CONTAGION AND EQUILIBRIUM SELECTION IN NETWORKS*

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Abstract: This paper develops methods for characterizing stochastic evolution in networks. We derive sufficient conditions for *asymptotic global convergence* to be *global* or *path-wise contagion*, and that the network must be *strongly connected*. Strategies that are either globally or path-wise contagious are then those that are asymptotically globally stable. Asymptotic global stability is robust to the model of mistakes and addition of strictly dominated strategies. We show that for a given payoff structure and hence relative payoff gains, a network can be designed to make at least one strategy asymptotically globally stable. Similarly, for a given network structure and set of strategies, one can determine the relative payoff gains that lead to a given strategy to be globally stable. We briefly discuss the practical and empirical relevance of these findings.

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I. Introduction

Stochastic evolutionary models provide the justification for Nash Equilibrium as well as a criterion for equilibrium selection. Under stochastic evolutionary dynamics, agents adjust their behavior over time after learning from their opponents' play. The adjustment

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process is such that players are assumed to best-respond to or imitate myopically their opponents' behaviors, but their assessments are subject to random shocks. In analyzing long-run outcomes of such dynamic processes, Foster and Young (1990) and Kandori et al. (1993) use the concept of *stochastic stability*. Stochastically stable outcomes are those that occur with positive probability at the limit of randomness. Fairly concrete results have been established with regard to stochastic stability in 2×2 coordination games. For example Young (1993) and Kandori et al. (1993), Blume (1995) show that in 2×2 coordination games and under global interactions, risk-dominant strategies are stochastically stable.[1] Maruta (1997) derives equivalent results for $m \times m$ coordination games, showing that *globally risk-dominant* strategies are selected in the long-run.[2] Kandori and Rob (1998) show that *globally pairwise risk-dominant* strategies are stable in the long-run only under strict conditions they refer to as *total bandwagon property* and *marginal bandwagon property*.[3] Under local interactions and 2×2 games, (Ellison, 2000), Lee and Valentinyi (2000) and Lee et al. (2003) show risk-dominant strategies are stable in the long-run.

In spite of these strong predictions, questions regarding robustness of and convergence rates to long-run stable outcomes do exist. For example Bergin and Lipman (1996) show that for given $m \times m$ asymmetric matrix games, the outcomes that are stochastically stable strictly depend on the assumptions made concerning the structure of experimentation by players. Kim and Wong (2010) show that for a given model of mistakes, any outcome can be made stochastically stable by appropriately adding strictly dominated strategies. Alós-Ferrer and Weidenholzer (2007) demonstrate that contrary to the predictions made in Kandori and Rob (1998) regarding globally pairwise risk dominant strategies under global interactions, under local interactions and beyond 4×4 coordination games, globally pairwise risk dominant strategies need not be selected. Ellison (1993) showed that under global interactions, the expected waiting times to stochastically stable outcomes are long.

This paper studies evolutionary processes in networks and $m \times m$ symmetric games. We follow the customary behavioral and dynamics assumptions of Darwinian dynamics and

1. In a 2 x2 symmetric game with two symmetric equilibria in pure strategies, one risk-dominates another if and only if the equilibrium strategy is a unique best response to any mixture that gives it at least a probability of one half.

2. In an $m \times m$ symmetric game, a strategy is globally risk-dominant if it is a unique best response to any mixture that gives it at least a probability of one half.

3. In an $m \times m$ symmetric game, a strategy is globally pairwise risk dominant if it risk-dominates each and every other strategy. Global pairwise risk dominance is a weaker notion compared to that of global risk dominance according to Maruta (1997).

with focus on establishing conditions for play to converge in the long-run and on how to identify stable strategies. More specifically, agents are assumed to base their decisions on the distribution of strategies in the previous period and not the entire history of play. Unlike in the case of global interactions, local interactions imply that information available to each agent is limited and is simply the distribution of strategies in their neighborhood. We establish conditions for *asymptotic global convergence* and *stability*, that is the long-run outcomes at the limit of population size rather than limit of noise. In so doing, we preserve the necessity of maintaining positive noise levels in evolutionary models. That is positive noise levels captures the general assumption of bounded rationality and experimentation embedded in the models.

These two fairly standard assumptions, limited information (local interactions) and positive noise levels, circumvent some of the above mentioned limitations of evolutionary processes in the following ways. First, several authors have shown that under local interactions the expected waiting times to the long-run stable state from any other state are bounded (e.g. Ellison (1993), Young (2011), Montanari and Saberi (2010)). The limitation concerning the convergence rates is thus not necessarily critical under local interactions, specially when the noise levels are kept positive.

Secondly, under local interactions asymptotic global convergence occurs for *strongly connected* networks and additional conditions we describe below. We show that for a given structure of interactions, strategies that are *globally* and/or *path-wise contagious* are globally stable for a sufficiently large population size. By contagious we mean a strategy spreads by best-response once a small fraction of players have adopted it. A strategy is globally contagious if it is uniquely contagious after pair-wise comparison with all other strategies. A strategy, say a, is path-wise contagious relative to another say b if there exists a directed path from b to a, such that each strategy on the path is contagious. For any given game however, even when no strategy is globally contagious it is possible to construct a range of network families for which at least one strategy is path-wise contagious. The relationship between global and path-wise contagion on one hand with interaction and the underlying game structures on the other hand is not linear. For a given game, sparsely connected networks tend to favor global and path-wise contagion. For a given network structure, strategies with the largest *relative payoff gains* are those that are potentially globally and path-wise

contagious.[4]

The notion of contagion in networks under strategic interactions as defined here is related to that in Morris (2000). Any given arbitrary network has a critical *contagion threshold* such that contagion occurs if and only if the relative payoff gain is below the contagion threshold. In this regard, the analysis in this paper is closely related to Morris (2000) in making use of the notion of contagion to characterize long-run outcomes of evolutionary processes in networks. The main difference resides in the fact that we focus on stochastic rather than deterministic dynamics. In so doing, we are able to make unique predictions of long-run stable outcomes for $m \times m$ coordination games. Similarly, we focus on characterizing long-run stable outcomes as opposed to determining the properties of networks that influence contagion.

Global contagion as we define here is related to the concept of *p-dominance* according to Morris et al. (1995). Generally, an action pair in a two-player game is said to be p-dominant if each action is a best response to any belief that the other player takes the action in this pair with probability at least p. For the local interaction game we consider, a strategy is p-dominant if for all players, it is the unique best-response when it is played by at least proportion p of the neighbors. This implies that for a network with contagion threshold p, a strategy that is p-dominant is also globally contagious. Path-wise contagion in the context of local interaction game as defined in this paper is however a novel notion, and is less restrictive compared to global contagion.

In relation to the analysis in Alós-Ferrer and Weidenholzer (2007), global and path-wise contagion are alternative methods that focus on the properties of the underlying network and game. Alós-Ferrer and Weidenholzer (2007) focus on establishing conditions for selection of $\frac{1}{2}$-dominant strategies, which occurs in networks with contagion threshold of $\frac{1}{2}$; for example the cyclic interaction structure. Here, we do not place restrictions on the contagion threshold and hence network topology. Most importantly however, global and path-wise contagion as opposed to the notion of Global pairwise risk-dominance and the partial bandwagon properties in Alós-Ferrer and Weidenholzer (2007) can be employed to make prediction for long-run outcomes in $m \times m$ and not just 3×3 coordination games.

The closely related literature with regard to p-dominance is the recent papers by Sand-

4. For any given matrix game, the relative payoff gain of strategy say a in relation to another say b, is equivalent to the fraction of opponents that must play a for that agent to switch from playing b to playing a.

holm (2001) and Sandholm et al. (2014). They show that the deterministic dynamics where players sample strategies of k-randomly chosen other players in the population leads to *almost global convergence* to $\frac{1}{k}$-dominant strategies. In relation to the definitions in this paper, $\frac{1}{k}$-dominant strategies would be those that are globally contagious whenever the maximum number of neighbors any player has is k. The contrast with what we do in this paper is that we study non-deterministic processes under general interaction structures, hence derive results for general interaction topologies and revision probabilities. Secondly, we emphasize evolutionary processes with positive noise levels. This enables us to derive results pertaining global convergence rather than almost global convergence.

Thirdly, we show that asymptotic globally stable outcomes are robust to addition of dominated strategies, circumventing the limitation of stochastic stability pointed out by Kim and Wong (2010). The reason for the robustness of asymptotic global stability to both addition of strictly dominated strategies and model of mistakes is that the factors that determine global stability under local interactions (global and path-wise contagion) are robust to both phenomena.

The most relevant aspect of our results is that for a given payoff structure and hence relative payoff gains, it is possible to design a network such that at least one strategy is asymptotically globally stable. Similarly, for a given network structure and set of strategies, one can determine the relative payoff gains that lead to a given strategy to be globally stable. Moreover, these findings are robust to the model of mistakes, circumventing the limitations pointed out by Bergin and Lipman (1996).

The findings in this paper have both practical and empirical implications. First, since the model of mistakes does not play a role in determining the long-run stable outcomes (but perhaps only the rates of convergence), then for any given game (e.g. institutional or technological adoption) if the network and payoff structures are known a priori, the level of noise/experimentation that is characteristic to the given interaction environment can be estimated. This can be done using historical data for competing technological products for example. For example Young (2009) fits adoption curves to data on diffusion of Hybrid Corn (based on the empirical work of Ryan and Gross (1943)) to distinguish between three diffusion processes; contagion, social influence and social learning. A similar exercise can be performed for a specific learning process then estimate the desirable level of experimentation.

This exercise is feasible since the network of interactions can be empirically determined. Recently, there has been a growing literature both theoretical and empirical in the field of social networks. Most of this literature is devoted to characterizing the distributional structure of real world social networks (see for example Newman et al. (2002) and Newman (2003)). Determining the level of experimentation that is characteristic to a given institutional structure or technology field is particularly relevant if we view the process of experimentation as an abstraction from the actual process through which new technologies and institutions emerge. The second practical relevance of our result is that, by relating network structure to relative payoff gains it is possible to determine for a given network of interaction the required level of incremental innovation for one product to take over the market. That is, for any given network one can determine the level of relative payoff gain for a given strategy to be globally contagious independently of the level of noise and model of mistakes. Similarly, if we think of competing scientific theories as exhibiting strategic complementarity, then for a given network of interactions between scientists (which can be constructed from co-authorship or cross-citations) one can determine the level of empirical evidence/support (hence relative payoff gains) that can lead to one theory to be firmly accepted.

The remainder of the paper is organized as follows. In section II. we introduce the general framework of stochastic evolutionary dynamics in networks. Section III. defines the solution concept and provides results for global convergence and stability. Sections IV. and V. developed the concepts of global and path-wise contagion, explicitly characterizing how the network and payoff structures interactively shape long-run stability.

II. The model

We consider an m strategy matrix coordination game $\Gamma(X, \{U_i\}_{i\in\mathcal{N}})$ played by a set $\mathcal{N} = \{1, \cdots, i, \cdots\}$ of players. Where $X = \{a, b, c, \cdots\}$ is the strategy set identical for all players and $U \in \mathbb{R}^{m\times m}$ is the associated payoff matrix such that $U_i(a, b)$ is the base payoff to i for playing a when the opponent plays b. Whenever the a finite population is referred N will denote the population size. Players revise their strategies simultaneously at discrete time intervals $t = 1, 2, \cdots$. At each t, each player evaluates the available strategies and chooses that which maximizes the expected payoffs. This evaluation process in based on strategies of opponents in the neighborhood. The neighborhoods form each player's social network.

Generally, the network of interactions can be modeled in a graph theoretical manner.

Let $G(N, E)$ be a graph with N vertices representing the number of agents and E edges linking different pairs of agents, such that a graph g_{ij} defines the connection between i and j. If $g_{ij} = 1$ then a directed link exists from i to j, and zero implies otherwise. $G(N, E)$ is thus a directed network describing the relationship of any one agent with every other agent in the population. The *adjacency matrix* $\mathscr{A}$ of $G(N, E)$ is defined as an $N \times N$ matrix with entries being the elements of g_{ij}. The *neighborhood* of agent i, $\mathcal{N}_i$, is defined as $\mathcal{N}_i = \{j \in N | g_{ij} = 1\}$, and gives the set of players to which i is linked to. The cardinality $\#\mathcal{N}_i = k_i$, is the *degree* of i.

We assume that each player plays the same strategy against all the neighbors. That is given state $\mathbf{x}$, where $\mathbf{x}_{-i}$ denotes the population state with i excluded, the expected payoff to i for playing strategy a is

$$U_i(a, \mathbf{x}_{-i}) = \sum_{j \in \mathcal{N}_i} J_{ij} U(a, x^j), \tag{1}$$

where x^j is the j^{th} coordinate of $\mathbf{x}$. The parameter J_{ij} takes on values in the closed interval $[0, 1]$. It is the weight that i attaches to the interaction with j, such that if i weights all the neighbors equally then $J_{ij} = \frac{1}{k_i}$ for all $j \in \mathcal{N}_i$. The model of stochastic evolution in networks is then defined as follows.

Definition 1. A model of stochastic evolution for an m-strategy coordination game in networks is a quadruple $(U^{m \times m}, \mathbf{X}_N, P_N, P_{N,\boldsymbol{\varepsilon}}, G_N)$ consisting of

1) A payoff function $U \in \mathbb{R}^{m \times m}$; a state space denoted by $\mathbf{X}_N$.

2) A family of interaction networks G_N indexed by N as the number of vertices and E_N as corresponding number of edges such that

$$\lim_{N \to \infty} \frac{|E_N|}{N(N-1)} < 1 \tag{2}$$

3) A family of Markov transition matrices P_N on $\mathbf{X}_N$ indexed by $N \geq 3$.

4) A family of Markov transition matrices $P_{N,\boldsymbol{\varepsilon}}$ on $\mathbf{X}_N$ indexed by $N \geq 3$ and the set $\boldsymbol{\varepsilon} = (\varepsilon_1, \cdots, \varepsilon_N)$, such that

   (i) $P_{N,\boldsymbol{\varepsilon}}$ is ergodic for all $\varepsilon_i > 0$.

(ii) $P_{N,\boldsymbol{\varepsilon}}$ is continuous in $\boldsymbol{\varepsilon}$ and $P_{N,0} = P_N$.

(iii) Each $\varepsilon_i(\mathbf{x})$ can be state dependent but are independent of N and the position in the network.

The state $\mathbf{X}_N$ is a function of both N and the network structure G_N. Condition (2) of the model places restriction on the structure of the network as the population size grows. It states that the density of the network as N grows should be bounded away from one. A complete network (in which each player interacts with every other player) has density of one; (2) therefore rules out complete networks and all network families for which the number (or mass) of edges grows proportionally with its volume: $N(N-1)$. As already established in Ellison (1993), for complete networks the radii of all basins of attraction are increasing functions of N. Condition (2) rules out these cases and is necessary for the validity of results in Theorem 9 (ii) and (iii) below.

The Markov transition matrix P_N is based on the unperturbed dynamics and $P_N(\mathbf{x}, \mathbf{y})$ is the probability that state $\mathbf{x}$ is followed by $\mathbf{y}$. Since we assume best response dynamics rather than say imitation, $P_N(\mathbf{x}, \mathbf{y})$ is the probability that state $\mathbf{y}$ is reached when each player switches to a strategy y^i which is best-response to $\mathbf{x}$. That is for each i

$$BR_i(y^i, \mathbf{x}) = \begin{cases} 1 & \text{if } y^i \in \arg\max_{b \in X} U_i(b, \mathbf{x}_{-i}) \\ 0 & \text{otherwise.} \end{cases} \tag{3}$$

The fourth element of the model specifies the nature of random perturbations. There are two main ways to capture the aspect of randomness. The mistakes resulting from experimentation (on strategies) and randomness resulting from expected payoffs perturbations. Under the former, the probability that player i chooses action a given $\mathbf{x}$ is

$$\mathbb{P}_i(a, \mathbf{x}) = (1 - \varepsilon_i(\mathbf{x}))BR_i(a, \mathbf{x}) + \varepsilon_i(\mathbf{x})\mathcal{P}_i(a, \mathbf{x}) \tag{4}$$

where $\sum_{a \in X} \mathcal{P}_i(a, \mathbf{x}) = 1$ for each $i \in \mathcal{N}$ and $a \in X$.

Condition (iii) of element 4 of the model implies that each $\varepsilon_i(\mathbf{x})$ and $\mathcal{P}_i(a, \mathbf{x})$ can be state dependent but are independent of N. This condition is necessary to rule out cases in which the likelihood of mistakes is a decreasing function of N. A distinction should however be made between the likelihood of mistakes and the number of mistakes. While the likelihood

of making a mistake to transition from one state to another is independent of N, the number of mistakes required to exit a subset of states can grow with N. The special case of dynamics (4) are Kandori et al. (1993) and Young (1993) where mutation rates are state and player independent.

Under the case of expected payoff perturbations, i's objective is to choose a strategy a that maximizes the perturbed payoff $U_i(a, \mathbf{x}_{-i}) + \varepsilon_a$, that is

$$a \in \arg\max_{b \in X} U_i(b, \mathbf{x}_{-i}) + \varepsilon_b$$

where ε_b's are the random components of the expected payoff. The special cases of expected payoff perturbations are those in which the components of $\boldsymbol{\varepsilon} = (\varepsilon_a, \varepsilon_b, \cdots)$ are assumed to be independently distributed. For example the logit and multinomial probit in Blume (2003) and Myatt and Wallace (2003) respectively.

III. Asymptotic global convergence

Given the conditions for random perturbations above, the process $P_{N,\boldsymbol{\varepsilon}}$ has a well defined unique invariant distribution $\pi_{N,\boldsymbol{\varepsilon}} = \lim_{t\to\infty} \mathbf{q}_0 P^t_{N,\boldsymbol{\varepsilon}}$, where $\mathbf{q}_t$ is the vector of probability mass functions at period t. It describes the amount of time the process spends in each state in the long-run or equivalently the long-run probability of each state. We denote by $\mathbf{l}$ for a typical limit states of the equivalent process without mistake, that derives from the dynamics in (3). The set of all such sets is denoted by $\mathbf{L}$. When interactions are localized, the number of limit states may increase depending on the network topology. Throughout the paper, we write $D(\mathbf{l})$ for the basin of attraction of $\mathbf{l}$.[5] We then define $\partial\mathbf{l}$ as a set of all states in the basin of attraction of $\mathbf{l}$ with $\mathbf{l}$ excluded and refer to it as the neighbourhood of the limit state $\mathbf{l}$.

Asymptotic global stability is then formally defined as follows

Definition 2. Given a family of networks G_N indexed by N, a subset of states $\mathbf{x}$ is said to be asymptotically globally stable if $\lim_{N\to\infty} \pi_{N,\boldsymbol{\varepsilon}}(\mathbf{x}) > 0$

5. For the process without noise P_N, a *basin of attraction* of a limit state $\mathbf{l}$ is formally defined as $D(\mathbf{l}) = \{\mathbf{x} \in \mathbf{X}_N | \mathbb{P}(\exists T \text{ s.t } \mathbf{x}_t \in \mathbf{l} \,\forall\, t > T | \mathbf{x}_0 = \mathbf{x}) = 1\}$. That is, the set of states from which the chain without noise converges to $\mathbf{l}$.

That is, asymptotically globally stable states are those where the probability with which it is played in the long-run is positive at the limit of the population size. The definition of asymptotic global stability above is different from that of stochastic stability commonly used as an equilibrium selection mechanism in evolutionary. A stochastically stable state is that in which $\lim_{\varepsilon\to 0}\pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l})>0$. In other models of stochastic evolution, such as Binmore et al. (1995), Binmore and Samuelson (1997) and Blume (2003), a limit of the population size is taken primarily to approximate the stochastic process by a deterministic form. The definition of long-run stable states in Blume (2003) is in the context of stochastic stability defined as $\lim_{\varepsilon\to 0}\lim_{N\to\infty}\pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l})>0$. Binmore et al. (1995) and Binmore and Samuelson (1997) on the other hand partly discuss equilibrium selection with positive noise levels in the context of asymptotic stability as defined above. They however do not refer to selected states as stochastically stable. Sandholm (2007) and Sandholm (2010) discusses equilibrium selection in deterministic evolutionary dynamics as in the above mentioned three papers, and defines stochastically stable states in the limit of population size, that is $\lim_{N\to\infty}\pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l})>0$. This in turn however prompted another definition, *limit stochastic stability* for states that are stable in the long-run at the limit of noise; that is states for which $\lim_{\varepsilon\to 0}\lim_{N\to\infty}\pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l})>0$. To avoid such redefinitions of stochastic stability, we refer to long-run stable states at the limit of population size as asymptotically globally stable.

The characterization of asymptotically globally stable states involves analysing the stationary distribution of $P_{N,\boldsymbol{\varepsilon}}$. The following definitions come handy in the characterization of the limit behaviour of $P_{N,\boldsymbol{\varepsilon}}$. First, we define $G(W)$-graphs for a subset $W\subset\mathbf{X}$ as a set of all oriented graphs $g\subset\mathbf{X}\times\mathbf{X}$ satisfying:

1. No arrows start from W and exactly one arrow starts from each state outside of W.

2. Each $g\in G(W)$ has no loops.

If W is a singleton set, say $\mathbf{x}$, then $G(\{\mathbf{x}\})$ is a set of all graphs linking every point outside of $\mathbf{x}$ to $\mathbf{x}$, also commonly referred to as $\mathbf{x}$-trees. Secondly, we define $g_{\mathbf{l},\mathbf{l}'}\in D(\mathbf{l})\times D(\mathbf{l}')$ graphs restricted to basins of attractions of $\mathbf{l}$ and $\mathbf{l}'$. Similarly, $G_{\mathbf{l},\mathbf{l}'}(W)$ graphs, where W is a subset of $D(\mathbf{l}')$ is a set of all graphs satisfying

1. No arrows start from W and exactly one arrow starts from each state outside of W.

2. Each $g_{\mathbf{l},\mathbf{l}'}\in G_{\mathbf{l},\mathbf{l}'}(W)$ has no loops.

For example if $\partial \mathbf{l} = \{\mathbf{x}, \mathbf{y}\}$ and $\partial \mathbf{l}' = \{\mathbf{w}, \mathbf{v}, \mathbf{z}\}$, then typical graphs in $G_{\mathbf{l},\mathbf{l}'}$ include $\mathbf{l} \to \mathbf{x} \to \mathbf{y} \to \mathbf{w} \to \mathbf{v} \to \mathbf{z} \to \mathbf{l}'$, e.t.c.

The third definition regards transition probabilities associated with graphs. We define $P_{N,\varepsilon}(g) = \prod_{(\mathbf{x},\mathbf{y})\in g} P_{N,\varepsilon}(\mathbf{x}, \mathbf{y})$. That is the product of probabilities of transitions in graph g. A similar definition follows for graphs in $G_{\mathbf{l},\mathbf{l}'}(W)$; where $P_{N,\varepsilon}(g_{\mathbf{l},\mathbf{l}'}) = \prod_{(\mathbf{x},\mathbf{y})\in g_{\mathbf{l},\mathbf{l}'}} P_{N,\varepsilon}(\mathbf{x}, \mathbf{y})$.

In characterizing $\pi_{N,\varepsilon}$ we make use of the following two lemmas, which are Lemma 3.1 and Theorem 4.1 of Freidlin and Wentzell (2012).

LEMMA 3. Given a process $P_{N,\varepsilon}$, the stationary distribution $\pi_{N,\varepsilon}(\mathbf{x})$ of some state $\mathbf{x}$ is given by

$$\pi_{N,\varepsilon}(\mathbf{x}) = \left(\sum_{g\in G(\{\mathbf{x}\})} P_\varepsilon(g) \right) \left(\sum_{\mathbf{y}\in\mathbf{X}} \sum_{g\in G(\{\mathbf{y}\})} P_\varepsilon(g) \right)^{-1} \tag{5}$$

LEMMA 4. Given a process $P_{N,\varepsilon}$, if probabilities $P_{N,\varepsilon}(\mathbf{x}, \mathbf{y})$ consist of numbers $\exp\left(-\varepsilon^{-2} v(\mathbf{x}, \mathbf{y})\right)$, then for ε sufficiently small and for some $\gamma > 0$

$$\pi_{N,\varepsilon}(\mathbf{x}) = \exp\left\{ -\varepsilon^{-2} \left(V(\mathbf{x}) - \min_{\mathbf{y}\in\mathbf{X}} V(\mathbf{y}) \pm \gamma \right) \right\} \tag{6}$$

where $V(\mathbf{x}) = \min_{g\in G(\{\mathbf{x}\})} \sum_{(\mathbf{x},\mathbf{y})\in g} v(\mathbf{x}, \mathbf{y})$

Lemma 4 derives from Lemma 3 and places lower and upper bounds on the stationary distribution in terms of the least cost graphs, where $V(\mathbf{x})$ is the total cost of the minimum cost $\mathbf{x}$-tree. Given the relation in Lemma 4, it is sufficient to focus on the $\mathbf{l}$-trees; that is, the $g \subset \mathbf{L} \times \mathbf{L}$ graphs defined on the state space of limit states. The first step in doing so is deriving probabilities $P_{N,\varepsilon}(g_{\mathbf{l},\mathbf{l}'})$ for graphs between limit states as defined above. Once these probabilities are expressed in the form $\exp(-c(\mathbf{l}, \mathbf{l}'))$, where $c(\mathbf{l}, \mathbf{l}')$ is a cost function of the graphs from $\mathbf{l}$ to $\mathbf{l}'$, we can then use Lemma 4 to characterize the stationary distribution of limit states.

For every graph $g_{\mathbf{l},\mathbf{l}'} \in G_{\mathbf{l},\mathbf{l}'}(\mathbf{l}')$, the process goes through two stages. First from $\mathbf{l} \to \partial\mathbf{l}'$, then from $\partial\mathbf{l}' \to \mathbf{l}'$. Denote by $g_{\mathbf{l},\partial\mathbf{l}'} \in G_{\mathbf{l},\partial\mathbf{l}'}(\mathbf{x})$ for graphs that start from $\mathbf{l}$ and end in a single state $\mathbf{x}$ of $\partial\mathbf{l}'$, and write $P_{N,\varepsilon}(g_{\mathbf{l},\partial\mathbf{l}'}) = \prod_{(\mathbf{x},\mathbf{y})\in g_{\mathbf{l},\partial\mathbf{l}'}} P_{N,\varepsilon}(\mathbf{x}, \mathbf{y})$. Similarly, we write $g_{\partial\mathbf{l}',\mathbf{l}'} \in G_{\partial\mathbf{l}',\mathbf{l}'}(\mathbf{l}')$ for graphs starting from states in $\partial\mathbf{l}'$ and end at $\mathbf{l}'$. For every graph $g_{\mathbf{l},\mathbf{l}'} \in G_{\mathbf{l},\mathbf{l}'}(\mathbf{l}')$, we can thus write $P_{N,\varepsilon}(g_{\mathbf{l},\mathbf{l}'})$ as a product $P_{N,\varepsilon}(g_{\mathbf{l},\mathbf{l}'}) = P_{N,\varepsilon}(g_{\mathbf{l},\partial\mathbf{l}'}) P_{N,\varepsilon}(g_{\partial\mathbf{l}',\mathbf{l}'})$. We refer to the probabilities $P_{N,\varepsilon}(g_{\mathbf{l},\partial\mathbf{l}'})$ as exit probabilities in the sense that they involve

exit from a basin of attraction, $P_{N,\boldsymbol{\varepsilon}}(g_{\partial \mathbf{l}',\mathbf{l}'})$ as contagion probabilities since they involve the dynamics within a basin of attraction and such dynamics is governed by the process of contagion or best-response. We now derive expressions for each.

III.A. Exit probabilities

As defined above, exit probabilities are probabilities of evolution along the graphs $g_{\mathbf{l},\partial \mathbf{l}'}$ for any given pair of limit states $(\mathbf{l},\mathbf{l}')$. Along paths of such graphs, the dynamics is governed by mutations and by definition each transition involves a single mutation. If mutation probabilities are uniform, for example the case in which probabilities of a transition by mistake from some state $\mathbf{x}$ to another $\mathbf{y}$ is given $P_{N,\boldsymbol{\varepsilon}}(\mathbf{x},\mathbf{y}) = \varepsilon^{v(\mathbf{x},\mathbf{y})}$, where $v(\mathbf{x},\mathbf{y})$ is some cost function that is greater than zero if the transition $\mathbf{x} \to \mathbf{y}$ requires a mutation and zero if it occurs under best-response. Then $P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\partial \mathbf{l}'}) = \varepsilon^{V(\mathbf{x},\mathbf{y})} = \exp\{V(\mathbf{x},\mathbf{y}) \ln \varepsilon\}$ where $V(\mathbf{x},\mathbf{y}) = \sum_{(\mathbf{x},\mathbf{y}) \in g_{\mathbf{l},\partial \mathbf{l}'}} v(\mathbf{x},\mathbf{y})$ is the total cost of graph $g_{\mathbf{l},\partial \mathbf{l}'}$. Under such homogeneous probabilities of mistakes, it becomes straightforward to apply results of Lemma 4. The first step in characterisation of exit probabilities thus involves expressing $P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\partial \mathbf{l}'})$ in exponential form. For the model defined above, the following lemma provides upper and lower bounds for $P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\partial \mathbf{l}'})$.

LEMMA 5. Suppose $(\mathbf{X}_N, P_{N,\boldsymbol{\varepsilon}}, G_N)$ is a model of evolution with noise and let $\mathbf{l}$ and $\mathbf{l}'$ be any two limit states of $(\mathbf{X}_N, P_N, G_N)$. Then

$$K \exp\left\{|g_{\mathbf{l},\partial \mathbf{l}'}| \ln\left(\mathbb{P}(x_{\mathbf{l}'},\mathbf{l})\right)\right\} \leq P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\partial \mathbf{l}'}) \leq \exp\left\{|g_{\mathbf{l},\partial \mathbf{l}'}| \ln\left(\mathbb{P}(x_{\mathbf{l}'},\mathbf{l})\right)\right\} \tag{7}$$

where $|g_{\mathbf{l},\partial \mathbf{l}'}|$ is the cardinality of $g_{\mathbf{l},\partial \mathbf{l}'}$, $\mathbb{P}_i(x_{\mathbf{l}'},\mathbf{l})$ is the probability that i plays action $x_{\mathbf{l}'}$ given that the process is in state $\mathbf{l}$, $x_{\mathbf{l}'}$ is the action played by all or a majority of players in state $\mathbf{l}'$ and $K > 0$ is some real number.

Proof.

See Appendix VII.A..

■

The quantity $|g_{\mathbf{l},\partial \mathbf{l}'}|$ is the number of mistakes required to exit the basin of attraction $D(\mathbf{l})$ starting from $\mathbf{l}$ into the basin of attraction $D(\mathbf{l}')$. Equivalently, it is the number of players required to play action $x_{\mathbf{l}'}$ by mistake either simultaneously or consecutively for evolution

from $\mathbf{l} \to \partial\mathbf{l}'$ to occur. For the remainder of the paper we write $R(\mathbf{l}, \partial\mathbf{l}')$ for $|g_{\mathbf{l},\partial\mathbf{l}'}|$ and the normalization $r(\mathbf{l}, \partial\mathbf{l}') = \frac{1}{N} R(\mathbf{l}, \partial\mathbf{l}')$. The quantity $c(\mathbf{l}, \partial\mathbf{l}') = -r(\mathbf{l}, \partial\mathbf{l}') \ln(\mathbb{P}(x_{\mathbf{l}'}, \mathbf{l}))$ is then the cost associated with the graph $g_{\mathbf{l},\partial\mathbf{l}'}$, or simply the cost of evolution from $\mathbf{l} \to \partial\mathbf{l}'$. The following example suffices to illustrate the implications of the measures contained in (7).

Consider a 2×2 symmetric coordination game with strategies a and b, where $U(a,a) = 3$, $U(a,b) = 2$, $U(b,a) = 0$, $U(b,b) = 4$ such that a is risk-dominant. Let the interaction structure be that of a ring network in which each player has two neighbours. There are two limit states in this case: that in which all players play a and that in which they all play b. Since a is risk-dominant, whenever a player has one neighbour playing a, his best-response is a. For $N \geq 4$, two mistakes are required to move from an all b state, $\mathbf{b}$, to the basin of attraction of an all a state, $\partial\mathbf{a}$. To move from $\mathbf{a}$ to $\partial\mathbf{b}$ requires more than $N/2$ mistakes. We then have $r(\mathbf{b}, \partial\mathbf{a}) = \frac{2}{N}$ and $r(\mathbf{a}, \partial\mathbf{b}) = \frac{1}{2}$. Now consider a model of mistakes in (4) and assume that $\varepsilon_i(\mathbf{x}) = \varepsilon(\mathbf{x})$ for all i and that $\varepsilon(\mathbf{x})$ follows a logit distribution such that $\varepsilon(a, \mathbf{b}) = \frac{\exp\{\beta U(a,\mathbf{b})\}}{\exp\{\beta U(a,\mathbf{b})\}+\exp\{\beta U(b,\mathbf{b})\}} = 0.018$ and $\varepsilon(b, \mathbf{a}) = \frac{\exp\{\beta U(b,\mathbf{a})\}}{\exp\{\beta U(b,\mathbf{a})\}+\exp\{\beta U(a,\mathbf{a})\}} = 0.0025$. Assume also $\mathcal{P}_i(a, \mathbf{b}) = \mathcal{P}_i(a, \mathbf{b}) = \frac{1}{2}$. That is, both strategies are equally likely whenever a mutation occurs. Combining $\varepsilon(.)$ and $\mathcal{P}(.)$ then gives $\mathbb{P}(b, \mathbf{a}) = 0.0013$ and $\mathbb{P}(a, \mathbf{b}) = 0.009$.

The costs of evolution between $\mathbf{a}$ and $\mathbf{b}$ are $c(\mathbf{b}, \partial\mathbf{a}) = -\frac{9.4}{N}$ and $c(\mathbf{a}, \partial\mathbf{b}) = -3.3$. The respective bounds for the exit probabilities are $K \exp(-3.3N) \leq P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{a},\partial\mathbf{b}}) \leq \exp(-3.3N)$ and $8.3 \times 10^{-5} K \leq P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{b},\partial\mathbf{a}}) \leq 8.3 \times 10^{-5}$. In other words, given the structure of perturbations, we can determine the rate at which exit probabilities decay with N. This is opposed to the case of limit noise analysis where the quantity $\ln \mathbb{P}(x_{\mathbf{l}'}, \mathbf{l})$ tends to negative infinity.

III.B. Contagion probabilities

The dynamics of the process from $\partial\mathbf{l}' \to \mathbf{l}'$ is driven by contagion or equivalently, by best-response. We use this property to derive the lower bounds for the probabilities $P_{N,\boldsymbol{\varepsilon}}(g_{\partial\mathbf{l}',\mathbf{l}'})$. The characterization is based on the notion that once the chain enters the neighbourhood of a limit state, it acquires a quasi-stationary distribution over the state space of a basin of attraction. The quasi-stationary distribution attained places most weight on the corresponding limit state. The convergence rate within a basin of attraction is precisely the rate at which the chain attains its quasi-stationary distribution. The following example will help illustrate this concept.

$$P_{N,\boldsymbol{\varepsilon}} = \left(\begin{array}{ccc:cccc} 0.91 & 0.05 & 0.03 & 0.003 & 0.003 & 0.004 & 0. \\ 0.85 & 0.075 & 0.07 & 0.0005 & 0.001 & 0.003 & 0.0005 \\ 0.1 & 0.84 & 0.05 & 0.004 & 0.0006 & 0.0004 & 0.005 \\ \hdashline 0.0006 & 0.003 & 0.0004 & 0.015 & 0.93 & 0.044 & 0.007 \\ 0.0005 & 0.0015 & 0.003 & 0.005 & 0.03 & 0.07 & 0.89 \\ 0. & 0.0002 & 0.0003 & 0.001 & 0.0005 & 0.99 & 0.008 \\ 0.0001 & 0.0003 & 0.0006 & 0.009 & 0.04 & 0.9 & 0.05 \end{array}\right) \tag{8}$$

Consider the Markov chain with transition matrix in (8). The state space is $\mathbf{X} = \{\mathbf{a}, \mathbf{b}, \mathbf{c}, \mathbf{d}, \mathbf{e}, \mathbf{f}, \mathbf{g}\}$. It consists of two limit states $\mathbf{a}$ and $\mathbf{f}$ and the corresponding basins of attraction are $\tilde{\mathbf{a}} = \{\mathbf{a}, \mathbf{b}, \mathbf{c}\}$ and $\tilde{\mathbf{f}} = \{\mathbf{d}, \mathbf{e}, \mathbf{f}, \mathbf{g}\}$ respectively. The basins of attraction thus form *almost invariant* subsets. The dashed lines partition the transition matrix into transitions within the states of almost invariant subsets (the upper left and lower right blocks of the matrix) and transitions from one invariant subset to another (upper right and lower left blocks). Whenever the process is in either of these subsets, it attains a quasi-stationary distribution that we denote by $\pi_{N,\boldsymbol{\varepsilon}}(\tilde{a})$ and $\pi_{N,\boldsymbol{\varepsilon}}(\tilde{f})$ respectively.

For the transition matrix (8), the respective invariant distributions rounded to the fourth decimal place are:

$$\pi_{N,\boldsymbol{\varepsilon}} = (0.0450, 0.0045, 0.0021, 0.0012, 0.0022, 0.9351, 0.0995),$$

$$\pi_{N,\boldsymbol{\varepsilon}}(\tilde{\mathbf{a}}) = (0.8700, 0.0865, 0.0435) \quad \text{and}$$

$$\pi_{N,\boldsymbol{\varepsilon}}(\tilde{\mathbf{f}}) = (0.0016, 0.0025, 0.9852, 0.0107).$$

The process thus spends 93.5% of the time in state $\mathbf{f}$ in the long-run. When in the basin of attraction $\tilde{\mathbf{a}}$, it spend 87% of the time in state $\mathbf{a}$; when in $\tilde{\mathbf{f}}$ it spends 98.5% of the time in $\mathbf{f}$. To fully characterize the dynamics of the process within each basin of attraction, we make use of the convergence rates to the quasi-stationary distributions. Closely related to the convergence rates are the mixing times within these almost invariant subsets, the time it takes the process to attain its stationary (quasi-stationary) distribution. For each $D(\mathbf{l})$, we denote the mixing time by $M_{D(\mathbf{l})}$. For the process (8) above, the mixing time for the entire process is $M = 1600$ periods, $M_{\tilde{\mathbf{a}}} = 12$ periods and $M_{\tilde{\mathbf{f}}} = 16$ periods.

Seneta (1993) showed that the convergence rates for finite Markov chains are always exponential. That is, for a given $P_{N,\boldsymbol{\varepsilon}}$ and probability mass function at time t, $\mathbf{q}_t$, $\left|\left|P^t_{N,\boldsymbol{\varepsilon}}\mathbf{q}_0 - \pi_{N,\boldsymbol{\varepsilon}}\right|\right| = \mathcal{O}(\mathcal{R}^t)$, for some $\mathcal{R} < 1$. We can thus generally define the convergence rate to the quasi-stationary distribution $\pi_{N,\boldsymbol{\varepsilon}}(D(\mathbf{l}))$ as,

$$\mathcal{R}(D(\mathbf{l})) = \limsup_{t\to\infty} \left|\left|P^t_{N,\boldsymbol{\varepsilon}}\mathbf{q}_{D(\mathbf{l})} - \pi_{N,\boldsymbol{\varepsilon}}(D(\mathbf{l}))\right|\right|^{\frac{1}{t}} \tag{9}$$

where $\mathbf{q}_{D(\mathbf{l})}$ is the probability mass function that places most weight on some initial state of the chain in $D(\mathbf{l})$.

Contagion probabilities (for transitions $\partial\mathbf{l} \to \mathbf{l}$) are then proportional to $1 - \mathcal{R}(D(\mathbf{l}))$. This is based on the fact that since $\mathcal{R}(D(\mathbf{l})) < 1$, the closer $\mathcal{R}(D(\mathbf{l}))$ is to one the longer the process takes to converge to its quasi-stationary distribution. We can then write $P_{N,\boldsymbol{\varepsilon}}(g_{\partial\mathbf{l},\mathbf{l}}) = (1 - \mathcal{R}(D(\mathbf{l})))^{K_\mathbf{l}}$, where $K_\mathbf{l} > 0$ is some real number. Equivalently,

$$P_{N,\boldsymbol{\varepsilon}}(g_{\partial\mathbf{l},\mathbf{l}}) = \exp\left(K_\mathbf{l} \ln\left(1 - \mathcal{R}(D(\mathbf{l}))\right)\right) \tag{10}$$

The parameters $\mathcal{R}(D(\mathbf{l}))$ are equivalent to the second largest eigenvalues of the block matrices describing the transitions within the states of almost invariant subsets (see proof of Proposition 6 below). For the process (8) the respective values are $\mathcal{R}(\tilde{\mathbf{a}}) = 0.2002$ and $\mathcal{R}(\tilde{\mathbf{f}}) = 0.2851$. Hence $P_{N,\boldsymbol{\varepsilon}}(g_{\partial\mathbf{a},\mathbf{a}}) = \exp(-0.22K_\mathbf{l})$ and $P_{N,\boldsymbol{\varepsilon}}(g_{\partial\mathbf{f},\mathbf{f}}) = \exp(-0.34K_\mathbf{l})$.

In what follows, we derive and expression for $\mathcal{R}(D(\mathbf{l}))$ in terms of computable parameters rather than using its relation to the eigenspectrum of the entire transition matrix. Here, we provide bounds in terms of the eigenspectrum of the network of interactions. We begin with the following definitions.

Denote the normalized adjacency matrix associated with the network of interactions by $\mathscr{A}$ (we omit the index N for notational simplicity). Let also $\rho(\mathscr{A}) = (\lambda^N_1, \cdots, \lambda^N_N)$ be its eigenvalue spectrum ordered in such away that $\lambda^N_1 = 1 \geq \lambda^N_2 \geq \cdots \geq \lambda^N_N$. Denote by $\Sigma_{\boldsymbol{\varepsilon}}$ for a player's individual transition matrix given an opponent's actions. That is let $\mathbb{P}(x_j|x_i)$ be the probability that a given player plays action $x_j \in X$ given that his opponent is playing

$x_i \in X$ in the current period. Then $\Sigma_{\boldsymbol{\varepsilon}}$ is given by

$$\Sigma_{\boldsymbol{\varepsilon}} = \begin{pmatrix} \mathbb{P}(x_1|x_1) & \mathbb{P}(x_2|x_1) & \cdots & \mathbb{P}(x_m|x_1) \\ \mathbb{P}(x_1|x_2) & \mathbb{P}(x_2|x_2) & \cdots & \mathbb{P}(x_m|x_2) \\ \vdots & \vdots & \ddots & \vdots \\ \mathbb{P}(x_1|x_m) & \mathbb{P}(x_2|x_m) & \cdots & \mathbb{P}(x_m|x_m) \end{pmatrix} \tag{11}$$

Let also $\rho(\Sigma_{\boldsymbol{\varepsilon}}) = (\vartheta_1, \cdots, \vartheta_m)$ be the eigenvalue spectrum of $\Sigma_{\boldsymbol{\varepsilon}}$. The following Lemma provides bounds for convergence rates.

LEMMA 6. For a given network of interactions G_N, the convergence rate $\mathcal{R}(D(\mathbf{l}))$ within a basin of attraction has the following bounds

$$1 - \lambda_2^N(G) \leq 1 - \mathcal{R}(D(\mathbf{l})) \leq 1 - \vartheta_m \lambda_2^N(G)$$

where $\lambda_2^N(G)$ is the second largest eigenvalue of the normalized adjacency matrix of network G_N.

*Proof.*See Appendix VII.B. ■

The eigenvalues of $\Sigma_{\boldsymbol{\varepsilon}}$, ϑ_m are functions of the underlying payoff structure and the level of noise. As the noise level tends to zero, ϑ_m tend to one.The quantity $1 - \lambda_2^N(G)$ is also generally referred to as the *spectral gap* of G_N. A bound on λ_2^N can be established through its relationship with the graph conductance $\phi(G)$. We give examples for specific graphs below.

EXAMPLE: The following relation between second the eigenvalue of a network graph G_N, $\lambda_2^N(G)$ and $\phi(G)$ can be derived from Cheeger inequality: See Appendix VII.C. for more detail concerning the relation plus derivations for the following examples.

$$\lambda_2^N(G) \leq 1 - \frac{\phi(G)^2}{2}. \tag{12}$$

(i) Complete network (G_{com}): a network structure in which every vertex is connected to every other vertex: $\lambda_2^N(G_{com}) \leq \frac{7}{8}$.

(ii) $1 - D$ cyclic network (G_{cyc}): a network in which vertices are arranged in a circle and

every vertex is connected to two other neighboring vertices; $\lambda_2^N(G_{cyc}) \leq \frac{N^2-2}{N^2}$.

(iii) $2D$ $N \times N$ lattice network (G_{2D}): a lattice structure constructed with periodic neighbourhood conditions such that each agent is connected to 4 neighbors: $\lambda_2^N(G_{2D}) \leq \frac{16N^2-1}{16N^2}$.

(iv) Random d-regular network (G_{d-r}): a network structure in which each of the N vertices is connected to d other vertices chosen at random: $\lambda_2^N(G_{d-r}) \leq \frac{7}{8}$.

(v) Newman's small world network (G_{nsw}): a network structure in which the mean shortest-path between nodes increases sufficiently slowly (logarithmically) as a function of the number of nodes in the network: $\lambda_2^N(G_{nsw}) = 1 - \mathcal{O}\left(\frac{c}{(\ln N)^2}\right)$, where c is a constant.

*Proof.*See Appendix VII.C. ■

In general, densely connected and random networks have higher second largest eigenvalues compared to sparsely connected network. For sufficiently small noise, ϑ_m is close to one such that $1 - \mathcal{R}(D(\mathbf{l}))$ is approximately equal to $1 - \lambda_2^N(G)$. This enables us to focus on the influence of the network on long-run stability.

III.C. Combining exit and contagion probabilities

The above discussion regarding the bounds for exit and contagion probabilities together yields the following lemma that provides bounds for $P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\mathbf{l}'})$.

LEMMA 7. Suppose $(U^{m\times m}, \mathbf{X}_N, P_{N,\boldsymbol{\varepsilon}}, G_N)$ is a model of evolution with noise and let $\mathbf{l}$ and $\mathbf{l}'$ be any two limit states of $((U^{m\times m}, \mathbf{X}_N, P_N, G_N)$. Given the network of interactions G_N, let the second eigenvalue of its normalized adjacency matrix be $\lambda_2^N(G)$, where for some real number $0 \leq K_{\mathbf{l}} \leq 1$, $\gamma^N(\mathbf{l}) = K_{\mathbf{l}} \ln(1 - \lambda_2^N(G))$. Then

$$K \exp\left\{-N\left[c(\mathbf{l}, \partial\mathbf{l}') - \frac{1}{N}\gamma^N(\mathbf{l}')\right]\right\} \leq P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\mathbf{l}'}) \leq \exp\left\{-N\left[c(\mathbf{l}, \partial\mathbf{l}') - \frac{1}{N}\gamma^N(\mathbf{l}')\right]\right\} \tag{13}$$

Given (13), we can then restates the results in Lemma 4 as follows.

LEMMA 8. Given a process $P_{N,\boldsymbol{\varepsilon}}$, if probabilities associated with graphs $g_{\mathbf{l},\mathbf{l}'}$ are as in (13),

then for sufficiently small rates of mutations and for some $\alpha > 0$

$$\pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l}) = \exp\left\{-\left(\psi^N(\mathbf{l}) - \min_{\mathbf{l}'\in\mathbf{L}} \psi^N(\mathbf{l}') \pm \alpha\right)\right\} \tag{14}$$

where $\psi^N(\mathbf{l}) = \min_{g\in G(\{\mathbf{l}\})} \sum_{(\mathbf{l}_i,\mathbf{l}_j)\in g} \psi^N(\mathbf{l}_i,\mathbf{l}_j)$ and $\psi^N(\mathbf{l}_i,\mathbf{l}_j) = N\left[c(\mathbf{l}_i,\partial\mathbf{l}_j) - \frac{1}{N}\gamma^N(\mathbf{l}_j)\right]$.

From relation (14), the network and payoff structures, the model of mistakes and the population size influence the stationary distribution through the cost functions $\psi^N(.)$. The relevant variables for characterising the long-run behaviour of the process are these cost functions, and since we seek to establish the behaviour of $\pi_{N,\boldsymbol{\varepsilon}}(.)$ for large population sizes, it is sufficient to focus on the properties of $\lim_{N\to\infty}\psi^N(.)$. The relationship between the two concepts are as follows. For a given $\mathbf{l}\in\mathbf{L}$, the limit $\lim_{N\to\infty}\pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l}) = 0$ if and only if $\lim_{N\to\infty}\left\{\psi^N(\mathbf{l}) - \min_{\mathbf{l}'\in\mathbf{L}}\psi^N(\mathbf{l}')\right\} = \infty$, implying that $\mathbf{l}$ is not asymptotically globally stable; if on the other hand $\lim_{N\to\infty}\left\{\psi^N(\mathbf{l}) - \min_{\mathbf{l}'\in\mathbf{L}}\psi^N(\mathbf{l}')\right\} = 0$, then $\lim_{N\to\infty}\pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l}) > 0$, which implies that $\mathbf{l}$ is asymptotically globally stable. We build on this relations to derive the theorem below that establishes sufficient conditions for asymptotic global convergence.

THEOREM 9. Suppose $(U^{m\times m}, \mathbf{X}_N, P_{N,\boldsymbol{\varepsilon}}, G_N)$ is a model of evolution with noise as described above. Let $g_{\min}(\mathbf{l}) \in \arg\min_{g\in G(\{\mathbf{l}\})} \sum_{(\mathbf{l}_i,\mathbf{l}_j)\in g}\psi^N(\mathbf{l}_i,\mathbf{l}_j)$; that is, $g_{\min}(\mathbf{l})$ is the minimum cost $\mathbf{l}$-tree. A state $\mathbf{l}^*$ is asymptotically globally stable if

(i) $\lim_{N\to\infty}\frac{1}{N}\ln(1-\lambda_2^N(G)) = 0$,

(ii) and for all $(\mathbf{l}_i,\mathbf{l}_j)\in g_{\min}(\mathbf{l}^*)$, $\lim_{N\to\infty} r(\mathbf{l}_j,\partial\mathbf{l}_j) = 0$.

Proof.

See Appendix VII.D.

■

Theorem 9 provides sufficient conditions on the interaction structure and the underlying base game for which asymptotic global convergence is feasible. It states that the unique asymptotically globally stable state is that in which the costs of transitions in its $\mathbf{l}^*$-tree are decreasing functions of population size. Incidentally, such an $\mathbf{l}^*$-tree is also the overall minimum cost graph. The use of minimum cost graphs analysis in stochastic evolutionary models has been employed before in the characterisation of stochastic stability (e.g. Young (1993) and Kandori et al. (1993)). In relation to the literature, there are two aspects worth

emphasizing in our analysis. First, rather considering $\mathbf{x}$-tree for the entire state space, we start by deriving probabilities and hence costs of evolution between pairs of limit states. This makes it possible to then focus on graphs defined on state space of limit states. In doing so, the size of $\mathbf{x}$-trees for which one has to analyse their cost functions is dramatically reduced.

Secondly, most studies of stochastic stability in the literature has been done for cases in which mutation probabilities are homogeneous. Under such scenarios, the cost of transition between any pair of limit states say $\mathbf{l}$ and $\mathbf{l}'$, is equal to the quantity $R(\mathbf{l}, \partial\mathbf{l}')$ as defined above. Here, since we study cases in which the population size grows rather than vanishing noise levels, the cost of transitions is $R(\mathbf{l}, \partial\mathbf{l}') \ln(\mathbb{P}(x_{\mathbf{l}'}, \mathbf{l}))$. This then enables one to study the effect of variations of models of mistakes and captured by the structure of probabilities $\mathbb{P}(x_{\mathbf{l}'}, \mathbf{l})$.

Both of the conditions stated in Theorem 9 are concerned with the structure of network/payoff combination and are independent of the model of mistakes. This results from the fact that for an asymptotically globally stable state, the quantities $r(\mathbf{l}, \partial\mathbf{l}')$ dominate the probabilities of mistakes at $\ln(\mathbb{P}(x_{\mathbf{l}'}, \mathbf{l}))$ at large population sizes. The first sufficient condition for asymptotic global convergence is that the rate at which the spectral gap of the interaction network grows with N must be negligible at the limit of N. This condition is valid for most *strongly connected* network structures. By strongly connected we mean networks in which there exists a directed path from any one player to every other player. Consider the examples in subsection III.B. above. For the case of random d-regular network (G_{d-r}), where $\lambda_2^N(G_{d-r}) \leq \frac{7}{8}$ we have $\ln(1-\lambda_2^N(G_{d-r})) = \ln\left(\frac{1}{8}\right)$. Thus $\lim_{N\to\infty} \frac{1}{N} \ln(1-\lambda_2^N(G_{d-r})) = 0$. Similarly, for the $2D$ $N \times N$ lattice network (G_{2D}), where $\lambda_2^N(G_{2D}) \leq \frac{16N^2-1}{16N^2}$, we have $\ln(1-\lambda_2^N(G_{2D})) = \ln\left(\frac{1}{8N^2}\right)$. The limit $\lim_{N\to\infty} \frac{1}{N} \ln(1-\lambda_2^N(G_{2D})) = -\frac{2\ln N}{N}$. From L'Hôpital's rule it follows that $\lim_{N\to\infty} \frac{1}{N} \ln(1-\lambda_2^N(G_{2D})) = 0$.

Conditions (ii) of Theorem 9 is influenced by not only the network structure but also the payoffs. The network/payoff combination interactively determines whether the quantities $r(\mathbf{l}, \partial\mathbf{l}')$ are decreasing functions of N. In what follows, we introduce a concept of *contagion*, that is sufficient but not necessary for Conditions (ii) of Theorem 9 to hold. We start by defining pairwise-contagion and then generalising it to $\mathbf{l}$-trees. A strategy is contagious relative to another for a given payoff and network it can spread by best-response once it has been adopted by a small fraction of the population. If a strategy $x_{\mathbf{l}'}$ played by all or

a majority of players in $\mathbf{l}'$ is contagious relative to $x_{\mathbf{l}}$ played in $\mathbf{l}$, then $r(\mathbf{l}, \partial\mathbf{l}')$ will be a decreasing function of N, and vice versa. The intuition behind this argument is that to evolve from limit state $\mathbf{l}$ directly to another $\mathbf{l}'$ without passing through other limit states, the process first exits the basin of attraction of $\mathbf{l}$ into the neighbourhood $\partial\mathbf{l}'$, and then from $\partial\mathbf{l}'$ to $\mathbf{l}'$. Since the quantity $r(\mathbf{l}, \partial\mathbf{l}')$ corresponds to the fraction of players that should initially play $x_{\mathbf{l}'}$ to trigger contagion, if $x_{\mathbf{l}'}$ is contagious relative to $x_{\mathbf{l}}$ then such a fraction is a decreasing function of N.

A generalization of pair-wise contagion to $\mathbf{l}$-trees leads to two additional concepts: *global* and *path-wise contagion*. A strategy $x_{\mathbf{l}}$ is globally contagious if it is pair-wise contagious relative to every other strategy $x_{\mathbf{l}'}$ for all $\mathbf{l}' \neq \mathbf{l}$. It is path-wise contagious if for every $x_{\mathbf{l}'}$ there exists a path $x_{\mathbf{l}'} \to x_{\mathbf{l}+\mathbf{1}'} \to \cdots \to x_{\mathbf{l}+\mathbf{i}'} \to \cdots \to x_{\mathbf{l}}$ from $x_{\mathbf{l}'}$ to $x_{\mathbf{l}}$ along which $x_{\mathbf{l}+\mathbf{i}+\mathbf{1}'}$ is pair-wise contagious relative to $x_{\mathbf{l}+\mathbf{i}'}$. We develop each of these concepts more formally in the following sections.

IV. Global contagion

We start the discussion of global contagion with a formal definition of pair-wise contagion.

Definition 10. Let $|\mathbf{x}|_a$ denote the number of players playing strategy a in state $\mathbf{x}$. For the transition $\mathbf{l} \to \mathbf{l}'$, $x_{\mathbf{l}'}$ is said to be contagious relative to $x_{\mathbf{l}}$ if $x_{\mathbf{l}'}$ spreads by best-response whenever $|\mathbf{x}|_{x_{\mathbf{l}'}} > R(\mathbf{l}, \partial\mathbf{l}')$. The strategy $x_{\mathbf{l}'}$ is globally contagious if it is contagious for all transitions $\mathbf{l} \to \mathbf{l}'$ for all $\mathbf{l} \neq \mathbf{l}'$.

That is, a strategy $x_{\mathbf{l}'}$ is contagious if it spreads by best-response once at least $R(\mathbf{l}, \partial\mathbf{l}')$ of the players have adopted it. The feasibility of global contagion depends on the properties of the interaction network and the payoff structure: That is *contagion threshold* and *relative payoff gains* respectively.

The relative payoff gain denoted by η_{ab}, for any pair of strategies a and b is defined by[6]

$$\eta_{ba} = \frac{U(b,b) - U(a,b)}{U(b,b) - U(b,a) + U(a,a) - U(a,b)} \tag{15}$$

6. Relation (15) follows from the condition for best-response; that is, given strategies a and b, if p is the fraction of i's neighbours playing strategy b and $1-p$ play strategy a, then i will switch to b if $pU(b,b) + (1-p)U(b,a) > pU(a,b) + (1-p)U(a,a)$. Rearranging for p yields $p > \frac{U(a,a)-U(a,a)}{U(b,b)-U(b,a)+U(a,a)-U(a,b)}$; hence the right hand side is the fraction of i's neighbours that must switch to b for i to do likewise.

and $\eta_{ab} = 1 - \eta_{ba}$. The quantities $U(b,b) - U(a,b)$ and $U(a,a) - U(a,b)$ are the private and social payoff gains of switching from b to a respectively. The measure of relative payoff gain η_{ba}, can also be interpreted as the fraction of neighbours that each player requires to play a for that player to switch from b to a through best-response, and vice versa for η_{ab}. We write $\lceil m \rceil$ for the smallest integer not less than m such that for each $i \in \mathcal{N}$ with respective degree k_i, the quantity $\lceil \eta_{ba} k_i \rceil$ is the minimum number of neighbours i requires to play a for i to do likewise.

For every network G_N there exists a real number $0 < \eta_G < 1$ such that for any pair of strategies say a and b, strategy a is contagious relative to b whenever $\eta_{ba} \leq \eta_G$. We then say that a strategy a is *globally contagious* under s network G_N whenever $\eta_{ba} \leq \eta_G$ for all $b \neq a$. Or equivalently, whenever $\eta_{\max,a} \leq \eta_G$, where $\eta_{\max,a} = \max_{b \neq a} \eta_{ba}$. This real number η_G is the *contagion threshold* of network G_N (Morris, 2000).

Every arbitrary network has a unique contagion threshold. Consider for example a cyclic network structure in which each player i has two neighbours $i-1$ and $i+1$. Such a network structure has the contagion threshold of $\frac{1}{2}$. Implying that for any underlying base game containing a unique strategy say a with maximum relative payoff gain $\eta_{\max,a} < \frac{1}{2}$ (that is a risk-dominant strategy), such a strategy is globally contagious under a cyclic network structure. Morris (2000) provides an explicit characterization of contagion threshold for various families of deterministic networks. Lelarge (2012) derives similar conditions for random networks.

The following example illustrate the selection of globally contagious strategies for given a network.

Example 11. For the 3×3 game of Table I, strategy b is globally contagious and hence asymptotically globally stable for all networks with contagion threshold $\eta_G \geq \frac{1}{3}$. This is true irrespective of the model of mistakes.

Proof.

The proof follows by first determining the relative payoff gains for each pair of strategies, which respectively are: $\eta_{ab} = \frac{1}{8}$. $\eta_{ba} = \frac{7}{8}$, $\eta_{bc} = \frac{2}{3}$, $\eta_{cb} = \frac{1}{3}$, $\eta_{ac} = \frac{5}{8}$, $\eta_{ca} = \frac{5}{6}$. Consequently, $\eta_{\max,a} = \frac{7}{8}$, $\eta_{\max,b} = \frac{1}{3}$ and $\eta_{\max,c} = \frac{2}{3}$. Implying that strategy b is globally contagious for all networks with contagion threshold $\eta_G \geq \frac{1}{3}$. Strategy b is thus uniquely asymptotically globally stable for all network with contagion threshold $\eta_G \geq \frac{1}{3}$.

TABLE I: For any pair of players the profile (b, b) is risk-dominant.

	a	b	c
a	6 , 6	0 , 5	0 , 0
b	5 , 0	7 , 7	6 , 3
c	0 , 0	3 , 6	8 , 8

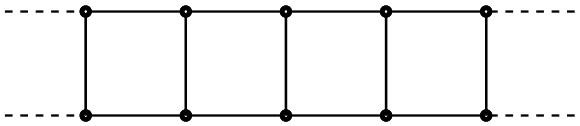

Figure I: The 2-dimensional network with contagion threshold of $\frac{1}{3}$.

■

Example 11 demonstrates the selection of globally contagious strategies and more specifically that there exists a range of families of networks for which global contagion and hence asymptotic global convergence is feasible. In this example, global contagion is feasible in all networks whose contagion threshold is $\frac{1}{3} \leq \eta_G \leq \frac{1}{2}$. The network in Figure I for example has a contagion threshold of $\frac{1}{3}$; and together with thes payoff structure in Table I imply that, $r(\mathbf{a}, \partial\mathbf{b}) = r(\mathbf{c}, \partial\mathbf{b}) = \frac{1}{N}$.

Now, consider the n-dimensions l-max distance interactions family of networks, which is an n-dimensional lattice network where each player interacts with all players who are within the distance of l steps away in all directions. See Figure II for the case of $n = 2$ and $l = 1$. Morris (2000) provides general expressions for contagion thresholds for this family of networks. For example when $n = 2$ the contagion thresholds are given by $\eta_G = \frac{l(2l+1)}{(2l+1)^2-1}$ for $l = 1, 2, 3, \cdots$. When $l = 1$, $\eta_G = \frac{3}{8}$. For this family of networks, the contagion threshold is $\eta_G \geq \frac{1}{3}$, implying global contagion of strategy b.

We conclude this section by noting that the definition of global contagion above is related to the notion of *p-dominance* according to Morris et al. (1995). An action pair in a two-player game is said to be p-dominant if each action is a best response to any belief that the other player takes the action in this pair with probability at least p. For the local interaction game we consider, a strategy is p-dominant if for all players, it is the unique best-response when

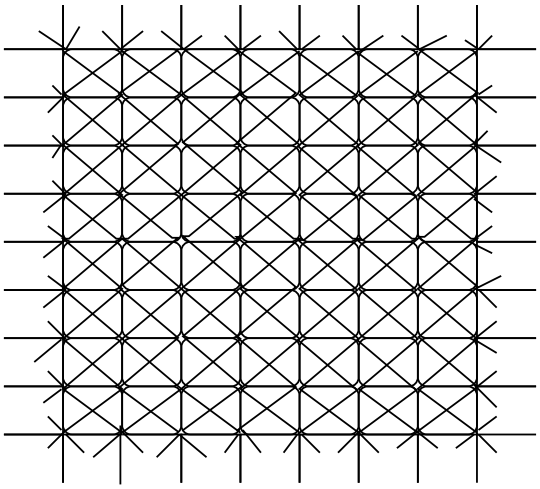

FIGURE II: THE 2-DIMENSIONS 1-MAX DISTANCE INTERACTIONS.

it is played by at least proportion p of the neighbors. This implies that for a network with contagion threshold p, a strategy that is p-dominant is also globally contagious.

V. PATH-WISE CONTAGION

As discussed above, path-wise contagion means pair-wise contagion along paths of $\mathbf{l}$-trees. The formal definition is as follows.

DEFINITION 12. Given a state space of limit states $\mathbf{L} = \{\mathbf{l}_1, \cdots, \mathbf{l}_j, \cdots, \mathbf{l}_J\}$, if $g_{\min}(\mathbf{l}_J) = \{\mathbf{l}_1 \to \cdots \to \mathbf{l}_j \to \cdots \to \mathbf{l}_J\}$ is the minimum cost $\mathbf{l}_J$-tree, then $x_{\mathbf{l}_J}$ is path-wise contagious if for each pair $(\mathbf{l}_j, \mathbf{l}_{j+1})$ along $g_{\min}(\mathbf{l}_J)$, $x_{\mathbf{l}_{j+1}}$ is pair-wise contagious relative to $x_{\mathbf{l}_j}$.

We provide three examples to illustrate application of the concept of path-wise contagion. The first example demonstrates selection of globally pair-wise risk-dominant strategies, the second example shows that it is feasible to appropriately design a network for a given payoff structure, to ensure that asymptotic global convergence occurs in a case where the process would otherwise exhibit cycles. The third example illustrate a case in which no strategy is uniquely path-wise contagious.

EXAMPLE 13. For the 3×3 game of Table II, strategy c is path-wise contagious and hence asymptotically globally stable for all network structures.

Proof.

TABLE II: For any pair of players the profile (c, c) is risk-dominant.

	a	b	c
a	6 , 6	0 , 5	0 , 0
b	5 , 0	7 , 7	5 , 5
c	0 , 0	5 , 5	8 , 8

The relative payoff gains for each pair of strategies are $\eta_{ab} = \frac{1}{8}$. $\eta_{ba} = \frac{7}{8}$, $\eta_{bc} = \frac{2}{5}$, $\eta_{cb} = \frac{3}{5}$, $\eta_{ac} = \frac{5}{8}$, $\eta_{ca} = \frac{5}{6}$. It follows that $\eta_{\max,a} = \frac{7}{8}$, $\eta_{\max,b} = \frac{3}{5}$ and $\eta_{\max,c} = \frac{5}{8}$. Since the maximum possible contagion threshold for any network structure is $\frac{1}{2}$, it follows that no single strategy is globally contagious for all network structures.

First consider the case of network structures with contagion threshold of $\eta_G \geq \frac{2}{5}$. For such networks b is pair-wise contagious relative to a and c is pair-wise contagious relative to b and not vice versa. The minimum cost graph is $g_{\min}(\mathbf{c}) = \{\mathbf{a} \to \mathbf{b} \to \mathbf{c}\}$. This implies that strategy c is path-wise contagious and hence $\mathbf{c}$ is the asymptotically globally stable state in such network families.

Now, consider the case of network structures with contagion threshold of $\eta_G \geq \frac{1}{8}$. For such networks b is contagious relative to a but c is no longer contagious relative b since $\eta_{bc} > \eta_G$. There however exist a series of intermediate limit states between $\mathbf{b}$ and $\mathbf{c}$ induced by the network structure. These states can be ordered in such a way that they are contagious relative to each other. The minimum cost graph is then $g_{\min}(\mathbf{c}) = \{\mathbf{b} \to \cdots \to \mathbf{l}_j \cdots \to \cdots \to \mathbf{c}\}$, where $\mathbf{l}_j$'s are the intermediate limit states. Consider the 2-dimensions nearest neighbor interactions network of Figure III for example. In this network structure, the intermediate states involve two players in each enclave of four simultaneously switching from playing b to playing c. More explicitly, if we consider the diagonal enclaves, then for an N size network we have $\sqrt{N}$ of such limit states, each with $r(\mathbf{l}_j, \partial\mathbf{l}_{j+1}) = \frac{2}{N}$; together with $r(\mathbf{a}, \partial\mathbf{b}) = \frac{1}{N}$ implies that along $g_{\min}(\mathbf{c})$, $\lim_{N\to\infty} r(.) = 0$ and hence $\mathbf{c}$ is asymptotically globally stable.

For the case of networks with $0 < \eta_G \leq \frac{1}{8}$, the similar argument of intermediate limit states that applies between $\mathbf{b}$ and $\mathbf{c}$ will apply between $\mathbf{a}$ and $\mathbf{b}$. Making $\mathbf{c}$ the asymptotically stable state in this family of networks as well.

■

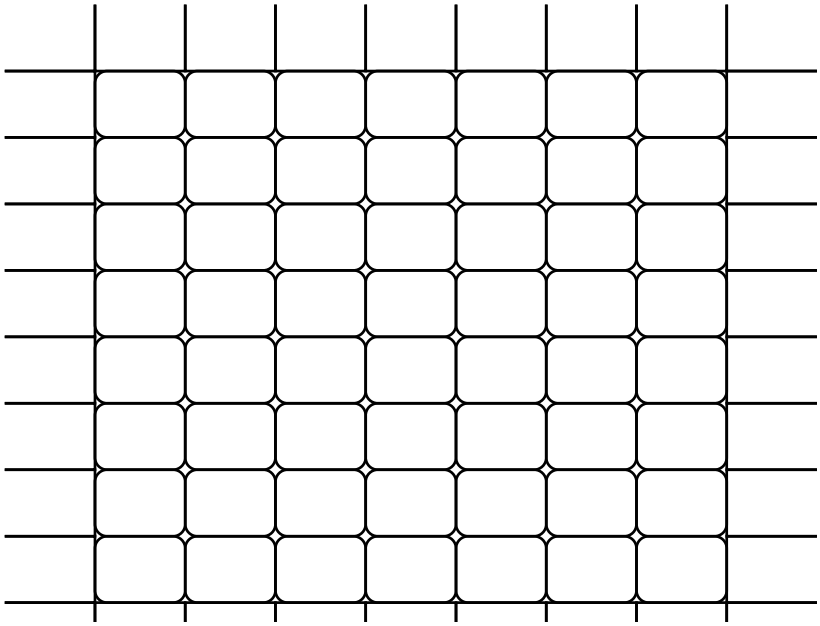

FIGURE III: THE 2-DIMENSIONS NEAREST NEIGHBOR INTERACTIONS NETWORK.

Example 13 acts to illustrate one of the main implications of Theorem 9 that if the underlying base game contains a globally pair-wise risk-dominant strategy, then it is always selected independently of the model of mistakes and network structure. This result generalizes earlier results by Lee and Valentinyi (2000) and Lee et al. (2003) to $m \times m$ matrix games, models of mistakes and to arbitrary networks. The result is contrary to the case of global interactions that crucially depends on the model of mistakes. For example Young (1993) showed that for the game in Table II the stochastically stable strategy is b under global interaction and mistakes model. Under multinomial logit model however, strategy c is stochastically stable. The main reason for the difference is that under global interactions, what matters for stochastic stability is simply the number of other players that must switch to a different strategy for any given player to do likewise. For example, in the game of Table II for any given player to switch from c to b, at least $\frac{3}{8}$ of the other players must play a. Since every player observes every other player's strategy, this process needs to occur only once. Under local interaction however, even if $\frac{3}{8}$ of any players neighbors switched to playing a, only that one player would switch to playing b and every other player keeps playing c. Moreover, over time the process can easily revert back to an all c state. In other words, what matters is whether or not the mistakes that occur can cause some form of relative contagion.

EXAMPLE 14. For the 3×3 game of Table III, strategy b is path-wise contagious and hence

asymptotically globally stable for network structures with $\eta_G = \frac{1}{3}$, such as that in Figure I.

TABLE III: In this game, no strategy is uniquely risk-dominant. Strategy a risk-dominates b, b risk-dominates c and c risk-dominates a

	a	b	c
a	5 , 5	3 , 1	0 , 3
b	1 , 3	6 , 6	2 , 2
c	3 , 0	2 , 2	4 , 4

Proof.

The relative payoff gains for each pair of strategies are $\eta_{ab} = \frac{4}{7}$, $\eta_{ba} = \frac{3}{7}$, $\eta_{bc} = \frac{2}{3}$, $\eta_{cb} = \frac{1}{3}$, $\eta_{ac} = \frac{1}{3}$, $\eta_{ca} = \frac{2}{3}$. It follows that $\eta_{\max,a} = \frac{2}{3}$, $\eta_{\max,b} = \frac{4}{7}$ and $\eta_{\max,c} = \frac{2}{3}$. Implying that no single strategy is globally stable for all network structures. For a network with contagion threshold $\eta_G = \frac{1}{3}$ however, c is contagious relative to a and b is contagious relative to c, and $g_{\min}(\mathbf{b}) = \{\mathbf{a} \to \mathbf{c} \to \mathbf{b}\}$ is the minimum cost graph; Hence, strategy b is asymptotically globally stable for this family of networks. It is then easy to check that for all networks with $\eta_G > \frac{1}{3}$, all strategies are contagious relative to each other, implying that the process indefinitely cycles around limit states, and hence global convergence does not occur. Similarly, for $\eta_G < \frac{1}{3}$ the network structure induces intermediate limit states between **a** and **c**, **c** and **b**, and **b** and **a**, equally leading to a cycle among limit states.

■

Example 14 acts to illustrate another main implications of Theorem 9, which is that for any given underlying game, it is possible to construct a network structure for which at least one strategy is globally stable provided that the relative payoff gains are not equivalent for all strategies. For example, for the game in Table III, strategy b is asymptotically globally stable under the network structure in Figure I, but for any network structure with contagion threshold $\eta_G > \frac{1}{3}$ or $\eta_G < \frac{1}{3}$, all the three strategies are almost equally likely in the long-run. This finding has quite strong implications even more so when viewed vice versa. That is, for a given network structure and set of strategies, it is possible to construct a payoff matrix hence relative payoff gains for which a given strategy gets globally adopted in the long-run.

Moreover, the result is independent of the model of mistakes.

The next example demonstrates that asymptotic global stability as defined in this paper is robust to addition of strictly dominated strategies. Kim and Wong (2010) first pointed out that addition of strictly dominated strategies may destabilise stochastically stable states. Global and path-wise contagion (hence asymptotic global stability) are however robust to this phenomenon. Addition of strictly dominated strategies does not make a strategy that was originally globally or path-wise contagious non-contagious. Similarly, addition of strictly dominated strategies does not make strategies that are not contagious contagious.

Consider the game in Table IV for example. The relative payoff gains are $\eta_{ab} = \frac{6}{13}$, $\eta_{ba} = \frac{7}{13}$, and hence under global interactions, $r(\mathbf{a}, \partial\mathbf{b}) = \frac{6}{13}$ and $r(\mathbf{b}, \partial\mathbf{a}) = \frac{7}{13}$. It can then easily be checked that $\mathbf{b}$ is stochastically stable under both the mistakes model with state independent mutations and the multinomial logit model. Similarly, since b is risk-dominant it is asymptotically globally stable for all network structures.

TABLE IV: Profile (b, b) is risk-dominant.

	a	b
a	8, 8	5, 5
b	5, 5	8.5, 8.5

Now, consider the game in Table V derived from the game in Table IV by addition of a strictly dominated strategy c. Under global interactions, $r(\mathbf{a}, \partial\mathbf{b}) = \frac{6}{13}$ and $r(\mathbf{b}, \partial\mathbf{a}) = \frac{1}{3}$, which means that $\mathbf{a}$ becomes stochastically stable. Under asymptotic global stability however, addition of a strictly dominated strategy does not affect the relative payoff gains and hence the values of $r(\mathbf{a}, \partial\mathbf{b})$ and $r(\mathbf{b}, \partial\mathbf{a})$ for any given network structure.

TABLE V: Game in Table IV with addition of strictly dominated strategy c.

	a	b	c
a	8, 8	5, 5	7 , 7
b	5 , 5	8.5, 8.5	0 , 6
c	7 , 7	6 , 0	0 , 0

Finally, the following examples act to illustrate the case in which no strategy is uniquely path-wise contagious, and hence there is more than one asymptotically globally stable.

TABLE VI: Strategy a is globally pairwise risk-dominant and $0 < \epsilon < \frac{1}{5}$.

	a	b	c
a	0	2	2
b	$-2+2\epsilon$	$3+2\epsilon$	4
c	-4	3	$5-2\epsilon$

Consider first the game in Table VI. The respective relative payoff gains are $\eta_{ab} = \frac{2(1-\epsilon)}{3}$, $\eta_{ba} = \frac{1+2\epsilon}{3}$, $\eta_{bc} = 2\epsilon$, $\eta_{cb} = 1-2\epsilon$, $\eta_{ac} = \frac{2(1+\epsilon)}{3}$, $\eta_{ca} = \frac{1}{2-\epsilon}$. Clearly, no strategy is uniquely globally contagious nor uniquely path-wise contagious even for networks with contagion threshold of $\frac{1}{2}$. For networks with contagion threshold of $\frac{1}{2}$, the only paths along which contagious occurs are: $\{\mathbf{b} \to \mathbf{a}\}$ and $\{\mathbf{b} \to \mathbf{c}\}$. Implying that the asymptotically stable states are **a** and **c** in such networks.

VI. Concluding remarks

This paper develops methods for stochastic evolutionary equilibrium selection in networks. We defined asymptotic global stability as an appropriate solution concept. We then defined two concepts that are compatible with asymptotic global stability: global and path-wise contagion. Strategies that are uniquely globally or path-wise contagious are also uniquely asymptotically globally stable. These two concepts are used to analyze how the network and payoff structures interactively influence asymptotic global convergence hence stability. We show that under local interactions, asymptotic global convergence is robust to the model of mistakes and addition of strictly dominated strategies. But perhaps most importantly, we show that for a given payoff structure and hence relative payoff gains, it is possible to design a network such that a unique strategy is asymptotically globally stable. Similarly, for a given network structure and set of strategies, one can determine the relative payoff gains that lead to a given strategy to be globally stable. The results we find have both practical and empirical implications that have been briefly discussed in the introduction.

VII. Appendix

VII.A. Proof of Lemma 5

For each pair $(\mathbf{l}, \mathbf{l}')$ of limit states, $P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\partial\mathbf{l}'})$ is by definition given by

$$P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\partial\mathbf{l}'}) = \prod_{(\mathbf{x},\mathbf{y})\in g_{\mathbf{l},\partial\mathbf{l}'}} P_{N,\boldsymbol{\varepsilon}}(\mathbf{x},\mathbf{y}) \tag{VII..1}$$

Notice that the right hand side (RHS) of (VII..1) can be expressed in terms of arithmetic mean. To see how, consider a vector $p = (p_1, \cdots, p_N)$ of real numbers, let $\mathbb{A}_m(p)$ and $\Pi_m(p)$ denote its arithmetic and geometric means respectively; defined formally as $\mathbb{A}_m(p) = \frac{1}{N}\sum_{i=1}^{N} p_i$ and $\Pi_m(p) = \left(\prod_{i=1}^{N} p_i\right)^{\frac{1}{N}}$. The difference $\mathbb{A}_m(p) - \Pi_m(p)$ between the two means has the following weak bounds: $0 \leq \mathbb{A}_m(p) - \Pi_m(p) \leq (p_{\max} - p_{\min})$, where $p_{\min}$ and $p_{\max}$ are the minimum and maximum entries of p (see for example Tung (1975) for a detailed discussion of such bounds). We can thus first rewrite the RHS of (VII..1) as $\left(\Pi_m(g_{\mathbf{l},\partial\mathbf{l}'})\right)^N$ where $\Pi_m(g_{\mathbf{l},\partial\mathbf{l}'})$ is the geometric mean of a vector of probabilities of transition in $g_{\mathbf{l},\partial\mathbf{l}'}$. From the above inequality for the difference between the two means, we then have that

$$K\exp\left\{|g_{\mathbf{l},\partial\mathbf{l}'}|\ln\left(\mathbb{A}_m(g_{\mathbf{l},\partial\mathbf{l}'})\right)\right\} \leq P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\partial\mathbf{l}'}) \leq \exp\left\{|g_{\mathbf{l},\partial\mathbf{l}'}|\ln\left(\mathbb{A}_m(g_{\mathbf{l},\partial\mathbf{l}'})\right)\right\} \tag{VII..2}$$

where $|g_{\mathbf{l},\partial\mathbf{l}'}|$ is the cardinality of $g_{\mathbf{l},\partial\mathbf{l}'}$, $\mathbb{A}_m(g_{\mathbf{l},\partial\mathbf{l}'})$ is arithmetic average of the probabilities of transitions in $g_{\mathbf{l},\partial\mathbf{l}'}$ and $K > 0$ is some real number. The quantity $|g_{\mathbf{l},\partial\mathbf{l}'}|$ is the number of mistakes required to exit the basin of attraction $D(\mathbf{l})$ starting from $\mathbf{l}$ into the basin of attraction $D(\mathbf{l}')$. Equivalently, it is the number of players required to play action $x_{\mathbf{l}'}$ by mistake either simultaneously or consecutively for evolution from $\mathbf{l} \to \partial\mathbf{l}'$ to occur.

For sufficiently small probabilities of mistakes, that is small rates of mutations, and since each transition in $g_{\mathbf{l},\partial\mathbf{l}'}$ involves a mutation, the probabilities of such transitions within a given basin of attraction, say $D(\mathbf{l})$, are approximately equal to the probabilities of transitions from $\mathbf{l}$ to it's immediate successive state $\mathbf{x}$; that is, t$\mathbf{x}$ is a state in which the transition $\mathbf{l} \to \mathbf{x}$ involves one mutation. The probabilities of transitions in $g_{\mathbf{l},\partial\mathbf{l}'}$ can thus be approximated by $\mathbb{P}_i(x_{\mathbf{l}'}, \mathbf{l})$, that is the probability that a given agent plays action $x_{\mathbf{l}'}$ given that the process is in state $\mathbf{l}$. Finally, since $\mathbb{P}_i(x_{\mathbf{l}'}, \mathbf{l})$ is by assumption independent of i's position in the network (see model definition above), then $\mathbb{P}_i(x_{\mathbf{l}'}, \mathbf{l}) = \mathbb{P}(x_{\mathbf{l}'}, \mathbf{l})$ for all i and hence $\mathbb{A}_m(g_{\mathbf{l},\partial\mathbf{l}'}) = \mathbb{P}(x_{\mathbf{l}'}, \mathbf{l})$.

Inequality (VII..2) then becomes.

$$K \exp\left\{|g_{\mathbf{l},\partial\mathbf{l}'}| \ln\left(\mathbb{P}(x_{\mathbf{l}'}, \mathbf{l})\right)\right\} \leq P_{N,\boldsymbol{\varepsilon}}(g_{\mathbf{l},\partial\mathbf{l}'}) \leq \exp\left\{|g_{\mathbf{l},\partial\mathbf{l}'}| \ln\left(\mathbb{P}(x_{\mathbf{l}'}, \mathbf{l})\right)\right\} \tag{VII..3}$$

VII.B. Proof of Lemma 6

We begin by proving the following lemma.

LEMMA 15. Let L be the number of closed communication classes and μ_j the jth eigenvalue of $P_{N,\boldsymbol{\varepsilon}}$. Then the contagion rate within any basin of attraction $\mathbf{l}_l$ has the following lower and upper bounds

$$1 - \mu_{L+1} \leq \mathcal{R}(\partial\mathbf{l}_l, \mathbf{l}_l) \leq 1 - \mu_{L+L}$$

*Proof.*The proof makes use of the spectral properties and near-complete decomposability of transition matrix $P_{N,\boldsymbol{\varepsilon}}$. Under chain $(\mathbf{X}_N, P_N, G_N)$, the transition matrix is completely decomposable into the form

$$P_N = \begin{pmatrix} M_1^* & & & & \\ & \ddots & & & \\ & & M_l^* & & \\ & & & \ddots & \\ & & & & M_L^* \end{pmatrix}$$

where M_l^* for $l = 1, \cdots, L$ is a block matrix describing the transitions within each basin of attraction under $(\mathbf{X}_N, P_N, G_N)$. The rest of the undisplayed elements are zeros and L is the number of closed communication classes. All leading eigenvalues of the block matrices are ones. The transition matrix $P_{N,\boldsymbol{\varepsilon}}$ on the other hand is near-completely decomposable into L "loosely" connected block matrices that we denote by M_l for $l = 1, \cdots, L$. $P_{N,\boldsymbol{\varepsilon}} = P_N + \epsilon P_N^*$, where ϵ is a small real number and P_N^* is an arbitrary $\#\mathbf{X}_N$ by $\#\mathbf{X}_N$ matrix. A more detailed exposition on the notion of near-complete decomposability can be found in Simon and Ando (1961). For ϵ small enough, the leading eigenvalues of the diagonal block matrices of $P_{N,\boldsymbol{\varepsilon}}$ are close to one.

Let μ_{i_l} denote the ith eigenvalue of the lth diagonal block matrix, such that $(\mu_{1_1}, \mu_{1_2}, \cdots, \mu_{1_L})$ are the largest eigenvalues in blocks 1 to L, and $(\mu_{2_1}, \mu_{2_2}, \cdots, \mu_{2_L})$ are the respective second largest eigenvalues. Index by n_l as the number of columns in diagonal block l such that the

eigenvalue spectrum $\rho(P_{N,\boldsymbol{\varepsilon}})$ of $P_{N,\boldsymbol{\varepsilon}}$ can be written as

$$\rho(P_{N,\boldsymbol{\varepsilon}}) = \left(\mu_{1_1}, \mu_{2_1}, \cdots, \mu_{n_{1_1}}, \cdots, \mu_{1_2}, \cdots, \mu_{1_l}, \cdots, \mu_{n_{l_l}}, \cdots, \mu_{1_L}, \cdots, \mu_{n_{L_L}}\right).$$

The spectral decomposition of $(\mathbf{X}_N, P_{N,\boldsymbol{\varepsilon}}, G_N)$ is then given by

$$\begin{aligned}\mathbf{q}_0 P_{N,\boldsymbol{\varepsilon}}^t = \mathbf{q}_0 \mathbf{r}_{1_1} \mathbf{z}_{1_1}^T + \sum_{j=2}^{n_1} \mu_{j_1}^t \mathbf{q}_0 \mathbf{r}_{j_1} \mathbf{z}_{j_1}^T + \mu_{1_2}^t \mathbf{q}_0 \mathbf{r}_{1_2} \mathbf{z}_{1_2}^T + \sum_{j=2}^{n_2} \mu_{j_2}^t \mathbf{q}_0 \mathbf{r}_{j_2} \mathbf{z}_{j_2}^T \\ + \cdots + \mu_{1_L}^t \mathbf{q}_0 \mathbf{r}_{1_L} \mathbf{z}_{1_L}^T + \sum_{j=2}^{n_L} \mu_{j_L}^t \mathbf{q}_0 \mathbf{r}_{j_L} \mathbf{z}_{j_L}^T \end{aligned} \tag{VII..4}$$

where $\mathbf{z}^T$ is the transpose of $\mathbf{z}$, and $\mathbf{r}_{j_l}$ and $\mathbf{z}_{j_l}$ are the right and left eigenvectors of μ_{j_l}.

Let $\mathbf{x}_l$ be the initial state of $(\mathbf{X}_N, P_{N,\boldsymbol{\varepsilon}}, G_N)$ in $\tilde{\mathbf{l}}_l$ and $\mathbf{q}_{\tilde{\mathbf{l}}_l}$ be the $\#\mathbf{X}_N$-dimensional vector of zeros except a one at the point corresponding to the state $\mathbf{x}_l$.

$$\begin{aligned}\mathbf{q}_t &= \mu_{1_l}^t \mathbf{q}_{\tilde{\mathbf{l}}_l} \mathbf{r}_{1_l} \mathbf{z}_{1_l}^T + \sum_{j=2}^{n_l} \mu_{j_l}^t \mathbf{q}_{\tilde{\mathbf{l}}_l} \mathbf{r}_{j_l} \mathbf{z}_{j_l}^T \\ \pi_{N,\boldsymbol{\varepsilon}}(\tilde{\mathbf{l}}_l) &= \lim_{t\to\infty} \mathbf{q}_t = \mu_{1_l}^\infty \mathbf{q}_{\tilde{\mathbf{l}}_l} \mathbf{r}_{1_l} \mathbf{z}_{1_l}^T \approx \mathbf{q}_{\tilde{\mathbf{l}}_l} \mathbf{r}_{1_l} \mathbf{z}_{1_l}^T \end{aligned}$$

where the approximation holds from the fact that μ_{1_l} is close to one for all l. It then follows that

$$\limsup_{t\to\infty} \left|\left| P_{N,\boldsymbol{\varepsilon}}^t \mathbf{q}_{\tilde{\mathbf{l}}_l} - \pi_{N,\boldsymbol{\varepsilon}}(\tilde{\mathbf{l}}_l) \right|\right|^{\frac{1}{t}} = |\mu_{2_l}| \limsup_{t\to\infty} \left|\left| \mathbf{q}_{\tilde{\mathbf{l}}_l} \mathbf{r}_{2_l} \mathbf{z}_{2_l}^T + \sum_{j=3}^{n_l} \left(\frac{\mu_{j_l}}{\mu_{2_l}}\right)^t \mathbf{q}_{\tilde{\mathbf{l}}_l} \mathbf{r}_{j_l} \mathbf{z}_{j_l}^T \right|\right|^{\frac{1}{t}} = |\mu_{2_l}|$$

Implying that $\mathcal{R}(\partial \mathbf{l}_l, \mathbf{l}_l) = |\mu_{2_l}|$ Since μ_j's are arranged in ascending order we then have that $\max_l \mu_{2_l} = |\mu_{L+1}|$ and $\min_l \mu_{2_l} = |\mu_{L+L}|$. For any $\mathbf{l}_l$,

$$1 - \mu_{L+1} \leq \mathcal{R}(\partial \mathbf{l}_l, \mathbf{l}_l) \leq 1 - \mu_{L+L}$$

■

To prove the second part of the theorem, we consider the linearization of $P_{N,\boldsymbol{\varepsilon}}$ of the form

$$\mathbf{q}_t \Psi = \mathbf{q}_0 P_{N,\boldsymbol{\varepsilon}}^t \Psi = \mathbf{q}_0 \Psi \Pi_{N,\boldsymbol{\varepsilon}}^t \tag{VII..5}$$

where Ψ is the event matrix derived by stacking into rows all possible realizations of states of $(\mathbf{X}_N, P_{N,\varepsilon}, G_N)$ written in the *basis vector* form. The choice basis vector for each player $i \in N$ is a vector of zeros except a one in a position corresponding to the action i is playing. For example for a binary action set $X = \{A, B\}$, a vector $(1, 0)$ implies that i is playing action A and $(0, 1)$ implies that i is playing action B. In the case of two players and binary action set, there are four possible realization such that

$$\Psi = \begin{pmatrix} 1 & 0 & 1 & 0 \\ 1 & 0 & 0 & 1 \\ 0 & 1 & 1 & 0 \\ 0 & 1 & 0 & 1 \end{pmatrix} \tag{VII..6}$$

where the first row corresponds to the state in which both players play action A, and so forth. Then $\Pi_{N,\varepsilon}$ is an $Nm \times Nm$ matrix defined by $\Pi_{N,\varepsilon} = \mathscr{A}^T \otimes \Sigma_{N,\varepsilon}$, where $\otimes$ is a Kronecker product, $\mathscr{A}^T$ is the transpose of the normalized adjacency matrix $\mathscr{A}$ and $\Sigma_{N,\varepsilon}$ is the action-transition matrix defined in (11). A detailed exposition on the validity of (VII..5) can be found in Asavathiratham (2001, Chapter 5). The following lemma follows directly from (VII..5) and the definition of $\Pi_{N,\varepsilon}$ above.

LEMMA 16. Let $\rho(\Pi_{N,\varepsilon}) = \tilde{\mu}_1, \cdots, \tilde{\mu}_{nm}$, $\rho(\mathscr{A}) = (\lambda_1, \cdots, \lambda_N)$ and $\rho(\Sigma_{N,\varepsilon}) = (\vartheta_1, \cdots, \vartheta_m)$ denote the eigenvalue spectra of $\Pi_{N,\varepsilon}$, $\mathscr{A}$ and $\Sigma_{N,\varepsilon}$ respectively.

(a) If μ_1 and $\tilde{\mu}_1$ are the unique largest eigenvalues of $P_{N,\varepsilon}$ and $\Pi_{N,\varepsilon}$ respectively, then $\mu_1 = \tilde{\mu}_1 = 1$.

(b) $\rho(\Pi_{N,\varepsilon}) = (\vartheta_i \lambda_j)\ \forall \vartheta_i \in \rho(\Sigma_{N,\varepsilon})$, $\lambda_j \in \rho(\mathscr{A})$.

*Proof.*Multiplying (VII..5) by the right eigenvector $\mathbf{r}_i$ of $P_{N,\varepsilon}$, we have $P_{N,\varepsilon}\Psi\mathbf{r}_1 = \Psi\Pi_{N,\varepsilon}\mathbf{r}_1$. Since $P_{N,\varepsilon}$ is a stochastic matrix, $\mu_1 = 1$, which implies that $P_{N,\varepsilon}\Psi\mathbf{r} = \Psi\mathbf{r}_1$, which is true if and only if $\Pi_{N,\varepsilon}\mathbf{r}_1 = \mathbf{r}_1$. That is $\tilde{\mu}_1 = \mu_1 = 1$. For the proof of Lemma 16 (*b*) see Horn and Johnson (1990, page 245, Theorem 4.2.12). ■

For sufficiently small noise, $|\mu_{L+1}| = |\tilde{\mu}_{L+1}| = \lambda_2\vartheta_1 = \lambda_2$ and $|\mu_{L+L}| = |\tilde{\mu}_{L+L}| = \lambda_2\vartheta_m$. This completes the proof.

VII.C. Proofs for the Example

Let $G = (\mathcal{N}, E)$ be a graph or network of N vertices. Denote by $\mathcal{S}$ a subset of $\mathcal{N}$ and S its cardinality. Let $e(S, N-S)$ be the number of interactions (for a weighted network graph its is the sum of weighted interactions) between $\mathcal{S}$ and its complement $\mathcal{N}-\mathcal{S}$. Also let $d(\mathcal{S})$ denote the total degree of $\mathcal{S}$. Then the conductance of G

$$\phi(G) = \min_{\mathcal{S}, S \leq \frac{N}{2}} \frac{e(S, N-S)}{d(\mathcal{S})} \tag{VII..7}$$

For regular network graphs (in which all vertices have the same degree), it is shown by (Alon and Milman, 1985) that

$$\lambda_2(G) \leq 1 - \frac{\phi(G)^2}{2}. \tag{VII..8}$$

For a complete graph, since every vertex is connected to every other vertex, we have that every vertex in $\mathcal{S}$ is connected to all other vertices in $\mathcal{N}-\mathcal{S}$. This implies that $e(S, N-S) = S \times \#(\mathcal{N}-\mathcal{S}) = S \times (N-S)$, and $d(\mathcal{S}) = N \times S$ such that

$$\phi(G_{com}) = \min_{\mathcal{S}, S \leq \frac{N}{2}} \frac{S \times (N-S)}{N \times S} \geq \frac{1}{2}, \tag{VII..9}$$

where the last inequality follows from the fact that $S \leq \frac{N}{2}$. We thus have that

$$\lambda_2(G_{com}) \leq \frac{7}{8} \tag{VII..10}$$

In the case of a $1-D$ cyclic network, $e(S, N-S) = 2$, and $d(\mathcal{S}) = 2 \times S$ such that

$$\phi(G_{cyc}) = \min_{\mathcal{S}, S \leq \frac{N}{2}} \frac{2}{2 \times S} \geq \frac{2}{N}. \tag{VII..11}$$

Hence $\lambda_2(G_{cyc}) \leq \frac{N^2-2}{N^2}$.

$2D$ network: Let the composition of $\mathcal{S}$ be chosen in such a way that the peripheral vertices (vertices at the perimeter or boundary of $\mathcal{S}$) contain approximately one edge each connecting it to the set $\mathcal{N}-\mathcal{S}$. Since it is a 2-dimensional structure there should be approximately $\sqrt{S}$ vertices forming such a boundary. This implies that $e(S, N-S) \approx \sqrt{S}$, and $d(\mathcal{S}) = 4 \times S$

such that

$$\phi(G_{2D}) = \min_{\mathcal{S}, S \leq \frac{N^2}{2}} \frac{\sqrt{S}}{4 \times S} \geq \frac{\sqrt{2}}{4N}. \tag{VII..12}$$

where the last inequality follows from the fact that $\sqrt{S} \leq \sqrt{\frac{N^2}{2}}$. It follows that

$$\lambda_2(G_{2D}) \leq \frac{16N^2 - 1}{16N^2}.$$

Random d-regular network: Since for each vertex the vertices to which it is connected are chosen at random, and that the maximum size of $\mathcal{S}$ is $\frac{N}{2}$, then a typical vertex in $\mathcal{S}$ is connected to approximately $\frac{d \times (N-S)}{N}$ other vertices in $\mathcal{N} - \mathcal{S}$ such that $e(S, N-S) \approx \frac{d \times S(N-S)}{N}$. We thus have

$$\phi(G_{d-r}) = \min_{\mathcal{S}, S \leq \frac{N}{2}} \frac{\frac{d \times S(N-S)}{N}}{d \times S} \geq 1. \tag{VII..13}$$

$$\lambda_2(G_{d-r}) \leq \frac{7}{8} \tag{VII..14}$$

For Newman's small world networks see Durrett (2006).

VII.D. Proof of Theorem 9

From the definition of asymptotic global convergence, we seek for conditions under which $\mathbf{l}^*$ satisfies the condition $\lim_{N\to\infty} \pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l}^*) > 0$. This is equivalent to the condition $\lim_{N\to\infty} \left\{\psi^N(\mathbf{l}) - \min_{\mathbf{l}' \in \mathbf{L}} \psi^N(\mathbf{l}')\right\} = 0$. Recall that $\psi^N(\mathbf{l}) = \sum_{(\mathbf{l}_i, \mathbf{l}_j) \in g_{\min}(\mathbf{l})} \psi^N(\mathbf{l}_i, \mathbf{l}_j)$, $\psi^N(\mathbf{l}_i, \mathbf{l}_j) = N\left[c(\mathbf{l}_i, \partial \mathbf{l}_j) - \frac{1}{N}\gamma^N(\mathbf{l}_j)\right]$, $c(\mathbf{l}, \partial \mathbf{l}') = -r(\mathbf{l}, \partial \mathbf{l}') \ln\left(\mathbb{P}(x_{\mathbf{l}'}, \mathbf{l})\right)$ and $\gamma^N(\mathbf{l}) = K_{\mathbf{l}} \ln(1 - \lambda_2^N(G))$, where $g_{\min}(\mathbf{l}) \in \arg\min_{g \in G(\{\mathbf{l}\})} \sum_{(\mathbf{l}_i, \mathbf{l}_j) \in g} \psi^N(\mathbf{l}_i, \mathbf{l}_j)$. Since for all $\mathbf{l}_i, \mathbf{l}_j, \mathbf{l} \in \mathbf{L}$, $\gamma^N(\mathbf{l}_j) > 0$, $c(\mathbf{l}, \partial \mathbf{l}') > 0$ and hence $\psi^N(\mathbf{l}_i, \mathbf{l}_j) > 0$, it must be that $\psi^N(\mathbf{l}) > 0$. This implies that one among states for which $\lim_{N\to\infty} \left\{\psi^N(\mathbf{l}) - \min_{\mathbf{l}' \in \mathbf{L}} \psi^N(\mathbf{l}')\right\} = 0$, is $\mathbf{l}^* \in \arg\min_{\mathbf{l} \in \mathbf{L}} \psi^N(\mathbf{l})$.

Given that $\mathbf{l}^*$ satisfies condition $\lim_{N\to\infty} \pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l}^*) > 0$, we then need to derive conditions under which it is the unique asymptotically stable state. That is conditions under which for every $\mathbf{l} \neq \mathbf{l}^*$, $\lim_{N\to\infty} \pi_{N,\boldsymbol{\varepsilon}}(\mathbf{l}) = 0$. This requires that $\lim_{N\to\infty} \left\{\psi^N(\mathbf{l}) - \psi^N(\mathbf{l}^*)\right\} > 0$, or equivalently $\lim_{N\to\infty} \psi^N(\mathbf{l}) > \lim_{N\to\infty} \psi^N(\mathbf{l}^*)$. Substituting for expressions of $\psi^N()$ yields

the inequality

$$\lim_{N\to\infty}\left\{\sum_{(\mathbf{l}_i,\mathbf{l}_j)\in g_{\min}(\mathbf{l})}\left(c(\mathbf{l}_i,\partial\mathbf{l}_j)-\frac{1}{N}\gamma^N(\mathbf{l}_j)\right)\right\}>\lim_{N\to\infty}\left\{\sum_{(\mathbf{l}_i,\mathbf{l}_j)\in g_{\min}(\mathbf{l}^*)}\left(c(\mathbf{l}_i,\partial\mathbf{l}_j)-\frac{1}{N}\gamma^N(\mathbf{l}_j)\right)\right\} \tag{VII..15}$$

Assumption 4 (*iii*) of model Definition 1 requires the probabilities of mistakes to be independent of population size, hence $\ln\left(\mathbb{P}(x_{\mathbf{l}'},\mathbf{l})\right)$ is a finite negative real number independent of N. For inequality (VII..15) to hold, it suffices for

$$\lim_{N\to\infty}\left(c(\mathbf{l}_i,\partial\mathbf{l}_j)-\frac{1}{N}\gamma^N(\mathbf{l}_j)\right)=0 \tag{VII..16}$$

for all $(\mathbf{l}_i,\mathbf{l}_j)\in g_{\min}(\mathbf{l}^*)$, and for at least one transition $(\mathbf{l}'_i,\mathbf{l}'_j)\in g_{\min}(\mathbf{l})$,

$$\lim_{N\to\infty}\left(c(\mathbf{l}'_i,\partial\mathbf{l}'_j)-\frac{1}{N}\gamma^N(\mathbf{l}'_j)\right)>0 \tag{VII..17}$$

Conditions (VII..16) and (VII..17) together are equivalent to requiring that $\lim_{N\to\infty}\frac{1}{N}\ln(1-\lambda_2^N(G))=0$, and $\lim_{N\to\infty}r(\mathbf{l}_j,\partial\mathbf{l}_j)=0$ for all $(\mathbf{l}_i,\mathbf{l}_j)\in g_{\min}(\mathbf{l}^*)$, and that for at least one transition $(\mathbf{l}'_i,\mathbf{l}'_j)\in g_{\min}(\mathbf{l})$, $\lim_{N\to\infty}r(\mathbf{l}'_i,\partial\mathbf{l}'_j)>0$.

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