Mathematical Modelling of Influenza-Meningitis under the Quarantine effect of influenza

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Abstract: In this research, the effect of influenza-infected populations on the spread of meningitis is examined in the nonlinear mathematical model. Influenza only, meningitis only, influenza-meningitis infectives, quarantine influenza fraction, and recovered fractions, the population of the host is classified into six sub-classes. We have examined the locally stable model utilizing non-linear differential equations stability theory. The Basic Reproduction Number of the coinfective system grows and lowers accordingly when contact and quarantine influenza rise. As quarantine rates, recovery rate of influenza alone and influenza meningitis increases, a portion of the recovered population also rises. The model is also numerically studied for the effects of different parameters on disease propagation.

Keywords: Influenza-meningitis coinfection, stability, disease free equilibrium, Basic reproduction number.

1. Introduction:

Influenza is a major risk for public health, an infectious disease of the respiratory system. This disease is a life threatening concern for vulnerable people in all age groups with various prognoses. Despite the vaccine-preventable disease, infection control requires yearly immunization programs and ongoing improvements. The influenza incubation period is on average 2 days, however it can be between 1 and 4 days. The transmission of aerosols may occur one day before the development of symptoms and can occur via asymptomatic individuals or folks who are not aware of their ailment being subjected to transmission.

Meningitis is a dangerous meninges, brain and spinal cord membranes infection. It remains the greatest public health challenge and is a terrible disease. Many pathogens, including bacteria, funguses or viruses, can cause the disease, although bacterial meningitis is the most severe global burden. Meningitis-related germs are spread from person to person through respiratory or throat droplets. Prolonged and close contact -for example, kissing,

cough, sneezing on a person or living with an infected person in the close proximity enhances disease spreading. The typical timeframe for incubation is 4 days but might vary from 2 to 10 days.

Hethcote (2000) evaluated a number of models analytically and applied to specific conditions for the transmission of infectious illnesses into communities. It examined threshold theorems for basic production number R_0, contact number σ and R substitution for conventional SIR epidemic and endemic models. A nonlinear mathematical model for influenza A (H1N1) spreading infectious disease, including vaccination role, has been proposed and analyzed by **Zhou and Guo (2012)**. **Khanh (2016)** has investigated the new paradigm of human-resistant transmission of influenza viruses. In showing the global stability of balance, he used Lyapunov's functional procedure and geometric technique. **Erdem et al. (2017)** have constructed a model of SIQR that includes quarantined individuals, with the potential for reducing the ability to generate secondary infection, to affect the process of the transmission-dynamics. The SIR deterministic model for mathematical co-infection of pneumonia and meningitis has been proposed by **Tilahun (2019)**. By employing normal differential equations, he created a seven-compartment model. A deterministic model for the Neisseria Meningitides, which causes meningitis, was provided by **Agusto and Leite (2019)**. The model was set by data from Nigeria's meningitis outbreak in 2017. The innovative deterministic model of the Listeriosis-Meningitis co-infection dynamics was created by **Chukwu et al. (2020)**. They used the sampling of Latin-Hypercubes to measure the parameters of the severity of the co-dynamic infection. The SVEIR model's dynamics were developed and examined by **Zephaniah et al. (2020)**, which contain saturated infection incidence force and a saturated pneumonia vaccine function.

The rest of the paper organization is: Section (2) contains an influenza-meningitis co-infection model, which consists of six suspected subclasses, influenza only, meningitis solely influenza infections, meningitis co-infective influenza quarantine, and rehabilitation. This section also contains a non-linear ODE system. We discussed the invariant region and the positive nature of the solution in subsection (3.1) of section (3). Free balance of disease was given in paragraph (3.2). The basic clothing replica number was calculated in sub-section by the next generation matrix method (3.3).

2. Influenza and Meningitis co-infection Model:

Let us consider the population of size $N(t)$ at time t, divided into six subclasses of suspectibles $S(t)$, influenza infectives only $I_1(t)$, meningistis infectives only $I_2(t)$, influenza-meningistis coinfectives $I_3(t)$, quarantine of influenza $Q(t)$ and recovered $R(t)$. The number of susceptible individuals recruited at the rate , recovered from influenza only , meningitis only and recovered from influenza-meningitis by losing their temporary immunity at the rate of δ_1, δ_2 and δ_3, respectively, are increased by the number of persons receiving through birth or immigration. One can obtain influenza with a_1 contact rate from an influenza only infected or co-infected individual with force of infection of influenza $g_1 = \frac{a_1(I_1+I_3)}{N}$ and join I_1 compartment in the entire susceptible population. Similarly, one can contact Meningitis with

a_2 contact rate from meningitis only infected or co-infected individual with Meningitis infection force $g_2 = \frac{a_2(I_2+I_3)}{N}$ and enter the I_2 compartment. Individuals who are just infected with influenza can develop a secondary meningitis infection with the power of infection g_2 and enter the co-infected subclass (I_3). Individuals who come from meningitis are only infected compartment when they are infected by influenza with g_1 force of infection, thus the coinfected compartment grows. There is a natural death rate of μ in all compartments, which equals. Furthermore, the death rates for Influenza, Meningitis, and Influenza-Meningitis are α_1, α_2 and $\alpha_3.\tau$ is the average duration spent in isolation, and d is the rate at which influenza infected is discovered and removed to quarantine.

The above description of the model is plotted in Fig. 1.

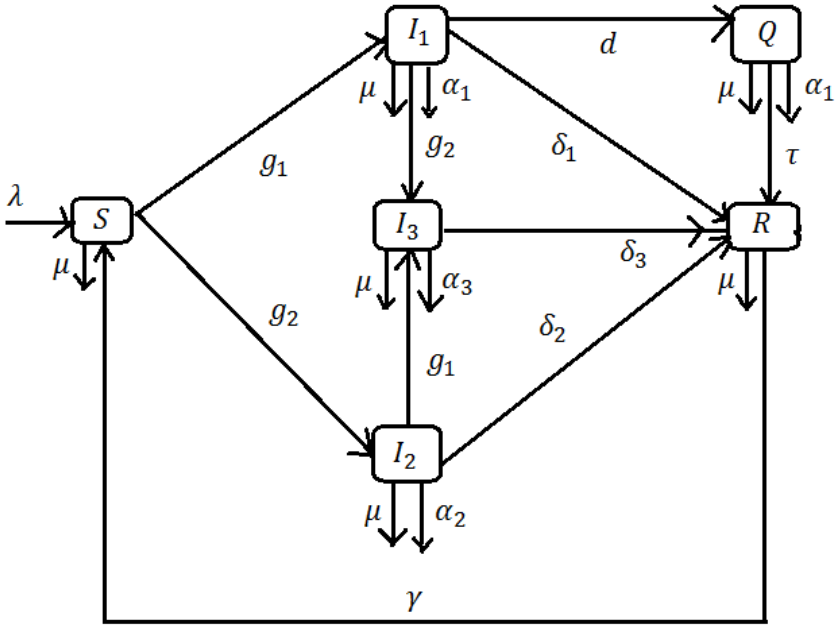


Figure 1: Flow Diagram of Influenza and Meningitis with Quarantine of Influenza infectious

We extract the following differential system from the model's flow graph (Fig. 1):

$$\left.\begin{aligned}
\frac{dS}{dt} &= \lambda - (g_1 + g_2 + \mu)S + \gamma R \\
\frac{dI_1}{dt} &= g_1 S - (g_2 + \mu + \alpha_1 + d + \delta_1)I_1 \\
\frac{dI_2}{dt} &= g_2 S - (g_1 + \mu + \alpha_2 + \delta_2)I_2 \\
\frac{dI_3}{dt} &= g_2 I_1 + g_1 I_2 - (\mu + \alpha_3 + \delta_3)I_3 \\
\frac{dQ}{dt} &= dI_1 - (\mu + \alpha_1 + \tau)Q \\
\frac{dR}{dt} &= \delta_1 I_1 + \delta_2 I_2 + \delta_3 I_3 - \mu R - \gamma R + \tau Q
\end{aligned}\right\} \quad (1)$$

$$N = S + I_1 + I_2 + I_3 + Q + R \quad (2)$$

Adding all equation of system (1), we get

$$\frac{dN}{dt} = \lambda - \mu N - \alpha_1 I_1 - \alpha_2 I_2 - \alpha_3 I_3 - \alpha_1 Q$$

$$\frac{dN}{dt} = \lambda - \mu N - \alpha_1 I_1 - \alpha_2 I_2 - (\alpha_1 + \alpha_2) I_3 - \alpha_1 Q$$

$$\frac{dN}{dt} = \lambda - \mu N - \alpha_1 (I_1 + I_3 + Q) - \alpha_2 (I_2 + I_3) \quad (3)$$

3. Quantitative analysis:

3.1 Invariant Region:

We use the entire population to get the invariant region as

$N = S + I_1 + I_2 + I_3 + Q + R$

$$\frac{dN}{dt} = \lambda - \mu N - \alpha_1 (I_1 + I_3 + Q) - \alpha_2 (I_2 + I_3) \quad (4)$$

If influenza and meningitis deaths are excluded, the (4) equation becomes

$$\frac{dN}{dt} \leq \lambda - \mu N \quad (5)$$

Solving equation (5) we get

$N \leq \frac{\lambda}{\mu} - c_1 e^{-\mu t}$ i.e. $0 \leq N \leq \frac{\lambda}{\mu}$

Theorem: If $S_0 > 0, I_{10} > 0, I_{20} > 0, I_{30} > 0, Q_0 > 0, R_0 > 0$ the set of the solution $[S(t), I_1(t), I_2(t), I_3(t), Q(t), R(t)]$ will be positive.

Proof:

Let

$t^* = \sup \{t > 0 : S(t_1) > 0, I_1(t_1) > 0, I_2(t_1) > 0, I_3(t_1) > 0, Q(t_1) > 0, R(t_1) > 0 \; \forall \; t_1 \in [0, t]\}$

Since $S_0 > 0, I_{10} > 0, I_{20} > 0, I_{30} > 0, Q_0 > 0, R_0 > 0$ Therefore $t^* > 0$

If $t^* < \infty$, then necessarily S or I_1 or I_2or I_3 or Q or R equal to 0 at t^*.

Using Equation (1), Let's look at the first equation.

$$\frac{dS}{dt} = \lambda - (g_1 + g_2 + \mu) S + \gamma R \quad (6)$$

To obtain the solution of (6), we use the variation of constant formula at t^*

$S(t^*) = S(0)exp\left[-\int_0^{t^*}(g_1+g_2+\mu)s\,ds\right] + \int_0^{t^*}(\lambda+\gamma R)exp\left[-\int_s^{t^*}(g_1+g_2+\mu)t_1 dt_1\right]ds$

Since all variables are positive in $[0, t^*]$ therefore $S(t^*) > 0$

Similarly we can show that

$I_1(t^*) > 0, I_2(t^*) > 0, I_3(t^*) > 0, Q(t^*) > 0, R(t^*) > 0$ which is a contradiction as we have assume $t^* < \infty$. Hence t^* must be equal to ∞.

3.2 Disease-free Equilibrium (DFE):

On putting $I_1 = I_2 = I_3 = 0$ in equation (1), we get DFE $E_0 = \left(\frac{\lambda}{\lambda}, 0,0,0,0,0\right)$

3.3 Basic Reproduction Number:

The infective compartment of the model is given by

$\frac{dI_1}{dt} = g_1 S - (g_2+\mu+\alpha_1+d+\delta_1)I_1$

$\frac{dI_2}{dt} = g_2 S - (g_1+\mu+\alpha_2+\delta_2)I_2$

$\frac{dI_3}{dt} = g_2 I_1 + g_1 I_2 - (\mu+\alpha_3+\delta_3)I_3$

$\frac{dQ}{dt} = dI_1 - (\mu+\alpha_1+\tau)Q$

From Next generation matrix of above infective compartment model, we get

$$F = \begin{bmatrix} \frac{a_1\lambda}{\mu} & 0 & \frac{a_1\lambda}{\mu} & 0 \\ 0 & \frac{a_2\lambda}{\mu} & \frac{a_2\lambda}{\mu} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}, V^{-1} = \begin{bmatrix} \frac{1}{\mu+\alpha_1+d+\delta_1} & 0 & 0 & 0 \\ 0 & \frac{1}{\mu+\alpha_2+\delta_2} & 0 & 0 \\ 0 & 0 & \frac{1}{\mu+\alpha_3+\delta_3} & 0 \\ 0 & 0 & 0 & \frac{1}{\mu+\alpha_1+\tau} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} \frac{a_1\lambda}{\mu(\mu+\alpha_1+d+\delta_1)} & 0 & \frac{a_1\lambda}{\mu(\mu+\alpha_3+\delta_3)} & 0 \\ 0 & \frac{a_2\lambda}{\mu(\mu+\alpha_2+\delta_2)} & \frac{a_2\lambda}{\mu(\mu+\alpha_3+\delta_3)} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

The Eigen values of FV^{-1} are

$\lambda_1 = \frac{a_1\lambda}{\mu(\mu+\alpha_1+d+\delta_1)} = R_1$

$$\lambda_2 = \frac{a_2\lambda}{\mu(\mu+\alpha_2+\delta_{2)}} = R_2$$

$$\lambda_3 = 0$$

$$R_{12} = max\{R_1, R_2\} \quad (7)$$

4. Numerical Results and discussion:

Table 1:

Parameters	Value	Units	Source
a_1	2.343	Per day	Supposed
δ_1	0.2, 0.3,0.4, 0.6	Per day	Supposed
d	0.5,1,1.5,2.0	Per day	Supposed
τ	0.244	Per day	Supposed
α_1	0.0002	Per day	Estimated
a_2	0.9	Per day	Fresnadillo Martínez (2013)
δ_2	0.8	Per day	Supposed
α_2	0.002 to 0.2	Per day	Estimated
δ_3	0.2,0.3,0.4	Per day	Supposed
λ	0.008	Per day	Nthiiri et al. (2015)
μ	0.02	Per day	Irving et al. (2012)

Fig.(2):Fraction of Population with time for d=0.5

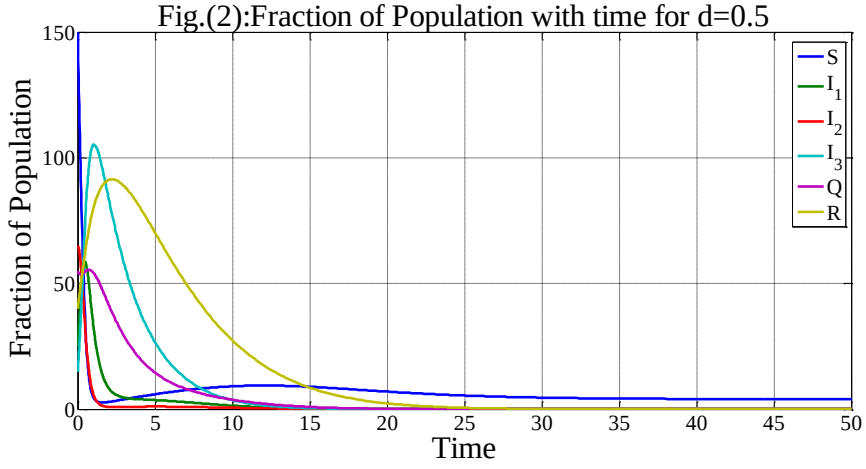


Fig.(3):Fraction of Population with time for d=1

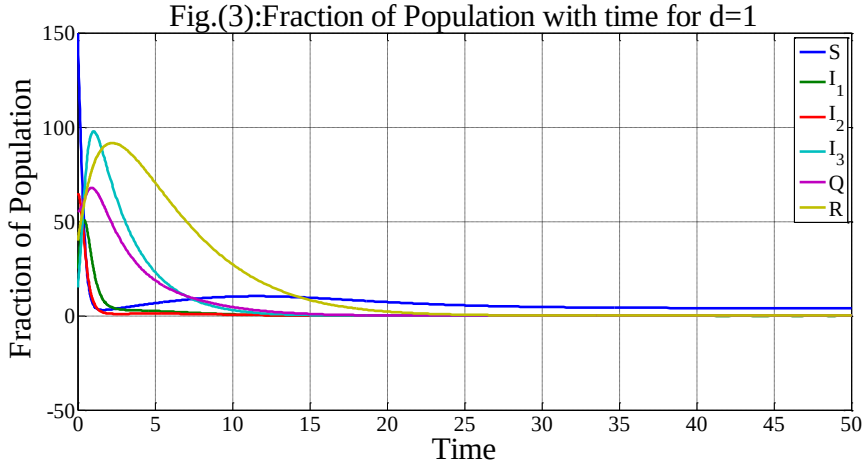


Fig. (4):Fraction of Population with time for d=1.5

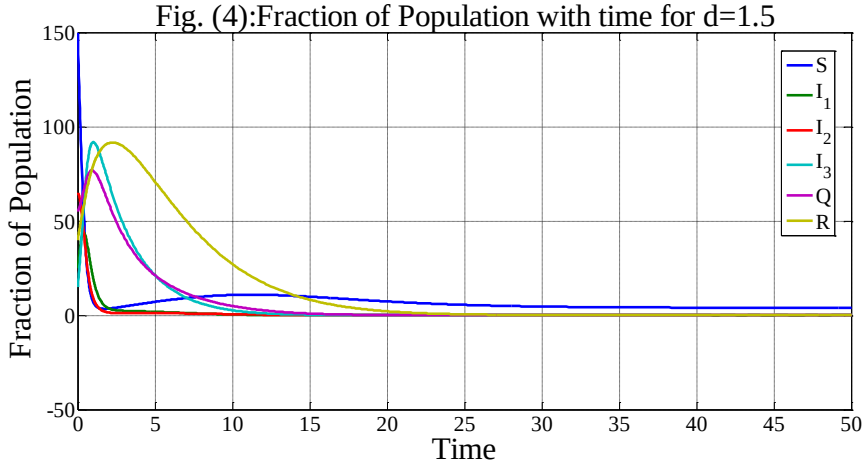


Fig. (5):Fraction of Population with time for d=2

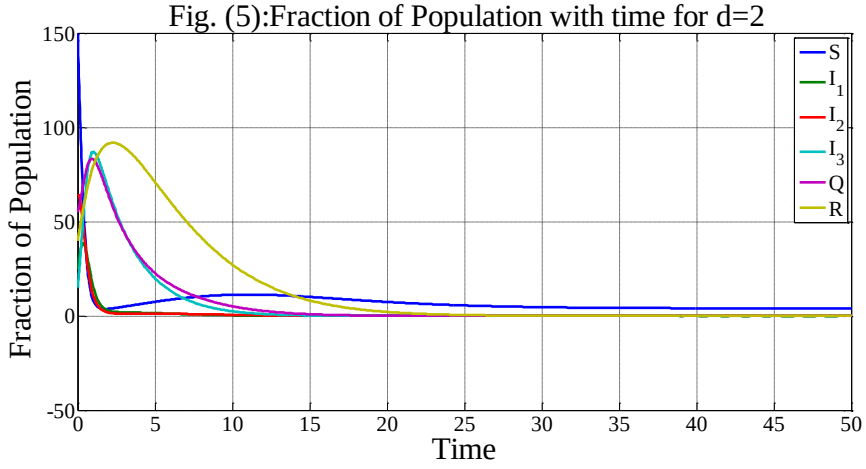


Fig. (6):Fraction of Population with time for δ_3=0.2

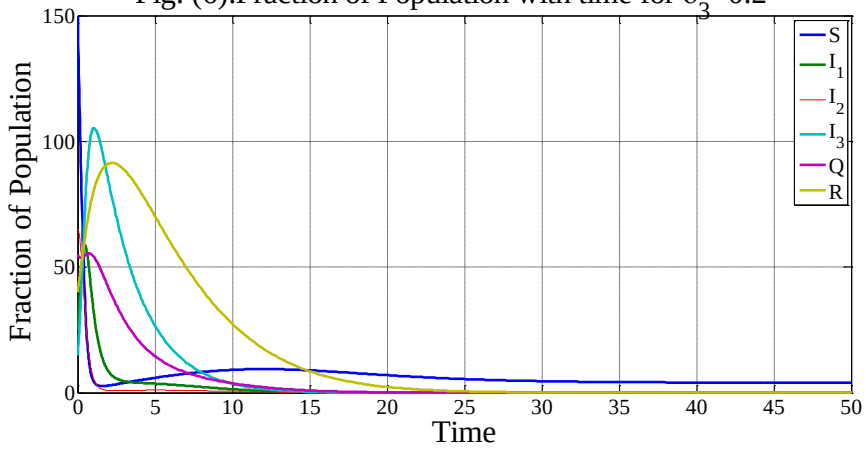


Fig. (7):Fraction of Population with time for δ_3=0.3

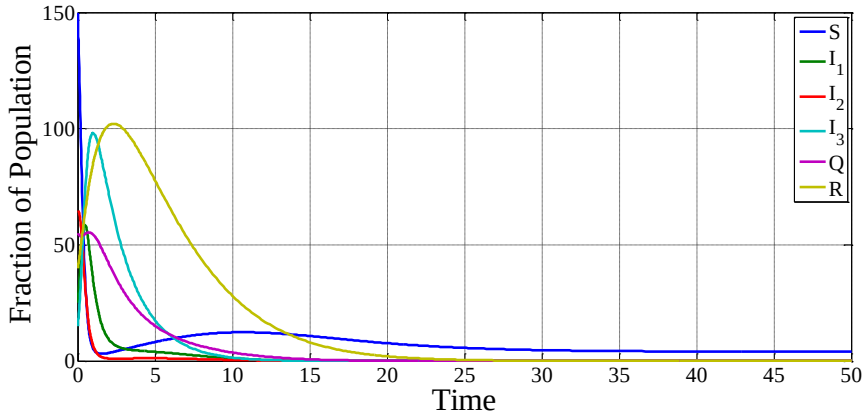


Fig. (8):Fraction of Population with time for δ_3=0.4

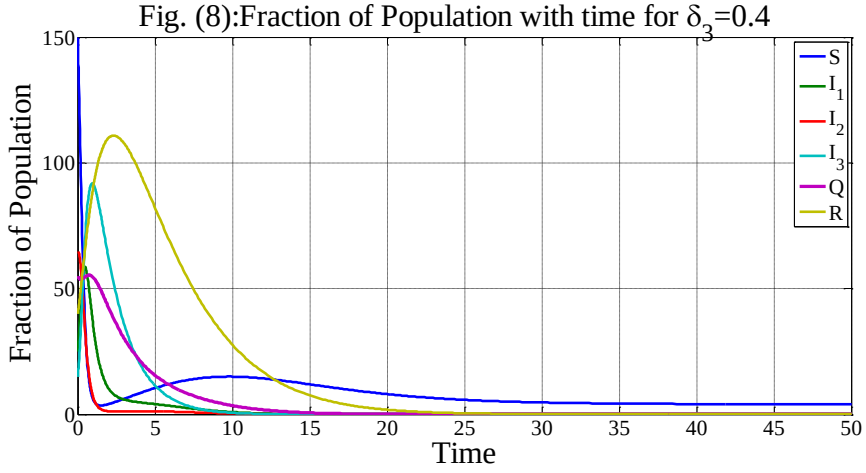


Fig. (9): Fraction of Population with time for δ_1=0.2

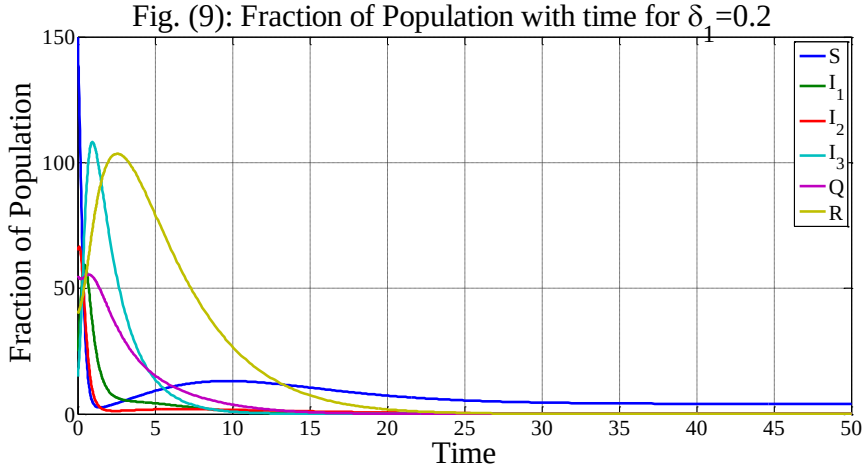


Fig. (10):Fraction of Population with time for δ_1=0.3

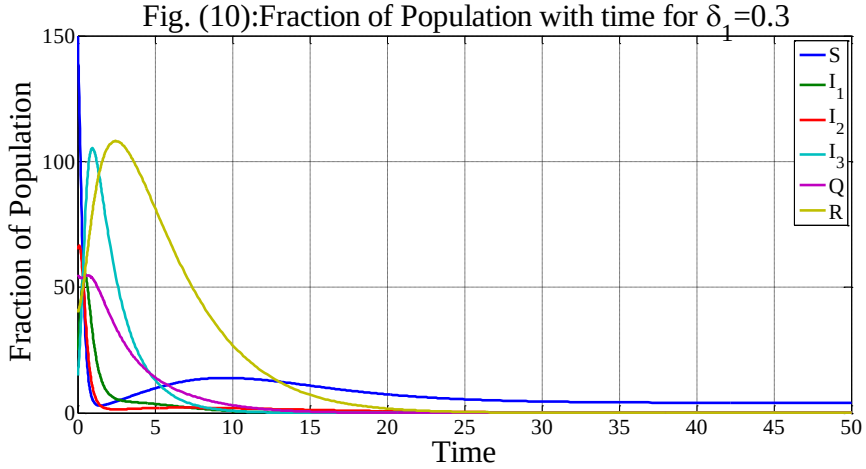


Fig.(11): Fraction of Population with time for δ_1=0.4

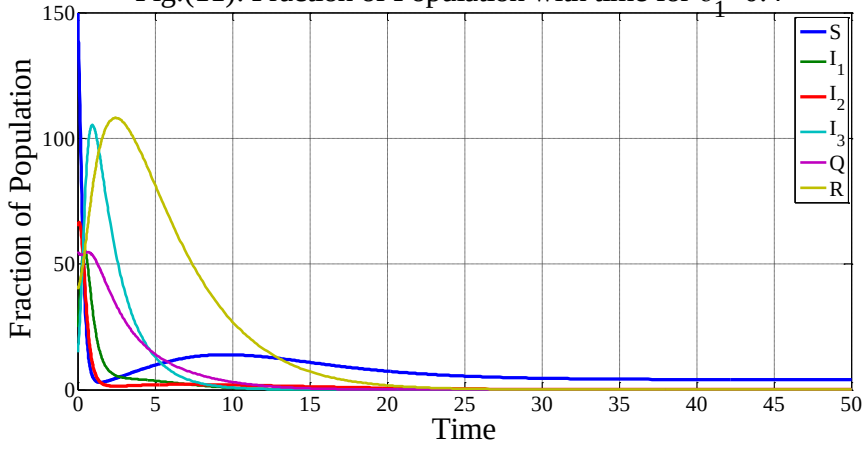


Fig. (12):Fraction of Population with time for δ_1=0.6

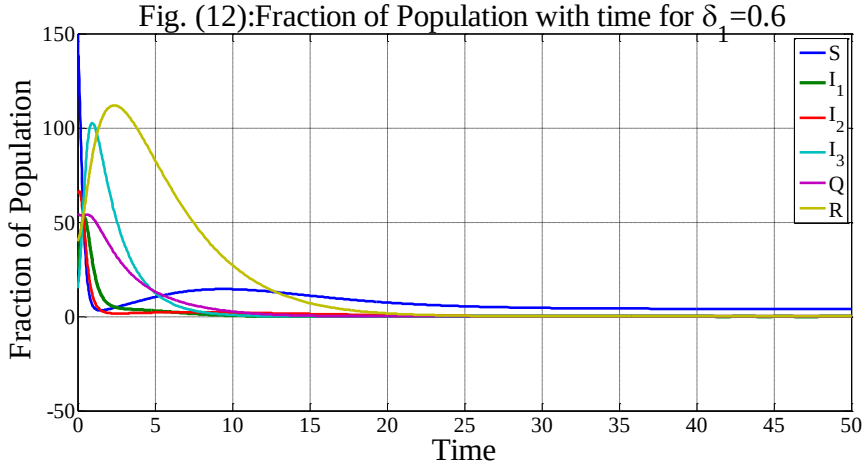


Fig. 13: Variation in Basic Reproduction number with the conatct rate from influenza for different Quarantine Rate of influenza

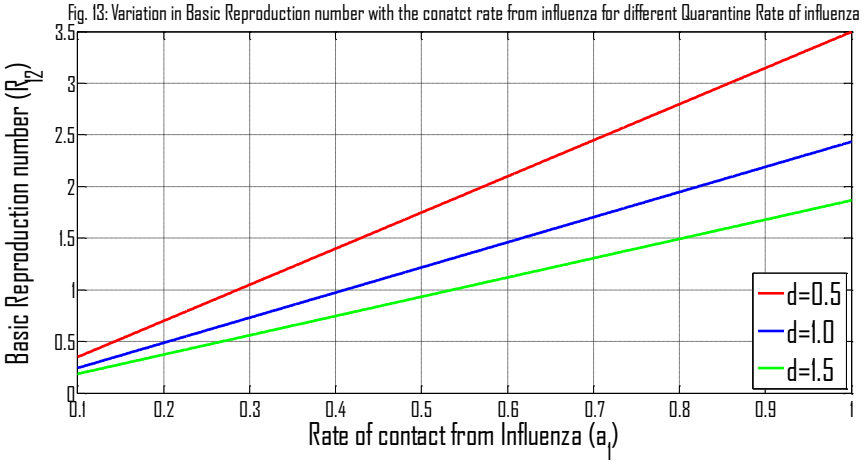


Fig. (14): Variation in Basic Reproduction number with the conatct rate from influenza for different recovery rate of influenza

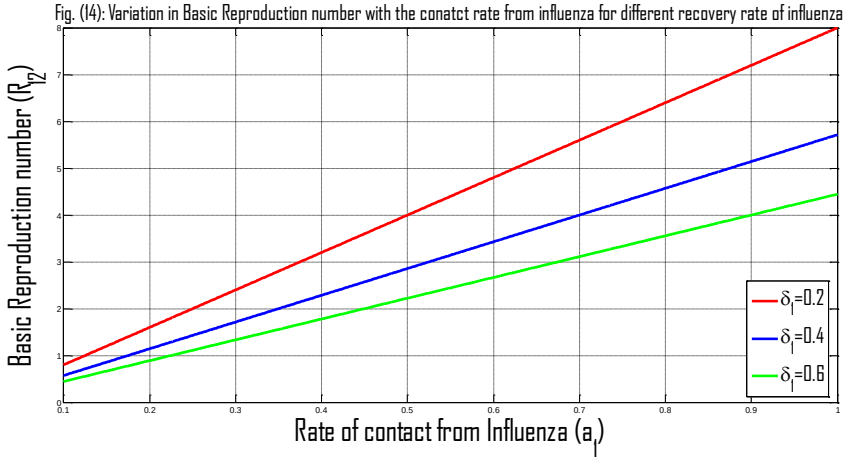
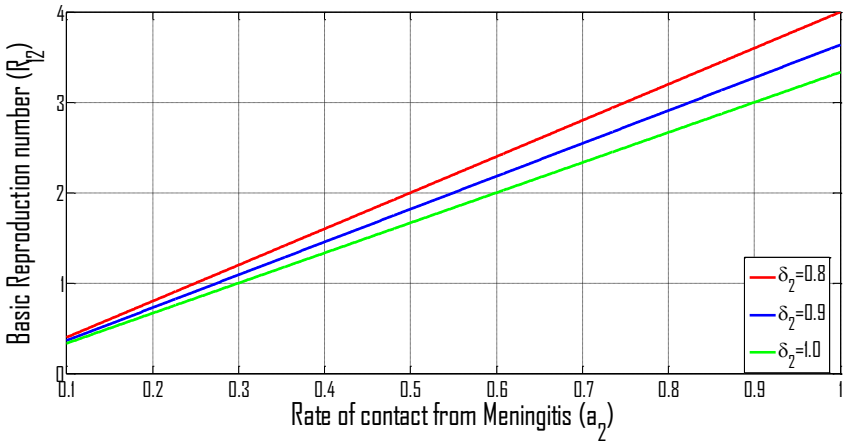


Fig. (15):Variation in Basic Reproduction number with the conatct rate from meningitis for different recovery rate of meningitis



In this part, numerical simulations for the influenza–meningitis co-infection model are done. We used MATLAB 7.0 to check the effect of several parameters in the expansion as well as to regulate the influenza and meningitis co-infection. The numerical values in Table 1 are utilized to calculate the parameters. The effect of time on the fraction of population of various compartments are shown in the figures (2)-(12). From these figures, one can easily observe the situation how fraction of various populations (susceptibles, influenza infectives only, Meningitis infectives only, influenza-Meningitis infectives, Quarantine and Recovered) are going down. Also it is obvious from the figures (2-5), Recovered fraction of the population increases as the quarantine rate (d) of influenza infectious population increases. As a result, public policymakers must focus on increasing the value of the influenza infectious population's quarantine rate. We concluded from Figures (6) to (8) that raising the recovery rate of the co-infectious population, which is δ_3, has a significant benefit in eradicating both diseases in the community. We have investigated from figures (9) to (12), that recovered fraction of the population increases as the recovery rate (δ_1) of influenza infectious population increases. This means that raising the influenza recovery rate is important for reducing influenza and meningitis co-infections. From Figures (13) to (15), we can see that as contact rate from influenza only and meningitis only increase, basic reproduction number of the co-infection model also increase. It is also obvious form these figures Basic reproduction number of co-infectious population decrease as the quarantine rate of influenza infectious, recovery rate from influenza only and meningitis only increases. Hence to reduce the infection, we have to increase the quarantine rate of influenza infectious, recovery rate from influenza only and meningitis only individually.

Conclusion:

We found that increasing the influenza infectious quarantine rate had a significant impact on reducing influenza infective only, meningitis infective only, and influenza-meningitis infectives in the community. Increasing the influenza-meningitis recovery rate and the influenza-only recovery rate, on the other hand, helps to eliminate infection. If the co-

infection recovery rate is enhanced, it has the effect of reducing the co-infectious population. It's worth noting that raising the influenza-only quarantine rate, influenza-only recovery rate, influenza only, meningitis only and decreasing the contact rate of either influenza or meningitis, we must enhance the influenza infectious quarantine rate, influenza recovery rate, and meningitis recovery rate all at the same time in order to reduce infection quickly.

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