On the relationship between p-dominance and stochastic stability in networks

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Abstract

Evolutionary models with persistent randomness employ stochastic stability as a solution concept to identify more reasonable outcomes in games with multiple equilibria. The complexity of computational methods used to identify stochastically stable outcomes and their lack of robustness to the interaction structure limit the applicability of evolutionary selection theories. This paper identifies *p-dominance* and *contagion threshold* as the properties of strategies and interaction structure respectively that robustly determine stochastically stable outcomes. Specifically, we show that *p-dominant strategies*, which are best responses to any distribution that assigns them a weight of at least p, are stochastically stable in networks with contagion threshold of at least p.

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1. Introduction

The concept of Nash equilibrium plays a central role in the field of game theory and economics. Many games (e.g. coordination games[1]) however have multiple strict Nash equilibria. This raises a question of which outcomes should be regarded more reasonable than others. To address this issue, Foster and Young (1990), Kandori et al. (1993) and Young (1993) proposed examining the process by which conventions (Nash equilibria of coordination games) become established using evolutionary models with persistent randomness. In their framework, randomness ensures that all outcomes are likely, but as the amount of noise vanishes, some outcomes are much more likely than others. Outcomes that retain a positive probability of being played in the long-run

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[1]Coordination games represent a class of games where players benefit most by choosing the same strategy. They are generally applied to model technology choice, social conventions, decisions on industry standards, and political actions such as protests

as the amount of noise vanishes are said to be *stochastically stable.*

A striking observation of the aforementioned papers is that stochastic stability as a selection mechanism not only rules out unstable mixed equilibria, but also selects a unique outcome in coordination games with two strategies: the risk-dominant equilibrium (i.e. a strategy that is a unique best response to any mixture that assigns it a weight of at least one half). Despite this interesting observation, there are two problems that limit the applicability of evolutionary selection theories: stochastic stability is not robust to the structure of social interactions,[2] and the computational methods used to identify stochastically stable outcomes are complex.[3] Thus, we do not have much knowledge about what kind of equilibria will be selected in coordination games with more than two strategies.

This paper contributes to the debate on the aforementioned limitations of evolutionary selection theories by focusing on the following question: what properties of strategies and interaction structure robustly determine stochastically stable outcomes? We consider an evolutionary model of best response with mutations (BRM) in which players interact locally through a social network. That is, players repeatedly choose strategies that are best responses to the distribution of strategies in their *neighbourhoods*—a fixed subset of the population whose strategies a player observes. Players' best responses are however subject to mutations (randomness) so that every strategy has a positive probability of being played.

Our analysis builds on and generalizes the concept of *pairwise contagion.* In the BRM model, a strategy a_2 is pairwise contagious relative to another a_1 if it can spread from a finite and *very small group* of players to the entire network through best response dynamics. The network property that determines whether contagion is feasible is the *contagion threshold.* Let $q \in (0, 1)$ be a critical number such that strategy a_2 is a best response whenever at least proportion q of a player's neighbours choose a_2. The contagion threshold of a network is a number p such that contagion occurs if and only if $q \leq p$ (Morris, 2000).

The property of strategies that naturally relates to the contagion threshold is *p-dominance.* A strategy is *p*-dominant if it is a best response whenever it is played by at least proportion p of

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[2]Young (1993) demonstrated that globally pairwise risk-dominant (GPRD) strategies need not be stochastically stable in global interactions (where each player observes strategies of every other player); Alós-Ferrer and Weidenholzer (2007) on the other hand showed that GPRD strategies are stochastically stable in 2-dimensional cyclic interactions.

[3] It employs a graph theoretic approach of Freidlin and Wentzell (1984), which involves constructing minimum cost spanning trees (Kandori et al., 1993; Young, 1993). This problem is exacerbated in local interactions since the network structure may induce additional equilibria which are also stochastically stable.

a player's neighbours. By definition, if a strategy is pairwise contagious in a coordination game with only two strategies, then it must be p-dominant. We generalize this relationship to coordination games with multiple strategies and derive an equivalence between p-dominant strategies and *globally pairwise contagious (GPRC) strategies*—strategies that are pairwise contagious relative to every other strategy. Using the relationship between p-dominance and $GPRC$ strategies, we show, in Theorem 1, that p-dominant strategies are stochastically stable in networks with a contagion threshold of at least p.

p-dominance is a Nash equilibrium refinement introduced by Morris et al. (1995) and has highly appealing properties that include: (i) uniqueness—if a p-dominant strategy exists, then it is unique. (ii) Independent of the number of strategies. (iii) monotonicity—for $p < p'$, any p-dominant strategy is also p'-dominant. Property (i) ensures that all equilibria that do not contain p-dominant strategies can be discarded (i.e. they are not stochastically stable). Properties (ii) and (iii) respectively ensure robustness of the predictions of Theorem 1 to the number of strategies, and their wider applicability. Consider for example the findings in Ellison (2000) showing that $\frac{1}{2}$-dominant strategies are stochastically stable in cyclic networks. Theorem 1 together with monotonicity of p-dominance imply that for all $p \leq \frac{1}{2}$, any p-dominant strategy is stochastically stable in cyclic networks. Theorem 1 also states that $\frac{1}{2}$-dominant strategies are stochastically stable in all networks with a contagion threshold of $\frac{1}{2}$, of which cyclic networks are a special case.

The present paper is closely related to Morris (2000), Ellison (2000), Sandholm (2001), Alós-Ferrer and Weidenholzer (2008) and Oyama et al. (2015).[4] Morris (2000) studies pairwise contagion in networks by examining deterministic best response dynamics in which players choose between two strategies. The focus is on identifying the key qualitative properties of networks that support contagion. We instead start from the premise that any interaction structure has a unique contagion threshold. We then exploit the properties of contagious strategies to establish a relationship between p-dominance, iterated p-best response sets and stochastic stability. Alós-Ferrer and Weidenholzer (2008) study contagion in an evolutionary process where players learn by imitating successful strategies. They find that the efficient strategy, and not the $\frac{1}{2}$-dominant strategy, is the only one which can spread contagiously to the whole population. Our paper is different in that we study best response dynamics and we employ contagion only as a means of establishing the relationship between p-dominance and stochastic stability.

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[4]Our results generalize Ellison (2000) who finds that $\frac{1}{2}$-dominant strategies are stochastically stable in cyclic network structures (see the discussion in the preceding paragraph).

Sandholm (2001) and Oyama et al. (2015) consider a deterministic dynamic process in which players choose strategies that are best responses to the empirical distribution of k others sampled randomly from an infinitely large population. They show that $\frac{1}{k}$-dominant strategies are almost globally stable. The key difference is that Sandholm (2001) and Oyama et al. (2015) consider deterministic dynamics which is opposed to stochastic dynamics considered in this paper. This in turn leads to differences in the solution concepts used (stochastic stability vs almost global convergence) and the respective analytical methods used in deriving results. Another difference concerns the interaction structure, where Oyama et al. (2015) consider a random sampling process and not deterministic networks. We discuss the implications of these differences in Sections 3.

Other papers that also study long-run stability of evolutionary process with local interactions include Ellison (1993, 2000), Blume (1995), Robson and Vega-Redondo (1996), Anderlini and Ianni (1996), Lee and Valentinyi (2000), Lee et al. (2003) and Alós-Ferrer and Weidenholzer (2007). These papers however consider specific network structures and/or 2-strategy coordination games. We instead derive predictions that are fairly robust to the network structure and the number of strategies.[5] Montanari and Saberi (2010), Young (2011) and Kreindler and Young (2013, 2014) study convergence rates of evolutionary dynamics in networks. Montanari and Saberi (2010) and Young (2011) show that convergence is fast in networks made up of cohesive subgroups; Kreindler and Young (2013, 2014) show that learning is fast if the level of experimentation is sufficiently large.[6] We discuss the implications of our results for convergence rates in Section 4.

The remainder of the paper is organized as follows. Section 2 outlines a typical model of evolutionary dynamics with best response and mutations. Section 3 establish the relationships between p-dominance and stochastic stability. Concluding remarks are offered in Section 4 and proofs are relegated to the Appendix.

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[5]There are also papers that study alternative classes of noisy best response choice rules to the BRM model considered in this paper (Bergin and Lipman, 1996; Maruta, 2002; Myatt and Wallace, 2003; Peski et al., 2010; Sandholm, 2010; Staudigl, 2012; Staudigl and Weidenholzer, 2014; Newton and Sawa, 2015; Klaus and Newton, 2016; Sandholm and Staudigl, 2016; Sawa and Wu, 2018). These papers however focus on global interactions, which makes comparison to our findings non-trivial.

[6]See also Newton and Angus (2015) and Ellison et al. (2016) who respectively study convergence rates for coalitional evolutionary dynamics and conditions for fast convergence.

2. Definitions and the learning model

2.1. The coordination game

We consider m-strategy 2-player coordination games. The set of pure strategies is denoted by $A = \{a_1, \cdots, a_j, \cdots, a_m\}$. Let $u(a_j, a_l)$ denote the payoff to a player playing strategy a_j against an opponent playing strategy a_l. We write Σ for the set of all mixed strategies over A, so that for any $a_j \in A$ and $\sigma \in \Sigma$, $\sigma(a_j)$ is the weight or probability σ assigns to a_j.

A coordination game is characterized by all pure strategies being strict Nash equilibrium. That is, $u(a_j, a_j) > u(a_j, a_l)$ for all $a_j, a_l \in A$ and $a_l \neq a_j$. Given that all pure strategies are strict Nash equilibria, we refer to the mapping $U : \Sigma \to \mathbb{R}^n$ of distributions over strategies to a vector of payoffs as *a strict coordination game*, where $U(\sigma) = (U(a_1 \mid \sigma), \cdots, U(a_m \mid \sigma))$, and $U(a_j \mid \sigma) = \sum_{a_k \in A} \sigma(a_k) u(a_j, a_k)$. The set of pure strategy best responses to σ is defined as

$$BR(\sigma) = \{a_j \in A \mid U(a_j \mid \sigma) \geq U(a_l \mid \sigma) \, \forall a_l \in A\}.$$

2.2. The social interaction structure

We consider a finitely large set $N = \{1, \cdots, i, \cdots, n\}$ of players interacting through a *social network*. The social network is represented by a graph $G(N, E)$, with N representing the number of players and E the set of edges linking different pairs of players. In $G(N, E)$, each player is identified by his *neighbourhood*—a fixed subset of N with whom a player directly interacts with. We place the following restrictions on the graph structure.

(i) $G(N, E)$ is undirected and unweighted: a link between any pair of agents i and j has a weight of one.

(ii) $G(N, E)$ is *strongly connected*: there exists a path of links connecting any pair of players $i, j \in N$.

(iii) The density $\mathcal{D}(G)$ of $G(N, E)$, defined as the ratio of the number of edges in $G(N, E)$ to the total possible number of edges among n players, which is equal to $n(n-1)/2$, is bounded by

$$\frac{2}{n} < \mathcal{D}(G) < 1.$$

Assumptions (i) and (ii) help simplify our analysis and avoids complexity that arise from heterogeneous weights and disconnected network structures. Networks that are not strongly connected may consist of disconnected subgroups, which raises complications regarding conditions under which an evolutionary process converges. We avoid such complications in order to focus on the main question regarding the robustness of stochastic stability to the network structure. In assumption (iii), the upper bound on the density rules out complete graphs where each player

directly plays against all other players. The lower bound rules out star-like networks with one player at the centre of other peripheral players. These two extreme cases of graph structures have special properties in relation to the notion of stochastic stability: they do not support the process of contagion that we use to derive the relationship between stochastic stability and the network structure.

Players simultaneously play the strict coordination game against their neighbours at discrete time, $t = 1, 2, \cdots$. At each period, a player selects a pure strategy in A and plays this strategy against all of his neighbours. We assume that $G(N, E)$ is exogenously given and fixed over time, so that each player repeatedly plays against the same set of neighbours. Let $\sigma_i = (\sigma_i(a_1), \cdots, \sigma_i(a_m))$ be the empirical distribution of strategies in i's neighbourhood. That is, σ_i is a mixed strategy representing the proportion of i's neighbours playing each pure strategy. Then the total payoff that i receives for playing strategy a_j against σ_i is

$$U(a_j \mid \sigma_i) = \sum_{a_l \in A} \sigma_i(a_l) u(a_j, a_l). \tag{1}$$

Note however that the total payoff is independent of a player's identity (the size of a player's neighbourhood) and depends only on the empirical distribution σ_i. If any two players have an identical empirical distribution σ, then their total payoffs are also identical. So, where no confusion arises, we simply write $U(a_j \mid \sigma)$ for the total payoff to any player playing strategy a_j against distribution σ. We then refer to the double (U, G) as a *local interaction strict coordination game*.

2.3. Unperturbed learning process

We consider *myopic best response dynamics* with simultaneous revision protocol. Let $\mathbf{x} = (x^1, \cdots, x^n)$ denote the profile of strategies, where x^i is the strategy of the ith player. Each strategy profile is a state of an evolutionary process, and we denote the set of all states by $\mathbf{X}$. For each $\mathbf{x}$, let $\sigma_i(a_l; \mathbf{x})$ be the proportion of i's neighbours playing strategy a_l in profile $\mathbf{x}$, and let $\sigma_i(\mathbf{x}) = (\sigma_i(a_1; \mathbf{x}), \cdots, \sigma_i(a_m; \mathbf{x}))$ be the empirical distribution over strategies in i's neighbourhood under strategy profile $\mathbf{x}$. In analogy to (1), $U\big(a_j \mid \sigma_i(\mathbf{x})\big) = \sum_{a_l \in A} \sigma_i(a_l; \mathbf{x}) u(a_j, a_l)$ is the payoff to i for adopting strategy a_j against a mixture $\sigma_i(\mathbf{x})$.

Let $\mathbf{x}(t)$ be the strategy profile at time t, and $x^i(t)$ the respective ith strategy in profile $\mathbf{x}(t)$. By myopic best response we mean, at time $t + 1$, each player chooses a strategy that is a best response to the strategy profile at time t. That is,

$$x^i(t+1) \in \arg\max_{a_j \in A} U\big(a_j \mid \sigma_i(\mathbf{x}(t))\big)$$

If the best response set to a given strategy profile consists of more than one strategy, we assume that a player randomly chooses one of them with equal probability. The assumption of myopia is standard in the literature of evolutionary game theory and it is used to model agents with bounded memory and rationality. That is, it assumes that agents are incapable of keeping track of the entire history of play and performing complex evaluations associated with forward-looking decisions.[7]

The dynamic framework described above leads to a finite Markov chain on the state space $\mathbf{X}$. Let P denote the transition probability matrix so that $P(\mathbf{x}, \mathbf{y})$ is the probability of transiting from state $\mathbf{x}$ to $\mathbf{y}$ in a single period. A subset $W \subseteq \mathbf{X}$ of states is an *absorbing set* of a Markov chain if, once entered, is never exited. If an absorbing set is a singleton then it is called an *absorbing state*; that is, any state $\mathbf{x} \in \mathbf{X}$ for which $P(\mathbf{x}, \mathbf{x}) = 1$ is an absorbing state.

The long-run behaviour of a Markov chain can be fully described by its *stationary distribution*, which is the probability distribution over the state space and describes the long-run average time spent in each state. That is, for any probability distribution ν whose support is contained in $\mathbf{X}$, if $\pi \in \Delta(\mathbf{X})$ is the stationary distribution, then $\lim_{t \to \infty} \nu P^t = \pi$, and that $\pi P = \pi$. For each $\mathbf{x} \in \mathbf{X}$, $\pi(\mathbf{x})$ is the proportion of time the process spends in state $\mathbf{x}$ along any path that ends up in an absorbing set. Note however that, for any P, the stationary distribution exists only if its absorbing sets are *aperiodic*, meaning that they do not contain deterministic non-trivial cycles.

A fundamental property of Markov chains that determines the structure of its stationary distribution is *ergodicity*. A Markov chain is *ergodic* if it consists of only one absorbing set. If a Markov chain is ergodic, then it has a unique stationary distribution. Non-ergodic Markov chains on the other hand have multiple stationary distributions, each describing the long-run behaviour of different sample paths. The long-run predictions in a non-ergodic Markov chain thus depends on the initial condition. The unperturbed process described above is non-ergodic since it consists of multiple absorbing states. The number of absorbing states of P is at least as many as the number of strategies. This is because each monomorphic state $\mathbf{a}_j = (a_j, \cdots, a_j)$ for all $a_j \in A$ is an absorbing state. In addition to monomorphic absorbing states, more absorbing states may exist depending on the network and payoff structures.

2.4. Perturbed learning process and stochastic stability

Following the literature, a *perturbed process* is derived from the unperturbed process described above by adding the possibility of rare mutations or experiments (Young, 1993; Kandori et al.,

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[7]An alternative justification is that a myopic decision maker is approximately rational if the adjustment rate is slower relative to the discount factor.

1993; Ellison, 2000). We specifically consider the model of best response with mutations (BRM) where, with a small fixed probability $\varepsilon > 0$, each player chooses at random a strategy that is different from that prescribed by the best reply process. Mutations ensure that every state is reached with a positive probability from every other state. The perturbed process is thus ergodic in that it has only one absorbing set, which also implies that it has a unique stationary distribution π_ε.

As the amount of noise tends to zero, the stationary distribution of the perturbed process tends to a limit distribution $\pi^* = \lim_{\varepsilon \to 0} \pi_\varepsilon$ that places most weight on one of the absorbing states of the unperturbed process. The absorbing states with the largest probability at the limit of ε are said to be *stochastically stable* (Foster and Young, 1990; Young, 1993; Kandori et al., 1993). Formally, let $\mathbf{A}$ be a set of all absorbing states of P. Then some $\mathbf{a}^* \in \mathbf{A}$ is stochastically stable if $\lim_{\varepsilon \to 0} \pi_\varepsilon(\mathbf{a}^*) > 0$.

To identify stochastically stable states, we employ a graph theoretic approach of Freidlin and Wentzell (1984).[8] The approach entails defining transition costs $C(\mathbf{a}, \mathbf{a}')$ between every pair of absorbing states $\mathbf{a}$ and $\mathbf{a}'$. For the model of best response with mutation considered in this paper, $C(\mathbf{a}, \mathbf{a}')$ is the minimal number of mutations needed for a transition from $\mathbf{a}$ to $\mathbf{a}'$ to occur. Such a transition need not occur in a single step and may entail a sequence of successive mutations that in turn lead the process to evolve out of $\mathbf{a}$ and eventually through best response to $\mathbf{a}'$. For each absorbing state $\mathbf{a}$, define an $\mathbf{a}$-tree as a directed spanning tree consisting of the set of all absorbing states as the set of nodes, and all links are directed to $\mathbf{a}$ as the end point. The cost $C(\mathbf{a})$ of an $\mathbf{a}$-tree is the sum of costs $C(\mathbf{a}, \mathbf{a}')$ of transitions between all pairs $\mathbf{a}, \mathbf{a}' \in \mathbf{A}$ of absorbing states making up the $\mathbf{a}$-tree. Kandori et al. (1993) and Young (1993) show that a stochastically stable state is the one at the root of a minimum cost tree; that is, $\mathbf{a}^* \in \mathbf{A}$ is stochastically stable if $C(\mathbf{a}^*) < C(\mathbf{a})$, for all $\mathbf{a} \in \mathbf{A}$.

3. *p*-dominance and stochastic stability

This section establish the relationship between stochastic stability and the refinement of Nash equilibrium called *p*-dominance. *p*-dominance was introduced by Morris et al. (1995) as an equilibrium refinement that is robust to incomplete information (Kajii and Morris, 1997). We aim to show that *p*-dominance is also a robust equilibrium selection mechanism in stochastic evolutionary dynamics.

Following Morris et al. (1995), a strategy a_l is *p*-dominant if for all $a_k \in A$, and all $\sigma \in \Sigma$

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[8]See Young (1993), Kandori et al. (1993) and Ellison (2000) for detailed discussions of this approach

with $\sigma(a_l) \geq p$,

$$\sum_{a_k \in A} \sigma(a_k)u(a_l, a_k) > \sum_{a_k \in A} \sigma(a_k)u(a_j, a_k) \quad \text{for all } a_j \neq a_l$$

Thus, a strategy is p-dominant if it is a unique best response whenever it is played with a probability of at least p. In analogy to the local interaction strict coordination game, a strategy is p-dominant if it is a best response whenever it is adopted by at least proportion p of a player's neighbours.[9]

3.1. Contagion and a contagion threshold

The derivation of the main results relies on the concept of pairwise contagion and its generalization. The *contagion threshold* is a network property that determines when contagion is feasible. Defined for a pair of strategies a_j and a_l, a strategy a_l is *pairwise contagious* relative to a_j ($a_l \mathrm{PRC} a_j$) if starting from a monomorphic absorbing state $\mathbf{a}_j$ where all players choose a_j, a_l can spread to the entire network through best response once it has been adopted by a *very small set* of players called *initial adopters*. The set of initial adopters should not be chosen *strategically*, that is, the number of initial adopters must be independent of the region of the network from which the set is picked; this ensures that any arbitrary non-regular network has a unique contagion threshold (we illustrate this point with an example below). We denote the set of initial adopters by $N(\mathbf{a}_j \to \mathbf{a}_l)$ and its cardinality by $n(\mathbf{a}_j \to \mathbf{a}_l)$. By a very small set of initial adopters, we mean $n(\mathbf{a}_j \to \mathbf{a}_l)$ is *independent* of n and *much smaller* than $\frac{1}{2}n$.

Definition 1. *Let $n(a_l; \mathbf{x})$ be the number of players playing strategy a_l in strategy profile $\mathbf{x}$. Then strategy $a_l PRC a_j$ if best response dynamics ensures that $n(a_l; \mathbf{x}(t+1)) > n(a_l; \mathbf{x}(t))$ for all $t \geq t'$, whenever $n(a_l; \mathbf{x}(t')) = n(\mathbf{a}_j \to \mathbf{a}_l)$, so that $\lim_{t \to \infty} n(a_l; \mathbf{x}(t)) = n$ and $\lim_{t \to \infty} n(a_j; \mathbf{x}(t)) = 0$.*

To define the contagion threshold, let $S \subset N$ be a subgroup of agents belonging to the same arbitrarily (and not strategically) chosen neighbourhood. That is, for each pair $i, j \in S$, either i and j are directly linked, or there exists a path $i = i_1 \to i_2 \to \cdots \to i_k \to i_{k+1} \to \cdots \to i_K = j$ and vice versa, whereby all $i_1, i_2, \cdots, i_k, \cdots, i_K \in S$. Let $\bar{S} = N \backslash S$ be the complement of S. We write $S(a_l)$ to imply that all agents in S choose a_l, and $\bar{S}^{[p,S]}(a_j)$ for a subset of agents in $\bar{S}$ choosing a_j for whom at least proportion p of their interactions are with agents in S.

Now, consider an increasing sequence $\{S_\tau(a_l)\}_{\tau \geq 1}$ whereby $S_\tau(a_l) \subset S_{\tau+1}(a_l)$. There exists a complementary decreasing sequence $\{\bar{S}_\tau(a_j)\}_{\tau \geq 1}$ with $\bar{S}_\tau(a_j) \supset \bar{S}_{\tau+1}(a_j)$, whereby for each

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[9]In 2×2 strict coordination games, $\frac{1}{2}$-dominance is equivalent to the notion of *risk-dominance* (Harsanyi and Selten, 1988). In $m \times m$ strict coordination games, $\frac{1}{2}$-dominance is equivalent to the notion of *global risk-dominance* according to Maruta (1997).

$\tau \geq 1$, $S_\tau(a_l) \cup \bar{S}_\tau(a_j) = N$ and $S_{\tau+1}(a_l) \backslash S_\tau(a_l) = \bar{S}_\tau(a_j) \backslash \bar{S}_{\tau+1}(a_j)$. Given sequences $\{S_\tau(a_l)\}_{\tau \geq 1}$ and $\{\bar{S}_\tau(a_j)\}_{\tau \geq 1}$, there exists a *maximum p*, called the *contagion threshold* of the underlying network, so that for a corresponding sequence $\{\bar{S}_\tau^{[p,S]}(a_j)\}_{\tau \geq 1}$, a_l is a best response for each $i \in \bar{S}_\tau^{[p,S]}(a_j)$ and for each $\tau \geq 1$. At each τ, $S_{\tau+1}(a_l) \backslash S_\tau(a_l) = \bar{S}_\tau(a_j) \backslash \bar{S}_{\tau+1}(a_j) = \bar{S}_\tau^{[p,S]}(a_j)$. In relation to the definition of pairwise contagion, if $a_l \text{PRC} a_j$, then contagion of strategy a_l gets triggered when $S(a_l) = N(\mathbf{a}_j \rightarrow \mathbf{a}_l)$.

The contagion threshold is a unique property of a network in that every network has a contagion threshold less or equal $\frac{1}{2}$ (Morris, 2000). Determining the contagion threshold is relatively easy for *deterministic regular networks* (networks where all player have the same number of neighbours), but may be a cumbersome process for non-regular networks. Morris (2000) provides a detailed characterization of contagion thresholds for various families of deterministic networks. For example, a cyclic interaction structure in which each player plays against k other players, $\frac{k}{2}$ to the left and right, has a contagion threshold of $\frac{1}{2}$. This is because a strategy can only spread around the ring, starting from a small neighbourhood, if each player requires only half of her neighbours, either on the left or right to adopt it for him to do likewise. In a similar vein, the contagion threshold for the nearest neighbour interactions in m-dimensions (where a 2-dimensional grid network is a special case) is $\frac{1}{m}$. Morris (2000) also develops bounds for contagion thresholds in terms of network characteristics: e.g. cohesiveness of subgroups, neighbourhood growth and uniformity.[10]

Example 1: To illustrate the notion of a strategically chosen set of initial adopters, consider a network in Figure 1 with $N = \{1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12\}$. The contagion threshold for this network is $\frac{1}{3}$ and the set of initial adopters is one player. To see why, let a_j, a_l be a pair of strategies where $a_l \text{PRC} a_j$. Given $p = \frac{1}{3}$, choose one player (an initial adopter) from any region of the network, say player 2, so that $S_1(a_l) = N(\mathbf{a}_j \rightarrow \mathbf{a}_l) = \{2\}$, $\bar{S}_1(a_j) = N \backslash \{2\}$ and $\bar{S}_1^{[p,S]}(a_j) = \{1, 3\}$. Here, $\bar{S}_1^{[p,S]}(a_j)$ is a subset of players in $\bar{S}_1(a_j)$ for whom at least proportion $p = \frac{1}{3}$ of their interactions are with players in $S_1(a_l)$. Since the contagion threshold is $\frac{1}{3}$, by definition, a_l is a best response for each $i \in \bar{S}_1^{[p,S]}(a_j)$, so that at $\tau = 2$, $S_2(a_l) = \{1, 2, 3\}$, $\bar{S}_2(a_j) = N \backslash \{1, 2, 3\}$ and $\bar{S}_2^{[p,S]}(a_j) = \{4, 5\}$. By iterating the process up to $\tau = 8$, we find that $S_8(a_l) = N$, $\bar{S}_8(a_j) = \emptyset$ and $\bar{S}_8^{[p,S]}(a_j) = \emptyset$. Provided $p = \frac{1}{3}$, the final outcome of this iterative process is the same, that is $S(a_l) = N$, $\bar{S}(a_j) = \emptyset$ and $\bar{S}^{[p,S]}(a_j) = \emptyset$, independently of the region of the network from which an initial adopter is picked.

Now, consider the case where $p > \frac{1}{3}$, say $p = \frac{1}{2}$. If we start with $S_1(a_l) = N(\mathbf{a}_j \rightarrow \mathbf{a}_l) = \{2\}$

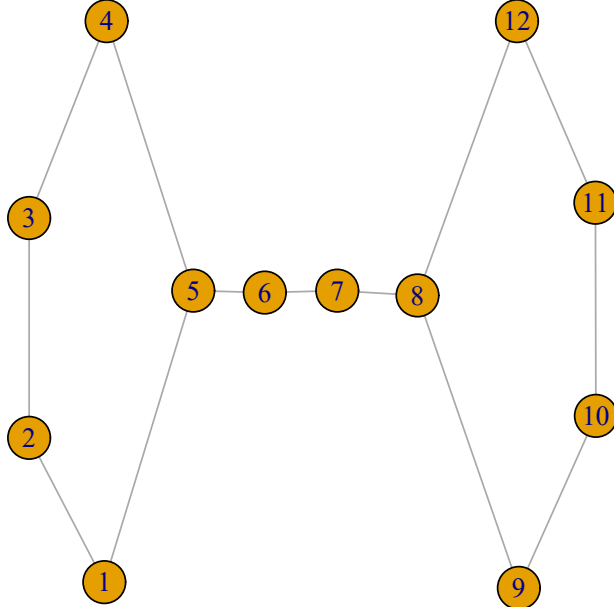[10]See also Lelarge (2012) for a related characterization for random networks.

Figure 1: An example of a network with contagion threshold of $\frac{1}{3}$.

as before, the iterative steps will be identical the case of $p = \frac{1}{3}$ until $\tau = 5$, where $S_5(a_l) = \{1, 2, 3, 4, 5, 6, 7\}$, $\bar{S}_5(a_j) = \{8, 9, 10, 11, 12\}$ and $\bar{S}_5^{[p,S]}(a_j) = \emptyset$. The set $\bar{S}_5^{[p,S]}(a_j)$ is empty because at $\tau = 5$, player 8 has only $\frac{1}{3}$ of its interactions with players in $S_5(a_l)$, and not $\frac{1}{2}$. So, contagion stops at $\tau = 5$. Note that when $p = \frac{1}{2}$, we can start with $S_1(a_l) = N(\mathbf{a}_j \to \mathbf{a}_l) = \{5, 8\}$ and the iteration would converge to $S(a_l) = N$, $\bar{S}(a_j) = \emptyset$ and $\bar{S}^{[p,S]}(a_j) = \emptyset$. The problem in that case however, is that $N(\mathbf{a}_j \to \mathbf{a}_l)$ is chosen strategically, and any other choice of the latter does not lead to convergence to a state where $S(a_l) = N$, $\bar{S}(a_j) = \emptyset$ and $\bar{S}^{[p,S]}(a_j) = \emptyset$.

3.2. p-dominance, contagion threshold and stochastic stability

The process of contagion brings about the connection between *p*-dominance and stochastic stability. The following theorem establishes the aforementioned relationship.

Theorem 1. *In an evolutionary model of best response with mutations, if n is sufficiently large, then a p-dominant strategy of U is stochastically stable in networks with contagion threshold of at least p.*

Proof. See Appendix B.1 □

The proof of Theorem 1 exploits the effects of pairwise contagion on the costs of transitions between absorbing states. That is, for a pair of strategies $a_j, a_l \in A$, if $a_l \mathrm{PRC} a_j$, then the cost $C(\mathbf{a}_j, \mathbf{a}_l)$ of transition from absorbing state $\mathbf{a}_j$, where all players choose a_j, to $\mathbf{a}_l$ is equivalent to $n(\mathbf{a}_j \to \mathbf{a}_l)$. Recall that $n(\mathbf{a}_j \to \mathbf{a}_l)$ is the number of initial adopters required to trigger contagion from $\mathbf{a}_j$ to $\mathbf{a}_l$, and by definition of pairwise contagion, it is independent of the population size and much smaller than $\frac{1}{2}n$. On the contrary, if $a_l \mathrm{PRC} a_j$ then the cost $C(\mathbf{a}_l, \mathbf{a}_j)$ of transition

from $\mathbf{a}_l$ to $\mathbf{a}_j$ is an increasing function of the population size. Thus, for n sufficiently large, $C(\mathbf{a}_j, \mathbf{a}_l) < C(\mathbf{a}_l, \mathbf{a}_j)$ whenever $a_l \mathrm{PRC} a_j$. The next step of the proof shows that if a strategy, say a_l, is pairwise contagious relative to every other strategy (globally pairwise contagious), then for any $\mathbf{a} \in \mathbf{A}$ in which two or more strategies other than a_l co-exist, $C(\mathbf{a}, \mathbf{a}_l) < C(\mathbf{a}_l, \mathbf{a})$ for n sufficiently large. This in turn implies that, the cost $C(\mathbf{a}_l)$ of the corresponding $\mathbf{a}_l$-tree is smaller than for trees of all other absorbing states, and hence, $\mathbf{a}_l$ is stochastically stable. The final step of the proof then establishes the equivalence between globally pairwise contagious strategies and p-dominant strategies.

An important question for the derivation of our results concerns the conditions under which pairwise contagion occurs in a given network. In other words, how can one tell from the payoff structure whether a strategy is pairwise contagious relative to another? The two important payoff-related measures that determine the condition for contagion are the *relative payoff-gains* η_{jl} and ϕ_{jl}. To define η_{jl} and ϕ_{jl}, let $\sigma_{jl}^q = (1-q, q, 0, \cdots, 0)$ be a distribution that assigns a weight of $1-q$ to strategy a_j, q to strategy a_l and zero to all other strategies. The expected payoff $U\left(a_k \mid \sigma_{jl}^q\right)$ to strategy a_k against distribution σ_{jl}^q is then

$$U\left(a_k \mid \sigma_{jl}^q\right) = (1-q)u(a_k, a_j) + qu(a_k, a_l) \tag{2}$$

Definition 2. *For a pair of strategies $a_j, a_l \in A$, the relative payoff gains are defined as follows:*

(i) η_{jl} is the maximum q above which a_l is a best response to σ_{jl}^q; that is, the q for which

$$U\left(a_l \mid \sigma_{jl}^q\right) > U\left(a_k \mid \sigma_{jl}^q\right) \quad \text{for all } a_k \neq a_l \tag{3}$$

(ii) ϕ_{jl} is the value of q for which

$$U\left(a_l \mid \sigma_{jl}^q\right) > U\left(a_j \mid \sigma_{jl}^q\right) \tag{4}$$

By substituting the expressions of expected utility from (2) into (3) and (4), we obtain the respective expressions for η_{jl} and ϕ_{jl} to be:[11]

$$\eta_{jl} = \max_{a_k \neq a_l} \left\{ \frac{u(a_k, a_j) - u(a_l, a_j)}{u(a_k, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_k, a_l)} \right\}$$

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[11]That is, $(1-q)u(a_l, a_j) + qu(a_l, a_l) > (1-q)u(a_k, a_j) + qu(a_k, a_l)$, for all $a_k \neq a_l$; which yields

$$q > \frac{u(a_k, a_j) - u(a_l, a_j)}{u(a_k, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_k, a_l)} \quad \text{for all } a_k \neq a_l$$

Hence, a_l is a best response to σ_{jl}^q whenever q is greater than

$$\eta_{jl} = \max_{a_k \neq a_l} \left\{ \frac{u(a_k, a_j) - u(a_l, a_j)}{u(a_k, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_k, a_l)} \right\}$$

The expression for ϕ_{jl} on the other hand is derived by solving for q in $(1-q)u(a_l, a_j) + qu(a_l, a_l) > (1-q)u(a_j, a_j) + qu(a_j, a_l)$.

$$\phi_{jl} = \frac{u(a_j, a_j) - u(a_l, a_j)}{u(a_j, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_j, a_l)},$$

Lemma 2. *For any pair of strategies $a_j, a_l \in A$ in coordination game U,*

(i) $\phi_{jl} = 1 - \phi_{lj}$

(ii) $\eta_{jl} \geq \phi_{jl}$

Proof. See Appendix A.1 and Appendix A.2 □

Comparing (3) and (4), we see that that $\eta_{jl} = \phi_{jl}$ in 2-strategy strict coordination games, and in m-strategy (with $m \geq 3$) games in which all best responses to σ_{jl}^q, for $0 \leq q \leq 1$, are in $\{a_j, a_l\}$.[12] When $\eta_{jl} \neq \phi_{jl}$ however, which from Lemma 2 (ii) implies that $\eta_{jl} > \phi_{jl}$, then there exists at least one $a_k \neq a_j, a_l$ that is a best response to σ_{jl}^q for values of q in the range $\phi_{jl} \leq q \leq \eta_{jl}$.[13]

To distinguish between the two scenarios, we write $a_j \times a_l \to \{a_j, a_l\}$ to refer to all cases in which $\eta_{jl} = \phi_{jl}$; and to be more specific, we write $a_j \times a_l \to a_l$ to mean that $\eta_{jl} = \phi_{jl} < \frac{1}{2}$; the latter also means that a_l is pairwise risk-dominant relative to a_j. When $\eta_{jl} \neq \phi_{jl}$, we write $a_j \times a_l \to a_k$ to mean that a_k is a best response to σ_{jl}^q when $\phi_{jl} \leq q \leq \eta_{jl}$, and respectively $a_j \times a_l \to A'$ when strategies in the subset $A' \subset A$ are best responses.

In analogy to the local interaction strict coordination game U, η_{jl} is the proportion of neighbours that should play a_l, while the complementary proportion plays a_j, above which a player chooses a_l. The quantity ϕ_{jl} has an identical interpretation but when the game is restricted to two strategies a_j and a_l. Relative payoff gains are so called because they contain relevant information about the relative benefits and costs of choosing one strategy over another. For example, we can think of strategies as a set of choices of information technology (IT) products (e.g. software products or telephone service providers) faced by consumers. For such products, there is a *social benefit* from coordinating choices with neighbours, and a *private benefit* (e.g. due to lower cost) of choosing an option regardless of neighbours' choices. The payoff of coordinating on a_l can be rewritten as $u(a_l, a_l) = u(a_j, a_j) + \alpha$, where α is the extra social benefit of

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[12]That is, for all values of q in the range $0 \leq q \leq 1$, $U\left(a_j \mid \sigma_{jl}^q\right) > U\left(a_k \mid \sigma_{jl}^q\right)$ for all $a_k \neq a_j, a_l$, so that when $q \leq \phi_{jl}$,

$$U\left(a_j \mid \sigma_{jl}^q\right) > U\left(a_l \mid \sigma_{jl}^q\right) > U\left(a_k \mid \sigma_{jl}^q\right) \quad \text{for all } a_k \neq a_j, a_l$$

and when $q > \phi_{jl}$,

$$U\left(a_l \mid \sigma_{jl}^q\right) > U\left(a_j \mid \sigma_{jl}^q\right) > U\left(a_k \mid \sigma_{jl}^q\right) \quad \text{for all } a_k \neq a_j, a_l$$

[13]That is, when $\phi_{jl} \leq q \leq \eta_{jl}$, $U\left(a_k \mid \sigma_{jl}^q\right) > U\left(a_j \mid \sigma_{jl}^q\right), U\left(a_l \mid \sigma_{jl}^q\right)$.

coordinating on a_l relative to a_j. The payoff to choosing a_l when all neighbours choose a_j can also be rewritten as $u(a_l, a_j) = u(a_j, a_l) + \lambda$, where λ is the extra net private benefit (intrinsic private benefit minus cost) of choice a_l relative to a_j. The quantity ϕ_{jl} can then be rewritten as

$$\phi_{jl} = \frac{\Big[u(a_j, a_j) - u(a_j, a_l)\Big] - \lambda}{2\Big[u(a_j, a_j) - u(a_j, a_l)\Big] - \lambda + \alpha} \tag{5}$$

Thus, from (5), a firm aiming to increase the likelihood with which consumers choose her product a_l, can do so by either increasing its relative social benefit α (through innovation), or increasing the relative private benefit λ (by cutting prices).

The following lemma establishes the conditions for pairwise contagion by relating relative payoff gains to the contagion threshold.

Lemma 3. *For an arbitrary network with contagion threshold p, pairwise contagion of strategy a_l relative to a_j occurs if and only if $\eta_{jl} = \phi_{jl} < p \leq \frac{1}{2}$.*

Proof. See Appendix A.3 □

Lemma 3 describes a necessary and sufficient condition for pair-wise contagion between any pair of strategies. The necessary condition is that the relative payoff-gain η_{jl} must be less or equal to the contagion threshold (i.e. $\eta_{jl} < p$). The sufficient condition is for $\eta_{jl} = \phi_{jl} < p$. The link between contagion and p-dominance is established by the following lemma.

Lemma 4. *If a strict coordination game U has a strategy, say a_l, that is globally pairwise contagious in a network with contagion threshold of p, then a_l is p-dominant.*

Proof. See Appendix B.2 □

Theorem 1 shows that if a p-dominant strategy exists in a strict coordination game, where $p \leq \frac{1}{2}$ is the contagion threshold of the underlying network, then it is uniquely stochastically stable. Moreover, if a p-dominant strategy exists then it is unique. To see why, notice from Lemmas 2 and 3 that if $a_l \mathrm{PRC} a_j$ then $\eta_{jl} = \phi_{jl} < \frac{1}{2}$, and hence $\eta_{lj} \geq \phi_{lj} > \frac{1}{2}$. If a_l is pairwise contagious relative to every other strategy, then $\eta_{lj} > \frac{1}{2}$ for all $a_j \neq a_l$, so that no other strategy is globally pairwise contagious. This makes a_l uniquely globally pairwise contagious, and from Lemma 4, uniquely p-dominant.

Since $\frac{1}{2}$-dominance is a special case of p-dominance, our results generalize those in the literature that establish the relationship between $\frac{1}{2}$-dominance and stochastic stability in cyclic network topologies (Ellison, 2000). A corollary to Theorem 1 is that $\frac{1}{2}$-dominant strategies are uniquely stochastically stable in network structures with contagion thresholds of $\frac{1}{2}$. As discussed in Morris (2000), cyclic network structures have a contagion threshold of $\frac{1}{2}$.

Our results are also comparable to Sandholm (2001) and Oyama et al. (2015). These two papers consider a dynamic process with an infinitely large population size where members of the population receive revision opportunities according to independent rate 1 Poisson processes. A player who receives a revision opportunity switches to a best response to the empirical distribution of strategies of k randomly sampled players. This dynamic protocol generates a deterministic evolutionary process as opposed to a stochastic process considered in this paper. They find that if a $\frac{1}{k}$-dominant strategy exists, then it is *almost globally stable.* That is, solution trajectories starting from *almost all* non-absorbing states converge to an absorbing state in which a $\frac{1}{k}$-dominant strategy is played.

The interaction structure in Sandholm (2001) and Oyama et al. (2015) is comparable to deterministic k-regular networks (i.e. networks where every player has k neighbours). Morris (2000) shows that k-regular deterministic networks have a contagion threshold of $\frac{1}{k}$. By virtue of Theorem 1, $\frac{1}{k}$-dominant strategies are stochastically stable in such interaction structures. The latter follows because a $\frac{1}{k}$-dominant strategy is globally pairwise contagious in k-regular networks. Note that if $a_l \mathrm{PRC} a_j$ then the basin of attraction of $\mathbf{a}_j$ is much smaller compared to that of $\mathbf{a}_l$. Thus, if a_l is globally pairwise contagious, then the basin of attraction of $\mathbf{a}_l$ contains *almost all* non-absorbing states. The results of Theorem 1 thus provide some intuition as to why a $\frac{1}{k}$-dominant strategy is almost globally stable in the model of k-sampling best response dynamics.

Despite the comparability of k-sampling best response dynamics to some families of deterministic network structures this paper covers, there is a fundamental difference between stochastic stability and almost global convergence; and even more so the analytical methods used in deriving the predictions of the two solution concepts. Stochastic stability relies on the presence of noise in the system while almost global convergence is defined as a global attractor of a deterministic system. This difference in turn leads to differences in the applicability of the results.

4. Concluding remarks

The lack of robustness of stochastic stability to the interaction structure and number of strategies, and the complexity of computational methods used to identify stochastically stable outcomes, limits the applicability of evolutionary selection theories. One approach, adopted in this paper, that can lead to relatively robust predictions is to identify aggregate network properties that directly relate to stochastic stability. We identify the contagion threshold as one such properties. Network structures can then be categorized based on their contagion thresholds and the predictions of stochastic stability will be identical for networks belonging to the same cate-

gory. We showed that p-dominant strategies are stochastic stability in networks with contagion threshold of p.

Our final remark concerns the implications of our results for the rate of convergence of stochastic evolutionary dynamics. As raised in Sandholm (2001), Oyama et al. (2015) and discussed in detail by Ellison (1993), the downside of stochastic evolutionary models is that the number of mutations required to exit the basin of attraction of a non-globally stable absorbing state may be an increasing function of the population size. This leads to questions regarding the applicability of the predictions of these models. For situations where pairwise contagion is feasible, as discussed above, the number of mutations needed to exit the basins of attraction of absorbing states in which non-contagious strategies are played is very small and independent of the population size. The expected waiting time of exit from such absorbing states, and convergence time to the stochastically stable states, are thus also independent of the population size. The derivation of the exact functional forms for convergence rates however remains an avenue for future research.

Appendix A. Preliminary lemmas and proofs

Appendix A.1. Proof of Lemma 2 (i)

For any pair of strategies $a_j, a_l \in A$,

$$
\begin{aligned}
\phi_{jl} &= \frac{u(a_j, a_j) - u(a_l, a_j)}{u(a_j, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_j, a_l)} \\
&= 1 - \frac{u(a_l, a_l) - u(a_j, a_l)}{u(a_j, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_j, a_l)} \\
&= 1 - \phi_{lj}.
\end{aligned}
\tag{A.1}
$$

Appendix A.2. Proof of Lemma 2 (ii)

Recall the definition of η_{jl} as

$$
\eta_{jl} = \max_{a_k \neq a_l} \left\{ \frac{u(a_k, a_j) - u(a_l, a_j)}{u(a_k, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_k, a_l)} \right\}
$$

From the expression of ϕ_{jl}, when $a_k = a_j$, we have $\eta_{jl} = \phi_{jl}$. Let η_{jl}^{-j} be derived from η_{jl} by excluding the jth row of the payoff matrix. That is,

$$
\eta_{jl}^{-j} = \max_{a_k \neq a_l, a_j} \left\{ \frac{u(a_k, a_j) - u(a_l, a_j)}{u(a_k, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_k, a_l)} \right\}
$$

Then η_{jl} can be rewritten as

$$
\eta_{jl} = \max \left\{ \phi_{jl}, \eta_{jl}^{-j} \right\}
$$

And hence, $\eta_{jl} \geq \phi_{jl}$.

Lemma 5. *For any pair of strategies $a_j, a_l \in A$ in coordination game U, let $\phi_{jl} < \frac{1}{2}$. If $a_j \times a_l \to a_k$ for some $a_k \neq a_j, a_l$, then $\eta_{lj} > \frac{1}{2}$ and $\eta_{jl} > \frac{1}{2}$.*

Proof. The first statement, $\eta_{lj} > \frac{1}{2}$, follows by definition. That is, if $\phi_{jl} < \frac{1}{2}$, then $\phi_{lj} = (1 - \phi_{jl}) > \frac{1}{2}$, and hence by Lemma 2, $\eta_{lj} \geq \phi_{lj} > \frac{1}{2}$. It remains to show that $\eta_{jl} > \frac{1}{2}$.

Recall also that ϕ_{jl} is the value of q above which $U\left(a_l \mid \sigma_{jl}^q\right) > U\left(a_j \mid \sigma_{jl}^q\right)$, and that when $a_j \times a_l \to a_k$ so that $\eta_{jl} > \phi_{jl}$, then for all values of q in the range $\phi_{jl} \leq q \leq \eta_{jl}$,

$$U\left(a_k \mid \sigma_{jl}^q\right) > U\left(a_l \mid \sigma_{jl}^q\right) > U\left(a_j \mid \sigma_{jl}^q\right) \tag{A.2}$$

Hence, when $a_j \times a_l \to a_k$, then for $q = \phi_{jl}$, we have

$$U\left(a_k \mid \sigma_{jl}^{\phi_{jl}}\right) > U\left(a_l \mid \sigma_{jl}^{\phi_{jl}}\right) \tag{A.3}$$

Substituting the expressions of $U\left(a_k \mid \sigma_{jl}^{\phi_{jl}}\right)$ and $U\left(a_l \mid \sigma_{jl}^{\phi_{jl}}\right)$ into (A.3) yields

$$(1 - \phi_{jl})u(a_k, a_j) + \phi_{jl}u(a_k, a_l) > (1 - \phi_{jl})u(a_l, a_j) + \phi_{jl}u(a_l, a_l) \tag{A.4}$$

Solving for ϕ_{jl} in (A.4) yields

$$\phi_{jl} > \frac{u(a_l, a_j) - u(a_k, a_j)}{u(a_l, a_j) - u(a_k, a_j) + u(a_k, a_l) - u(a_l, a_l)} \tag{A.5}$$

Substituting the expression for ϕ_{jl} from (A.1) into (A.5), and after simplifying, gives the following inequality

$$\Big(u(a_j, a_j) - u(a_l, a_j)\Big)\Big(u(a_k, a_l) - u(a_l, a_l)\Big) > \Big(u(a_l, a_j) - u(a_k, a_j)\Big)\Big(u(a_l, a_l) - u(a_j, a_l)\Big) \tag{A.6}$$

By definition of coordination games $u(a_j, a_j) > u(a_l, a_j)$ and $u(a_l, a_l) > u(a_j, a_l)$. We started with the assumption that $\phi_{jl} < \frac{1}{2}$, that is,

$$\phi_{jl} = \frac{u(a_j, a_j) - u(a_l, a_j)}{u(a_j, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_j, a_l)} < \frac{1}{2} \tag{A.7}$$

which implies $u(a_j, a_j) - u(a_l, a_j) < u(a_l, a_l) - u(a_j, a_l)$. For inequality (A.6) to hold, it must then be the case that $u(a_k, a_l) - u(a_l, a_l) > u(a_l, a_j) - u(a_k, a_j)$, or equivalently $u(a_l, a_l) - u(a_k, a_l) < u(a_k, a_j) - u(a_l, a_j)$, which in turn implies that

$$\frac{u(a_k, a_j) - u(a_l, a_j)}{u(a_k, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_k, a_l)} > \frac{1}{2} \tag{A.8}$$

Recall that η_{jl} is given by

$$\eta_{jl} = \max_{a_k \neq a_l} \left\{ \frac{u(a_k, a_j) - u(a_l, a_j)}{u(a_k, a_j) - u(a_l, a_j) + u(a_l, a_l) - u(a_k, a_l)} \right\}$$

It follows from (A.8) that $\eta_{jl} > \frac{1}{2}$; hence, if $a_j \times a_l \to a_k$, then $\eta_{lj} > \frac{1}{2}$ and $\eta_{jl} > \frac{1}{2}$.

$\square$

Appendix A.3. Proof of Lemma 3

Recall the definition of contagion threshold: starting from a monomorphic absorbing state $\mathbf{a}_j$, define a sequence $\{S_\tau(a_l)\}_{\tau \geq 1}$ whereby $S_\tau(a_l) \subset S_{\tau+1}(a_l)$, and a complementary sequence $\{\bar{S}_\tau(a_j)\}_{\tau \geq 1}$ for which $\bar{S}_\tau(a_j) \supset \bar{S}_{\tau+1}(a_j)$. The contagion threshold of the underlying network is the *largest p*, so that for a corresponding sequence $\{\bar{S}_\tau^{[p,S]}(a_j)\}_{\tau \geq 1}$ (each $\bar{S}_\tau^{[p,S]}(a_l)$ is a subset of players in $\bar{S}_\tau(a_l)$ for whom at least proportion p of their interactions are with players in $S_\tau(a_j)$), a_l is a best response for each $i \in \bar{S}_\tau^{[p,S]}(a_j)$. Pairwise contagion of a_l relative to a_j, starting from $\mathbf{a}_j$, is then triggered whenever $S(a_l) = N(\mathbf{a}_j \to \mathbf{a}_l)$.

By definition, a contagion threshold is equivalent to the minimum proportion of neighbours any player requires to play a_l, with the complementary proportion playing a_j, for him to switch from a_j to a_l. That is, if p is the contagion threshold, then for all $q \geq p$, a_l is a best response to σ_{jl}^q for all players. Recall the definition of η_{jl} as a minimum q (i.e. $q > \eta_{jl}$) above which a_l is the best response to σ_{jl}^q. Hence, pairwise contagion of a_l relative to a_j is feasible if and only if $\eta_{jl} < p$.

The complete the proof, we use results from Lemma 5 and Morris (2000, Proporition 3). Morris (2000, Proposition 3) proves that every network has a contagion threshold $p \leq \frac{1}{2}$. It follows from Lemma 5 that contagion is not feasible whenever $a_j \times a_l \to a_k$ for some $a_k \neq a_j, a_l$; this is because under such conditions $\eta_{lj} > \frac{1}{2}$. Hence, contagion is feasible only when $a_j \times a_l \to a_l$, or equivalently, $\eta_{jl} = \phi_{jl}$.

Appendix A.4. Monomorphic and polymorphic absorbing states

This section discusses the nature of absorbing states in a local interaction strict coordination game (U, G). We denote by $\mathbf{A}$ a set of all absorbing states. We first categorize $\mathbf{A}$ into classes of *monomorphic absorbing states* $M(\mathbf{A})$, corresponding to all strategies in A, and *polymorphic absorbing states* $Q(\mathbf{A}) = \mathbf{A} \backslash M(\mathbf{A})$, where two or more strategies co-exist. The set of polymorphic absorbing states is further subdivided into a set of *tipping points* $\mathcal{T}(\mathbf{A})$ and a set of *relatively stable* polymorphic absorbing states $S(\mathbf{A}) = Q(\mathbf{A}) \backslash \mathcal{T}(\mathbf{A})$.

An absorbing state $\mathbf{a} \in \mathcal{T}(\mathbf{A})$ is a tipping point if it contains a strategy that is pairwise contagious relative to every other strategy contained in $\mathbf{a}$. That is, if A' is a subset of strategies that co-exist in $\mathbf{a}$, then there exists some $a_l \in A'$ that is pairwise contagious relative to every other $a_j \in A'$ with $a_j \neq a_l$. If A' consists of only two strategies, say a_j and a_l, then $\mathbf{a}$ corresponds to a mixed strategy equilibrium in which a pair of players randomize between a_j and a_l with probabilities $1 - \phi_{jl}$ and ϕ_{jl} respectively. That is, $\mathbf{a}$ is an absorbing state whereby each player choosing a_j has proportion $\eta_{jl} = \phi_{jl}$ of neighbours choosing a_l. Thus, $\mathbf{a}$ is a tipping point

because if at least one player switches to a_l (to a_j), the process converges to $\mathbf{a}_l$ (to $\mathbf{a}_j$) through best response dynamics. This also directly implies that if $a_l \text{PRC} a_j$ then there are no other absorbing states where only a_j and a_l co-exist except for the tipping point. A set of tipping points is empty in most local interaction strict coordination games.

The absorbing states in $S(\mathbf{A})$ are *relatively stable* because once reached, none of the strategies co-existing in some $\mathbf{a}' \in S(\mathbf{A})$ can spread by contagion. And hence, many mutations (depending on the network topology) may be needed for the process to transit from some $\mathbf{a}' \in S(\mathbf{A})$ to a monomorphic absorbing state corresponding to either of the strategies played in $\mathbf{a}'$. If $\mathbf{a}' \in S(\mathbf{A})$ consists of only two strategies a_j and a_l, then (by definition of tipping points above) they are not pairwise contagious relative to each other. As an example, consider the network in Figure 1 which has a contagion threshold of $\frac{1}{3}$, if $\frac{1}{3} < \phi_{jl} < \frac{1}{2}$ (meaning that a_l is not pairwise contagious relative to a_j), then there exists an absorbing state (see Example 1) where players $\{1, 2, 3, 4, 5, 6, 7\}$ choose a_l while $\{8, 9, 10, 11, 12\}$ choose a_j, and an absorbing state where $\{1, 2, 3, 4, 5\}$ choose a_j while $\{6, 7, 8, 9, 10, 11, 12\}$ choose a_l.
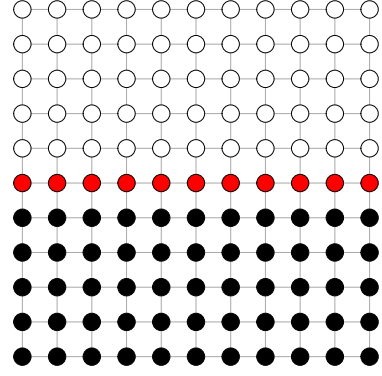
The necessary condition for strategies a_j and a_k to co-exist with a third strategy a_l in some absorbing state $\mathbf{a}' \in S(\mathbf{A})$, is for $a_j \times a_k \to a_l$ (i.e. a_j and a_k must not be pairwise contagious relative to each other). Under this condition, it is possible to have absorbing states (that are not tipping points) in which players choosing a_l are surrounded by players choosing a_j and a_k. Examples of such configurations are presented in Figure A.2b, where red dots represent players choosing a_l, and are surrounded by players choosing a_j in black and players choosing a_k in white. The condition $a_j \times a_k \to a_l$ is necessary but not sufficient. The following Lemma provides specific conditions for three strategies to co-exist in some $\mathbf{a}' \in S(\mathbf{A})$.

Lemma 6. *Let $\mathbf{a}' \in S(\mathbf{A})$ be a relatively stable absorbing state in which three strategies in the subset $A' = \{a_j, a_k, a_l\}$ co-exist. If $a_j \times a_k \to a_l$, then a_j and a_k will co-exists with a_l in $\mathbf{a}'$ if $a_j \text{PRC} a_l$ and $a_k \text{PRC} a_l$.*

Proof. To prove Lemma 6 (*i*), consider a network with contagion threshold of p. $a_j \text{PRC} a_l$ implies that $a_l \times a_j \to a_j$ and $\eta_{lj} = \phi_{lj} < p$, while $a_k \text{PRC} a_l$ implies that $a_l \times a_k \to a_k$ and $\eta_{lk} = \phi_{lk} < p$. Now, let $a_j \times a_k \to a_l$; strategy a_l will be a best response to any player who is surrounded by neighbours where proportion q play a_k and $1 - q$ play a_j, for values of q in the range $\phi_{jk} \leq q \leq \eta_{jk}$. Strategy a_j will be a best response to all players playing a_j provided at least proportion p of neighbours also play a_j, and at most $1 - p$ play a_l. Similarly, strategy a_k will be a best response to all players playing a_k provided at least proportion p of neighbours also play a_k, and at most $1 - p$ play a_l. Thus, it is possible to have a relatively stable absorbing state
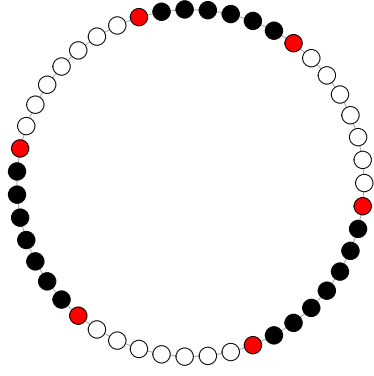
(a) A 2-dimensional cyclic network   (b) A 2-dimensional grid network

Figure A.2: This figure represents a strategy configuration where three strategies a_j, a_k, a_l co-exist. The red dots represent players choosing a_l, who are surrounded by players choosing a_j (in black) and players choosing a_k (in white).

$\mathbf{a}'$ in which a subgroup of players playing a_l is surrounded by subgroups playing a_j and a_l.

$\square$

To see why absorbing states in $S(\mathbf{A})$ are relatively stable, consider the configurations in Figure A.2 where players choosing a_l (in red) are surrounded by players choosing a_j (in black) and a_k in white. Since $a_j \mathrm{PRC} a_l$ and $a_k \mathrm{PRC} a_l$, strategy a_l cannot spread through pairwise contagion (i.e. best response dynamics). Even if all red players mutate to playing either a_j or a_k, neither a_j or a_k can spread through contagion. In fact, all players at the intersection of subgroups of a_j and a_l players will all switch to playing a_l again by best response. Hence, many mutation are required to turn the configurations of the form in Figure A.2 into a monomorphic absorbing state, making them relatively stable.

Consider instead the case in which a_l is pairwise contagious relative to both a_j and a_k. Configurations taking the form in Figure A.2 would be tipping points because a_l will spread to the black and white dots (players choosing a_j and a_k respectively) through contagion.

Appendix B. Proofs of main results

Appendix B.1. Proof of Theorem 1

We first show that for a pair of strategies $a_j, a_l \in A$ and their respective monomorphic absorbing states $\mathbf{a}_j$ and $\mathbf{a}_l$, if $a_l \mathrm{PRC} a_j$ then the costs $C(\mathbf{a}_j, \mathbf{a}_l) < C(\mathbf{a}_l, \mathbf{a}_j)$ for n sufficiently large. Recall that $C(\mathbf{a}_j, \mathbf{a}_l)$ is the minimal number of mutations needed for the transition from $\mathbf{a}_j$ to $\mathbf{a}_l$ to occur. From the definition of pairwise contagion, we noted that if $a_l \mathrm{PRC} a_j$ then

$C(\mathbf{a}_j, \mathbf{a}_l) = n(\mathbf{a}_j \to \mathbf{a}_l)$, the number of initial adopters of a_l needed to trigger contagion of a_l starting from $\mathbf{a}_j$. By definition, $n(\mathbf{a}_j \to \mathbf{a}_l)$ is independent of n and is much smaller than $\frac{n}{2}$.

From Lemma 3, we saw that if $a_l \mathrm{PRC} a_j$, then for each $a_j \neq a_l$, $\eta_{jl} = \phi_{jl} < p \leq \frac{1}{2}$, which also implies that $\eta_{lj} \geq \phi_{lj} > \frac{1}{2}$. Thus, each player requires more than half of his neighbours to switch from a_l to a_j for him to do likewise. The transition from $\mathbf{a}_l$ to $\mathbf{a}_j$ then requires a large number of mutation that ensures the each player has more than half of his neighbours playing a_l. In this case, although the total number of mutations required depends on the network density, in general, it is a function of the network size n. For highly sparse networks (with very low density), the number of mutations required is close to $\frac{n}{2}$. As the network density tends to one (i.e. to a complete network), the number of mutations needed approaches to $\eta_{jl}.(n-1) > \frac{1}{2}$; this is because in a complete network, each player has $n-1$ neighbours. If each player requires more than η_{jl} of his neighbours to switch from a_j to a_l for him to do likewise, then the whole population will switch from a_j to a_l once proportion $\eta_{jl}.(n-1)$ does so.

An example of a network with a very low density is a ring network, in which each player i has two neighbours $i-1$ on the left and $i+1$ on the right. In this network, the number of mutations required is $\frac{n}{2}$. This is because if $\eta_{lj} > \frac{1}{2}$ then a player requires both of his neighbours to switch to a_l for him to do likewise. Thus, starting from $\mathbf{a}_j$, a mutation arrangement where for examples players $0, 2, 4, \cdots, i-1, i+2, \cdots n-1$ experiment to play a_l is sufficient to switch the population from $\mathbf{a}_j$ to $\mathbf{a}_l$. Pairwise contagion of a_l relative to a_j therefore implies that the cost $C(\mathbf{a}_l, \mathbf{a}_j)$ is an increasing function of n; hence, for n sufficiently large, $C(\mathbf{a}_j, \mathbf{a}_l) < C(\mathbf{a}_l, \mathbf{a}_j)$.

Let $Q(\mathbf{A})$ be non-empty. We first consider the set of tipping points $\mathcal{T}(\mathbf{A})$. Let A' be a set of strategies that co-exist in some $\mathbf{a} \in \mathcal{T}(\mathbf{A})$. Since a_l is globally pairwise contagious, it must be pairwise contagious relative to every other $a_j \in A'$ with $a_j \neq a_l$. Given all $a_j \in A'$ contained in $\mathbf{a}$, the cost $C(\mathbf{a}, \mathbf{a}_l) \leq \sum_{a_j \in A'} C(\mathbf{a}_j, \mathbf{a}_l)$, or simply, $C(\mathbf{a}, \mathbf{a}_l) = \gamma \sum_{a_j \in A'} C(\mathbf{a}_j, \mathbf{a}_l)$ for some $\gamma \in (0, 1]$. But since each $C(\mathbf{a}_j, \mathbf{a}_l)$ is very small and independent of the population size n, i.e. $\mathcal{O}(1)$, it follows that $C(\mathbf{a}, \mathbf{a}_l) = \gamma \mathcal{O}(1)$. Now, consider the cost $C(\mathbf{a}_l, \mathbf{a})$ of a reverse transition from $\mathbf{a}_l$ to $\mathbf{a}$. It can also be written as $C(\mathbf{a}_l, \mathbf{a}) = \alpha \sum_{a_j \in A'} C(\mathbf{a}_l, \mathbf{a}_j)$ for some $\alpha \in (0, 1]$. Each $C(\mathbf{a}_l, \mathbf{a}_j)$ is an increasing function of n, i.e. $\mathcal{O}(n)$, so that $C(\mathbf{a}_l, \mathbf{a}) = \alpha \mathcal{O}(n)$. Hence, for n sufficiently large,

$$\gamma \mathcal{O}(1) < \alpha \mathcal{O}(n) \implies C(\mathbf{a}, \mathbf{a}_l) < C(\mathbf{a}_l, \mathbf{a})$$

Next, consider a subset $S(\mathbf{A})$ of $Q(\mathbf{A})$. Since each a_l is globally pairwise contagious, it follows from Section Appendix A.4 that each $\mathbf{a}' \in S(\mathbf{A})$ does not contain a_l. Since a_l is pairwise contagious relative to every $a_j \neq a_l$ contained in $\mathbf{a}' \in S(\mathbf{A})$, it follows from the arguments of the preceding paragraph that for n sufficiently large, $C(\mathbf{a}', \mathbf{a}_l) < C(\mathbf{a}_l, \mathbf{a}')$.

To conclude this part of the proof, we claim that if a_l is globally pairwise contagious, then the $\mathbf{a}_l$-tree is the least cost tree. That is, for each absorbing state $\mathbf{a} \in \mathbf{A}$, $C(\mathbf{a}_l) < C(\mathbf{a})$. For any $\mathbf{a}$, let $G(\mathbf{a})$ be a set of all $\mathbf{a}$-trees and $g \in G(\mathbf{a})$ a typical $\mathbf{a}$-tree. Let $g(\mathbf{a})$ be the least cost $\mathbf{a}$-tree so that

$$C(\mathbf{a}_l) = \sum_{(\mathbf{a},\mathbf{a}') \in g(\mathbf{a}_l)} C(\mathbf{a}, \mathbf{a}') \tag{B.1}$$

We have just shown above that if a_l is globally pairwise contagious, then for each $\mathbf{a}_j \in M(\mathbf{A})$ and any $\mathbf{a} \in Q(\mathbf{A})$, $C(\mathbf{a}_j, \mathbf{a}_l) < C(\mathbf{a}_l, \mathbf{a}_j)$ and $C(\mathbf{a}, \mathbf{a}_l) < C(\mathbf{a}_l, \mathbf{a})$ respectively. The structure of an $\mathbf{a}_l$-tree then involves direct arrows from every other absorbing state $\mathbf{a} \in \mathbf{A}$, where $\mathbf{a} \neq \mathbf{a}_l$, to $\mathbf{a}_l$, so that

$$C(\mathbf{a}_l) = \sum_{\mathbf{a} \neq \mathbf{a}_l} C(\mathbf{a}, \mathbf{a}_l) \tag{B.2}$$

For any other $\mathbf{a} \neq \mathbf{a}_l$, the least cost $\mathbf{a}$-tree, $g(\mathbf{a})$, involves replacing an arrow starting from some $\mathbf{a}''$ to $\mathbf{a}_l$ with an arrow starting from $\mathbf{a}_l$ to $\mathbf{a}''$. The associated transition costs are $C(\mathbf{a}_l, \mathbf{a}'') > C(\mathbf{a}'', \mathbf{a}_l)$, and hence,

$$C(\mathbf{a}) = C(\mathbf{a}_l) + \big(C(\mathbf{a}_l, \mathbf{a}'') - C(\mathbf{a}'', \mathbf{a}_l)\big) > C(\mathbf{a}_l) \tag{B.3}$$

Thus, $C(\mathbf{a}_l) < C(\mathbf{a})$ for all $\mathbf{a} \neq \mathbf{a}_l$. This completes the proof showing that a monomorphic absorbing state corresponding to a globally pairwise contagious strategy is stochastically stable. We next prove Lemma 4, which shows that if a strategy is pairwise contagious relative to every other strategy in a network with contagion threshold of p, then it is p-dominant.

Appendix B.2. Proof of Lemma 4

Recall the definition of η_{jl} as the minimum q above which a_l is a best response to σ_{jl}^q. Let $\eta_l = \max_{j \neq l} \{\eta_{jl}\}$ and $\phi_l = \max_{j \neq l} \{\phi_{jl}\}$. If a_l is globally pairwise contagious in a network with contagion threshold of p, then $\eta_{jl} = \phi_{jl} < p \leq \frac{1}{2}$ for all $a_j \neq a_l$; and hence, $\eta_l = \phi_l < p \leq \frac{1}{2}$. Given any other distribution $\sigma \in \Sigma$ that is not of the form σ_{jl}^p, let $\eta_l(\sigma)$ be the maximum $\sigma(a_l)$ above which a_l is a best response to σ. To prove Lemma 4, it is sufficient to show that for all $\sigma \in \Sigma$, $\eta_l(\sigma) < \eta_l$. The following steps are a proof of the latter.

For notational convenience, we write σ_j for $\sigma(a_j)$, and u_{jl} for $u(a_j, a_l)$. In analogy to σ_{jl}^q, let $\sigma_l = q$ and $\sigma_j = 1 - q - \bar{\sigma}_k$, where $\bar{\sigma}_k = \sum_{k \neq j,l} \sigma_k$, so that

$$\sigma = (1 - q - \bar{\sigma}_k, q, \cdots, \sigma_k, \cdots, \sigma_m), \tag{B.4}$$

Note that we are able to write $\sigma_j = 1 - q - \bar{\sigma}_k$ because $\sum_{k=1}^m \sigma_k = 1$.

In analogy to η_{jl}, let $\eta_{jl}(\sigma)$, for all distributions σ taking the form defined in (B.4), be the q above which a_l is a best response to σ. Given σ, a player chooses a_l whenever

$$qu_{ll} + (1 - q - \bar{\sigma}_k)u_{lj} + \sum_{k \neq l,j} \sigma_k u_{lk} > qu_{rl} + (1 - q - \bar{\sigma}_k)u_{rj} + \sum_{k \neq l,j} \sigma_k u_{jk} \quad \text{for all } r \neq l$$

Solving for q yields

$$q > \frac{u_{rj} - u_{lj}}{u_{rj} - u_{lj} + u_{ll} - u_{rl}} + \bar{\sigma}_k \frac{u_{lj} - u_{rj}}{u_{rj} - u_{lj} + u_{ll} - u_{rl}} + \frac{\sum_{k \neq l,j} \sigma_k (u_{rk} - u_{lk})}{u_{rj} - u_{lj} + u_{ll} - u_{rl}} \quad \text{for all } r \neq l$$

$$= \frac{u_{rj} - u_{lj}}{u_{rj} - u_{lj} + u_{ll} - u_{rl}} + \sum_{k \neq l,j} \sigma_k \left(\frac{(u_{rk} - u_{lk}) - (u_{rj} - u_{lj})}{u_{rj} - u_{lj} + u_{ll} - u_{rl}} \right) \quad \text{for all } r \neq l \tag{B.5}$$

Hence, the maximum q above which a player chooses a_l given distribution σ is

$$\eta_{jl}(\sigma) = \max_{r \neq l} \left\{ \frac{u_{rj} - u_{lj}}{u_{rj} - u_{lj} + u_{ll} - u_{rl}} + \sum_{k \neq l,j} \sigma_k \left(\frac{(u_{rk} - u_{lk}) - (u_{rj} - u_{lj})}{u_{rj} - u_{lj} + u_{ll} - u_{rl}} \right) \right\} \tag{B.6}$$

The first term on the right hand side of (B.6) is equivalent to η_{jl}, that is,

$$\eta_{jl} = \max_{r \neq l} \left\{ \frac{u_{rj} - u_{lj}}{u_{rj} - u_{lj} + u_{ll} - u_{rl}} \right\} \tag{B.7}$$

If a_l is pairwise contagious relative to a_j, then

$$\eta_{jl} = \phi_{jl} = \frac{u_{jj} - u_{lj}}{u_{jj} - u_{lj} + u_{ll} - u_{jl}} \tag{B.8}$$

Thus, pairwise contagion of a_l relative to a_j implies that the maximum on the right hand side of (B.6) obtains when $r = j$, such that

$$\eta_{jl}(\sigma) = \phi_{jl} + \sum_{k \neq l,j} \sigma_k \left(\frac{(u_{jk} - u_{lk}) - (u_{jj} - u_{lj})}{u_{jj} - u_{lj} + u_{ll} - u_{jl}} \right) \tag{B.9}$$

Note also that pairwise contagion of a_l relative to a_j implies that $\eta_{jl} = \phi_{jl} < \frac{1}{2}$. This implies from (B.8) that $u_{jj} - u_{lj} < u_{ll} - u_{jl}$. Substitute inequality $u_{jj} - u_{lj} < u_{ll} - u_{jl}$ to (B.9) yields

$$\eta_{jl}(\sigma) < \phi_{jl} + \sum_{k \neq l,j} \sigma_k \left(\frac{(u_{jk} - u_{lk}) - (u_{ll} - u_{jl})}{u_{jj} - u_{lj} + u_{ll} - u_{jl}} \right) \tag{B.10}$$

From (B.10), $\eta_{jl}(\sigma) \geq \phi_{jl}$ if and only if there exist some k's for which $(u_{jk} - u_{lk}) - (u_{ll} - u_{jl}) > 0$, that is, $u_{jk} - u_{lk} > u_{ll} - u_{jl}$. Note that the denominator in the second term on the right hand side of (B.10) is positive since by definition of coordination games, $u_{jj} - u_{lj} > 0$ and $u_{ll} - u_{jl} > 0$. Assume for a moment that $u_{jk} - u_{lk} > u_{ll} - u_{jl}$. Then

$$\eta_{kl} = \max_{r \neq l} \left\{ \frac{u_{rk} - u_{lk}}{u_{rk} - u_{lk} + u_{ll} - u_{rl}} \right\} > \frac{1}{2} \tag{B.11}$$

The inequality on the right hand side of (B.11) is because when $r = j$, then $u_{jk} - u_{lk} > u_{ll} - u_{jl}$ implies that

$$\frac{u_{jk} - u_{lk}}{u_{jk} - u_{lk} + u_{ll} - u_{jl}} > \frac{1}{2}.$$

Inequality (B.11) however violates the condition for pairwise contagion of a_l relative to a_k. But since we started out by assuming that a_l is pairwise contagious relative to every other strategy, it must then be the case that $u_{jk} - u_{lk} < u_{ll} - u_{jl}$. This inequality in turn makes the second term on the right hand side of (B.10) negative, and hence $\eta_{jl}(\sigma) < \phi_{jl}$. Taking a maximum over all $j \neq l$, we find that

$$\eta_l(\sigma) = \max_{j \neq l} \left\{ \eta_{jl}(\sigma) \right\} < \max_{j \neq l} \left\{ \phi_{jl} \right\} = \max_{j \neq l} \left\{ \eta_{jl} \right\} = \eta_l \tag{B.12}$$

Inequality (B.12) implies that if a_l is pairwise contagious relative to every other strategy $a_j \neq a_l$, then a player will choose a_l whenever a proportion $\eta_l = \phi_l$ of his neighbours do so. Thus, a_l is p-dominant *for all $p > \eta_l$*. The phrase "for all $p > \eta_l$" is due to monotonicity of p-dominance, whereby if $p < p'$, then any p-dominant strategy is also p'-dominant.

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