\}$  do remain in  $\Omega \forall t > 0$ . That is, the set  $\Omega$  is positively invariant and attracting.

#### 2.4 Scaling the population

Introducing new variables  $v = \frac{V}{N}$ ,  $s = \frac{s}{N}$ ,  $h_r = \frac{H_r}{N}$ ,  $l_r = \frac{L_r}{N}$ ,  $s_T = \frac{T}{N}$ ,  $i = \frac{I}{N}$ ,  $i_T = \frac{I_T}{N}$ ,  $r = \frac{R}{N}$  and  $\frac{dV}{dt} = v\frac{dN}{dt} + N\frac{dv}{dt}$  which implies that  $\frac{dv}{dt} = \frac{1}{N} \left\{ \frac{dV}{dt} - v\frac{dN}{dt} \right\}$  and similar derivation for  $\frac{ds}{dt}$ ,  $\frac{dh_r}{dt}$ ,  $\frac{dl_r}{dt}$ ,  $\frac{ds_T}{dt}$ ,  $\frac{di_T}{dt}$ ,  $\frac{di_T}{$ 

$$= \frac{1}{N} \left\{ \frac{dV}{dt} - v \frac{dN}{dt} \right\} = \psi \zeta - (\zeta + \sigma \lambda + \theta - di)v$$
(9)

$$\frac{dt}{dt} = \frac{1}{N} \left\{ \frac{dt}{dt} - v \frac{dt}{dt} \right\} = \psi \zeta - (\zeta + \sigma \lambda + \theta - dt) v \qquad (10)$$

$$\frac{ds}{dt} = \frac{1}{N} \left\{ \frac{ds}{dt} - s \frac{dN}{dt} \right\} = (1 - \psi) \zeta + \theta v - (\lambda + \zeta - di) s \qquad (10)$$

$$\frac{dh_r}{dt} = \frac{1}{V} \left\{ \frac{dH_r}{dt} - h_r \frac{dN}{dt} \right\} = \lambda (s + \sigma v + \kappa r) - (\zeta + \alpha - di) h_r \qquad (11)$$

$$\frac{dl}{dt} = \frac{1}{N} \left\{ \frac{dL_r}{dt} - l_r \frac{dN}{dt} \right\} = \alpha \varepsilon (1-p)h_r - (\zeta + \gamma - di)l_r$$
(12)

$$-s_T \frac{dN}{dt} = \delta \gamma l_r + \alpha (1-\varepsilon)(1-p)h_r - (\zeta + \rho + d - di)i$$
(13)

$$= \alpha p h_r - (\zeta + \phi - di)s_T \tag{14}$$

$$= q\rho i - (\zeta + \varphi - di)i_T \tag{15}$$

$$\frac{ds_T}{dt} = \frac{1}{N} \left\{ \frac{dt}{dt} - s_T \frac{dt}{dt} \right\} = \delta \gamma l_r + \alpha (1 - \varepsilon) (1 - p) h_r - (\zeta + \rho + d - di) i \qquad (13)$$

$$\frac{di_T}{dt} = \frac{1}{N} \left\{ \frac{dl_T}{dt} - i_T \frac{dN}{dt} \right\} = \alpha p h_r - (\zeta + \phi - di) s_T$$

$$\frac{di}{dt} = \frac{1}{N} \left\{ \frac{dl}{dt} - i \frac{dN}{dt} \right\} = q\rho i - (\zeta + \phi - di) i_T$$

$$= q\rho i - (\zeta + \phi - di) i_T$$

$$= \phi s_T + (1 - q)\rho i + (1 - \delta)\gamma l_r + \phi i_T - (\zeta + \kappa \lambda - di)r \qquad (16)$$

#### 2.5 Equilibrium points and their stability analysis

**Disease Free Equilibrium point**  $E^0 = (v^0, s^0, h_r^0, l_r^0, i^0, s_T^0, i_T^0, r^0)$ 

The disease free equilibrium point  $E^{-1} = (v^{-}, s^{-}, t^{-}, t^{-}, t^{-}, t^{-}, t^{-}, t^{-})$ The disease free equilibrium point is obtained by assuming that  $h_r^{-0} = l_r^{-0} = i^0 = s_T^{-0} = i_T^{-0} = r^0 = 0$  and by making the right hand side of the dynamical system (9) - (16) equal to zero we get the disease free equilibrium point is:  $E^{0} = (v^{0}, s^{0}, h_r^{-0}, l_r^{-0}, i^{0}, s_T^{-0}, i_T^{-0}, r^{0}) = \left(\frac{\psi\zeta}{\zeta + \theta}, \frac{(1-\psi)\zeta + \theta}{\zeta + \theta}, 0, 0, 0, 0, 0, 0\right).$ 

#### **Basic Reproduction Number** $R_0$

The basic reproduction number is defined as the average number of secondary infections caused by typical infected individual during his entire period of infectiousness. We calculate the basic reproduction number  $R_0$  by using the next generation operator method in the dynamical system (9)-(16) with the rate of appearance of new infections  $\mathcal{F}$  and the transfer rate of individuals V at the disease free steady  $E^0 = \left(\frac{\psi\zeta}{\zeta+\theta}, \frac{(1-\psi)\zeta+\theta}{\zeta+\theta}, 0, 0, 0, 0, 0, 0\right)$  is state

$$F = \begin{bmatrix} 0 & 0 & c\omega \left( \frac{\sigma\psi\zeta + (1-\psi)\zeta + \theta}{\zeta + \theta} \right) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} (\zeta + \alpha) & 0 & 0 \\ -\alpha\varepsilon(1-p) & (\zeta + \gamma) & 0 \\ -\alpha(1-\varepsilon)(1-p) & -\delta\gamma & (\zeta + \rho + d) \end{bmatrix}$$
and

$$V^{-1} = \begin{bmatrix} \frac{1}{(\zeta + \alpha)} & 0 & 0\\ \frac{\alpha\varepsilon(1-p)}{(\zeta + \alpha)(\zeta + \gamma)} & \frac{1}{(\zeta + \gamma)} & 0\\ \frac{\alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta + \gamma)}{(\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d)} & \frac{\delta\gamma}{(\zeta + \gamma)(\zeta + \rho + d)} & \frac{1}{(\zeta + \rho + d)} \end{bmatrix}$$

So that  $_{FV^{-1}}$ 

$$= \begin{bmatrix} c\omega \left(\frac{\sigma\psi\zeta + (1-\psi)\zeta + \theta}{\zeta + \theta}\right) \frac{\alpha\varepsilon(1-p)\delta\gamma + (\zeta + \rho + d)(\zeta + \gamma)}{(\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d)} & c\omega \left(\frac{\sigma\psi\zeta + (1-\psi)\zeta + \theta}{\zeta + \theta}\right) \frac{\delta\gamma}{(\zeta + \gamma)(\zeta + \rho + d)} & c\omega \left(\frac{\sigma\psi\zeta + (1-\psi)\zeta + \theta}{\zeta + \theta}\right) \frac{1}{(\zeta + \rho + d)} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

Thus the basic reproduction number  $R_0$  is the spectral radius of  $FV^{-1}$ 

.

$$R_{0} = \frac{c\omega((1-\psi)\zeta + \theta)\alpha\varepsilon(1-p)\delta\gamma}{(\zeta + \theta)(\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d)} + \frac{c\omega\sigma\psi\zeta\alpha\varepsilon(1-p)\delta\gamma}{(\zeta + \theta)(\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d)} + \frac{c\omega((1-\psi)\zeta + \theta)\alpha(1-\varepsilon)(1-p)}{(\zeta + \theta)(\zeta + \alpha)(\zeta + \rho + d)} + \frac{c\omega\sigma\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta + \theta)(\zeta + \alpha)(\zeta + \rho + d)}$$

**Endemic Equilibrium Point**  $E^* = (v^*, s^*, h_r^*, l_r^*, s_T^*, i^*, i_T^*, r^*)$ 

The endemic equilibrium point  $E^* = (v^*, s^*, h_r^*, l_r^*, s_T^*, i^*, i_T^*, r^*)$  obtained by setting the right hand side of each equation of the dynamical system (9)-(16) equal to zero. That is

$$\psi\zeta - (\zeta + \sigma\lambda + \theta - \operatorname{di})v = 0$$
  
(1 - \psi)\zeta + \theta v - (\lambda + \zeta - \operatorname{di})s = 0  
\lambda(s + \sigma v + \kappa r) - (\zeta + \alpha - \operatorname{di})h\_r = 0

 $\begin{aligned} \alpha \varepsilon (1-p)h_r - (\zeta + \gamma - di)l_r &= 0\\ \delta \gamma l_r + \alpha (1-\varepsilon)(1-p)h_r - (\zeta + \rho + d - di)i &= 0\\ \alpha ph_r - (\zeta + \phi - di)s_T &= 0\\ q\rho i - (\zeta + \phi - di)i_T &= 0\\ \phi s_T + (1-q)\rho i + (1-\delta)\gamma l_r + \phi i_T - (\zeta + \kappa\lambda - di)r &= 0\\ \text{Let}\pi &= \zeta - di^* \text{and } \lambda^* = c\omega i^*. \end{aligned}$ 

Thus after some calculation we get the endemic equilibrium point  $E^* = (v^*, s^*, h_r^*, l_r^*, s_T^*, i^*, i_T^*, r^*)$  where  $\frac{1}{\sqrt{2}}$ 

$$\begin{aligned} v^* &= \frac{q\cdot y}{\pi + \sigma\lambda^* + \theta} \\ s^* &= \frac{(1-\psi)\zeta(\pi + \sigma\lambda^* + \theta) + \theta\psi\zeta}{(\lambda^* + \pi)(\pi + \sigma\lambda + \theta)} \\ l_r^* &= \frac{B\lambda^*\varepsilon(1-p)}{(A_1\lambda^* + A_2)(\pi + \gamma)} \left( \frac{(\pi + \kappa\lambda^*)(1-\psi)\zeta(\pi + \sigma\lambda^* + \theta) + \theta\psi\zeta}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} + \frac{(\pi + \kappa\lambda^*)\sigma\psi\zeta}{\kappa(\pi + \sigma\lambda^* + \theta)} \right), \\ s_T^* &= \frac{B\lambda^*(\delta\gamma\varepsilon(1-p) + (\pi + \gamma)(1-\varepsilon)(1-p))}{(A_1\lambda^* + A_2)(\pi + \gamma)(\pi + \rho + d)} \left( \frac{(\pi + \kappa\lambda^*)(1-\psi)\zeta(\pi + \sigma\lambda^* + \theta) + \theta\psi\zeta}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} + \frac{(\pi + \kappa\lambda^*)\sigma\psi\zeta}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} \right) \\ i_r^* &= \frac{B\lambda^*(\phi\rho\delta\gamma\varepsilon(1-p) + (\pi + \gamma)(\pi + \rho + d)}{(A_1\lambda^* + A_2)(\pi + \gamma)(\pi + \rho + d)} \left( \frac{(\pi + \kappa\lambda^*)(1-\psi)\zeta(\pi + \sigma\lambda^* + \theta) + \theta\psi\zeta}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} + \frac{(\pi + \kappa\lambda^*)\sigma\psi\zeta}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} \right) \\ i_T^* &= \frac{B\lambda^*(\phi\rho\delta\gamma\varepsilon(1-p) + (\pi + \gamma)(1-\varepsilon)(1-p))}{(A_1\lambda^* + A_2)(\pi + \varphi)(\pi + \gamma)(\pi + \rho + d)} \left( \frac{(\pi + \kappa\lambda^*)(1-\psi)\zeta(\pi + \sigma\lambda^* + \theta) + \theta\psi\zeta}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} + \frac{(\pi + \kappa\lambda^*)\sigma\psi\zeta}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} \right) \\ r^* &= \frac{B\lambda^*(\pi + \alpha)}{(A_1\lambda^* + A_2)\lambda^*\kappa} \left( \frac{(\pi + \kappa\lambda^*)(1-\psi)\zeta(\pi + \sigma\lambda^* + \theta) + \theta\psi\zeta}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} + \frac{(\pi + \kappa\lambda^*)\sigma\psi\zeta}{\kappa(\pi + \sigma\lambda^* + \theta)} \right) \\ - \left( \frac{(1-\psi)\zeta(\pi + \sigma\lambda^* + \theta)}{\kappa(\lambda^* + \pi)(\pi + \sigma\lambda^* + \theta)} + \frac{\sigma\psi\zeta}{\kappa(\pi + \sigma\lambda^* + \theta)} \right) \\ Where, A_1 &= \begin{cases} \kappa(\pi + \alpha)(\pi + \varphi)(\pi + \gamma)(\pi + \rho + d) - \kappa\phi\phi\rho(\pi + \gamma)(\pi + \rho + d) - \kappa\phi\rho(\pi + \gamma)(1 - \varepsilon)(1 - p) - \kappa\phi\rho(\pi + \gamma)(\pi + \rho + d) - \kappa(\pi + \varphi)(\pi + \gamma)(\pi + \rho + d) - \kappa(\pi + \varphi)(\pi + \gamma)(\pi + \rho + d) \end{cases} \right)$$

## 2.5.1 Local Stability of the Disease Free Equilibrium *E*<sup>0</sup> Theorem-3:

The disease free equilibrium point  $E^0 = \left(\frac{\psi\zeta}{\zeta+\theta}, \frac{(1-\psi)\zeta+\theta}{\zeta+\theta}, 0, 0, 0, 0, 0, 0\right)$  of the dynamical system (9)-(16) is locally asymptotically stable if the basic reproduction number  $R_0 < 1$  and  $E^0$  is unstable if  $R_0 > 1$ . **Proof:** 

The Jacobean matrix of the dynamical system (9)-(16) at the disease free equilibrium point  $E^0 = (v^0, s^0, h_r^0, l_r^0, i^0, s_T^0, i_T^0, r^0) = (\frac{\psi\zeta}{z+\theta}, \frac{(1-\psi)\zeta+\theta}{z+\theta}, 0, 0, 0, 0, 0, 0)$  is

$$J(E^{0}) = \left(\frac{\psi\zeta}{\zeta+\theta}, \frac{(1-\psi)\zeta+\theta}{\zeta+\theta}, 0, 0, 0, 0, 0, 0, 0\right)$$
 is  
$$J(E^{0}) = \begin{bmatrix} m_{1} & 0 & 0 & 0 & m_{2} & 0 & 0\\ \theta & -\zeta & 0 & 0 & m_{3} & 0 & 0\\ 0 & 0 & m_{4} & 0 & 0 & m_{5} & 0 & 0\\ 0 & 0 & m_{6} & m_{7} & 0 & 0 & 0 & 0\\ 0 & 0 & m_{6} & m_{7} & 0 & 0 & 0 & 0\\ 0 & 0 & m_{9} & \delta\gamma & 0 & m_{10} & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & q\rho & m_{11} & 0\\ 0 & 0 & 0 & m_{12} & \phi & m_{13} & \varphi & -\zeta \end{bmatrix}$$

Where,

$$m_{1} = -(\zeta + \theta), m_{2} = -(\sigma c \omega - d) \frac{\psi \zeta}{\zeta + \theta}, m_{3} = -(\sigma c \omega - d) \frac{(1 - \psi)\zeta + \theta}{\zeta + \theta},$$

$$m_{4} = -(\zeta + \alpha), m_{5} = c \omega \left(\frac{(1 - \psi)\zeta + \theta}{\zeta + \theta} + \frac{\sigma \psi \zeta}{\zeta + \theta}\right), m_{6} = \alpha \varepsilon (1 - p),$$

$$m_{7} = -(\zeta + \gamma), m_{8} = -(\zeta + \phi), m_{9} = \alpha (1 - \varepsilon)(1 - p),$$

$$m_{10} = -(\zeta + \rho + d), m_{11} = -(\zeta + \varphi), m_{12} = (1 - \delta)\gamma, m_{13} = (1 - q)\rho$$
The corresponding characteristic equation of the Jacobean matrix at the disease equilibrium point is:
$$\left. \begin{array}{c} m_{1} - \lambda & 0 & 0 & 0 & m_{2} & 0 & 0 \\ \theta & -\zeta - \lambda & 0 & 0 & 0 & m_{3} & 0 & 0 \\ 0 & 0 & m_{4} - \lambda & 0 & 0 & m_{5} & 0 & 0 \\ 0 & 0 & m_{6} & m_{7} - \lambda & 0 & 0 & 0 & 0 \\ 0 & 0 & m_{9} & \delta \gamma & 0 & m_{10} - \lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & q\rho & m_{11} - \lambda & 0 \end{array} \right| = 0$$

$$\left[ \begin{pmatrix} 0 & 0 & m_{12} & \phi & m_{13} & \varphi & -\zeta - \lambda \\ & [(\lambda + \zeta)^2 (\lambda + \zeta + \theta)(\lambda + \zeta + \phi)(\lambda + \zeta + \varphi)] * \\ & -(\lambda^3 + (3\xi + \alpha + \gamma + \rho + d)\lambda^2) + \\ & (\zeta + \alpha)(\zeta + \gamma) + (2\zeta + \alpha + \gamma)(\zeta + \rho + d) + \alpha(1 - \varepsilon)(1 - p)c\omega \left(\frac{(1 - \psi)\zeta + \theta}{\zeta + \theta} + \frac{\sigma\psi\zeta}{\zeta + \theta}\right) \right)\lambda + \right] + \right]$$

$$\left[ \begin{pmatrix} (\zeta + \alpha)(\zeta + \gamma) + (2\zeta + \alpha + \gamma)(\zeta + \rho + d) + \alpha(1 - \varepsilon)(1 - p)c\omega \left(\frac{(1 - \psi)\zeta + \theta}{\zeta + \theta} + \frac{\sigma\psi\zeta}{\zeta + \theta}\right) \right)\lambda + \\ & (\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d) + \alpha(1 - \varepsilon)(1 - p)(\zeta + \gamma) + \\ & c\omega \left(\frac{(1 - \psi)\zeta + \theta}{\zeta + \theta} + \frac{\sigma\psi\zeta}{\zeta + \theta}\right) \left(\delta\gamma\alpha\varepsilon(1 - p) - \alpha(1 - \varepsilon)(1 - p)(\zeta + \gamma)\right) \\ & = 0 \end{pmatrix} \right]$$

Thus the roots of the characteristic equation are:  

$$\lambda_{1} = -\zeta, \lambda_{2} = -, \lambda_{3} = -(\zeta + \theta), \quad \lambda_{4} = -(\zeta + \theta), \quad \lambda_{5} = -(\zeta + \gamma) \text{ or } \lambda^{3} + c_{1}\lambda^{2} + c_{2}\lambda + c_{3} = 0$$
Where,  

$$c_{1} = (3\zeta + \alpha + \gamma + \rho + d),$$

$$c_{2} = (\zeta + \alpha)(\zeta + \gamma) + (2\zeta + \alpha + \gamma)(\zeta + \rho + d) + \alpha(1 - \varepsilon)(1 - p)c\omega\left(\frac{(1 - \psi)\zeta + \theta}{\zeta + \theta} + \frac{\sigma\psi\zeta}{\zeta + \theta}\right),$$

$$c_{3} = (\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d) - c\omega\left(\frac{(1 - \psi)\zeta + \theta}{\zeta + \theta} + \frac{\sigma\psi\zeta}{\zeta + \theta}\right)\left(\delta\gamma\alpha\varepsilon(1 - p) + \alpha(1 - \varepsilon)(1 - p)(\zeta + \gamma)\right).$$
Now we are going to show 
$$c_{3} > 0.$$

$$(\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d) - c\omega\left(\frac{(1 - \psi)\zeta + \theta}{\zeta + \theta} + \frac{\sigma\psi\zeta}{\zeta + \theta}\right)\left(\delta\gamma\alpha\varepsilon(1 - p) + \alpha(1 - \varepsilon)(1 - p)(\zeta + \gamma)\right) > 0$$

$$\Rightarrow 1 - c\omega \left(\frac{(1-\psi)\zeta+\theta}{\zeta+\theta} + \frac{\sigma\psi\zeta}{\zeta+\theta}\right) \frac{\delta\gamma\alpha\varepsilon (1-p)+\alpha(1-\varepsilon)(1-p)(\zeta+\gamma)}{(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)} > 0 \text{ that is } 1 - R_0 > 0$$
  
And therefore  $R_0 < 1$ . Since these conditions ensure that all roots of the polynomial have negative real parts and thus by RouthHurwitz stability criterion we found that all of the eigenvalues of the Jacobean matrix have negative real parts when  $R_0 < 1$ ,  $(c_3 > 0)$ . Thus, the disease free equilibriumpoint  $E^0$ , of the dynamical system

(9)-(16) is locally asymptotical stable if  $R_0 < 1$ .

### 2.5.2 Global stability of Diseases free Equilibrium point Theorem-4:

The diseases free equilibrium  $E^0$  of the model (9)-(16) is globally asymptotically stable in  $\Omega$  whenever $R_0 < 1 - \frac{(c\omega \kappa r + dh_r)[\alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta+\gamma)] + \delta\gamma(\zeta+\alpha)dl_r + (\zeta+\gamma)(\zeta+\alpha)di}{(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)}$ .

#### **Proof:**

Define a Liapunov function  $W(l_r, h_r, i) = A_1 l_r + A_2 h_r + A_3 i, for all A_1 > 0, for i = 1,2,3.$  $\Rightarrow W(l_r, h_r, i) = \begin{cases} A_1 \left\{ L_r(0)M_L + M_L \int_0^t \alpha \varepsilon (1-p)H_r exp[\gamma t + \mu t] dw \right\} + A_2 \left\{ H_r(0)M_H + M_H \int_0^t \lambda(t)(S(t) + \sigma V(t) + \kappa R(t))exp[\alpha t + \mu t] dw \right\} + A_3 \left\{ I(0)M_I + M_I \int_0^t [\delta \gamma L_r + \alpha (1-\varepsilon)(1-p)H_r]exp[\rho t + dt + \mu t] dw \right\} \end{cases}$ 

Where  $M_L = M_H = exp - [\alpha t + \mu t] \text{and} M_I = exp - [\rho t + dt + \mu t]$ . Here we do have  $W(x) \ge 0$ , for  $x \in int\Omega$  since  $l_r(t) > 0$ ,  $h_r(t) > 0$ , i(t) > 0 and  $W(E^0) = 0$ , since  $l_r = h_r = 0$ ; so the function W is positive definite with respect to the disease free equilibrium point. The derivative of W at the diseases free equilibrium point is  $\begin{pmatrix} A_1[c\omega i(s + \sigma v + \kappa r) - (\zeta + \alpha - di)h_r] + \end{pmatrix}$ 

$$\begin{split} \dot{W} &= \begin{cases} A_1[\cos((\zeta + \sigma) + \alpha)^{-1}(\zeta + \gamma - di)l_r] + \\ A_2[\alpha\varepsilon(1-p)h_r - (\zeta + \gamma - di)l_r] + \\ A_3[\delta\gamma l_r + \alpha(1-\varepsilon)(1-p)h_r - (\zeta + \rho + d - di)i] \end{cases} \\ By choosing A_1 &= \alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta + \gamma), A_2 = \delta\gamma(\zeta + \alpha), A_3 = (\zeta + \gamma)(\zeta + \alpha) \text{we do have} \\ \dot{W} &\leq (\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d) \left[ c\omega(s^* + \sigma v^*) \frac{\alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta + \gamma)}{(\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d)} - 1 \right] i \\ &+ \left[ A_1(c\omega\kappa r + dh_r) + A_2dl_r + A_3di \right] i \\ &= (\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d)[R_0 - 1] i \\ &+ \left[ \left[ \alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta + \gamma) \right] (c\omega\kappa r + dh_r) + \delta\gamma(\zeta + \alpha)dl_r \\ &+ (\zeta + \gamma)(\zeta + \alpha)di \right] i \end{aligned}$$
Hence  $\dot{W} \leq 0$ , provided that  $(\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d)[R_0 - 1] + \left[ \left[ \alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta + \gamma) \right] (c\omega\kappa r + dh_r) + \delta\gamma(\zeta + \alpha)dl_r + (\zeta + \gamma)(\zeta + \alpha)di \right] i \end{aligned}$ 

Hence  $\dot{W} < 0$ , provided that  $(\zeta + \alpha)(\zeta + \gamma)(\zeta + \rho + d)[R_0 - 1] + [[\alpha \varepsilon (1 - p)\delta \gamma + \alpha(1 - \varepsilon)(1 - p)(\zeta + \rho \omega \kappa r + dhr + \delta \gamma \zeta + \alpha dlr + \zeta + \gamma \zeta + \alpha di < 0$ . That is,  $W < 0 \Leftrightarrow R0 - 1 < -\alpha \varepsilon 1 - p\delta \gamma + \alpha 1 - \varepsilon 1 - p\zeta + \gamma \omega \kappa r + dhr + \delta \gamma \zeta + \alpha dlr + \zeta + \gamma \zeta + \alpha dl \zeta + \alpha \zeta + \gamma \zeta + \rho + d$ 

$$\Leftrightarrow R_0 < 1 - \frac{\left[ [\alpha \varepsilon (1-p) \delta \gamma + \alpha (1-\varepsilon) (1-p) (\zeta + \gamma)] (c \omega \, \kappa r + dh_r) + \delta \gamma (\zeta + \alpha) dl_r + (\zeta + \gamma) (\zeta + \alpha) di \right]}{(\zeta + \alpha) (\zeta + \gamma) (\zeta + \rho + d)}$$

# 2.5.3 Local Stability of endemic equilibrium point Theorem-5:

The endemic equilibrium point  $E^* = (v^*, s^*, h_r^*, l_r^*, s_T^*, i^*, i_T^*, r^*)$  of the dynamical (9)-(16) is locally asymptotically stable if  $R_0 > 1, C_{ii} < 0$ , for i = 1:8 and  $d > c\omega$ . **Proof:** 

The Jacobean matrix of the dynamical system (9)-(16) at the endemic equilibrium point  $E^* = (v^*, s^*, h_r^*, l_r^*, s_T^*, i^*, i_r^*, r^*)$  is

$$J(E^*) = \begin{cases} C_{11} & 0 & 0 & 0 & 0 & C_{16} & 0 & 0 \\ C_{12}C_{22} & 0 & 0 & 0 & C_{26} & 0 & 0 \\ C_{31}C_{32}C_{33} & 0 & 0 & C_{36} & 0 & C_{38} \\ 0 & 0 & C_{43}C_{44} & 0 & C_{46} & 0 & 0 \\ 0 & 0 & C_{53} & 0 & C_{55}C_{56} & 0 & 0 \\ 0 & 0 & C_{63}C_{64} & 0 & C_{66} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & C_{76}C_{77} & 0 \\ 0 & 0 & 0 & C_{84}C_{85}C_{86}C_{87}C_{88} \end{cases}$$

Where,

 $\begin{array}{l} C_{11}=-(\zeta+\sigma c\omega i^*+\theta-di^*), \ C_{22}=-(c\omega i^*+\zeta-di^*), \ C_{16}=(d-\sigma c\omega)v^*, \ C_{21}=\theta, \ C_{32}=c\omega i^*, \ C_{26}=(d-c\omega)s^*, \ C_{31}=\sigma c\omega i^*, \ C_{33}=-(\zeta+\alpha-di^*), \ C_{36}=c\omega (s^*+\sigma v^*+\kappa r^*)+dh_r^*, \ C_{38}=c\omega ki^*, \ C_{43}=\alpha \varepsilon (1-p), \ C_{44}=-(\zeta+\gamma-di^*), \ C_{46}=dl_r^*, \ C_{53}=\alpha p, \ C_{55}=-(\zeta+\phi-di^*), \ C_{56}=ds_T^*, \ C_{63}=\alpha (1-\varepsilon)(1-p), \ C_{64}=\delta \gamma, \ C_{66}=-(\zeta+\rho+d-2di^*), \ C_{75}=q\rho+di_r^*, \ C_{77}=-(\zeta+\varphi-di^*), \ C_{85}=\phi, \ C_{86}=(1-q)\rho+dr^*, \ C_{87}=\varphi \text{and} \ C_{88}=-(\zeta+\kappa c\omega i^*-di^*) \end{array}$ 

The corresponding characteristic equation of the Jacobean matrix is:

$$\begin{vmatrix} C_{11} - \lambda & 0 & 0 & 0 & 0 & C_{16} & 0 & 0 \\ C_{12} & C_{22} - \lambda & 0 & 0 & 0 & C_{26} & 0 & 0 \\ C_{31} & C_{32} & C_{33} - \lambda & 0 & 0 & C_{36} & 0 & C_{38} \\ 0 & 0 & C_{43} & C_{44} - \lambda & 0 & C_{46} & 0 & 0 \\ 0 & 0 & C_{53} & 0 & C_{55} - \lambda & C_{56} & 0 & 0 \\ 0 & 0 & C_{63} & C_{64} & 0 & C_{66} - \lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & C_{76} & C_{77} - \lambda & 0 \\ 0 & 0 & 0 & 0 & C_{84} & C_{85} & C_{86} & C_{87} & C_{88} - \lambda \end{vmatrix} = 0$$

Or we can rewrite in form of:

 $\lambda^{8} + A_{7}\lambda^{7} + A_{6}\lambda^{6} + A_{5}\lambda^{5} + A_{4}\lambda^{4} + A_{3}\lambda^{3} + A_{2}\lambda^{2} + A_{1}\lambda + A_{0} = 0$ 

We have set conditions that  $d > c\omega$  and diagonal elements of  $J(E_2)$  (i.e,  $C_{ii} < 0$ ) are negative, for i = 1, 2, ..., 8, and then the coefficients from  $A_0 to A_7$  are all positive. Finally we found that the elements in first columnof the Routh-Hurwitharrayare all positive, it follows from the Routh–Hurwitz criteria that all the eigenvalues associated to the Jacobean matrix of the dynamical system at the endemic equilibrium have negative real part. Therefore the endemic equilibrium point is locally asymptotically stable for  $R_0 > 1$  with the conditions  $d > c\omega$  and diagonal elements of  $J(E_2)$  are negative.

### 2.5.4 Global stability of Endemic Equilibrium point Theorem-6:

The endemic equilibrium  $E^*$  of the tuberculosis dynamical system is globally asymptotically stable if  $R_0 > 1$ . **Proof:** 

We define a Liapunovfunction  $V(x) = \sum_{i=1}^{8} A_i \left( x_i - x_i^* - x_i^* ln \frac{x_i}{x_i^*} \right)$ , where  $A_i$  properly selected positive is constant,  $x_i$  is the population of  $i^{th}$  compartment and  $x_i^*$  is the population of  $i^{th}$  compartment at the endemic equilibrium point. We note that  $V(x) \ge 0$ , for  $x \ne E^*$  and the Liapunov function at the endemic equilibrium point is zero i.eV  $(E^*) = 0$ . Now differentiating the Liapunov function with respect to time we get:

$$\dot{V} = A_1 \left( 1 - \frac{v^*}{v} \right) \dot{v} + A_2 \left( 1 - \frac{s^*}{s} \right) \dot{s} + A_3 \left( 1 - \frac{h_r^*}{h_r} \right) \dot{h_r} + A_4 \left( 1 - \frac{l_r^*}{l_r} \right) \dot{l_r} + A_5 \left( 1 - \frac{s_T^*}{s_T} \right) \dot{s_T} + A_6 \left( 1 - \frac{i^*}{i} \right) \dot{i_r} + A_7 \left( 1 - \frac{i_T^*}{i_T} \right) \dot{i_T} + A_8 \left( 1 - \frac{r^*}{r} \right) \dot{r}$$

Substituting their respective values and some calculation gives

$$\begin{split} \dot{V} &= -(\zeta + \theta)A_1 v \left(1 - \frac{v^*}{v}\right)^2 - \zeta A_2 s \left(1 - \frac{s^*}{s}\right)^2 - A_8 \zeta r - A_1 i^* v^* (1 - x_1) \left(1 - \frac{x_3}{x_1 x_5}\right) [d - \sigma c \omega] \\ &\quad - \theta A_2 v^* \left(1 - \frac{1}{x_1}\right) (1 - x_2) + i^* s^* A_2 (1 - x_2) \left(1 - \frac{1}{x_2 x_5}\right) (c \omega - d) \\ &\quad + A_3 c \omega i^* s^* \left(1 - \frac{x_3}{x_2 x_5} + \frac{1}{x_2 x_5}\right) + A_3 \sigma c \omega i^* v^* \left(1 - \frac{x_3}{x_1 x_5} + \frac{1}{x_1 x_5}\right) \\ &\quad + A_3 \kappa c \omega i^* r^* \left(1 - \frac{x_3}{x_2 x_8} + \frac{1}{x_2 x_8}\right) + + A_4 \alpha \varepsilon (1 - p) h_r^* \left(1 - \frac{x_4}{x_3}\right) + A_3 d i^* h_r^* \left(1 - \frac{1}{x_5} + \frac{1}{x_3 x_5}\right) \\ &\quad + A_4 d i^* l_r^* \left(1 - \frac{1}{x_5} + \frac{1}{x_4 x_5}\right) + A_5 \alpha p h_r^* \left(1 - \frac{x_6}{x_3}\right) + A_5 d i^* s_T^* \left(1 - \frac{1}{x_5} + \frac{1}{x_5 x_6}\right) \\ &\quad + A_6 d i^* i^* \left(1 - \frac{1}{x_5} + \frac{1}{x_5} \frac{1}{x_5}\right) + A_7 d i^* i_T^* \left(1 - \frac{1}{x_5} + \frac{1}{x_5 x_7}\right) \\ &\quad + A_6 \delta \gamma l_r^* \left(1 - \frac{x_5}{x_4}\right) + A_6 \alpha (1 - \varepsilon) (1 - p) h_r^* \left(1 - \frac{x_5}{x_3}\right) + A_7 q \rho i^* \left(1 - \frac{x_7}{x_5}\right) + A_8 \phi s_T^* \left(1 - \frac{x_8}{x_6}\right) + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) + A_8 (1 - \frac{x_8}{x_6}) + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_6}) + A_8 (1 - \frac{x_8}{x_6}) \\ &\quad + A_8 (1 - \frac{x_8}{x_$$

 $qpi*1-x8x5+A81-\delta \gamma lr*1-x8x4+A8\varphi iT*1-x8x7+A8d-\kappa c \omega i*r*1-1x5+1x5x8$ . Where, x1, x2, x3, x4, x5, x6, x7, x8=v\*v, s\*s, hr\*hr, lr\*lr, i\*i, sT\*sT, iT\*iT, r\*r

After some simplification we get  $\dot{V}(x) < 0$  if  $R_0 > 1$ .

#### **III. Numerical Simulations**

This numerical simulation is done by using a set of parameter values whose sources are mainly from related literatures, WHO and Federal Democratic Republic of Ethiopia Ministry of Healthreports.

Parameter Symbols	Value	Source						
$\psi$	0.9	[13]						
σ	0.2	[13]						
θ	0.0667	[10, 13]						
$\phi$	2	Estimated						
ω	0.5	[8]						
С	2	Estimated						
α	0.03	[8]						
<i>d</i>	0.00025	[13]						
p	0.2	Estimated						
γ	0.03	[8]						
δ	0.1	Estimated						
ε	0.5	Estimated						
ρ	0.3	[8]						
<i>q</i>	0.94	[13]						
$\varphi$	1.33	Estimated						
ζ	0.0183	Estimated						
κ	0.99	Estimated						
Table 2. Dependent actimation								

Table-2: Parameter estimation

#### Numerical simulation for basic reproduction number

We discussed on the relation between basic reproduction number  $R_0$  and the parameters involved in it. Accordingly, Figer-2 represents the graph of basic reproduction number  $R_0$  versus contact rate c bykeeping other parameters constant, and shows the lines  $R_0(c) = 0.510027891273821c$  and  $R_0 = 1$  intersect at c = 1.960677086. Therefore, $R_0 < 1$  when the contact rate, c < 1.960677086 and  $R_0 > 1$  when c > 1.960677086. Figer-3 represents the graph of basic reproduction number  $R_0$  versus probability of transmission  $\omega$  bykeeping other parameters constant, shows the lines  $R_0(\omega) = 2.040111564909529\omega$  and  $R_0 = 1$  intersect at  $\omega = 0.490169272$ , then  $R_0 < 1$  when  $\omega < 0.490169272$  and  $R_0 > 1$  when 0.490169272 <  $\omega$ .



**Figure-2:**the basic reproduction number  $R_0$  versus contact rate *c* 



**Figure-3:**graph the basic reproduction number  $R_0$  versus probability of transmission  $\omega$ 

Figure-4 represents the graph of the basic reproduction number  $R_0$  versus rate of vaccine waning  $\theta$  by keeping other parameters constant. This graph shows the curve  $R_0(\theta) = 1.20718341374268 \frac{0.005124 + \theta}{0.0183 + \theta}$  and the line  $R_0 = 1$  intersect at  $\theta = 0.05849180491849$ , then  $R_0 < 1$  when  $\theta < 0.05849180491849$  and  $R_0 > 1$ when  $\theta > 0.05849180491849$ . Figure-5 represents the graph of the basic reproduction number  $R_0$  versus proportions of new born vaccinated  $\psi$  by keeping other parameters constant and then this shows the lines  $R_0(\psi) = -0.2079195903199174\psi + 1.20718341374269$  and  $R_0 = 1$  intersect at  $\psi = 0.9964593$ , then  $R_0 < 1$  when  $\theta > 0.9964593$  and  $R_0 > 1$  when  $\theta < 0.9964593$ 



rate of vaccine waning  $\theta$ 

proportions new born vaccinated  $\psi$ 

The basic reproduction number  $R_0$  is given as a function of progression rate  $\alpha$  of individuals from early latently infected bykeeping other parameters constant  $R_0(\alpha) = \frac{1.126946446858242 \alpha}{\alpha + 0.0183}$ . In figure-6the curve  $R_0(\alpha) = \frac{1.126946446858242 \alpha}{\alpha + 0.0183}$ .  $\alpha + 0.0183$ 1.126946446858242 α and  $R_0 = 1$  intersect at  $\alpha = 0.14415528$ , the line then  $R_0 < 1$  $\alpha + 0.0183$ when  $\alpha < 0.14415528$  and  $R_0 > 1$  when  $\alpha > 0.14415528$ . In figure-7, the basic reproduction number,  $R_0 < 1$  when  $\gamma < 0.02870644$  and  $R_0 > 1$  when  $\gamma > 0.02870644$  by taking the value of all other parameters from table-2 respectively.



**Figure-6:**the basic reproduction number  $R_0$  versus progression rate  $\alpha$  of individuals from early latently infected

**Figure-7:** the basic reproduction number  $R_0$  versus progression rate from long latently infected

The basic reproduction number  $R_0$  is given as a function of proportion of individuals who do not get  $H_r$  and who go to  $L_r$  class  $\varepsilon$  by keeping other parameters chance for screened at constant  $R_0(\varepsilon) = -1.236198565079491\varepsilon + 1.318066019717244$ . In figure-8 the lines  $R_0(\varepsilon) =$  $-1.236198565079491\varepsilon + 1.318066019717244$  and  $R_0 = 1$  intersect at  $\varepsilon = 0.257293632$  and then  $R_0 < 1$ when  $\varepsilon > 0.257293633$  and  $R_0 > 1$  when  $\varepsilon < 0.257293633$ . The basic reproduction number  $R_0$  is also given as a function of death rate d by keeping other parameters constant  $R_0(d) = \frac{2.229744041283815}{d+0.085}$ . By figure-9the curve $R_0(d) = \frac{2.229744041283815}{d \pm 0.085}$  and the line  $R_0 = 1$  intersect at d = 2.144744041, then  $R_0 < 1$  when d > 0.005d+0.0852.144744041 and  $R_0 > 1$  when d < 2.144744041.





**Figure-8:** the basic reproduction number  $R_0$  versus Proportion of individuals who do not get chance for screened at  $H_r, \varepsilon$ 



The basic reproduction number  $R_0$  can also be given as a function of the rate  $\rho$  at which individuals leave infectious class bykeeping other parameters constant  $R_0(\rho) = \frac{2.229744041283815}{\rho + 0.0185}$ . As figure-10, the curve  $R_0(\rho) = \frac{2.229744041283815}{2.229744041283815}$ the  $line R_0 = 1$  $at\rho = 2.211194$ ,  $R_{0}(\rho) = \frac{2.229744041203013}{\rho + 0.0185} \text{ and the } \lim_{\alpha \to 0} R_{0} = 1 \text{ intersect } \operatorname{at} \rho = 2.211194, \text{ then} \kappa_{0} < 1$ when  $\rho > 2.211194$  and  $R_{0} > 1$  when  $\rho < 2.211194$ . Figure-11 shows that the curve  $R_{0}(\zeta) = \frac{(0.28\zeta + 0.0667)(0.012\zeta + 0.00036)}{(\zeta + 0.0667)(\zeta + 0.03)^{2}(\zeta + 0.30025)}$  and the line  $R_{0} = 1$  intersect at  $\zeta = 4.015$ , then  $R_{0} < 1$  when  $\zeta < 4.015$  and  $R_{0} > 1$  when  $\zeta > 4.015$ . And the curve  $R_{0}(p) = (1 - p)0.8749584214737915$  and the line  $R_{0} = 1$  for all  $p_{0}[0, 1]$ and intersect then  $R_0 < 1$ 1 have no intersection in the first quadrant however  $R_0 < 1$  for all  $p \in [0,1]$ .



rate at which individuals leave infectious class  $\rho$ 



#### **IV. Sensitivity Analysis**

We perform sensitivity analyses on a mathematical model of tuberculosis transmission to determine the relative importance of model parameters to disease transmission and control. We apply the normalized forward sensitivity index of  $R_0$  to a parameter is the ratio of the relative change in the variable to the relative change in the parameter <sup>[10]</sup>. We do have an explicit formula for sensitivity index:  $\Pi_x^{R_0} = \frac{\partial R_0}{\partial x} \times \frac{x}{R_0}$  where x is the parameter of the dynamical system

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$$\Pi_{c}^{R_{0}} = \frac{\partial}{\partial c} \frac{R_{0}}{c} \times \frac{c}{R_{0}} = 1; \quad \Pi_{\omega}^{R_{0}} = \frac{\partial}{\partial c} \times \frac{\omega}{R_{0}} = 1$$

$$\Pi_{\psi}^{R_{0}} = \frac{\partial}{\partial \psi} \times \frac{\psi}{R_{0}} = \frac{(\sigma-1)\psi\zeta}{\sigma\psi\zeta+(1-\psi)\zeta+\theta}; \quad \Pi_{\sigma}^{R_{0}} = \frac{\partial}{\partial \sigma} \times \frac{\sigma}{R_{0}} = \frac{\sigma\psi\zeta}{\sigma\psi\zeta+(1-\psi)\zeta+\theta},$$

$$\Pi_{\theta}^{R_{0}} = \frac{\partial}{\partial \sigma} \times \frac{\theta}{R_{0}} = \frac{(1-\sigma)\psi\zeta}{(\zeta+\theta)(\sigma\psi\zeta+(1-\psi)\zeta+\theta)}; \quad \Pi_{\alpha}^{R_{0}} = \frac{\partial}{\partial \alpha} \times \frac{\alpha}{R_{0}} = \frac{\zeta}{(\zeta+\alpha)},$$

$$\Pi_{\gamma}^{R_{0}} = \frac{\partial}{\partial \gamma} \times \frac{\gamma}{R_{0}} = \frac{\gamma[\alpha\varepsilon(1-p)\delta + \alpha(1-\varepsilon)(1-p)]}{\alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta+\gamma)} - \frac{\gamma}{(\zeta+\gamma)}$$

$$\Pi_{p}^{R_{0}} = \frac{\partial}{\partial p} \times \frac{p}{R_{0}} = -\frac{p[\alpha\varepsilon\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta+\gamma)]}{\alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta+\gamma)}$$

$$\begin{split} \Pi_{\varepsilon}^{R_{0}} &= \frac{\partial}{\partial \varepsilon} \times \frac{\varepsilon}{R_{0}} = \frac{\alpha(1-p)\varepsilon[\delta\gamma - (\zeta+\gamma)]}{\alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta+\gamma)}; \\ \Pi_{\rho}^{R_{0}} &= \frac{\partial}{\partial \rho} \times \frac{\rho}{R_{0}} = -\frac{\rho}{(\zeta+\rho+d)} \\ \Pi_{\delta}^{R_{0}} &= \frac{\partial}{\delta\delta} \times \frac{\delta}{R_{0}} = \frac{\delta\alpha\varepsilon(1-p)\gamma}{\alpha\varepsilon(1-p)\delta\gamma + \alpha(1-\varepsilon)(1-p)(\zeta+\gamma)}; \\ \Pi_{d}^{R_{0}} &= \frac{\partial}{\partial d} \times \frac{d}{R_{0}} = -\frac{d}{(\zeta+\rho+d)} \\ \Pi_{\zeta}^{R_{0}} &= \frac{\partial}{\delta\zeta} \times \frac{\zeta}{R_{0}} \\ &= \zeta \bigg[ \frac{(1+(\sigma-1)\psi)}{(1+(\sigma-1)\psi)\zeta + \theta} + \frac{(1-\varepsilon)}{(1-\varepsilon)\zeta + \varepsilon\delta\gamma + (1-\varepsilon)\gamma} - \frac{1}{\zeta+\theta} - \frac{1}{\zeta+\theta} - \frac{1}{\zeta+\gamma} \\ &- \frac{1}{\zeta+d+\rho} \bigg] \end{split}$$

Using the data in table-2the resulting sensitivity indices of  $R_0$  to the different parameters in the model are shown in the following table in the order from most sensitive to the least.

Parameters	θ	γ	С	ω	α	ζ	δ	σ	d	$\psi$	Е	ρ	p
sensitivity index	2.16	1.26	1	1	0.38	0.13	0.06	0.05	-0.00075	-0.18	-0.88	-0.94	-1.25

Table-3: Sensitivity indices

#### V. Results and discussion

In this work we considered non-linear dynamical system to study the dynamics of Tuberculosis disease. The basic reproduction number is:  $R_{0} = \frac{c\omega((1-\psi)\zeta+\theta)\alpha\varepsilon(1-p)\delta\gamma}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)} + \frac{c\omega\sigma\psi\zeta\alpha\varepsilon(1-p)\delta\gamma}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)} + \frac{c\omega\sigma\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)} + \frac{c\omega\sigma\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)}$ which depends on thirteen parameters. We have evaluated the effect of each parameter on the basic reproduction number  $R_{0}$  by keeping all other parameters that involved in it are constants. Consequently, Figure 2 shows that if the contact rate, c < 1.960677086 then  $R_{0} < 1$  and if c > 1.960677086 then  $R_{0} > 1$ . Implies that the disease does not spread in the community when c < 1.960677086 and spreads in the community when c > 1.960677086. Figure 3 illustrates that  $R_{0} < 1$  when  $\omega < 0.490169272$  and  $R_{0} > 1$  when  $0.490169272 < \omega < 1$  and does not spread in the community if  $\omega < 0.490169272$ . In figure  $6, R_{0} < 1$  if  $\alpha < 0.0.14415528$  and  $R_{0} > 1$  if  $\alpha > 0.14415528$  and is not spread in the community when  $\alpha > 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.14415528$  and is not spread in the community when  $\omega < 0.1441552$ 

community if  $\alpha < 0.14415528$ . Figure-7 also shows that the tuberculosis disease does not spread in the society when  $\gamma > 0.02870644$ . Figure-4 confirms that the tuberculosis disease spreads in the society if  $\theta > 0.05849180491849$  and does not spread in the society if  $\theta < 0.0584918049184.$ Figure-5 shows that  $R_0 < 1$  if  $\psi > 0.9964593$  and  $R_0 > 1$  if  $\psi < 0.9964593$  implies that the disease does not spread in the society when  $\psi < 0.9964593.$   $R_0 < 1$  for all  $p \in [0,1]$  and then the disease does not spread in the society when  $\psi < 0.9964593.$   $R_0 < 1$  for all  $p \in [0,1]$  and then the disease does not spread in the society when  $\varepsilon > 0.257293633$  and the disease spreads in the society when  $\delta > 2.144744041$  and spreads in the society when d < 2.144744041. Figure-10 shows the tuberculosis disease does not spread in the society when  $\rho > 2.211194$  and spreads in the society when  $\rho < 2.211194$  by keeping other parameters are constant. Figure-11 tells us the disease does not spread in the society when  $\zeta < 4.015$  and spreads in the society when  $\zeta > 4.015$  by keeping other parameters are constant.

From table-2, we found that the parameters contact rat of susceptible or vaccinated individuals makes with infectious individuals c, probability of tuberculosis disease transmission from infectious person to another person  $\omega$ , the rate of inefficacy of Bacilli Calmette-Guérin (BCG) vaccine  $\sigma$ , the rate of Bacilli Calmette-Guérin (BCG) vaccine waning  $\theta$ , the rate of individuals leave from early latently infected class  $\alpha$ , the rate of individuals leave from long latently infected class have positive contributions for the transmission of tuberculosis, implies that, the value of  $R_0$  increases when those parameters increase. While the parameters, the proportion of vaccinated new born individuals leave infectious class will help to decrease the value of  $R_0$  as they increase.

The most sensitive parameter in the spread and control of tuberculosis disease is the waning rate of Bacilli Calmette-Guérin(BCG) vaccine,  $\theta$ , followed by the progression rate from long latently infected tuberculosis to active tuberculosis,  $\gamma$  and the proportion *p* of early stage latently infected individuals who have got the chance for screened and treatment.

#### **VI.** Conclusion

This study presents a deterministic model for the dynamics of tuberculosis Mathematical model with interventions: vaccination, chemoprophylaxis and therapeuticstreatments. The total population is divided in to ten compartments. We found the dynamical system has disease free equilibrium point and endemic equilibrium point. We also found that the basic reproduction number of the considered dynamical system is

 $R_{0} = \frac{c\omega\left((1-\psi)\zeta+\theta\right)\alpha\varepsilon(1-p)\delta\gamma}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)} + \frac{c\omega\sigma\,\psi\zeta\alpha\varepsilon(1-p)\delta\gamma}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)} + \frac{c\omega\left((1-\psi)\zeta+\theta\right)\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\rho+d)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-p)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\zeta\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\alpha(1-\varepsilon)(1-\varphi)}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\alpha)(\zeta+\alpha)} + \frac{c\omega\sigma\,\psi\alpha(1-\varepsilon)(1-\varphi$ 

 $\frac{K_0 - \frac{1}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)} + \frac{1}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)} + \frac{1}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)} + \frac{1}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)} + \frac{1}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)}}{(\zeta+\theta)(\zeta+\alpha)(\zeta+\rho+d)}}$ We proved that the disease free equilibrium is locally asymptotically stable if the basic reproduction number is less than unity and globally asymptotically stable if the basic reproduction number  $R_0 < 1 - \frac{(cw \kappa r + dh_r)[\alpha \varepsilon (1-p)\delta \gamma + \alpha (1-\varepsilon)(1-p)(\zeta+\gamma)] + \delta \gamma (\zeta+\alpha) dl_r + (\zeta+\gamma)(\zeta+\alpha) dl}{(\zeta+\alpha)(\zeta+\gamma)(\zeta+\rho+d)}$ . We also proved the local stability of the endemic

equilibrium point and also its global stability using a Liapunov function. Using standard data collected from different sources we found the numerical value of the basic reproduction number is  $R_0 = 0.7$  which shows that the tuberculosis disease not spreads in the community. We have done the numerical simulation of the dynamical system. The waning rate of Bacilli Calmette-Guérin (BCG) vaccine,  $\theta$ , followed by the progression rate from long latently infected tuberculosis to active tuberculosis,  $\gamma$  and the proportion p of early stage latently infected individuals who go for treatment are the most sensitive parameter the most influential parameter to change the basic reproduction number. The result shows that vaccination alone cannot eliminate tuberculosis disease from a population, but can slow the rate of transmission from long stage latently infected; and increasing the portion screened and treating of early stage latently infected.

#### VII. Recommendation

To study the dynamics of tuberculosis we considered vaccination, chemoprophylaxis and therapeutics treatments. The next researchers may found more findings by considering drug resistant tuberculosis on the infection pattern.

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