DYNAMICAL ANALYSIS FOR EPIDEMIC MODELS OF COVID-19 AND INFLUENZA

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The dynamical analysis of epidemic models for COVID-19 [2] and influenza involves the application of mathematical models that accurately depict the dynamics of these diseases. These models are characterized by the use of fractional derivatives, particularly the Caputo fractional derivative, which allows for the incorporation of memory and hereditary effects in the modeling process.

COVID-19 Model formulation:

We modified and investigated the extended COVID-19 model $(S_p\ Q_p\ E_p\ A_p\ I_p\ D_p\ R_p\ V_p)$ with the addition of vaccination effect.

$$
\begin{aligned}
&{}_0^cD_\tau^z\ S_p(\tau) = -\alpha^z\ S_p(\tau)\ (I_p(\tau) + \delta^z\ A_p(\tau)) - (\kappa^z + \eta)S_p(\tau) + \gamma^z\ Q_p(\tau) - \rho_I^z\ S_p(\tau),\\
&{}_0^cD_\tau^z\ Q_p(\tau) = \kappa^z\ S_p(\tau) - \gamma^z\ Q_p(\tau) - \rho_I^z\ Q_p(\tau),\\
&{}_0^cD_\tau^z\ E_p(\tau) = \alpha^z\ S_p(\tau)\ (I_p(\tau) + \delta^z\ A_p(\tau)) - \psi^z\ E_p(\tau) + \sigma^z\ \eta\ V_p(\tau)I_p(\tau) - \rho_I^z\ E_p(\tau),\\
&{}_0^cD_\tau^z\ A_p(\tau) = \psi^z\ (1 - \eta^z)E_p(\tau) - \mu_A^z\ A_p(\tau) - \varphi_A^z\ A_p(\tau) - \rho_I^z\ A_p(\tau),\\
&{}_0^cD_\tau^z\ I_p(\tau) = \psi^z\ \eta^z\ E_p(\tau) - \varphi_I^z\ I_p(\tau) - \rho_I^z\ I_p(\tau) - \mu_I^z\ I_p(\tau),\\
&{}_0^cD_\tau^z\ D_p(\tau) = \mu_A^z\ A_p(\tau) + \mu_I^z\ I_p(\tau) - \rho_D^z\ D_p(\tau) - \varphi_D^z\ D_p(\tau) - \rho_I^z\ D_p(\tau),\\
&{}_0^cD_\tau^z\ R_p(\tau) = \varphi_A^z\ A_p(\tau) + \varphi_I^z\ I_p(\tau) + \varphi_D^z\ D_p(\tau) - \rho_I^z\ R_p(\tau),\\
&{}_0^cD_\tau^z\ V_p(\tau) = \eta\ S_p(\tau) - \sigma^z\ V_p(\tau)I_p(\tau) - \rho_I^z\ R_p(\tau).
\end{aligned}
$$

starting with initial conditions that are non-negative

$$S_p\ (0) = S_{p_0} \geq 0, \quad Q_p\ (0) = Q_{p_0} \geq 0, \quad E_p\ (0) = E_{p_0} \geq 0, \quad A_p\ (0) = A_{p_0} \geq 0$$

$$I_p\ (0) = I_{p_0} \geq 0, \quad D_p\ (0) = D_{p_0} \geq 0, \quad R_p\ (0) = R_{p_0} \geq 0, \quad V_p\ (0) = V_{p_0} \geq 0$$

Stability Analysis:

We generally seek steady-state (equilibrium) solutions. Models contain at least a “disease-free” steady state and an “endemic” steady state. The disease-free steady state represents clearance of disease. The goal of treatment is to reduce spread of disease or at the very least to ensure that solutions remain close to the disease-free steady state. When this steady state becomes unstable, disease may spread unboundedly and this represents progression to spread of viruses. For this purpose, the stability analysis is performed.

Basic Reproduction Number:

A very threshold quantity is the basic reproduction number, sometimes called the basic reproductive number or basic reproductive ratio which is usually denoted by R_0 which is average number of cases produced by one infected individual introduced into a population of susceptible individuals. We find the condition of R_o to reduce or eradicate the disease. If $R_o < 1$, then disease can be eradicated from the population. But if $R_o > 1$, then the disease will spread in the population. We used next generation matrix approach [3] to get the basic

reproduction number R_0 which is equal to the spectral radius of $K = FV^{-1}$ where F is the non-negative matrix of infected terms and V is the singular matrix of the transmission terms.

Lemma (Generalized Mean Value Theorem): Consider a function $\xi(\tau) \in \mathbb{C}[a,b]$. Fractional derivative with Caputo operators is denoted as ${}_0^cD_\tau^z\ \xi\ (\tau)$, for $0 < z \leq 1$, then $\xi(\tau) = \xi(s) + \frac{1}{\Gamma(z)}\ {}_0^cD_\tau^z\ \xi\ (\theta)(\tau - s)^z$, with $0 \leq \theta \leq \tau,\ \forall\ \tau \in (a,b]$.

Remark: Suppose that $\xi(\tau) \in \mathbb{C}[a,b]$ and the Caputo derivative of ${}_0^cD_\tau^z \in (0, \mathrm{b})$ for $0 < z \leq 1$. *Lemma* show that

- If ${}_0^cD_\tau^z\ \xi\ (\tau) \geq 0, \forall\ \tau \in [0,b]$, then the $\xi(\tau)$ function is non-decreasing.
- If ${}_0^cD_\tau^z\ \xi\ (\tau) \leq 0, \forall\ \tau \in [0,b]$, then the $\xi(\tau)$ function is non-increasing.

We modified some theorems to find the existence and uniqueness of the solution.

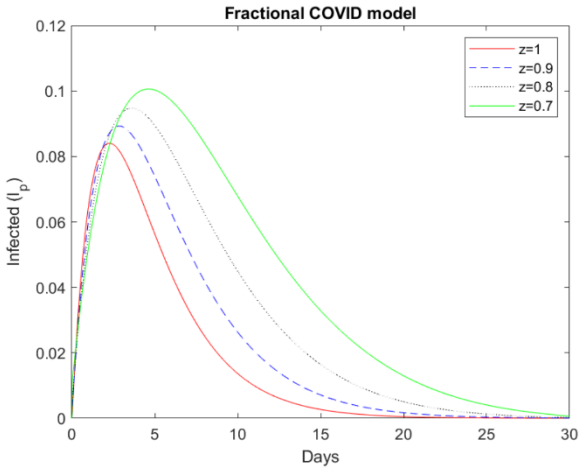
i. The solution to the initial condition of the proposed fractional order COVID model is unique and limited in R_+^8.

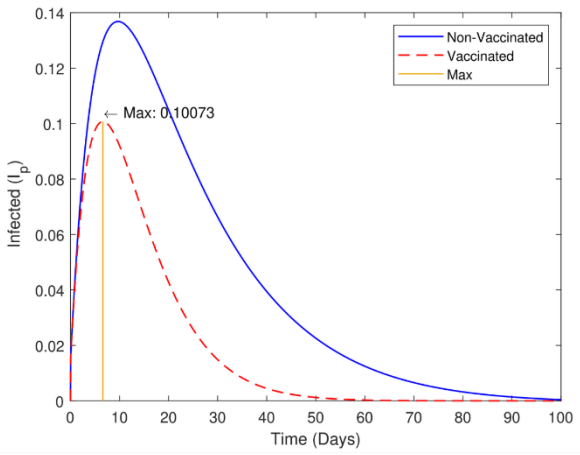
ii. If the following inequality holds $0 \leq r_i < 1$, then the function F_i for $i = 1,2,3,4,5,6,7,8$ fulfill with the condition of Lipschitz and contraction mapping as well.

iii. If there exists $r_1 > 1$ such that $\frac{r_i}{\Gamma(z)} r_1 \leq 1$, for $i = 1,2,3,4,5,6,7,8$ then there exists at least one solution of the system given by the fractional COVID-19 model $(S_p\ Q_p\ E_p\ A_p\ I_p\ D_p\ R_p\ V_p)$.

iv. If the condition $\left(1 - \frac{r_i}{\Gamma(z)} r_1\right) > 0$, for $i = 1,2,3,4,5,6,7,8$ holds then the model $(S_p\ Q_p\ E_p\ A_p\ I_p\ D_p\ R_p\ V_p)$ has unique solution.

The model is solved numerically using the Fractional Trapezoidal method [1], and the results are presented in the form of graphs for each compartment using MATLAB. The simulations at different fractional orders and comparison of vaccinated and non-vaccinated population for the infected compartment are given below:





Based on the data and figures analyzed, it appears that fractional-order models offer a superior approach to modeling COVID-19 transmission. As we can see from the figure (right), vaccination proves effective across infected compartment within the model. The data clearly indicates a decrease in the infected population following vaccine application. In the light of all these mentioned facts and figure it is found fractional order can be better approach for modeling.

Influenza Model formulation:

The $SVIR$ Influenza model that differentiates between certain subtypes of influenza. We possess three indices: $n = A^{m2}(H1), A^{m2}(H3), and\ B^{m2}$, denoting the influenza $A^{m2}(H1), A^{m2}(H3), and\ B^{m2}$ viruses, respectively.

$$\frac{dS}{d\tau} = -\sum_{n=1}^{3} \eta_n I_n(\tau) S(\tau) - \mu\left(1 - \frac{Ve(\tau)}{A^*}\right),$$

$$\frac{dV}{d\tau} = \mu\left(1 - \frac{Ve(\tau)}{A^*}\right) - \sum_{n=1}^{3} \lambda_n I_n(\tau) V_p(\tau) \quad with\ \lambda_n = \eta_n(1 - \nu_n),$$

$$\frac{dI_n}{d\tau} = \eta_n I_n(\tau) S(\tau) + \lambda_n I_n(\tau) V_p(\tau) - \rho_n I_n(\tau),$$

$$\frac{dR}{d\tau} = \sum_{n=1}^{3} \rho_n I_n(\tau),$$

$$\frac{dVe}{d\tau} = \mu\left(1 - \frac{Ve(\tau)}{A^*}\right).$$

where λ_n is determined by the vaccine effectiveness ν_n and the transmission rate η_n:

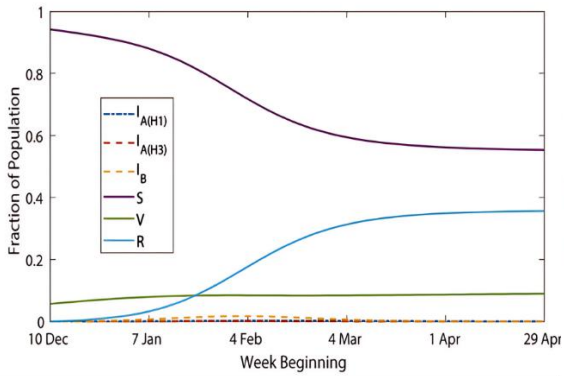
$$\lambda_n = \eta_n(1 - \nu_n), \qquad where \qquad n = A^{m2}(H1), A^{m2}(H3), B^{m2}.$$

that represents a vaccine with a leaky characteristic, offering partial protection to each recipient.

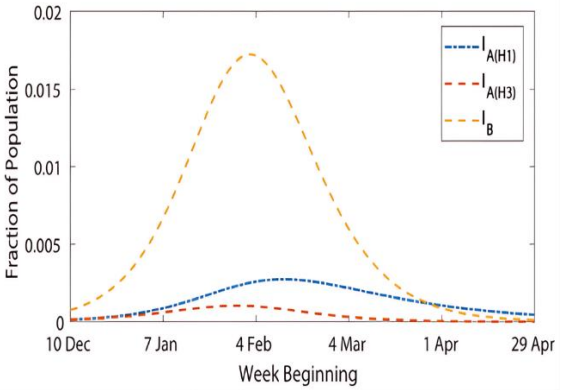
Analysis:

We investigated the influenza model by applying similar methodologies used in the COVID-19 model. Some key points are:

- The threshold quantity value R_0 similar to the basic reproduction number [4] is obtained using the Jacobian matrix approach.
- It can be shown that if $R_0 < 1$ the infection will disappear, but if $R_0 > 1$, the infection exists and the disease persists.
- We applied Euler method for the numerical scheme and simulations using MATLAB.



All compartments



Infected compartments

- We analyzed the stability of Influenza model.
- Given that $\nu_{A^{m2}(H1)} = \nu_{A^{m2}(H3)} = \nu_{B^{m2}}$. The disease-free equilibrium is unstable. This means that the transmission of influenza [5] may be initiated by a single infection case.

This is evident when we consider the situation where the initial number of susceptible individuals $V(0)$ and the initial number of infected individuals $R(0)$ are equal to zero at the beginning of the season.

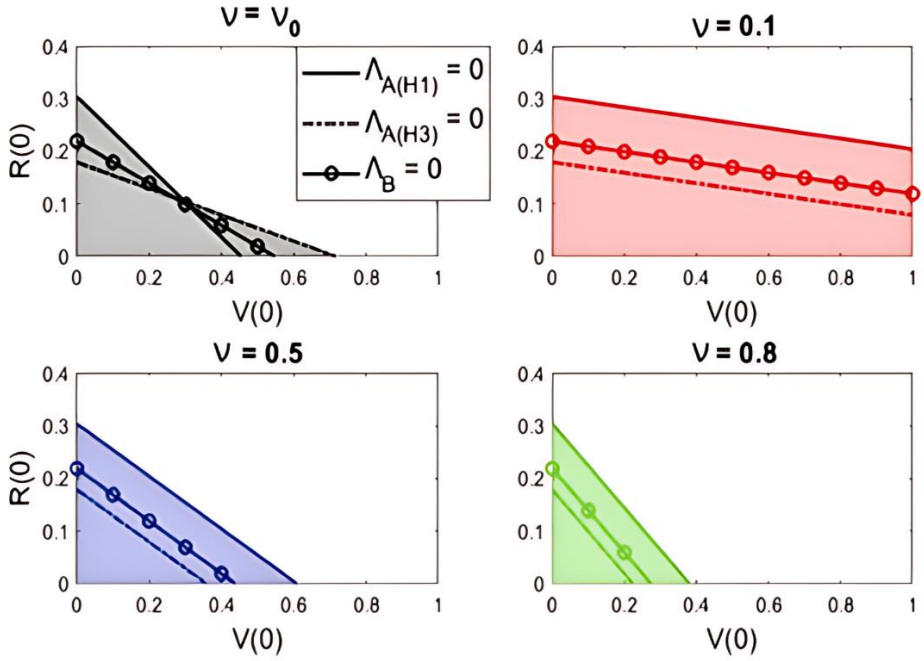


Figure: The deciding eigenvalues Λ_j in the space $(V^*, R^*) = (V(0), R(0))$ vary with influenza subtypes j and vaccination efficiency. $\nu_n = \nu_{A^{m2}(H1)} = \nu_{A^{m2}(H3)} = \nu_{B^{m2}}$

- The increase in vaccination efficiency $(\nu = 0.1 \rightarrow 0.5 \rightarrow 0.8)$ leads to a drop in the initial vaccinated population $V(0)$ to maintain stable, steady states. This shift can be seen in the unshaded area of Figure, which moves towards the left. Even if the whole population has been vaccinated $(V(0) = 1)$, the disease-free equilibrium remains unstable when $\nu = 0.1$ and $R(0) \approx 0$.
- at least 72% of the population get herd immunity vaccinations to prevent seasonal epidemics. At 11.6%, immunization rates are low.
- The study shows that vaccine effectiveness grows, but essential immunization coverage falls. In addition, improving a vaccine against one influenza subtype may increase the incidence of another.

References:

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[4]. Nikbakht, R., Baneshi, M.R., Bahrampour, A. and Hosseinnataj, A., 2019. Comparison of methods to estimate basic reproduction number (R_0) of influenza, using Canada 2009 and 2017-18 A (H1N1) data. *Journal of Research in Medical Sciences*, *24*(1), p.67.

[5]. Neumann, G. and Kawaoka, Y., 2015. Transmission of influenza A viruses. *Virology*, *479*, pp.234-246.