

# THE SPREAD OF AN EPIDEMIC: A GAME-THEORETIC APPROACH

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ABSTRACT. We introduce and study a game-theoretic model to understand the spread of an epidemic in a homogeneous population. A discrete-time stochastic process is considered where, in each epoch, first a randomly chosen agent updates their action trying to maximize a proposed utility function, and then agents who have viral exposures beyond their immunity get infected. Our main results discuss asymptotic limiting distributions of both the cardinality of the subset of infected agents and the action profile, considered under various values of two parameters (initial action and immunity profile). We also show that the theoretical distributions are almost always achieved in the first few epochs.

## 1. INTRODUCTION

### 1.1 OVERVIEW OF THE PAPER

The primary motivation that fuels our work in this paper is the need to understand how an infectious disease spreads through a homogeneous population comprising intelligent, pragmatically thinking individuals who decide upon their actions (such as distancing oneself from possibly infected acquaintances via voluntary confinement to one's home) on a day-to-day basis, with the aim to maximize their respective *utility functions*. The key novelty of our work lies in being able to capture, via our model, the fact that the population we consider is made up of rational beings referred to as *agents* or *players*. We emphasize here the need for investigation in understanding the spread of a contagion through a population whose members are not just helpless entities exposed to the infection at the whim of nature alone (see §1.2 for a brief discussion of the existing literature on models devised for studying the spread and control of epidemics, based on game theory).

Our model is firmly based on the premise of game theory, constituting a population  $N = \{1, 2, \dots, n\}$  of  $n$  agents, each of whom is allowed to choose from a set  $A = [0, 1]$  of available *actions*. Choosing action 0 is equivalent to the agent confining themselves to their home and coming in contact with no other agent, whereas choosing action 1 is tantamount to the agent going about their day as usual, with no restrictions imposed. An *action profile*  $a_N = (a_1, \dots, a_n)$  is an element of the set  $A^n$ , with  $a_i$  indicating the most recent action undertaken by agent  $i$ , for each  $i \in N$ . The agents are represented by the vertices of an undirected weighted graph, and the *interaction* between agent  $i$  and agent  $j$ , for distinct  $i, j \in N$ , is captured by the weight  $g_{i,j} \in [0, 1]$  of the edge connecting the

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vertices  $i$  and  $j$ . We further endow agent  $i$ , for each  $i \in N$ , with an *immunity power*  $\tau(i) \in (0, 1)$ . We consider a discrete-time stochastic process indexed by  $\mathbb{N}_0$ , the set of all non-negative integers. At the beginning of the  $t$ -th *epoch* of time, for each  $t \in \mathbb{N}_0$ , an agent  $v_t$  is chosen uniformly randomly out of  $N$  and permitted to update their action. The chosen agent decides upon their action by taking stock of the *state* the process is in at the beginning of that epoch, and their own *utility function*, both of which are formally defined in §2. We mention here that the state  $S_t$  of the process, at the start of epoch  $t \in \mathbb{N}_0$ , is made up of two crucial components: (i) the set  $I(S_t)$  comprising all the agents who are infected at the beginning of epoch  $t$ , (ii) and the action profile  $a_N(S_t)$  of the agents at the beginning of epoch  $t$ .

The process mentioned above shall, henceforth, be referred to as the *stochastic virus spread process* (SVSP). In addition, we shall consider, for some of our preliminary investigations of the SVSP, a *deterministic virus spread process* (DVSP) (see §2 for a more formal definition) in which the sequence  $\underline{v} = (v_t : t \in \mathbb{N}_0)$  of agents is specified fully (i.e. the agent  $v_t$  chosen to update their action at the start of epoch  $t$ , for each  $t \in \mathbb{N}_0$ , is predetermined, and *not* random).

The principal questions we aim to answer in this work are those concerning the limiting distribution of the infected set  $I(S_t)$  and the limiting distribution of the action profile  $a_N(S_t)$  of all agents concerned, as  $t \rightarrow \infty$ , provided such limits exist. Such questions are pertinent not just theoretically, but also from a very practical perspective in that, in any country, the departments under the federal government that are tasked with overseeing the provision of healthcare for the population must be able to reliably predict the approximate proportion of citizens to get infected in the long run (i.e. when the epidemic has continued for a considerably long duration). This is necessary because such knowledge can aid in the decision of how much resources (medicines and medical equipment, hospital beds etc.) to set aside for the treatment of infected patients in the long run. The investigation of the limiting behaviour of the action profile  $a_N(S_t)$  as  $t \rightarrow \infty$  goes on to reveal how, when such a limit exists, individuals in a population typically tend to behave once the epidemic has prevailed for a sufficiently long time.

## 1.2 A BRIEF REVIEW OF PERTINENT LITERATURE

The classical *compartmental models* of epidemiology (see [5] for a comprehensive survey) date as far back as the early 1900s (see [34]). Some of the most notable ones out of these are *Susceptible-Infectious-Removed* (SIR) model (see [17]), the *Susceptible-Infectious-Susceptible* (SIS) model (see [13]) and the *Susceptible-Exposed-Infectious-Removed* (SEIR) model (see [1]). In the recent years, *network models* have become more popular, with the vertices or *nodes* of a network representing the individuals of a population under consideration, and the edge between any two distinct nodes denoting the relationship or interaction between the two individuals those nodes represent, in such models (for instance, see [30], [33], [9], [16], [23], [26], [38], [36], [4], [10], [6] etc.).

We now begin a discussion of research articles that are closely aligned in flavour with our work in this paper. We begin with [2], which investigates a game for a continuum of non-identical players evolving on a finite state space, with their heterogeneous interactions with other players represented via a *graphon* (viewed as the limit of a dense random graph). A player's transition rates between the states depend on their control and the strength of their interaction with other players. Sufficient conditions for the existence of Nash equilibria are studied in [2], and the existence of solutions to a continuum of fully coupled forward-backward ordinary differential equations characterizing the Nash equilibria is proved. In [39], spectral properties of graphons are used to study stability and sensitivity to noise of deterministic SIS epidemics over large networks. In particular, the presence of additive noise in a linearized SIS model is considered and a noise index is derived to quantify the deviation from the disease-free state due to noise.

In the next couple of paragraphs, we focus on citing a few of the articles out of the vast literature that concerns itself with applying the theory of mean field games to the study of the spread of an epidemic throughout a population. In [3], motivated by models of epidemic control in large populations, a *Stackelberg mean field game* model between a principal and a mean field of agents evolving on a finite state space is considered, with the agents playing a non-cooperative game in which they can control their transition rates between states to minimize individual costs. An application is then proposed to an epidemic model of the SIR type in which the agents control their interaction rate and the principal is a regulator acting with non pharmaceutical interventions. In [24], a mean-field game model in controlling the propagation of epidemics on a spatial domain is introduced, with the control variable being the spatial velocity (introduced at first for the classical disease models, such as SIR), and fast numerical algorithms based on proximal primal-dual methods are provided. In [25], a mean-field variational problem in a spatial domain, controlling the propagation of a pandemic by the optimal transportation strategy of vaccine distribution, is investigated. In [32], an agent's decision as to whether to be socially active in the midst of an epidemic is modeled as a mean-field game with health-related costs and activity-related rewards. By considering the fully and partially observed versions of this problem, the role of information in guiding an agent's rational decision is highlighted. In [31], how the evolution of an infectious disease in a large heterogeneous population is governed by the self-interested decisions (to be socially active) of individual agents is studied based on a mean-field type optimal control model. The model is used to investigate the role of partial information on an agent's decision-making, and study the impact of such decisions by a large number of agents on the spread of the virus in the population.

In [7], a mean-field game model is proposed in which each of the agents chooses a dynamic strategy of making contacts, given the trade-off of gaining utility but also risking infection from additional contacts. Both the *mean-field equilibrium strategy*, which assumes that each agent acts selfishly to maximize their own utility, and the *socially optimal strategy*, which maximizes the total utility of the population, are computed and compared with each other. An additional cost is also included as an incentive to the agents to change their strategies, when computing the socially optimal strategies. The *price of anarchy* of this system is computed to understand the conditions under which large discrepancies between the mean-field equilibrium strategies and the socially optimal strategies arise, which is when intervening public policy would be most effective. In [11], a mean field game model of SIR dynamics is proposed in which players choose when to get vaccinated. It is shown that this game admits a unique mean-field equilibrium that consists of vaccinating aggressively at a maximal rate for a certain amount of time and then not vaccinating, and it is shown that this equilibrium has the same structure as the vaccination strategy that minimizes the total cost. A very similar problem is studied in [12] that focuses on a virus propagation dynamics in a large population of agents, with each agent being in one of three possible states (namely, susceptible, infected and recovered) and with each agent allowed to choose when to get vaccinated. It is shown that this system admits a unique symmetric equilibrium when the number of agents goes to infinity, and that the vaccination strategy that minimizes the social cost has the same threshold structure as the mean field equilibrium, though the latter has a shorter threshold. In [14], the newborn, non-compulsory vaccination in an SIR model with vital dynamics is studied, with the evolution of each individual modeled as a Markov chain and their decision to vaccinate aimed at optimizing a criterion depending on the time-dependent aggregate (societal) vaccination rate and the future epidemic dynamics. The existence of a Nash mean field game equilibrium among all individuals in the population is established. In [18], techniques from the mean field game theory are used to examine whether, in an SIR model, egocentric individuals (i.e. whose actions

are driven by self-interest when it comes to getting vaccinated) can reach an equilibrium with the rest of the society, and it is shown that an equilibrium exists. The individual best vaccination strategy (with as well as without discounting) is completely characterized, a comparison is made with a strategy based only on overall societal optimization, and a situation with a non-negative price of anarchy is exhibited. In [19], individual optimal vaccination strategies in an SIR model are analyzed. It is assumed that the individuals vaccinate according to a criterion taking into account the risk of infection, the possible side effects of the vaccine and the overall epidemic course, that the vaccination capacity is limited, and that the individual discounts the future at a given positive rate. Under these assumptions, an equilibrium between the individual decisions and the epidemic evolution is shown to exist. In [37], a model of agent-based vaccination campaign against influenza with imperfect vaccine efficacy and durability of protection is considered. The existence of a Nash equilibrium is proved and a novel numerical method is proposed to find said equilibrium. Various aspects of the model are also discussed, such as the dependence of the optimal policy on the imperfections of the vaccine, the best vaccination timing etc.

In [15], a general mathematical formalism is introduced to study the optimal control of an epidemic via incentives to lockdown and testing, and the interplay between the government and the population, while an epidemic is spreading according to the dynamics given by a stochastic SIS model or a stochastic SIR model, is modeled as a principal–agent problem with moral hazard. Although, to limit the spread of the virus, individuals within a given population can choose to reduce interactions among themselves, this cannot be perfectly monitored by the government and it comes with certain social and monetary costs for the population. One way to mitigate such costs and encourage social distancing, lockdown etc., is to put in place an incentive policy in the form of a tax or subsidy. In addition, the government may also implement a testing policy in order to know more precisely the spread of the epidemic within the country, and to isolate infected individuals. It is verified via numerical results that if a tax policy is implemented, the individuals in the population are encouraged to significantly reduce interactions among themselves, and if the government also adjusts its testing policy, less effort is required on the part of the population to enforce social distancing, lockdown upon itself, and the epidemic is largely contained by the targeted isolation of positively-tested individuals. In [8], a model for the evolution of sociality strategies in the presence of both a beneficial and costly contagion is investigated, and a social dilemma is identified in that the evolutionarily-stable sociality strategy is distinct from the collective optimum (i.e. the level of sociality that would be best for all individuals) – in particular, the level of social interaction in the former is greater (respectively less) than the social optimum when the good contagion spreads more (respectively less) readily than the bad contagion. Finally, we cite [35], which provides a state-of-the-art update on recent advances in the mean field approach that can be used very effectively in analyzing a dynamical modeling framework, known as a continuous time Markov decision process, for epidemic modeling and control.

### 1.3 ORGANIZATION OF THE PAPER

The model that we investigate in this paper, along with all the pertinent definitions, has been described formally in §2, although we did allude to it briefly in §1. §2 also includes some observations and lemmas concerning the the deterministic virus spread process (also mentioned previously in §1). The main results of this paper, namely Theorems 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10 are stated in §3, along with relevant discussions regarding the conclusions drawn from them. Simulations exploring the cardinality of the infected set for the first several epochs of the process, thereby yielding good approximations to the limit that it converges to, are given in §6. A summary of what we have been

able to achieve in this paper, along with directions of research on this as well as related topics that we wish to pursue in the future, is provided in §7.

We would like to emphasize to our readers that we have included the proofs of Theorem 1, Theorem 2, and Theorem 7 in the main body of the paper, immediately following their respective statements in §3. We have done so in order to illustrate some of the most fundamental ideas used in our proof techniques. However, we have deferred the proofs of the remaining main results to §B and §D in the Appendix, to keep the paper as uncluttered as possible for the reader. Our aim is to ensure that our readers fully understand the key steps of the analysis carried out to prove our results, without being burdened with technical details every step of the way.

## 2. FORMAL DESCRIPTION OF THE MODEL

Recall, from the second paragraph of §1.1, the brief introduction to the model we consider in this paper. Here, we formalize the model by providing mathematical definitions to the crucial quantities involved in it.

The process described in §1.1 is said to be in the *state*  $S = (I, a_N)$  if  $I \subseteq N$  denotes the set of infected agents and  $a_N$  denotes the action profile at that time. Given a state  $S$ , we denote by  $I(S)$  the corresponding set of infected agents, and by  $a_{\hat{N}}(S) = (a_i(S) : i \in \hat{N})$  the tuple in which  $a_i(S)$  represents the action of the  $i$ -th agent for all  $i \in \hat{N}$ , for any subset  $\hat{N}$  of  $N$ . In particular, if  $\hat{N} = N \setminus \{j\}$ , we abbreviate the notation  $a_{N \setminus \{j\}}(S)$  by  $a_{-j}(S)$ , and for any  $a \in A$ , we denote by  $(a \vee a_{-j}(S))$  the tuple  $(a_1(S), \dots, a_{j-1}(S), a, a_{j+1}(S), \dots, a_n(S))$ . We denote by  $\mathcal{S}$  the set of all possible states.

The viral exposure  $r_i(S)$  that agent  $i$  is subjected to, when the process is in state  $S$ , is defined as

$$r_i(S) = \begin{cases} \left( \frac{\sum_{j \in I \setminus \{i\}} g_{ij} a_j(S)}{\sum_{j \in N \setminus \{i\}} g_{ij} a_j(S)} \right) & \text{if } \sum_{j \in N \setminus \{i\}} g_{ij} a_j(S) \neq 0, \\ 0 & \text{if } \sum_{j \in N \setminus \{i\}} g_{ij} a_j(S) = 0. \end{cases}$$

For an intuitive understanding of viral exposure, consider the interpretation that  $a_j(S)$  determines how much (say, how many units of time), the  $j$ -th individual goes out at state  $S$ , and  $g_{ij}$  represents the amount of interaction  $i$  has with  $j$  when both are outside. Therefore,  $g_{ij} a_j(S)$  is the amount of interaction the  $i$ -th individual will have with the  $j$ -th individual when they both are outside. Now, the denominator captures the fact that with more uninfected people roaming around, the amount of interaction an individual does with an infected person proportionally reduces, and so does their chance of being infected.<sup>1</sup>

We assume that an individual  $i$  gets infected if  $a_i r_i(S) > \tau$ . For a justification of the same, note that the viral exposure  $r_i(S)$  of an individual  $i$  does not take care of the precaution (through staying at home) taken by  $i$ . However, the amount of virus individual  $i$  receives will naturally depend on the amount they go out (that is,  $a_i$ ), together with the effective amount of virus present outside in  $i$ 's network (that is,  $r_i(S)$ ). Therefore, the product of  $r_i(S)$  and  $a_i$  measures the total amount of virus that  $i$ 's body receives when  $i$  chooses  $a_i$ . One could also potentially see this product being interpreted as follows: with the maximum possible risk of exposure being  $r_i(S)$ , if the  $i$  th individual

<sup>1</sup>One can probabilistically interpret the model by assuming that for any individual  $j$ ,  $a_j$  is the probability that they go out, and  $\frac{g_{ij}}{\sum_{j \in N \setminus \{i\}} g_{ij}}$  is the probability that individual  $i$  interacts with individual  $j$  when they both are out. Then,  $r_i(S)$  is the probability that individual  $i$  interacts with an infected person, conditional on  $i$  goes out (that is,  $a_i = 1$ ).

does not go out at all (Read  $a = 0$ ) then they are not exposed at all, whereas if they choose to fully go out (Read  $a = 1$ ) then they get exposed to the max possible amount which is  $r_i(S)$ . Now, since the immunity power  $\tau$  measures the maximum amount of virus that an individual's body can withstand, this implies that an individual  $i$  would be infected if  $a_i r_i(S) > \tau$ .

Next, we introduce the utility function of an agent. The utility of an agent  $i$ , when the process is in state  $S$ , is defined as

$$u_i(S) = \begin{cases} 1 + f(a_i(S)) & \text{if } i \notin I(S) \text{ and } a_i(S)r_i(S) \leq \tau(i), \\ f(a_i(S)) & \text{if either } i \in I(S) \text{ or } a_i(S)r_i(S) > \tau(i) \end{cases} \quad (2.1)$$

where  $f : [0,1] \rightarrow [0,1]$  is a strictly increasing function. Intuitively, if agent  $i$  is neither already infected during the current epoch (which is indicated by the condition  $i \notin I(S)$ ) nor runs the risk of being infected in the next epoch (which is indicated by the condition  $a_i(S)r_i(S) \leq \tau(i)$ , i.e. their action multiplied by the viral exposure they have been subjected to does not exceed their immunity power), they enjoy a 'reward' of amount 1 in addition to the utility  $f(a_i(S))$  that they receive because of their chosen action (note that the strictly increasing nature of  $f$  ensures that the more they go out in society, the more utility they get). Else, they are deprived of such a reward and must settle for the utility value  $f(a_i(S))$ .<sup>2</sup>

We now formally describe how agent  $i$  responds if they are chosen to update their action at the beginning of an epoch when the system is in state  $S$ . We call this the *best response* by agent  $i$  at state  $S$ , denoted  $b_i(S)$ , and it is defined as

$$b_i(S) = \operatorname{argmax}_{a \in [0,1]} u_i(I(S), (a \vee a_{-i}(S))). \quad (2.2)$$

In words, this is the set of actions  $a$  by agent  $i$  that allow them to maximize their utility function (note that the utility function, as defined in (2.1), is a function of the state, and the state here constitutes  $I(S)$  as the infected set and  $(a \vee a_{-i}(S))$  as the action profile).

The following lemma summarizes the best response of an agent at a state depending on whether or not they are infected at that state. It, in particular, says that the best response always exists and is unique.

**Lemma 1.** *Let  $i \in N$  be an agent and  $S \in \mathcal{S}$  be a state. Then,*

$$b_i(S) = \begin{cases} 1 & \text{if } i \in I(S), \\ 1 & \text{if } i \notin I(S) \text{ and } r_i(S) = 0, \\ \min \left\{ 1, \frac{\tau(i)}{r_i(S)} \right\} & \text{if } i \notin I(S) \text{ and } r_i(S) \neq 0. \end{cases}$$

**Proof:** We provide the proof by distinguishing three cases as considered in the statement of the lemma.

**Case 1.**  $i \in I(S)$ .

By (2.1),  $u_i(I(S), (a_i, a_{-i}(S))) = f(a_i)$ . As  $f$  is an increasing function, their best response is

$$b_i(S) = \operatorname{argmax}_{a_i \in [0,1]} f(a_i) = 1.$$

**Case 2.**  $i \notin I(S)$  and  $r_i(S) = 0$ .

Since  $r_i(S) = 0$ ,  $a r_i(S) \leq \tau(i)$  for all  $a \in [0,1]$ , and hence by (2.1),  $u_i(I(S), (a, a_{-i}(S))) = 1 + f(a)$  for all  $a \in [0,1]$ . As  $f$  is an increasing function, this implies  $b_i(S) = 1$ .

<sup>2</sup>One can interpret the (negative) reward as the cost of the viral infection.

**Case 3.**  $i \notin I(S)$  and  $r_i(S) > 0$ .

Consider the quantity  $\frac{\tau(i)}{r_i(S)}$ . It follows from (2.1) that  $u_i(I(S), (a, a_{-i}(S)))$  is increasing in  $a$  in both the regions  $\left[0, \min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}\right]$  and  $\left(\min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}, 1\right]$ . The maximum value of  $u_i(I(S), (a, a_{-i}(S)))$  when  $a$  lies in the region  $\left[0, \min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}\right]$  is  $1 + f\left(\min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}\right)$  and that when  $a$  lies in the region  $\left[\min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}, 1\right]$  is  $f(1)$ . Because  $\tau(i) > 0$ , we have  $\frac{\tau(i)}{r_i(S)} > 0$ . This, together with the fact that  $f$  is strictly increasing, implies  $f\left(\min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}\right) > 0$ . Hence,  $1 + f\left(\min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}\right) > 1$ . Additionally, as  $f(1) \leq 1$ , we have  $1 + f\left(\min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}\right) > f(1)$ . Therefore,  $u_i(I(S), (a, a_{-i}(S)))$  will be uniquely maximum at  $\min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}$  implying  $b_i(S) = \min\left\{1, \frac{\tau(i)}{r_i(S)}\right\}$ . Combining all these, we have the following form of  $b_i(S)$ .

$$b_i(S) = \begin{cases} 1 & \text{if } i \in I(S), \\ 1 & \text{if } i \notin I(S) \text{ and } r_i(S) = 0, \\ \min\left\{1, \frac{\tau(i)}{r_i(S)}\right\} & \text{if } i \notin I(S) \text{ and } r_i(S) \neq 0. \end{cases}$$

There are two key messages to take away from Lemma 1. The first of these is that the best response of an agent  $i$  at any state  $S$  is unique, which is why we have, henceforth, presented  $b_i(S)$  as an element of  $A$  (which is more convenient than writing it as a singleton subset of  $A$ ). The second is that once an agent is infected or runs no risk of becoming infected (i.e. the viral exposure is 0), they choose to go out with no restrictions imposed on their movements. ■

We now summarize the stochastic process we focus on in this paper. We denote by  $S_t = (I(S_t), a_N(S_t))$  the state of the process at the start of epoch  $t$ , for  $t \in \mathbb{N}_0$ . At the beginning of the epoch  $t$ , an agent  $\tilde{v}_t$  is uniformly randomly chosen, then the chosen agent takes the best response  $b_{\tilde{v}_t}(S_t)$  as defined in (2.2) based on the number of agents  $I(S_t)$  and the action profile  $a_{-\tilde{v}_t}(S_t)$  of all agents except  $\tilde{v}_t$  at epoch  $t$ . Then the action profile is updated from  $a_N(S_t)$  to  $(b_{\tilde{v}_t}(S_t) \vee a_{-\tilde{v}_t}(S_t))$ . Let us define an *intermediate* state  $\hat{S}_t = (I(S_t), (b_{\tilde{v}_t}(S_t) \vee a_{-\tilde{v}_t}(S_t)))$ . As a consequence, due to the change of the action profile, the viral exposure  $(r_i(S_t))_{1 \leq i \leq N}$  changes accordingly to  $(r_i(\hat{S}_t))_{1 \leq i \leq N}$ , and therefore, those uninfected agents satisfy  $a_j(\hat{S}_t)r_j(\hat{S}_t) > \tau(j)$  will also be infected and added to the set of infected agents. Thus, the updated infected set becomes  $I(S_{t+1}) = I(S_t) \cup \{j : a_j(\hat{S}_t)r_j(\hat{S}_t) > \tau(j)\}$ , and at the beginning of epoch  $t + 1$ , the process is in state  $S_{t+1} = (I(S_{t+1}), (b_{\tilde{v}_t}(S_t) \vee a_{-\tilde{v}_t}(S_t)))$  (which tells us that  $a_N(S_{t+1}) = (b_{\tilde{v}_t}(S_t) \vee a_{-\tilde{v}_t}(S_t))$ ).

Although we alluded to it in §1, we recall here the definition of the deterministic virus spread process (DVSP). Given a (deterministic) agent sequence  $\underline{v}$ , the DVSP  $S = (S_t : t \in \mathbb{N}_0)$  induced by  $\underline{v} = (\underline{v}_t : t \in \mathbb{N}_0)$ , with  $S_t$  indicating the state of the process just before epoch  $t$  commences, is defined in a manner identical to the stochastic virus spread process (SVSP) described above, with the only difference being that, instead of choosing an agent randomly at the start of each epoch, the agent  $\underline{v}_t$  is chosen at the start of epoch  $t$  to update their action, for each  $t \in \mathbb{N}_0$ . Whenever the agent sequence  $\underline{v}$  is not clear from the context, we shall denote the DVSP  $S$  (induced by  $\underline{v}$ ) by  $S(\underline{v})$ .

to emphasize its dependence on  $\underline{v}$ . In this case,  $S_t(\underline{v})$  will denote the state of the process at the start of epoch  $t$ .

In what follows, we make a few observations about the DVSP  $S(\underline{v})$  that we shall use frequently throughout the paper. Recall that  $\hat{S}_t$  indicates the intermediate state of the process at the midpoint of epoch  $t$ , for each  $t \in \mathbb{N}_0$ .

**Observation 1.** *Let  $S$  be the DVSP induced by  $\underline{v}$ . Then, for all  $t \in \mathbb{N}_0$ ,*

- (i)  $I(S_t) = I(\hat{S}_t)$  and  $a_N(\hat{S}_t) = a_N(S_{t+1})$ ,
- (ii) if  $b_{\underline{v}_t}(S_t) = a_{\underline{v}_t}(S_t)$ , then  $S_t = \hat{S}_t = S_{t+1}$ ,
- (iii) if  $I(S_t) = I(S_{t+1})$ , then  $\hat{S}_t = S_{t+1}$ .

**Observation 2.** *For any fixed  $i \in N$ , if  $\underline{v}_t \neq i$  for some  $t \in \mathbb{N}_0$ , then  $a_i(S_t) = a_i(\hat{S}_t) = a_i(S_{t+1})$ . By repeated applications of this observation, we are able to conclude the following: if  $\underline{v}_t \neq i$  for all  $t \in [t', t'']$  with  $t' < t''$ , then this yields  $a_i(S_t) = a_i(S_{t'})$  for all  $t \in [t', t'']$ .*

**Observation 3.** *Since the best response of an infected agent is always 1 (see Lemma 1),  $i \in I(S(t))$  and  $\underline{v}_t = i$  together imply that  $a_i(S_{t'}) = 1$  for all  $t' > t$ .*

**Observation 4.** *Since the best response of an uninfected agent  $i$  is*

$$b_i(S) = \begin{cases} 1 & \text{if } r_i(S) = 0, \\ \min \left\{ 1, \frac{\tau(i)}{r_i(S)} \right\} & \text{if } r_i(S) \neq 0, \end{cases}$$

by Lemma 1, hence  $\underline{v}_t = i$  and  $i \notin I(S_t)$  together imply that  $i \notin I(S_{t+1})$  as well.

Recall that our main goal in this paper is to explore the limiting behaviours of both the cardinality of the infected set of agents and the action profile of all the agents in our population. We now show that such limits are well-defined, at the very least, for a deterministic sequence of agents:

**Lemma 2.** *The DVSP  $S(\underline{v})$  converges for each agent sequence  $\underline{v} \in N^{\mathbb{N}_0}$ . In other words, both  $\lim_{t \rightarrow \infty} I(S_t(\underline{v}))$  and  $\lim_{t \rightarrow \infty} a_N(S_t(\underline{v}))$  exist.*

**Proof:** Let  $\underline{v}$  be a DVSP. It follows from the definition of  $S(\underline{v})$  that  $I(S_1(\underline{v})) \subseteq I(S_2(\underline{v})) \subseteq \dots \subseteq I(S_t(\underline{v}))$  for any  $t \in \mathbb{N}_0$ . As  $I(S_t) \subseteq N$  for all  $t$ , this means  $\lim_{t \rightarrow \infty} I(S_t(\underline{v}))$  exists. Also, as  $|N|$  is finite, there exists  $t_0$  such that  $I(S_{t_0}(\underline{v})) = I(S_t(\underline{v}))$  for all  $t \geq t_0$ . Consider  $\bar{t} \geq t_0 + 1$ . In the next claim, we show that for all  $i \in N$ ,  $a_i(S_{\bar{t}+1}) \geq a_i(S_{\bar{t}})$ .

**Claim 1.**  $a_i(S_{\bar{t}+1}) \geq a_i(S_{\bar{t}})$  for all  $i \in N$ .

**Proof of the claim:** Let  $\underline{v}_{\bar{t}} = j$ . By the definition of the process, for any other agent  $i$  we have  $a_i(S_{\bar{t}+1}) = a_i(S_{\bar{t}})$ , and hence the claim holds for them. We proceed show that the claim holds for agent  $j$ . Recall that  $a_j(\hat{S}_{\bar{t}}) = a_j(S_{\bar{t}+1})$  (see Observation 1). If  $j \in I(S_{\bar{t}})$  then  $a_j(\hat{S}_{\bar{t}}) = 1$  (see Observation 3), and hence  $a_j(\hat{S}_{\bar{t}}) \geq a_j(S_{\bar{t}})$ . As  $a_j(\hat{S}_{\bar{t}}) = a_j(S_{\bar{t}+1})$ , this means  $a_j(S_{\bar{t}+1}) \geq a_j(S_{\bar{t}})$ . If  $j \notin I(S_{\bar{t}})$ , by the definition of the process,  $j$  will choose their action as  $a_j(\hat{S}_{\bar{t}}) = b_j(S_{\bar{t}})$ . If  $b_j(S_{\bar{t}}) = 1$  then there is nothing to show. Assume  $b_j(S_{\bar{t}}) < 1$ . This implies  $a_j(\hat{S}_{\bar{t}}) = \frac{\tau(j)}{r_j(S_{\bar{t}})}$ . As  $j \notin I(S_{\bar{t}})$ , we have  $a_j(\hat{S}_{\bar{t}-1})r_j(\hat{S}_{\bar{t}-1}) \leq \tau(j)$ . Also, as  $\bar{t} \geq t_0 + 1$ , it follows that  $I(S_{\bar{t}-1}) = I(S_{\bar{t}})$ , which implies  $\hat{S}_{\bar{t}-1} = S_{\bar{t}}$  (see (iii) of Observation 1) and hence  $r_j(\hat{S}_{\bar{t}-1}) = r_j(S_{\bar{t}})$ . Combining this with the fact



that  $a_j(S_{\bar{t}}) = a_j(\hat{S}_{\bar{t}-1})$ , we obtain  $a_j(S_{\bar{t}}) \leq \frac{\tau(j)}{r_j(S_{\bar{t}})}$ . Since  $a_j(\hat{S}_{\bar{t}}) = \frac{\tau(j)}{r_j(S_{\bar{t}})}$  and  $a_j(S_{\bar{t}}) \leq \frac{\tau(j)}{r_j(S_{\bar{t}})}$ , we have  $a_j(\hat{S}_{\bar{t}}) \geq a_j(S_{\bar{t}})$ . This completes the proof of the claim.  $\square$

Since  $a_i(S_t) \leq 1$  for all  $i \in N$ , by Claim 1, we have the convergence of  $a_N(S_t(\underline{v}))$ .  $\blacksquare$

In view of Lemma 2, we set  $S_\infty(\underline{v}) = \lim_{t \rightarrow \infty} S_t(\underline{v})$ .

The set  $N^{\mathbb{N}_0}$  is the set of all agent-sequences indexed by  $\mathbb{N}_0$ . We consider the probability space  $(N^{\mathbb{N}_0}, \mathcal{F}, \mathbb{P})$  where  $\mathcal{F}$  is the sigma-field generated by the cylindrical sets of  $N^{\mathbb{N}_0}$  and  $\mathbb{P}$  is the uniform probability distribution.

**Remark 1.** Let  $N_\infty$  be the subset of  $N^{\mathbb{N}_0}$  consisting of the agent-sequences where each agent moves an infinite number of times. In other words,  $N_\infty = \{\underline{v} \in N^{\mathbb{N}_0} : v_t = i \text{ for infinitely many } t, \text{ for all } i \in N\}$ . It is straightforward to see that the set  $N_\infty$  has probability 1 under  $\mathbb{P}$ , since the probability of the set  $N^{\mathbb{N}_0} \setminus N_\infty$  is 0.

In view of Remark 1, for the rest of the paper, we shall work with the probability space  $(N_\infty, \mathcal{F}, \mathbb{P})$ .<sup>3</sup> Recall that in the stochastic virus spread process (SVSP), before each epoch commences, an agent is chosen randomly, following the discrete uniform distribution on the set  $N$ , and they are allowed to update their action by playing their best response (see (2.2)) to the current state. Consequently, the SVSP is a random variable  $S$  supported on the probability space  $(N_\infty, \mathcal{F}, \mathbb{P})$ .

For an agent  $i \in N$ , the random variable  $t_i$  is defined as follows with respect to  $(N_\infty, \mathcal{F}, \mathbb{P})$ : for  $\underline{v} \in N_\infty$ , we set  $t_i(\underline{v}) = l$  if  $l \in \mathbb{N}_0$  is such that  $v_l = i$  and  $v_k \neq i$  for all  $k < l$ . Note that for any  $\underline{v} \in N_\infty$ ,  $i \in N$ , and  $t \in \mathbb{N}_0$  with  $t \leq t_i(\underline{v})$ , we have  $a_i(S_0) = a_i(S_t(\underline{v}))$ . Let  $N_1$  be the measurable function on  $(N_\infty, \mathcal{F}, \mathbb{P})$  that describes the (random) set of agents who had been chosen before agent 1 was chosen for the first time, that is,  $N_1(\underline{v}) = \{i \in N \mid t_i(\underline{v}) < t_1(\underline{v})\}$ .

We now establish that  $|N_1|$  follows the uniform distribution on  $\{0, 1, \dots, n-1\}$  where  $|S|$  denotes the cardinality of the set  $S$ . Lemma 3 will be used in the proofs of the main results of this paper.

**Lemma 3.**  $\mathbb{P}(|N_1| = l) = \frac{1}{n}$  for all  $l \in \{0, 1, \dots, n-1\}$ .

**Proof:** Since  $\mathbb{P}$  is uniform and there are  $n!$  possible orderings of the random times  $t_1, \dots, t_n$ , each ordering of  $t_1, \dots, t_n$  has an equal probability of  $\frac{1}{n!}$  to occur. We can choose  $m-1$  random variables from the set  $\{t_2, \dots, t_n\}$  of  $n-1$  random times in  ${}^{n-1}C_{m-1}$  ways where  ${}^nC_r = \frac{n!}{r!(n-r)!}$  denotes the number of ways to choose  $r$  objects out of  $n$  without replacement. Therefore, the number of orderings that correspond to the event  $|\{i \in N \mid t_i < t_1\}| = m-1$  is  ${}^{n-1}C_{m-1} \times (m-1)! \times (n-m)!$ , and hence, the probability of the said event is  $\frac{{}^{n-1}C_{m-1} \times (m-1)! \times (n-m)!}{n!}$ , which is  $\frac{1}{n}$ . This completes the proof of the lemma.  $\blacksquare$

### 3. MAIN RESULTS

Before stating our main results we formally state assumptions for all the main results of the paper. As mentioned in §1, here we consider a homogeneous population to study the spread of an epidemic. To be specific, the homogeneity of the population is spelt through the following assumptions.

<sup>3</sup>With a slight abuse of notation, we keep using the notation  $\mathcal{F}$  for the induced  $\sigma$ -field  $\mathcal{F} \cap N_\infty$  on  $N_\infty$ .

- All individuals have the same action at the beginning of the epidemic (that is before they started deciding their actions strategically in response to the present state of the epidemic),
- All individuals have the same immunity power,
- Every pair of individuals have the same level of interaction.

We also intend to study the spread of an epidemic from the very beginning, and to capture that we assume,

- Exactly one individual is infected at the beginning of the epidemic.

Below, we present the assumptions formally. Recall that  $S_0$  denotes the initial state at which the process starts, and  $a_i(S_0)$  and  $I(S_0)$  denote the action of individual  $i$  and the set of infected people, respectively, at the state  $S_0$ .

- (i)  $a_i(S_0) = a$ ,  $\tau(i) = \tau$ , and  $g_{ij} = c$  for all  $i, j \in N$  with  $i \neq j$  for some  $a \in [0, 1]$ ,  $c \in \mathbb{R}^+$ ,  $\tau \in (0, 1]$ .
- (ii)  $I(S_0) = \{1\}$ .

We will assume the above assumptions throughout the paper without specifically mentioning everywhere.

A natural discussion is in order as to how realistic such assumptions are. Note that, from a technical point of view, the assumption of every individual having their initial actions and immunity profile potentially different is difficult to characterize. To bring some more realism, assume if the action (and immunity) profiles were all random, it is very natural to assume that distribution is identical throughout the population. Then our homogeneity assumption can be seen as a special case when the distributions assume a degenerate value. Also, the assumption of only one infected individual in the entire population is pretty realistic as that is exactly how contagious diseases spread. Our intuition says that more than one infected individual at the beginning will lead to more infected people with a higher probability and such cases can be analyzed using similar techniques as used in the paper. Since, to the best of our knowledge, this is the first paper to look at such a stochastic process, we wanted to stick to very concise yet important and insightful findings with the means of the above assumptions.

We adopt the following notations to state our results. For  $a \in \mathbb{R}$ , we let  $\lceil a \rceil = \min\{k \in \mathbb{Z} : a \leq k\}$  and  $\lfloor a \rfloor = \max\{k \in \mathbb{Z} : a \geq k\}$ . For  $a, b \in \mathbb{N}_0$ ,  $[a, b]$  denotes the set  $\{a, a + 1, \dots, b\}$  if  $a \leq b$ , and denotes the null set if  $a > b$ . For  $m \geq \lfloor \tau(n - 1) \rfloor + 1$ , we define the set  $A_m$  to be the set of all ordered tuples  $\underline{x} = (x_1, \dots, x_n)$  that satisfy the following properties:

- (i)  $x_1 = 1$ ,
- (ii) there are precisely  $m - 1$  coordinates  $i \in \{2, \dots, n\}$  such that  $x_i = 1$ ,
- (iii) each of the remaining coordinates equals  $\frac{\tau m}{(1 + \tau)m - \tau(n - 1)}$ .<sup>4</sup>

A couple of facts follow immediately from the above definition. The first is that  $A_n$  is the singleton set  $\{\underline{1}\}$ , where  $\underline{1}$  is the  $n$ -dimensional tuple in which each coordinate equals 1. The second is that  $|A_m| = {}^{n-1}C_{m-1}$  for each  $m$  for which  $A_m$  is well-defined, since we need only choose the  $m - 1$  coordinates out of  $2, \dots, n$  that equal 1.

<sup>4</sup>As  $m > (n - 1)\tau$ ,  $\frac{\tau m}{(1 + \tau)m - \tau(n - 1)}$  is strictly less than 1.

### 3.1 RESULTS WHEN $a = 0$

Here, we consider the situation where the (common) initial action  $a$  equals 0. Theorem 1 provides the limiting distribution of the infected set for arbitrary values of  $\tau$ . Let

$$\alpha = \min \left\{ \left\lceil \frac{1}{\tau} \right\rceil, n \right\}. \quad (3.1)$$

**Theorem 1.** *Suppose  $a = 0$ . Then the limiting distribution of the infected set is given by*

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\alpha - 1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \alpha], \\ 0 & \text{otherwise,} \end{cases}$$

where  $\alpha$  as defined in (3.1).

**Proof:** We complete the proof in two steps. In Step 1, we explore how the infection spreads when agents update their actions according to a fixed agent sequence, and in Step 2 we use this to explore how infection spreads when agents update their actions randomly.

**Step 1.** Fix an agent sequence  $\underline{v} \in N_\infty$  and let  $S$  be the DVSP induced by  $\underline{v}$ . To shorten notation, for all  $i \in N$ , let us denote  $t_i(\underline{v})$  by  $k_i$ . The following claim demonstrates how an agent  $i$  with  $k_i < k_1$  will update their action.

**Claim 1:** Suppose  $k_i < k_1$  for some  $i \in N$ . Then,  $a_i(S_t) = 1$  for all  $t = k_i + 1, \dots, k_1$ .

**Proof of the claim.** By Lemma 7,  $I(S_t) = \{1\}$  for all  $t \leq k_1$ . Since  $k_1 < \infty$  and  $k_i < k_1$ , we have  $k_i < \infty$ . Consider any time point  $l$  such that  $k_i \leq l < k_1$ . By the definition of the process, we need to show that the Claim holds for  $l$  such that  $\underline{v}_l = i$  (see Observation 2). Since  $l < k_1$ , we have  $a_1(S_l) = a_1(S_0) = 0$ . This together with  $I(S_l) = \{1\}$  implies  $r_i(S_l) = 0$ . Hence, by Lemma 1, agent  $i$  will update their action to 1 at  $\hat{S}_l$ . Since  $a_i(\hat{S}_l) = a_i(S_{l+1})$ , this means,  $a_i(S_{l+1}) = 1$ . This completes the proof of the Claim.  $\square$

**Case 1:**  $|N_1(\underline{v})| \geq \alpha$ .

As  $|N_1(\underline{v})| \leq n - 1$ , the assumption of the case implies  $\alpha = \left\lceil \frac{1}{\tau} \right\rceil$ . Hence,  $\alpha\tau \geq 1$ . By Claim 1,  $a_i(S_{k_1}) = 1$  for all  $i \in N_1(\underline{v})$ . Also, by the definition of the process,  $a_i(S_{k_1}) = 0$  for all  $i \notin N_1(\underline{v}) \cup \{1\}$  as they have not updated their actions till the time point  $k_1$ . Recall that  $\hat{S}_{k_1}$  denotes the intermediate state where the only change from  $S_{k_1}$  is that agent  $\underline{v}_{k_1}$  has updated their action to  $b_{\underline{v}_{k_1}}(S_{k_1})$ . Since  $\underline{v}_{k_1} = 1$ , we have  $a_i(S_{k_1}) = a_i(\hat{S}_{k_1})$  for all  $i \neq 1$ . Thus,  $a_i(\hat{S}_{k_1}) = 1$  for all  $i \in N_1(\underline{v})$  and  $a_i(\hat{S}_{k_1}) = 0$  for all  $i \notin N_1(\underline{v}) \cup \{1\}$ .

By Remark 1 and the definition of the process,  $a_1(\hat{S}_{k_1}) = 1$ . Consider the time point  $k_1 + 1$ . By the definition of the process, an agent  $i \neq 1$  will be in  $I(S_{k_1+1})$  if  $a_i(\hat{S}_{k_1})r_i(\hat{S}_{k_1}) > \tau$ . Since  $I(S_{k_1}) = \{1\}$ ,  $a_i(\hat{S}_{k_1}) = 1$  for all  $i \in N_1(\underline{v}) \cup \{1\}$ ,  $a_i(\hat{S}_{k_1}) = 0$  for all  $i \notin N_1(\underline{v}) \cup \{1\}$ , and  $g_{ij} = c$  for all  $i \neq j$ , it follows that  $r_i(\hat{S}_{k_1}) \leq \frac{1}{\alpha}$  for all  $i \in N_1(\underline{v})$ . Because  $\alpha\tau \geq 1$ , this implies that no agent in  $N_1(\underline{v})$  gets infected at the time point  $k_1 + 1$ . Moreover, since  $a_i(\hat{S}_{k_1}) = 0$  for each agent  $i \notin N_1(\underline{v}) \cup \{1\}$ , we have  $a_i(\hat{S}_{k_1})r_i(\hat{S}_{k_1}) = 0 \leq \tau$ . Thus, no new agent gets infected at the time point  $k_1 + 1$ , and hence,  $I(S_{k_1+1}) = \{1\}$ .

We show that no new agent would get infected after this. We first show that  $I(S_{k_1+2}) = \{1\}$ . Let  $v_{k_1+1} = i$ . If  $i \notin I(S_{k_1+1})$  then as  $I(S_{k_1}) = I(S_{k_1+1})$  by Lemma 6, we have  $I(S_{k_1+1}) = I(S_{k_1+2})$ . If  $i \in I(S_{k_1+1})$  then  $i = 1$ . Moreover,  $a_1(S_{k_1+1}) = a_1(\hat{S}_{k_1}) = 1$ . Hence, by Lemma 6,  $I(S_{k_1+1}) = I(S_{k_1+2})$ . Therefore,  $I(S_{k_1+2}) = \{1\}$ . Using the same arguments repeatedly, it follows that  $I(S_t) = \{1\}$  for all  $t \geq k_1 + 2$ . Thus,  $I(S_\infty) = \{1\}$ .

**Case 2:**  $|N_1(v)| \leq \alpha - 1$ .

Using similar arguments as in Case 1, we have  $a_i(\hat{S}_{k_1}) = 1$  for all  $i \in N_1(v)$  and  $a_i(\hat{S}_{k_1}) = 0$  for all  $i \notin N_1(v) \cup \{1\}$ . This, together with  $g_{ij} = c$  for all  $i \neq j$ , implies  $r_i(\hat{S}_{k_1}) \geq \frac{1}{\alpha - 1}$  for all  $i \in N_1(v)$ .

As  $\alpha = \min \left\{ \left\lceil \frac{1}{\tau} \right\rceil, n \right\}$ , we have  $(\alpha - 1)\tau < 1$ . Hence, all agents in  $N_1(v)$  will get infected at time point  $k_1 + 1$ . Moreover, as  $a_i(\hat{S}_{k_1}) = 0$  for all  $i \notin N_1(v) \cup \{1\}$ , the agents outside  $N_1(v) \cup \{1\}$  will not get infected at time point  $k_1 + 1$ . Thus, we have  $I(S_{k_1+1}) = N_1(v) \cup \{1\}$ . Because,  $a_i(S_{k_1+1}) = a_i(\hat{S}_{k_1}) = 1$  for all  $i \in I(S_{k_1+1})$  and  $a_i(S_{k_1+1}) = 0 \leq \tau$  for all  $i \notin I(S_{k_1+1})$ , by Lemma 8 it follows that  $I(S_{k_1+1}) = I(S_\infty)$ . Hence,  $I(S_\infty) = N_1(v) \cup \{1\}$ .

**Step 2.** Consider the probability space  $(N_\infty, \mathcal{F}, \mathbb{P})$  and random variables  $S$  and  $t_1, \dots, t_n$ . Let  $m \in \{2, \dots, n\}$  be such that  $m \leq \alpha$ . In view Case 1 and Case 2 of the current proof, we have (i)  $|I(S_\infty)| \leq \alpha$ , and (ii)  $|I(S_\infty)| = m$  with  $1 \in I(S_\infty)$  if and only if  $|\{i \in N \mid t_i < t_1\}| = m - 1$ . Also,  $I(S_\infty) = \{1\}$  if and only if  $|\{i \in N \mid t_i < t_1\}| \geq \alpha$ . Moreover, as  $\mathbb{P}$  is uniform, any two subsets of  $N$  with same cardinality have the same probability. These observations together yield

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\alpha - 1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \alpha], \\ 0 & \text{otherwise.} \end{cases}$$

This completes the proof of the theorem. ■

Next, we proceed to explore the limiting distribution of the action profile, and this is found to be dependent on the value of  $\tau$ . Accordingly, the statement of Theorem 2 is split into two parts on the basis of whether  $\tau$  exceeds  $(n - 1)^{-1}$  or not. We introduce the quantity

$$\beta = \min\{\lfloor (n - 1)\tau \rfloor + 1, \alpha + 1\}. \quad (3.2)$$

**Theorem 2.** Suppose  $a = 0$ . For  $\tau \geq \frac{1}{n - 1}$ , the limiting distribution of the action profile is given by

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{\alpha - \beta + 1}{n} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [\beta, \alpha], \\ 0 & \text{otherwise,} \end{cases}$$

whereas for  $\tau < \frac{1}{n-1}$ , the limiting distribution of the action profile is given by

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [1, n], \\ 0 & \text{otherwise,} \end{cases}$$

with  $\alpha$  and  $\beta$  as defined in (3.1) and (3.2) respectively.

A brief discussion is in order regarding some of the startling findings that may be deduced from the two theorems of §3.1. Theorem 1 reveals that, if we consider *any* two *different* subsets  $J_1$  and  $J_2$  of  $N$ , the probabilities  $\mathbb{P}(I(S_\infty) = J_1)$  and  $\mathbb{P}(I(S_\infty) = J_2)$  are the same as long as  $J_1$  and  $J_2$  have the same cardinality and either both of them contain agent 1 or neither contains agent 1. We note that the number of subsets  $J$  of  $N$  with  $1 \in J$  and  $|J| = m$  is given by  ${}^{n-1}C_{m-1}$ , so that summing  $\mathbb{P}(I(S_\infty) = J)$  over all such  $J$  yields  $\mathbb{P}(|I(S_\infty)| = m) = n^{-1}$  for *each*  $m \in [2, \alpha]$ . These observations suggest a rather close resemblance that the limiting distribution of the infected set, as well as the limiting distribution of its cardinality, bears with suitably defined discrete uniform distributions. In fact, for  $\tau \leq n^{-1}$ , we have  $\alpha = n$ , reducing the distribution of  $|I(S_\infty)|$  to precisely the discrete uniform distribution on  $\{1, 2, \dots, n\}$ . This uniform structure is somewhat marred when  $\tau > n^{-1}$ . For example, when  $n = 5$ ,  $a = 0$  and  $\tau = 0.25$ , we have

$$\begin{aligned} \mathbb{P}(|I(S_\infty)| = 1) &= \frac{2}{5}, \quad \mathbb{P}(|I(S_\infty)| = 2) = \frac{1}{5}, \quad \mathbb{P}(|I(S_\infty)| = 3) = \frac{1}{5}, \\ \mathbb{P}(|I(S_\infty)| = 4) &= \frac{1}{5}, \quad \mathbb{P}(|I(S_\infty)| = 5) = 0, \end{aligned} \tag{3.3}$$

whereas if  $\tau = 0.4$ , the probability distribution changes to

$$\begin{aligned} \mathbb{P}(|I(S_\infty)| = 1) &= \frac{3}{5}, \quad \mathbb{P}(|I(S_\infty)| = 2) = \frac{1}{5}, \quad \mathbb{P}(|I(S_\infty)| = 3) = \frac{1}{5}, \\ \mathbb{P}(|I(S_\infty)| = 4) &= 0, \quad \mathbb{P}(|I(S_\infty)| = 5) = 0. \end{aligned} \tag{3.4}$$

An intuitive explanation for this phenomenon is that with higher immunity, i.e. higher value of  $\tau$ , the disease is less likely to spread to the entire community, instead having a higher probability of remaining confined to the initial infected set.

Conclusions of a similar flavour can be drawn as a consequence of Theorem 2. For *any* two *different* ordered tuples  $\underline{x}$  and  $\underline{y}$  that belong to the same  $A_m$ , the probabilities  $\mathbb{P}(a_N(S_\infty) = \underline{x})$  and  $\mathbb{P}(a_N(S_\infty) = \underline{y})$  are equal, for both the cases  $\tau \geq (n-1)^{-1}$  and  $\tau < (n-1)^{-1}$ . Moreover, since  $|A_m| = {}^{n-1}C_{m-1}$ , we obtain  $\mathbb{P}(a_N(S_\infty) \in A_m) = n^{-1}$  for *every*  $m \in [\beta, \alpha]$  when  $\tau \geq (n-1)^{-1}$  and for every  $m \in [1, n]$  when  $\tau < (n-1)^{-1}$ . These are, once again, reminiscent of suitably defined discrete uniform distributions.

A connection may be established between Theorem 1 and Theorem 2, for the case where  $\tau \geq (n-1)^{-1}$ , via the following fact whose justification has been included in the proof of Theorem 2: for any DVSP  $S(\underline{v})$ , if the limiting infected set has cardinality  $m \in [\beta, \alpha]$  (note that  $\beta \geq 2$ ), the limiting action profile will be a tuple in  $A_m$ , with all infected agents choosing action 1 and all uninfected agents choosing action  $\tau m[(1+\tau)m - \tau(n-1)]^{-1}$ . On the other hand, if the limiting infected set for the DVSP  $S(\underline{v})$  has cardinality strictly less than  $\beta$ , the final action profile becomes  $\underline{1}$ , signifying that *all* agents choose action 1 in the long run.

**Proof:** First assume  $\tau \geq \frac{1}{n-1}$ . We first explore the limiting actions for a fixed agent sequence, and then we use this to find the limiting probability distribution. Let  $\underline{v}$  be an agent sequence and  $S$  be the DVSP induced by  $\underline{v}$ . Note that by Remark 1, it is enough to assume  $\underline{v} \in N_\infty$ . Therefore, by Lemma 10, all the agents outside  $I(S_\infty)$  have the same action limit, and all the agents in  $I(S_\infty)$  have the action limit 1. Let us denote the common limit for all agents outside  $I(S_\infty)$  by  $\gamma$ . We distinguish two cases based on the value of  $N_1(\underline{v})$  (as in the proof of Theorem 1) to find  $\gamma$ . Note that by the assumption of the theorem  $\alpha \leq n-1$ .

**Case 1:**  $|N_1(\underline{v})| \geq \alpha$ .

Recall that for this case the final infected set is  $\{1\}$ . Moreover, by the assumption of the theorem,  $\tau(n-1) \geq 1$ . Therefore, by Lemma 11,  $\gamma = 1$ . Hence,  $a_N(S_\infty) = \underline{1}$ .

**Case 2:**  $|N_1(\underline{v})| \leq \alpha - 1$ .

Recall that for this case, the final infected set is  $N_1(\underline{v}) \cup \{1\}$ . Therefore, by Lemma 11, if  $(n-1)\tau \geq |N_1(\underline{v})| + 1$  then  $a_N(S_\infty) = \underline{1}$ , and if  $(n-1)\tau < |N_1(\underline{v})| + 1$  then

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \frac{\tau(|N_1(\underline{v})| + 1)}{(1 + \tau)(|N_1(\underline{v})| + 1) - \tau(n-1)} & \text{if } i \notin I(S_\infty). \end{cases}$$

Recall that  $\beta = \min\{\lfloor (n-1)\tau \rfloor + 1, \alpha + 1\}$ . Hence, combining Cases 1 and 2, we have the following:

(i)  $|N_1(\underline{v})| + 1 \in [\beta, \alpha]$  implies

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \frac{\tau(|N_1(\underline{v})| + 1)}{(1 + \tau)(|N_1(\underline{v})| + 1) - \tau(n-1)} & \text{if } i \notin I(S_\infty). \end{cases}$$

(ii)  $|N_1(\underline{v})| + 1 \in [1, \beta - 1] \cup [\alpha + 1, n]$  implies  $a_N(S_\infty) = \underline{1}$ .

Note that (i) implies  $a_N(S_\infty) \in A_{(|N_1(\underline{v})| + 1)}$  when  $|N_1(\underline{v})| + 1 \in [\beta, \alpha]$ . Also, as  $\mathbb{P}$  is uniform, any two vectors in  $A_m$ , for  $m \in [\beta, \alpha]$ , have the same probability. Thus, we have the following distribution

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{\alpha - \beta + 1}{n} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [\beta, \alpha], \\ 0 & \text{otherwise.} \end{cases}$$

Now assume  $\tau < \frac{1}{n-1}$ . We follow the same structure as in the previous case, that is, we first explore the limiting actions for a fixed agent sequence, and then we use this to find the limiting probability distribution. Let  $\underline{v}$  be an agent sequence and  $S$  be the DVSP induced by  $\underline{v}$ . Note that by Remark 1, it is enough to assume  $\underline{v} \in N_\infty$ . Therefore, by Lemma 10, all the agents outside  $I(S_\infty)$  have the same action limit, and all the agents in  $I(S_\infty)$  have the action limit 1. Let us denote the common limit by  $\gamma$ . As by the assumption of the theorem,  $(n-1)\tau < 1$ , we have  $\alpha = n$ , and hence,

$|N_1(\varrho)| \leq \alpha - 1$ . Moreover, for  $|N_1(\varrho)| \leq \alpha - 1$  (shown in the proof of Theorem 1), the final infected set is  $N_1(\varrho) \cup \{1\}$ . Thus,  $|I(S_\infty)| > (n - 1)\tau$ . Hence, by Lemma 11 if  $|N_1(\varrho)| + 1 < n$

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \frac{\tau(|N_1(\varrho)| + 1)}{(1 + \tau)(|N_1(\varrho)| + 1) - \tau(n - 1)} & \text{if } i \notin I(S_\infty). \end{cases}$$

and if  $|N_1(\varrho)| + 1 = n$ ,  $a_N(S_\infty) = \underline{1}$ . Recall the notation  $A_m$ . By the above arguments, we have  $a_N(S_\infty) \in A_{[|N_1(\varrho)|+1]}$  when  $|N_1(\varrho)| + 1 < n$ . Moreover, as  $\mathbb{P}$  is uniform, any two vectors in  $A_m$ , for  $m \in [1, (n - 1)]$ , have the same probability. Thus, by Theorem 1, we have the following distribution

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} \frac{1}{n} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [1, n - 1], \\ 0 & \text{otherwise.} \end{cases}$$

■

### 3.2 RESULTS WHEN $a = 1$

Here, we consider the situation where the (common) initial action  $a$  equals 1. The following theorem provides the limiting distribution of the set of infected agents:

**Theorem 3.** *Suppose  $a = 1$ . If  $\tau \geq \frac{1}{n - 1}$ , the limiting distribution of the infected set is given by*

$$\mathbb{P}(I(S_\infty) = \{1\}) = 1,$$

whereas if  $\tau < \frac{1}{n - 1}$ , the limiting distribution is given by

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} \frac{1}{n^2} & \text{if } 1 \in J \text{ and } |J| = n - 1, \\ 1 - \frac{n - 1}{n^2} & \text{if } |J| = n, \text{ i.e., } J = N, \\ 0 & \text{otherwise.} \end{cases}$$

The proof of this theorem can be found in Appendix B (subsection B.1). Note that since there are  $n - 1$  many sets  $J$  such that  $1 \in J$  and  $|J| = n - 1$ , the above display exhibits a valid probability distribution.

**Theorem 4.** *Suppose  $a = 1$ . If  $\tau \geq \frac{1}{n - 1}$ , the limiting distribution of the action profile is given by*

$$\mathbb{P}(a_N(S_\infty) = \underline{1}) = 1,$$

whereas if  $\tau < \frac{1}{n-1}$ , the limiting distribution is given by

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{n-1}{n^2} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n^2} & \text{if } \underline{x} \in A_{n-1}, \\ 0 & \text{otherwise.} \end{cases}$$

The proof of this theorem can be found in Appendix D (subsection D.1). We draw the reader's attention to the fact that the results of §3.2 differ quite a bit in appearance from those in §3.1. While the limiting distribution of the infected set, for  $a = 0$ , is supported on *all* subsets of  $N$  that contain 1 and that have sizes bounded above by  $\alpha$  (Theorem 1), the infected set, for  $a = 1$ , converges to the singleton  $\{1\}$  when  $\tau \geq (n-1)^{-1}$ , and its limiting distribution is supported on *only* those subsets of  $N$  that contain 1 and have cardinality at least  $n-1$  when  $\tau < (n-1)^{-1}$  (Theorem 3). In some sense, for  $a = 0$ , the limiting distribution is "spread out" over a wider support, while for  $a = 1$ , it is more "concentrated".

Likewise, for  $a = 0$ , the limiting distribution of the action profile is supported on *all*  $A_m$  with  $m \in \{n\} \cup [\beta, \alpha]$  when  $\tau \geq (n-1)^{-1}$ , and it is supported on *all*  $A_m$  with  $m \in \{1, \dots, n\}$  when  $\tau < (n-1)^{-1}$  (Theorem 2). In contrast, for  $a = 1$ , the action profile converges to  $\underline{1}$  when  $\tau \geq (n-1)^{-1}$ , and the limiting distribution of the action profile is supported on *just*  $A_n \cup A_{n-1}$  when  $\tau < (n-1)^{-1}$  (Theorem 4).

### 3.3 RESULTS WHEN $0 < a \leq \tau$ AND $a \neq 1$

In this subsection, we consider the case where the (common) initial action  $a$  lies strictly between 0 and 1, and is bounded above by  $\tau$ . Let

$$\hat{a} = \max \left\{ 1, \left\lceil \frac{\frac{1}{\tau} - (n-1)a}{1-a} \right\rceil \right\}. \quad (3.5)$$

**Theorem 5.** *Suppose  $0 < a \leq \tau$  and  $a \neq 1$ . Further, suppose  $\tau \geq \frac{1}{n-1}$ . Then the limiting distribution of the infected set is given by*

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\hat{a}-1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \hat{a}], \\ 0 & \text{otherwise.} \end{cases}$$

The proof of this theorem can be found in Appendix B (subsection B.2). Next, we proceed to describe the limiting distribution of the action profile. We introduce the following notation in order to state our next result:

$$\hat{\beta} = \min\{\lfloor (n-1)\tau \rfloor + 1, \hat{a} + 1\}. \quad (3.6)$$



**Theorem 6.** Suppose  $0 < a \leq \tau$  and  $a \neq 1$ . Further, suppose  $\tau \geq \frac{1}{n-1}$ . Then the limiting distribution of the action profile is given by

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{\hat{\alpha} - \hat{\beta} + 1}{n} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [\hat{\beta}, \hat{\alpha}], \\ 0 & \text{otherwise.} \end{cases}$$

The proof of the theorem can be found in Appendix D (subsection D.2).

**Remark 2.** If one sets  $a = 0$  in the conclusion of Theorem 5, one gets back the conclusion of Theorem 1 for  $\tau \geq (n-1)^{-1}$ . However, Theorem 1 is more general in terms of its coverage of the values of  $\tau$ . In a similar manner, setting  $a = 0$  in Theorem 6 yields Theorem 2 for the case of  $\tau \geq (n-1)^{-1}$ .

Discussions of findings of a flavour similar to those in §3.1 can be included here as well. Even if  $J_1$  and  $J_2$  are two *different* subsets of  $N$ , Theorem 5 shows that the probabilities  $\mathbb{P}(I(S_\infty) = J_1)$  and  $\mathbb{P}(I(S_\infty) = J_2)$  are the same as long as  $J_1$  and  $J_2$  have the same cardinality and either both contain 1 or neither does. Summing over all subsets of  $N$  that contain 1 and are of cardinality  $m$ , we obtain  $\mathbb{P}(|I(S_\infty)| = m) = n^{-1}$  for each  $2 \leq m \leq \hat{\alpha}$ . Likewise, for any two *different* ordered tuples  $\underline{x}$  and  $\underline{y}$ , Theorem 6 shows that the probabilities  $\mathbb{P}(a_N(S_\infty) = \underline{x})$  and  $\mathbb{P}(a_N(S_\infty) = \underline{y})$  are the same as long as both  $\underline{x}$  and  $\underline{y}$  belong to the same  $A_m$ . Summing over all members of an  $A_m$  yields  $\mathbb{P}(a_N(S_\infty) \in A_m) = n^{-1}$  for every  $\hat{\beta} \leq m \leq \hat{\alpha}$ .

### 3.4 RESULTS WHEN $\tau < a < 1$ .

In this subsection, we consider the scenario where the (common) initial action  $a$  is strictly greater than  $\tau$ . We introduce the following notations to facilitate the presentation of the results that follow: Let

$$\tilde{\alpha} = \max \left\{ 1, \left\lceil \frac{1 - (n-1)a\tau}{\tau(1-a)} \right\rceil \right\} \quad \text{and} \quad \bar{\alpha} = \left\lfloor \frac{(n-1)a\tau}{a - \tau(1-a)} \right\rfloor + 1. \quad (3.7)$$

Note that, in this regime,  $\tau < a < a/(1-a)$  and thus  $a - \tau(1-a) > 0$ . Now since,  $(n-1)a\tau/(a - \tau(1-a))$  is increasing in  $\tau$ , we have, for  $\tau \geq 1/(n-1)$ ,

$$\frac{(n-1)a\tau}{a - \tau(1-a)} \geq \frac{(n-1)a\left(\frac{1}{n-1}\right)}{a - \frac{1-a}{n-1}} = \frac{a}{a - \frac{1-a}{n-1}} > 1.$$

This yields  $\bar{\alpha} \geq 2$ .

**Theorem 7.** Suppose  $\frac{1}{n-1} \leq \tau < a < 1$ . If  $\tilde{\alpha} + 1 \leq \bar{\alpha}$ , the limiting distribution of the infected set is given by

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\tilde{\alpha} - 1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \tilde{\alpha}], \\ 0 & \text{otherwise,} \end{cases}$$

whereas if  $2 \leq \bar{\alpha} < \tilde{\alpha} + 1$ , the limiting distribution is given by

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\tilde{\alpha} - 1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \bar{\alpha} - 1], \\ \frac{\eta(\tilde{\alpha}, \bar{\alpha}, n)}{n-1} & \text{if } 1 \in J \text{ and } |J| = n-1, \\ \frac{\tilde{\alpha} - (\bar{\alpha} - 1)}{n} - \eta(\tilde{\alpha}, \bar{\alpha}, n) & \text{if } |J| = n, \text{ i.e., } J = N, \\ 0 & \text{otherwise,} \end{cases}$$

where  $\eta(\tilde{\alpha}, \bar{\alpha}, n) = \frac{(n-1)!}{n^3} \sum_{w=\bar{\alpha}-1}^{\tilde{\alpha}-1} \frac{1}{(n-w-2)!} \sum_{t=w+1}^{\infty} \binom{\{t-1\}_w}{n^{t-1}}$ , and  $\left\{ \begin{matrix} p \\ q \end{matrix} \right\}$  is the Stirling number of the second kind with parameters  $p$  and  $q$ .

**Proof:** We start with a lemma that shows for an agent sequence, the infected set remains the same till agent 1 appears for the first time.

**Lemma 4.** Let  $\varrho \in N_\infty$  and  $\hat{t} \in \mathbb{N}_0$  be such that  $\varrho_t \neq 1$  for all  $t < \hat{t}$ . Then,  $I(S_t) = \{1\}$  for all  $t \leq \hat{t}$ .

**Proof:** Note that if  $\hat{t} = 0$  then there is nothing to show. So, assume  $\hat{t} \geq 1$ . We use induction to prove this. As the base case, we show that  $I(S_1) = \{1\}$ . Let  $\varrho_0 = i$ . Since  $\hat{t} \geq 1$ ,  $i \neq 1$ . Moreover, as  $g_{ij} = c$  for all  $i \neq j$ ,  $r_i(S_0) = \frac{1}{(n-1)}$ . Hence,

$$b_i(S_0) = \min \left\{ 1, \frac{\tau}{\frac{1}{(n-1)}} \right\} = \min\{1, (n-1)\tau\} = 1$$

as by our assumption  $\tau \geq \frac{1}{(n-1)}$ . This means agent  $i$  will not get infected. For any  $j \notin \{1, i\}$ ,

$a_j(\hat{S}_0) = a_j(S_0) = a$  and  $r_j(\hat{S}_0) = \frac{a}{(n-2)a+1} \leq \frac{1}{(n-1)}$ . Thus,

$$a_j(\hat{S}_0)r_j(\hat{S}_0) = a \frac{a}{(n-2)a+1} \leq \frac{a}{(n-1)} \leq \frac{1}{(n-1)} \leq \tau.$$

So, agent  $j$  will also not get infected at  $t = 1$ . Thus,  $I(S_1) = \{1\}$ . Next we introduce an induction hypothesis.

*Induction Hypothesis:* Given  $\bar{t} \in \mathbb{N}_0$  with  $\hat{t} \geq \bar{t} > 1$ , we have  $I(S_1) = \dots = I(S_{\bar{t}-1}) = \{1\}$ .

We show that  $I(S_{\bar{t}}) = \{1\}$ . Let  $\underline{v}_{\bar{t}-1} = i$ . Since  $\hat{t} \geq \bar{t}$ , this means  $i \neq 1$ . Hence,  $i \notin I(S_{\bar{t}-1})$ . As  $\bar{t} > 1$ , we have  $I(S_{\bar{t}-2}) = I(S_{\bar{t}-1})$ . This together with Lemma 6, implies  $I(S_{\bar{t}}) = I(S_{\bar{t}-1}) = \{1\}$ . Thus, by induction, we have  $I(S_{\bar{t}}) = \{1\}$ . This completes the proof of the lemma. ■

We complete the proof in two steps. In Step 1, we explore how the infection spreads when agents update their actions according to a fixed agent sequence, and in Step 2 we use this to explore how infection spreads when agents update their actions randomly.

**Step 1:** Fix an agent sequence  $\underline{v} \in N_\infty$  and let  $S$  be the DVSP induced by  $\underline{v}$ . To shorten notation, for all  $i \in N$ , let us denote  $t_i(\underline{v})$  by  $k_i$ .

**Claim 1:** For all  $0 \leq t < k_1$ ,  $a_i(S_{t+1}) = 1$  where  $\underline{v}_t = i$ .

**Proof of the claim.** Let  $\underline{v}_0 = i$ . As  $k_1 > 0$ ,  $i \neq 1$ . Since  $a_j(S_0) = a > 0$  for all  $j \in N$ ,  $I(S_0) = \{1\}$ , and  $g_{ij} = c$  for all  $i \neq j$ , we have  $r_i(S_0) = \frac{1}{(n-1)}$ . This means

$$b_i(S_0) = \min \left\{ 1, \frac{\tau}{\frac{1}{(n-1)}} \right\} = \min\{1, (n-1)\tau\} = 1,$$

as by our assumption  $\tau \geq \frac{1}{(n-1)}$ . Thus,  $a_i(S_1) = a_i(\hat{S}_0) = 1$ . Next we introduce an induction hypothesis.

*Induction Hypothesis:* Given  $\bar{t} \in \mathbb{N}_0$  with  $\bar{t} < k_1$ , we have for all  $t < \bar{t}$ ,  $a_j(S_{t+1}) = 1$  where  $\underline{v}_t = j$ .

Let  $\underline{v}_{\bar{t}} = i'$  and we show that  $a_{i'}(S_{\bar{t}+1}) = 1$ . Note that by Lemma 4,  $I(S_{\bar{t}}) = \{1\}$ . Moreover, by the induction hypothesis,  $a_j(S_{\bar{t}}) \geq a$  for all  $j \in N \setminus \{1\}$ . Also, as  $\bar{t} < k_1$ , we have  $a_1(S_{\bar{t}}) = a$ . Combining all these observations we have,

$$\frac{1}{(n-1)} \geq r_{i'}(S_{\bar{t}}) \geq \frac{a}{(n-1)}. \quad (3.8)$$

Since  $r_{i'}(S_{\bar{t}}) > 0$ ,  $b_{i'}(S_{\bar{t}}) = \min \left\{ 1, \frac{\tau}{r_{i'}(S_{\bar{t}})} \right\}$ ; see Lemma 1. Therefore, using (3.8) and the fact

$\tau \geq \frac{1}{(n-1)}$ , we have  $b_{i'}(S_{\bar{t}}) = 1$ . Thus,  $a_{i'}(S_{\bar{t}+1}) = a_{i'}(\hat{S}_{\bar{t}}) = 1$ . □

We distinguish some cases based on  $|N_1(\underline{v})|$ .

**Case 1:**  $|N_1(\underline{v})| \geq \tilde{\alpha}$ .

We show that no new agent will get infected and  $I(S_\infty) = \{1\}$ . By Claim 1,  $a_i(S_{k_1}) = 1$  for all  $i \in N_1(\underline{v})$ . By the definition of the process,  $a_i(S_{k_1}) = a$  for all  $i \notin N_1(\underline{v}) \cup \{1\}$  as they have not updated their actions till the time point  $k_1$ . Recall that  $\hat{S}_{k_1}$  denotes the intermediate state where the only change from  $S_{k_1}$  is that agent  $\underline{v}_{k_1}$  has updated their action to  $b_{\underline{v}_{k_1}}(S_{k_1})$ . Since  $\underline{v}_{k_1} = 1$ , we have  $a_i(S_{k_1}) = a_i(\hat{S}_{k_1})$  for all  $i \neq 1$ . Thus,  $a_i(\hat{S}_{k_1}) = a$  for all  $i \in |N_1(\underline{v})|$  and  $a_i(\hat{S}_{k_1}) = 1$  for all  $i \notin N_1(\underline{v}) \cup \{1\}$ .

By Lemma 1 and the definition of the process,  $a_1(\hat{S}_{k_1}) = 1$ . Consider the time point  $k_1 + 1$ . By the definition of the process, an agent  $i \neq 1$  will be in  $I(S_{k_1+1})$  if  $a_i(\hat{S}_{k_1})r_i(\hat{S}_{k_1}) > \tau$ . Since  $I(S_{k_1}) = \{1\}$ ,  $a_i(\hat{S}_{k_1}) = 1$  for all  $i \in N_1(\underline{v}) \cup \{1\}$ ,  $a_i(\hat{S}_{k_1}) = a$  for all  $i \notin N_1(\underline{v}) \cup \{1\}$ , and  $g_{ij} = c$  for all  $i \neq j$ , it

follows that for all  $i \in N_1(\vartheta)$

$$r_i(\hat{S}_{k_1}) = \frac{1}{|N_1(\vartheta)| + (n-1 - |N_1(\vartheta)|)a}$$

and

$$\begin{aligned} a_i(\hat{S}_{k_1})r_i(\hat{S}_{k_1}) &= \frac{1}{|N_1(\vartheta)| + (n-1 - |N_1(\vartheta)|)a} \\ &= \frac{1}{|N_1(\vartheta)|(1-a) + (n-1)a}. \end{aligned} \quad (3.9)$$

Recall that by the assumption of the case,  $|N_1(\vartheta)| \geq \tilde{\alpha}$ . This together with  $\tilde{\alpha} = \max\left\{1, \left\lceil \frac{1 - (n-1)a\tau}{\tau(1-a)} \right\rceil\right\}$  implies

$$|N_1(\vartheta)| \geq \frac{1 - (n-1)a\tau}{\tau(1-a)} \implies \tau \geq \frac{1}{|N_1(\vartheta)|(1-a) + (n-1)a}. \quad (3.10)$$

Combining (3.9) and (3.10), we may conclude that agent  $i$  will not be infected at the time point  $t+1$ . Similar arguments show that any agent  $j \notin N_1(\vartheta) \cup \{1\}$  will not be infected at the time point  $t+1$ . Hence,  $I(S_{k_1+1}) = \{1\}$ .

We show that no new agent would get infected after this. We first show that  $I(S_{k_1+2}) = \{1\}$ . Let  $\vartheta_{k_1+1} = i$ . If  $i \notin I(S_{k_1+1})$  then as  $I(S_{k_1}) = I(S_{k_1+1})$  by Lemma 6, we have  $I(S_{k_1+1}) = I(S_{k_1+2})$ . If  $i \in I(S_{k_1+1})$  then  $i = 1$ . Moreover,  $a_1(S_{k_1+1}) = a_1(\hat{S}_{k_1}) = 1$ . Hence, by Lemma 6,  $I(S_{k_1+1}) = I(S_{k_1+2})$ . Therefore,  $I(S_{k_1+2}) = \{1\}$ . Using the same arguments repeatedly, it follows that  $I(S_t) = \{1\}$  for all  $t \geq k_1 + 2$ . Thus,  $I(S_\infty) = \{1\}$ .

**Case 2:**  $|N_1(\vartheta)| \leq \tilde{\alpha} - 1$ .

In the following claim, we show that at time point  $k_1 + 1$ , the infected set is  $N_1(\vartheta) \cup \{1\}$ .

**Claim 2.**  $I(S_{k_1+1}) = N_1(\vartheta) \cup \{1\}$ .

**Proof of the claim:** Recall that  $\tilde{\alpha} = \max\left\{1, \left\lceil \frac{1 - (n-1)a\tau}{\tau(1-a)} \right\rceil\right\}$ . First assume  $\tilde{\alpha} \neq \left\lceil \frac{1 - (n-1)a\tau}{\tau(1-a)} \right\rceil$ , i.e.,  $\tilde{\alpha} = 1$  and  $1 - (n-1)a\tau \leq 0$ . This, together with the assumption of the case, implies  $|N_1(\vartheta)| = 0$ . Therefore,  $k_1 = 1$ . Hence, to prove the claim, it is enough to show that  $I(S_1) = \{1\}$ . Note that by the definition of the process,  $a_1(\hat{S}_0) = 1$ ,  $a_i(\hat{S}_0) = a$  for all  $i \neq 1$ , and  $g_{ij} = c$  for all  $i \neq j$ . Thus,

$$\begin{aligned} r_i(\hat{S}_0) &= \frac{1}{1 + (n-2)a} \\ &\leq \frac{1}{(n-1)a} \\ &\leq \tau. \end{aligned} \quad (\text{since } 1 - (n-1)a\tau \leq 0)$$

This implies  $I(S_1) = \{1\}$ . Now assume  $\tilde{\alpha} = \left\lceil \frac{1 - (n-1)a\tau}{\tau(1-a)} \right\rceil$ . Consider an agent  $i \in N_1(\vartheta)$ . Using similar arguments as in (3.9), we may show that

$$a_i(\hat{S}_{k_1})r_i(\hat{S}_{k_1}) = \frac{1}{|N_1(\vartheta)|(1-a) + (n-1)a}.$$

This, together with  $\tilde{\alpha} = \left\lceil \frac{1 - (n-1)a\tau}{\tau(1-a)} \right\rceil$  and  $|N_1(\varrho)| \leq \tilde{\alpha} - 1$ , implies  $a_i(\hat{S}_{k_1})r_i(\hat{S}_{k_1}) > \tau$  and hence, agent  $i$  will get infected at the time point  $t + 1$ . For any  $j \notin N_1(\varrho) \cup \{1\}$ ,

$$r_j(\hat{S}_{k_1}) = \frac{1}{|N_1(\varrho)| + 1 + (n-1 - |N_1(\varrho)| - 1)a}$$

and

$$\begin{aligned} a_j(\hat{S}_{k_1})r_j(\hat{S}_{k_1}) &= \frac{a}{|N_1(\varrho)| + 1 + (n-1 - |N_1(\varrho)| - 1)a} \\ &= \frac{a}{|N_1(\varrho)|(1-a) + (n-2)a + 1}. \end{aligned}$$

Hence,  $j$  gets infected at  $t + 1$  if

$$\frac{a}{|N_1(\varrho)|(1-a) + (n-2)a + 1} > \tau \implies \frac{a - \tau(n-1)a}{\tau(1-a)} > |N_1(\varrho)|.$$

But this does not hold as  $\frac{a - \tau(n-1)a}{\tau(1-a)} \leq 0$  and  $|N_1(\varrho)| \geq 0$ . So, agent  $j$  does not get infected at  $t + 1$ . Thus,  $I(S_{k_1+1}) = N_1(\varrho) \cup \{1\}$ . This completes the proof of the claim.  $\square$

We now determine the final infected set. To do so we consider two sub-cases based on the value of  $|N_1(\varrho)|$ .

**Case 2.1:**  $|N_1(\varrho)| + 1 < \tilde{\alpha}$ .

We show that no new agent would get infected after  $k_1 + 1$ . We first show that  $I(S_{k_1+2}) = N_1(\varrho) \cup \{1\}$ . Let  $\varrho_{k_1+1} = i$ . If  $i \in I(S_{k_1+1})$  then  $i \in N_1(\varrho) \cup \{1\}$ . Moreover,  $a_i(S_{k_1+1}) = a_i(\hat{S}_{k_1}) = 1$ . Hence, by

Lemma 6,  $I(S_{k_1+1}) = I(S_{k_1+2})$ . If  $i \notin I(S_{k_1+1})$  then since  $r_i(S_{k_1+1}) = \frac{|N_1(\varrho)| + 1}{|N_1(\varrho)| + 1 + (n-1 - |N_1(\varrho)| - 1)a} \neq$

0, agent  $i$  will choose  $\min \left\{ 1, \frac{\tau}{r_i(S_{k_1+1})} \right\}$  as their action  $a_i(\hat{S}_{k_1+1})$  at  $\hat{S}_{k_1+1}$ . This means  $a_i(\hat{S}_{k_1+1})r_i(\hat{S}_{k_1+1}) \leq \tau$  and agent  $i$  will not get infected at  $k_1 + 2$ . To show that any agent  $j \in I(S_{k_1+1}) \setminus \{i\}$  will not get infected at  $k_1 + 2$ , we first prove a claim.

**Claim 3.**  $a_i(\hat{S}_{k_1+1}) \geq a$ .

**Proof of the claim:** Note that if  $a_i(\hat{S}_{k_1+1}) = 1$  then the claim holds as  $a \leq 1$ . If  $a_i(\hat{S}_{k_1+1}) = \frac{\tau}{r_i(S_{k_1+1})}$  then

$$\begin{aligned} a_i(\hat{S}_{k_1+1}) &= \frac{\tau}{r_i(S_{k_1+1})} \\ &= \tau(1-a) + \frac{\tau a(n-1)}{|N_1(\varrho)| + 1}. \end{aligned} \tag{3.11}$$

Moreover, by the assumption of the case  $|N_1(\varrho)| + 1 < \tilde{\alpha}$ . This together with  $\tilde{\alpha} = \left\lceil \frac{(n-1)a\tau}{a - \tau(1-a)} \right\rceil + 1$  and (3.11) implies

$$\begin{aligned} a_i(\hat{S}_{k_1+1}) &\geq \tau(1-a) + \frac{[\tau a(n-1)](a - \tau(1-a))}{(n-1)a\tau} \\ &= a. \end{aligned}$$

This completes the proof of the claim. □

For any  $j \notin I(S_{k_1+1}) \setminus \{i\}$ ,  $a_j(\hat{S}_{k_1+1}) = a$  and

$$r_j(\hat{S}_{k_1+1}) = \frac{|N_1(\varrho)| + 1}{|N_1(\varrho)| + 1 + (n - 1 - |N_1(\varrho)| - 2)a + a_i(\hat{S}_{k_1+1})} \quad (\text{as } g_{ij} = c \text{ for all } i \neq j).$$

Thus,

$$\begin{aligned} a_j(\hat{S}_{k_1+1})r_j(\hat{S}_{k_1+1}) &= \frac{a(|N_1(\varrho)| + 1)}{|N_1(\varrho)| + 1 + (n - 1 - |N_1(\varrho)| - 2)a + a_i(\hat{S}_{k_1+1})} \\ &\leq \frac{a(|N_1(\varrho)| + 1)}{|N_1(\varrho)| + 1 + (n - 1 - |N_1(\varrho)| - 1)a} \quad (\text{as by Claim 3, } a_i(\hat{S}_{k_1+1}) \geq a) \\ &= ar_i(\hat{S}_{k_1+1}) \\ &\leq \tau \quad (\text{as } a_i(\hat{S}_{k_1+1})r_i(\hat{S}_{k_1+1}) \leq \tau \text{ and } a_i(\hat{S}_{k_1+1}) \geq a). \end{aligned}$$

Hence, agent  $j$  will not get infected at  $k_1 + 2$ . This concludes that  $I(S_{k_1+2}) = N_1(\varrho) \cup \{1\}$ . Now using similar logic as in Case 1, we may show that no agent would get infected after this and  $I(S_\infty) = N_1(\varrho) \cup \{1\}$ .

**Case 2.2:**  $|N_1(\varrho)| + 1 \geq \bar{a}$ .

First assume that  $\varrho_{k_1+1} = i$  where  $i \in N_1(\varrho) \cup \{1\}$ . We show that  $I(S_\infty) = N$ . Note that as  $i \in N_1(\varrho) \cup \{1\}$ ,  $a_i(\hat{S}_{k_1+1}) = 1$ . Thus, for any  $j \notin N_1(\varrho) \cup \{1\}$ ,

$$r_j(\hat{S}_{k_1+1}) = \frac{|N_1(\varrho)| + 1}{|N_1(\varrho)| + 1 + (n - 1 - |N_1(\varrho)| - 1)a} \quad (\text{as } g_{ij} = c \text{ for all } i \neq j)$$

and hence,

$$\begin{aligned} a_j(\hat{S}_{k_1+1})r_j(\hat{S}_{k_1+1}) &= \frac{a(|N_1(\varrho)| + 1)}{|N_1(\varrho)| + 1 + (n - 1 - |N_1(\varrho)| - 1)a} \\ &= \frac{a(|N_1(\varrho)| + 1)}{(|N_1(\varrho)| + 1)(1 - a) + (n - 1)a} \\ &\geq \frac{a\bar{a}}{\bar{a}(1 - a) + (n - 1)a} \quad (\text{as } |N_1(\varrho)| + 1 \geq \bar{a}) \\ &> \tau. \quad (\text{as } \bar{a} > \frac{(n - 1)a\tau}{a - \tau(1 - a)}) \end{aligned}$$

Therefore,  $I(S_{k_1+2}) = N$  and  $I(S_\infty) = N$ .

Now assume that  $\varrho_{k_1+1} = i$  where  $i \notin N_1(\varrho) \cup \{1\}$ . We show that  $I(S_{k_1+2}) = N \setminus i$ . Since  $i \notin I(S_{k_1+1})$  and  $\varrho_{k_1+1} = i$ , agent  $i$  will not get infected at  $k_1 + 2$  (Observation 4). Consider  $j \notin N_1(\varrho) \cup \{1\}$  with  $j \neq i$ . We first prove a claim.

**Claim 4.**  $\tau < a_i(\hat{S}_{k_1+1}) < a$ .

**Proof of the claim:** We show that  $\tau < \frac{\tau}{r_i(S_{k_1+1})} < a$ . This together with  $a < 1$  proves the claim. As

$$r_i(S_{k_1+1}) = \frac{|N_1(\varrho)| + 1}{|N_1(\varrho)| + 1 + (n - 1 - |N_1(\varrho)| - 1)a} < 1, \text{ we have } \tau < \frac{\tau}{r_i(S_{k_1+1})}. \text{ To see } \frac{\tau}{r_i(S_{k_1+1})} < a,$$

recall that by (3.11)

$$a_i(\hat{S}_{k_1+1}) = \tau(1-a) + \frac{\tau a(n-1)}{|N_1(\varrho)| + 1}.$$

Moreover, by the assumption of the case  $|N_1(\varrho)| + 1 \geq \bar{a}$ . This, together with  $\bar{a} > \frac{(n-1)a\tau}{a - \tau(1-a)}$ , implies

$$\begin{aligned} a_i(\hat{S}_{k_1+1}) &< \tau(1-a) + \frac{[\tau a(n-1)](a - \tau(1-a))}{(n-1)a\tau} \\ &= a. \end{aligned}$$

This completes the proof of the claim.  $\square$

For any  $j \notin I(S_{k_1+1}) \setminus \{i\}$ ,  $a_j(\hat{S}_{k_1+1}) = a$  and

$$r_j(\hat{S}_{k_1+1}) = \frac{|N_1(\varrho)| + 1}{|N_1(\varrho)| + 1 + (n-1 - |N_1(\varrho)| - 2)a + a_i(\hat{S}_{k_1+1})} \quad (\text{as } g_{ij} = c \text{ for all } i \neq j).$$

Thus,

$$\begin{aligned} a_j(\hat{S}_{k_1+1})r_j(\hat{S}_{k_1+1}) &= \frac{a(|N_1(\varrho)| + 1)}{|N_1(\varrho)| + 1 + (n-1 - |N_1(\varrho)| - 2)a + a_i(\hat{S}_{k_1+1})} \\ &> \frac{a(|N_1(\varrho)| + 1)}{|N_1(\varrho)| + 1 + (n-1 - |N_1(\varrho)| - 1)a} \quad (\text{as by Claim 4, } a_i(\hat{S}_{k_1+1}) < a) \\ &= \frac{a(|N_1(\varrho)| + 1)}{(|N_1(\varrho)| + 1)(1-a) + (n-1)a} \\ &\geq \frac{a\bar{a}}{\bar{a}(1-a) + (n-1)a} \quad (\text{as } |N_1(\varrho)| + 1 \geq \bar{a}) \\ &> \tau. \quad (\text{as } \bar{a} > \frac{(n-1)a\tau}{a - \tau(1-a)}) \end{aligned}$$

Hence, agent  $j$  will get infected at  $k_1 + 2$ . This concludes that  $I(S_{k_1+2}) = N \setminus \{i\}$ .

To determine the final infected set, we now distinguish two cases based on whether  $\varrho_{k_1+2} = i$  or not.

**Case 2.2.1:**  $\varrho_{k_1+2} = i$

We show that the final infected set will be  $N \setminus \{i\}$ . Since by our assumption  $\varrho_{k_1+2} = i$  and  $i \notin I(S_{k_1+2})$ , by Observation 4,  $i \notin I(S_{k_1+3})$ . Hence,  $I(S_{k_1+3}) = N \setminus \{i\}$ . We now show that  $i$  will not get infected after this. At time point  $k_1 + 2$ ,

$$r_i(\hat{S}_{k_1+2}) = \frac{(|N_1(\varrho)| + 1) + a(n-1 - |N_1(\varrho)| - 1)}{(|N_1(\varrho)| + 1) + (n-1 - |N_1(\varrho)| - 1)a} = 1.$$

Therefore,  $a_i(\hat{S}_{k_1+2}) = \tau$ . At  $k_1 + 3$ , if  $\varrho_{k_1+3} = i$ , then agent  $i$  would not get infected at  $k_1 + 4$  (Observation 4). On the other hand, if  $\varrho_{k_1+3} \neq i$  then as  $a_i(\hat{S}_{k_1+3}) = a_i(\hat{S}_{k_1+2}) = \tau$ , agent  $i$  would remain uninfected at  $k_1 + 4$ . Continuing in this manner, we may show that  $i$  will not get infected after this. Thus,  $I(S_\infty) = N \setminus \{i\}$ .

**Case 2.2.2:**  $\varrho_{k_1+2} \neq i$

We show that the final infected set will be  $N$ . Since  $I(S_{k_1+2}) = N \setminus \{i\}$ ,  $r_i(\hat{S}_{k_1+2}) = 1$ . Moreover as  $a_i(S_{k_1+2}) = a_i(\hat{S}_{k_1+1}) > \tau$  (by Claim 4) and  $\varrho_{k_1+2} \neq i$ , it follows that  $a_i(\hat{S}_{k_1+2}) > \tau$ . Combining this

two we have  $a_i(\hat{S}_{k_1+2})r_i(\hat{S}_{k_1+2}) > \tau$ . Thus, agent  $i$  will get infected at  $k_1 + 3$ . Hence,  $I(S_{k_1+3}) = N$  and  $I(S_\infty) = N$ .

**Step 2:** To begin with we claim  $\tilde{\alpha} \leq n - 1$ . To see this, observe that  $\left\lceil \frac{1 - (n-1)a\tau}{\tau(1-a)} \right\rceil \leq \left\lceil \frac{1-a}{\tau(1-a)} \right\rceil \leq n - 1$  as  $(n-1)\tau \geq 1$ . Hence,  $\tilde{\alpha} \leq n - 1$ . Moreover, recall that  $\bar{\alpha} \geq 2$ . We now find the distribution of  $I(S_\infty)$ . First, assume that  $\tilde{\alpha} + 1 \leq \bar{\alpha}$ . Therefore, by the above cases we have

- $I(S_\infty) = \{1\}$  if  $|N_1(\underline{v})| \in \{0, \tilde{\alpha}, \tilde{\alpha} + 1, \dots, n - 1\}$ ,
- $I(S_\infty) = N_1(\underline{v}) \cup \{1\}$  if  $|N_1(\underline{v})| \in \{1, 2, \dots, \tilde{\alpha} - 1\}$ .

Moreover, as  $\mathbb{P}$  is uniform, any two subsets of  $N$  with same cardinality have the same probability. These observations together with Lemma 3 yield

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\tilde{\alpha} - 1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \tilde{\alpha}], \\ 0 & \text{otherwise.} \end{cases}$$

Now assume that  $\tilde{\alpha} + 1 > \bar{\alpha} \geq 2$ . By Case 1 and Case 2, we have

- (i)  $I(S_\infty) = \{1\}$  if  $|N_1(\underline{v})| \in \{0, \tilde{\alpha}, \tilde{\alpha} + 1, \dots, n - 1\}$ ,
- (ii)  $|I(S_\infty)| = |N_1(\underline{v})| + 1$  with  $1 \in I(S_\infty)$  if  $|N_1(\underline{v})| \in \{1, 2, \dots, \bar{\alpha} - 2\}$ ,
- (iii)  $|I(S_\infty)| = n$  if  $|N_1(\underline{v})| \in \{\bar{\alpha} - 1, \dots, \tilde{\alpha} - 1\}$  and there is no  $i \in N$  such that  $k_i = k_1 + 1$  and  $\underline{v}_{k_1+2} = i$ , and
- (iv)  $|I(S_\infty)| = n - 1$  with  $1 \in I(S_\infty)$  if  $|N_1(\underline{v})| \in \{\bar{\alpha} - 1, \dots, \tilde{\alpha} - 1\}$  and there is  $i \in N$  such that  $k_i = k_1 + 1$  and  $\underline{v}_{k_1+2} = i$ .

Since  $|N_1|$  follows uniform distribution on  $\{0, 1, \dots, n - 1\}$  and any two subsets of  $N$  with the same cardinality have the same probability, by (i) and (ii) we have

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\tilde{\alpha} - 1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \bar{\alpha} - 1]. \end{cases}$$

We calculate the probability of  $|I(S_\infty)| = n - 1$ . By (iv) we have

$$\begin{aligned} & \mathbb{P}(\underline{v} \mid |N_1(\underline{v})| \in \{\bar{\alpha} - 1, \dots, \tilde{\alpha} - 1\} \text{ and } \exists i \neq 1 \text{ such that } k_i = k_1 + 1 \text{ and } \underline{v}_{k_1+2} = i) \\ &= \sum_{w=\bar{\alpha}-1}^{\tilde{\alpha}-1} P(\underline{v} \mid |N_1(\underline{v})| = w \text{ and } \exists i \neq 1 \text{ such that } k_i = k_1 + 1 \text{ and } \underline{v}_{k_1+2} = i) \\ &= \sum_{w=\bar{\alpha}-1}^{\tilde{\alpha}-1} \sum_{t=w+1}^{\infty} P(\underline{v} \mid |N_1(\underline{v})| = w \text{ and } k_1 = t \text{ and } \exists i \neq 1 \text{ such that } k_i = t + 1 \text{ and } \underline{v}_{t+2} = i) \\ &= \sum_{w=\bar{\alpha}-1}^{\tilde{\alpha}-1} \sum_{t=w+1}^{\infty} {}^{n-1}C_w \times \left( \frac{w! \binom{t-1}{w}}{n^{t-1}} \right) \times \frac{1}{n} \times {}^{(n-w-1)}C_1 \times \frac{1}{n^2} \end{aligned}$$



$$\begin{aligned}
 &= \frac{(n-1)!}{n^3} \sum_{w=\bar{\alpha}-1}^{\bar{\alpha}-1} \frac{1}{(n-w-2)!} \sum_{t=w+1}^{\infty} \binom{\{t-1\}_w}{n^{t-1}} \\
 &= \eta(\tilde{\alpha}, \bar{\alpha}, n).
 \end{aligned}$$

Note that by (i)-(iv),

$$\sum_{m=1}^{\bar{\alpha}-1} P(|I(S_\infty)| = m) + P(|I(S_\infty)| = n-1) + P(|I(S_\infty)| = n) = 1.$$

Therefore,

$$\begin{aligned}
 P(|I(S_\infty)| = n) &= 1 - \sum_{m=1}^{\bar{\alpha}-1} P(|I(S_\infty)| = m) - P(|I(S_\infty)| = n-1) \\
 &= \frac{\tilde{\alpha} - (\bar{\alpha} - 1)}{n} - \eta(\tilde{\alpha}, \bar{\alpha}, n).
 \end{aligned}$$

Since any two subsets of  $N$  with the same cardinality have the same probability, combining all the above observations, we have the following distribution of the infected set.

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\tilde{\alpha} - 1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \bar{\alpha} - 1], \\ \frac{\eta(\tilde{\alpha}, \bar{\alpha}, n)}{n-1} & \text{if } 1 \in J \text{ and } |J| = n-1, \\ \frac{\tilde{\alpha} - (\bar{\alpha} - 1)}{n} - \eta(\tilde{\alpha}, \bar{\alpha}, n) & \text{if } |J| = n, \text{ i.e., } J = N, \\ 0 & \text{otherwise.} \end{cases}$$

This completes the proof of the theorem. ■

As in the previous subsections, we now proceed to explore the limiting distribution of the action profile. The following notations will be helpful in presenting the results:

$$\tilde{\beta} = \min\{\lfloor (n-1)\tau \rfloor + 1, \tilde{\alpha} + 1\} \text{ and } \bar{\beta} = \min\{\lfloor (n-1)\tau \rfloor + 1, \bar{\alpha}\}. \quad (3.12)$$

**Theorem 8.** Suppose  $\frac{1}{n-1} \leq \tau < a < 1$ . If  $\tilde{\alpha} + 1 \leq \bar{\alpha}$ , the limiting distribution of the action profile is given by

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{\tilde{\alpha} - \tilde{\beta} + 1}{n} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [\tilde{\beta}, \tilde{\alpha}], \\ 0 & \text{otherwise,} \end{cases}$$

whereas if  $2 \leq \bar{\alpha} < \tilde{\alpha} + 1$ , the limiting distribution is given by

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 + \frac{\bar{\beta} - \bar{\alpha}}{n} - \eta(\tilde{\alpha}, \bar{\alpha}, n) & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [\bar{\beta}, \bar{\alpha} - 1], \\ \frac{\eta(\tilde{\alpha}, \bar{\alpha}, n)}{n-1} & \text{if } \underline{x} \in A_{n-1}, \\ 0 & \text{otherwise,} \end{cases}$$

where  $\eta(\tilde{\alpha}, \bar{\alpha}, n) = \frac{(n-1)!}{n^3} \sum_{w=\bar{\alpha}-1}^{\tilde{\alpha}-1} \frac{1}{(n-w-2)!} \sum_{t=w+1}^{\infty} \binom{\{w\}^{t-1}}{n^{t-1}}$ , and  $\left\{ \begin{matrix} p \\ q \end{matrix} \right\}$  is the Stirling number of the second kind with parameters  $p$  and  $q$ .

The proof of this theorem can be found in Appendix D (subsection D.3). Once again, observations similar to those made in §3.1 and §3.3 can be noted here for Theorem 7 and Theorem 8 as well, but we do not elaborate upon them to avoid the possibility of sounding repetitive.

The next two theorems deal with situation when  $\tau$  is less than or equal to  $\frac{a}{(n-1)}$ . Theorem 9 characterizes the limiting distribution of the infected set and Theorem 10 characterizes the limiting distribution of the action profile.

**Theorem 9.** Suppose  $\tau < a < 1$ . If  $\tau = \frac{a}{n-1}$ , the limiting distribution of the infected set is given by

$$\mathbb{P}(I(S_\infty) = N) = 1,$$

whereas if  $\tau < \frac{a}{n-1}$ , the limiting distribution is given by

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} \frac{1}{n^2} & \text{if } 1 \in J \text{ and } |J| = n-1, \\ 1 - \frac{n-1}{n^2} & \text{if } |J| = n, \text{ i.e., } J = N, \\ 0 & \text{otherwise.} \end{cases}$$

The proof of this theorem can be found in Appendix B (subsection B.3).

**Theorem 10.** Suppose  $\tau < a < 1$ . If  $\tau = \frac{a}{n-1}$ , the limiting distribution of the action profile is given by

$$\mathbb{P}(a_N(S_\infty) = \underline{1}) = 1,$$

whereas if  $\tau < \frac{a}{n-1}$ , the limiting distribution is given by

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{n-1}{n^2} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n^2} & \text{if } \underline{x} \in A_{n-1}, \\ 0 & \text{otherwise.} \end{cases}$$

The proof of this theorem can be found in Appendix D (subsection D.4). The results in these final set of theorems are also consistent with our intuition. It says that if  $\tau$  is small enough, the eventually infected set is either of size  $n-1$  or  $n$  with probability 1.

**Remark 3.** The connection between the initial action and the limiting distribution is an important question that may come to a reader's mind. In fact, it may intuitively seem at a quick thought that for every  $k \leq n$ , the probability that  $k$  or more people are infected in the long run will be weakly increasing in the initial action  $a$ . In other words, a higher value of the initial action  $a$  makes it likely to have more infected people in the limit. The intuition is (kind of) natural as a higher value of  $a$  at the initial epoch means people are roaming more freely initially, and thus leads to a higher risk of spreading the virus initially, which may then multiply over time. However, this intuition does not go through the game theoretical nature of the model. The reason is people are strategic, and they take more precautions (by lowering their  $a$ ) at the next epoch when they realize the virus has already spread (more) at the first epoch. For example, when  $n = 5$ , for  $\tau = 0.05$  and  $a = 0.2$ , the disease spreads completely, i.e., all the agents are infected in the long run. However, keeping  $\tau$  at 0.05, for  $a = 0.35$ , the probability of all the agents being infected is 0.84. Similarly, for  $\tau = 0.35$ , three or more are infected in limit with probability 0.2 for  $a = 0$ , but for  $a = 0.8$ , the same event has a probability of 0. Note that, the counter intuition, that is, fewer people are infected in the long run as  $a$  increases, is not true either.

#### 4. RESULTS UNDER RECOVERY

In this section, we consider situations where an infected agent recovers after  $\kappa$ ,  $\kappa \in \mathbb{N}$ , epochs of time from the time of getting the infection, and analyze the corresponding stochastic process. Let the set of agents who recover from the infection at time  $t$  be denoted by  $R_t$ . Thus,  $R_t$  is the set of agents  $I(S_{t-\kappa})$  who got the virus at time  $t - \kappa$ . If  $t - \kappa$  is negative,  $R_t$  is defined as the empty set. Furthermore, the agents who are infected at the beginning (that is, at time  $t = 0$ ) recover at time  $t = \kappa$ .<sup>5</sup> We additionally assume that an agent decides to stay (completely) at home (that is, goes for the action 0) on the day they recover. This is a simplifying assumption but not unrealistic.

We now detail the changes in the stochastic process considered before under the current setup. The infected set at time  $t + 1$  is given by  $I(S_{t+1}) = I(S_t) \cup \{j : a_j(\hat{S}_t)r_j(\hat{S}_t) > \tau(j)\} \setminus R_{t+1}$ , and the actions at time  $t + 1$  is given by  $a_j(S_{t+1}) = 0$  for all  $j \in R_{t+1}$ , and  $a_j(S_{t+1}) = a_j(\hat{S}_t)$  for all  $j \notin R_{t+1}$ .

In what follows, we present our results under recovery. Except for the recovery component, we stick to the assumptions we made in Section 3 for the case of non-recovery. Recall that  $a$  denotes the (common) initial action of the agents. We provide results for the cases for every  $\tau$  where  $a$  is 0 and

<sup>5</sup>In other words, we assume that the agents who are infected at  $t = 0$ , actually have got infected at  $t = 0$  only (and were not infected from the past).

1. For both these extreme cases, we show that the epidemic ends in the long run (and consequently, people roam freely).

We first prove a general lemma that shows that irrespective of the initial action, if it happens at some epoch of a(ny) DVSP that all the infected agents have actions 1 and no new agent gets infected at the immediate next epoch, then all agents will eventually recover.

**Lemma 5.** *Consider  $\underline{v} \in N_\infty$  and let  $\hat{t} \in \mathbb{N}_0$  be such that  $a_i(\hat{S}_{\hat{t}}) = 1$  for all  $i \in I(\hat{S}_{\hat{t}})$  and  $I(\hat{S}_{\hat{t}}) \supseteq I(\hat{S}_{\hat{t}+1})$ . Then,  $I(S_\infty) = \emptyset$ .*

**Proof:** We prove the lemma by showing that for all  $r, s \in \mathbb{N}_0$  with  $r < s$ ,  $I(\hat{S}_{\hat{t}+1+r}) \supseteq I(\hat{S}_{\hat{t}+1+s})$ . Assume for contradiction there exists  $p \in \mathbb{N}$  such that  $I(\hat{S}_{\hat{t}+1}) \supseteq \dots \supseteq I(\hat{S}_{\hat{t}+p})$  but  $I(\hat{S}_{\hat{t}+p}) \not\supseteq I(\hat{S}_{\hat{t}+p+1})$ , i.e., after epoch  $\hat{t}$  there was no new infection till  $\hat{t} + p$ , and at  $\hat{t} + p + 1$  some new agents are infected. Let  $i \in N$  be such that  $i \in I(\hat{S}_{\hat{t}+p+1})$  but  $i \notin I(\hat{S}_{\hat{t}+p})$ . This means  $\underline{v}_{\hat{t}+p} \neq i$  and  $a_i(\hat{S}_{\hat{t}+p-1})r_i(\hat{S}_{\hat{t}+p-1}) \leq \tau < a_i(\hat{S}_{\hat{t}+p})r_i(\hat{S}_{\hat{t}+p})$ . As  $\underline{v}_{\hat{t}+p} \neq i$ , we have  $a_i(\hat{S}_{\hat{t}+p-1}) = a_i(\hat{S}_{\hat{t}+p})$ . Thus,

$$r_i(\hat{S}_{\hat{t}+p-1}) < r_i(\hat{S}_{\hat{t}+p}). \quad (4.1)$$

Let  $\underline{v}_{\hat{t}+p} = j$ . As  $a_k(\hat{S}_{\hat{t}}) = 1$  for all  $k \in I(\hat{S}_{\hat{t}})$  and  $I(\hat{S}_{\hat{t}}) \supseteq \dots \supseteq I(\hat{S}_{\hat{t}+p})$ , (4.1) and the Definition of the process together imply that  $j \notin I(\hat{S}_{\hat{t}+p-1})$  and  $a_j(\hat{S}_{\hat{t}+p-1}) > a_j(\hat{S}_{\hat{t}+p})$ . Further, as  $I(\hat{S}_{\hat{t}+p-1}) \supseteq I(\hat{S}_{\hat{t}+p})$  and  $\underline{v}_{\hat{t}+p} = j$ , it must be that  $a_j(\hat{S}_{\hat{t}+p-1})r_j(\hat{S}_{\hat{t}+p-1}) \leq \tau$  and  $a_j(\hat{S}_{\hat{t}+p})r_j(\hat{S}_{\hat{t}+p}) = \tau$ . Combining the two observations, we have  $r_j(\hat{S}_{\hat{t}+p-1}) < r_j(\hat{S}_{\hat{t}+p})$ . But this is a contradiction. To see this first note that  $I(\hat{S}_{\hat{t}+p-1}) \supseteq I(\hat{S}_{\hat{t}+p})$  and  $a_h(\hat{S}_{\hat{t}+p-1}) = 1$  for all  $h \in I(\hat{S}_{\hat{t}+p-1})$ . Moreover, as  $\underline{v}_{\hat{t}+p} = j$ , we have  $a_k(\hat{S}_{\hat{t}+p-1}) = a_k(\hat{S}_{\hat{t}+p})$  for all  $k \in N \setminus I(\hat{S}_{\hat{t}+p-1})$  and  $a_l(\hat{S}_{\hat{t}+p}) = 0$  for all  $l \in I(\hat{S}_{\hat{t}+p-1}) \setminus I(\hat{S}_{\hat{t}+p})$ . Thus, it follows that  $r_j(\hat{S}_{\hat{t}+p-1}) \geq r_j(\hat{S}_{\hat{t}+p})$ . ■

We are now ready to present and prove our results for the cases  $a = 0$  and  $a = 1$ .

#### 4.1 RESULTS WHEN $a = 0$

In this subsection, we consider the situation where the (common) initial action  $a$  equals 0. The next theorem describes the limiting distribution of the infected set of agents and their action profiles. As we have stated earlier, it shows that all the agents will recover in the long run, and the action profile will have a degenerate distribution at  $\underline{1}$ .

**Theorem 11.** *Suppose  $a = 0$ . Then the limiting distribution of the infected set is given by*

$$\mathbb{P}(I(S_\infty) = \emptyset) = 1,$$

*and the limiting distribution of the action profile is given by*

$$\mathbb{P}(a_N(S_\infty) = \underline{1}) = 1.$$

**Proof:** We first prove the distribution of the infected set. Fix an agent sequence  $\underline{v} \in N_\infty$  and let  $S$  be the DVSP induced by  $\underline{v}$ . We show that  $I(S_\infty) = \emptyset$ . Observe that Claim 1 in the proof of Theorem 1 holds in the setup of this theorem as well. We distinguish two cases based on the values of  $k_1$ .

**Case 1:**  $k_1 \geq \kappa$ .

The assumption of the claim implies that agent 1 will get recovered before getting a chance to update their action. As their initial action is 0 and they are the only agent infected at the beginning, it means that for any other agent  $i$ ,  $r_i(\hat{S}_t) = 0$  for all  $t$  with  $0 \leq t \leq \kappa$ . Therefore, no new agent will be infected till  $\kappa$ . At  $\kappa$ , agent 1 will recover as per the process, and no one will get infected further.

**Case 2:**  $k_1 < \kappa$ .

Note that the assumption implies agent 1 gets a chance to update their action before they recover. Thus, as in Theorem 1, we consider two sub-cases. Recall the definition of  $\alpha$  as defined in (3.1).

**Case 2.1:**  $|N_1(\underline{v})| \geq \alpha$ .

As in Case 1 of Theorem 1, we can show that  $I(S_1) = \dots = I(S_{k_1+1}) = \{1\}$  and  $a_1(\hat{S}_{k_1}) = 1$ . Hence, by Lemma 5,  $I(S_\infty) = \emptyset$ .

**Case 2.2:**  $|N_1(\underline{v})| \leq \alpha - 1$ .

As  $k_1 < \kappa$ , using similar arguments as in Case 2 of Theorem 1, we can show that  $N_1(\underline{v}) \subseteq I(S_{k_1+1}) \subseteq N_1(\underline{v}) \cup \{1\}$  with  $a_i(S_{k_1+1}) = 1$  for all  $i \in I(S_{k_1+1})$  and  $a_i(S_{k_1+1}) = 0$  for all  $i \notin I(S_{k_1+1})$ . At  $k_1 + 1$  epoch, if  $\underline{v}_{k_1+1} \in I(S_{k_1+1})$  then they will choose the the same action 1, and we will have  $I(S_{k_1+2}) \subseteq I(S_{k_1+1})$ . If  $\underline{v}_{k_1+1} \notin I(S_{k_1+1})$ , they will choose their action  $b_{\underline{v}_{k_1+1}}(S_{k_1+1}) = \tau$  as all the uninfected agents have action 0 and all the infected agents have action 1. Therefore, no new agent will get infected at  $k_1 + 2$ , and we have  $I(S_{k_1+2}) \subseteq I(S_{k_1+1})$ . As  $a_i(\hat{S}_{k_1+1}) = 1$  for all  $i \in I(S_{k_1+1})$ , by Lemma 5, it follows that  $I(S_\infty) = \emptyset$ .

As  $\underline{v}$  is an arbitrary agent sequence in  $N_\infty$  and the cases are exhaustive, we have  $\mathbb{P}(I(S_\infty) = \emptyset) = 1$ .

For the second part of the theorem, take any agent sequence  $\underline{v} \in N_\infty$ . Then we have  $I(S_\infty) = \emptyset$ . This means there exists  $\hat{t}$  such that  $I(S_{\hat{t}}) = I(S_{\hat{t}+1}) = \dots = \emptyset$ . As there is no infected agent after epoch  $\hat{t}$ , any agent who updates their action after epoch  $\hat{t}$  will choose their best response as 1. This together with the fact that at  $\underline{v}$ , every agent appears infinitely many times, we conclude that  $a_N(S_\infty) = \underline{1}$ . Therefore,  $\mathbb{P}(a_N(S_\infty) = \underline{1}) = 1$ . ■

## 4.2 RESULTS WHEN $a = 1$

This subsection considers the situation where the (common) initial action  $a$  equals 1. As was the case for  $a = 0$ , here too, we show that in the long run, the epidemic vanishes, and people roam freely.

**Theorem 12.** *Suppose  $a = 1$ . Then the limiting distribution of the infected set is given by*

$$\mathbb{P}(I(S_\infty) = \emptyset) = 1,$$

*and the limiting distribution of the action profile is given by*

$$\mathbb{P}(a_N(S_\infty) = \underline{1}) = 1.$$

**Proof:** We prove the theorem by showing that for any agent sequence  $\underline{v}$  in  $N_\infty$ ,  $I(S_\infty) = \emptyset$  where  $S$  is the DVSP induced by  $\underline{v}$ . Consider an agent sequence  $\underline{v}$  and the DVSP  $S$  induced by  $\underline{v}$ . First, assume that  $\kappa \geq 2$ . Because of this assumption, using similar arguments as in the proof of Theorem 3, we can show that

- (i) if  $\tau \geq \frac{1}{n-1}$ , then  $I(S_1) = \{1\}$ , and
- (ii) if  $\tau < \frac{1}{n-1}$ , then
  - (a) either  $I(S_1) = N$  and  $a_j(S_1) = 1$  for all  $j \in N$
  - or
  - (b) there exists  $i \in N \setminus 1$  with  $a_j(S_1) = a_j(S_2) = 1$  for all  $j \in N \setminus i$  such that either  $I(S_1) = I(S_2) = N \setminus i$  or  $I(S_1) = N \setminus i$  and  $I(S_2) = N$ .

It's easy to see that if either (i) or (ii)-(a) holds, by Lemma 5, we will have  $I(S_\infty) = \emptyset$ . Suppose (ii)-(b) holds with  $I(S_1) = I(S_2) = N \setminus i$ ,  $a_j(S_1) = a_j(S_2) = 1$  for all  $j \in N \setminus i$ . This means  $I(S_1) = I(S_2) = N \setminus i$  and  $a_j(\hat{S}_1) = 1$  for all  $j \in N \setminus i$ . Thus, by Lemma 5,  $I(S_\infty) = \emptyset$ . Now, suppose (ii)-(b) holds with  $I(S_1) = N \setminus i$ ,  $I(S_2) = N$  with  $a_j(S_1) = a_j(S_2) = 1$  for all  $j \in N \setminus i$ . At epoch  $\kappa \geq 2$ , agent 1 recovers, i.e.,  $I(S_\kappa) = N \setminus 1$ . This means  $r_i(S_\kappa) = 1$ . So, if agent 1 gets a chance to update their action, they would choose  $a_1(\hat{S}_\kappa) = \tau$  as their best response. Otherwise, it would be  $a_1(\hat{S}_\kappa) = 0$ . Thus, agent 1 will not get infected at  $\kappa + 1$ . Hence,  $I(S_{\kappa+1}) = i$  as all the agents except  $i$  will recover at  $\kappa + 1$ . At epoch  $\kappa + 1$ , all the uninfected agents have action less than or equal to  $\tau$ , thus, whoever agent updates their action at  $\kappa + 1$ , no one will get infected at  $\kappa + 2$ . Further, at epoch  $\kappa + 2$  agent  $i$  will get infected. Therefore,  $I(S_{\kappa+2}) = \emptyset$ . No one will get infected after this, hence,  $I(S_\infty) = \emptyset$ . This shows that if  $\kappa \geq 2$ ,  $I(S_\infty) = \emptyset$ .

Now, assume that  $\kappa = 1$ . This means agent 1 will recover at epoch 1 and  $a_1(S_1) = 0$ . Suppose  $\tau \geq \frac{1}{n-1}$ . Using similar arguments as in the proof of Theorem 3, we can show that at epoch 1,

no new agent will get infected, implying  $I(S_1) = \emptyset$ . Therefore,  $I(S_\infty) = \emptyset$ . Suppose  $\tau < \frac{1}{n-1}$ . If  $v_0 = 1$  then using similar arguments as in the proof of Theorem 3, it can be shown that at epoch 1, all the agents other than 1 will get infected. We claim that  $I(S_2) = \emptyset$  yielding  $I(S_\infty) = \emptyset$ . To see this, observe that if agent 1 updates their action at epoch 2, they would change it to  $\tau$  as all the other agents are infected with non-zero actions. Otherwise, their action would remain the same, i.e.,  $a_1(\hat{S}_1) = 0$ . Thus, agent 1 will not get further infected at epoch 2. Also, as  $\kappa = 1$ , all the other agents will recover at epoch 2. Hence,  $I(S_2) = \emptyset$ .

If  $v_0 = i$  ( $\neq 1$ ) then at epoch 1, all the agents other except agents  $i$  and 1 will get infected (using similar arguments as in Case 2 of Theorem 3). Moreover, agent  $i$  will update their action to  $(n-1)\tau$ , i.e.,  $a_i(S_1) = (n-1)\tau$ . We consider different possibilities for  $v_1$ . First, consider  $v_1 = i$ . This means at epoch 2, agent  $i$  will not get infected, and as  $a_1(S_1) = 0$ , agent 1 will not get infected either. Further, all the other agents recover at epoch 2. Combining all these, we have  $I(S_2) = \emptyset$ . Now, consider  $v_1 = j$  ( $\notin \{1, i\}$ ). As  $j \in I(S_1)$  and  $a_j(S_1) = 1$ , it means  $a_j(\hat{S}_1) = 1$ . Thus, at epoch 2, agent  $i$  will get infected (see Case 2.2 in the proof of Theorem 3). Also, as  $\kappa = 1$ , all agents except 1 and  $i$  will get recovered at this epoch. This means  $a_k(S_2) = 0$  for all  $k \neq i$  (recall that  $a_1(S_1) = 0$  and  $v_1 \neq 1$ ). Therefore, none of these agents will get infected at the next epoch, i.e., at epoch 3. In addition, agent  $i$  will be recovered implying  $I(S_3) = \emptyset$ .

Finally, consider  $v_1 = 1$ . As  $I(S_1) = N \setminus \{1, i\}$  with  $a_k(S_1) = 1$  for all  $k \in I(S_1)$  and  $a_i(S_1) = (n-1)\tau$ , agent 1 will choose their action as  $a_1(\hat{S}_1) = \tau \frac{(n-2) + (n-1)\tau}{(n-2)}$ . Also, at epoch 2, agent  $i$  will get infected (see Case 2.2 in the proof of Theorem 3), and all the agents in  $N \setminus \{1, i\}$  will be recovered. Thus,  $a_1(S_2) = \tau \frac{(n-2) + (n-1)\tau}{(n-2)}$  and  $a_k(S_2) = 0$  for all  $k \in N \setminus \{1, i\}$ . If  $v_2 = 1$ , then as  $I(S_2) = i$ ,  $a_i(S_2) > 0$ , and  $a_k(S_2) = 0$  for all  $k \in N \setminus \{1, i\}$ , agent 1 will update their action to  $\tau$ , and will not get infected in the next epoch. Further, as  $i$  will be recovered at the next epoch implying that  $I(S_3) = \emptyset$ . If  $v_2 = i$ , as  $I(S_2) = i$ ,  $i$  will update their action to 1, and as a result agent 1 will get infected again at epoch 3. However, as  $\kappa = 1$ , agent  $i$  will get recovered at epoch 3. This means all the uninfected agents at epoch 3 have action as 0. Hence, at epoch 4, no new agent will get infected and agent 1 will recover, implying  $I(S_4) = \emptyset$ . If  $v_2 = r$  ( $\notin \{1, i\}$ ), agent  $r$  will update their action to  $\frac{\tau}{b_r(S_2)} = \frac{\tau((n-1)\tau + a_1(S_2))}{(n-1)\tau}$ . We claim  $I(S_3) = \emptyset$ . To see this, note that agent  $i$  will be recovered

at 3. Among other agents, only agents 1 and  $r$  have positive actions. So, it is enough to show agents 1 and  $r$  will not get infected. As agent  $r$  updates their action to  $a_r(\hat{S}_2) = \frac{\tau}{b_r(S_2)}$ , they will not get infected. For agent 1, we show that they will not get infected by showing that  $a_r(\hat{S}_2) > a_1(\hat{S}_2)$ . Note that  $a_1(\hat{S}_2) = a_1(\hat{S}_1)$  and  $a_r(\hat{S}_2) = \frac{\tau((n-1)\tau + a_1(S_2))}{(n-1)\tau}$ . Thus,  $a_r(\hat{S}_2) > a_1(\hat{S}_2)$  holds iff

$$\begin{aligned} & \tau \left( \frac{(n-1)\tau + \tau \frac{(n-2)+(n-1)\tau}{(n-2)}}{(n-1)\tau} \right) > \tau \frac{(n-2) + (n-1)\tau}{(n-2)} \\ \iff & 1 + \frac{(n-2) + (n-1)\tau}{(n-2)(n-1)} > \frac{(n-2) + (n-1)\tau}{(n-2)} \\ \iff & \frac{(n-2) + (n-1)\tau}{(n-2)(n-1)} > \frac{(n-1)\tau}{(n-2)} \\ \iff & \frac{1}{(n-1)} > \tau. \end{aligned}$$

Therefore,  $I(S_3) = \emptyset$ . This shows that  $I(S_\infty) = \emptyset$  for  $\kappa = 1$  and completes the first part of the theorem. The second part of the theorem follows from the same arguments used in the proof of Theorem 11. ■

### 4.3 EVIDENCE FROM SIMULATION

Although we furnish a thorough simulation study for the model without recovery in Section 6, here we briefly mention that we also ran a simulation study for this general model with recovery and the following are our findings

- For any  $0 < \tau < 1$  and  $\kappa > 0$ , both  $a = 0$  and  $a = 1$ , indeed the population becomes completely uninfected.
- Consistent with our intuition, the time it takes to become disease-free is monotonic with  $\kappa$ , i.e. with higher recovery time, it takes longer for the disease to vanish.
- Similar results of disease-free population seem to be true for  $0 < a < 1$  cases as well, however, since we leave the proofs for these scenarios of general  $a$  for future, we do not comment here on the time it takes depending on small or large value of  $a$

## 5. A MODEL UNDER SIMULTANEOUS RESPONSE

In our model (as defined in Section 2), exactly one agent is chosen randomly at every epoch, who then plays their best response to the current state. In this section, we discuss another model where agents respond simultaneously at every epoch. Before we proceed to analyze this model, we point out some aspects of the same.

While simultaneous response by all players is considered in static games and evolutionary games, such a model may violate the common belief in rationality for dynamic games like ours.<sup>6</sup> This is because, if all agents are (best) responding to the current state simultaneously, then each agent knows that the state will change at the next epoch, and whatever is a/the best response for the current state may not continue to be optimal at the next epoch where the action will be practically

<sup>6</sup>The common belief in rationality says that each player is rational (utility maximizer), each player believes that every other player is rational, each player believes that every other player believes that every other player is rational, and so on. See Chapter 4 in [27] for a formal definition of the common belief in rationality.

executed.<sup>7</sup> So, playing a/the best response to the current state is not consistent with the common belief in rationality. One reasonable way to model such a situation is to assume that the players play actions corresponding to a Nash equilibrium (NE), whenever that exists.<sup>8</sup> If there is a unique NE of the game at the initial state, then a plausible model would be to assume that the players play the corresponding actions. However, if there are multiple equilibria, different agents may play actions corresponding to different equilibria resulting in an action profile that is perhaps ‘far’ from any equilibrium. Even if we assume that agents somehow coordinate to one particular NE, there is no clear way to identify that equilibrium as a function of the current state. This is particularly because an NE may not give equal utility (or even relatively higher utility) to every player, and there is no clear way to decide whom to favor. This also raises the question as to whether the players will stick to any particular NE forever for the dynamic situation we consider. Nevertheless, it is known that playing an NE of a static game repeatedly constitutes an NE of the corresponding repeated game, and therefore, we compute all the NE of the game at the initial state in this section. Needless to say, we lose the dynamic nature of the problem in this approach.

Before we proceed to characterize the NE, we discuss the connection of this model with evolutionary games. In evolutionary games, according to the best response dynamics (or, its subsequent modification as logit dynamics), each population chooses a strategy that is a (or, the) best response to the current state.<sup>9</sup> However, in evolutionary games, the whole population is considered as one player, and actions are considered as different species in that population. In particular, in contrast to our model, actions cannot be treated as rational players in evolutionary games, and consequently the common belief in rationality does not apply to the actions. Nevertheless, we feel a (suitable) evolutionary approach to the virus spread model would be an interesting problem for future research.

### 5.1 NASH EQUILIBRIA OF THE GAME AT THE INITIAL STATE

We now investigate the NE of the game induced at the initial state. Since we treat it as a static game (in particular, the state is not allowed to change), we consider a general setup where an

<sup>7</sup>One can add one more level of rationality by assuming that each agent  $i$  responds to the state obtained by replacing the actions of every other agent  $j$  with their best responses. However, that too will not be consistent as while  $i$  is responding to the modified state (as stated above), they believe that  $j$  is responding to the current state. This inconsistency will continue no matter how many levels of rationality we consider, and it is hard to determine if the common belief in rationality will lead to some action profile in the limit.

<sup>8</sup>A collection of strategies, one for each player, is a Nash equilibrium of a game if for each player, the corresponding strategy is a best response to the strategies of other players given in the Nash equilibrium. It is worth noting that players do not play a best response to the ‘current state’ (in fact, there is no such state in a static game) in an NE, instead, they play a best response to the perceived equilibrium state.

<sup>9</sup>An evolutionary game consists of a class of populations each of which has a set of actions. A strategy of a population is to choose a distribution of its mass over its actions. In best response dynamics, each population plays a best response strategy to the current state. Since there need not be a unique best response, utilities are perturbed to achieve the unique best response at every state. When the utilities are perturbed using a Gumbel distribution, the corresponding dynamic is called the logit best response dynamic. One important question in evolutionary games is whether every time playing a/the best response to the previous state leads to converging to an NE. [20] establish this fact under logit best response dynamic, and [21] do it for arbitrary lower semicontinuous, strongly convex perturbations (for example, Tsallis and Burg entropy) of the utilities. A connection between the approach we have taken in this paper and the logit dynamic in evolutionary games can be drawn from [22]. They show that the logit dynamic can be achieved by starting with populations with finite size, allowing one randomly chosen action to respond at each time, and then letting the population size go to infinity. Recently, [28] and [29] have considered Bayesian evolutionary games and established the convergence to an NE for finite and continuum strategies, respectively, under the different perturbed Bayesian best response dynamics.



arbitrary set of agents  $S$ ,  $S \subseteq N$ , is infected at the initial state. Following the formulation in Section 2 (and simplifying certain expressions for the present case), the game at the initial state of the infection is defined as  $G = \langle N, (A_i)_{i \in N}, (v_i)_{i \in N} \rangle$ , where

- $N = \{1, 2, \dots, n\}$  is the set of payers,
- $A_i = [0, 1]$  is the set of actions of each player  $i \in N$ ,
- for each action profile  $\underline{a} := (a_1, \dots, a_n) \in [0, 1]^n$ ,
  - for  $i \in S$ ,  $v_i(\underline{a}) = f(a_i)$ , and
  - for  $i \in N \setminus S$ ,

$$v_i(\underline{a}) = \begin{cases} 1 + f(a_i) & \text{if } a_i r_i(\underline{a}) \leq \tau, \\ f(a_i) & \text{if } a_i r_i(\underline{a}) > \tau \end{cases} \quad (5.1)$$

where  $f : [0, 1] \rightarrow [0, 1]$  is a strictly increasing function, and

$$r_i(\underline{a}) = \begin{cases} \left( \frac{\sum_{j \in S} a_j}{\sum_{j \in N \setminus \{i\}} a_j} \right) & \text{if } \sum_{j \in N \setminus \{i\}} a_j \neq 0, \\ 0 & \text{if } \sum_{j \in N \setminus \{i\}} a_j = 0. \end{cases}$$

We now define the notion of (pure) Nash equilibrium (NE) for static games.

**Definition 1.** An action profile  $a_N = (a_1, \dots, a_n)$  is a (pure) Nash equilibrium of a game  $G = \langle N, (A_i)_{i \in N}, (v_i)_{i \in N} \rangle$  for all  $i \in N$  and all  $a'_i \in A_i$

$$v_i(a_N) \geq v_i(a'_i, a_{-i}).$$

The following theorem characterizes all NE of the game  $G$ .

**Theorem 13.** For the game  $G$ , if  $\tau < \frac{|S|}{n-1}$ , then there is a unique NE where agents in  $S$  play the action 1 and every other agent plays the action  $\frac{\tau|S|}{|S| - (n - |S| - 1)\tau}$ , and if  $\tau \geq \frac{|S|}{n-1}$ , then there is a unique NE where every agent plays the action 1.

**Proof:** We first show that in any NE of the game  $G$ , an uninfected agent will remain uninfected. Assume for contradiction there is an NE  $\underline{a} = (a_1, \dots, a_n)$  where uninfected agent  $i$  becomes infected. Since  $\underline{a}$  is a NE, we have

$$u_i(\underline{a}) \geq u_i(a'_i, a_{-i}) \text{ for all } a'_i \in [0, 1]. \quad (5.2)$$

As by our assumption, agent  $i$  is infected at  $\underline{a}$ , we have  $u_i(\underline{a}) = f(a_i)$ . Consider  $a'_i = \tau$ . This means agent  $i$  will remain uninfected at  $(a'_i, a_{-i})$  and hence,  $u_i(a'_i, a_{-i}) = 1 + f(a'_i)$ . But this contradicts (5.2) as  $f : [0, 1] \rightarrow [0, 1]$  is a strictly increasing function. Therefore, in any NE of the game  $G$ , all the agents other than agents in  $S$  will remain uninfected. Also, as agents in  $S$  have the utility function  $f$ , they will always choose the action 1 in an NE.

Next, we show that in any NE of the game  $G$ , two uninfected agents will have the same action. Assume for contradiction there is a NE of the game  $\underline{a} = (a_1, \dots, a_n)$  where two uninfected agents  $i$  and  $j$  have different actions, i.e.,  $a_i \neq a_j$ . WLG we may assume that  $a_i > a_j$ . We show that  $u_j(\underline{a}) < u_j(a'_j, a_{-j})$  where  $a'_j = a_i$ , a contradiction to the fact that  $\underline{a}$  is a NE. Note that as  $\underline{a}$  is a NE, agent  $j$  will remain uninfected and hence,  $u_j(\underline{a}) = 1 + f(a_j)$ . For the profile  $(a'_j, a_{-j})$ ,

$$a'_j r_j((a'_j, a_{-j})) = \frac{a'_j |S|}{|S| + \sum_{k \notin S \cup j} a_k} = \frac{a'_j |S|}{1 + \sum_{k \notin S \cup \{i, j\}} a_k + a_i}$$

$$\begin{aligned}
&< \frac{a'_j}{1 + \sum_{k \notin S \cup \{i,j\}} a_k + a_j} && \text{( as } a_i > a_j \text{)} \\
&= \frac{a_i}{1 + \sum_{k \notin S \cup \{i,j\}} a_k + a_j} && \text{( as } a'_j = a_i \text{)} \\
&\leq \tau && \text{( as agent } i \text{ is uninfected at } \underline{a} \text{)}
\end{aligned}$$

This means agent  $j$  will get infected at  $(a'_j, a_{-j})$ . Hence,  $u_j(a'_j, a_{-j}) = 1 + f(a'_j) > 1 + f(a_j) = u_j(\underline{a})$ . This shows that in any NE of the game  $G$ , all the uninfected agents will have the same action.

We are now ready to complete the proof of the lemma. Let  $\underline{a}$  be a NE of the game  $G$ . First, assume that  $\tau < \frac{|S|}{n-1}$ . As discussed before all the agents in  $S$  will choose their action as 1. Therefore,  $a_i = 1$  for all  $i \in S$ . Consider  $i \notin S$ . As agent  $i$  will remain uninfected at  $\underline{a}$  and  $a_i$  is their best action given the actions of the others, it must be that

$$a_i r_i(\underline{a}) = a_i \frac{|S|}{|S| + \sum_{k \notin S \cup i} a_k} = \tau.$$

This together with the fact that  $a_j = a_l$  for all  $j, l \in N \setminus S$  implies

$$\begin{aligned}
a_i \frac{|S|}{|S| + \sum_{k \notin S \cup i} a_k} = \tau &\implies x \frac{|S|}{|S| + \sum_{k \notin S \cup i} x} = \tau && \text{( where } a_j = x \text{ for all } j \neq i \text{)} \\
&\implies x = \frac{\tau |S|}{|S| - (n - |S| - 1)\tau}.
\end{aligned}$$

Note that as  $\tau < \frac{|S|}{n-1}$ , the following holds.

$$x = \frac{\tau |S|}{|S| - (n - |S| - 1)\tau} \leq \frac{\tau |S|}{|S| - (n - |S| - 1) \frac{|S|}{n-1}} = \frac{\tau(n-1)}{|S|} \leq 1,$$

$$\text{and } |S| - (n - |S| - 1)\tau \geq |S| - (n - |S| - 1) \frac{|S|}{n-1} = \frac{|S|^2}{n-1} \geq 0.$$

Thus,  $0 \leq x \leq 1$ . Now assume that  $\tau \geq \frac{|S|}{n-1}$ . As for the action profile  $\underline{a} = \underline{1}$ ,  $a_i r_i(\underline{a}) = \frac{|S|}{n-1} \leq \tau$  for all  $i \in N \setminus S$ , no agent in  $N \setminus S$  will get infected if they choose the action as 1. As 1 is the maximum possible action, the unique NE will be  $\underline{1}$ . ■

## 6. SIMULATION STUDIES

In this section, we corroborate our theoretical results with some simulation evidences. Our focus remains on the following three aspects.

- Completely enumerate the empirical distribution of number of infected agents for a small  $n$  (total number of agents) upto a few epochs.
- For the same  $n$ , we obtain the reported theoretical action profile limits by increasing the epochs. We achieve this by selecting a large number of sequences of the particular epoch length.

- For large  $n$ , using the same approach of random permutations, we explore some special cases of  $a$  and  $\tau$  and show we match the reported asymptotic distribution for the cardinality of the infected set.

### 6.1 EMPIRICAL DISTRIBUTION OF NUMBER OF INFECTED AGENTS UPTO FEW EPOCHS

In our paper so far, we have provided the asymptotic distribution of the cardinality of the final infected set but it remains to understand how fast such distributions or its close approximations are reached. In this section, we provide a very thorough exploration for the cardinality of the infected set up to a few epochs of time. Note that, for the distribution of the total number of infected people in the population, we required an exact enumeration of all possible sequences and thus it becomes difficult to compute this beyond 10 or 11 epochs. So the numbers we will report for this case is exact probability enumeration based on 10 epochs. We set  $n = 5$  and various values of  $a$  and  $\tau$  in Table 1.

In particular, we see that after only 10 epochs for  $n = 5$ , we are able to reach very good approximations to the final distributions. Moreover, the number of epochs to get a close approximation is much smaller. One can see that except for the very first case of  $a = 0, \tau = 0.12$ , we have pretty good convergence to the actual distribution in 10 steps. Generally speaking, for smaller  $a$  and  $\tau$  it takes longer to approximately reach close to the asymptotic distribution.

### 6.2 EMPIRICAL DISTRIBUTION OF ACTION PROFILE

A very pertinent question about some simulation evidence for the asymptotic distribution of the final action set distribution was asked by one reviewer. First, we must say that, even for  $n = 5$  exactly tabulating all possible empirical distribution of a 5-dimensional vector is a challenging problem. Moreover, while we did the simulation, we saw for most cases, the empirical distribution (with complete enumeration) after 10 or 11 epochs was slightly far from the theoretical ones. For this reason, we decided to extend our empirical probability calculation to larger number of epochs. As complete enumeration was computationally challenging, even for  $n = 5$ , we decided to randomly sample 50000 sequences of epoch length 50, 200 and 400. After a lot of deliberation on how to concisely report the average performance of the 5-dimensional vector after these epochs, we decided to report the following

- The theoretical distributions in Table 2 and
- The empirical distribution of the sum of the action profiles after 50, 200 and 400 epochs.

We choose the following cases

- $a = 0$ , with  $\tau = 0.1, 0.3, 0.6$  and  $0.9$ ,
- $a = 0.4$ , with  $\tau = 0.05, 0.3, 0.4$  and  $0.9$ ,
- $a = 0.7$ , with  $\tau = 0.1, 0.3, 0.6$  and  $0.9$ ,
- $a = 1$ , with  $\tau = 0.1, 0.5, 0.6$  and  $0.9$ .

For solely presentation purpose, we omitted a few cases from Table 2 and present them in Figure 1, 2, 3 and 4. One could see in Figure 1, for very small  $\tau$  the uniform distribution in the five possible classes was reached after 200 epochs whereas for larger  $\tau$  the theoretical distributions were reached pretty fast. For large  $a$  however, say  $a = 1$  in Figure 4, the convergence is faster. This is consistent with our finding in Table 1 where a complete enumeration was performed.

Apart from matching the sum of actions in each case, we present visually, we want to draw the attention of the reader to the following cases

- $a = 0.4, \tau = 0.3$  and
- $a = 0.7, \tau = 0.3$

$a$	Range of $\tau$	$\tau$	Theoretical distribution	Empirical distribution
0	(0,0.25) [0.25,0.334) [0.334,0.5) [0.5,1)	0.12 0.3 0.4 0.6	(0.2,0.2,0.2,0.2,0.2) (0.4,0.2,0.2,0.2,0) (0.6,0.2,0.2,0,0) (0.8,0.2,0,0,0)	(0.3340,0.2,0.199,0.181,0.085) (0.42,0.2,0.199,0.181,0) (0.601,0.2,0.199,0,0) (0.8,0.2,0,0,0)
0.2	(0,0.05) 0.05 (0.05,0.25) [0.25,0.3125] (0.3125,0.4166] (0.4166,0.6249] (0.6249,1)	0.02 0.05 * 0.3 0.35 0.5 0.7	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.4,0.2,0.2,0.2,0) (0.6,0.2,0.2,0,0) (0.8,0.2,0,0,0) (1,0,0,0,0)	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.42,0.2,0.199,0.181,0) (0.601,0.2,0.199,0,0) (0.8,0.2,0,0,0) (1,0,0,0,0)
0.35	(0,0.0875) 0.0875 (0.0875,0.25) [0.25-0.2592] (0.2592,0.2985] (0.2985,0.3134] (0.3134,0.3704) [0.3704,0.4878] (0.4878,1]	0.05 0.0875 * 0.255 0.27 0.3 0.36 0.4 0.5	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.4,0,0,0.048,0.552) (0.4, 0.2,0, 0.024,0.376) (0.6, 0.2,0, 0.016,0.184) (0.5,0.2,0.2,0,0) (0.8,0.2,0,0,0) (1,0,0,0,0)	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.420,0,0.001, 0.086, 0.493) (0.420, 0.200, 0.001, 0.062, 0.317) (0.601, 0.200, 0.001, 0.017, 0.182) (0.601,0.2,0.199,0,0) (0.8,0.2,0,0,0) (1,0,0,0,0)
0.45	(0,0.1125) 0.1125 (0.1125,0.25) [0.25,0.2898] (0.2898,0.3103] (0.3103,0.3448] (0.3448,0.4225] (0.4255,1)	0.1 0.1125 * 0.27 0.3 0.32 0.4 0.5	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.4,0,0,0.048,0.552) (0.6,0,0, 0.04,0.360) (0.6,0.2,0, 0.016,0.184) (0.8,0.2,0,0,0) (1,0,0,0,0)	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.420, 0.000, 0.001, 0.086, 0.493) (0.601, 0.000, 0.001, 0.041, 0.358) (0.601, 0.200, 0.001, 0.017, 0.182) (0.8,0.2,0,0,0) (1,0,0,0,0)
0.6	(0,0.15) 0.15 (0.15,0.25) [0.25,0.2777] (0.2777,0.3124] (0.3124,0.3571] (0.3571,1)	0.1 0.15 * 0.26 0.3 0.34 0.4	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.4,0,0, 0.048,0.552) (0.6,0,0, 0.04,0.360) (0.8,0,0,0.024,0.176) (1,0,0,0,0)	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.420, 0.000, 0.001, 0.086, 0.493) (0.601, 0.000, 0.001, 0.041, 0.358) (0.800, 0.000, 0.000, 0.024, 0.176) (1,0,0,0,0)
0.8	(0,0.2) 0.2 (0.2,0.25) [0.25,0.2631] (0.2631,0.2777] (0.2777,0.2941] [0.2941,1)	0.1 0.2 * 0.26 0.27 0.28 0.5	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.4,0,0, 0.024,0.576) (0.6,0,0, 0.04,0.360) (0.8,0,0,0.024,0.176) (1,0,0,0,0)	(0,0,0,0.16,0.84) (0,0,0,0,1) * (0.420, 0.000, 0.001, 0.086, 0.493) (0.601, 0.000, 0.001, 0.041, 0.358) (0.800, 0.000, 0.000, 0.024, 0.176) (1,0,0,0,0)
1	(0,0.25) [0.25,1)	0.12 0.5	(0,0,0,0.16,0.84) (1,0,0,0,0)	(0,0,0,0.16,0.84) (1,0,0,0,0)

TABLE 1. Exact enumeration of empirical distribution after 10 epochs. Here  $(p_1, \dots, p_5)$  denotes  $(\mathbb{P}(|I(S_\infty)| = 1), \dots, \mathbb{P}(|I(S_\infty)| = 5))$  and \* denotes that those regions are not covered by our theoretical results.

$a$	$\tau$	Distribution: Class (prob)	Sum of actions (prob)
0	0.1	(1,0.14,0.14,0.14,0.14) (0.2)	1.56 (0.2)
		(1,1,0.11,0.11,0.11) (0.2)	2.33 (0.2)
		(1,1,1,0.103,0.103) (0.2)	3.203 (0.2)
		(1,1,1,1,0.1) (0.2)	4.1 (0.2)
		(1,1,1,1,1) (0.2)	5 (0.2)
	0.3	(1,1,0.43,0.43,0.43) (0.2)	3.29 (0.2)
		(1,1,1,0.33,0.33) (0.2)	3.66 (0.2)
		(1,1,1,1,0.3) (0.2)	4.3 (0.2)
		(1,1,1,1,1) (0.4)	5 (0.4)
	0.6	(1,1,1,1,1) (1)	5 (1)
	0.9	(1,1,1,1,1) (1)	5 (1)
0.4	0.05	(1,1,1,1,0.05) (0.16)	4.05 (0.16)
		(1,1,1,1,1) (0.84)	5 (0.84)
	0.3	(1,1,0.43,0.43,0.43) (0.2)	3.29 (0.2)
		(1,1,1,1,0.3) (0.006)	4.3 (0.006)
		(1,1,1,1,1) (0.794)	5 (0.794)
	0.4	(1,1,0.67,0.67,0.67) (0.2)	4.01 (0.2)
		(1,1,1,1,1) (0.8)	5 (0.8)
	0.9	(1,1,1,1,1) (1)	5 (1)
0.7	0.1	(1,1,1,1,0.1) (0.16)	4.1 (0.16)
		(1,1,1,1,1) (0.84)	5 (0.84)
	0.3	(1,1,1,1,0.3) (0.01)	4.3 (0.01)
		(1,1,1,1,1) (0.99)	5 (0.99)
		(1,1,1,1,1) (1)	5 (1)
	0.6	(1,1,1,1,1) (1)	5 (1)
	0.9	(1,1,1,1,1) (1)	5 (1)
1	0.1	(1,1,1,1,0.1) (0.16)	4.1 (0.16)
		(1,1,1,1,1) (0.84)	4 (0.84)
	0.5	(1,1,1,1,1) (1)	5 (1)
	0.6	(1,1,1,1,1) (1)	5 (1)
	0.9	(1,1,1,1,1) (1)	5 (1)

TABLE 2. Theoretical distribution of action profile and their sum. Here vectors stand for the class where last 4 entries can be permuted. For example, (1,1,1,0.33,0.33) stands for the class containing six vectors (1,1,1,0.33,0.33), (1,1,0.33,0.33,1), (1,0.33,0.33,1,1), (1,1,0.33,1,0.33), (1,0.33,1,0.33,1), (1,0.33,1,1,0.33)

In both, the theoretical distribution from Table 2 reads a class with a negligible theoretical probability of 0.006 and 0.01 respectively. One could see, that even though these small classes were not prominent after 50 epochs, they became so after 200 epochs. Such strong empirical evidence bolsters that our theoretical findings are accurate. Moreover, it says that based on values of  $a$  and  $\tau$ , it might take different time for the action profile to eventually reach the limiting distributions.

### 6.3 LARGE SAMPLE SIZE

Lastly, we want to understand, for a large population, how well does our result hold empirically and more importantly how fast do we converge to the theoretical distribution. For this as well,

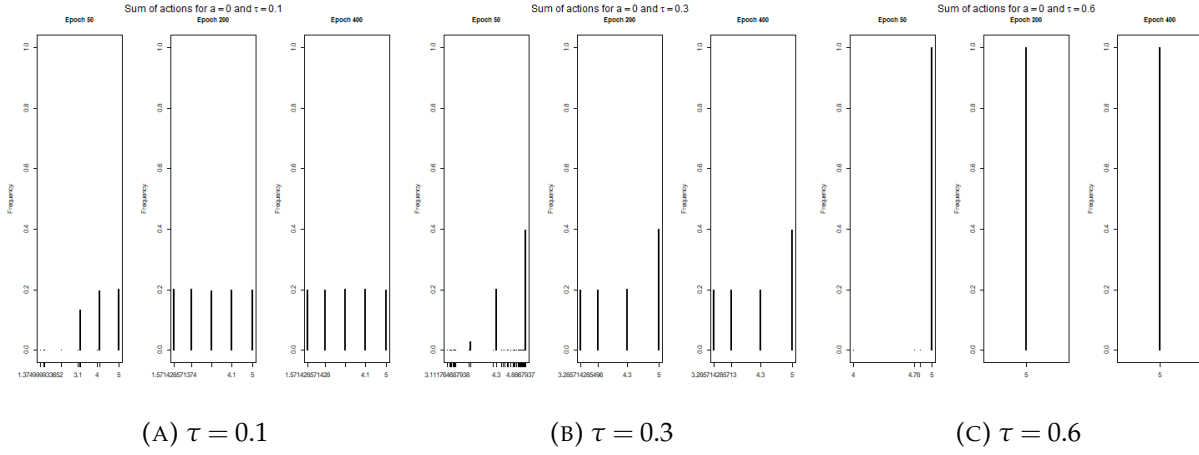


FIGURE 1. Sum of action profiles for  $a = 0$  for  $n = 5$

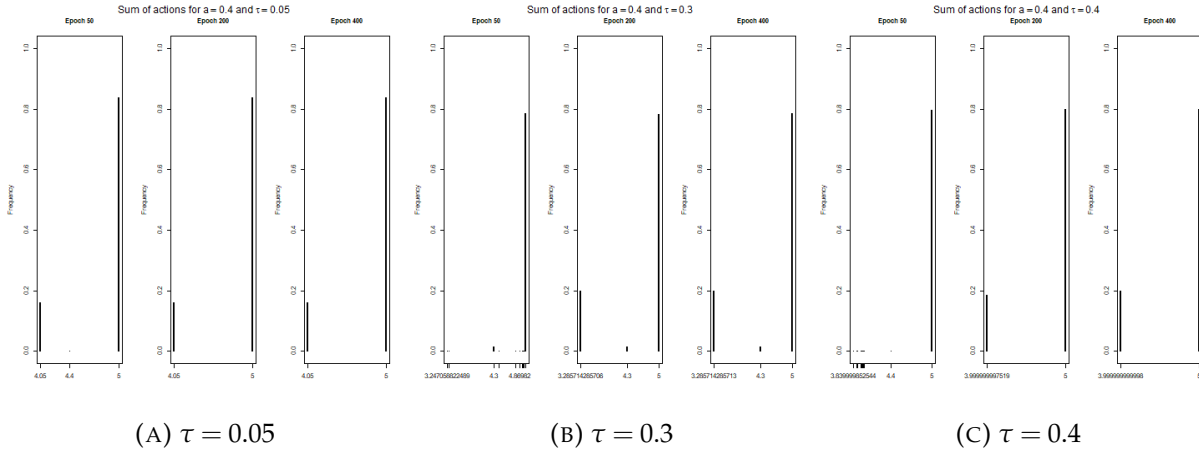


FIGURE 2. Sum of action profiles for  $a = 0.4$  for  $n = 5$

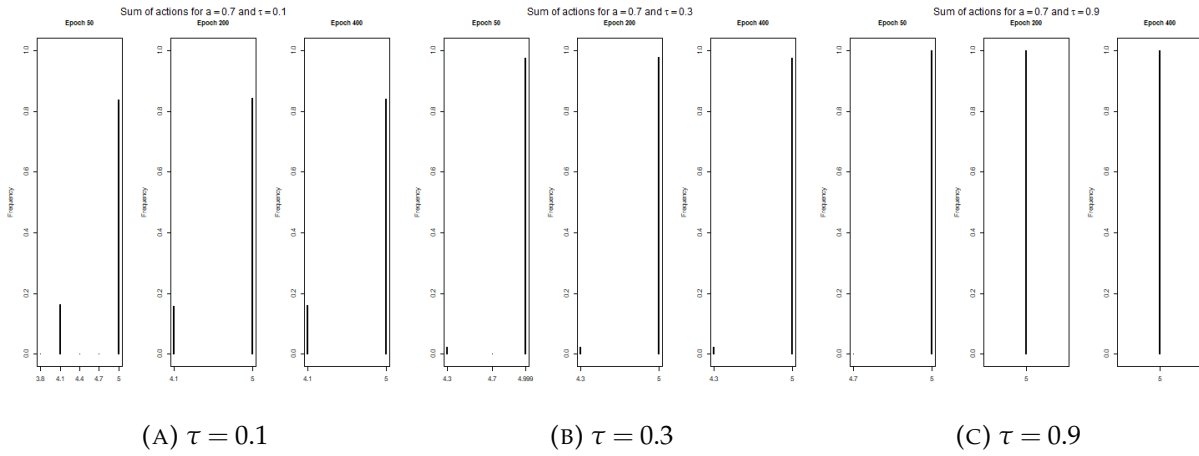


FIGURE 3. Sum of action profiles for  $a = 0.7$  for  $n = 5$

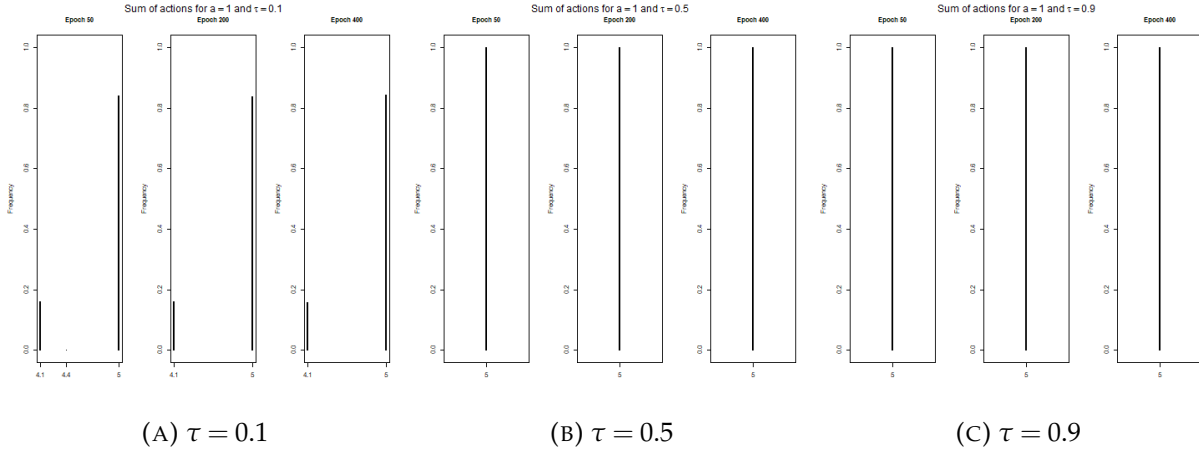


FIGURE 4. Sum of action profiles for  $a = 1$  for  $n = 5$

we have to rely on evaluating a random sample of sequences as complete enumeration for even  $n$  moderately large as 20 or 50 is nearly impossible to achieve. That said, we were able to achieve the said theoretical distributions through evaluating a large number (50000) of permutations of the same length as the corresponding epoch. We choose the scenario  $a = 0, \tau < 1/(n - 1)$  to exhibit this dynamics. Our theory in Theorem 1 says that the number of infected agents asymptotically converges to  $\text{Uniform}(1, \dots, n)$ . In Figure 5, we choose  $n = 5, 20$  and 50 and obtain the dynamics at epoch lengths 20, 50, 100 and 200.

One could see for each  $n$ , initially, the infected set remains just 1 with a somewhat significant probability whereas the probability of having all agents infected is negligible. However, as time progresses, the distribution of the number of agents becomes more uniform. While for small  $n$ , the distribution becomes almost uniform at smaller epochs like 20, but for larger  $n$ , it takes significantly longer. This finding is consistent with our intuition and initial setting. Since we begin with one infected individual, initially the number of infected agents remains 1 with nontrivial probability. At the same time, the chance that it would spread to everyone is quite small. We also ran it for different  $n, a$  and  $\tau$  settings and obtained similar findings. However, for large  $n$ , it is very difficult to summarize every possible exhaustive case as we did for  $n = 5$  in Table 1 and thus we skip those discussions here.

## 7. CONCLUSION

In this article, we propose a graph-theoretic model to describe the spread of a contagious disease allowing for rational interventions from agents sitting at the nodes of the graph. The agents act based on a reasonable utility function and they may (or may not) get affected if their exposure increases. We obtain the asymptotic distribution of the cardinality of the infected set as well as that of the action profile. The results reveal several interesting patterns that exhibit proximity to uniformity, as well as results that are intuitively justifiable (such as if everyone’s immunity ( $\tau$  value) is low to begin with, then eventually the whole population gets affected). We have given an almost complete picture of how the values of  $\tau$  and  $a$  impact the final distribution of the infected set and the action profile. We also observe several fascinating phase transition phenomena in our results. Through exact enumeration of all possible sequences in which the agents are picked randomly, we also show that the empirical distributions obtained mimic the corresponding empirical distributions rather closely after only around 10 epochs from the start of the process.

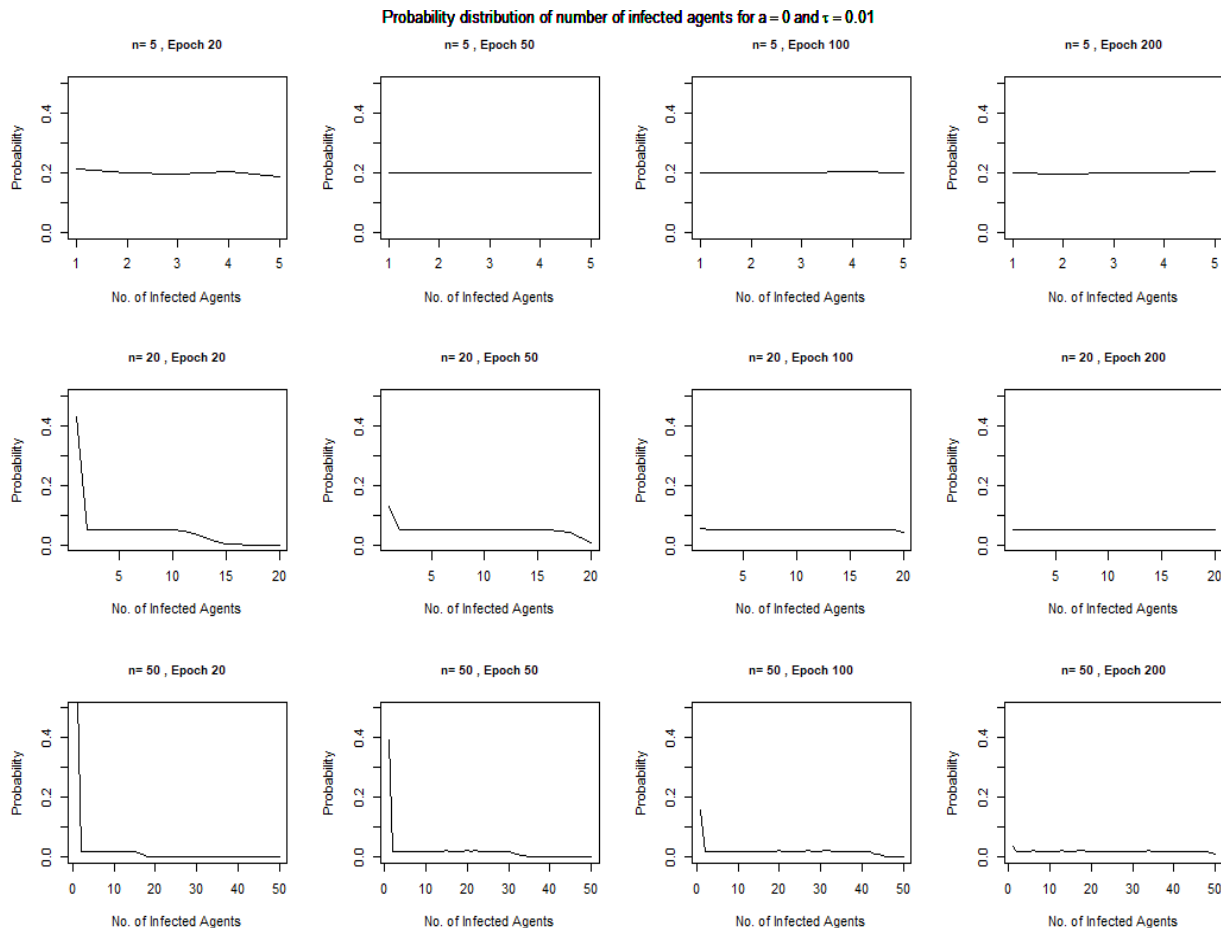


FIGURE 5. Empirical probability distributions of number of infected agents for  $a = 0, \tau = 0.01$  for sample size  $n = 5, 20, 50$  (Different rows) at Epochs 20, 50, 100, 200 (Different columns). For each  $n$ , it eventually becomes uniform however for small  $n$ , it is attained faster.

However, there are a number of questions that remain to be addressed that seem to be beyond the scope of this paper. We give the readers a brief overview of the questions we intend to pursue for similar or related models in the future. So far, we have been unable to obtain, theoretically at least, the limiting distributions for the case where  $a/(n-1) < \tau < 1/(n-1)$ . The length of this interval, for any given  $\tau$ , is negligible for large  $n$ . However, our simulation studies show that there are possibly only two different distributions that could lie in this space. Second, we want to relax the restriction that all agents start with the same initial action  $a$  or the same initial immunity  $\tau$ . Again, some numerical explorations revealed that for fixed  $a$  and uniform  $\tau$  or for fixed  $\tau$  and uniform  $a$ , the contagion tends to spread throughout the population, yielding a rather interesting phenomenon. However, the current mathematical tools will fail to encompass such levels of randomness and proving the occurrence of the phenomena mentioned above rigorously may require completely different mathematical machinery. Finally, we would also like to explore the situation where  $g_{ij}$  is allowed to change over time or have its own model of evolution. That would also bring significant changes to our computations and thus left for future persuasion.



Finally, from the model perspective, one could potentially think of incorporating a cost function for infected individual when they go out and thus this would put some restrictions on  $f(\cdot)$  in the utility function to be not always monotonic. This would constitute an interesting direction in terms of how the dynamics is affected by such a cost.

## 8. ACKNOWLEDGEMENT

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## REFERENCES

- [1] Joan L Aron and Ira B Schwartz. Seasonality and period-doubling bifurcations in an epidemic model. *Journal of theoretical biology*, 110(4):665–679, 1984.
- [2] Alexander Aurell, René Carmona, Gökçe Dayanıklı, and Mathieu Laurière. Finite state graphon games with applications to epidemics. *Dynamic Games and Applications*, 12(1):49–81, 2022.
- [3] Alexander Aurell, Rene Carmona, Gokce Dayanikli, and Mathieu Lauriere. Optimal incentives to mitigate epidemics: a stackelberg mean field game approach. *SIAM Journal on Control and Optimization*, 60(2):S294–S322, 2022.
- [4] Asma Azizi, Cesar Montalvo, Baltazar Espinoza, Yun Kang, and Carlos Castillo-Chavez. Epidemics on networks: Reducing disease transmission using health emergency declarations and peer communication. *Infectious Disease Modelling*, 5:12–22, 2020.
- [5] Fred Brauer. Compartmental models in epidemiology. In *Mathematical epidemiology*, pages 19–79. Springer, 2008.
- [6] Christopher A Browne, Daniel B Amchin, Joanna Schneider, and Sujit S Datta. Infection percolation: A dynamic network model of disease spreading. *Frontiers in Physics*, 9:645954, 2021.
- [7] Samuel Cho. Mean-field game analysis of sir model with social distancing. *arXiv preprint arXiv:2005.06758*, 2020.
- [8] Daniel B Cooney, Dylan H Morris, Simon A Levin, Daniel I Rubenstein, and Pawel Romanczuk. Social dilemmas of sociality due to beneficial and costly contagion. *PLoS computational biology*, 18(11):e1010670, 2022.
- [9] Ben R Craig, Tom Phelan, Jan-Peter Siedlarek, and Jared Steinberg. Improving epidemic modeling with networks. *Economic Commentary*, (2020-23), 2020.
- [10] Yapeng Cui, Shunjiang Ni, and Shifei Shen. A network-based model to explore the role of testing in the epidemiological control of the covid-19 pandemic. *BMC Infectious Diseases*, 21(1): 1–12, 2021.
- [11] Josu Doncel, Nicolas Gast, and Bruno Gaujal. A mean field game analysis of sir dynamics with vaccination. *Probability in the Engineering and Informational Sciences*, 36(2):482–499, 2022.
- [12] Bruno Gaujal, Josu Doncel, and Nicolas Gast. Vaccination in a large population: mean field equilibrium versus social optimum. In *NETGCOOP 2020-10th International Conference on NETwork Games, COnTrol and OPTimization*, pages 1–9, 2021.
- [13] Herbert W Hethcote. Asymptotic behavior in a deterministic epidemic model. *Bulletin of Mathematical Biology*, 35:607–614, 1973.
- [14] Emma Hubert and Gabriel Turinici. Nash-mfg equilibrium in a sir model with time dependent newborn vaccination. *Ricerche di matematica*, 67:227–246, 2018.
- [15] Emma Hubert, Thibaut Mastrolia, Dylan Possamaï, and Xavier Warin. Incentives, lockdown, and testing: from thucydides’ analysis to the covid-19 pandemic. *Journal of mathematical biology*, 84(5):37, 2022.
- [16] Matt J Keeling and Ken TD Eames. Networks and epidemic models. *Journal of the royal society interface*, 2(4):295–307, 2005.
- [17] William Ogilvy Kermack and Anderson G McKendrick. A contribution to the mathematical theory of epidemics. *Proceedings of the royal society of london. Series A, Containing papers of a mathematical and physical character*, 115(772):700–721, 1927.
- [18] Laetitia Laguzet and Gabriel Turinici. Individual vaccination as nash equilibrium in a sir model with application to the 2009–2010 influenza a (h1n1) epidemic in france. *Bulletin of*

- Mathematical Biology*, 77:1955–1984, 2015.
- [19] Laetitia Laguzet, Gabriel Turinici, and Ghozlane Yahiaoui. Equilibrium in an individual-societal sir vaccination model in presence of discounting and finite vaccination capacity. In *New trends in differential equations, control theory and optimization: proceedings of the 8th congress of Romanian mathematicians*, pages 201–214. World Scientific, 2016.
- [20] Ratul Lahkar and Frank Riedel. The logit dynamic for games with continuous strategy sets. *Games and Economic Behavior*, 91:268–282, 2015.
- [21] Ratul Lahkar, Sayan Mukherjee, and Souvik Roy. Generalized perturbed best response dynamics with a continuum of strategies. *Journal of Economic Theory*, 200:105398, 2022.
- [22] Ratul Lahkar, Sayan Mukherjee, and Souvik Roy. The logit dynamic in supermodular games with a continuum of strategies: A deterministic approximation approach. *Games and Economic Behavior*, 139:133–160, 2023.
- [23] John C Lang, Hans De Sterck, Jamieson L Kaiser, and Joel C Miller. Analytic models for sir disease spread on random spatial networks. *Journal of Complex Networks*, 6(6):948–970, 2018.
- [24] Wonjun Lee, Siting Liu, Hamidou Tembine, Wuchen Li, and Stanley Osher. Controlling propagation of epidemics via mean-field control. *SIAM Journal on Applied Mathematics*, 81(1):190–207, 2021.
- [25] Wonjun Lee, Siting Liu, Wuchen Li, and Stanley Osher. Mean field control problems for vaccine distribution. *Research in the Mathematical Sciences*, 9(3):51, 2022.
- [26] Parul Maheshwari and Réka Albert. Network model and analysis of the spread of covid-19 with social distancing. *Applied network science*, 5(1):1–13, 2020.
- [27] Michael Maschler, Shmuel Zamir, and Eilon Solan. *Game theory*. Cambridge University Press, 2020.
- [28] Sayan Mukherjee and Souvik Roy. Regularized bayesian best response learning in finite games. *arXiv preprint arXiv:2111.13687*, 2021.
- [29] Sayan Mukherjee and Souvik Roy. Perturbed bayesian best response dynamic in continuum games. *Working Paper*, 2024.
- [30] Mark EJ Newman. Spread of epidemic disease on networks. *Physical review E*, 66(1):016128, 2002.
- [31] S Yagiz Olmez, Shubham Aggarwal, Jin Won Kim, Erik Miebling, Tamer Başar, Matthew West, and Prashant G Mehta. How does a rational agent act in an epidemic? In *2022 IEEE 61st Conference on Decision and Control (CDC)*, pages 5536–5543. IEEE, 2022.
- [32] S Yagiz Olmez, Shubham Aggarwal, Jin Won Kim, Erik Miebling, Tamer Başar, Matthew West, and Prashant G Mehta. Modeling presymptomatic spread in epidemics via mean-field games. In *2022 American Control Conference (ACC)*, pages 3648–3655. IEEE, 2022.
- [33] Romualdo Pastor-Satorras, Claudio Castellano, Piet Van Mieghem, and Alessandro Vespignani. Epidemic processes in complex networks. *Reviews of modern physics*, 87(3):925, 2015.
- [34] Ronald Ross and Hilda P Hudson. An application of the theory of probabilities to the study of a priori pathometry. *Proceedings of the Royal Society of London. Series A, Containing papers of a mathematical and physical character*, 93(650):225–240, 1917.
- [35] Amal Roy, Chandramani Singh, and Y Narahari. Recent advances in modeling and control of epidemics using a mean field approach. *arXiv preprint arXiv:2208.14765*, 2022.
- [36] Pratha Sah, Michael Otterstatter, Stephan T Leu, Sivan Levijang, and Shweta Bansal. Revealing mechanisms of infectious disease spread through empirical contact networks. *PLoS computational biology*, 17(12):e1009604, 2021.
- [37] Francesco Salvarani and Gabriel Turinici. Optimal individual strategies for influenza vaccines with imperfect efficacy and durability of protection. *Mathematical Biosciences and Engineering*,

- 15(3), 2018.
- [38] M Small and Chi Kong Tse. Complex network models of disease propagation: modelling, predicting and assessing the transmission of sars. *Hong Kong Medical Journal*, 16(5 SUPP4): 43–44, 2010.
- [39] Renato Vizuete, Paolo Frasca, and Federica Garin. Graphon-based sensitivity analysis of sis epidemics. *IEEE Control Systems Letters*, 4(3):542–547, 2020.

## A. A FEW IMPORTANT LEMMAS

**Lemma 6.** Suppose  $\varrho \in N_\infty$  and let  $\bar{t} \in \mathbb{N}_0$  be such that either

$$\varrho_{\bar{t}} \in I(S_{\bar{t}}) \text{ and } a_{\varrho_{\bar{t}}}(S_{\bar{t}}) = 1,$$

or,

$$\varrho_{\bar{t}} \notin I(S_{\bar{t}}) \text{ and } I(S_{\bar{t}-1}) = I(S_{\bar{t}}).$$

Then  $I(S_{\bar{t}}) = I(S_{\bar{t}+1})$ .

**Proof:** First assume that  $I(S_{\bar{t}-1}) = I(S_{\bar{t}})$  and  $\varrho_{\bar{t}} = i$  with  $i \notin I(S_{\bar{t}})$ . Since  $i \notin I(S_{\bar{t}})$ ,  $i$  will choose their action as

$$b_i(S_{\bar{t}}) = \begin{cases} 1 & \text{if } r_i(S_{\bar{t}}) = 0, \\ \min \left\{ 1, \frac{\tau(i)}{r_i(S_{\bar{t}})} \right\} & \text{if } r_i(S_{\bar{t}}) \neq 0. \end{cases}$$

If  $r_i(S_{\bar{t}}) = 0$  then  $r_i(\hat{S}_{\bar{t}}) = r_i(S_{\bar{t}}) = 0$ , and agent  $i$  will not get infected as  $1 \times r_i(\hat{S}_{\bar{t}}) = 0 \leq \tau(i)$ . Suppose  $r_i(S_{\bar{t}}) > 0$ . Since  $a_i(\hat{S}_{\bar{t}}) = b_i(S_{\bar{t}})$  and  $r_i(S_{\bar{t}}) = r_i(\hat{S}_{\bar{t}})$ , this means agent  $i$  will not get infected at  $\bar{t} + 1$ . To show that any other agent  $j \notin I(S_{\bar{t}})$  will not get infected at  $\bar{t} + 1$ , we first claim that  $a_i(\hat{S}_{\bar{t}}) \geq a_i(S_{\bar{t}})$ . If  $a_i(\hat{S}_{\bar{t}}) = 1$  then there is nothing to show, so, assume  $a_i(\hat{S}_{\bar{t}}) = \frac{\tau(i)}{r_i(S_{\bar{t}})}$ . As  $i \notin I(S_{\bar{t}})$ , we have  $a_i(\hat{S}_{\bar{t}-1})r_i(\hat{S}_{\bar{t}-1}) \leq \tau(i)$ . Moreover, as  $I(S_{\bar{t}-1}) = I(S_{\bar{t}})$ , it follows that  $\hat{S}_{\bar{t}-1} = S_{\bar{t}}$  (see (iii) of Observation 1) and hence,  $r_i(\hat{S}_{\bar{t}-1}) = r_i(S_{\bar{t}})$ . Combining it with  $a_i(S_{\bar{t}}) = a_i(\hat{S}_{\bar{t}-1})$ , we get  $a_i(S_{\bar{t}})r_i(S_{\bar{t}}) \leq \tau(i)$ . So,  $a_i(\hat{S}_{\bar{t}}) \geq a_i(S_{\bar{t}})$ .

Take  $j \notin I(S_{\bar{t}})$  with  $j \neq i$ . Since  $j \notin I(S_{\bar{t}})$ , it means  $a_j(\hat{S}_{\bar{t}-1})r_j(\hat{S}_{\bar{t}-1}) \leq \tau(j)$ . Additionally,  $j \neq i$  implies  $a_j(\hat{S}_{\bar{t}-1}) = a_j(S_{\bar{t}}) = a_j(\hat{S}_{\bar{t}})$ . Therefore, to show that  $a_j(\hat{S}_{\bar{t}})r_j(\hat{S}_{\bar{t}}) \leq \tau(j)$ , it is enough to show  $r_j(\hat{S}_{\bar{t}-1}) \geq r_j(\hat{S}_{\bar{t}})$ . Note that

$$\begin{aligned} r_j(\hat{S}_{\bar{t}-1}) &= \frac{\sum_{k \in I(\hat{S}_{\bar{t}-1}) \setminus j} a_k(\hat{S}_{\bar{t}-1}) g_{jk}}{\sum_{k \in N \setminus j} a_k(\hat{S}_{\bar{t}-1}) g_{jk}} \\ &= \frac{\sum_{k \in I(\hat{S}_{\bar{t}-1}) \setminus j} a_k(\hat{S}_{\bar{t}}) g_{jk}}{a_i(\hat{S}_{\bar{t}-1}) g_{ji} + \sum_{k \in N \setminus \{i,j\}} a_k(\hat{S}_{\bar{t}}) g_{jk}} \quad (\text{as } i \notin I(\hat{S}_{\bar{t}-1}) \text{ and } a_k(\hat{S}_{\bar{t}-1}) = a_k(\hat{S}_{\bar{t}}) \forall k \neq i) \\ &= \frac{\sum_{k \in I(\hat{S}_{\bar{t}}) \setminus j} a_k(\hat{S}_{\bar{t}}) g_{jk}}{a_i(\hat{S}_{\bar{t}-1}) g_{ji} + \sum_{k \in N \setminus \{i,j\}} a_k(\hat{S}_{\bar{t}}) g_{jk}} \quad (\text{as } I(\hat{S}_{\bar{t}-1}) = I(S_{\bar{t}-1}) = I(S_{\bar{t}}) = I(\hat{S}_{\bar{t}})) \\ &\geq \frac{\sum_{k \in I(\hat{S}_{\bar{t}}) \setminus j} a_k(\hat{S}_{\bar{t}}) g_{jk}}{a_i(\hat{S}_{\bar{t}}) g_{ji} + \sum_{k \in N \setminus \{i,j\}} a_k(\hat{S}_{\bar{t}}) g_{jk}} \quad (\text{as } a_i(\hat{S}_{\bar{t}}) \geq a_i(S_{\bar{t}}) = a_i(\hat{S}_{\bar{t}-1})) \\ &= r_j(\hat{S}_{\bar{t}}). \end{aligned}$$

So, agent  $j$  will not get infected at  $\bar{t} + 1$  and hence,  $I(S_{\bar{t}+1}) = I(S_{\bar{t}})$ .

Now assume  $i \in I(S_{\bar{t}})$  with  $a_i(S_{\bar{t}}) = 1$ . This means  $a_i(\hat{S}_{\bar{t}}) = b_i(S_{\bar{t}}) = 1$ . As  $b_i(S_{\bar{t}}) = a_i(S_{\bar{t}})$  and  $\varrho_{\bar{t}} = i$ , we have  $S_{\bar{t}} = S_{\bar{t}+1}$  (see Observation 1). Hence,  $I(S_{\bar{t}}) = I(S_{\bar{t}+1})$ . This completes the proof of the lemma.  $\blacksquare$

**Lemma 7.** Suppose that  $I(S_0) = \{1\}$  and  $a_i(S_0) \leq \tau(i)$  for all  $i \in N$ . Let  $\varrho \in N_\infty$  and  $\hat{t} \in \mathbb{N}_0$  be such that  $\varrho_t \neq 1$  for all  $t < \hat{t}$ . Then,  $I(S_t) = \{1\}$  for all  $t \leq \hat{t}$ .

**Proof:** Note that if  $\hat{t} = 0$  then there is nothing to show. So, assume  $\hat{t} \geq 1$ . We use induction to prove this. As the base case, we show that  $I(S_1) = \{1\}$ . Let  $v_0 = i$ . Since  $\hat{t} \geq 1$ ,  $i \neq 1$ . Agent  $i$  will choose their action as

$$b_i(S_0) = \begin{cases} 1 & \text{if } r_i(S_0) = 0, \\ \min \left\{ 1, \frac{\tau(i)}{r_i(S_0)} \right\} & \text{if } r_i(S_0) \neq 0. \end{cases}$$

If  $r_i(S_0) = 0$  then  $r_i(\hat{S}_0) = r_i(S_0) = 0$ , and agent  $i$  will not get infected as  $1 \times r_i(\hat{S}_0) = 0 \leq \tau(i)$ . Suppose  $r_i(S_0) > 0$ . Since  $a_i(\hat{S}_0) = b_i(S_0)$ ,  $r_i(\hat{S}_0) = r_i(S_0)$ , and  $b_i(S_0) \leq \frac{\tau(i)}{r_i(S_0)}$ , this means agent  $i$  will not get infected at  $t = 1$ . For any  $j \notin \{1, i\}$ ,  $a_j(\hat{S}_0) = a_j(S_0) \leq \tau(j)$ , so, agent  $j$  will also not get infected at  $t = 1$ . Thus,  $I(S_1) = \{1\}$ . Next we introduce an induction hypothesis.

*Induction Hypothesis:* Given  $\bar{t} \in \mathbb{N}_0$  with  $\hat{t} \geq \bar{t} > 1$ , we have  $I(S_1) = \dots = I(S_{\bar{t}-1}) = \{1\}$ .

We show that  $I(S_{\bar{t}}) = \{1\}$ . Let  $v_{\bar{t}-1} = i$ . Since  $\hat{t} \geq \bar{t}$ , this means  $i \neq 1$ . Hence,  $i \notin I(S_{\bar{t}-1})$ . As  $\bar{t} > 1$ , we have  $I(S_{\bar{t}-2}) = I(S_{\bar{t}-1})$ . This together with Lemma 6, implies  $I(S_{\bar{t}}) = I(S_{\bar{t}-1}) = \{1\}$ . Thus, by induction, we have  $I(S_{\hat{t}}) = \{1\}$ . This completes the proof of the lemma. ■

**Remark 4.** It follows from Lemma 7 that  $I(S_{t_1(v)}) = \{1\}$  for all  $v \in N_\infty$ .

**Lemma 8.** Consider  $v \in N_\infty$  and let  $\hat{t} \in \mathbb{N}_0$  be such that  $a_i(S_{\hat{t}}) = 1$  for all  $i \in I(S_{\hat{t}})$  and  $a_i(S_{\hat{t}}) \leq \tau(i)$  for all  $i \notin I(S_{\hat{t}})$ . Then,  $I(S_{\hat{t}}) = I(S_\infty)$ .

**Proof:** We first show that  $I(S_{\hat{t}+1}) = I(S_{\hat{t}})$ . Let  $v_{\hat{t}} = i$ . Suppose  $i \in I(S_{\hat{t}})$ . Thus by Lemma 1,  $a_i(\hat{S}_{\hat{t}}) = b_i(S_{\hat{t}}) = 1$ . This implies  $S_{\hat{t}} = S_{\hat{t}+1}$  (see Observation 1) and hence,  $I(S_{\hat{t}+1}) = I(S_{\hat{t}})$ . Now suppose  $i \notin I(S_{\hat{t}})$ . Agent  $i$  will choose their action as

$$b_i(S_{\hat{t}}) = \begin{cases} 1 & \text{if } r_i(S_{\hat{t}}) = 0, \\ \min \left\{ 1, \frac{\tau(i)}{r_i(S_{\hat{t}})} \right\} & \text{if } r_i(S_{\hat{t}}) \neq 0. \end{cases}$$

If  $r_i(S_{\hat{t}}) = 0$  then  $r_i(\hat{S}_{\hat{t}}) = r_i(S_{\hat{t}}) = 0$ , and agent  $i$  will not get infected as  $a_i(\hat{S}_{\hat{t}}) \times r_i(\hat{S}_{\hat{t}}) = 0 \leq \tau(i)$ . Suppose  $r_i(S_{\hat{t}}) > 0$ . Since  $a_i(\hat{S}_{\hat{t}}) = b_i(S_{\hat{t}})$  and  $r_i(S_{\hat{t}}) = r_i(\hat{S}_{\hat{t}})$ , this means agent  $i$  will not get infected at  $\hat{t} + 1$ . Take  $j \notin I(S_{\hat{t}})$  and  $j \neq i$ . Note that by the assumption of the lemma,  $a_j(S_{\hat{t}}) \leq \tau(j)$ . Since  $j \neq i$ , we have  $a_j(S_{\hat{t}}) = a_j(\hat{S}_{\hat{t}})$ . Combining these two, we have  $a_j(\hat{S}_{\hat{t}}) \leq \tau(j)$ . As  $r_j(\hat{S}_{\hat{t}}) \leq 1$  this implies  $a_j(\hat{S}_{\hat{t}})r_j(\hat{S}_{\hat{t}}) \leq \tau(j)$ . Thus, agent  $j$  will not get infected at  $\hat{t} + 1$ . Hence,  $I(S_{\hat{t}+1}) = I(S_{\hat{t}})$ .

We now show that for any  $t \in \mathbb{N}_0$  with  $t > \hat{t} + 1$ ,  $I(S_{\hat{t}}) = I(S_t)$  holds. Assume for contradiction there exists  $\bar{t} \in \mathbb{N}_0$  with  $\bar{t} > \hat{t} + 1$  such that  $I(S_{\hat{t}}) \subsetneq I(S_{\bar{t}})$ . Without loss of generality we can assume that  $I(S_{\hat{t}}) = I(S_{\hat{t}+1}) = \dots = I(S_{\bar{t}-1})$ . Let  $v_{\bar{t}-1} = i$ . Suppose  $i \in I(S_{\bar{t}-1})$ . We first show

$$a_i(S_{\bar{t}-1}) = 1. \tag{A.1}$$

As  $i \in I(S_{\bar{t}-1})$  and  $I(S_{\bar{t}-1}) = I(S_{\hat{t}})$ , we have  $i \in I(S_{\hat{t}})$ . Thus, by the assumption of the lemma,  $a_i(S_{\hat{t}}) = 1$ . Since  $\hat{t} \leq \bar{t} - 1$ , this implies  $a_i(S_{\bar{t}-1}) = 1$ ; see Observation 3.

By (A.1), we have  $a_i(S_{\bar{t}-1}) = 1$ . Since  $v_{\bar{t}-1} = i$  and  $i \in I(S_{\bar{t}-1})$ , this implies  $a_i(\hat{S}_{\bar{t}-1}) = 1$ . Thus,  $S_{\bar{t}-1} = \hat{S}_{\bar{t}-1}$ , and hence,  $I(S_{\bar{t}-1}) = I(S_{\bar{t}})$  (see Observation 1), a contradiction to  $I(S_{\hat{t}}) \subsetneq I(S_{\bar{t}})$ . Hence,  $I(S_{\bar{t}}) = I(S_{\hat{t}})$ .

Now suppose  $i \notin I(S_{\bar{t}-1})$ . As  $\bar{t} > \hat{t} + 1$ , we have  $I(S_{\bar{t}-1}) = I(S_{\bar{t}-2})$ . This together with Lemma 6 implies  $I(S_{\bar{t}-1}) = I(S_{\bar{t}})$ , a contradiction to  $I(S_{\hat{t}}) \subsetneq I(S_{\bar{t}})$ . Hence,  $I(S_{\bar{t}}) = I(S_{\hat{t}})$ . This completes the proof of the lemma. ■

## B. PROOF OF THEOREM 3, THEOREM 5, AND THEOREM 9

## B.1 PROOF OF THEOREM 3

**Proof:** We follow the same structure that we used in the proof of Theorem 1.

**Step 1.** Fix an agent sequence  $\underline{v} \in N_\infty$  and let  $S$  be the DVSP induced by  $\underline{v}$ . To shorten notation, for all  $i \in N$ , let us denote  $t_i(\underline{v})$  by  $k_i$ . The following claim demonstrates how an agent  $i$  with  $k_i < k_1$  will update their action. Recall the set  $N_1(\underline{v})$ . We distinguish two cases based on the value of  $|N_1(\underline{v})|$ .

**Case 1:**  $|N_1(\underline{v})| = 0$ .

First assume  $\tau \geq \frac{1}{n-1}$ . We show that no agent will get infected under this assumption, i.e.,  $I(S_\infty) = \{1\}$ . Note that by the assumption of the case,  $v_0 = 1$ . Also, as  $a = 1$ ,  $a_i(S_0) = 1$  for all  $i \in N$ . Recall that  $\hat{S}_0$  denotes the intermediate state where the only change from  $S_0$  is that agent  $v_0$  has updated their action to  $b_{v_0}(S_0)$ . Since  $v_0 = 1$ , we have  $a_i(S_0) = a_i(\hat{S}_0)$  for all  $i \neq 1$ . Thus,  $a_i(\hat{S}_0) = 1$  for all  $i \in N \setminus \{1\}$ . Moreover, by Lemma 1 and the definition of the process,  $a_1(\hat{S}_0) = 1$ . Consider the time point 1. By the definition of the process, an agent  $i \neq 1$  will be in  $I(S_1)$  if  $a_i(\hat{S}_0)r_i(\hat{S}_0) > \tau$ . Since  $I(S_0) = \{1\}$ ,  $a_i(\hat{S}_0) = 1$  for all  $i \in N$ , and  $g_{ij} = c$  for all  $i \neq j$ , it follows that  $r_i(\hat{S}_0) = \frac{1}{n-1}$  for all  $i \in N \setminus \{1\}$ . Because  $\tau \geq \frac{1}{n-1}$ , this implies that no agent in  $N \setminus \{1\}$  gets infected at the time point 1. Hence,  $I(S_1) = \{1\}$ .

We now show that no new agent would get infected after this. We first show that  $I(S_2) = \{1\}$ . Let  $v_1 = i$ . If  $i \notin I(S_1)$  then as  $I(S_0) = I(S_1)$  by Lemma 6, we have  $I(S_1) = I(S_2)$ . If  $i \in I(S_1)$  then  $i = 1$ . Moreover,  $a_1(S_1) = a_1(\hat{S}_0) = 1$ . Hence, by Lemma 6,  $I(S_1) = I(S_2)$ . Therefore,  $I(S_2) = \{1\}$ . Using the same arguments repeatedly, it follows that  $I(S_t) = \{1\}$  for all  $t \geq 2$ . Thus,  $I(S_\infty) = \{1\}$ .

Now assume  $\tau < \frac{1}{n-1}$ . We show that all the agent gets infected under this assumption. Using similar arguments as before, we get  $r_i(\hat{S}_0) = \frac{1}{n-1}$  for all  $i \in N \setminus \{1\}$ . As  $\tau < \frac{1}{n-1}$ , this means each  $i \in N \setminus \{1\}$  will get infected at time point 1. Therefore,  $I(S_\infty) = N$ .

**Case 2:**  $|N_1(\underline{v})| \geq 1$ .

This means  $v_0 \neq 1$ . Let  $v_0 = i \notin \{1\}$ . Hence, by the definition of the process, agent  $i$  will choose their action as  $b_i(S_0)$  at the intermediate state  $\hat{S}_0$ . As  $a_j(S_0) = 1$  for all  $j \in N$  and  $I(S_0) = \{1\}$ , it follows that  $r_i(S_0) \neq 0$ . Therefore,

$$b_i(S_0) = \min \left\{ 1, \frac{\tau}{r_i(S_0)} \right\} = \min \{1, (n-1)\tau\}. \quad (\text{B.1})$$

Since by our assumption  $v_0 = i$  and  $i \notin I(S_0)$ , by Observation 4,  $i \notin I(S_1)$ . For any other uninfected agent  $j$ ,

$$r_j(\hat{S}_0) = \frac{1}{(n-2) + b_i(S_0)}.$$

This together with the fact that  $a_j(\hat{S}_0) = 1$  implies

$$(i) \text{ if } \tau \geq \frac{1}{n-1} \text{ then } b_i(S_0) = 1 \text{ and hence, } a_j(\hat{S}_0)r_j(\hat{S}_0) = \frac{1}{n-1} \leq \tau, \text{ and}$$

(ii) if  $\tau < \frac{1}{n-1}$  then  $b_i(S_0) < 1$  and hence,  $a_j(\hat{S}_0)r_j(\hat{S}_0) > \frac{1}{n-1} > \tau$ .

Combining the above observations, we may write if  $\tau \geq \frac{1}{n-1}$  then agent  $j$  will not get infected at time point 1 and if  $\tau < \frac{1}{n-1}$  then agent  $j$  will get infected at time point 1. Hence, we have

$$\tau \geq \frac{1}{n-1} \implies I(S_1) = \{1\} \text{ and } \tau < \frac{1}{n-1} \implies I(S_1) = N \setminus \{i\}.$$

If  $\tau \geq \frac{1}{n-1}$  then using similar arguments as in Case 1, we can show that  $I(S_\infty) = \{1\}$ . If  $\tau < \frac{1}{n-1}$  then to decide the final infected set we distinguish two subcases.

**Case 2.1.**  $v_1 = i$ .

We show that the final infected set will be  $N \setminus i$ . Since by our assumption  $v_1 = i$  and  $i \notin I(S_1)$ , by Observation 4,  $i \notin I(S_2)$ . Hence,  $I(S_2) = N \setminus \{i\}$ . We now show that  $i$  will not get infected after this. At time point 2,

$$r_i(\hat{S}_2) = \frac{(n-1)}{(n-1)} = 1.$$

Therefore,  $a_i(\hat{S}_2) = \tau$  (see Observation 4). At time point 3, if  $v_3 = i$ , then agent  $i$  would not get infected at time point 4 (Observation 4). On the other hand, if  $v_3 \neq i$  then as  $a_i(\hat{S}_3) = a_i(\hat{S}_2) = \tau$ , it follows that  $a_i(\hat{S}_3)r_i(\hat{S}_3) \leq \tau$ . Hence, agent  $i$  would remain uninfected at time point 4. Continuing in this manner, we may show that  $i$  will not get infected after this. Thus,  $I(S_\infty) = N \setminus \{i\}$ .

**Case 2.2.:**  $v_1 \neq i$

We show that the final infected set will be  $N$ . Since  $I(S_1) = N \setminus \{i\}$ ,  $r_i(\hat{S}_1) = 1$ . Moreover, as  $a_i(S_1) = a_i(\hat{S}_0) = b_i(S_0) = (n-1)\tau > \tau$  (see B.5) and  $v_1 \neq i$ , it follows that  $a_i(\hat{S}_1) > \tau$ . Combining this two we have  $a_i(\hat{S}_1)r_i(\hat{S}_1) > \tau$ . Thus, agent  $i$  will get infected at time point 2. Hence,  $I(S_2) = N$  and  $I(S_\infty) = N$ .

**Step 2.** First assume  $\tau \geq \frac{1}{n-1}$ . Therefore, in view Case 1 and Case 2 of the current proof, we have  $I(S_\infty) = \{1\}$ .

Now assume  $\tau < \frac{1}{n-1}$ . By Case 1 and Case 2 above, we have

- (i)  $|I(S_\infty)| = n-1$  with  $1 \in I(S_\infty)$  if  $|N_1(v)| \geq 1$  and there is  $i \in N \setminus \{1\}$  such that  $k_i = 0$  and  $v_1 = i$ , and
- (ii)  $I(S_\infty) = N$  if either  $|N_1(v)| = 0$  or  $|N_1(v)| \geq 1$  and there is no  $i \in N \setminus \{1\}$  such that  $k_i = 0$  and  $v_1 = i$ .

We calculate the probability of  $|I(S_\infty)| = n-1$ . By (i) we have

$$\begin{aligned} & P(v \mid |N_1(v)| \geq 1 \text{ and } \exists i \neq 1 \text{ such that } k_i = 0 \text{ and } v_1 = i) \\ &= P(v \mid \exists i \neq 1 \text{ such that } k_i = 0 \text{ and } v_1 = i) \\ &= {}^{n-1}C_1 \times \frac{1}{n^2} \\ &= \frac{n-1}{n^2}. \end{aligned}$$



Note that by (i) and (ii),

$$P(|I(S_\infty)| = n - 1) + P(I(S_\infty) = N) = 1.$$

Therefore,

$$\begin{aligned} P(I(S_\infty) = N) &= 1 - P(|I(S_\infty)| = n - 1) \\ &= 1 - \frac{n - 1}{n^2}. \end{aligned}$$

Since any two subsets of  $N$  with the cardinality  $n - 1$  have the same probability, combining all the above observations, we have the following distribution of the infected set.

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} \frac{1}{n^2} & \text{if } 1 \in J \text{ and } |J| = n - 1, \\ 1 - \frac{n - 1}{n^2} & \text{if } |J| = n, \text{ i.e., } J = N, \\ 0 & \text{otherwise.} \end{cases}$$

This completes the proof of the theorem. ■

## B.2 PROOF OF THEOREM 5

**Proof:** Note that

$$\left[ \hat{a} \geq \left\lceil \frac{\frac{1}{\tau} - (n - 1)a}{1 - a} \right\rceil \right] \iff \left[ \tau \geq \frac{1}{\hat{a} + (n - 1 - \hat{a})a} \right], \quad (\text{B.2})$$

and

$$\left[ \hat{a} = \left\lceil \frac{\frac{1}{\tau} - (n - 1)a}{1 - a} \right\rceil \right] \iff \left[ \frac{1}{\hat{a} - 1 + (n - \hat{a})a} > \tau \geq \frac{1}{\hat{a} + (n - 1 - \hat{a})a} \right]. \quad (\text{B.3})$$

Also, as  $\tau \geq \frac{1}{n - 1}$ , we have  $\hat{a} \leq n - 1$ . We follow the same structure that we used in the proof of Theorem 1.

**Step 1** Fix an agent sequence  $\underline{v} \in N_\infty$  and let  $S$  be the virus spread process induced by  $\underline{v}$ . To shorten notation, for all  $i \in N$ , let us denote  $t_i(\underline{v})$  by  $k_i$ . We first prove a claim similar to Claim 1 as in Step 1 of the proof of Theorem 1.

**Claim 1:** For all  $0 \leq t < k_1$ ,  $a_i(S_{t+1}) = 1$  where  $\underline{v}_t = i$ .

**Proof of the claim.** Let  $\underline{v}_0 = i$ . As  $k_1 > 0$ ,  $i \neq 1$ . Since  $a_j(S_0) = a > 0$  for all  $j \in N$ ,  $I(S_0) = \{1\}$ , and  $g_{ij} = c$  for all  $i \neq j$ , we have  $r_i(S_0) = \frac{1}{(n - 1)}$ . This means

$$b_i(S_0) = \min \left\{ 1, \frac{\tau}{\frac{1}{(n-1)}} \right\} = \min \{1, (n - 1)\tau\} = 1$$

as by the assumption of the lemma  $\tau \geq \frac{1}{(n - 1)}$ . Thus,  $a_i(S_1) = a_i(\hat{S}_0) = 1$ . Next we introduce an induction hypothesis.

*Induction Hypothesis:* Given  $\bar{t} \in \mathbb{N}_0$  with  $\bar{t} < k_1$ , we have for all  $t < \bar{t}$ ,  $a_j(S_{t+1}) = 1$  where  $\underline{v}_t = j$ .

Let  $\varrho_{\bar{t}} = i'$  and we show that  $a_{i'}(S_{\bar{t}+1}) = 1$ . Note that by Lemma 7,  $I(S_{\bar{t}}) = \{1\}$ . Moreover, by the induction hypothesis,  $a_j(S_{\bar{t}}) \geq a$  for all  $j \in N \setminus \{1\}$ . Also, as  $\bar{t} < k_1$ , we have  $a_1(S_{\bar{t}}) = a$ . Combining all these observations we have,

$$\frac{1}{(n-1)} \geq r_{i'}(S_{\bar{t}}) \geq \frac{a}{(n-1)}. \quad (\text{B.4})$$

Since  $r_{i'}(S_{\bar{t}}) > 0$ ,  $b_{i'}(S_{\bar{t}}) = \min\left\{1, \frac{\tau}{r_{i'}(S_{\bar{t}})}\right\}$ ; see Lemma 1. Therefore, using (B.4) and the fact  $\tau \geq \frac{1}{(n-1)}$ , we have  $b_{i'}(S_{\bar{t}}) = 1$ . Thus,  $a_{i'}(S_{\bar{t}+1}) = a_{i'}(\hat{S}_{\bar{t}}) = 1$ . This completes the proof of the claim.  $\square$

We now determine the final infection set. Note that by Claim 1,  $a_i(S_{k_1}) = 1$  for all  $i \in N_1(\varrho)$ . Also, by the definition of the process,  $a_i(S_{k_1}) = a$  for all  $i \notin N_1(\varrho) \cup \{1\}$  as they have not updated their actions till the time point  $k_1$ . Recall that  $\hat{S}_{k_1}$  denotes the intermediate state where the only change from  $S_{k_1}$  is that agent  $\varrho_{k_1}$  has updated their action to  $b_{\varrho_{k_1}}(S_{k_1})$ . Since  $\varrho_{k_1} = 1$ , we have  $a_i(S_{k_1}) = a_i(\hat{S}_{k_1})$  for all  $i \neq 1$ . Thus,  $a_i(\hat{S}_{k_1}) = 1$  for all  $i \in N_1(\varrho)$  and  $a_i(\hat{S}_{k_1}) = a$  for all  $i \notin N_1(\varrho) \cup \{1\}$ .

Moreover, by Remark 1 and the definition of the process,  $a_1(\hat{S}_{k_1}) = 1$ . Consider the time point  $k_1 + 1$ . By the definition of the process, an agent  $i \neq 1$  will be in  $I(S_{k_1+1})$  if  $a_i(\hat{S}_{k_1})r_i(\hat{S}_{k_1}) > \tau$ . For any  $i \notin N_1(\varrho) \cup \{1\}$ ,  $a_i(\hat{S}_{k_1}) = a \leq \tau$ . Thus,  $a_i(\hat{S}_{k_1})r_i(\hat{S}_{k_1}) \leq \tau$  and any agent in  $N_1(\varrho) \cup \{1\}$  will not get infected at  $k_1 + 1$ . For agents in  $N_1(\varrho)$ , we distinguish two cases.

**Case 1:**  $|N_1(\varrho)| \geq \hat{\alpha}$ .

Since  $I(S_{k_1}) = \{1\}$ ,  $a_i(\hat{S}_{k_1}) = 1$  for all  $i \in N_1(\varrho) \cup \{1\}$ ,  $a_i(\hat{S}_{k_1}) = a$  for all  $i \notin N_1(\varrho) \cup \{1\}$ , and  $g_{ij} = c$  for all  $i \neq j$ , it follows that

$$\begin{aligned} r_i(\hat{S}_{k_1}) &= \frac{1}{|N_1(\varrho)| + (n-1 - |N_1(\varrho)|)a} \\ &= \frac{1}{|N_1(\varrho)|(1-a) + (n-1)a} \\ &\leq \frac{1}{\hat{\alpha}(1-a) + (n-1)a} && (\text{since } |N_1(\varrho)| \geq \hat{\alpha}) \\ &\leq \tau && (\text{by (B.2)}) \end{aligned}$$

for all  $i \in N_1(\varrho)$ . This implies that no agent in  $N_1(\varrho)$  gets infected at the time point  $k_1 + 1$ .

We show that no new agent would get infected after this. We first show that  $I(S_{k_1+2}) = \{1\}$ . Let  $\varrho_{k_1+1} = i$ . If  $i \notin I(S_{k_1+1})$  then as  $I(S_{k_1}) = I(S_{k_1+1})$  by Lemma 6, we have  $I(S_{k_1+1}) = I(S_{k_1+2})$ . If  $i \in I(S_{k_1+1})$  then  $i = 1$ . Moreover,  $a_1(S_{k_1+1}) = a_1(\hat{S}_{k_1}) = 1$ . Hence, by Lemma 6,  $I(S_{k_1+1}) = I(S_{k_1+2})$ . Therefore,  $I(S_{k_1+2}) = \{1\}$ . Using the same arguments repeatedly, it follows that  $I(S_t) = \{1\}$  for all  $t \geq k_1 + 2$ . Thus,  $I(S_\infty) = \{1\}$ .

**Case 2:**  $|N_1(\varrho)| \leq \hat{\alpha} - 1$ .

By the assumption of the case,  $\hat{\alpha} \geq 1$ . First assume  $\hat{\alpha} = 1$ . This, together with  $|N_1(\varrho)| \leq \hat{\alpha} - 1$ , implies  $|N_1(\varrho)| = 0$ . Therefore,  $k_1 = 1$ . We show that  $I(S_\infty) = \{1\}$ . Note that by the definition of the process,  $a_i(\hat{S}_0) = a$  for all  $i \neq 1$ . As  $a \leq \tau$ , this means no agent in the set  $\{2, \dots, n\}$  will get infected at the time point 1. Hence,  $I(S_1) = \{1\}$ . Moreover, as  $I(S_1) = \{1\}$  with  $a_1(S_1) = 1$  and  $a_i(S_1) = a \leq \tau$  for all  $i \neq 1$ , by Lemma 8 it follows that  $I(S_1) = I(S_\infty)$ . Hence,  $I(S_\infty) = \{1\}$ .

Now assume  $\hat{a} \geq 2$ . Thus by the definition of  $\hat{a}$ , we have  $\hat{a} = \left\lceil \frac{\frac{1}{\tau} - (n-1)a}{1-a} \right\rceil$ . As  $I(S_{k_1}) = 1$ ,  $a_i(\hat{S}_{k_1}) = 1$  for all  $i \in N_1(\underline{v}) \cup \{1\}$ ,  $a_i(\hat{S}_{k_1}) = a$  for all  $i \notin N_1(\underline{v}) \cup \{1\}$ , and  $g_{ij} = c$  for all  $i \neq j$ , we have for all  $i \in N_1(\underline{v})$

$$\begin{aligned} r_i(\hat{S}_{k_1}) &= \frac{1}{|N_1(\underline{v})| + (n-1 - |N_1(\underline{v})|)a} \\ &= \frac{1}{|N_1(\underline{v})|(1-a) + (n-1)a} \\ &\geq \frac{1}{(\hat{a}-1)(1-a) + (n-1)a} && \text{(since } |N_1(\underline{v})| \leq (\hat{a}-1)\text{)} \\ &= \frac{1}{(\hat{a}-1) + (n-\hat{a})a} \\ &> \tau. && \text{(by (B.3))} \end{aligned}$$

This implies all agents in  $N_1(\underline{v})$  will get infected at time point  $k_1 + 1$ . Thus, we have  $I(S_{k_1+1}) = N_1(\underline{v}) \cup \{1\}$ . Further, as,  $a_i(S_{k_1+1}) = a_i(\hat{S}_{k_1}) = 1$  for all  $i \in I(S_{k_1+1})$  and  $a_i(S_{k_1+1}) = a \leq \tau$  for all  $i \notin I(S_{k_1+1})$ , by Lemma 8 it follows that  $I(S_{k_1+1}) = I(S_\infty)$ . Hence,  $I(S_\infty) = N_1(\underline{v}) \cup \{1\}$ .

**Step 2.** Consider the probability space  $(N_\infty, \mathcal{F}, \mathbb{P})$  and random variables  $S$  and  $t_1, \dots, t_n$ . Let  $m \in \{2, \dots, n\}$  be such that  $m \leq \hat{a}$ . In view of Case 1 and Case 2 of the current proof, we have (i)  $|I(S_\infty)| \leq \hat{a}$ , and (ii)  $|I(S_\infty)| = m$  with  $1 \in I(S_\infty)$  if and only if  $|\{i \in N \mid t_i < t_1\}| = m - 1$ . Also,  $|I(S_\infty)| = 1$  if and only if either  $\{i \in N \mid t_i < t_1\} = \emptyset$  or  $|\{i \in N \mid t_i < t_1\}| \geq \hat{a}$ . Moreover, as  $\mathbb{P}$  is uniform, any two subsets of  $N$  with same cardinality have the same probability. These observations together yield

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} 1 - \frac{\hat{a}-1}{n} & \text{if } J = \{1\}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } 1 \in J \text{ and } |J| = m \text{ where } m \in [2, \hat{a}], \\ 0 & \text{otherwise.} \end{cases}$$

This completes the proof of the theorem. ■

### B.3 PROOF OF THEOREM 9

**Proof:** We follow the same structure that we used in the proof of Theorem 1.

**Step 1.** Fix an agent sequence  $\underline{v} \in N_\infty$  and let  $S$  be the DVSP induced by  $\underline{v}$ . To shorten notation, for all  $i \in N$ , let us denote  $t_i(\underline{v})$  by  $k_i$ . The following claim demonstrates how an agent  $i$  with  $k_i < k_1$  will update their action. Recall the set  $N_1(\underline{v})$ . We distinguish two cases based on the value of  $|N_1(\underline{v})|$ .

**Case 1:**  $|N_1(\underline{v})| = 0$ .

We show that, for  $\tau \leq \frac{a}{n-1}$ , all the agents will get infected under this assumption, i.e.,  $I(S_\infty) = N$ .

Note that by the assumption of the case,  $\underline{v}_0 = 1$ . Recall that  $\hat{S}_0$  denotes the intermediate state where the only change from  $S_0$  is that agent  $\underline{v}_0$  has updated their action to  $b_{\underline{v}_0}(S_0)$ . Since  $\underline{v}_0 = 1$ ,

we have  $a_i(S_0) = a_i(\hat{S}_0) = a$  for all  $i \neq 1$ . Moreover, by Remark 1 and the definition of the process,  $a_1(\hat{S}_0) = 1$ . Consider the time point 1. By the definition of the process, an agent  $i \neq 1$  will be in  $I(S_1)$  if  $a_i(\hat{S}_0)r_i(\hat{S}_0) > \tau$ . Since  $I(S_0) = \{1\}$ ,  $a_i(\hat{S}_0) = a$  for all  $i \in N$ , and  $g_{ij} = c$  for all  $i \neq j$ , it follows that for all  $i \in N \setminus \{1\}$

$$ar_i(\hat{S}_0) = \frac{a}{(n-2)a+1} > \frac{a}{(n-1)}.$$

Because  $\tau \leq \frac{a}{n-1}$ , this implies that all the agents in  $N \setminus \{1\}$  gets infected at the time point 1. Hence,  $I(S_1) = N$ . Therefore, by the definition of the process  $I(S_\infty) = N$ .

**Case 2:**  $|N_1(\varrho)| \geq 1$ .

This means  $\varrho_0 \neq 1$ . Let  $\varrho_0 = i \in N \setminus 1$ . Hence, by the definition of the process, agent  $i$  will choose their action as  $b_i(S_0)$  at the intermediate state  $\hat{S}_0$ . As  $a_j(S_0) = a > 0$  for all  $j \in N$  and  $I(S_0) = \{1\}$ , it follows that  $r_i(S_0) \neq 0$ . Therefore,

$$b_i(S_0) = \min \left\{ 1, \frac{\tau}{r_i(S_0)} \right\} = \min \{1, (n-1)\tau\} = (n-1)\tau. \quad (\text{B.5})$$

Since by our assumption  $\varrho_0 = i$  and  $i \notin I(S_0)$ , by Observation 4,  $i \notin I(S_1)$ . For any other uninfected agent  $j$ ,

$$r_j(\hat{S}_0) = \frac{a}{(n-2)a + b_i(S_0)} = \frac{a}{(n-2)a + (n-1)\tau}.$$

This together with the fact that  $a_j(\hat{S}_0) = a$  implies

- (i) if  $\tau = \frac{a}{n-1}$  then  $a_j(\hat{S}_0)r_j(\hat{S}_0) = \frac{a}{n-1} = \tau$ , and
- (ii) if  $\tau < \frac{a}{n-1}$  then  $a_j(\hat{S}_0)r_j(\hat{S}_0) > \frac{a}{n-1} > \tau$ .

Combining the above observations, we may write if  $\tau = \frac{1}{n-1}$  then agent  $j$  will not get infected at time point 1 and if  $\tau < \frac{a}{n-1}$  then agent  $j$  will get infected at time point 1. Hence, we have

$$\tau = \frac{a}{n-1} \implies I(S_1) = \{1\} \text{ and } \tau < \frac{a}{n-1} \implies I(S_1) = N \setminus \{i\}.$$

To decide the final outcome, we first assume  $\tau = \frac{a}{n-1}$ . Note that by (B.5),  $b_i(S_0) = a$ . This means  $a_i(S_1) = a$ . Moreover, as  $\varrho_0 = i$ , we have  $a_j(S_1) = a$  for all  $j \neq i$ . Using similar arguments, we can show that  $a_k(S_{k_1}) = a$  for all  $k \in N$  and  $I(S_{k_1}) = \{1\}$ . By the definition of the process,  $a_1(\hat{S}_{k_1}) = 1$  and  $a_k(\hat{S}_{k_1}) = a$  for all  $k \neq 1$ . Therefore, for any  $k \neq 1$

$$a_k(\hat{S}_{k_1})r_k(\hat{S}_{k_1}) = \frac{a}{(n-2)a+1} > \frac{a}{(n-1)} = \tau.$$

Thus, all the agents other than agent 1 will get infected at  $k_1 + 1$ . Hence,  $I(S_\infty) = N$ .

Now assume  $\tau < \frac{a}{n-1}$ . We distinguish two subcases.

**Case 2.1.**  $\varrho_1 = i$ .

We show that the final infected set will be  $N \setminus i$ . Since by our assumption  $\varrho_1 = i$  and  $i \notin I(S_1)$ , by

Observation 4,  $i \notin I(S_2)$ . Hence,  $I(S_2) = N \setminus \{i\}$ . We now show that  $i$  will not get infected after this. At time point 2,

$$r_i(\hat{S}_2) = \frac{(n-1)}{(n-1)} = 1.$$

Therefore,  $a_i(\hat{S}_2) = \tau$  (see Observation 4). At time point 3, if  $v_3 = i$ , then agent  $i$  would not get infected at time point 4 (Observation 4). On the other hand, if  $v_3 \neq i$  then as  $a_i(\hat{S}_3) = a_i(\hat{S}_2) = \tau$ , it follows that  $a_i(\hat{S}_3)r_i(\hat{S}_3) \leq \tau$ . Hence, agent  $i$  would remain uninfected at time point 4. Continuing in this manner, we may show that  $i$  will not get infected after this. Thus,  $I(S_\infty) = N \setminus \{i\}$ .

**Case 2.2.:**  $v_1 \neq i$

We show that the final infected set will be  $N$ . Since  $I(S_1) = N \setminus \{i\}$ ,  $r_i(\hat{S}_1) = 1$ . Moreover, as  $a_i(S_1) = a_i(\hat{S}_0) = b_i(S_0) = (n-1)\tau > \tau$  (see B.5) and  $v_1 \neq i$ , it follows that  $a_i(\hat{S}_1) > \tau$ . Combining this two we have  $a_i(\hat{S}_1)r_i(\hat{S}_1) > \tau$ . Thus, agent  $i$  will get infected at time point 2. Hence,  $I(S_2) = N$  and  $I(S_\infty) = N$ .

**Step 2.** First assume  $\tau = \frac{a}{n-1}$ . Therefore, in view Case 1 and Case 2 of the current proof, we have  $I(S_\infty) = N$ .

Now assume  $\tau < \frac{a}{n-1}$ . By Case 1 and Case 2 above, we have

- (i)  $I(S_\infty) = N \setminus i$  with  $1 \in I(S_\infty)$  if  $|N_1(v)| \geq 1$  and there is  $i \in N \setminus \{1\}$  such that  $k_i = 0$  and  $v_1 = i$ , and
- (ii)  $I(S_\infty) = N$  if either  $|N_1(v)| = 0$  or  $|N_1(v)| \geq 1$  and there is no  $i \in N \setminus \{1\}$  such that  $k_i = 0$  and  $v_1 = i$ .

We calculate the probability of  $|I(S_\infty)| = n-1$ . By (i) we have

$$\begin{aligned} & P(v \mid |N_1(v)| \geq 1 \text{ and } \exists i \neq 1 \text{ such that } k_i = 0 \text{ and } v_1 = i) \\ &= P(v \mid \exists i \neq 1 \text{ such that } k_i = 0 \text{ and } v_1 = i) \\ &= {}^{n-1}C_1 \times \frac{1}{n^2} \\ &= \frac{n-1}{n^2}. \end{aligned}$$

Note that by (i) and (ii),

$$P(|I(S_\infty)| = n-1) + P(I(S_\infty) = N) = 1.$$

Therefore,

$$\begin{aligned} P(I(S_\infty) = N) &= 1 - P(|I(S_\infty)| = n-1) \\ &= 1 - \frac{n-1}{n^2}. \end{aligned}$$

Since any two subsets of  $N$  with the cardinality  $n-1$  have the same probability, combining all the above observations, we have the following distribution of the infected set.

$$\mathbb{P}(I(S_\infty) = J) = \begin{cases} \frac{1}{n^2} & \text{if } 1 \in J \text{ and } |J| = n - 1, \\ 1 - \frac{n-1}{n^2} & \text{if } |J| = n, \text{ i.e., } J = N, \\ 0 & \text{otherwise.} \end{cases}$$

This completes the proof of the theorem. ■

### C. A FEW IMPORTANT LEMMAS

**Lemma 9.** *Let  $\varrho \in N_\infty$  and let  $S$  be the DVSP induced by  $\varrho$ . Suppose  $t_0$  is such that  $I(S_{t_0}) = I(S_t)$  for all  $t \geq t_0$  and  $a_k(S_{t_0}) = 1$  for all  $k \in I(S_{t_0})$ . Then for  $i \notin I(S_{t_0})$  and  $\bar{t} > t_0$  with  $\varrho_{\bar{t}} = i$  implies*

$$a_i(\hat{S}_{\bar{t}}) \geq a_j(\hat{S}_{\bar{t}}) \text{ for all } j \notin I(S_{t_0}) \text{ with } \varrho_t = j \text{ for some } t \in (t_0, \bar{t}].$$

**Proof:** We use induction on  $\bar{t}$  to prove the lemma. Note that for the base case, that is, for  $\bar{t} = t_0 + 1$ , the lemma holds vacuously. Next we introduce an induction hypothesis.

*Induction Hypothesis:* Given  $\bar{t} \in \mathbb{N}_0$  with  $\bar{t} > t_0 + 1$ , the lemma holds for all  $t$  with  $t_0 + 1 \leq t < \bar{t}$ .

We show that the lemma holds for  $\bar{t}$ . Suppose  $\varrho_{\bar{t}} = i$  where  $i \notin I(S_{t_0})$ . If there is no  $t \in (t_0, \bar{t})$  such that  $\varrho_t \notin I(S_{t_0})$ , the lemma holds vacuously. So, assume that  $\hat{t}$  is the last time point before  $\bar{t}$  such that  $\varrho_{\hat{t}} = j$  for some  $j \notin I(S_{t_0})$ . This, together with the induction hypothesis, implies  $a_j(\hat{S}_{\hat{t}}) \geq a_k(\hat{S}_{\hat{t}})$  for all  $k \notin I(S_{t_0})$  with  $\varrho_t = k$  for some  $t \in (t_0, \hat{t})$ . Also, by the definition of the process,  $a_l(\hat{S}_{\hat{t}}) = a_l(\hat{S}_{\bar{t}})$  for all  $l \in I(S_{t_0}) \setminus i$ . Therefore, to prove the lemma it is enough to show that  $a_i(\hat{S}_{\bar{t}}) \geq a_j(\hat{S}_{\bar{t}})$ . Additionally, as  $a_j(\hat{S}_{\bar{t}}) \leq 1$ , we may assume that  $a_i(\hat{S}_{\bar{t}}) = \frac{\tau}{r_i(\hat{S}_{\bar{t}})}$ . Moreover, as  $j \notin I(S_{t_0})$ ,  $a_j(\hat{S}_{\bar{t}}) \leq \frac{\tau}{r_j(\hat{S}_{\bar{t}})}$ . Now

$$\begin{aligned} \frac{\tau}{r_j(\hat{S}_{\bar{t}})} &= \frac{\tau}{\frac{|I(S_{t_0})|}{|I(S_{t_0})| + \sum_{k \notin I(S_{t_0}) \setminus j} a_k(\hat{S}_{\bar{t}})}} \quad (\text{as } g_{ij} = c \text{ for all } i \neq j) \\ &= \frac{\tau[|I(S_{t_0})| + \sum_{k \notin I(S_{t_0}) \setminus j} a_k(\hat{S}_{\bar{t}})]}{|I(S_{t_0})|} \quad (\text{as } I(S_{t_0}) = I(S_{\hat{t}}) \text{ and for } k \in I(S_{t_0}), a_k(S_{\hat{t}}) = 1) \\ &= \frac{\tau[|I(S_{t_0})| + \sum_{k \notin I(S_{t_0}) \setminus \{i, j\}} a_k(\hat{S}_{\bar{t}}) + a_i(\hat{S}_{\bar{t}})]}{|I(S_{t_0})|} \\ &\leq \frac{\tau[|I(S_{t_0})| + \sum_{k \notin I(S_{t_0}) \setminus \{i, j\}} a_k(\hat{S}_{\bar{t}}) + a_j(\hat{S}_{\bar{t}})]}{|I(S_{t_0})|} \quad (\text{as } a_j(\hat{S}_{\bar{t}}) \geq a_i(\hat{S}_{\bar{t}})) \\ &= \frac{\tau[|I(S_{t_0})| + \sum_{k \notin I(S_{t_0}) \setminus \{i, j\}} a_k(\hat{S}_{\bar{t}}) + a_j(\hat{S}_{\bar{t}})]}{|I(S_{t_0})|} \quad (\text{as } a_k(\hat{S}_{\bar{t}}) = a_k(\hat{S}_{\hat{t}}) \text{ for all } k \notin I(S_{t_0}) \setminus i) \\ &= \frac{\tau[|I(S_{t_0})| + \sum_{k \notin I(S_{t_0}) \setminus i} a_k(\hat{S}_{\bar{t}})]}{|I(S_{t_0})|} \\ &= \frac{\tau}{\frac{|I(S_{t_0})|}{|I(S_{t_0})| + \sum_{k \notin I(S_{t_0}) \setminus i} a_k(\hat{S}_{\bar{t}})}} \quad (\text{as } I(S_{t_0}) = I(S_{\bar{t}}) \text{ and for } k \in I(S_{t_0}), a_k(S_{\bar{t}}) = 1) \end{aligned}$$

$$= \frac{\tau}{r_i(\hat{S}_{\bar{t}})} \text{ (as } g_{ij} = c \text{ for all } i \neq j). \quad (\text{C.1})$$

(C.1) together with  $a_i(\hat{S}_{\bar{t}}) = \frac{\tau}{r_i(\hat{S}_{\bar{t}})}$  and  $a_j(\hat{S}_{\bar{t}}) \leq \frac{\tau}{r_j(\hat{S}_{\bar{t}})}$  implies  $a_i(\hat{S}_{\bar{t}}) \geq a_j(\hat{S}_{\bar{t}})$ . Hence,  $a_i(\hat{S}_{\bar{t}}) \geq a_j(\hat{S}_{\bar{t}})$ .

This completes the proof of the lemma.  $\blacksquare$

The following lemma provides an important property of the final action limit for both infected and uninfected agents. It shows that an infected agent will have the action limit 1 whereas any two uninfected agents will have the same action limit, that is, for  $i, j \notin I(S_\infty)$ ,  $a_i(S_\infty) = a_j(S_\infty)$ .

**Lemma 10.** *Let  $\underline{v} \in N_\infty$  and let  $S$  be the DVSP induced by  $\underline{v}$ . Then, for*

$$[k \in I(S_\infty)] \implies [a_k(S_\infty) = 1]$$

and

$$[i, j \notin I(S_\infty)] \implies [a_i(S_\infty) = a_j(S_\infty)].$$

**Proof:** Let  $\underline{v} \in N_\infty$  and let  $S$  be the DVSP induced by  $\underline{v}$ . Consider  $k \in I(S_\infty)$ . As  $\underline{v} \in N_\infty$ , agent  $k$  appears infinitely many times in  $\underline{v}$ . And, after getting infected whenever they update their action, they will choose it as 1. Thus,  $a_k(S_\infty) = 1$ . Now consider  $i, j \notin I(S_\infty)$ . Let  $b = a_i(S_\infty)$  and consider  $\epsilon > 0$ . This means there exists  $t_0$  such that  $a_i(S_t) \geq b - \epsilon$  for all  $t \geq t_0$ . Note that as  $N$  is a finite set and  $I(S_\infty)$  exists, there exists  $\bar{t} \in \mathbb{N}_0$  such that  $I(S_{\bar{t}}) = I(S_\infty)$ . In view of this, we may assume that  $I(S_{t_0}) = I(S_\infty)$ . Consider a time point  $\hat{t}$  such that

- (i)  $\hat{t} > t_0$  and  $\underline{v}_{\hat{t}} = j$  and
- (ii) there exists  $\bar{t} \in [t_0, \hat{t}]$  such that  $\underline{v}_{\bar{t}} = i$ .

Such a time point  $\hat{t}$  exists as  $\underline{v} \in N_\infty$ . Therefore, by Lemma 9,  $a_j(S_{\hat{t}}) \geq a_i(S_{\hat{t}})$ . As  $\hat{t} > t_0$ , this means  $a_j(S_{\hat{t}}) \geq b - \epsilon$ . Further, as  $I(S_{t_0}) = I(S_\infty)$  and  $\hat{t} > t_0$ , by Claim 1 in Lemma 2,  $a_j(S_t) \geq a_j(S_{\hat{t}})$  for all  $t \geq \hat{t}$ . Thus,  $a_j(S_t) \geq b - \epsilon$  for all  $t \geq \hat{t}$ . Since  $\epsilon$  is arbitrary, this gives  $a_j(S_\infty) \geq b$ . Similarly, we can show that  $a_i(S_\infty) \geq a_j(S_\infty)$ . Hence,  $a_i(S_\infty) = a_j(S_\infty)$ .  $\blacksquare$

The next lemma determines the common action limit of the uninfected agents.

**Lemma 11.** *Let  $\underline{v} \in N_\infty$  and let  $S$  be the DVSP induced by  $\underline{v}$ . Further, let  $\gamma$  be the common action limit of the uninfected agents. Then,*

$$[(n-1)\tau < |I(S_\infty)|] \implies \left[ \gamma = \frac{\tau |I(S_\infty)|}{(1+\tau)|I(S_\infty)| - \tau(n-1)} < 1 \right],$$

and

$$[(n-1)\tau \geq |I(S_\infty)|] \implies [\gamma = 1].$$

**Proof:** Let  $t_0 \in \mathbb{N}_0$  be such that  $I(S_{t_0}) = I(S_\infty)$  and  $a_k(S_{t_0}) = 1$  for all  $k \in I(S_{t_0})$ . First assume that  $(n-1)\tau < |I(S_\infty)|$ . This implies  $\frac{\tau}{|I(S_\infty)|} < \frac{1}{n-1}$ . We first show that for any time point  $\bar{t} \geq t_0$ , if  $\underline{v}_{\bar{t}} \notin I(S_\infty)$  then  $a_{\underline{v}_{\bar{t}}}(\hat{S}_{\bar{t}}) < 1$ . Let  $\underline{v}_{\bar{t}} = i$ . Since  $a_i(\hat{S}_{\bar{t}}) = \min\{\frac{\tau}{r_i(\hat{S}_{\bar{t}})}, 1\}$ , it is enough to show that  $\frac{\tau}{r_i(\hat{S}_{\bar{t}})} < 1$ .

$$\frac{\tau}{r_i(\hat{S}_{\bar{t}})} = \frac{\tau}{|I(\hat{S}_{\bar{t}})|} \left( |I(\hat{S}_{\bar{t}})| + \sum_{j \notin I(\hat{S}_{\bar{t}}) \cup \{i\}} a_j(\hat{S}_{\bar{t}}) \right) \text{ (as } g_{ij} = c \text{ for all } i \neq j)$$

$$\begin{aligned}
&= \frac{\tau}{|I(S_\infty)|} \left( |I(S_\infty)| + \sum_{j \notin I(S_\infty) \cup \{i\}} a_j(\hat{S}_{\bar{t}}) \right) \text{ (as } I(S_{t_0}) = I(S_\infty) \text{ and } \bar{t} \geq t_0) \\
&< \frac{1}{n-1} \left( |I(S_\infty)| + \sum_{j \notin I(S_\infty) \cup \{i\}} a_j(\hat{S}_{\bar{t}}) \right) \text{ (as } \frac{\tau}{|I(S_\infty)|} < \frac{1}{n-1}) \\
&\leq 1 \text{ (as } a_j(\hat{S}_{\bar{t}}) \leq 1 \text{ for all } j \notin I(S_\infty) \cup \{i\}).
\end{aligned}$$

Since  $\bar{t}$  is arbitrary, it follows that  $a_i(\hat{S}_t) = \frac{\tau}{r_i(\hat{S}_t)}$  for all  $t \geq t_0$  with  $\varrho_t = i$ . Hence,

$$\begin{aligned}
a_i(\hat{S}_t) &= \frac{\tau}{r_i(\hat{S}_t)} \\
&= \frac{\tau}{|I(\hat{S}_t)|} \left( |I(\hat{S}_t)| + \sum_{j \notin I(\hat{S}_t) \cup \{i\}} a_j(\hat{S}_t) \right) \text{ (as } g_{ij} = c \text{ for all } i \neq j) \\
&= \frac{\tau}{|I(S_\infty)|} \left( |I(S_\infty)| + \sum_{j \notin I(S_\infty) \cup \{i\}} a_j(\hat{S}_t) \right). \tag{C.2}
\end{aligned}$$

Taking limit on both the sides of C.2, we have

$$\begin{aligned}
\gamma &= \frac{\tau}{|I(S_\infty)|} \left( |I(S_\infty)| + \sum_{j \notin I(S_\infty) \cup \{i\}} \gamma \right) \\
\implies \gamma &= \frac{\tau |I(S_\infty)|}{(1 + \tau) |I(S_\infty)| - \tau(n-1)} \\
\implies \gamma &< \frac{\tau |I(S_\infty)|}{(1 + \tau) |I(S_\infty)| - |I(S_\infty)|} = 1.
\end{aligned}$$

Now assume  $(n-1)\tau \geq |I(S_\infty)|$ . We have to show that  $\gamma = 1$ . Assume  $\gamma < 1$ . Consider  $i \notin I(S_\infty)$ . Since by Claim 1 in Lemma 2,  $a_i(S_t)$  is an increasing sequence for  $t > t_0$ ,  $\gamma < 1$  implies  $a_i(S_t) < 1$  for all  $t > t_0$ . This means  $a_i(\hat{S}_t) = \frac{\tau}{r_i(\hat{S}_t)}$  for  $t > t_0$  with  $\varrho_t = i$ . Therefore, using similar arguments as before we have

$$\begin{aligned}
\gamma &= \frac{\tau |I(S_\infty)|}{(1 + \tau) |I(S_\infty)| - \tau(n-1)} \\
\implies \gamma &\geq \frac{\tau |I(S_\infty)|}{(1 + \tau) |I(S_\infty)| - |I(S_\infty)|} = 1.
\end{aligned}$$

But this is a contradiction to  $\gamma < 1$ . Therefore,  $\gamma = 1$ . ■



## D. PROOF OF THEOREM 4, THEOREM 6, THEOREM 8, AND THEOREM 10

### D.1 PROOF OF THEOREM 4

**Proof:** We first explore the limiting actions for a fixed agent sequence, and then we use this to find the limiting probability distribution. Let  $\underline{v}$  be an agent sequence and  $S$  be the DVSP induced by  $\underline{v}$ . Note that by Remark 1, it is enough to assume  $\underline{v} \in N_\infty$ . Therefore, by Lemma 10, all the agents outside  $I(S_\infty)$  have the same action limit, and all the agents in  $I(S_\infty)$  have the action limit 1. Let us denote the common limit by  $\gamma$ . First assume  $\tau \geq \frac{1}{n-1}$ . By Theorem 3,  $I(S_\infty) = \{1\}$ . Therefore,  $(n-1)\tau \geq |I(S_\infty)|$ , and hence, by Lemma 11,  $\gamma = 1$ . Thus,  $a_N(S_\infty) = \underline{1}$ .

Now assume that  $\tau < \frac{1}{n-1}$ . We distinguish two cases based on the value of  $N_1(\underline{v})$  (as in the proof of Theorem 3) to find  $\gamma$ .

**Case 1:**  $|N_1(\underline{v})| = 0$ .

Recall that for this case the final infected set is  $N$ . Hence,  $a_N(S_\infty) = \underline{1}$ .

**Case 2:**  $|N_1(\underline{v})| \geq 1$ .

Recall that for this case, the final infected set has cardinality either  $n$  or  $n-1$ . If cardinality is  $n$  then  $a_N(S_\infty) = \underline{1}$ . If cardinality is  $n-1$ , then as  $(n-1)\tau < 1$ , by Lemma 11,  $\gamma = \tau$ . Hence,

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \tau & \text{if } i \notin I(S_\infty). \end{cases}$$

Note that this implies  $a_N(S_\infty) \in A_{n-1}$ . Also, as  $\mathbb{P}$  is uniform, any two vectors in  $A_{n-1}$  have the same probability. Thus, by Theorem 3, we have the following distribution

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{n-1}{n^2} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n^2} & \text{if } \underline{x} \in A_{n-1}, \\ 0 & \text{otherwise.} \end{cases}$$

■

### D.2 PROOF OF THEOREM 6

**Proof:** We first explore the limiting actions for a fixed agent sequence, and then we use this to find the limiting probability distribution. Let  $\underline{v}$  be an agent sequence and  $S$  be the DVSP induced by  $\underline{v}$ . Note that by Remark 1, it is enough to assume  $\underline{v} \in N_\infty$ . Therefore, by Lemma 10, all the agents outside  $I(S_\infty)$  have the same action limit, and all the agents in  $I(S_\infty)$  have the action limit 1. Let us denote the common limit by  $\gamma$ . We distinguish two cases based on the value of  $N_1(\underline{v})$  (as in the proof of Theorem 5) to find  $\gamma$ .

**Case 1:**  $|N_1(\underline{v})| \geq \hat{\alpha}$ .

Recall that for this case the final infected set is  $\{1\}$ . Moreover, by the assumption of the theorem,  $(n-1)\tau \geq 1$ . Therefore, by Lemma 6,  $\gamma = 1$ . Hence,  $a_N(S_\infty) = \underline{1}$ .

**Case 2:**  $|N_1(\underline{v})| \leq \hat{\alpha} - 1$ .

Recall that for this case, the final infected set is  $N_1(\underline{v}) \cup \{1\}$ . Note that as  $\hat{\alpha} \leq n-1$ ,  $N_1(\underline{v}) \cup \{1\} \leq n-1$ . Therefore, by Lemma 6, if  $(n-1)\tau \geq |N_1(\underline{v})| + 1$  then  $a_N(S_\infty) = \underline{1}$ , and if  $(n-1)\tau < |N_1(\underline{v})| + 1$  then

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \frac{\tau(|N_1(\underline{v})| + 1)}{(1 + \tau)(|N_1(\underline{v})| + 1) - \tau(n - 1)} & \text{if } i \notin I(S_\infty). \end{cases}$$

Recall that  $\hat{\beta} = \min\{\lfloor (n - 1)\tau \rfloor + 1, \hat{\alpha} + 1\}$ . Thus, combining Cases 1 and 2, we have the following:

(i)  $|N_1(\underline{v})| + 1 \in [\hat{\beta}, \hat{\alpha}]$  implies

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \frac{\tau(|N_1(\underline{v})| + 1)}{(1 + \tau)(|N_1(\underline{v})| + 1) - \tau(n - 1)} & \text{if } i \notin I(S_\infty). \end{cases}$$

Note that (i) implies  $a_N(S_\infty) \in A_{\lfloor |N_1(\underline{v})| + 1 \rfloor}$  when  $|N_1(\underline{v})| + 1 \in [\hat{\beta}, \hat{\alpha}]$ . Also, as  $\mathbb{P}$  is uniform, any two vectors in  $A_m$ , for  $m \in [\hat{\beta}, \hat{\alpha}]$ , have the same probability. Thus, we have the following distribution

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{\hat{\alpha} - \hat{\beta} + 1}{n} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [\hat{\beta}, \hat{\alpha}], \\ 0 & \text{otherwise.} \end{cases}$$

■

### D.3 PROOF OF THEOREM 8

**Proof:** We first explore the limiting actions for a fixed agent sequence, and then we use this to find the limiting probability distribution. Let  $\underline{v}$  be an agent sequence and  $S$  be the DVSP induced by  $\underline{v}$ . Note that by Remark 1, it is enough to assume  $\underline{v} \in N_\infty$ . Therefore, by Lemma 10, all the agents outside  $I(S_\infty)$  have the same action limit, and all the agents in  $I(S_\infty)$  have the action limit 1. Let us denote the common limit by  $\gamma$ . First assume  $\tilde{\alpha} + 1 < \bar{\alpha}$ . As shown in the proof of Theorem 7, the infected set is either  $\{1\}$  or  $|N_1(\underline{v})| + 1$  where  $N_1(\underline{v}) \in [1, \tilde{\alpha}]$ . Since by the assumption of the theorem,  $(n - 1)\tau \geq 1$ , we have  $(n - 1)\tau \geq |I(S_\infty)|$  when the infected set is  $\{1\}$ . Therefore, by Lemma 11,  $\gamma = 1$  and hence,  $a_N(S_\infty) = \underline{1}$ . On the other hand, if the final infected set is  $N_1(\underline{v}) \cup \{1\}$ , the limiting action depends on  $|N_1(\underline{v})|$ . By Lemma 6, if  $(n - 1)\tau \geq |N_1(\underline{v})| + 1$  then  $a_N(S_\infty) = \underline{1}$ , and if  $(n - 1)\tau < |N_1(\underline{v})| + 1$  then

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \frac{\tau(|N_1(\underline{v})| + 1)}{(1 + \tau)(|N_1(\underline{v})| + 1) - \tau(n - 1)} & \text{if } i \notin I(S_\infty). \end{cases}$$

Recall that the following was shown in the proof of Theorem 7 when  $\tilde{\alpha} + 1 \leq \bar{\alpha}$ :

- $|I(S_\infty)| = 1$  if  $|N_1(\underline{v})| \in \{0, \tilde{\alpha}, \tilde{\alpha} + 1, \dots, n - 1\}$  and
- $|I(S_\infty)| = |N_1(\underline{v})| + 1$  if  $|N_1(\underline{v})| \in \{1, 2, \dots, \tilde{\alpha} - 1\}$ .

Recall that  $\tilde{\beta} = \min\{\lfloor (n - 1)\tau \rfloor + 1, \tilde{\alpha} + 1\}$ . Therefore, we have the following:

(i)  $|N_1(\underline{v})| + 1 \in [\tilde{\beta}, \tilde{\alpha}]$  implies

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \frac{\tau(|N_1(\underline{v})| + 1)}{(1 + \tau)(|N_1(\underline{v})| + 1) - \tau(n - 1)} & \text{if } i \notin I(S_\infty). \end{cases}$$

(ii)  $|N_1(\underline{v})| + 1 \in [1, \tilde{\beta} - 1] \cup [\tilde{\alpha} + 1, n]$  implies  $a_N(S_\infty) = \underline{1}$ .

Note that (i) implies  $a_N(S_\infty) \in A_{[|N_1(\underline{v})|+1]}$  when  $|N_1(\underline{v})| + 1 \in [\tilde{\beta}, \tilde{\alpha}]$ . Also, as  $\mathbb{P}$  is uniform, any two vectors in  $A_m$ , for  $m \in [\tilde{\beta}, \tilde{\alpha}]$ , have the same probability. Thus, we have the following distribution

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{\tilde{\alpha} - \tilde{\beta} + 1}{n} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [\tilde{\beta}, \tilde{\alpha}], \\ 0 & \text{otherwise.} \end{cases}$$

Now assume  $2 \leq \tilde{\alpha} < \tilde{\alpha} + 1$ . Recall that the following was shown in the proof of Theorem 7 when  $2 \leq \tilde{\alpha} < \tilde{\alpha} + 1$ :

- (i)  $|I(S_\infty)| = 1$  if  $|N_1(\underline{v})| \in \{0, \tilde{\alpha}, \tilde{\alpha} + 1, \dots, n - 1\}$ ,
- (ii)  $|I(S_\infty)| = |N_1(\underline{v})| + 1$  if  $|N_1(\underline{v})| \in \{1, 2, \dots, \tilde{\alpha} - 2\}$ ,
- (iii)  $|I(S_\infty)| = n$  if  $|N_1(\underline{v})| \in \{\tilde{\alpha} - 1, \dots, \tilde{\alpha} - 1\}$  and there is no  $i \in N$  such that  $k_i = k_1 + 1$  and  $v_{k_1+2} = i$ , and
- (iv)  $|I(S_\infty)| = n - 1$  if  $|N_1(\underline{v})| \in \{\tilde{\alpha} - 1, \dots, \tilde{\alpha} - 1\}$  and there is  $i \in N$  such that  $k_i = k_1 + 1$  and  $v_{k_1+2} = i$ .

By the assumption of the theorem,  $(n - 1)\tau \geq 1$  and  $\tau < 1$ . Thus, if  $|I(S_\infty)| = 1$  we have  $(n - 1)\tau \geq |I(S_\infty)|$ , and if  $|I(S_\infty)| = (n - 1)$  we have  $(n - 1)\tau < |I(S_\infty)|$ . Recall that  $\tilde{\beta} = \min\{\lfloor (n - 1)\tau \rfloor + 1, \tilde{\alpha}\}$ . Combining all these observations, we may write the following

(i)  $|I(S_\infty)| \in [\tilde{\beta}, \tilde{\alpha} - 1] \cup \{n - 1\}$  implies

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \frac{\tau(|I(S_\infty)|)}{(1 + \tau)(|I(S_\infty)|) - \tau(n - 1)} & \text{if } i \notin I(S_\infty). \end{cases}$$

(ii)  $|I(S_\infty)| \in [1, \tilde{\beta} - 1] \cup \{n\}$  implies  $a_N(S_\infty) = \underline{1}$ .

Note that (i) implies  $a_N(S_\infty) \in A_{(|I(S_\infty)|)}$  when  $|I(S_\infty)| \in [\tilde{\beta}, \tilde{\alpha} - 1] \cup \{n - 1\}$ . Also, as  $\mathbb{P}$  is uniform, any two vectors in  $A_m$ , for  $m \in [\tilde{\beta}, \tilde{\alpha} - 1] \cup \{n - 1\}$ , have the same probability. Therefore, using Theorem 7, we have the following distribution

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 + \frac{\bar{\beta} - \bar{\alpha}}{n} - \eta(\bar{\alpha}, \bar{\alpha}, n) & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n \times {}^{n-1}C_{m-1}} & \text{if } \underline{x} \in A_m \text{ for some } m \in [\bar{\beta}, \bar{\alpha} - 1], \\ \frac{\eta(\bar{\alpha}, \bar{\alpha}, n)}{n-1} & \text{if } \underline{x} \in A_{n-1}, \\ 0 & \text{otherwise.} \end{cases}$$

■

#### D.4 PROOF OF THEOREM 10

**Proof:** We first explore the limiting actions for a fixed agent sequence, and then we use this to find the limiting probability distribution. Let  $\underline{v}$  be an agent sequence and  $S$  be the DVSP induced by  $\underline{v}$ . Note that by Remark 1, it is enough to assume  $\underline{v} \in N_\infty$ . Therefore, by Lemma 10, all the agents outside  $I(S_\infty)$  have the same action limit, and all the agents in  $I(S_\infty)$  have the action limit 1. Let us denote the common limit by  $\gamma$ . First assume  $\tau = \frac{a}{n-1}$ . By Theorem 9,  $I(S_\infty) = N$ . Therefore, by Lemma 10,  $a_N(S_\infty) = \underline{1}$ .

Now assume that  $\tau < \frac{a}{n-1}$ . We distinguish two cases based on the value of  $N_1(\underline{v})$  (as in the proof of Theorem 9) to find  $\gamma$ .

**Case 1:**  $|N_1(\underline{v})| = 0$ .

Recall that for this case the final infected set is  $N$ . Hence,  $a_N(S_\infty) = \underline{1}$ .

**Case 2:**  $|N_1(\underline{v})| \geq 1$ .

Recall that for this case, the final infected set has cardinality either  $n$  or  $n-1$ . If cardinality is  $n$  then  $a_N(S_\infty) = \underline{1}$ . If cardinality is  $n-1$ , then as  $(n-1)\tau < 1$ , by Lemma C.2,  $\gamma = \tau$ . Hence,

$$a_i(S_\infty) = \begin{cases} 1 & \text{if } i \in I(S_\infty), \\ \tau & \text{if } i \notin I(S_\infty). \end{cases}$$

Note that this implies  $a_N(S_\infty) \in A_{n-1}$ . Also, as  $\mathbb{P}$  is uniform, any two vectors in  $A_{n-1}$  have the same probability. Thus, by Theorem 9, we have the following distribution

$$\mathbb{P}(a_N(S_\infty) = \underline{x}) = \begin{cases} 1 - \frac{n-1}{n^2} & \text{if } \underline{x} \in A_n, \text{ i.e., } \underline{x} \in A_n, \text{ i.e., } \underline{x} = \underline{1}, \\ \frac{1}{n^2} & \text{if } \underline{x} \in A_{n-1}, \\ 0 & \text{otherwise.} \end{cases}$$

■