

The vaccination game: insights on role of Fake-News Game Theory project

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Abstract—In this work we apply Evolutionary Game Theory to the vaccination dilemma, where individuals in a finite-size network voluntarily decide to uptake a perfectly efficient vaccine. Their choice depends on the adaptation that is fixed. The dynamics of an epidemics in such network is simulated by the means of a Gillespie Algorithm. Moreover, we model Fake-News spreading process using a basic complex contagion model, and see how and whether it affects the vaccination coverage.

We simulated an evolution of two 50×50 2-dim lattice networks for different costs of vaccination, different adaptation rules and the eventual presence of Fake-News spreaders.

We find that there might be a dependence on the outcome, but has to be further studied using longer, and more in numbers, simulations to avoid statistical fluctuations that appear to be quite relevant. However, it seems that the presence of Fake-News spreaders might play a role.

Index Terms—Epidemiology, Evolutionary Game Theory, Fake-news, Two-Dimensional lattice, Complex Contagion Model, Vaccination Game

I. INTRODUCTION

In 2020, COVID-19 pandemic definitely changed everyone's life, therefore epidemiology and its models started to play an important role in policy making. In particular, they can predict the fraction of infected [1] people in a network once both some parameters peculiar of the pathogen and the topology of the network are known. This is possible only if one approximates society as a network whose nodes are people. Being able to collect this information turns out to be useful to ensure administrations allocate enough resources to healthcare facilities and efficiently treat a certain amount of infected people.

A possible tool that can be exploited in preventing the spread of a disease and lower the number of infections is a vaccine. In addition, many actual debates mainly deal with the possibility to introduce a public coercion to take vaccine in order to maximize its uptake among the whole population. On the counterpart, some might object that coercion goes against individual's freedom, that is a fundamental principle on which a democracy is based on. However, the latter comes with a price: there may be individuals that decide to vaccinate or not depending on proselytism based on non-scientific facts. Therefore, assuming no coercion is possible, one should make

the vaccination coverage among the population as high as possible.

In order to model efficiently human behavior, a new branch has arisen in the very past few years: that is called sociophysics [2]. It mainly deals with applying mathematical and physical tools to different fields related to society, that is obviously different from the topics where they were firstly introduced. Based on the assumption that an individual is free to take or not a vaccine, our work discusses the so called "Vaccination Game" [3] applying both concepts of epidemiology and evolutionary game theory, tested in a 2-dim lattice network. In this work, we want to further investigate whether Fake-News spreaders eventually play a role in this game and affect the vaccine coverage, once having introduced them by the means of a complex contagion threshold model [4]. Basically, we defined as a spreader of a Fake News a node that when come in touch with any other node will convince it not to vaccinate. In addition, if many of these contacts occur successfully in a short amount of time, the other node will start to spread Fake-News itself. In order to pursue this goal, we simulated the spread of a given disease according to a compartmental $SIR - V$ model, by the means of an implementation of the Gillespie algorithm [5].

Any worthy results of this work can be further studied and better analyzed, also from a theoretical point of view, on more complex networks such as for instance Poisson, Free-Scale, Small-World, higher dimensional lattices, in order to understand where and how system dynamics at equilibrium will tend to. Moreover, once eventual effects of Fake-News spreaders in vaccine coverage are known, one may want to study and apply different countermeasures to them, such as introducing subsidies to people willing to take vaccine or awareness raising pro-vaccine campaigns.

II. METHODS

A. Compartmental Models - $SIR - V$

In an epidemiological model, nodes in a network (e.g. individuals) can be characterized into different groups (e.g. compartments) according to their actual state of the disease. Hence nodes can be labelled as:

- Susceptible: a node can contract a disease when it comes into contact with an infected node, according to some rate β .
- Infected: a node is infectious and can spread the disease to susceptible nodes.
- Recovered: a node recovers from the disease and acquires full immunity, according to some rate μ . It cannot be infected anymore, unless immunity wanes.
- Vaccinated: a node is vaccinated and has acquired immunity. Therefore it cannot contract the disease.

If we assume that there are no deaths nor births (closed population assumption) and a well-mixed population, that is to say everyone has the same probability to be infected, the differential equations that describe the flux of people between $SIR - V$ compartments are [1]:

$$\frac{ds}{dt} = -\beta \langle k \rangle si \quad (1)$$

$$\frac{di}{dt} = \beta \langle k \rangle si - \mu i \quad (2)$$

$$\frac{dr}{dt} = \mu i \quad (3)$$

$$\frac{dv}{dt} = 0 \quad (4)$$

where β is the *per contact transmissibility*, μ is the *recovery rate*: these are typical quantities of a disease. Moreover, $\langle k \rangle$ is the average number of contacts that an individual may have or, alternatively, it represents the average degree of the network. In addition, $s = S/N$, $i = I/N$, $r = R/N$, and $v = V/N$ are the fractions of susceptible, infected, recovered and vaccinated nodes over the whole population N , respectively. v is also known as *vaccination coverage*. Under these assumptions, it holds that $i + s + r + v = 1$.

The *basic reproductive ratio* $R_0 = \frac{\beta \langle k \rangle}{\mu}$ drives the dynamics of the system: when $R_0 \geq 1$ the infection will spread to the whole network, except for some statistical fluctuations that might lead to the early extinction of the disease. One can note that it depends both on quantities related to the disease (β, μ), and on the topology of the network ($\langle k \rangle$). Solving (4) and computing $R(t \rightarrow \infty)$, namely the number of infected nodes in the long-run, one can easily compute the *herd immunity threshold*. The latter is the least fraction of vaccinated nodes according to which $R(t \rightarrow \infty) = 0$. Above this threshold, epidemics is suppressed, on the contrary a disease will be able to spread to the whole network. According to statistical mechanics formalism, one observes a 2-nd order phase transition in $R_0 = 1$ for the prevalence of the disease (i.e. i/N) as $t \rightarrow \infty$.

B. Evolutionary Game Theory

Evolutionary game theory is the application of Game Theory that models the time evolution of a system, focusing especially on the dynamical change of the strategies chosen by different players. This tool comes handy to explain why sometimes we empirically observe systems at an equilibrium that differs from the ones we would expect simply applying GT framework.

We recall that a dilemma is defined as a situation wherein the choice each individual makes among their possible strategies does not accord with the preferred state from the social point of view. More formally, the Nash Equilibrium (NE) of the problem is not consistent with the social optimum. In a Public Good Game (PGG) there is a public good that can be restored only when moral-mind individuals cooperate and donate (*co-operators*). At the end, the public good result of donations is finally split among all players, including defectors. This implies that players have an incentive not to donate (*defectors*), but at the same time they want to obtain cooperative fruits brought about by the donations of others.

In this framework, let us introduce the so called "vaccination game", where both epidemiological concepts and dynamics of human decision making are applied. For the sake of simplicity, we assume the vaccine to be 100% efficient: a person that decides to be vaccinated, i.e. to *cooperate* (C), faces a vaccination cost $0 \leq C_r \leq 1$ and cannot be infected in any case. The vaccination "cost" implies a direct cost and the potential risk of side-effects and psychological negative-costs brought about by vaccination. On the other hand, one may choose to not vaccinate, or to *defect* (D), at *no* cost thus facing the possibility to be infected. We refer to these nodes as "*free riders*". Two possibilities now arise, depending on whether the node is infected or not at the end of the spreading process. If it contracts the infection, i.e. at the end of the epidemics season, the node belongs to the recovered compartment the cost to be paid is 1. Otherwise it might not contract the disease due to eventual herd immunity or early extinction of the disease, and this comes with no cost. Payoff matrix for this problem is depicted in table (I).

Obviously, a conflict between individual and social benefits arises, in which, every individual has to face a conflict: either avoiding vaccination and free riding, or everyone in the society taking the vaccine thus reaching the fair Pareto optimum. It is the best solution where everyone equally bears the cost to maintain public goods, that in this case is the herd immunity. This conflict explains us why we are allowed to mix evolutionary game theory and epidemiology: vaccination indeed can be viewed as a game on a complex social network. This specific dilemma is also known as "vaccination" dilemma [6].

	Not infected	Infected
Not Vaccined (D)	0	-1
Vaccined (C)	$-C_r$	—

Table I

PAYOFF MATRIX FOR THE VACCINATION GAME. WE ASSUMED A PERFECTLY EFFICIENT VACCINE: THEREFORE A NODE WHICH VACCINES CANNOT BE INFECTED, HENCE NO VALUE IS PRESENT.

The problem was modelled as it is shown in Fig.1. We assume that individuals in a network chooses its own strategy that can be either to vaccinate or not. Then, a given disease spreads in a network according to mathematical epidemiology dynamics. It is assumed that the immunity acquired by vaccination vanishes after this stage: this is realistic due to

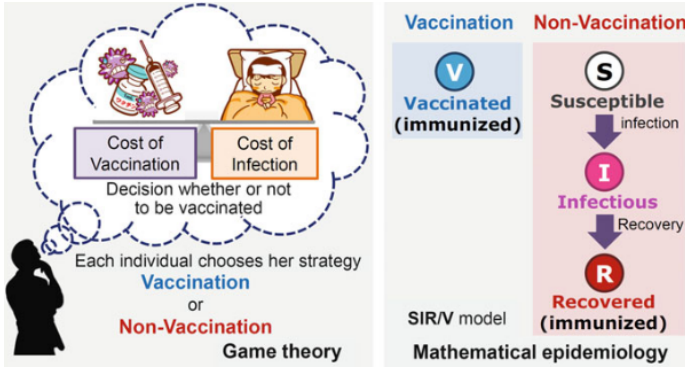


Figure 1. Our work considers both Epidemiological and Game Theory concepts. [6]

antibodies waning or to the disease genomic evolution, and indeed this is what happens every year with influenza. After the occurrence of epidemics every individual has to decide whether to vaccinate or not, depending on the comparison between its own payoff and other's, according to some strategy updating rules. Every season consists of two stages (see Fig.2) cyclically repeating: the *vaccination campaign* and the *epidemic season*. We assume that, changing many seasons, the system will have settled to equilibrium as can be seen in figure (3).

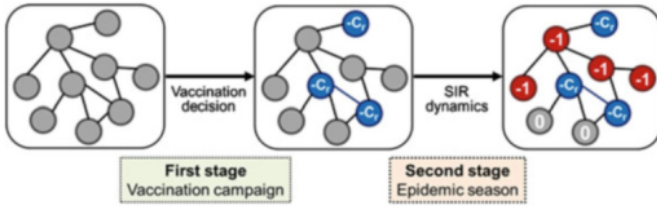


Figure 2. A season is composed by two stages, vaccination campaign and epidemic season. [6]

After one cycle, an individual examines again the vaccination decision-making at the beginning of next season based on some strategy update rule. We compared three different strategy adaptations: the first two were already present in literature [6], while the last one was introduced to take into account the eventual presence of Fake-News spreaders, by the means of a complex contagion model. At every vaccination campaign, each i -th node in the network picks randomly a j -th neighbor of itself and then, according to the strategy updating rule, computes the probability $P(s_i \leftarrow s_j)$, that is the probability for the node i to adopt the strategy s_j that node j played, given it previously chose the strategy s_i . Probabilities are computed depending on the updated rule as follows:

- Individual-Based Risk-Assessment (IB-RA) [6]: node i compares its own payoff π_i with the individual payoff π_j of node j . The probability is computed by the means of a Fermi-Sigmoid function:

$$P(s_i \leftarrow s_j) = \frac{1}{1 + e^{\frac{\pi_i - \pi_j}{\kappa}}} \quad (5)$$

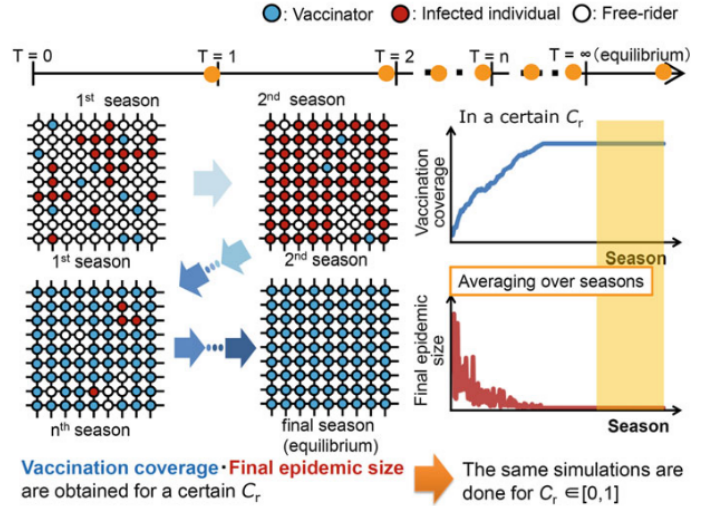


Figure 3. Every season is repeated many times until the system will reach an equilibrium. [6]

- Strategy-Based Risk-Assessment (SB-RA) [6]: node i compares its own payoff π_i with the average society payoff $\langle \pi_j \rangle$, resulting of adopting the strategy of node j . If node j has vaccinated, then $\langle \pi_j \rangle = -C_r$, otherwise it is proportional to the number of free riders that contracted the infection: $\langle \pi_j \rangle = 0 \cdot \frac{S}{N} + (-1) \cdot \frac{R}{N}$. Formally:

$$P(s_i \leftarrow s_j) = \frac{1}{1 + e^{\frac{\pi_i - \langle \pi_j \rangle}{\kappa}}} \quad (6)$$

- Strategy-Based Risk-Assessment (SB-RA) + Fake-News: node i picks randomly a neighbor j of itself. If j is a spreader of fake news, i will not vaccine no matter what. Otherwise, it will follow the update strategy rule (SB-RA). However, it comes to explain how to model a fake-news spreader and what are the effects on the nodes that come into contact with it, which is done later in II-C.

where κ is the *selection pressure*. If $\kappa \rightarrow 0$, i -th node will copy any strategy resulting in a higher payoff. For lower selection pressures, namely higher κ , individual is less sensitive to payoffs difference. Therefore there is chance that a node adopts the strategy that returned a lower payoff.

C. Complex Contagion model

Following epidemiological formalism, one may want to model viral spreading of information in a network as an epidemics spreading: indeed these processes behave in a very similar way. Epidemic models indeed can be adapted to social systems and this comes handy in our case. We used the so called complex contagion framework, since we are modelling the possible effects of multiple exposures to a source of Fake News.

Firstly, we need to introduce a quantity under the name of "dose" d , that answers to the question "how much infection" an infected node gives to other individuals after a successful

contact. Moreover, the *cumulated dose* $d_i(t)$, as suggested by the name, is the dose that node i -th has received at time t from other infected nodes.

Generally a complex contagion model is based on the following assumptions:

- A spreader of Fake-News is defined as a node whose *cumulated dose* d overcomes a certain threshold d^* .
- Every time a Fake-news spreader has a contact with a given node i , this contact can be successful with probability p . If the contact is successful, then the spreader gives node i a dose d , otherwise nothing happens.
- At every time step, that in our case is the first stage of every season, the cumulated dose of all nodes decreases by a fixed amount of quantity. This is done to take into account that if for a certain amount of time a node is not exposed to Fake-News, there is the possibility for it to "recover" even though being a Fake-News spreader, but only in the case when its cumulated dose is relatively low.

Note that the dose d resulting from successful contact can follow any distribution, and p , d^* are parameters of the model that are fixed.

D. Theoretical Expectations

Applying Evolutionary Game Theory to our problem, depending on the relative magnitude of elements in the payoff matrix, we can uniquely characterize a game and predict whether there will be a dilemma. Elements of the payoff matrix can be rescaled and compared to certain universal values, according to which one can tell to what class of games our problem belongs to. This theory is known as "universal scaling theory" [7], and is really similar to the "universality" concept of statistical mechanics. For the latter it was observed that, for systems large enough, some properties were independent of the dynamical details of the system and were shared among systems of the same class. The same argument can be applied to our framework: depending on the payoff matrix one is able to compute these universal values and, according to their relative magnitude, uniquely characterize the type of game of our problem.

Moreover, using some algebraic analysis we can also compute the equilibria of some observables in the system when playing such games repeatedly. These are indeed found by computing the eigenvalues of the Jacobian matrix describing the dynamics of the system, which depends on the average payoff in the system and consequently in the change of the fraction of people that decides to vaccinate at every season [3]. In our game the main observable we account for is the vaccination coverage, that is the fraction of nodes that decide to vaccinate or, in other words, the fraction of cooperators. In this way we are able to characterize also the dynamics of the system and predict its equilibria. According to the value of C_r our game can turn into three different classes:

- Trivial game: it is not a dilemma, therefore Nash Equilibrium coincides with the fair Pareto optimum where

everyone cooperates and vaccine. Also intuitively we can expect that this is achieved for lowest C_r .

- Prisoner's Dilemma: it is a dilemma. Fair Pareto optimum Equilibrium does not coincide with Nash Equilibrium, since network will tend to have all defectors. This is obviously achieved for high C_r , when the cost of vaccinations is almost as large as the one of being infected.
- Chicken: it is a dilemma, since the Nash Equilibrium for such system will settle to a state where cooperation and defection members exist in certain proportions. This scenario is called coexistence or polymorphic equilibrium: indeed agents will periodically alternate phases of cooperation and defections, keeping oscillating once having settled on a certain equilibrium fraction. This is achieved for intermediate values of C_r .

For all of these three classes, the initial fraction of cooperators is not important in the evolution of the system.

III. RESULTS

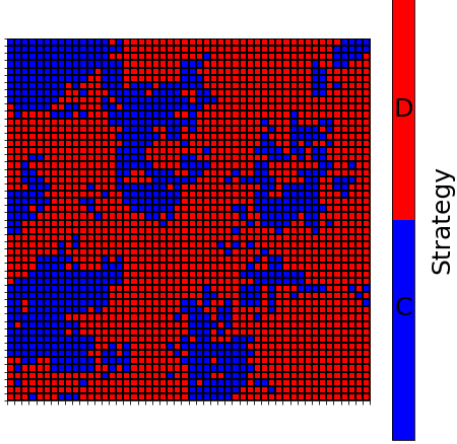
For the present study we used Google Colab interactive environment, which was running Python 3.6.9, and the package *networkx*[8] version 2.5. Simulations were performed implementing a Gillespie algorithm for this specific *SIR* – *V* model.

The network considered is a regular 2-dim graph of dimension 50×50 with no boundary conditions. Total the number of iterations is set to 200. We assume that already at the 100-th iteration the system would reach equilibrium, therefore all the results were the mean of last 100 iterations, even though this finding is empirically based. Nevertheless, we expect that the behaviour of the system should have already ended its noisiest phases and lost its dependency on the starting conditions. Finally, quantities such as vaccine coverage, fraction of nodes infected, maximum number of infected and average social payoff for different C_r obtained from different simulations, were mediated when referring to a unique update rule. $C_r \in [0, 1]$ in step of $\Delta C_r = 0.05$. In our work, we set social pressure to $\kappa = 0.1$: individual in *most* cases will choose the strategy that returns a higher payoff.

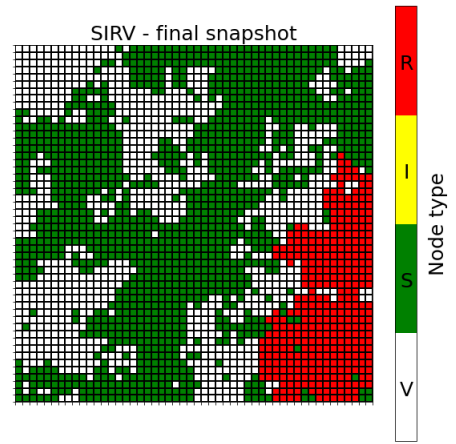
In addition, we set $\beta = 1$ that is to say every contact was successful, and the recovery rate to $\mu = 0.4$. With regards to the fake-news spreaders simulations, probability for a contact to be successful was $p = 0.5$, while the threshold was set to an amount of dose of $d^* = 2$. Every successful contact would increase the dose by $d = 1$ and, at every season, all nodes saw their cumulated dose decreasing by 0.25. In this way the number of fake-news spreaders would oscillate, around the starting value, without diverging. Number of initial fake news spreaders is set to $N_0 = 1$ and $N_0 = 2$, results for these adaption rules were labelled respectively as "*FN_1*" and "*FN_2*".

IV. DISCUSSION

From Fig. 4, one can clearly spot clusters that are theoretically grounded theory[6]. They appear due to the topology of the network and to the strategy adaptation rule. Every node



(a) During the vaccination campaign stage, every node makes a decision to either vaccinate. In blue there are cooperators (C), i.e. nodes that vaccinate, and in red defectors (D), i.e. the ones who decide to free ride.



(b) Green nodes are susceptible nodes, yellow infected ones (at the end of dynamics there will be none), red the ones that were infected and white the vaccinated ones.

Figure 4. Typical snapshots of the system after the vaccination campaign, when strategies have been updated, and after SIR-V dynamical stage.

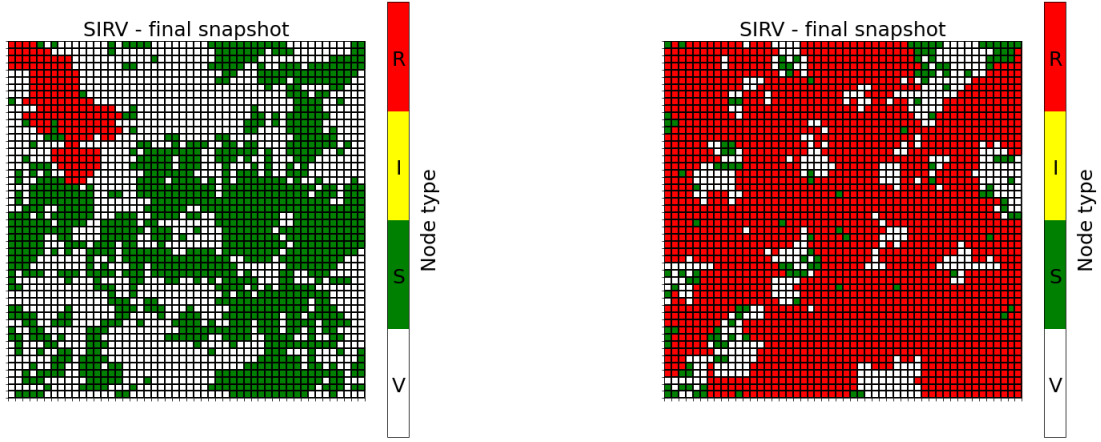
indeed can imitate strategies that are played by neighbors of it: a node in the center of a cluster will play almost surely the same strategy that characterizes its own cluster. Moreover, one can see that their size depends on the vaccination cost C_r (see Fig. 5): the higher it is, the more we expect defectors cluster to increase their size. The converse holds, too. These most generic statements follow from results in [9], where more pictures for different costs C_r and iterations have been uploaded. Moreover we would expect that clusters behavior would depend also on the strategy adaptation: nodes indeed change their strategy according to their nearest neighbors. For IB-RA dynamics develops slowly and, considering the case where a node is surrounded by vaccinated nodes, most likely it will imitate them. On the contrary for SB-RA adaption rule, nodes can change their strategy even if surrounding neighbors are all either defectors or cooperators. All these considerations directly follow from percolation theory framework, that can be applied to our problem. From a theoretical point of view the existence of a giant component and the possibility for the disease to spread all along the network, given some nodes might be vaccinated and act as "obstacles", is directly related to it. Including Fake-News spreaders must be treated carefully, however, since we might be introducing some sort of discontinuities in our problem. Theoretical implications about it are far from the goals of this report.

Figures in 6 explain us that our simulations were run correctly, since the fraction of people that vaccine behaves as expected: for very low C_r the system settles to the Nash Equilibrium that coincides with the fair Pareto optimum where everyone cooperates. On the other hand, for high vaccine

cost and after a low number of iteration one can easily see that everyone defects. In between we mainly note that for $C_r = 0.8$ the system has reached equilibrium and oscillations occur with respect to a fixed value, that we assumed to be the equilibrium fraction of cooperators/defectors. Averaging over a large number of iterations, we are therefore able to obtain this value thanks to the law of large numbers. On the contrary, for $C_r = 0.5$ we still observe fluctuations. However, the just aforementioned fixed value seems to increase with respect to time. This actually tells us that even after 100 iterations the system dynamics have not reached equilibrium, therefore the assumption that we could average over last 100 iterations was not totally correct for some values of C_r . Hence, our simulations had to be run for more time since some transiency was still present.

Averaging the final results of the two simulations runs, we obtain what is represented in Fig. 7. Results are coherent from what it is already present in the literature, with the disclaimer that both simulations were run for a shorter time, and the number of simulations was less. Nevertheless results are meaningful. This is a possible reason why we observe such statistical oscillations shown in picture.

However, one can observe that for all strategies of adaptations, and very low C_r , the fraction of people that vaccines is the largest ($C - trivial$ class). Increasing C_r , however, leads the curve related to IB - RA to a plateau that is present up to $C_r \sim 0.8$. On the contrary, the other curves show very strong oscillations as we already stated, but still being above IB - RA result. This is a very important results, since SB - RA based adaptations rules lead to a larger fraction



(a) Final snapshot after 47-th season of the simulation of epidemics and $C_r = 0.1$ and $SB - RA$ adaptation rule.

(b) Final snapshot after 47-th season of the simulation of epidemics and $C_r = 0.9$ and $SB - RA$ adaptation rule.

Figure 5. Intermediate snapshots of the final epidemics spread in the network for different for different vaccination costs. They refer to the same simulation (seed set to 10) and after 47 seasons.

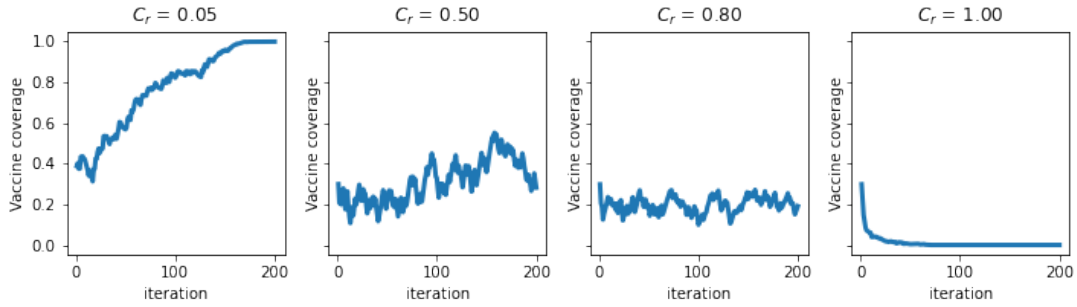


Figure 6. Vaccine coverage for each timestep using Strategy-Based Risk-Assessment (SB-RA) adaptation rule.

of cooperators. Socially speaking, in order to increase the vaccine coverage, a government should run awareness raising campaigns to make individuals be sensitive to the payoff of the whole society, rather than leaving them comparing its own payoff with their nearest neighbors. This is specially valid for intermediate C_r , when dealing with *Chicken* class of problems. Presence of Fake-News spreaders does not affect so much the vaccine coverage, despite the curves tend to lower as number of initial spreader increase. For higher values of C_r (*PD* class) curves collapse into a unique one, and the presence of Fake-News spreaders is not relevant.

Fraction of final infected people seems to depend only on the type of adaptation rule we used as a base, whether it is either $IB - RA$ or $SB - RA$. The same argument can be pointed out also for the maximal fraction of infected people: the higher the peak of the prevalence of the disease, the more pressure to the hospitalization facilities is present. This is why it should be as low as possible. $SB - RA$ seems to lead to

results that are closer to the social optimum.

One last argument worth to be noted is that the average payoff society scales linearly with respect to the vaccination cost for $SB - RA$. This can be due to the fact that $SB - RA$ indeed takes into account the average social payoff when a node has to update the strategy, but it is worth to be noted that all curves for $SB - RA$ almost coincide. Indeed it does not show any dependence on the initial number of Fake-News spreaders.

V. CONCLUSION

Results we have obtained so far are coherent with literature, and we used this fact as benchmark for the goodness of the simulation. However this was strongly affected by the fact that sometimes system did not reach its equilibrium: it can be a reason such large fluctuations are present. Moreover, for further works one could change the type of network and see how topology affects these results for different adaptations

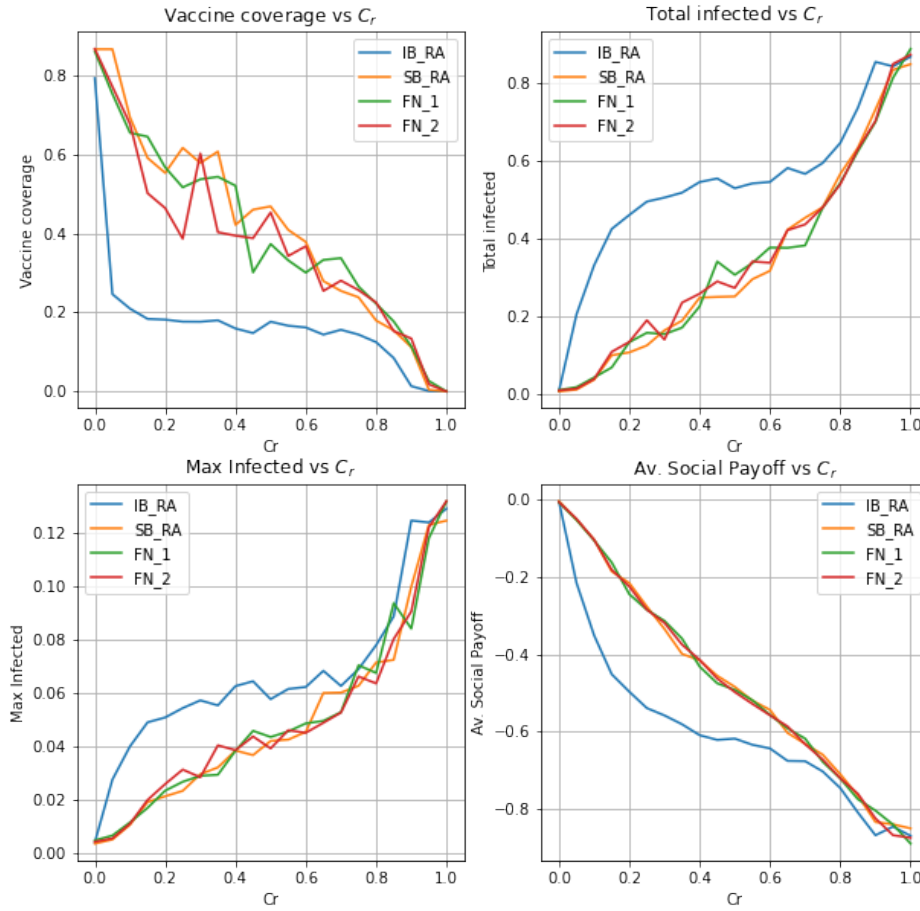


Figure 7. These results were obtained by making the average between of two simulations that were run.

rules. The latter ones can be modified, too. The choice of 2-dim lattice was made for the sake of simplicity, in addition it could be easily represented on a 2×2 grid with colors to highlight how clusters evolve in time, but in principle network can be of any kind. Indeed one possible improvement would be to see to compute clustering coefficients and homophily, or any other cluster-related metrics, and see its dependence on the type and on the size of the network. This can be studied using statistical mechanics formalism and percolation theory.

Introducing Fake-News spreaders, according to our modelling, does not seem to affect our results in a strong way. So there are two possible explanations for it: either the model was implemented correctly but the topology of the network did not allow a realistic spreading of Fake-News, or they are not so relevant in a vaccination game. We would slightly tend to the first possibility. They indeed affect only the vaccination coverage, but it is needed to understand whether they are only statistical fluctuations or they really play a role. Obviously, a

deeper sight on literature should be given, in order to tune and use more realistic parameters, such as probability of success per contact p , dose threshold d^* and so forth, for our problem.

Moreover, herd immunity threshold value strongly depends both on the network and on the disease. Nevertheless it is quite always reached for low vaccination costs, that is why the risk perception correlated to vaccination has to be low as possible or, conversely, there should be some subsidies from side of the government to decrease vaccination cost. Finally, another interesting topic would be to apply our Fake-News modelling on more complex models that modify the payoff matrix, in such way to take into account the eventual failure of the vaccine or eventual presence of state subsidies, which in turn were already developed in literature.

REFERENCES

- [1] A. Pagano and A. Nicolai, "Lecture Notes of Data Epidemiology," 2020, accessed: 01-11-

2021. [Online]. Available: <https://github.com/AlicePagano/Lecture-Notes-of-Life-Data-Epidemiology/blob/main/main/main.pdf>
- [2] J. Tanimoto, "Evolutionary Games with Sociophysics Analysis of Traffic Flow and Epidemics," 2018.
 - [3] F. Bai, "Uniqueness of Nash equilibrium in vaccination games," *Journal of Biological Dynamics*, vol. 10, pp. 395–415, 2016.
 - [4] C. C. V. M. P. Pastor-Satorras, R. and R. e. a. Vespignani, A. Pastor-Satorras, "Epidemic processes in complex networks," *American Physical Society*, vol. 87, pp. 925–979, 2015.
 - [5] A. Nicolai, "Vaccination game - game theory project," https://github.com/andrybicio/EGT_VaccinationGame, 2021.
 - [6] J. Tanimoto, "Fundamentals of Evolutionary Game Theory and its Applications," 2015.
 - [7] Z. Wang, S. Kokubo, M. Jusup, and J. Tanimoto, "Universal scaling for the dilemma strength in evolutionary games," *Physics of Life Reviews*, vol. 14, pp. 1 – 30, 2015. [Online]. Available: <http://www.sciencedirect.com/science/article/pii/S1571064515000949>
 - [8] A. A. Hagberg, D. A. Schult, and P. J. Swart, "Exploring network structure, dynamics, and function using networkx," in *Proceedings of the 7th Python in Science Conference*, G. Varoquaux, T. Vaught, and J. Millman, Eds., Pasadena, CA USA, 2008, pp. 11 – 15.
 - [9] A. Nicolai, "Vaccination game - images and results repo," <https://drive.google.com/drive/folders/1GWZvID2Vc4hqI09DgHqAgbKkE9k89xX1?usp=sharing>, 2021.