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Impact of Vaccination on the Dynamics of Infectious Diseases

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Abstract: **In this paper, we consider a highly simplified deterministic model that incorporates a vaccination compartment to the classical SI epidemic model to study the impact of vaccination on the dynamics of infectious diseases. We have established results about the stability of the disease free and the endemic equilibria of the model as it relates to the basic reproduction number (R_0) and numerical simulations have supported our analytical results that when $R_0 < 1$, the disease free equilibrium becomes stable and the disease dies out of the population and for $R_0 > 1$, the endemic equilibrium becomes stable showing that the disease will spread and persist within its host population. Numerical simulations have been used to support the importance of vaccination to a susceptible population and suggest a minimum vaccination rate and vaccine loss rate to target in a vaccination campaign.**

Keywords: **Vaccination, Epidemic model, Basic Reproduction number, Stability, Disease free equilibrium, Endemic equilibrium.**

I. INTRODUCTION

In the WHO bulletin, Andre et al [1] acknowledges that only clean water performs better than vaccination in the reduction of the burden of infectious disease in a population. Vaccination has been so successful that an estimated 20.3 million deaths were prevented by the measles vaccine alone between 2000 and 2015[2]. Unfortunately, despite all the progress achieved in the developed world, infectious diseases still account for the death of millions of people around the world especially in developing countries. Vaccination model like the one developed in this paper therefore becomes a veritable tool in the design and understanding of vaccination strategies in such countries with limited resources.

Mathematical models of the effect of vaccination on the transmission dynamics of infectious diseases can help interpret the trial result and generalize the findings to the long term impact of vaccination on the population at various coverage levels (see [3 - 9]). In [10], Fred Brauer formulated a simple model for disease transmission with Vaccination based on the SIS model with constant birth rate. They studied the properties of the solution, establishing a criterion for its stability. They found out that the equilibrium point corresponding to a point on the bifurcation curve with negative slope is unstable, and an equilibrium corresponding to a point on the bifurcation curve with positive slope is asymptotically stable and also that the system does not admit oscillations about an unstable endemic equilibrium. In this paper, we have adapted a classical SI epidemiological model consisting of the infectives (I) and the susceptibles (S) by adding a vaccination compartment (V) to have an SIV model. We have shown that if $R_0 < 1$ then the disease free equilibrium is locally asymptotically stable and when $R_0 > 1$, then the endemic equilibrium is locally asymptotically stable. Numerical simulations support our analytical calculations and also show that we have global asymptotic stability of the disease free equilibrium for $R_0 < 1$ and the endemic equilibrium for $R_0 > 1$. The paper is organized as follows: The model is described in Section II. The basic reproduction number and relevant results for the stabilities of the disease free and endemic equilibria could be found in Section III. We have numerical simulations in IV and conclusion in Section V.

II. DERIVATION OF THE MODEL

In the derivation of this model, we consider a highly simplified deterministic model that incorporates a vaccination compartment to the classical SI epidemic model. Individuals are assumed to be in one of the following epidemiological states: Susceptibles (at risk of contracting the disease), Infectives (infected and capable of transmitting the disease), and Vaccinated (population vaccinated and are immune to the infection). All recruitment is into the susceptible class, and occurs at a constant rate β. A susceptible individual has an average ϕI contacts that would be sufficient to transmit the disease. Thus, the rate at which susceptibles in the population are infected is ϕSI. We present the model as follows:

$$\begin{aligned}\frac{dS}{dt} &= \beta - \mu S - \kappa S - \phi SI + \sigma V + \Upsilon I \\ \frac{dI}{dt} &= \phi SI - (\mu + \Upsilon)I \\ \frac{dV}{dt} &= \kappa S - (\mu + \sigma)V\end{aligned} \tag{1}$$

Where

β : Birth rate.

μ : Natural death rate.

ϕ: Rate of infection.

ϒ : Recovery rate.

κ: Vaccination rate

σ: Rate vaccination loses effect

The variables S, I and V represent the population of susceptible, infected and vaccinated individuals respectively. This model has the death rate, μ which represent death rate as a result of natural causes. In developing the model, we have taken into cognizance the fact that vaccinated individuals lose the effect of the vaccine at a constant rate σ to become susceptible again. Since this model is for human population, we assume that all its state variables and parameters are nonnegative for all t ≥ 0. The region biologically relevant is given by

$$\Omega = \left\{(S, I, V) \in \mathcal{R}_+^3 : 0 \leq S + I + V \leq \frac{\beta}{\mu}\right\} \tag{2}$$

The total human population is given by N = S + I + V, so that $dN/dt \leq \beta - \mu N$, thus $N \to \beta/\mu$ as $t \to$ ∞ .

III. STABILITY ANALYSIS

The basic reproduction number for the model is given as

$$R_0 = \frac{\phi\beta(\mu + \sigma)}{\mu(\mu^2 + \mu\Upsilon + \mu\kappa + \mu\sigma + \Upsilon\kappa + \Upsilon\sigma)} \tag{3}$$

The disease-free equilibrium given by $E^0 = (S^0, I^0, V^0)$ is the only equilibrium for $R_0 \leq 1$, where

$$S^0 = \frac{\beta(\mu + \sigma)}{\mu(\mu + \kappa + \sigma)}, \quad I^0 = 0, \qquad V^0 = \frac{\beta\kappa}{\mu(\mu + \kappa + \sigma)}$$

If $R_0 > 1$, then there is also a unique endemic equilibrium given by $E^* = (S^*, I^*, V^*)$, where

$$\begin{aligned}S^* &= \frac{\Upsilon + \mu}{\phi} \\ I^* &= -\frac{\mu^3 + \mu^2\Upsilon + \mu^2\kappa + \mu^2\sigma - \mu\phi\beta + \mu\Upsilon\kappa + \mu\Upsilon\sigma - \phi\beta\sigma}{\mu\phi(\mu + \sigma)} \\ V^* &= \frac{\kappa(\Upsilon + \mu)}{\phi(\mu + \sigma)}\end{aligned} \tag{4}$$

Local Stability of the Disease Free Equilibrium.

The characteristics equation after linearizing (1) about the disease free equilibrium E^0 gives

$$(\lambda+\mu)(\lambda+\mu+\kappa+\sigma)(\mu^2\lambda+\mu\kappa\lambda+\mu\sigma\lambda+\mu^3+\mu^2\Upsilon+\mu^2\kappa+\mu^2\sigma-\mu\phi\beta+\mu\Upsilon\kappa+\mu\Upsilon\sigma-\phi\beta\sigma)=0 \quad (5)$$

This gives

$$\lambda_1=-\mu, \qquad \lambda_2=-(\mu+\kappa+\sigma), \text{ and } \lambda_3=\{\mu+\Upsilon\}(R_0-1)$$

The first two eigenvalues λ_1 and λ_2 are negative and if $R_0 < 1$, λ_3 is also negative giving us the following theorem.

Theorem 1.

The disease-free equilibrium point is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$.

Local Stability of the Endemic Equilibrium

We analyse the local stability of the endemic equilibrium point in this section. The characteristics equation at the endemic equilibrium point E^* gives

$$(\lambda+\mu)(\mu^4+\mu^3\Upsilon+\mu^3\kappa+2\mu^3\sigma-\mu^2\phi\beta+\mu^2\Upsilon\kappa+\mu^2\Upsilon\lambda+2\mu^2\Upsilon\sigma+\mu^2\kappa\sigma-\mu^2\lambda^2-\mu^2\lambda\sigma+\mu^2\sigma^2-\mu\phi\beta\lambda$$
$$-2\mu\phi\beta\sigma+\mu\Upsilon\kappa\lambda+\mu\Upsilon\kappa\sigma+\mu\Upsilon\lambda\sigma+\mu\Upsilon\sigma^2-\mu\kappa\lambda\sigma-\mu\lambda^2\sigma-\mu\lambda\sigma^2-\phi\beta\lambda\sigma-\phi\beta\sigma^2)=0 \quad (6)$$

This gives $\lambda=-\mu$ and the solution to the following

$$\mu^4+\mu^3\Upsilon+\mu^3\kappa+2\mu^3\sigma-\mu^2\phi\beta+\mu^2\Upsilon\kappa+\mu^2\Upsilon\lambda+2\mu^2\Upsilon\sigma+\mu^2\kappa\sigma-\mu^2\lambda^2-\mu^2\lambda\sigma+\mu^2\sigma^2-\mu\phi\beta\lambda$$
$$-2\mu\phi\beta\sigma+\mu\Upsilon\kappa\lambda+\mu\Upsilon\kappa\sigma+\mu\Upsilon\lambda\sigma+\mu\Upsilon\sigma^2-\mu\kappa\lambda\sigma-\mu\lambda^2\sigma-\mu\lambda\sigma^2-\phi\beta\lambda\sigma-\phi\beta\sigma^2=0 \quad (7)$$

Equation (7) simplifies to

$$(\mu^2+\mu\sigma)\lambda^2+(\mu^3+\mu^2\kappa+2\mu^2\sigma+\mu\kappa\sigma+\mu\sigma^2+\mu(\mu^2+\mu\Upsilon+\mu\kappa+\mu\sigma+\Upsilon\kappa+\Upsilon\sigma)\{R_0-1\})\lambda$$
$$+\mu(\mu+\sigma)(\mu^2+\mu\Upsilon+\mu\kappa+\mu\sigma+\Upsilon\kappa+\Upsilon\sigma)\{R_0-1\}=0 \quad (8)$$

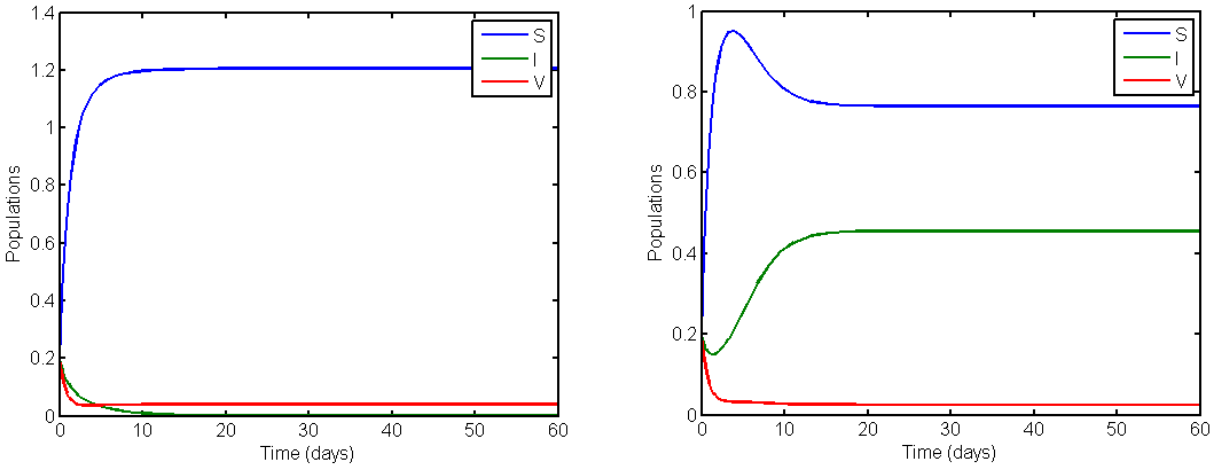
(8) satisfy the Routh Hurwitz stability criterion when $R_0 > 1$, hence all roots of (6) have negative real parts. This gives rise to the following theorem.

Theorem 2.

The endemic equilibrium point (E^*) of (1) is locally asymptotically stable when $R_0 > 1$.

IV. NUMERICAL SIMULATION

In this section, we show numerically the established results in earlier sections about the stability of the disease free and the endemic equilibria of the model as it relates to the basic reproduction number (R_0). The importance of vaccination to a susceptible population is highlighted and the plot of the infectives for different values of the vaccination rate has suggested a minimum vaccination rate and vaccine loss rate to target in a vaccination campaign. We use the ode23 suite in Matlab to simulate system (1) with the parameters as shown below the figures. The parameters are chosen solely for simulation convenience and do not reflect actual collected data.

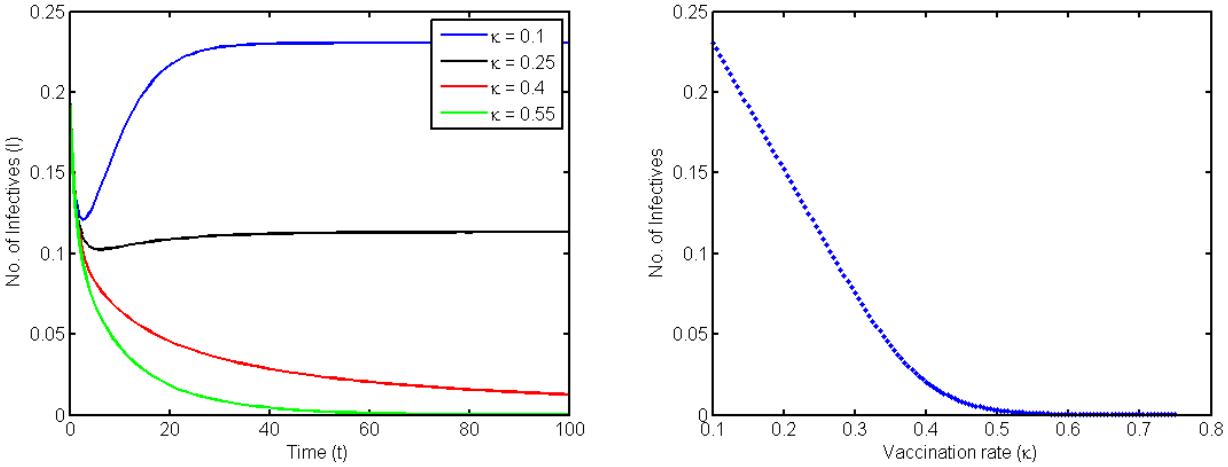


(a) $R_0 = 0.6753 < 1$, $\phi = 0.42$ (b) $R_0 = 1.5758 > 1$, $\phi = 0.98$

Figure 1: Other parameters are: β = 0.81, μ = 0.65, κ = 0.04, Υ= 0.1 and σ=0.55.

In figure 1(a), $R_0 = 0.6753 < 1$, hence the disease free equilibrium becomes stable which shows that the infection dies out of the population. Figure 1(b) shows the stable endemic equilibrium for $R_0 = 1.5758 > 1$, this means that the disease will persist in the population. This simulation agrees with theorems (1) and (2).

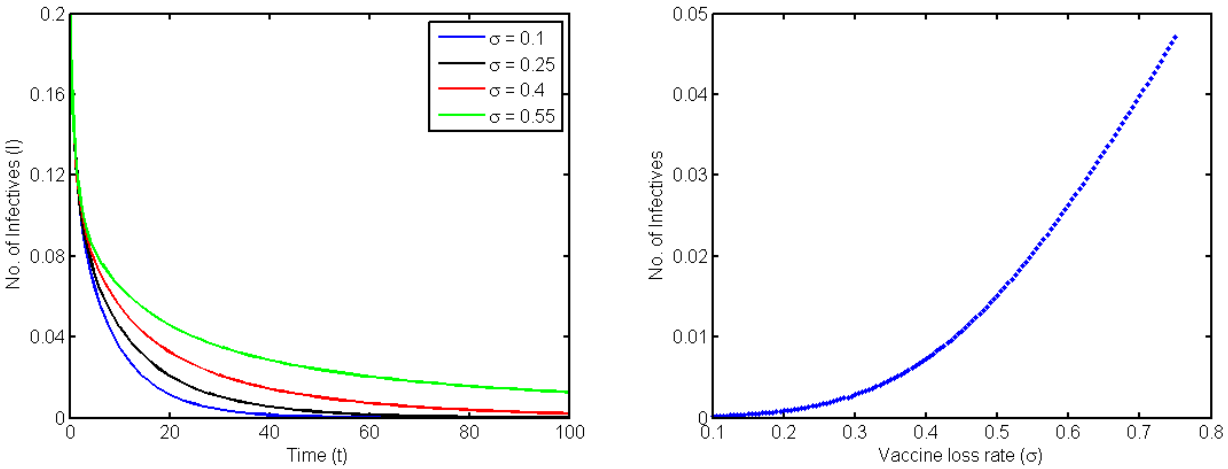
In the next figure, we show the effect the vaccination rate (κ) has on the dynamics of system (1) by plotting the number of infectives with varying vaccination rate in fig 2(a) and the vaccination rate against the steady states of the infectives in fig 2(b).



(a) $\kappa = \{0.1, 0.25, 0.4, 0.55\}$ (b) $\kappa \in [0.1: 0.75]$

Figure 2: Simulation of the evolution of the infected individuals for different values of vaccination rate κ. Other parameters are: $\beta = 0.81$, $\mu = 0.65$, $\varphi = 0.8$, $\Upsilon = 0.1$ and $\sigma = 0.55$.

In the figure below, we simulate the effect the vaccine loss rate (σ) has on the dynamics of system (1) by plotting the number of infected individuals with varying vaccine loss rate in fig 3(a) and the vaccine loss rate against the steady states of the infectives in fig 3(b).



(a) $\sigma = \{0.1, 0.25, 0.4, 0.55\}$ (b) $\sigma \in [0.1: 0.75]$

Figure 3: Simulation of the evolution of the infected individuals for different values of vaccine loss rate σ. Other parameters are: $\beta = 0.81$, $\mu = 0.65$, $\phi = 0.8$, $\Upsilon = 0.1$ and $\kappa = 0.4$.

V. CONCLUSION

We conclude that system (1) gives a good mathematical model to study the effect of vaccination in a population and could be used with actual data collected from endemic regions for the purpose of strategic planning and control of infectious diseases. Targeted vaccination on a population could provide an effective tool in the control of an epidemic as could be

seen in fig. 2(a). The infection was eradicated at the choice of the vaccination rate $\kappa = 0.55$. Effort in this case has to be made to keep the vaccine loss rate σ below 0.25 to achieve this as seen in fig. 3(a).

REFERENCES

[1] FE Andre, R Booy, HL Bock, J Clemens, SK Datta, TJ John, BW Lee, S Lolekha, H Peltola, TA Ruff, M Santosham, HJ Schmitt "Vaccination greatly reduces disease, disability, death and inequity worldwide", Bulletin of the World Health Organization, Volume 86, Number 2, February 2008, 81-160

[2] Patel MK, Gacic-Dobo M, Strebel PM, et al. "Progress Toward Regional Measles Elimination — Worldwide, 2000–2015". MMWR Morb Mortal Wkly Rep 2016; 65:1228–1233. DOI: http://dx.doi.org/10.15585/mmwr.mm6544a6

[3] C.M. Kribs-Zaleta, J.X. Velasco-Hernández, "A simple vaccination model with multiple endemic states", Math. Biosci. 164 (2000) 183–201.

[4] S.M. Blower, A.R. Mclean, "Prophylactic vaccines, risk behavior change, and the probability of eradicating HIV in San Francisco", Science 265 (1994) 1451.

[5] B. Reade, R. Bowers, M. Begon, R. Gaskell, "A model of disease and vaccination for infection with acute and chronic phases", Journ. Theor. Biol. 190 (1998) 355.

[6] J. MULLER, "Optimal Vaccination Patterns in Age-Structured Populations: Endemic Case", ELSEVIER, Mathematical a Computer Modelling 31 (2000) 149-160

[7] E. C. Yuan, D. L. Alderson, S. Stromberg and J. M. Carlson, "Optimal Vaccination in a Stochastic Epidemic Model of Two Non- Interacting Populations". PLoS ONE 10(2): e0115826. https://doi.org/10.1371/journal (2015)

[8] B. Shulgin, L. Stone and A. Z. Bull, "Pulse vaccination strategy in the SIR epidemic model", Math. Biol. (1998) 60: 1123. doi:10.1006/S0092-8240(98)90005-2

[9] J. Arino, C. Connell McCluskey, and P. van den Driessche, "Global Results for an Epidemic Model with Vaccination that Exhibits Backward Bifurcation", SIAM J. Appl. Math., 64(1), 260–276 (2003).

[10] Fred Brauer "Backward bifurcations in simple vaccination models", ELSEVIER, J. Math. Anal. Appl. 298 (2004) 418–431