Imitation dynamics predict vaccinating behaviour. - Chris T. Bauch

(Presented by Siddhant Kamble and Gokuleshwor Pokharel for the Final Paper for Math 437: Mathematical Biology, in Spring 2024, in the University of Idaho, Moscow Campus.)

Abstract: Until now, when we talk about vaccinations, we have often considered the scenario in which we consider the *SIR* model where the vaccinated group is put under R, and their offspring are put in either S or R. In this paper, the author is implying that if we can actually nullify the effect of vaccination by taking another drug, then we can extend the general SIR model by the addition of another variable x, which measures the level of vaccinated people in the population.

Introduction: Vaccines always benefit the society, as long as it does not have any major side effects. Due to the dilemma between the associated cost of vaccinations that come mostly through the side effects and direct monetary cost, and the associated preventive as well as curative measures of the vaccinations, along with the 'free riding' for 'herd immunity', people decide whether to take the vaccinations or not. In this paper, the author presents a model of "imitation dynamics": *SIR* model is presented with the additional 'x' variable, which measures the proportion of population, and who will also vaccinate their offspring at birth.

Model: The 'players' of this game are parents, who decide whether to vaccinate their child at birth or not. According to the author, the 'rumors' like MMR vaccine causing autism in children serve as a hindering mechanism for the parents to vaccinate their offspring. The (negative) payoff of vaccination is : $f_v = -r_v$, where r_v is the probability of significant injury to the children due to the side effects from the vaccination, whereas the (negative) payoff of not vaccinating a child is the associated probability of suffering significant injury due to the infection from the concerned disease under discussion, and the associated probability of being infected, which is taken to be directly proportional to the proportion of Infected in the population: $f_n(I) = -r_i mI$, where mI = probability of infection with proportionality constant m, and r_i = probability of significant injury once infected.

For the "imitation game", it is assumed that the individuals randomly sample the other individuals, and a decision is taken if they find "switching the side from vaccination to non-vaccination" is beneficial, or vice versa. Here, $\Delta E = f_v - f_n(I)$. If $\Delta E > 0$, then non-vaccinators will want to be vaccinators. We have, $dx/dt = (1 - x) \cdot \sigma \cdot x \cdot \rho \cdot \Delta E$: *"(1-x)"* non vaccinator, samples at the rate σ, to find total of *"$\sigma . x$"* sample vaccinators , and switches to the vaccination strategy with probability "$\rho . \Delta E$" with the proportionality constant ρ. Similarly, if $\Delta E < 0$, $dx/dt = (-) x \cdot \sigma (1 - x) \cdot \rho (- \Delta E)$. In any case, we can get to $dx/dt = kx (1 - x) [-r_v + r_i mI]$, where $k = \sigma\rho$. ***This is how the rate equation for the new-introduced variable 'x' is derived!***

The SIR model governing this study is:
$dS/dt = \mu(1 - x) - \beta SI - \mu S$, $dI/dt = \beta SI - \gamma I - \mu I$, $dR/dt = \mu x + \gamma I - \mu R$, and $dx/dt = kx (1 - x) [-r_v + r_i mI]$.
Since $S + I + R = 1$, the system can be written as:
$dS/dt = \mu(1 - x) - \beta SI - \mu S$, $dI/dt = \beta SI - \gamma I - \mu I$, and

$dx/dt = kx\,(1 - x)\ [-r_v + r_i mI] = k\,r_v\,(1 - x)\ [-1 + \{r_i m / r_v\}\,I] = \kappa x\,(1 - x)\ [-1 + \omega I]$ taking $\kappa = k\,r_v = \sigma\rho\,r_v$ and $\omega = (mr_i / r_v)$.

Equilibrium points under the necessary conditions

For Equilibrium points, we compute:

$dI/dt = \beta.SI - \gamma.I - \mu.I = I\{\beta SI - \gamma I - \mu I\} = 0$ if, $I = 0$ or, $S = (\mu + \gamma)/\beta$
$dx/dt = \kappa x\,(1 - x)\ [-1 + \omega I] = 0$ with $I = 0$ gives $\kappa x\,(1 - x)\ [-1] = 0$,
which is true if $x = 0$, or $x = 1$.
$dx/dt = \kappa x\,(1 - x)\ [-1 + \omega I] = 0$ with $S = (\mu + \gamma)/\beta$ is true if
$x = 0$, or $x = 1$, or, $I = 1/\omega$.

Case I: $dS/dt = \mu(1 - x) - \beta SI - \mu S = 0$ with $I = 0$ and $x = 0$ gives $\mu - \mu S = 0$, or,
$\mu(1 - S) = 0$, which is true if $S = 1$.
This gives the first Equilibrium point: $\boldsymbol{\xi_1 = (S_1, I_1, x_1) = (1, 0, 0)}$.

Case II: $dS/dt = \mu(1 - x) - \beta SI - \mu S = 0$ with $I = 0$ and $x = 1$ gives $-\mu S = 0$, which is true if $S = 0$ since $\mu > 0$.
This gives the second Equilibrium point: $\boldsymbol{\xi_2 = (S_2, I_2, x_2) = (0, 0, 1)}$.

Case III: $dS/dt = \mu(1 - x) - \beta SI - \mu S = 0$ with $S = (\mu + \gamma)/\beta$ and $x = 1$ gives
$-S(\beta I + \mu) = 0$, or, $I = -\mu/\beta$ since, $S = (\mu + \gamma)/\beta$ cannot be 0.
This gives the Equilibrium point: $\xi = (S, I, x) = ((\mu + \gamma)/\beta,\ -\mu/\beta,\ 1)$, which has negative I, and thus is out of the domain / scope of the problem.

Case IV: $dS/dt = \mu(1 - x) - \beta SI - \mu S = 0$ with $S = (\mu + \gamma)/\beta = 1/R_0$ and $x = 0$ gives $\mu - \beta SI - \mu S = 0$
or, $\mu - I.\beta.[(\mu + \gamma)/\beta] - \mu.[(\mu + \gamma)/\beta] = 0$,
or, $\mu - I(\mu + \gamma) - \mu.[(\mu + \gamma)/\beta] = 0$,
or, $\mu - \mu.[(\mu + \gamma)/\beta] = I(\mu + \gamma)$,
or, $\mu[1 - [(\mu + \gamma)/\beta]] = (\mu + \gamma)I$,
or, $\mu[1 - 1/R_0] = (\mu + \gamma)I$.
Therefore, $I = [\mu/(\mu + \gamma)][1 - 1/R_0]$, which is valid only when $1 - 1/R_0 > 0$, or when $R_0 > 1$ (else $I = 0$ when $R_0 = 1$ with $S = 1$ which is already included in ξ_1, and I is negative when $R_0 < 1$).
So, we have $\xi_3 = (S_3, I_3, x_3) = (1/R_0,\ [\mu/(\mu + \gamma)][1 - 1/R_0],\ 0)$
or, $\boldsymbol{\xi_3 = (S_3, I_3, x_3) = (1/R_0,\ 1/\omega_0,\ 0)}$ **when** $\boldsymbol{R_0 > 1}$, where
$\omega_0 = [(\mu + \gamma)/(\mu)]\ /\ [1 - [1/R_0]]$ (notation given by the author).

Case V: $dS/dt = \mu(1 - x) - \beta SI - \mu S = 0$ with $S = (\mu + \gamma)/\beta = 1/R_0$ and
$I = 1/\omega$ gives $\mu(1 - x) - \beta(1/R_0)(1/\omega) - \mu(1/R_0) = 0$
or, $\mu(1 - x) = \beta(1/R_0)(1/\omega) + \mu(1/R_0)$
or, $\mu(1 - x) = \mu[\beta/(R_0\,\mu\,\omega)) + (1/R_0)]$
or, $1 - x = \beta/(R_0\,\mu\,\omega) + (1/R_0)$
or, $x = 1 - [1/R_0] - [\beta/(R_0\,\mu\,\omega)]$

or, $x = 1 - [1 / R_0] - [(\mu + \gamma) / \beta][\beta / (\mu \omega)]$ *since* $S = (\mu + \gamma) / \beta = 1/R_0$
or, $x = 1 - [1 / R_0] - [(\mu + \gamma) / (\mu \omega)]$ *when*
$1 - [1 / R_0] - [(\mu + \gamma) / (\mu \omega)] > 0$, *else x becomes negative, which does not make sense.*
or, when $[1 - [1 / R_0]] > [(\mu + \gamma) / (\mu \omega)]$
or, when $\omega > \omega_0$.
So, we have $\boldsymbol{\xi_4 = (S_4, I_4, x_4) = (1/R_0, \quad 1/\omega, \quad 1 - [1 / R_0] - [(\mu + \gamma) / (\mu \omega)])}$
when $\boldsymbol{\omega > \omega_0}$ ***with*** $\boldsymbol{R > R_0}$.

Therefore, the four equilibrium points for the system are: $\xi_1 = (S_1, I_1, x_1) = (1, 0, 0)$, $\xi_2 = (S_2, I_2, x_2) = (0, 0, 1)$, $\xi_3 = (S_3, I_3, x_3) = (1/R_0, 1/\omega_0, 0)$, which exists when $R_0 > 1$, *and* $\xi_4 = (S_4, I_4, x_4) = (1 / R_0, 1 / \omega, 1 - 1 / R_0 - (\gamma + \mu) / (\omega\mu))$, which exists when $R_0 > 1$, *and* $\omega > \omega_0$.

Stability Analysis – Extension of The Paper

The paper presents the stability analysis without proper mathematical foundation. So, as the extension of the paper, we have performed the Jacobian analysis of each of the equilibrium points in the 3 * 3 system for the stability analysis of each of the four presented equilibrium points.

Stability Analysis via linearization

Given that
$dS/dt = \mu(1 - x) - \beta SI - \mu S$
$dI/dt = \beta.SI - \gamma.I - \mu.I$
$dx/dt = \kappa x (1 - x) [-1 + \omega I]$

$$J(S, I, X) = \begin{bmatrix} -\beta I - \mu & -\beta S & -\mu \\ \beta I & \beta S - \gamma - \mu & 0 \\ 0 & \kappa x (1 - x)\omega & \kappa(1 - 2x) [-1 + \omega I] \end{bmatrix}$$

At Equilibrium Points

1. $\xi_1 = (S_1, I_1, x_1) = (1, 0, 0)$

$$J(1, 0, 0) = \begin{bmatrix} -\mu & -\beta & -\mu \\ 0 & \beta - \gamma - \mu & 0 \\ 0 & 0 & -\kappa \end{bmatrix}$$

Therefore, $(S_1, I_1, x_1) = (1, 0, 0)$ *is stable if* $\beta - \gamma - \mu < 0$, *or, when* $R_0 < 1$.

When $R_0 > 1$, $\beta - \gamma - \mu > 0$ *making* $(1, 0, 0)$ *unstable – saddle.*

2. $\xi_2 = (S_2, I_2, x_2) = (0, 0, 1)$

$$J(0, 0, 1) = \begin{bmatrix} -\mu & 0 & -\mu \\ 0 & -\gamma - \mu & 0 \\ 0 & 0 & +\kappa \end{bmatrix}$$

Therefore, $\xi_2 = (S_2, I_2, x_2) = (0, 0, 1)$ *unstable – saddle.*

3. $\xi_3 = (S_3, I_3, x_3) = (1/R_0, 1/\omega_0, 0)$ *when* $R_0 > 1$

$$J(1/R_0, 1/\omega_0, 0) = \begin{bmatrix} (-\beta/\omega 0) - \mu & (-\beta/R0) & -\mu \\ (\beta/\omega 0) & 0 & 0 \\ 0 & 0 & +\kappa((\omega/\omega 0) - 1) \end{bmatrix}$$

For eigenvalues of the Jacobian $J(1/R_0, 1/\omega_0, 0)$, we solve det (J - λI) = 0 to get:

$[\lambda - \kappa((\omega/\omega 0) - 1)]\ [\lambda^2 + \{\mu + (\beta/\omega 0)\}\lambda + \{\mu + (\beta/\omega 0)\}] = 0.$

The first eigenvalue $\lambda_1 = \kappa((\omega/\omega 0) - 1)$ is < 0 when

$(\omega/\omega 0) - 1 < 0,\ i.e.,\ when\ 0 < \omega < \omega 0$.

The two eigenvalues that come from the stated quadratic equation gives:

$\lambda = [-\{\mu + (\beta/\omega 0)\} \quad (+/-) \quad \sqrt{(\mu + (\beta/\omega 0))^2 - 4(\beta(\gamma + \mu)/\omega 0))}\ ] / 2$

Note that $\omega 0$ is a positive constant for $R_0 > 1$. So, both of these eigenvalues have negative real parts, no matter whether they are real valued, or complex.

Hence, the third equilibrium point, $\xi_3 = (S_3, I_3, x_3) = (1/R_0, 1/\omega_0, 0)$ *when* $R_0 > 1$, *is* ***stable*** **when** $\mathbf{0 < \omega < \omega 0}$, *whereas* ***unstable-saddle when*** $\boldsymbol{\omega > \omega 0}$.

4. $\xi_4 = (S_4, I_4, x_4) = (1/R_0, 1/\omega, 1 - [1/R_0] - (\gamma + \mu)/(\omega\mu))$ *when* $R_0 > 1$ *and* $\omega > \omega 0$ *(i.e., it exists when* ξ_3 *is unstable-saddle)*

$J(1/R_0, 1/\omega, x_4) =$

$$\begin{bmatrix} (-\beta/\omega) - \mu & (-\beta/R0) & -\mu \\ (\beta/\omega) & 0 & 0 \\ 0 & \kappa\{[1/R0] + (\gamma + \mu)/(\omega\mu)\}\{1 - [1/R0] - (\gamma + \mu)/(\omega\mu)\} & 0 \end{bmatrix}$$

For eigenvalues of the Jacobian $J(1/R_0, 1/\omega, 1 - [1/R_0] - (\gamma + \mu)/(\omega\mu))$, we solve det (J - λI) = 0 to get:

$$\lambda^3 + \{ (\beta / \omega) + \mu \}\lambda^2 + \{ \beta^2 / (R0\,\omega) \}\lambda$$

$$+ \{\mu\beta\kappa / \omega\}\{ [1 / R0] + (\gamma + \mu) / (\omega\mu)\}\{1 - [1 / R0] - (\gamma + \mu) / (\omega\mu)\} = 0$$

This equation could not be solved by us directly; Thus, we purpose the following method:
Plug in the given parameters for analysis by case by case. Then, use "bisection method" numerically to get the first real root; The first root is guaranteed to be real since it is a cubic equation, and complex roots always come in pairs. Then, we can get the quadratic factor by "matching the parameters" of the main cubic root equation (after plugging in the given parameters). This tells us whether the remaining quadratic roots will have complex or real roots. Then, use quadratic formula to obtain the remaining roots.

Analysis

Let's discuss the dynamics of disease prevalence and vaccination behavior in populations, emphasizing the significance of different equilibrium states and the emergence of various dynamical regimes in the κ–ω parameter plane.
We basically found four equilibriums ξ_1, ξ_2, ξ_3, ξ_4 and they are as follows :

1. $\xi_1 = (S_1, I_1, x_1) = (1, 0, 0)$ is called a disease free, pure non-vaccinator equilibrium When the basic reproduction number (Ro) of the disease is less than 1, ξ_1 is globally stable. In this scenario, each infected individual yields fewer than one secondary infection on average, leading to the eventual disappearance of the disease from the population. Therefore, there's no incentive for vaccination. This equilibrium experiments with the idea that there are multiple ways to eradicate a disease from a population and vaccination is not the only way. If enough people develop immunity to the disease and the basic reproduction number(Ro) is less than one the disease will eventually cease to exist globally and hence it is called a pure non-vaccinator equilibrium that is globally stable.

2. $\xi_2 = (S_2, I_2, x_2) = (0, 0, 1)$ is called the pure vaccinator equilibrium This equilibrium is always unstable due to the disincentive to vaccinate when coverage is high. When vaccination coverage is high, individuals may perceive that they are already protected by herd immunity, leading to a decline in vaccination rates.

3. $\xi_3 = (S_3, I_3, x_3) = (1/R_0, [\mu/(\mu + \gamma)][1 - 1/R_0], 0) = (1/R_0 , 1/\omega_0 , 0)$ is only locally stable equilibrium which means the population does not want to vaccinate and hence the disease is prevalent in the environment.

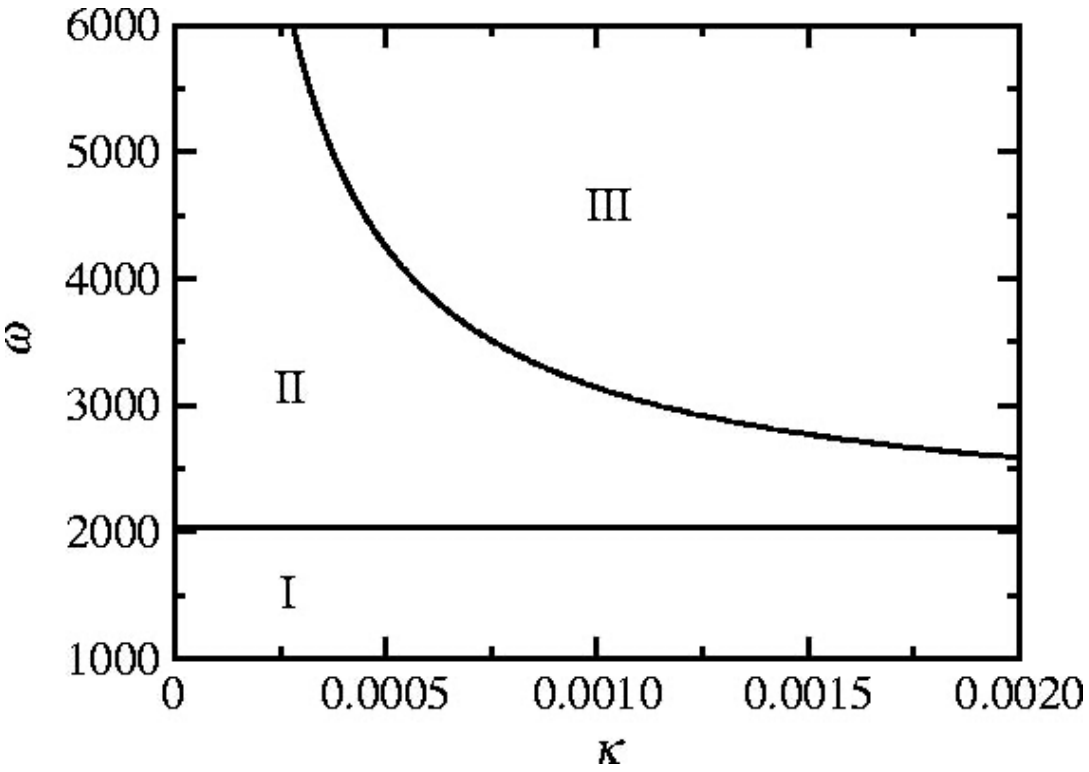
4. $\xi_4 = (S_4, I_4, x_4) = (1/R_0 , 1/\omega , 1 - [1 / R_0] - (\gamma + \mu) / (\omega\mu))$ only exits when Ro>1 and ω> ωo is again locally stable because vaccination rate does not keep up with the infection rate and eventually the vaccination rate and the disease in the population goes to a non-zero constant.

The SIX model that we are left with after everything is as follows:

$dS/dt = \mu(1 - x) - \beta SI - \mu S$

$dI/dt = \beta.SI - \gamma.I - \mu.I$

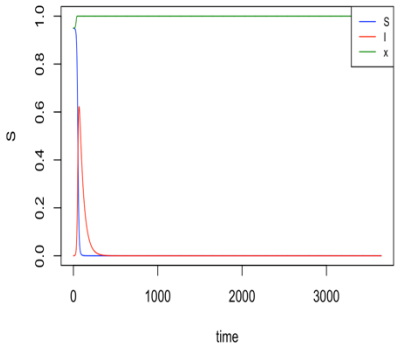
$dx/dt = \kappa x\ (1 - x)\ [\ -1 + \omega I\ ]$



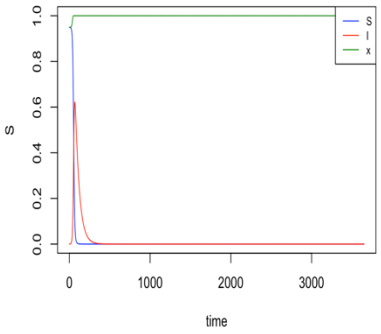
The graph above is the k-w parameter plane for the vaccination game with imitation dynamics, and the plane gets dissected into three regions.
Let's discuss what those regions are and how the stability of the equilibrium in those planes and what effects vaccination has on the population.

1. Region I ($0<\omega<\omega o$): In this region, the endemic, pure non-vaccinator equilibrium is stable, and no one chooses to vaccinate. The prevalence of the disease remains constant and non-zero.
2. Region II: In this region, the endemic, mixed equilibrium is stable, leading to stable oscillations in both the frequency of vaccinators and disease prevalence.
3. Region III: In this region, the mixed equilibrium destabilizes, leading to stable limit cycles. The frequency of vaccinators and disease prevalence oscillate in a repeating pattern over time.

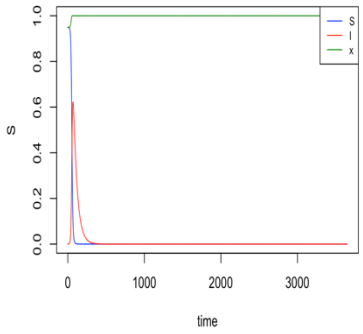
The Hopf curve can be seen as well, the Hopf curve separates regions where the system exhibits different types of behavior. Specifically, it separates regions where stable equilibria exist from regions where stable limit cycles occur.



w=6000

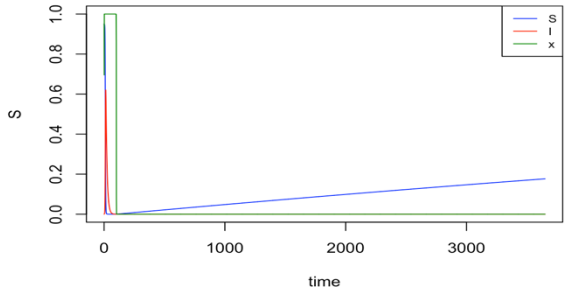


w=2500

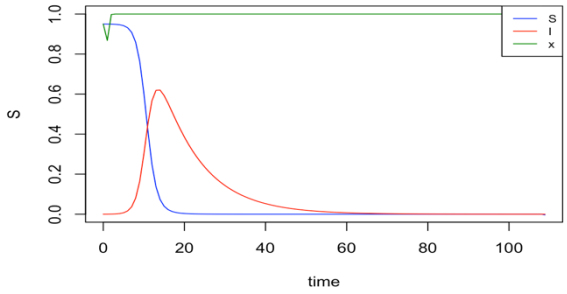


w=1000

The above graph is reproduced using the parameter values as following in order to produce a time-series of x ,1/μ=50 years is the recovery rate, 1/γ=10 days, Ro=10, k=0.001, with initial conditions as S=0.05, I=0.0001, x=0.95 is the frequency of vaccinators and disease prevalence.
Figure 1 has w=6000, Figure 2 has w=2500 and Figure 3 has w=1000. time-series that represents the frequency of vaccinator over time with respect to x and as you can see. For w=6000 when you start with a higher w parameter value it goes to a higher steady state and keeps oscillating between 0.4 and 0.8, for w=2500 it dips down and keeps oscillating between 0.1 and 0.3 for a while and then goes to 0.2vand for w=1000 it eventually exponentially very quickly goes to zero.
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1560180/)



w=5000, k=10



w=5000, k=5

The above graph is reproduced using the parameter values as following in order to produce a time-series of x ,1/μ=50 years is the recovery rate, 1/γ=10 days, Ro=10, k=0.001, with initial conditions as S=0.05, I=0.0001, x=0.95 is the frequency of vaccinators and disease prevalence.

The above graphs have been produced by changing the imitation rate(k) and there is clear relation between the imitation rate, frequency of vaccinators and disease prevalence.
This proves that the frequency of vaccinators increases as you increase the imitation number and hence the disease prevalence becomes negligible over time.

The interpretation of the time-series data helps simplify and understand the complex dynamics of vaccination behavior and disease transmission under different parameter settings, providing valuable insights into the stability and oscillatory behavior of the system in different regions.

Discussion

The introduction of a vaccination game with imitation dynamics offers insights into the complex dynamics of vaccine uptake. This model successfully reproduces several key features, including oscillations in vaccine uptake in response to disease outbreaks and the gradual recovery of vaccine uptake following a vaccine scare. Additionally, it highlights the importance of individual factors such as vaccination and disease prevalence rate. The factors Influencing oscillations in vaccine uptake are higher values of parameters k and w increase the probability and amplitude of oscillations in vaccine uptake. This suggests that individuals who are more prone to imitating others or who are more responsive to changes in disease prevalence are likely to exhibit greater fluctuations in vaccination behavior over time. Although the disease-free, pure vaccinator equilibrium (ξ_2) is not stable in the vaccination game with imitation dynamics, real-world populations often exhibit sustained high vaccine uptake over extended periods of time. This stability may be attributed to factors such as trust in medical authorities, mandatory vaccination policies. This model acknowledges that other factors beyond those considered, such as stochasticity, seasonality, and spatial structure, can influence epidemic dynamics. These factors may be crucial in understanding real-world vaccination dynamics and may need to be incorporated into more complex models. The application of game theory to vaccination policy holds promise for public health but is limited by the availability of suitable data. Understanding the interplay between disease prevalence, vaccine coverage, and individual vaccinating behavior remains a critical area of research, with game theory providing a valuable framework for addressing these complex dynamics and informing public health strategies.

In summary, the integration of game theory with epidemiological models offers a valuable approach for understanding and managing the population dynamics of vaccination behavior, with implications for improving public health outcomes.

References

1. Bauch, C. T. (2005). Imitation dynamics predict vaccinating behavior. *Proceedings of the Royal Society (2005); 272, 1669 – 1675.*
2. Chauhan, S., Misra, O.P., & Dhar, J. (2014). Stability Analysis of Sir Model with Vaccination. *American Journal of Computational and Applied Mathematics 2014; 4(1): 17 – 23.*
3. Scherer, A., & McLean, A. (2002). Mathematical models of vaccination. *British Medical Bulletin (2002); 62: 187 – 199.*

Code for the Graphs (written by Siddhant)

```
library(deSolve)

## Parameters
gam <- 1/10  # recovery rate
N <- 1  # population size
r0 <- 10     # basic reproduction number
mu <- 1/(50*365)  # death rate
bet <- r0*(gam+mu)/N
k <- 10 # imitation rate
w <-5000


## Initial conditions
state <- c(S=N-0.05, I=0.0001, x=0.95)  # Initial proportions

## Function defining the differential equations
vaccination_game <- function(t, state, parameters) {
  with(as.list(c(state, parameters)), {
    dS <- mu*(1-x) - bet*S*I - mu*S
    dI <- bet*S*I - gam*I - mu*I
    dx <- k*x*(1-x)*(-1 + w*I)
    return(list(c(dS, dI, dx)))
  })
}

## Parameters list
parameters <- list(gam = gam, bet = bet, mu = mu, w=w)

## Time points for solving the equations
times <- seq(0, 365*10, by = 1)

## Solve the differential equations
out <- as.data.frame(ode(y = state, times = times, func = vaccination_game, parms = parameters))

## Plotting
library(ggplot2)
plot(S ~ time, out, type = "l", col = "blue", ylim = c(0, N))
lines(I ~ time, out, col = "red")
lines(x ~ time, out, col = "green4")
legend("topright", c("S", "I", "x"), lwd = 1, col = c("blue", "red", "green4"), cex = 0.75)

  plot(I ~ S, out, type = "l", xlim = c(0, N), ylim = c(0, 5000))
```