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Natural Models for Evolution on Networks

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Abstract. Evolutionary dynamics have been traditionally studied in the context of homogeneous populations, mainly described by the Moran process [15]. Recently, this approach has been generalized in [13] by arranging individuals on the nodes of a network (in general, directed). In this setting, the existence of directed arcs enables the simulation of extreme phenomena, where the fixation probability of a randomly placed mutant (i.e. the probability that the offsprings of the mutant eventually spread over the whole population) is arbitrarily small or large. On the other hand, undirected networks (i.e. undirected graphs) seem to have a smoother behavior, and thus it is more challenging to find suppressors/amplifiers of selection, that is, graphs with smaller/greater fixation probability than the complete graph (i.e. the homogeneous population). In this paper we focus on undirected graphs. We present the first class of undirected graphs which act as suppressors of selection, by achieving a fixation probability that is at most one half of that of the complete graph, as the number of vertices increases. Moreover, we provide some generic upper and lower bounds for the fixation probability of general undirected graphs. As our main contribution, we introduce the natural alternative of the model proposed in [13]. In our new evolutionary model, all individuals interact *simultaneously* and the result is a compromise between aggressive and non-aggressive individuals. That is, the behavior of the individuals in our new model and in the model of [13] can be interpreted as an “*aggregation*” vs. an “*all-or-nothing*” strategy, respectively. We prove that our new model of mutual influences admits a *potential function*, which guarantees the convergence of the system for any graph topology and any initial fitness vector of the individuals. Furthermore, we prove fast convergence to the stable state for the case of the complete graph, as well as we provide almost tight bounds on the limit fitness of the individuals. Apart from being important on its own, this new evolutionary model appears to be useful also in the abstract modeling of control mechanisms over invading populations in networks. We demonstrate this by introducing and analyzing two alternative control approaches, for which we bound the time needed to stabilize to the “healthy” state of the system.

Keywords: Evolutionary dynamics, undirected graphs, fixation probability, potential function, Markov chain, fitness, population structure.

1 Introduction

Evolutionary dynamics have been well studied (see [1,6,7,19,21,22]), mainly in the context of homogeneous populations, described by the Moran process [15,17]. In addition, population dynamics have been extensively studied also from the perspective of the strategic interaction in evolutionary game theory, cf. for instance [8,9,10,11,20]. One of the main targets of evolutionary game theory is evolutionary dynamics (see [9,23]). Such dynamics usually examine the propagation of intruders with a given *fitness* to a population, whose initial members (resident individuals) have a different fitness. In fact, “evolutionary stability” is the case where no dissident behaviour can invade and dominate the population. The evolutionary models and the dynamics we consider here belong to this framework. In addition, however, we consider structured populations (i.e. in the form of an undirected graph) and we study how the underlying graph structure affects the evolutionary dynamics. We study in this paper two kinds of evolutionary dynamics. Namely, the “all or nothing” case (where either the intruder overtakes the whole graph or die out) and the “aggregation” case (more similar in spirit to classical evolutionary game theory, where the intruder’s fitness aggregates with the population fitness and generates eventually a homogeneous crowd with a new fitness).

In a recent article, Lieberman, Hauert, and Nowak proposed a generalization of the Moran process by arranging individuals on a connected network (i.e. graph) [13] (see also [18]). In this model, vertices correspond to individuals of the population and weighted edges represent the reproductive rates between the adjacent vertices. That is, the population structure is translated into a network (i.e. graph) structure. Furthermore, individuals (i.e. vertices) are partitioned into two types: *aggressive* and *non-aggressive*. The degree of (relative) aggressiveness of an individual is measured by its *relative fitness*; in particular, non-aggressive and aggressive individuals are assumed to have relative fitness 1 and $r \geq 1$, respectively. This modeling approach initiates an ambitious direction of interdisciplinary research, which combines classical aspects of computer science (such as combinatorial structures and complex network topologies), probabilistic calculus (discrete Markov chains), and fundamental aspects of evolutionary game theory (such as evolutionary dynamics).

In the model of [13], one *mutant* (or *invader*) with relative fitness $r \geq 1$ is introduced into a given population of *resident* individuals, each of whom having relative fitness 1. For simplicity, a vertex of the graph that is occupied by a mutant will be referred to as *black*, while the rest of the vertices will be referred to as *white*. At each time step, an individual is chosen for reproduction with a probability proportional to its fitness, while its offspring replaces a randomly chosen neighboring individual in the population. Once u has been selected for reproduction, the probability that vertex u places its offspring into position v is given by the weight w_{uv} of the directed arc $\langle uv \rangle$. This process stops when either all vertices of the graph become black (resulting to a *fixation* of the graph) or they all become white (resulting to *extinction* of the mutants). Several similar models have been previously studied, describing for instance influence

propagation in social networks (such as the decreasing cascade model [12,16]), dynamic monopolies [2], particle interactions (such as the voter model, the antivoter model, and the exclusion process), etc. However, the dynamics emerging from these models do not consider different fitnesses for the individuals.

The *fixation probability* f_G of a graph $G = (V, E)$ is the probability that eventually fixation occurs, i.e. the probability that an initially introduced mutant, placed uniformly at random on a vertex of G , eventually spreads over the whole population V , replacing all resident individuals. One of the main characteristics in this model is that at every iteration of the process, a “battle” takes place between aggressive and non-aggressive individuals, while the process stabilizes only when one of the two teams takes over the whole population. This kind of behavior of the individuals can be interpreted as an *all-or-nothing* strategy.

Lieberman et al. [13] proved that the fixation probability for every symmetric directed graph (i.e. when $w_{uv} = w_{vu}$ for every u, v) is equal to that of the complete graph (i.e. the homogeneous population of the Moran process), which tends to $1 - \frac{1}{r}$ as the size n of the population grows. Moreover, exploiting vertices with zero in-degree or zero out-degree (“upstream” and “downstream” populations, respectively), they provided several examples of *directed* graphs with arbitrarily small and arbitrarily large fixation probability [13]. Furthermore, the existence of directions on the arcs leads to examples where neither fixation nor extinction is possible (e.g. a graph with two sources).

In contrast, general *undirected* graphs (i.e. when $\langle uv \rangle \in E$ if and only if $\langle vu \rangle \in E$ for every u, v) appear to have a smoother behavior, as the above process eventually reaches fixation or extinction with probability 1. Furthermore, the coexistence of both directions at every edge in an undirected graph seems to make it more difficult to find *suppressors* or *amplifiers* of selection (i.e. graphs with smaller or greater fixation probability than the complete graph, respectively), or even to derive non-trivial upper and lower bound for the fixation probability on general undirected graphs. This is the main reason why only little progress has been done so far in this direction and why most of the recent work focuses mainly on the exact or numerical computation of the fixation probability for very special cases of undirected graphs, e.g. the star and the path [3,4,5].

Our Contribution. In this paper we overcome this difficulty for undirected graphs and we provide the first class of undirected graphs that act as suppressors of selection in the model of [13], as the number of vertices increases. This is a very simple class of graphs (called *clique-wheels*), where each member G_n has a clique of size $n \geq 3$ and an induced cycle of the same size n with a perfect matching between them. We prove that, when the mutant is introduced to a clique vertex of G_n , then the probability of fixation tends to zero as n grows. Furthermore, we prove that, when the mutant is introduced to a cycle vertex of G_n , then the probability of fixation is at most $1 - \frac{1}{r}$ as n grows (i.e. to the same value with the homogeneous population of the Moran process). Therefore, since the clique and the cycle have the same number n of vertices in G_n , the fixation probability f_{G_n} of G_n is at most $\frac{1}{2}(1 - \frac{1}{r})$ as n increases, i.e. G_n is a suppressor of selection. Furthermore, we provide for the model of [13] the first non-trivial upper and lower

bounds for the fixation probability in general undirected graphs. In particular, we first provide a generic upper bound depending on the degrees of some local neighborhood. Second, we present another upper and lower bound, depending on the ratio between the minimum and the maximum degree of the vertices.

As our main contribution, we introduce in this paper the natural alternative of the *all-or-nothing* approach of [13], which can be interpreted as an *aggregation* strategy. In this aggregation model, all individuals interact *simultaneously* and the result is a compromise between the aggressive and non-aggressive individuals. Both these two alternative models for evolutionary dynamics coexist in several domains of interaction between individuals, e.g. in society (dictatorship vs. democracy, war vs. negotiation) and biology (natural selection vs. mutation of species). In particular, another motivation for our models comes from biological networks, in which the interacting individuals (vertices) correspond to cells of an organ and advantageous mutants correspond to viral cells or cancer. Regarding the proposed model of mutual influences, we first prove that it admits a *potential* function. This potential function guarantees that for any graph topology and any initial fitness vector, the system converges to a stable state, where all individuals have the same fitness. Furthermore, we analyze the telescopic behavior of this model for the complete graph. In particular, we prove fast convergence to the stable state, as well as we provide almost tight bounds on the *limit fitness* of the individuals.

Apart from being important on its own, this new evolutionary model enables also the abstract modeling of new control mechanisms over invading populations in networks. We demonstrate this by introducing and analyzing the behavior of two alternative control approaches. In both scenarios we periodically modify the fitness of a small fraction of individuals in the current population, which is arranged on a complete graph with n vertices. In the first scenario, we proceed in phases. Namely, after each modification, we let the system stabilize before we perform the next modification. In the second scenario, we modify the fitness of a small fraction of individuals at each step. In both alternatives, we stop performing these modifications of the population whenever the fitness of every individual becomes sufficiently close to 1 (which is considered to be the “healthy” state of the system). For the first scenario, we prove that the number of *phases* needed for the system to stabilize in the healthy state is logarithmic in $r - 1$ and independent of n . For the second scenario, we prove that the number of *iterations* needed for the system to stabilize in the healthy state is linear in n and proportional to $r \ln(r - 1)$. Due to space limitations we omit the proofs of the results, which can be found in [14].

Notation. In an undirected graph $G = (V, E)$, the edge between vertices $u \in V$ and $v \in V$ is denoted by $uv \in E$, and in this case u and v are said to be *adjacent* in G . If the graph G is directed, we denote by $\langle uv \rangle$ the arc from u to v . For every vertex $u \in V$ in an undirected graph $G = (V, E)$, we denote by $N(u) = \{v \in V \mid uv \in E\}$ the set of neighbors of u in G and by $\deg(u) = |N(u)|$. Furthermore, for any $k \geq 1$, we denote for simplicity $[k] = \{1, 2, \dots, k\}$.

2 All-or-Nothing vs. Aggregation

In this section we formally define the model of [13] for undirected graphs and we introduce our new model of mutual influences. Similarly to [13], we assume for every edge uv of an undirected graph that $w_{uv} = \frac{1}{\deg u}$ and $w_{vu} = \frac{1}{\deg v}$, i.e. once a vertex u has been chosen for reproduction, it chooses one of its neighbors uniformly at random.

2.1 The Model of Lieberman, Hauert, and Nowak (An All-or-Nothing Approach)

Let $G = (V, E)$ be a connected undirected graph with n vertices. Then, the stochastic process defined in [13] can be described by a Markov chain with state space $\mathcal{S} = 2^V$ (i.e. the set of all subsets of V) and transition probability matrix P , where for any two states $S_1, S_2 \subseteq V$,

$$P_{S_1, S_2} = \begin{cases} \frac{1}{|S_1| r + n - |S_1|} \cdot \sum_{u \in N(v) \cap S_1} \frac{r}{\deg(u)}, & \text{if } S_2 = S_1 \cup \{v\} \text{ and } v \notin S_1 \\ \frac{1}{|S_1| r + n - |S_1|} \cdot \sum_{u \in N(v) \setminus S_2} \frac{1}{\deg(u)}, & \text{if } S_1 = S_2 \cup \{v\} \text{ and } v \notin S_2 \\ \frac{1}{|S_1| r + n - |S_1|} \left(\sum_{u \in S_1} \frac{r \cdot |N(u) \cap S_1|}{\deg(u)} + \sum_{u \in V \setminus S_1} \frac{|N(u) \cap (V \setminus S_1)|}{\deg(u)} \right), & \text{if } S_2 = S_1 \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

Notice that in the above Markov chain there are two absorbing states, namely \emptyset and V , which describe the cases where the vertices of G are all white or all black, respectively. Since G is connected, the above Markov chain will eventually reach one of these two absorbing states with probability 1. If we denote by h_v the probability of absorption at state V , given that we start with a single mutant placed on vertex v , then by definition $f_G = \frac{\sum_v h_v}{n}$. Generalizing this notation, let h_S be the probability of absorption at V given that we start at state $S \subseteq V$, and let $h = [h_S]_{S \subseteq V}$. Then, it follows that vector h is the unique solution of the linear system $h = P \cdot h$ with boundary conditions $h_\emptyset = 0$ and $h_V = 1$.

However, observe that the state space $\mathcal{S} = 2^V$ of this Markov chain has size 2^n , i.e. the matrix $P = [P_{S_1, S_2}]$ in (1) has dimension $2^n \times 2^n$. This indicates that the problem of computing the fixation probability f_G of a given graph G is hard, as also mentioned in [13]. This is the main reason why, to the best of our knowledge, all known results so far regarding the computation of the fixation probability of undirected graphs are restricted to regular graphs, stars, and paths [3,4,5,13,18]. In particular, for the case of regular graphs, the above Markov chain is equivalent to a birth-death process with $n - 1$ transient (non-absorbing) states, where the forward bias at every state (i.e. the ratio of the forward probability over the backward probability) is equal to r . In this case, the fixation probability is equal to $\rho = \frac{1}{1 + \sum_{i=1}^{n-1} \frac{1}{r^i}} = \frac{1 - \frac{1}{r^n}}{1 - \frac{1}{r}}$. cf. [18], chapter 8. It is worth mentioning that, even for the case of paths, there is no known exact or approximate formula for the fixation probability [5].

2.2 An Evolutionary Model of Mutual Influences (An Aggregation Approach)

The evolutionary model of [13] constitutes a sequential process, in every step of which only two individuals interact and the process eventually reaches one of two extreme states. However, in many evolutionary processes, all individuals may interact simultaneously at each time step, while some individuals have greater influence to the rest of the population than others. This observation leads naturally to the following model for evolution on graphs, which can be thought as a smooth version of the model presented in [13].

Consider a population of size n and a portion $\alpha \in [0, 1]$ of newly introduced mutants with relative fitness r . The topology of the population is given in general by a directed graph $G = (V, E)$ with $|V| = n$ vertices, where the directed arcs of E describe the allowed interactions between the individuals. At each time step, every individual $u \in V$ of the population influences every individual $v \in V$, for which $\langle uv \rangle \in E$, while the degree of this influence is proportional to the fitness of u and to the weight w_{uv} of the arc $\langle uv \rangle$. Note that we can assume without loss of generality that the weights w_{uv} on the arcs are normalized, i.e. for every fixed vertex $u \in V$ it holds $\sum_{\langle uv \rangle \in E} w_{uv} = 1$. Although this model can be defined in general for directed graphs with arbitrary arc weights w_{uv} , we will focus in the following to the case where G is an undirected graph (i.e. $\langle u_i u_j \rangle \in E$ if and only if $\langle u_j u_i \rangle \in E$, for every i, j) and $w_{uv} = \frac{1}{\text{deg}(u)}$ for all edges $uv \in E$.

Formally, let $V = \{u_1, u_2, \dots, u_n\}$ be the set of vertices and $r_{u_i}(k)$ be the fitness of the vertex $u_i \in V$ at iteration $k \geq 0$. Let $\Sigma(k)$ denote the sum of the fitnesses of all vertices at iteration k , i.e. $\Sigma(k) = \sum_{i=1}^n r_{u_i}(k)$. Then the vector $r(k+1)$ with the fitnesses $r_{u_i}(k+1)$ of the vertices $u_i \in V$ at the next iteration $k+1$ is given by $[r_{u_1}(k+1), r_{u_2}(k+1), \dots, r_{u_n}(k+1)]^T = P \cdot [r_{u_1}(k), r_{u_2}(k), \dots, r_{u_n}(k)]^T$, i.e.

$$r(k+1) = P \cdot r(k) \tag{2}$$

In the latter equation, the elements of the square matrix $P = [P_{ij}]_{i,j=1}^n$ depend on the iteration k and they are given as follows:

$$P_{ij} = \begin{cases} \frac{r_{u_j}(k)}{\text{deg}(u_j)\Sigma(k)}, & \text{if } i \neq j \text{ and } u_i u_j \in E \\ 0, & \text{if } i \neq j \text{ and } u_i u_j \notin E \\ 1 - \sum_{j \neq i} P_{ij}, & \text{if } i = j \end{cases} \tag{3}$$

Note by (2) and (3) that after the first iteration, the fitness of every individual in our new evolutionary model of mutual influences equals the expected fitness of this individual in the model of [13] (cf. Section 2.1). However, this correlation of the two models is not maintained in the next iterations and the two models behave differently as the processes evolve.

In particular, in the case where G is the complete graph, i.e. $\text{deg}(u_i) = n - 1$ for every vertex u_i , the matrix P becomes

$$P = \begin{bmatrix} 1 - \frac{r_{u_2}(k) + \dots + r_{u_n}(k)}{(n-1)\Sigma(k)} & \dots & \frac{r_{u_1}(k)}{(n-1)\Sigma(k)} \\ \frac{r_{u_1}(k)}{(n-1)\Sigma(k)} & \dots & \frac{r_{u_n}(k)}{(n-1)\Sigma(k)} \\ \dots & \dots & \dots \\ \frac{r_{u_1}(k)}{(n-1)\Sigma(k)} & \dots & 1 - \frac{r_{u_1}(k) + \dots + r_{u_{n-1}}(k)}{(n-1)\Sigma(k)} \end{bmatrix} \quad (4)$$

The system given by (2) and (3) can be defined for every initial fitness vector $r(0)$. However, in the case where there is initially a portion $\alpha \in [0, 1]$ of newly introduced mutants with relative fitness r , the initial condition $r(0)$ of the system in (2) is a vector with αn entries equal to r and with $(1 - \alpha)n$ entries equal to 1. Note that the recursive equation (2) is a *non-linear* equation on the fitness values $r_{u_j}(k)$ of the vertices at iteration k .

Since by (3) the sum of every row of the matrix P equals to one, the fitness $r_{u_i}(k)$ of vertex u_i after the $(k + 1)$ -th iteration of the process is a convex combination of the fitnesses of the neighbors of u_i after the k -th iteration. Therefore, in particular, the fitness of every vertex u_i at every iteration $k \geq 0$ lies between the smallest and the greatest initial fitness of the vertices. That is, if r_{\min} and r_{\max} denote the smallest and the greatest initial fitness in $r(0)$, respectively, then $r_{\min} \leq r_{u_i}(k) \leq r_{\max}$ for every $u_i \in V$ and every $k \geq 0$.

Degree of influence. Suppose that initially αn mutants (for some $\alpha \in [0, 1]$) with relative fitness $r \geq 1$ are introduced in graph G on a subset $S \subseteq V$ of its vertices. Then, as we prove in Theorem 4, after a certain number of iterations the fitness vector $r(k)$ converges to a vector $[r_0^S, r_0^S, \dots, r_0^S]^T$, for some value r_0^S . This *limit fitness* r_0^S depends in general on the initial relative fitness r of the mutants, on their initial number αn , as well as on their initial position on the vertices of $S \subseteq V$. The relative fitness r of the initially introduced mutants can be thought as having the “black” color, while the initial fitness of all the other vertices can be thought as having the “white” color. Then, the limit fitness r_0^S can be thought as the “degree of gray color” that all the vertices obtain after sufficiently many iterations, given that the mutants are initially placed at the vertices of S . In the case where the αn mutants are initially placed with *uniform* probability to the vertices of G , we can define the *limit fitness* r_0 of G as $r_0 = \frac{1}{\binom{n}{\alpha n}} \cdot \sum_{S \subseteq V, |S|=\alpha n} r_0^S$. For a given initial value of r , the bigger is r_0 the stronger is the effect of natural selection in G .

Since r_0^S is a convex combination of r and 1, there exists a value $f_{G,S}(r) \in [0, 1]$, such that $r_0^S = f_{G,S}(r) \cdot r + (1 - f_{G,S}(r)) \cdot 1$. Then, the value $f_{G,S}(r)$ is the *degree of influence* of the graph G , given that the mutants are initially placed at the vertices of S . In the case where the mutants are initially placed with uniform probability at the vertices of G , we can define the degree of influence of G as $f_G(r) = \frac{1}{\binom{n}{\alpha n}} \sum_{S \subseteq V, |S|=\alpha n} f_{G,S}(r)$.

Number of iterations to stability. For some graphs G , the fitness vector $r(k)$ reaches *exactly* the *limit fitness vector* $[r_0, r_0, \dots, r_0]^T$ (for instance, the complete

graph with two vertices and one mutant not only reaches this limit in exactly one iteration, but also the degree of influence is exactly the fixation probability of this simple graph). However, for other graphs G the fitness vector $r(k)$ converges to $[r_0, r_0, \dots, r_0]^T$ (cf. Theorem 4 below), but it never becomes equal to it. In the first case, one can compute (exactly or approximately) the number of iterations needed to reach the limit fitness vector. In the second case, given an arbitrary $\varepsilon > 0$, one can compute the number of iterations needed to come ε -close to the limit fitness vector.

3 Analysis of the All-or-Nothing Model

In this section we present analytic results on the evolutionary model of [13], which is based on the sequential interaction among the individuals. In particular, we first present non-trivial upper and lower bounds for the fixation probability, depending on the degrees of vertices. Then we present the first class of undirected graphs that act as suppressors of selection in the model of [13], as the number of vertices increases.

Recall by the preamble of Section 2.2 that, similarly to [13], we assumed that $w_{uv} = \frac{1}{\deg u}$ and $w_{vu} = \frac{1}{\deg v}$ for every edge uv of an undirected graph $G = (V, E)$. It is easy to see that this formulation is equivalent to assigning to every edge $e = uv \in E$ the weight $w_e = w_{uv} = w_{vu} = 1$, since also in this case, once a vertex u has been chosen for reproduction, it chooses one of its neighbors uniformly at random. A natural generalization of this weight assignment is to consider G as a complete graph, where every edge e in the clique is assigned a non-negative weight $w_e \geq 0$, and w_e is not necessarily an integer. Note that, whenever $w_e = 0$, it is as if the edge e is not present in G . Then, once a vertex u has been chosen for reproduction, u chooses any other vertex v with probability $\frac{w_{uv}}{\sum_{x \neq u} w_{ux}}$.

Note that, if we do not impose any additional constraint on the weights, we can simulate multigraphs by just setting the weight of an edge to be equal to the multiplicity of this edge. Furthermore, we can construct graphs with arbitrary small fixation probability. For instance, consider an undirected star with n leaves, where one of the edges has weight an arbitrary small $\varepsilon > 0$ and all the other edges have weight 1. Then, the leaf that is incident to the edge with weight ε acts as a source in the graph as $\varepsilon \rightarrow 0$. Thus, the only chance to reach fixation is when we initially place the mutant at the source, i.e. the fixation probability of this graph tends to $\frac{1}{n+1}$ as $\varepsilon \rightarrow 0$. Therefore, it seems that the difficulty to construct strong suppressors lies in the fact that unweighted undirected graphs can not simulate sources. For this reason, we consider in the remainder of this paper only unweighted undirected graphs.

3.1 A Generic Upper Bound Approach

In the next theorem we provide a generic upper bound of the fixation probability of undirected graphs, depending on the degrees of the vertices in some local neighborhood.

Theorem 1. *Let $G = (V, E)$ be an undirected graph. For any $uv \in E$, let $Q_u = \sum_{x \in N(u)} \frac{1}{\deg x}$ and $Q_{uv} = \sum_{x \in N(u) \setminus \{v\}} \frac{1}{\deg x} + \sum_{x \in N(v) \setminus \{u\}} \frac{1}{\deg x}$. Then $f_G \leq \max_{uv \in E} \left\{ \frac{r^2}{r^2 + rQ_u + Q_u Q_{uv}} \right\}$.*

3.2 Upper and Lower Bounds Depending on Degrees

In the following theorem we provide upper and lower bounds of the fixation probability of undirected graphs, depending on the minimum and the maximum degree of the vertices.

Theorem 2. *Let $G = (V, E)$ be an undirected graph, where $\delta \leq \deg(u) \leq \Delta$ for every $u \in V$. Then, the fixation probability f_G of G , when the fitness of the mutant is r , is upper (resp. lower) bounded by the fixation probability of the clique for mutant fitness $r_u = \frac{r\Delta}{\delta}$ (resp. for mutant fitness $r_l = \frac{r\delta}{\Delta}$).*

3.3 The Undirected Suppressor

In this section we provide the first class of undirected graphs (which we call *clique-wheels*) that act as suppressors of selection as the number of vertices increases. In particular, we prove that the fixation probability of the members of this class is at most $\frac{1}{2}(1 - \frac{1}{r})$, i.e. the half of the fixation probability of the complete graph, as $n \rightarrow \infty$. The clique-wheel graph G_n consists of a clique of size $n \geq 3$ and an induced cycle of the same size n with a perfect matching between them. We refer to the vertices of the inner clique as *clique vertices* and to the vertices of the outer cycle as *ring vertices*. The proof of the main results of this section (cf. Lemma 1 and Theorem 3) is technically involved. However, due to space limitations, we omit here the proofs; for a full version see [14].

Denote by h_{clique} (resp. h_{ring}) the probability that all the vertices of G_n become black, given that we start with one black clique vertex (resp. with one black ring vertex). We first provide in the next lemma an upper bound on h_{clique} .

Lemma 1. *For any $r \in (1, \frac{4}{3})$, $h_{clique} \leq \frac{7}{6n(\frac{4}{3r}-1)} + o(\frac{1}{n})$.*

In the next theorem we provide also an upper bound on h_{ring} , thus bounding the fixation probability f_{G_n} of G_n (cf. Theorem 3).

Theorem 3. *For any $r \in (1, \frac{4}{3})$, $h_{ring} \leq (1 + o(1))(1 - \frac{1}{r})$. Therefore, by Lemma 1, the fixation probability of the clique-wheel graph G_n is $f_{G_n} \leq \frac{1}{2}(1 - \frac{1}{r}) + o(1)$ as $n \rightarrow \infty$.*

4 Analysis of the Aggregation Model

In this section, we provide analytic results on the new evolutionary model of mutual influences. More specifically, in Section 4.1 we prove that this model admits a *potential function* for arbitrary undirected graphs and arbitrary initial fitness vector, which implies that the corresponding dynamic system converges to a stable state. Furthermore, in Section 4.2 we prove fast convergence of the dynamic system for the case of a complete graph, as well as we provide almost tight upper and lower bounds on the limit fitness, to which the system converges.

4.1 Potential and Convergence in General Undirected Graphs

In the following theorem we prove convergence of the new model of mutual influences using a potential function.

Theorem 4. *Let $G = (V, E)$ be a connected undirected graph. Let $r(0)$ be an initial fitness vector of G , and let r_{\min} and r_{\max} be the smallest and the greatest initial fitness in $r(0)$, respectively. Then, in the model of mutual influences, the fitness vector $r(k)$ converges to a vector $[r_0, r_0, \dots, r_0]^T$ as $k \rightarrow \infty$, for some value $r_0 \in [r_{\min}, r_{\max}]$.*

4.2 Analysis of the Complete Graph

The next theorem provides an almost tight analysis for the limit fitness value r_0 and the convergence time to this value, in the case of a complete graph (i.e. a homogeneous population).

Theorem 5. *Let $G = (V, E)$ be the complete graph with n vertices and $\varepsilon > 0$. Let $\alpha \in [0, 1]$ be the portion of initially introduced mutants with relative fitness $r \geq 1$ in G , and let r_0 be the limit fitness of G . Then $|r_u(k) - r_v(k)| < \varepsilon$ for every $u, v \in V$, when $k \geq (n - 2) \cdot \ln(\frac{r-1}{\varepsilon})$. Furthermore, for the limit fitness r_0 ,*

$$1 + \alpha(r - 1) \leq r_0 \leq 1 + \alpha(r - 1) + \frac{\alpha(1 - \alpha)}{1 + \alpha(r - 1)} \cdot \frac{(r - 1)^2}{2} \tag{5}$$

Corollary 1. *Let $G = (V, E)$ be the complete graph with n vertices. Suppose that initially exactly one mutant with relative fitness $r \geq 1$ is placed in G and let r_0 be the limit fitness of G . Then $1 + \frac{r-1}{n} \leq r_0 \leq 1 + \frac{r^2-1}{2n}$.*

5 Invasion Control Mechanisms

As stated in the introduction of this paper, our new evolutionary model of mutual influences can be used to model control mechanisms over invading populations in networks. We demonstrate this by presenting two alternative scenarios in Sections 5.1 and 5.2. In both considered scenarios, we assume that αn individuals of relative fitness r (the rest being of fitness 1) are introduced in the complete graph with n vertices. Then, as the process evolves, we periodically choose (arbitrarily) a small fraction $\beta \in [0, 1]$ of individuals in the current population and we reduce their current fitnesses to a value that is considered to correspond to the healthy state of the system (without loss of generality, this value in our setting is 1). In the remainder of this section, we call these modified individuals as “stabilizers”, as they help the population resist to the invasion of the mutants.

5.1 Control of Invasion in Phases

In the first scenario of controlling the invasion of advantageous mutants in networks, we insert stabilizers to the population in phases, as follows. In each phase $k \geq 1$, we let the process evolve until all fitnesses $\{r_v \mid v \in V\}$ become ε -relatively-close to their fixed point $r_0^{(k)}$ (i.e. until they ε -approximate $r_0^{(k)}$). That is, until $\frac{|r_v - r_0^{(k)}|}{r_0^{(k)}} < \varepsilon$ for every $v \in V$. Note by Theorem 4 that, at every phase, the fitness values always ε -approximate such a limit fitness $r_0^{(k)}$. After the end of each phase, we introduce βn stabilizers, where $\beta \in [0, 1]$. That is, we replace βn vertices (arbitrarily chosen) by individuals of fitness 1, i.e. by resident individuals. Clearly, the more the number of phases, the closer the fixed point at the end of each phase will be to 1. In the following theorem we bound the number of phases needed until the system stabilizes, i.e. until the fitness of *every* vertex becomes sufficiently close to 1.

Theorem 6. *Let $G = (V, E)$ be the complete graph with n vertices. Let $\alpha \in [0, 1]$ be the portion of initially introduced mutants with relative fitness $r \geq 1$ in G and let $\beta \in [0, 1]$ be the portion of the stabilizers introduced at every phase. Let $r_0^{(k)}$ be the limit fitness after phase k and let $\varepsilon, \delta > 0$, be such that $\frac{\beta}{2} > \sqrt{\varepsilon}$ and $\delta > \frac{4}{3}\sqrt{\varepsilon}$. Finally, let each phase k run until the fitnesses ε -approximate their fixed point $r_0^{(k)}$. Then, after $k \geq 1 + \ln\left(\frac{\varepsilon + (1+\varepsilon)\frac{1+\alpha}{2}(r-1)}{\delta - \frac{4}{3}\sqrt{\varepsilon}}\right) / \ln\left(\frac{1}{(1+\varepsilon)(1-\frac{\beta}{2})}\right)$ phases, the relative fitness of every vertex $u \in V$ is at most $1 + \delta$.*

5.2 Continuous Control of Invasion

In this section we present another variation of controlling the invasion of advantageous mutants, using our new evolutionary model. In this variation, we do not proceed in phases; we rather introduce *at every single iteration* of the process βn stabilizers, where $\beta \in [0, 1]$ is a small portion of the individuals of the population. For simplicity of the presentation, we assume that at every iteration the βn stabilizers with relative fitness 1 are the same.

Theorem 7. *Let $G = (V, E)$ be the complete graph with n vertices. Let $\alpha \in [0, 1]$ be the portion of initially introduced mutants with relative fitness $r \geq 1$ in G and let $\beta \in [0, 1]$ be the portion of the stabilizers introduced at every iteration. Then, for every $\delta > 0$, after $k \geq \frac{n}{\beta}(n-1) \cdot \ln\left(\frac{r-1}{\delta}\right)$ iterations, the relative fitness of every vertex $u \in V$ is at most $1 + \delta$.*

Observation 1. *The bound in Theorem 7 of the number of iterations needed to achieve everywhere a sufficiently small relative fitness is independent of the portion $\alpha \in [0, 1]$ of initially placed mutants in the graph. Instead, it depends only on the initial relative fitness r of the mutants and on the portion $\beta \in [0, 1]$ of the vertices, to which we introduce the stabilizers.*

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