

MATHEMATICAL MODEL ON TUBERCULOSIS ERADICATION

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Abstract:

Lung is one of the organs of human body which perform many functions and have related diseases which can affect the lung. One of such diseases is tuberculosis which is a respiratory disease and can be treated using vaccine called Bacillus Calmette Guerin(BCG). This work is aimed at proposing a mathematical model on the spread of tuberculosis to determine the possibility of eradicating the disease. The model reveals that the disease can be eradicated in a finite time.

Key Words: Tuberculosis, Endemic, Contagious, Eradication, Asymptotic stability, Disease-free equilibrium and Mathematical model.

INTRODUCTION:

Tuberculosis is a contagious disease caused by inhaling the tubercle bacillus in the droplet nucleus form; it is an air borne disease Yusuf (2008).

Christopher Murray(1998), Harvard School of Public Health, described a mathematical model developed to forecast the future impact of improvements in tuberculosis prevention and control, this model projected the number of tuberculosis cases and deaths averted through the year 2050. Different scenarios were simulated to project the effect of adding tuberculosis vaccines to existing interventions. Six specific scenarios assessed the effect of vaccines (with efficacy levels of 20%, 50% and 80%).

Another research work conducted by Dye, et al.(2000) developed a Mathematical model that makes use of

routinely-collected data to calculate the number of death directly prevented by tuberculosis treatment. The method applied to over 500 million people in China. The result was that the short course chemotherapy has substantially reduced tuberculosis mortality in half of China.

According to Caroline (2006), in many such models, there is a sharp threshold behavior and the asymptotic dynamics are determined by a parameter R_0 when $R_0 < 1$, the disease-free equilibrium is (usually globally) asymptotically stable and when $R_0 > 1$ there exists a unique endemic equilibrium which is also (usually globally) stable. There are some common terms related to this topic such as:

Endemic is a disease that last for long period of time in a population.

Contagious is a disease that can spread to others by touch or contact.

Eradication to get rid of the disease in a population.

Asymptotic stability a system of differential equation is said to have asymptotic stable equilibrium whenever the eigenvalues of the characteristics equation are real negative or have a negative real part.

In this paper, we will present a mathematical model for the Tuberculosis disease population dynamics using Susceptible-Infected - Recovered (SIR) and use equilibrium analysis approach. In fact results may be interrelated and can help to confirm or refute the earlier findings.

Model assumptions

In building our model, we make the following assumptions by dividing the population in to Susceptible, Infected and Recovered (SIR).

- i. The population is homogenous.
- ii. The newborns are susceptible.
- iii. The susceptible individuals become infected due to interaction with infected.
- iv. The infected die due to the disease.
- v. The rate of recruitment of the infected into recovered is proportional

$$S'(t) = bp - [\alpha I(t) + d] s(t) \dots \dots \dots 1.$$

$$\begin{aligned} I'(t) &= [\alpha s(t) - d - \delta \\ &- \beta] I(t) \dots \dots \dots 2. \end{aligned}$$

$$R'(t) = \beta I(t) - (d + k)R(t) \dots \dots \dots 3.$$

Model analysis:

We use equilibrium analysis of the above equations to determine or

to the infected that acquired good treatment.

- vi. When recovered lose immunity they become susceptible.
- vii. Common birth rate and death rate are equal.

Model Building:

Parameters;

$S(t)$ = Number of susceptible at time t.

$I(t)$ = Number of susceptible infected at time t.

$R(t)$ = Number of susceptible recovered at time t.

$P(t)$ =Total population .

α = Infectious rate of the disease.

b = Recruitment rate.

d = Natural death rate

δ = Death rate due to the disease.

K = Immunity lose rate.

β = transmission parameter

Based on our assumptions and the defined parameters the following differential equations are obtained.

investigate whether the disease could be wiped out or not? Equating each of the three (3) ordinary differential equations to zero,

$$bp - [\alpha I(t) + d]s(t) = 0 \dots \dots \dots 4$$

$$[\alpha s(t) - d - \delta - \beta] I(t) = 0 \dots \dots \dots 5$$

$$\beta I(t) - (d - k) R(t) = 0 \dots \dots \dots 6$$

$$P(0) = p, I(0) \geq 0, R(0) \geq 0.$$

Let us consider equation (5)

$(\alpha s - d - \delta - \beta)I = 0$, implies either

$I = 0$ or $\alpha s - d - \delta - \beta = 0$.

Now let substitute I into equation (4) we have

$$bp - ds = 0$$

$$\Rightarrow S = \frac{bp}{d}.$$

Also considering equation (6) we have

$$-(d + k)R = 0, \text{ if } -(d + k) \neq 0$$

$$\Rightarrow R = 0.$$

It is obvious that at disease-free situation infectious is zero as well as recovered zero, ($I = R = 0$).

Hence, the disease-free equilibrium is $(\frac{bp}{d}, 0, 0)$.

Suppose S_0, I_0, R_0 , are our equilibrium points, then we have

$$S_0, I_0, R_0 = (\frac{bp}{d}, 0, 0).$$

If we equate equations 1,2,3 equal to $q_1(S,I,R)$, $q_2(S,I,R)$ and $q_3(S,I,R)$ respectively and find the Jacobian matrix of the equations; we obtain

$$J = \begin{bmatrix} -(\alpha I + d) & -\alpha s & 0 \\ \alpha I & \alpha s - (d + \delta + \beta) & 0 \\ 0 & \beta & -(d + k) \end{bmatrix}$$

i.e $J(\frac{bp}{d}, 0, 0) =$

$$\begin{bmatrix} -d & \frac{bpa}{d} & 0 \\ 0 & bpa - (d + \delta + \beta)d & 0 \\ 0 & \beta & -(d + k) \end{bmatrix}$$

We went as far as to obtain the eigenvalues $\lambda_1, \lambda_2, \lambda_3$ as

$$\lambda_1 = -d, \lambda_2 = -(d + k)$$

$$\lambda_3 = (bp\alpha - (d + \delta + \beta)d) = 0.$$

$$\Rightarrow P < \frac{(d + \delta + \beta)d}{b}.$$

The values of λ_1 and λ_2 are obvious, satisfying the necessary conditions for stability.

Result discussion:

In the stability analysis of the model we have established the disease-free equilibrium denoted by $S_0, I_0, R_0 = (\frac{bp}{d}, 0, 0)$, the situation in which the disease does not exist completely in the host population through continuous vaccination of the new born after a single mass vaccination of the susceptible population. We also obtain eigenvalues λ_1, λ_2 and λ_3 to determine whether the disease can be eradicated or not and since both λ_1 and λ_2 are negative this shows that the disease free equilibrium is asymptotically stable, meaning that the disease can be eradicated in a finite time.

In general, we say that tuberculosis can be eradicated in a population under a specified condition.

We recommend the result of the work for predict of spread and controlling by epidemiologists and continuous vaccination of newly born babies after a massive vaccination of the susceptible population.

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