

MATHEMATICAL MODELLING ON INDUSTRIAL POLLUTION AND SPREAD OF INFECTION DISEASE USING POPULATION GROWTH MODEL FOR EPIDEMICS

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Abstract: Mathematical model on the industrial pollution and spread of infection diseases using population growth model for epidemic has been studied. Epidemics have ever been a great concern of human kind and we are still moved by the dramatic descriptions that arrive to us from the past, as in Lucretius's sixth book of "De Rerum Natura" or as in other more recent descriptions that we find in the literature. The "Black Death", the plague that spread across Europe and from 1347 to 1352 and made 25 millions of victims, seems to be far from our lives, but more recent events remind us that epidemics are an actual problem for health institution that are continuously facing emerging and reemerging diseases. The model presented in terms of ordinary differential equations have been studied to investigate the long term effect of population in terms of spread of diseases based on working environment, social and other effects.

Key words:infection, epidemic occlusion, pollution .

I. INTRODUCTION

The effect of industrial pollution on the surrounding vegetation and life can always be determined by estimating the extent of pollution in a given industrial domain or land area, the pollution may be in terms of chemical, biological gases and polluted land and water resources.

In addition to above types of pollutants there are many indirect pollutants in industrial habituate areas which also cause health hazards. The affected population becomes prone to catch viral and bacterial infections and is susceptible for uniform in the entire industrial population.

Mathematical study of the infectious diseases including epidemics is mostly confined to homogeneous population consisting of single group [1][2]. The population model are concerned we have considered and analysed biological populations with two or more compartments in the same species. The same model is carried out to investigate on the effect of human population.

II. MATHEMATICAL MODEL

The basic elements for the description of infectious diseases, have been the three epidemiological classes of susceptible, infective and removed individuals, respectively defined as those individuals who are healthy and can be infected; those individuals who are infected and are able to transmit the disease; those individuals who are immune because have been infected and now have recovered; Thus the basic variables identifying the state of the population in the epidemiological perspective are

$S(t)$ the number of susceptible at time t , $I(t)$ the number of infective at time t

$R(t)$ the number of immune at time t

For the epidemic model the following assumptions can be made

- i) The rate at which members become infective is proportional to the product of the number of susceptibles and the numbers of infectives.
- ii) The population is closed with no births no deaths except from the disease and no migration.
- iii) The rate of passage from infective to removed class through recovery or death is proportional to the number of infectives.

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$N(t) = S(t) + I(t) + R(t) = \text{total population.}$

$$\begin{aligned} \frac{dI}{dt} &= \beta S I - \frac{1}{\alpha} I \\ \frac{dS}{dt} &= -\beta S I \\ \frac{dR}{dt} &= \frac{1}{\alpha} I \end{aligned} \tag{1}$$

Moreover, the removal rate $R(t)$ is usually assumed to be a constant indeed, the epidemiological classes characterizing a disease may be more than these, but considerable insight into the phenomena can however be achieved on the basis of the above description. After the basic state variables introduced above, further gross simplification may be introduced concerning the disease progression and effect. Namely, a basic distinction may be done between those diseases that impart lifelong immunity and those which do not. The rest case leads to the so called SIR type model, the second to SIS type models. In fact, the individual path through. In the set of equations (1) The values of parameters will depend on the following assumptions

- a) Every individual who contracts the diseases is immediately capable of communicating it to others

$$p(t) = \{ s(t) \ I(t) \ R(t) \} \tag{2}$$
 where $p(t)$ is the population composition vector which contains the relevant information on the composition of the population at time t .

- b) The population of the fixed size which gives an equation

$$S(t) + I(t) + R(t) = n \text{ (constant) } \tag{3}$$

The mathematical model (1) is proposed by Kermack and M C Kewrudrick [6] for the recovery which gives the immunity. But the recovery does not give immunity then this model is called SIS model in which the individuals move from the susceptible class to the infective class and then back to the infective class and then back to susceptible class upon recovery the model is

$$\begin{aligned} \frac{dS}{dt} &= -\beta S I - \frac{1}{\alpha} I \\ \frac{dI}{dt} &= \beta S I - \frac{1}{\alpha} I \end{aligned} \tag{4}$$

Considering equation (3) as $S + I + R = n$, the total population size is constant. The equations (1) to (4) are hold good for the infected one then we can take that the average number of contacts are sufficient to transmit infection per infective in unit time is constant. The number of time such contacts in unit time is λI then each constant with susceptible one can be taken as s/k the infection rate is $\beta S I$ with $\beta = \frac{\lambda}{k}$ equation (4) are the modified equations of Kermack and mc Kendrick [6]. The basic concept of epidemiology is the existence of thresholds. The value of thresholds are responsible for quantification of the effective parameters such as contact number, population size or vector density that must be exceeded in order for an epidemic to occur or for a disease to remain epidemic.

The rate of growth of the infected sub population is propositional to the number of contacts per unit time between of groups S and I then $\frac{ds}{dt} = -K S(t) I(t)$

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$$\frac{ds}{dt} = -K S(t) [n+1-s(t)] \tag{5}$$

where K is a non-negative constant determined by the initial condition

$$\text{when } t = 0, I(t) = I(0) = 0 \tag{6}$$

The epidemic will be said to end at time t_c . The condition (6) gives the epidemic is in the initial stage and the affected one is moving towards the susceptible one then $I(t) = 0$. There are no infected individuals at time t_c then no one is available to continue spreading the infection. At time $t = 0$, there is exactly one infected individual then the condition to be satisfied by the solution $S = S(t)$ of equation (5) at time $t = 0$ is $S(0) = n$.

III. ANALYSIS

Equations (5) and (6) form a mathematical model for the simple situation characterized by equations (1),(3) and(4). On solving equation (5)

$$\frac{1}{n+1} \{ \log S - \log(n+1-s) \} = -Kt + C_1$$

$$S(t) = \frac{n+1}{1 + c_2 e^{(k+1)t}} \quad \text{Where } c_2 = \frac{1}{n} \tag{7}$$

Equation (7) represents the mathematical model for susceptible one. In the same way we can also obtain the mathematical model for I(t). Since we expect the rate of change of size of sub population S to be very small initially (assumed that there is only one infected individual) to increase as the size of I(t) increases and to decrease as almost all individuals become infected. Thus equation (5) can be taken as

$$-\frac{ds}{dt} = K S(t) I(t)$$

$$-\frac{ds}{dt} = \frac{K n(n+1)^2}{[n + e^{k(n+1)t}]^2} \tag{8}$$

Then using the condition $S(0) = n$

$$-\frac{ds}{dt} = K S(0) I(0)$$

$$-\frac{ds}{dt} = K n$$

$$-\frac{d^2s}{dt^2} = K \left[S(0) \frac{dI(0)}{dt} + I(0) \frac{dS(0)}{dt} \right]$$

$$-\frac{d^2S}{dt^2} = k^2 n(n-1) \tag{9}$$

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Where $I(0) > 1$, for definiteness we assume $I(0)=1$ from equation (8) ds/dt becomes infinity as t approaches to infinity. It follows that the epidemic curve has at least one relative maximum. To obtain the coordinates of one of these maxima, we differentiate ds/dt in equation (8) and we try for the zeros of the resulting expression. Then the maximum value of ds/dt is determined by the equation.

$$n + e^{k(n+1)t} = 0$$

Then the time t_m is

$$t_m = \frac{1}{k(n-1)} \log n \tag{10}$$

The maximum rate of infection varies inversely with the parameter k and is a decreasing function of the size of the total population. The size of the group of susceptible at time t_m and also the maximum rate infection.

$$-\left(\frac{ds}{dt}\right)_{t=t_m}$$

We get

$$[S(t)]_{t=t_m} = \frac{n+1}{2} \text{ and } -\left[\frac{ds}{dt}\right]_{t=t_m} = \frac{k(n+1)^2}{2} \tag{11}$$

Therefore the growth models for epidemic for infected and susceptible have been analysed using deterministic mathematical models.

IV. CONCLUSION

Mathematical modelling on industrial pollution and spread of infection disease using population growth model for epidemics have been studied through a mathematical models described in the equations 1 to 11 are directly related with human population. The whole population is active (instead, for some, diseases either part or all of the removed class does not participate in the mixing), that the contact rate is independent of the size of the active population and that contacts with infectives are equally infective. We note that in (1) the factor $I(t)/N(t)$ stands for the probability that the contacted individual is infective. Also, assumption (3) means that the progression of the disease is the same within any infective and γ measures the average fraction of recovering individuals in the time unit. With this assumption, a given group of infectives would decrease exponentially with time constant.

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