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# On Validation of Pneumonia Model with Infected population and Vaccination

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***Abstract :***

*In this paper, we present the pneumonia model on the basis of its validation with infected population & vaccination. We have formulated and described the pneumonia model. To validate this model we have studied the following properties existence and uniqueness of solution invariant region and the positivity of solution and the results are established.*

***Keywords :*** *Mathematics modeling, pneumonia, reproduction number, endemic equilibrium*

## 1. Introduction :

In the report of WHO 2013, "Infectious diseases are the leading cause of death in human beings." According to the fact sheet of WHO, 2013 sixteen percent of all deaths each year are from infectious diseases that means over 9.5 million deaths annually attribute to infectious diseases, with most of them in developing countries from 9.5 million annual death, "Pneumonia and other respiratory infectious cause about 2 million child deaths yearly in developing countries." (WHO 2015)

Pneumonia is an inflammatory condition of the lungs affecting the microscopic air sacs (alveoli) and is usually associated with fever, chest symptoms and lack of air space (cosmolidation) on a chest (MC Lucke and Leach 2009). It is typically caused by infection. Infectious agents include; bacteria, viruses, fungi and parasites (Luckie, 20090). Classic pneumonia is normally caused by streptococuss pneumoniae (Pnemococcocus) (Dum, 2005). Pneumocystosis is commonly found in the lungs of healthy people with a weak immune system. here we have studied and developed a pneumonia model with infected population and vaccination.

## 2. Model Formulation and Description :

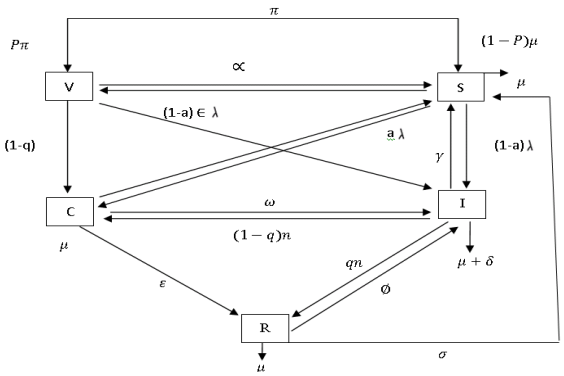


Fig. : A Compartmental Diagram for the Pneumonia Transmission dynamics

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**Model Equations :**

$\frac{dv}{dt} = p\pi + \beta s - (\alpha + \epsilon\lambda + \mu)V$ ---------(2.1)

$\frac{ds}{dt} = (1-p)\pi + \alpha V + \gamma C + vI + \sigma R - (\beta + \ +\mu)s$ -----(2.2)

$\frac{dc}{dt} = \in a \quad V + a \quad s + (1-q)nI - (\gamma + \omega + \varepsilon + \mu)c$ --------(2.3)

$\frac{dI}{dt} = (1-a) \quad S + (1-a) \in \lambda V + wc + \emptyset R - (v + n + \mu + \delta)I$ …. (2.4)

$\frac{dR}{dt} = \varepsilon c + qnI - (\emptyset + \sigma + \mu)R$ --------(2.5)

With initial condition $S(0)=S_0$, $(V_0)=V_0$, $C(0)=C_0$, $I(0)=I_0$, $R(0)=R_0$

Table I : Description of Variable and parameters of the model

| Variable | Description |
|---|---|
| V(t) | No. of vaccinated individuals at time t |
| S(t) | No. of susceptible individuals at time t |
| C(t) | No. of Carrier individuals at time t |
| I(t) | No. of infected individuals at time t |
| R(t) | No. of recovered individuals at time t |

| Parameters | Interpretation |
|---|---|
| $\pi$ | Recruitment rate |
| $\mu$ | Natural death rate |
| $\delta$ | Disease induced death rate for I class |
| $\lambda$ | Force of infection |
| a | Probability that newly infected individuals are asymptomatic / carrier. |
| $\alpha$ | Waning rate of vaccine |
| $\beta$ | Rate of vaccination from S to V |
| $\in\lambda$ | Rate of vaccinated getting carrier and infected |
| $\gamma$ | Rate at which carrier transform to susceptible class |
| $\omega$ | Rate at which carrier transform in infected class |
| $\eta$ | Rate of infected getting carrier and infected. |
| $\xi$ | Recovery rate due to prompt treatment |
| $\emptyset$ | Recovery rate due to infected class |
| v | Rate at which infected transferring to susceptible class. |
| $\sigma$ | Rate at which recovered person getting susceptible. |

The model divides the total population into five subclasses namely susceptible S(t), Vaccinated V(t), Carrier C(t), Infected I (t) and recovered R(t). The individuals are recruited into the vaccinated and susceptible class either by immigration or by birth rate $\pi. Let\ \mu$ be the natural death at any compartment. Let p$\pi$ be the number of vaccinated persons. Let (1-p)$\pi$ $be\ the$ susceptible number of people. Since vaccines wanes with time the protected individuals after its expiry return backs to susceptible compartment at the rate $\alpha$. Individuals move from susceptible class to vaccinated class with vaccination rate of $\beta$. The susceptible class is infected either by carrier or symptomatically infected individuals with a force of infection

$$\lambda = x\left(\frac{I(t) + pc(t)}{N}\right)$$

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where$x = K\tau$, K is constant rate, $\tau$ is the probability that contact is effective to cause infection and $\rho$ is transmission coefficient for the carrier. If $\rho$ >1 then, the carriers infect susceptible more highly than infective. If $\rho$=1, then both carriers and infective have good chance to infect susceptible than carriers. It is assumed that the model is not 100% effective, so vaccinated classes (V) also have a chance of being infection or carrier with small proportion and the force of infection for the vaccinated class be $\lambda_u = \lambda\epsilon$ where $0 \leq \epsilon < 1$ and $\epsilon$ is the proportion of the serotype not covered by the vaccine newly infected individuals by the force of infection become either carrier with a probability of a to join the carrier class C or move to the infected class I with probably of 1-a. The carrier class can develop and join the infected class with a rate of $\omega$ or recover by gaining natural immunity at $\varepsilon$ rate. Individuals in the infected class move to recovered compartment at a per capita rate of $n$ by treatment, with treatment efficiency of q proportion of individuals join the recovered class or join the carrier class with (1-q) proportion by adapting the treatment, or die from the disease at the rate $\delta$. Individuals from recovered class lose their temporary immunity by $\sigma$ rate . Recovery rate from infected class be $\emptyset$. Let $\gamma$ be the rate at which carriers gets back to susceptible class.

## 3. Model Analysis :

### 3.1 Existence and uniqueness of solution :

The validity and authenticity of any mathematical model depends on whether the given system of equations has a solution, and if it has there is a need to check if the solution is unique. We shall use the Lipschitz condition to verify the existence and uniqueness of solution for the system of equations (2.1) to (2.5)

**Theorem 3.1 : (Derrick and Grossman, 1976)**

Derrick and Grossman theorem is used to verify the existence and uniqueness of solution of the model. Let $\Omega$ denotes the region $|t-t_0| \leq a, ||x-x_0|| \leq b$, $x_0=(x_{10}, x_{20}..... x_{n0})$, satisfies the Lipschitz condition.$||f(t, x_1) - f(t, x_2)|| \leq K||x_1-x_2||$

The pairs $(t, x_1)$ and $(t, x_2)$ belongs to $\Omega$ and K is the positive constant hence there is a constant $\underset{\delta}{\rightarrow} > 0$ such that there exists a unique continuous vector solution x(t) of the system in the interval $t-t_0 \leq \underset{\delta}{\rightarrow}$. It is important to note that the condition is satisfied by $\frac{df_i}{dx_i}$, i, j,=1, 2 ... be continuous and bounded in Ω .Let the system of equation (2.1) to (2.5) be as follows.

$F_1 = P\pi + \beta s - (\alpha + \epsilon\lambda + \mu)V$ .....(2.6)

$F_2 = (1-P)\pi + \alpha V + \gamma C + vI + \sigma R - (\beta + \lambda + \mu)s$ .....(2.7)

$F_3 = \epsilon a \lambda V + q\lambda s + (1-q)nI - (\gamma + \omega + \varepsilon + \mu)c$ .....(2.8)

$F_4 = (1-a)\lambda S + (1-a)\epsilon\lambda V + \omega c + \emptyset R - (v + n + \mu + \delta)I$ .....(2.9)

$F_4 = \varepsilon c + qnI - (\emptyset + \sigma + \mu)R$ .....(2.10)

Considering the model eqution (2.1) to (2.5) we are interested in the region $0 \leq \varepsilon \leq R$. We look for the bounded solution in the region and whose partial derivatives satisfy $f \leq \theta \leq 0$ when $\underset{\delta}{\rightarrow}$ and $\theta$ are positive constants.

**Theorem 3.2 :**

Let $\Omega$ denote the region $0 \leq \varepsilon \leq R$, then the eqution (2.6) to (2.10) have a unique solution if $\frac{df_i}{dx_j}$ i, j = 1, 2, .... 5 are continuous and bounded in $\Omega$

**Proof :**

The equation from (2.6) to (2.10) are represented by $F_1$, $F_2$, $F_3$, $F_4$, $F_5$ respectively then from the system of equations, we obtain the following partical derivatives

$\left|\frac{dF_1}{dv}\right| = |-(\alpha + \epsilon\lambda + \mu)| < \infty$; $\left|\frac{dF_1}{ds}\right| = |\beta| < \infty$

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$|\frac{dF_2}{dv}| = |\alpha| < \infty$; $|\frac{dF_2}{ds}| = |-(\beta + \lambda + \mu)| < \infty$ ;

$|\frac{dF_2}{dc}| = |\gamma| < \infty$; $|\frac{dF_2}{dI}| = |v| < \infty$; $|\frac{dF_2}{dR}| = |\sigma| < \infty$;

$|\frac{dF_3}{dV}| = |\epsilon a\lambda| < \infty$; $|\frac{dF_3}{ds}| = |a\lambda| < \infty$;

$|\frac{dF_3}{dc}| = |-(\gamma + \omega + \varepsilon + \mu)| < \infty$;

$|\frac{dF_3}{dI}| = |(1-q)n| < \infty$;

$|\frac{dF_4}{dV}| = |(1-a)\epsilon\lambda| < \infty$; $|\frac{dF_4}{ds}| = |(1-a)\lambda| < \infty$;

$|\frac{dF_4}{dR}| = |\emptyset| < \infty$;

$|\frac{dF_5}{dC}| = |\varepsilon| < \infty$; $|\frac{dF_5}{dI}| = |qn| < \infty$;

$|\frac{dF_5}{dR}| = |-(\emptyset + \sigma + \mu)| < \infty$;

These partial derivates exists, continuous and are bounded. Hence the model (2.6) to (2.10) has a unique solution.

**3.2 Invariant Region / Feasibility Region :**

In this section a region in which soluti8on of the model are uniformly bounded is the proper subset $\Omega \subset R_+^5$ The Total population at any time t is given by N = V+S+C+I+R.

Differentiating both sides of N,

$\frac{dN}{dt} = \frac{dV}{dt} + \frac{dS}{dt} + \frac{dC}{dt} + \frac{dI}{dt} + \frac{dR}{dt}$

Which gives $\frac{dN}{dt} = \pi - \mu N - \delta I(t)$ ..... (3.1)

In the absence of mortality due to Pneumonia (3.1) becomes,

$\frac{dN}{dt} \leq \pi - \mu N$ ..... (3.2)

By the separation of variable rule equation (3.2) becomes

$\frac{dN}{\pi - \mu N} \leq dt$ .....(3.3)

Integrating both side of equation (3.3)

$\int \frac{dN}{\pi - \mu N} = \int dt$ ..... (3.4)

$\frac{1}{\mu}\ln(\pi - \mu N) \leq t + c$

$\pi - \mu \geq Ae^{-\mu t}$ ..... (3.5)

Where A is constant by applying the initial condition N(0)=$N_0$ in equation (3.5), we get,

$A = (\pi - \mu N_0)$

and upon substituion in (3.5) gives

$(\pi - \mu N) \geq (\pi - \mu N_0)\, e^{-\mu t}$ ..... (3.6)

On rearranging, we get

$N \leq \frac{\pi}{\mu} - \left(\frac{\pi - \mu N_0}{\mu}\right) e^{-\mu t}$ ..... (3.7)

as t$\rightarrow \infty$ in equation (3.7) the population size N$\rightarrow \frac{\pi}{\mu}$. Thus the feasible solution set of the system equation of the model enter and remain in the region.

$\Omega = \left\{(V, S, C, I, R) \in R_+^5 : N \leq \frac{\pi}{\mu}\right\}$ .....(3.8)

Therefore, the basic model is well posed epidemiologically and mathematically. Hence, it is sufficient to study the dynamics of the basic model in

**3.3 Positivity of the Solution :**

**Theorem 3.3 :**

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Let$\Omega$= $\{(V,S,C,I,R) \ \epsilon R_+^5 : V_0 > 0,\ S_0 > 0,\ C_0 > 0, I_0 > 0, R_0 > 0\}$ then the solution of $\{V,S,C,I,R\}$ are positive for $t \geq 0$.

**Proof :**

From the system of differential equation (1) to (5) let us take first equation

$\frac{dv}{dt} = p\pi + \beta s - (\alpha + \epsilon\lambda + \mu)V$

$\frac{dv(t)}{dt} \geq -(\alpha + \epsilon\,\lambda + \mu)V(t)$

$\frac{dv(t)}{v(t)} \geq -(\alpha + \epsilon\,\lambda + \mu)d(t)$

$\int \frac{dv(t)}{v(t)} = \int -(\alpha + \epsilon\lambda + \mu)d(t)$

by using separation of varible and applying condition we obtain,

v(t) $\geq V_0\ e^{-(\alpha+\epsilon\lambda\,+\mu)t}$ ..... (3.9)

Similarly taking second, third, fourth and fifth equations & solving by variable separable method, we get,

S(t) $\geq S_0\ e^{-(\beta+\epsilon\lambda+\mu)t} \geq 0$ ..... (3.10)

C(t) $\geq C_0\ e^{-(\gamma+\omega+\varepsilon+\mu)t} \geq 0$..... (3.11)

I(t) $\geq I_0\ e^{-(v+n\,+\mu+\delta)t} \geq 0$..... (3.12)

R(t) $\geq R_0\ e^{-(\emptyset+\sigma\,+\mu)t} \geq 0$ ..... (3.13)

Thus the solution of $(V,S,C,I,R)$ are positive for t $\geq 0$

**Conclusion and Discussion :**

We proved there exists unique solution for the model using the Lipschitz Condition, boundedness of the model using Derrick and Grossman theorem, invariant set in which the solution of the model are biologically meaningful was derived. Positivity of the solution is also established. All the basic properties of the epidemiological models are satisfied by the model presented .Based on that, the model is suitable to study transmission dynamics of pneumonia disease.

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