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► **To cite this version:**

Eitan Altman. The vaccination Game in Susceptible-Infected-Susceptible (SIS) networks with multipopulations. Game Theory for Networks (Gamenets) 2021, Dec 2021, Virtual, France. hal-03484177

HAL Id: hal-03484177

<https://inria.hal.science/hal-03484177>

Submitted on 16 Dec 2021

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The vaccination Game in Susceptible-Infected-Susceptible (SIS) networks with multipopulations

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Abstract. We model in this paper the multipopulation vaccination game over a fully connected graph. Each player decides whether to purchase a vaccine or not, and if they do, then they further decide which vaccine to purchase among a finite number of vaccine producers. The players need not be indistinguishable. A potential consumer belongs to a risk type that characterizes how important it is for them to be vaccinated. The cost of a vaccine may depend on the demand, on the cost of the production, and on the consumer's class. We prove the existence of an equilibrium within pure policies in the general multipopulation case. We further derive some properties of the equilibria in the case of a single risk-class.

Keywords: Vaccination Game, Multipopulation

1 Introduction

Vaccination has turned out to be a major prevention method to fight both biological epidemics [14] as well as malware attacks [4, 17, 13]. Like many other viral pandemics, there is discrimination between the victims of the epidemics, and different infected persons may develop the disease in different forms or of degree of severity. But unlike other epidemics, getting infected with covid is correlated with belonging to some well defined risk groups such as sex, age group, other diseases etc. We call these groups sub-populations or risk classes. Members of each sub-population have similar properties and are assumed to be interchangeable. The knowledge of the above correlation has permitted decision makers to better treat higher risk groups and to avoid giving inappropriate treatments to specific risk groups.

In this vaccination game, each node in the network is a player faced with the decision of whether to buy a vaccine or not. We assume that any consumer may purchase any vaccine within some finite set of available candidates. If they buy a vaccine then they are immuned and do not infect themselves, nor other players.

We show that this game is equivalent to a crowding game (but not to a congestion game, as is the case for a single population [15]) and has therefore an

equilibrium within pure strategies. We then identify the structure of equilibrium policies.

The structure of the paper is as follows. After a short Introduction, we present the model in Section 2. We recall the mean field approximation of the health quasi stationary probability distribution and model the health and the risk states. We then model the actions and the costs as a function of each vaccine and of the different risk-state (after averaging over the the health states that are assumed to be in the quasi stationary regime). The main results appear in Section 3. Further structural characterisation are derived for the spetial case of one population in Section 4. A concluding Section ends this paepr.

2 The model

2.1 Background: Quasi-stationary infection probability

We consider the Susceptible-Infected-Susceptible (SIS) compartment model on a non-directed graph. A node on this graph represents a (potntial) consumer of a vaccine. The total number of nodes is denoted by N . The total number of consumers that decide to purchase the vaccine is given by n_v .

Let $V_i(t)$ denote the event that node i is infected at time t . S and I stand for the health state of a node: I is infected and S stands for Susceptible. $v_i(t)$ is the expectation of the indicator of (or simply the probability of) this event and A_{ij} is the incidence matrix. Its value is 1 if there is a link between node j and note i . Otherwize its value is zero. We assume that $A_{ij} = A_{ji}$. In the malware application, it means that the links are bi-directional. In the applications to pandemics propagation, this means that a node i is a potential contact of nofe j if and only if node j is a potential contact of node i .

The following holds:

$$\frac{dv_i(t)}{dt} = -\delta v_i(t) + \beta E \left[(1 - V_i(t)) \sum_{j=1}^N A_{ij} V_j(t) \right] \quad (1)$$

where δ is the rate of healing at an infected node, and β is the rate at which a susceptible node becomes infected by a contact with an infected neighbour. For any nodes i and j , we have $E[V_i(t)V_j(t)] \geq v_i v_j$ [5]. Hence for all i ,

$$\frac{dv_i(t)}{dt} \leq -\delta v_i(t) + \beta(1 - v_i(t)) \sum_{j=1}^N A_{ij} v_j(t)^T \quad (2)$$

The NIMFA mean field approximation v' is defined as the solution of (2) when replacing the inequality with an equality. The vector v' is a bound on the quasi stationary vector v and it becomes tight as the initial number of nodes N tends to infinity, see [4, 9, 15].

Let $\tau = \beta/\delta$ be the virality constant.

Proposition 1. $v(t) = 0$ is a stationary solution of (2). Assume throughout that all nodes are interconnected; i.e. all entries of the incident matrix are 1. $v = 0$ is the only solution of (2) if $\tau < 1/N$. A second symmetric vector solution whose entries are denoted by v_∞ is obtained when $\tau > 1/N$. It is given by

$$v_\infty = \frac{\tau N - 1}{\tau N} = 1 - \frac{1}{\tau N} \quad (3)$$

and it is called the quasi stationary solution.

Proof. We obtain the quasi stationary solutions by equating the time derivative to 0. Indeed, we get

$$v_\infty = 1 - \frac{1}{1 + \tau A v_\infty}$$

which implies

$$v_\infty = 1 - \frac{1}{1 + \tau N v_\infty} = \frac{\tau N v_\infty}{1 + \tau N v_\infty}$$

We conclude that

$$1 = \frac{\tau N}{1 + \tau N v_\infty}$$

thus getting condition (3).

2.2 States and actions

We assume that the system is already in its quasi stationary regime which implies that the health states S and I of an individual are not used as part of a feedback control.

There are several ways in which one could obtain a multipopulation model. For example, it could be through the topology of the underlying network or through different time scales: a set of states such that every two nodes in the set are quickly reachable from a node are said to be from the same sub-population [15, 10]. Below we introduce another classification into risk types according to the cost. This is motivated by risk states in covid and we say that all nodes with a similar cost have the same risk state. Risk state may stand for genre, age, other health problems etc. = We consider competition both between producers of vaccines as well as between consumers of vaccines. There are M vaccine producers and K risk classes of consumers. In this paper we study the competition between consumers of various risk-types; the competition is induced by given cost functions of the vaccine producers. We do not study here how these functions are formed, which would lead to price formation issues.

The action in this game for a consumer is a number m between 1 to $M + 1$; action m then stands for purchasing a vaccine from producer m . In addition, action $M + 1$ stands for not purchasing any vaccine.

The state in this game is given by the combination of a local component k which stands for the risk state of the player, and a global component \mathbf{n} . \mathbf{n} is a matrix of dimension $(M + 1) \times K$. $n(m, k)$ is the number of players of type k that choose vaccine of producer m , $m = 1, \dots, M$. Let $n(M + 1)$ be the number of consumers who do not vaccinate. Thus $n(M + 1) + n_v = n$.

2.3 The cost

The cost of type m vaccine is given as a function $C(m, k, n(m))$. The cost is to be understood in a wide sense. It is not just the monetary cost but may include also the risk of complications; which is why the cost depends on the consumer type k . The cost of type m vaccine is assumed to be a function of the total number $n(m)$ of individuals that purchase type m vaccine.

Remark 1. [15] study a similar game but the model there restricts to a single type of consumer and of vaccine. the vaccination comes at a fixed cost C that does not depend on the demand for the vaccine. Note that (3) implies that v is monotone increasing.

A node that invests in a vaccine is assumed not only to acquire resistance against the virus but also not to carry the virus anymore and thus to stop being contagious. We assume that all n nodes are initially connected (the incident matrix has one in all links) and thus if the number of nodes who purchase a vaccine is n_v then we are left with a fully connected graph with $n(M+1)$ nodes.

3 Main result: a multipopulation equilibrium in pure strategies

The multipopulation game with multi-vaccine types that we have defined can be seen to be equivalent to the congestion game defined in Milchtech [6]. This class of games is known today as crowding games where as the term "congestion game" is used for games as defined in [11]. A crowding game is concerned with a network of parallel links all with a common source and a common destination. Players are atomic and each has to decide what link in the parallel link network to choose. A player belongs to one of K types. The cost for routing an agent through a given link is allowed to depend on the total load on that link, but this cost function may vary depending on the player (or on the class it belongs to). On the other hand, the contribution of a player to congestion in a link depends only on the total load on the link, and not on the class it belongs to. Nor is it a function of the class k of any other player in the network. The vaccine game is indeed equivalent to a crowding game in which link m corresponds to buying a vaccine of type m and where the choice $m = M+1$ corresponds to not purchasing any vaccine.

From the equivalence of this game to the vaccine game, we conclude the main result:

Theorem 1. *The multipopulation game has an equilibrium within pure policies in the multipopulation game.*

4 Further structure in the single population case

4.1 Existence of a potential

We next derive the structure of policies in the case of a single risk class. We delete the risk-class from the notation. The cost functions for any player to

purchase a type m vaccine is given by $C(m, n(m))$, it thus depends on the total number of consumers that choose vaccin m . This is seen to be equivalent to a congestion game which describes routing games between atomic players. There is a restriction in these games that the cost of choosing to route through a given path should only depend on how many agents use that route and should not depend on other characteristics which are agent specific. Under this condition as well as the monotonicity of C in its second argument, the game is known to have a potential [11]. The potential of this game is given by

$$pot(\mathbf{n}) = \sum_{m=1}^{M+1} pot(\mathbf{n}, m) \quad \text{where} \quad (4)$$

$$pot(\mathbf{n}, m) = \sum_{\ell=1}^{n(m)} C(m, n(m))$$

This allows us to conclude that any local minimum of the potential is an equilibrium in the original game [12]. This further implies that the game has an equilibrium in pure policies. Furthermore, the equilibrium can be obtained by solving best response algorithms in a finite number of iterations.

4.2 Threshold equilibrium policies.

A map u from the set of states to the set of actions is said to be a multi-policy. An equilibrium is a multi-policy from which no unilateral deviation is profitable for any player.

We present conditions in this section for equilibria policies to be of threshold type.

Definition 1. *A threshold policy for a player with a threshold value (n, q) , where n is an integer number and q is a nonnegative real number smaller than 1, is a policy that vaccinates if the number of players who are vaccinated is lower than n , and it does not vaccinate if the number of vaccinated is above n . At n the individual randomizes so that with probability q it vaccinates.*

Definition 2. *A symmetric multistrategy is said to be of a threshold type with parameter (n, q) if each player uses a threshold policy with that parameter.*

We restrict here to single type m of vaccine and a single type k of consumers. Each player has to decide whether to buy a vaccine or not. We shall assume that $C(n) - v(n)$ is increasing in n . This is the case in particular when C is taken to be a constant (corresponding to the cost of a vaccination).

Theorem 2. *Assume that n is the smallest integer such that $v(n) \geq C(n)$, i.e. when n purchase one vaccination each, then the cost $C(n)$ per vaccination is lower than the cost for getting infected by the virus. Then $v(\ell) > C(\ell)$ for all $\ell > n$ and $v(\ell) < C(\ell)$ for all $\ell < n$. Hence there is a symmetric threshold equilibrium multipolicy with parameter (n, q) for some q .*

Sketch of proof: Denote by $z = n + q$ the threshold policy with parameter (n, q) . We observe that if all players use a symmetric threshold policy z then the best response policy $z' = n' + q'$ for a player, say player i , is a threshold policy, monotonely decreasing in z . The Proof then follows Tarski fixed point Theorem [16].

Remark 2. i) Note that the equilibrium need not be unique. Indeed, this is the case if the symmetric equilibrium is not in pure policies.

ii) A detailed proof of Theorem 2 can be adapted from the proof of Theorem 1 in [2].

5 Conclusion

Many free riding phenomena and competition may occur during pandemics. For fixed policy of health authority (in case of biological viruses) or of regulation bodies (in the case of e-viruses), individuals may respond in a cooperative or a non cooperative way. At a higher level, there may or there may not be cooperation and coordination between regulation bodies or public health institutions. we have started working on modeling these phenomena so as to better provide incentives to pursue cooperative behavior. This is important in view of the fact that the Covid 19 pandemic has had very different impacts in different countries- (less than 5 victims per 100000 in some countries (China, New Zealand, Australia) and more than a hundred in others (USA, France, Italy). In this paper we have studied the source of non-cooperation in the use of vaccines.

We focused on the game between potential consumers of vaccines who may be tempted not to vaccinate themselves thus adopting a free riding behavior. We modeled further the impact of pricing strategies of the producers of the vaccines on the equilibrium. We established existence of an equilibrium within pure policies. We obtain further structure of equilibria for the case of a single risk class.

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