

# Influence of Metapopulation traffic model with vaccination game approach to suppress the disease spreading on different graphs

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## Abstract

The SIR/V epidemic diffusion model is incorporated with a metapopulation traffic model for random walkers to study the effect of contagious disease for the evolutionary vaccination game approach. Each node in metapopulation designated a subpopulation where the individuals move from one node to another by random walk following different graphs; star, cycle, wheel and complete. The framework of human traffic flow induced by the epidemic in vaccination game is observed in one single season as well as generation by considering individual based risk assessment (IB-RA) strategy update rule for an individual either taking vaccination or not. We successfully built a new analytical framework and Multi Agent Simulation (MAS) model for metapopulation for a vaccination game combined with susceptible-infected-recovered (SIR) model to explore how different graphs of an underlying social network giving impact on the final epidemic size, vaccination coverage and average social payoff.

## 1. Introduction

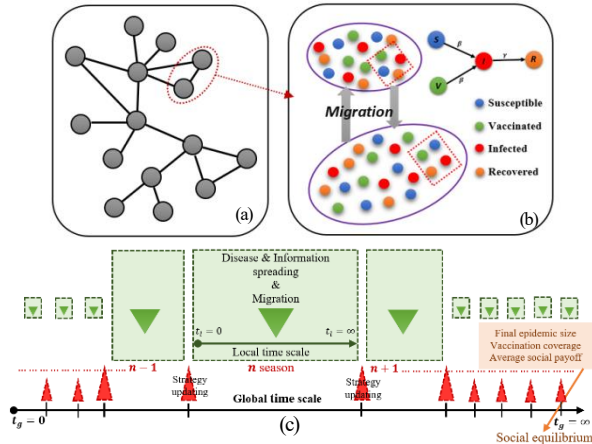
In ecosystem, the human traffic occurred in insecure local population for human activities like war, infectious diseases and natural disasters that make the total population into several patches (subpopulation) is called metapopulation [1], where, the individual walk randomly from one patch to another by following some graphs. Moreover, the connection between nodes are connected with unidirectional graphs to show the migration effect of the disease and information occurred concurrently in a node obtained by *Colizza et al.* [2]. At present, random movement of human is considered that have a fundamental mechanism for many disease diffusion on graphs that studied several researchers [3-6]. In order to explain the impact of human traffic or called migration in epidemiology, the voluntary vaccination game theoretical approach is deliberated to explain the decision making process to take self-protection before disease or quarantine in a safe place after being infected. Previously, many researchers [7-11] investigated the evolutionary game theoretical framework in epidemiological dynamics to study the human decision and the behavior of changing strategies in a population. Meanwhile, the decision about taking vaccination as well as migration, are

depending on one self-interest, risk, cost, consciousness and others behavior that helps people to decide the mortality and morbidity to lessen the risk of infections treat and also vaccination cost or random walk in a safe place. Most of the work related to the vaccination game is relied on multi-agent simulation (MAS) approach that is very powerful dynamics of a complex social system rather than a theoretical approach. Recently, *Kuga et al.* [12] presented an analytical compared with MAS approach epidemic vaccination game model that described the effect of imperfect vaccination with intermediate defense measure. Inspired by the investigation of the [13] work for metapopulation model in star, cycle and complete graphs, we developed metapopulation SIR/V epidemic model with disease diffusion for the vaccination game approach.

In current work, the analytical model for SIR/V on metapopulation is explored for four graphs by using the compartmental model with the mean field approach. The numerical simulation is analyzed for mathematical model and validated by a MAS approach to explore the impact of migration by drawing the 2D full phase diagrams.

## 2. Model

The susceptible-vaccinated-infected-recovered epidemic dynamic is considered on metapopulation for several graphs. Each graph has subpopulations denoted by respective nodes in the topology with well-mixed and infinite number of individuals. Meanwhile, the metapopulation is divided into  $N$  subpopulations named node, where individuals randomly walk from one node to another by maintaining the path of some graphs. In a single season, the susceptible and vaccinated individuals may become infected by the disease spreading rate  $\beta$  and the infected become recovered at the rate of  $\gamma$ . The vaccinated individuals are divided into two modules as perfect immune individuals and non-immune individuals by the vaccination effectiveness  $e$  ( $0 \leq e \leq 1$ ). For simplicity, we assumed constant migration rate  $m$  to expose the most fundamental idea of random walk.



**Figure 1.** Schematic diagram of (a) metapopulation model, (b) subpopulation, (c) total evaluation process for local ( $t_l$ ) and global ( $t_g$ ) time scale.

In metapopulation (Figure 1), the total population is distributed into  $N$  subpopulations, while the local population at respective nodes are,  $\rho_1, \rho_2, \rho_3 \dots \rho_N$ . The individuals in each subpopulation are classified into four states as susceptible ( $S_k$ ), vaccinated ( $V_k$ ), infected ( $I_k$ ) and recovered ( $R_k$ ) designated at the beginning of each season. As constraint,  $\rho_k = S_k + V_k + I_k + R_k$  and  $\rho_{Total} = \sum_{k \in N} (S_k + V_k + I_k + R_k) = 1$ , where,  $k=1, 2, 3, \dots, N$  and  $N$  is the maximum number of subpopulations. Throughout, we presume that only infected individuals can move randomly from one node to another, and individuals can update their strategy relied on own

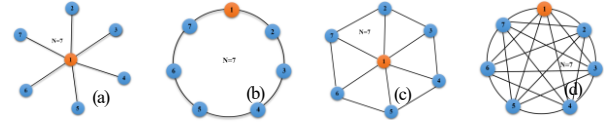
information. Because of, the fraction of infected individual performance as a key role in epidemiology as well as quarantine policy. The schematic of SIR/V (Figure 1) and the differential equations of metapopulation model into four different graphs; star, cycle, wheel and complete (Figure 2) based on update rule individuals based risk assessment (IB-RA) are as follows:

$$\dot{S}_k(t) = -\beta(\rho_k(t) - I_k(t))I_k(t) \quad (1)$$

$$\dot{V}_k(t) = -\beta(V_k(t) - eV_k(0))I_k(t) \quad (2)$$

$$\dot{I}_k(t) = \beta(\rho_k(t) - I_k(t))I_k(t) + \beta(V_k(t) - eV_k(0))I_k(t) - \gamma I_k(t) + MI(t) \quad (3)$$

$$\dot{R}_k(t) = \gamma I_k(t). \quad (4)$$



**Figure 2.** The metapopulation model of seven nodes ( $N=7$ ) for four different graphs: (a) star, (b) cycle, (c) wheel and (d) complete. Node 1 is considered as a hub nodes for all graphs.

The metapopulation dynamics for each subpopulation is presented in Table 1 and the migration fractions are depicted in

Table 2 as follows:

**Table 1.** SIR/V-UA migration dynamics for star, cycle, wheel and complete graph.

| Graphs(Nodes)    | Subpopulation dynamics   |
|------------------|--|
| Star( $k = 1$ )  | $\dot{\rho}_1(t) = \sum_{i \in N, i \neq 1} m \rho_i(t) - m \rho_1(t),$  |
| Star( $k > 1$ )  | $\dot{\rho}_k(t) = \frac{1}{N-1} m \rho_1(t) - m \rho_k(t)$  |
| Cycle            | $\dot{\rho}_k(t) = \frac{1}{2} m \rho_{k-1}(t) + \frac{1}{2} m \rho_{k+1}(t) - m \rho_k(t),$                             |
| Wheel( $k = 1$ ) | $\dot{\rho}_1(t) = \sum_{i \in N, i \neq 1} \frac{1}{3} m \rho_i(t) - m \rho_1(t),$                                      |
| Wheel( $k > 1$ ) | $\dot{\rho}_k(t) = \frac{1}{N-1} m \rho_1(t) + \frac{1}{3} m \rho_{k-1}(t) + \frac{1}{3} m \rho_{k+1}(t) - m \rho_k(t),$ |
| Complete         | $\dot{\rho}_k(t) = \sum_{i \in N, i \neq k} \frac{1}{N-1} m \rho_i(t) - m \rho_k(t),$                                    |

**Table 2.** SIR/V-UA model migration dynamics for star, cycle, wheel and complete graph.

| Graphs (Nodes)   | Migration equation ( $MI(t)$ )  |
|------------------|---|
| Star( $k = 1$ )  | $\sum_{i \in N, i \neq 1} m AI_i(t) - m AI_1(t)$  |
| Star( $k > 1$ )  | $\frac{1}{N-1} m AI_1(t) - m AI_k(t)$   |
| Cycle            | $\frac{1}{2} m AI_{k-1}(t) + \frac{1}{2} m AI_{k+1}(t) - m AI_k(t)$                           |
| Wheel( $k = 1$ ) | $\sum_{i \in N, i \neq 1} \frac{1}{3} m AI_i(t) - m AI_1(t)$                                  |
| Wheel( $k > 1$ ) | $\frac{1}{N-1} m AI_1(t) - m AI_k(t) + \frac{1}{3} m AI_{k+1}(t) + \frac{1}{3} m AI_{k-1}(t)$ |
| Complete         | $\sum_{i \in N, i \neq k} \frac{1}{N-1} m AI_i(t) - m AI_k(t)$                                |

At equilibrium, the total individuals are divided into four groups as; healthy and vaccinated (HV), infected and vaccinated (IV), healthy and non-vaccinated (called successfully free rider, SFR) and infected and non-vaccinated (called failed free rider, FFR). The corresponding fractions and payoff (relative cost) are illustrated in Table 3.

**Table 3.** Fraction of individuals and payoff structure

|          | Healthy & Vaccinated | Infected & Vaccinated | Healthy & Unvaccinated | Infected & Unvaccinated |
|----------|----------------------|-----------------------|------------------------|-------------------------|
| Payoff   | $-C_r$               | $-C_r - 1$            | 0                      | -1                      |
| Fraction | $HV_k(x, \infty)$    | $IV_k(x, \infty)$     | $SFR_k(x, \infty)$     | $FFR_k(x, \infty)$      |

The social average payoff and the transition probability affecting by the relative cost and based on the Fermi Function [14], the dynamical equation for individual based risk assessment is as follows:

$$\langle \pi \rangle = -C_r HV_k(x, \infty) - (C_r + 1) IV_k(x, \infty) - FFR_k(x, \infty) \quad (5)$$

$$\dot{x}_k = -HV_k(x, \infty) SFR_k(t, \infty) P(HV \leftarrow SFR)$$

$$-HV_k(x, \infty) FFR_k(t) P(HV \leftarrow FFR)$$

$$-IV_k(x, \infty) SFR_k(t) P(IV \leftarrow SFR) - IV_k(x, \infty) FFR_k(t) P(IV \leftarrow FFR)$$

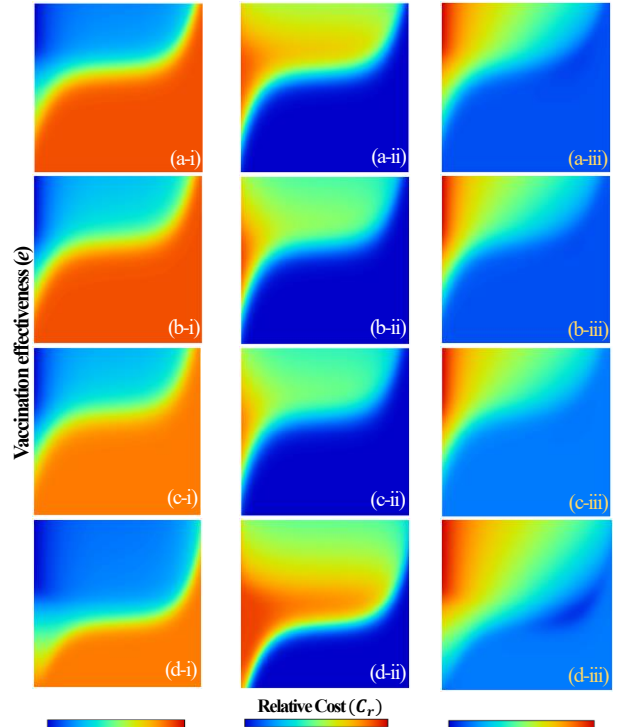
$$+ SFR_k(x, \infty) HV_k(t) P(SFR \leftarrow HV) + FFR_k(x, \infty) HV_k(t) P(FFR \leftarrow HV)$$

$$+ SFR_k(x, \infty) IV_k(t) P(SFR \leftarrow IV) + FFR_k(x, \infty) IV_k(t) P(FFR \leftarrow IV). \quad (6)$$

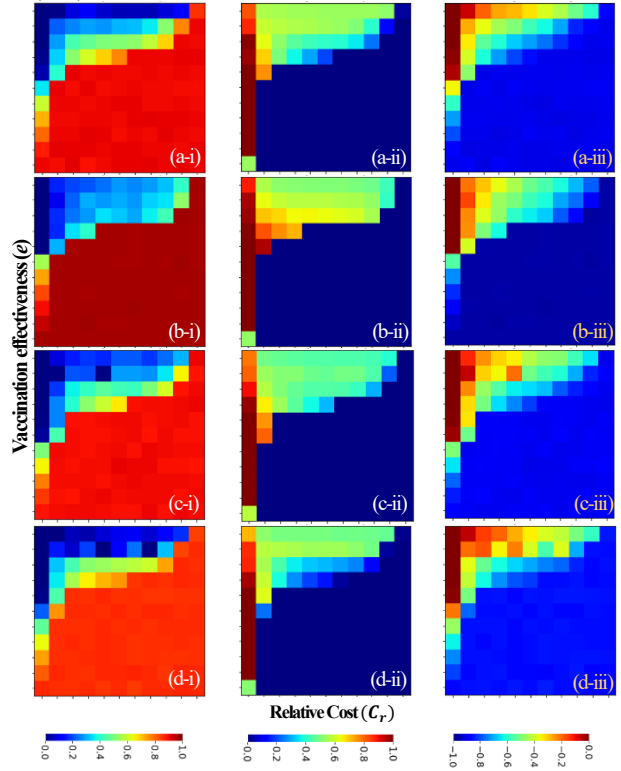
### 3. Result and discussion

The presented numerical results of the SIR/V on metapopulation model according to the concept of vaccination game theory explain the random walk induced by infection. To validate the propose model, we display the analysis of diffusion model by portraying the final epidemic size, vaccination coverage and average social payoff for both analytical and MAS approach. In figures 3 & 4, the subpopulation in the metapopulation model is displayed by the star graphs in figure (a-\*), the cycle graphs in figure (b-\*), the wheel graphs in figure (c-\*) and the complete graph in figure (\*-d). Meanwhile, figure (\*-i), (\*-ii) & (\*-iii) show the final epidemic size (FES); the fraction of individuals who infected and now recovered, vaccination coverage (VC); all individuals (both healthy and infected) who take vaccination and social average payoff (SAP) (eqn. 5), respectively.

From figure 3, the varying propensity from star to complete graph show the significant reduce of final epidemic sizes, (red to yellow).



**Figure 3.** The phase diagram of (a-\*) Star, (b-\*) Cycle, (c-\*) Wheel and (d-\*) Complete graph of (\*-i) FES, (\*-ii) VC and (\*-iii) SAP.



**Figure 4.** The MAS results of (a-\*) Star, (b-\*) Cycle, (c-\*) Wheel and (d-\*) Complete graph of (\*-i) FES, (\*-ii) VC and (\*-iii) SAP.

This monotonic declining tendency is happened because of the graphs properties: the isolated graph has none of links, each node (other than hub) of star graph has only one connection with hub node, in the case of cycle and wheel have two and

three edges respectively for each node, on the other hand, complete graph have maximum links according to the number of nodes.

Thus, it incurs that the network structure of complete graph can lessened the thread of infection considerably compared with other graphs. This is because every node is connected each other, which ensures the maximum number of places for migration, regardless being infected or not, i.e., it has maximal number of heading subpopulations.

To validate our theoretical framework, we conducted a series of numerical simulations based on the MAS approach ([7], [8]) in figure 4. In MAS approach, we presumed a finite population size of  $N=14000$  (2000 for each node). The contradicting point is observed for the case of cycle graph by comparing analytical and MAS results (figure 3(b-\*) & 4(b-\*)). The cycle graph displays worse situation compare with other graphs in MAS results. The cycle graph has no hub node, but the star, wheel and complete have the hub nodes surrounded by peripheral nodes. In MAS process the impact of hub node is very influential, due to the high density of vaccination is presented there. On the other hand, theoretical analysis is very superficial assumption than MAS approach that explore the differences.

#### 4. Conclusion

The intension of current work is to build a metapopulation migration model combined with vaccination game on star, cycle, wheel and complete graph as a prototype of complex network. We successfully established the respective evolutionary formulas with showing numerical results that validated by comparing with MAS results. It is exposed from the examine of different graphs, obviously, the complete graph shows the maximum improved results to reduce disease by comparing with star, cycle and wheel graph due to the number of large amount of edges in each node. Thus, migration can reduce the dangerous situation of disease in a subpopulation by taking vaccination or self-protection or even individuals or government can take quarantine policy.

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