Networked Bio-Inspired Evolutionary Dynamics on a Multi-Population (I)

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Wouter Baar[1] and Dario Bauso[2]

Abstract— **We consider a multi-population, represented by a network of groups of individuals. Every player of each group can choose between two options, and we study the problem of reaching consensus. The dynamics not only depend on the dynamics within the group, but they also depend on the topology of the network, so neighboring groups influence individuals as well. First, we develop a mathematical model of this networked bio-inspired evolutionary behavior and we study its steady-state. We look at the special case where the underlying network topology is a regular and unweighted graph and show that the steady-state is a consensus equilibrium. A sufficient condition for exponential stability is given. Finally, a related networked dynamical system with connections to the Bass model is studied and we conclude the paper with simulations.**

Keywords— **Multi-agent systems, networked systems, collective decision-making, consensus.**

I. INTRODUCTION

In this paper we study networked bio-inspired models, where a group of individuals has the objective of reaching consensus on one of the available options. In recent years there has already been a surge in amount of published literature on this topic, see for example [1], [3], [8] and [9]. Usually, a group of individuals is considered and every player of the group can choose between two options, 1 or 2, or can choose to be uncommitted. Rather than studying individual behavior of each player, we are only interested in how many players choose a certain strategy, i.e., we model the mean-field approximation, by taking the population size very large.

The evolutionary dynamics are now as follows. Every player can spontaneously decide to commit to an option, or can decide to commit to an option by means of imitation: since in general individuals are crowd-seeking, individuals are attracted to the option that has the most committed players. Players can also decide to leave their choice, by either spontaneously abandonment, or they are lured to become uncommitted by other players. We then also talk about cross-inhibitory signals that are send to opposing players to attract them to become uncommitted. Finally, when modeling the dynamics of such systems, the states of the model are the fraction of committed individuals to option 1, the fraction of committed individuals to option 2 and the fraction of uncommitted individuals.

As an element of novelty in comparison with the existing literature, in this paper we will deal with multi-population evolutionary dynamics, as displayed in Figure 1. Committed players to option 1 and option 2 are displayed in red and blue, respectively, while uncommitted players are displayed in green. The idea here is that we have groups of individuals, and the dynamics of every player now not only depends on the fractions of committed and uncommitted players within the group, but it also depends on the distribution in neighboring groups. The topology of the network thus plays a central role in this paper.
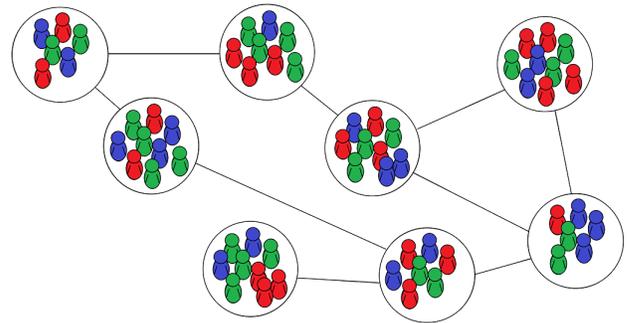

Fig. 1. Depiction of a multi-population.

A. Highlights of the Contribution

The main contributions of this paper are the following. First of all, a mathematical model of the networked bio-inspired dynamics will be presented. This mathematical model takes into account the structure of the network, and the states of the model are the fractions of committed and uncommitted individuals in every group of the multi-population. Secondly, the steady-state of this system is studied, as well as the steady-state of a simplified network where we assume that the topology is regular and unweighted. We then provide a sufficient condition to ensure exponential stability of this equilibrium. Furthermore, we highlight similarities with the well-known Bass model, which is widely used to simulate the diffusion of a new technology.

B. Related Work

In the existing literature, often the dynamics of a single group of individuals is studied, [1], [3], [9]. Here, the evolutionary dynamics are inspired on a biological model on swarms of bees, see e.g. [4], [5], [6].

The underlying idea in those papers is in general the following: we have a colony of bees, and the bees need to

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decide on a new home, and bees can choose between two options. Some bees will commit to option 1 while others commit to option 2. Bees can either spontaneously commit to an option or they imitate the rest (bees are crowd-seeking and are attracted to the home where most bees already are). Bees can also decide to leave their choice and become uncommitted, either by spontaneously uncommitment or by cross-inhibitory signals send by the bees in the opposing camp. A lot of research is about the behavior on the long run, since the desired final state would be where the total bee population has committed to a single option.

Another use of the bio-inspired model is in economic markets. Here, two companies put a similar product on the market, and the companies must compete for the largest market share. Consumers can be attracted to either option 1 or option 2. The cross-inhibitory signals can now be thought of as advertisements of the opposing company.

Networked bio-inspired evolutionary models also arise in consensus networks [2], [7], [8]. Here, we can think of groups of individuals that need to decide between the Democratic or Republican Party, or between left and right politics. The cross-inhibitory signals are then smear campaigns by the opposing team.

Finally, networked systems can be used to study diffusion models. For example, in [10], they are used to study how a disease spreads of a population. Individuals are now either susceptible or infected. Infected individuals can recover and they become susceptible again.

This paper is now organized as follows. In Section II we discuss the needed preliminaries. Then, in Section III, we discuss the networked bio-inspired model and its steady-state. In Section IV we study a simplified case where the graph of the underlying network is assumed to be unweighted and regular. In Section V we look at a related model with applications in diffusion models. Finally, we perform some simulations in Section VI and Section VII provides the conclusions and directions for future research.

II. PRELIMINARIES

In this section we will present the mathematical preliminaries and the notation used throughout this paper.

The real numbers are denoted by $\mathbb{R}$. The n-dimensional vector consisting of all ones is denoted by $\mathbb{1}_n \in \mathbb{R}^n$ and the zero n-dimensional vector is denoted by $\mathbb{0}_n \in \mathbb{R}^n$. The transpose of a matrix A is denoted as A^T and I_n denotes the $n \times n$ identity matrix. Finally, the cardinality of a set S is denoted by $|S|$.

A *directed graph* $G = (V, E)$ is a pair of two sets, the *node set* $V = \{1, 2, \ldots, n\}$ and the *edge set* E, which consists of ordered pairs $(i, j) \in V \times V$. If for every edge (i, j) we also have that $(j, i) \in E$, we call the graph *undirected*. In this case an edge is also denoted as $\{i, j\}$. A graph is *simple* if there are no self loops, that is, $(i, i) \notin E$ for all $1 \le i \le n$.

For an undirected graph G, if $\{i, j\} \in E$, we call i and j *neighbors*. The set of neighbors of node i is denoted as $N_i = \{j \in V \mid \{i, j\} \in E\}$. The *degree* d_i of node i is the number of neighbors of i, i.e., the cardinality of the neighbor

set $|N_i| = d_i$. If every node has the same degree we say that the graph G is *regular*.

To any simple and undirected graph $G = (V, E)$ we can assign a set of matrices as follows

$$\mathcal{A}(G) = \{A \in \mathbb{R}^{n \times n} \mid A = A^T \text{ and } a_{ij} \ne 0 \Leftrightarrow \{i, j\} \in E\}.$$

Any such matrix A is called a *weighted adjacency matrix*. A nonzero entry a_{ij} is called the *weight* of edge $\{i, j\}$. A *weighted graph* is a triple (V, E, A). If all the nonzero entries in A are the same, we call the graph *unweighted*. Without loss of generality all nonzero entries are set to one, then.

In the remainder of this paper, unless stated otherwise, whenever we talk about a graph $G = (V, E)$, we mean that the graph is simple and undirected.

III. THE NETWORKED BIO-MODEL

We have a large population of individuals. The population is divided into groups. Every group is located at a position i. At every position i, the individuals from that group can either be committed to option 1 or option 2, or they are uncommitted. The dynamics of a group of individuals at location i are presented in Figure 2. Here, x_i is the fraction of individuals committed to option 1, y_i is the fraction of individuals committed to option 2 and z_i is the fraction of uncommitted individuals. Uncommitted individuals can spontaneously decide to commit to an option (quantified by a parameter γ in Figure 2). Uncommitted individuals can also be attracted to an option by other individuals, since individuals are crowd-seeking: the more individuals committed to an option, the more people are attracted to that option (quantified by r). Individuals from option 1 can send cross-inhibitory signals σ to the people committed to 2, to lure them to become uncommitted. Individuals at option 2 can attract individuals from option 1 as well by using opposite cross-inhibitory signals σ. Finally, individuals can also decide to spontaneously abandon their choice and become uncommitted (quantified by α). These dynamics and the role of the parameters are summarized in Figure 2. The
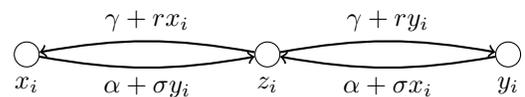
Fig. 2. The evolutionary dynamics at the node level (microscopic level).

microscopic dynamics describe the evolution at the group level. As stated, to each group we assign three variables: x_i, y_i and z_i, denoting the fractions of committed and uncommitted individuals. Note that we have $x_i + y_i + z_i = 1$ at all times. These groups of individuals interact with each other over a given network topology. This structure is captured in a graph. Every node represents a group of individuals and the edges represent the connections between the groups. An example of this is given in Figure 3.

Another interpretation of the model in Figure 3 is as follows. Let generic node i now represent a single individual.

Fig. 3. An example of a networked bio-model, at the macroscopic level. Every node has three states, x_i, y_i and z_i.
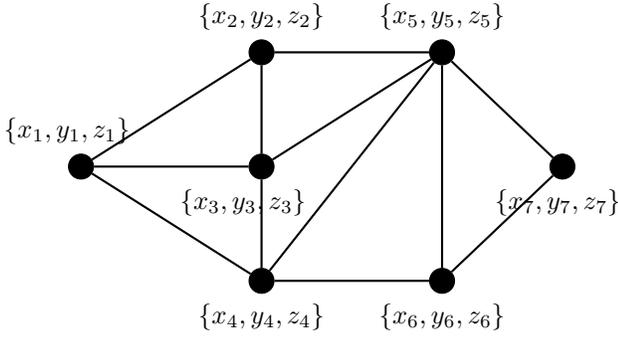
Then, the states x_i, y_i and z_i represent the probability of commitment to option 1, 2 or no option, respectively.

In either case, the dynamics of node i are described by

$$\dot{x}_i = \left(\gamma + r \sum_{j \in N_i} a_{ij} x_j\right) z_i - x_i \left(\alpha + \sigma \sum_{j \in N_i} a_{ij} y_i\right),$$
$$\dot{y}_i = \left(\gamma + r \sum_{j \in N_i} a_{ij} y_j\right) z_i - y_i \left(\alpha + \sigma \sum_{j \in N_i} a_{ij} x_i\right), \quad (1)$$
$$\dot{z}_i = -\dot{x}_i - \dot{y}_i.$$

To simplify our notation we use the following local averages

$$\sum_{j \in N_i} a_{ij} x_j = \bar{x}_i, \quad \sum_{j \in N_i} a_{ij} y_i = \bar{y}_i.$$

Note that $z_i = 1 - x_i - y_i$ and using this, the dynamics of (1) can be described solely in terms of x_i and y_i. The network dynamics at the microscopic level are now

$$\dot{x}_i = (\gamma + r\bar{x}_i)(1 - x_i - y_i) - x_i(\alpha + \sigma\bar{y}_i),$$
$$\dot{y}_i = (\gamma + r\bar{y}_i)(1 - x_i - y_i) - y_i(\alpha + \sigma\bar{x}_i). \quad (2)$$

The next theorem gives us insight in the steady-state of the above dynamical system.

Theorem 1: Let $t > 0$ and let $(x^0, y^0, z^0) \in \mathbb{R}^{3n}$ be the initial state. The equilibrium of (2) is given by (x^*, y^*, z^*) with

$$x_i^* = \frac{(\alpha + \sigma\bar{y}_i)(\gamma + r\bar{x}_i)}{\substack{(\alpha + \sigma\bar{y}_i)(\alpha + \sigma\bar{x}_i) + (\gamma + r\bar{x}_i)(\alpha + \sigma\bar{x}_i) + \\ (\alpha + \sigma\bar{y}_i)(\gamma + r\bar{y}_i)}},$$
$$y_i^* = \frac{(\alpha + \sigma\bar{y}_i)(\gamma + r\bar{y}_i)}{\substack{(\alpha + \sigma\bar{y}_i)(\alpha + \sigma\bar{x}_i) + (\gamma + r\bar{x}_i)(\alpha + \sigma\bar{x}_i) + \\ (\alpha + \sigma\bar{y}_i)(\gamma + r\bar{y}_i)}}. \quad (3)$$

And $z_i^* = 1 - x_i^* - y_i^*$. In the above, $\bar{x}_i$ is the sum over the equilibrium values x_j^*, and likewise for $\bar{y}_i$.

Proof: For an equilibrium we require $\dot{x}_i = 0$ and $\dot{y}_i = 0$. For $\dot{x}_i = 0$ we obtain

$$\gamma - \gamma x_i - \gamma y_i + r\bar{x}_i - rx_i\bar{x}_i - ry_i\bar{x}_i - \alpha x_i - \sigma x_i\bar{y}_i = 0.$$

Note that in the sum $\bar{x}_i$ the term x_i does not appear, since $a_{ii} = 0$ because we have a simple graph. We can isolate x_i and y_i easily and obtain

$$(\gamma + r\bar{x}_i + \alpha + \sigma\bar{y}_i)x_i + (\gamma + r\bar{x}_i)y_i = \gamma + r\bar{x}_i. \quad (4)$$

Rewriting $\dot{y}_i = 0$ from equation (2) one obtains

$$(\gamma + r\bar{y}_i)x_i + (\gamma + r\bar{y}_i + \alpha + \sigma\bar{x}_i)y_i = \gamma + r\bar{y}_i. \quad (5)$$

Combining equations (4) and (5) we obtain a non-homogeneous linear system of two equations in two unknowns, x_i and y_i, as follows

$$\begin{bmatrix} \gamma + r\bar{x}_i + \alpha + \sigma\bar{y}_i & \gamma + r\bar{x}_i \\ \gamma + r\bar{y}_i & \gamma + r\bar{y}_i + \alpha + \sigma\bar{x}_i \end{bmatrix} \begin{bmatrix} x_i \\ y_i \end{bmatrix} = \begin{bmatrix} \gamma + r\bar{x}_i \\ \gamma + r\bar{y}_i \end{bmatrix}.$$

The solution of the above set of equations is given by

$$x_i = \frac{(\gamma + r\bar{y}_i + \alpha + \sigma\bar{x}_i)(\gamma + r\bar{x}_i) - (\gamma + r\bar{x}_i)(\gamma + r\bar{y}_i)}{\left(\substack{(\gamma + r\bar{x}_i + \alpha + \sigma\bar{y}_i)(\gamma + r\bar{y}_i + \alpha + \sigma\bar{x}_i) - \\ (\gamma + r\bar{x}_i)(\gamma + r\bar{y}_i)}\right)},$$
$$y_i = \frac{(\gamma + r\bar{x}_i + \alpha + \sigma\bar{y}_i)(\gamma + r\bar{y}_i) - (\gamma + r\bar{x}_i)(\gamma + r\bar{y}_i)}{\left(\substack{(\gamma + r\bar{x}_i + \alpha + \sigma\bar{y}_i)(\gamma + r\bar{y}_i + \alpha + \sigma\bar{x}_i) - \\ (\gamma + r\bar{x}_i)(\gamma + r\bar{y}_i)}\right)}.$$

Note that these expressions can be simplified to the equations in (3). Furthermore, the denominator is always strictly positive, so the above solution is indeed well-defined. This completes the proof. ∎

We now give an interpretation of the above result. We define $\Gamma_{x_i} = (\gamma + r\bar{x}_i)$ and $\Lambda_{x_i} = (\alpha + \sigma\bar{y}_i)$ as the gain and loss of x_i, respectively. Analogously, we set $\Gamma_{y_i} = (\gamma + r\bar{y}_i)$ and $\Lambda_{y_i} = (\alpha + \sigma\bar{x}_i)$. With respect to Figure 2, the arc from z_i to x_i carries the weight Γ_{x_i}, and the amount of uncommitted individuals that become committed to option 1 is precisely proportional to the gain Γ_{x_i}. Similarly, Λ_{x_i} can be thought of as the loss of x_i, since it is proportional to the amount of individuals that become uncommitted. Note that the microscopic dynamics as explained in (2) can be rewritten as

$$\dot{x}_i = \Gamma_{x_i}(1 - x_i - y_i) - \Lambda_{x_i} x_i,$$
$$\dot{y}_i = \Gamma_{y_i}(1 - x_i - y_i) - \Lambda_{y_i} y_i.$$

Then, the equilibrium (3) is

$$x_i^* = \frac{\Lambda_{y_i}\Gamma_{x_i}}{\Lambda_{x_i}\Lambda_{y_i} + \Gamma_{x_i}\Lambda_{y_i} + \Lambda_{x_i}\Gamma_{y_i}},$$
$$y_i^* = \frac{\Lambda_{x_i}\Gamma_{y_i}}{\Lambda_{x_i}\Lambda_{y_i} + \Gamma_{x_i}\Lambda_{y_i} + \Lambda_{x_i}\Gamma_{y_i}},$$
$$z_i^* = 1 - x_i^* - y_i^* = \frac{\Lambda_{x_i}\Lambda_{y_i}}{\Lambda_{x_i}\Lambda_{y_i} + \Gamma_{x_i}\Lambda_{y_i} + \Lambda_{x_i}\Gamma_{y_i}}.$$

To shed light on the relevance of this result, we remark the following. Regarding the value of x_i^*, the quantity $\Lambda_{y_i}\Gamma_{x_i}$ can be seen as the total beneficial factor of growth for x_i. The meaning of this is that x_i increases by either direct gain Γ_{x_i} or by indirect loss Λ_{y_i}, since individuals that leave y_i and become uncommitted, might later on become committed to x_i. We see that higher values of Λ_{y_i} and higher values of Γ_{x_i} lead to higher values of x_i as expected. Of course the final value of x_i^* depicts how the value of total gain for x_i, $\Lambda_{y_i}\Gamma_{x_i}$, compares to the sum of total gain for x_i, total gain for y_i and total gain for z_i.

IV. Regular and Unweighted Graphs

In this section, we assume that we have an unweighted and regular graph. Hence all nonzero a_{ij} are equal to 1 and every node has the same degree d. The micro-dynamics at the node level are now described by

$$\dot{x}_i = (\gamma + r\sum x_j)(1 - x_i - y_i) - x_i(\alpha + \sigma\sum y_j),$$
$$\dot{y}_i = (\gamma + r\sum y_j)(1 - x_i - y_i) - y_i(\alpha + \sigma\sum x_j), \quad (6)$$

where each sum is over all $j \in N_i$. Also $\dot{z}_i = -\dot{x}_i - \dot{y}_i$ since $z_i = 1 - x_i - y_i$. We are ready to establish the following.

Theorem 2: Suppose the network is regular and unweighted, and let the dynamics be described by (6). Let $t > 0$ and let $(x^0, y^0, z^0) \in \mathbb{R}^{3n}$ be the initial state. A consensus equilibrium $(x^*, y^*, z^*) = (\xi\mathbb{1}_n, \mu\mathbb{1}_n, \zeta\mathbb{1}_n)$ is reached with

- Case 1. If $\xi = \mu$,

$$\xi = \mu = \frac{-(2\gamma - rd + \alpha) + \sqrt{(2\gamma - rd + \alpha)^2 + 4\gamma(2rd + \sigma d)}}{2(2rd + \sigma d)},$$

$$\zeta = 1 - \frac{-(2\gamma - rd + \alpha) + \sqrt{(2\gamma - rd + \alpha)^2 + 4\gamma(2rd + \sigma d)}}{(2rd + \sigma d)}.$$

- Case 2. If $\zeta = \frac{\alpha}{dr}$,

$$\xi = \frac{-(\frac{\alpha}{r} - d) \pm \sqrt{(\frac{\alpha}{r} - d)^2 - \frac{4\gamma\alpha}{r\sigma}}}{2d},$$

$$\mu = 1 - \frac{-(\frac{\alpha}{r} - d) \pm \sqrt{(\frac{\alpha}{r} - d)^2 - \frac{4\gamma\alpha}{r\sigma}}}{2d} - \frac{\alpha}{rd},$$

$$\zeta = \frac{\alpha}{rd}.$$

- Case 3. If $\xi = \mu$ and $\zeta = \frac{\alpha}{dr}$,

$$\xi = \mu = \sqrt{\frac{\gamma\alpha}{\sigma rd^2}} = \frac{rd - \alpha}{2rd},$$

$$\zeta = \frac{\alpha}{rd}.$$

Proof: Let the consensus equilibrium be given by $(x^*, y^*, z^*) = (\xi\mathbb{1}_n, \mu\mathbb{1}_n, \zeta\mathbb{1}_n)$, with $\zeta = 1 - \xi - \mu$. At this equilibrium, and since $\dot{x}_i = 0$ and $\dot{y}_i = 0$ at an equilibrium, the equations in (6) reduce to

$$0 = \dot{x}_i = (\gamma + rd\xi)\zeta - \xi(\alpha + \sigma d\mu),$$
$$0 = \dot{y}_i = (\gamma + rd\mu)\zeta - \mu(\alpha + \sigma d\xi). \quad (7)$$

From (7) it also follows that

$$0 = \dot{x}_i - \dot{y}_i = rd(\xi - \mu)\zeta - \xi\alpha + \mu\alpha = (rd\zeta - \alpha)(\xi - \mu).$$

From this expression we obtain that $\xi = \mu$, or $\zeta = \frac{\alpha}{rd}$, or we have both $\xi = \mu$ and $\zeta = \frac{\alpha}{rd}$. We distinguish three cases.

- Case 1. If $\xi = \mu$, the first equation of (7) reduces to

$$0 = \dot{x}_i = (\gamma + rd\xi)(1 - 2\xi) - \xi(\alpha + \sigma d\xi)$$
$$= \gamma - 2\gamma\xi + rd\xi - 2rd\xi^2 - \alpha\xi - \sigma d\xi^2$$
$$= (2rd + \sigma d)\xi^2 + (2\gamma - rd + \alpha)\xi - \gamma.$$

This is a quadratic equation in ξ and the solution is

$$\xi = \frac{-(2\gamma - rd + \alpha) \pm \sqrt{(2\gamma - rd + \alpha)^2 + 4\gamma(2rd + \sigma d)}}{2(2rd + \sigma d)}.$$

Note that in general one obtains two solution to a quadratic equation, however the solution with a minus sign in front of the square root cannot be an equilibrium since in that case the value of ξ would be strictly negative. Finally, $\mu = \xi$ and $\zeta = 1 - 2\xi$.

- Case 2. If $\zeta = \frac{\alpha}{rd}$, using the fact that $\mu = 1 - \xi - \frac{\alpha}{rd}$ now, we obtain

$$0 = \dot{x}_i = (\gamma + rd\xi)\frac{\alpha}{rd} - \xi(\alpha + \sigma d(1 - \xi - \frac{\alpha}{rd}))$$
$$= d\xi^2 + (\frac{\alpha}{r} - d)\xi + \frac{\gamma\alpha}{rd\sigma}.$$

This is a quadratic equation in ξ and the solution is

$$\xi = \frac{-(\frac{\alpha}{r} - d) \pm \sqrt{(\frac{\alpha}{r} - d)^2 - \frac{4\gamma\alpha}{r\sigma}}}{2d}.$$

It can happen that for some values of parameters both solutions are within the interval $[0, 1]$. In that case we do not have a unique equilibrium.

- Case 3. If $\xi = \mu$ and $\zeta = \frac{\alpha}{rd}$, we obtain

$$0 = \dot{x}_i = (\gamma + rd\xi)\frac{\alpha}{rd} - \xi(\alpha + \sigma d\xi)$$
$$= \frac{\gamma\alpha}{rd} + \xi\alpha - \xi\alpha - \xi^2\sigma d$$
$$= \frac{\gamma\alpha}{rd} - \xi^2\sigma d,$$

which implies

$$\xi = \sqrt{\frac{\gamma\alpha}{\sigma rd^2}}.$$

Note that we could have also computed this equilibrium value differently. Using $\zeta = 1 - \xi - \mu$, we get $\frac{\alpha}{rd} = 1 - 2\xi$, so $\xi = \frac{1 - \frac{\alpha}{rd}}{2} = \frac{rd - \alpha}{2rd}$.

This completes the proof. ∎

In the case there is no spontaneously uncommitment, so letting α go to zero, we obtain the following corollary.

Corollary 3: Let $\alpha \to 0$. The consensus equilibrium values (ξ, μ, ζ) in case 2 converge to $(1, 0, 0)$ and $(0, 1, 0)$ and in case 3 they converge to $(\frac{1}{2}, \frac{1}{2}, 0)$.

This corollary has the following meaning and interpretation. In case 2 the equilibrium points are $(\mathbb{1}_n, \mathbb{0}_n, \mathbb{0}_n)$ and $(\mathbb{0}_n, \mathbb{1}_n, \mathbb{0}_n)$. This means that all individuals are committed to option 1 and option 2, respectively. In case 3, the equilibrium is given by $(\frac{1}{2}\mathbb{1}_n, \frac{1}{2}\mathbb{1}_n, \mathbb{0}_n)$. This means that individuals are uniformly distributed over option 1 and 2. This situation is referred to as a symmetric equilibrium.

For the consensus equilibrium established in Theorem 2, we have the following sufficient condition for exponential stability. We will show that two inequalities must hold on the strength of the cross-inhibitory signals, and these conditions can be checked a priori.

Theorem 4: Suppose the network is regular and unweighted. Let the dynamics be described by equation (6). The consensus equilibrium $x^* = (\xi\mathbb{1}_n, \mu\mathbb{1}_n, \zeta\mathbb{1}_n)$ is exponentially stable if the following inequalities on the cross-inhibitory signal σ hold:

$$\sigma > \frac{\alpha - rd(1 - \xi - \mu)}{d(1 - \mu)} \quad \text{and} \quad \sigma > \frac{\alpha - rd(1 - \xi - \mu)}{d(1 - \xi)}.$$

Proof: We compute the Jacobian and evaluate it at the equilibrium $x^* = (\xi\mathbb{1}_n, \mu\mathbb{1}_n, \zeta\mathbb{1}_n)$. Consider the dynamics described by (6), then the partial derivatives of $\dot{x}_i$ are given

by the following expressions

$$\frac{\partial \dot{x}_i}{\partial x_i} = -\gamma - r \sum_{j \in N_i} x_j - \alpha - \sigma \sum_{j \in N_i} y_j,$$

$$\frac{\partial \dot{x}_i}{\partial x_j} = \begin{cases} 0 \text{ if } j \notin N_i, \\ r - rx_i - ry_i \text{ if } j \in N_i, \end{cases}$$

$$\frac{\partial \dot{x}_i}{\partial y_i} = -\gamma - r \sum_{j \in N_i} x_j,$$

$$\frac{\partial \dot{x}_i}{\partial y_j} = \begin{cases} 0 \text{ if } j \notin N_i, \\ -\sigma x_i \text{ if } j \in N_i. \end{cases}$$

The partial derivatives of $\dot{y}_i$ are obtained in a similar fashion. We evaluate the expressions of the partial derivatives at the equilibrium $x^* = (\xi \mathbb{1}_n, \mu \mathbb{1}_n, \zeta \mathbb{1}_n)$ and we make use of the fact that $1 - \xi - \mu = \zeta$. This gives the following Jacobian

$$J = \left[\frac{\partial(\dot{x}_1, \cdots, \dot{x}_n, \dot{y}_1, \cdots, \dot{y}_n)}{\partial(x_1, \cdots, x_n, y_1, \cdots, y_n)} \right] \Bigg|_{x=x^*}$$

$$= \left[\begin{matrix} \frac{\partial(\dot{x}_1, \cdots, \dot{x}_n)}{\partial(x_1, \cdots, x_n)} & \frac{\partial(\dot{x}_1, \cdots, \dot{x}_n)}{\partial(y_1, \cdots, y_n)} \\ \frac{\partial(\dot{y}_1, \cdots, \dot{y}_n)}{\partial(x_1, \cdots, x_n)} & \frac{\partial(\dot{y}_1, \cdots, \dot{y}_n)}{\partial(y_1, \cdots, y_n)} \end{matrix} \right] \Bigg|_{x=x^*}$$

$$= \begin{bmatrix} (r - r\xi - r\mu)A - & -\sigma A - (\gamma + rd\xi)I_n \\ (\gamma + rd\xi + \alpha + \sigma d\mu)I_n & \\ & (r - r\xi - r\mu)A - \\ -\sigma A - (\gamma + rd\mu)I_n & (\gamma + rd\mu + \alpha + \sigma d\xi)I_n \end{bmatrix}$$

$$= \begin{bmatrix} r\zeta A & -\sigma A \\ -\sigma A & r\zeta A \end{bmatrix}$$

$$- \begin{bmatrix} (\gamma + rd\xi + \alpha + \sigma d\mu)I_n & (\gamma + rd\xi)I_n \\ (\gamma + rd\mu)I_n & (\gamma + rd\mu + \alpha + \sigma d\xi)I_n \end{bmatrix}$$

To prove exponential stability the eigenvalues of the above matrix should be contained in the open left half of the complex plane. Computing the eigenvalues of the above $2n \times 2n$ Jacobian matrix is rather difficult, however, we can find an estimate using the Gershgorin circle theorem. Gershgorin circle theorem tells us that each eigenvalue λ_i is contained in a circle around J_{ii} with radius $\sum_{i \neq j} |J_{ij}|$. We note that all diagonal entries J_{ii} are strictly negative, so if we require that the radius of the circle does not cross the imaginary axis we know that the eigenvalue has a strictly negative real part. Using this, we find a sufficient condition for stability. So for $i = 1, \ldots, n$ we require

$$-J_{ii} > \sum_{j \neq i} |J_{ij}|$$

$$\gamma + rd\xi + \alpha + \sigma d\mu > rd\zeta + \sigma d + \gamma + rd\xi$$

$$\sigma > \frac{rd\zeta - \alpha}{d\mu - d} = \frac{\alpha - rd\zeta}{d(1 - \mu)}.$$

Analogously, for $i = n + 1, \ldots, 2n$ we must have $-J_{ii} > \sum_{j \neq i} |J_{ij}|$ and simple computations show that this gives the second constraint. This completes the proof. ∎

V. A RELATED NETWORKED SIS-MODEL

We will now move our attention towards a related model that shares striking similarities with a commonly used dif-

fusion model known as the Bass model, [11]. The idea is that we have a multi-population and each individual of every group can be classified as a susceptible or infected player. Infected agents can recover by some recovery rate γ, and susceptible agents can become infected by either spontaneously infection r or by infection due to other players, with some infection rate β. The dynamics at the node level are represented in Figure 4.
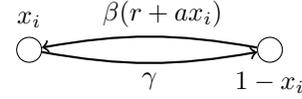
$$x_i \quad \beta(r + ax_i)$$
$$\gamma \quad 1 - x_i$$

Fig. 4. The game theoretic network with only one option at the node level (microscopic level).

This model can be used to study for example the way in which a disease spreads over a population, or the way in which consumers adapt to a new technology. The dynamics of each group is given by

$$\dot{x}_i = \beta(1 - x_i)\Big(\sum_{j=1}^{n} a_{ij} x_j + r \Big) - \gamma x_i, \qquad (8)$$

where β and γ denote the infection and recovery rate, respectively. Here x_i denotes the fraction of infected people in a group, or it denotes the probability that individual i is infected. So $1 - x_i$ is the fraction of individuals that are susceptible at location i, or it denotes the probability that individual i is susceptible. In the following theorem we derive a result for the equilibrium of the dynamics in (8).

Theorem 5: Let the evolutionary dynamics be given by (8). An equilibrium is obtained at $x^* \in \mathbb{R}^n$ with

$$x_i^* = \frac{\sum_{j=1}^{n} a_{ij} x_j^* + r}{\sum_{j=1}^{n} a_{ij} x_j^* + r + \frac{\gamma}{\beta}}. \qquad (9)$$

Proof: The proof follows immediately from $\dot{x}_i = 0$. ∎
It is noteworthy to observe that if there is no recovery, i.e., $\gamma = 0$, the equilibrium value is $x_i^* = 1$. This makes sense intuitively, since there is no recovery taking place so every agent must be infected at some point. Also note that if the recovery rate γ is much stronger than the infection rate β, we see that x_i tends to 0, which is to be expected as well.

Note that in practice it is hard to compute the equilibrium value (9) explicitly, since for the calculation of component x_i^* one needs the other equilibrium values x_j^*.

In the special case of an unweighted and regular graph, it is however easy to compute x_i^*. We have the following:

Corollary 6: Let the topology of the network be an unweighted and regular graph. Then, we reach a consensus equilibrium $x^* = \xi \mathbb{1}_n$ with

$$\xi = \frac{-(r - d + \frac{\gamma}{\beta}) + \sqrt{(r - d + \frac{\gamma}{\beta})^2 + 4dr}}{2d}, \qquad (10)$$

where d is the degree of a single node.

Proof: In the case of an unweighted and regular graph, equation (9) reduces to $\xi = \frac{d\xi + r}{d\xi + r + \frac{\gamma}{\beta}}$, or equivalently $d\xi^2 + \xi r + \xi \frac{\gamma}{\beta} = d\xi + r$. The solution to this quadratic equation is (10). ∎

VI. Numerical Simulations

Two simulations are run to support our findings. First, we show the validity of Theorem 1. To do so, we consider the network depicted in Figure 3, with the following weights:

$$a_{1,2} = 1, \quad a_{1,3} = 1, \quad a_{1,4} = 2, \quad a_{2,3} = 1,$$
$$a_{2,5} = 9, \quad a_{3,4} = 5, \quad a_{3,5} = 1, \quad a_{4,5} = 1,$$
$$a_{4,6} = 8, \quad a_{5,6} = 1, \quad a_{5,7} = 1, \quad a_{6,7} = 1.$$

Furthermore we set $\gamma = 0.5, \alpha = 0.6, r = 0.4$ and $\sigma = 0.3$. The evolution of the states $x_i(t)$ and $y_i(t)$ are presented in Figure 5 in dashed blue and solid red lines, respectively.
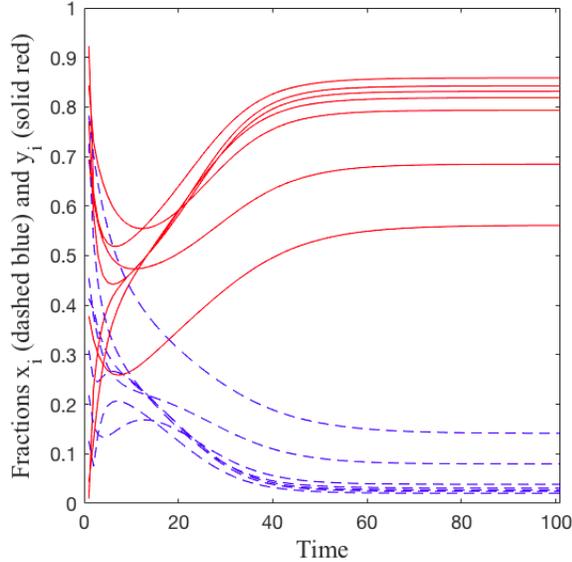

Fig. 5. Dynamics on a network consisting of 7 nodes. The trajectories of $x_i(t)$ are shown in dashed blue, and $y_i(t)$ is presented in solid red.

We see that we reach a steady-state situation. The values of this steady-state are compared to the expected equilibrium values according to equation (3), and they are equal.

Another simulation is performed to show the validity of Theorem 3. We look at a regular and unweighted network given by the Buckminster Fuller geodesic dome, which is a regular graph on 60 nodes where each node has degree 3. We performed the simulation and the results are shown in Figure 6. The values of the parameters were set as follows: $\gamma = 0.2, \alpha = 0.4, r = 0.3$ and $\sigma = 0.4$.

The trajectories of x_i are presented in dashed blue lines, while the trajectories of y_i are presented in solid red lines. We observe that we reach a consensus equilibrium with $x_i = \xi = 0.222$ and $y_i = \mu = 0.333$. We note that $\zeta = 1 - \xi - \mu = 0.444$. This is equal to $\frac{\alpha}{rd}$. Computing the values of ξ and μ using the formulas in case 2 of Theorem 2 yield the same values as the found results of the simulation.

VII. Conclusions

In this paper we studied bio-inspired evolutionary dynamics on a network representing a multi-population. The dynamics of an individual of each group now not only changes due to changes at the micro-level, but it takes into account the states of its neighbors as well. We presented
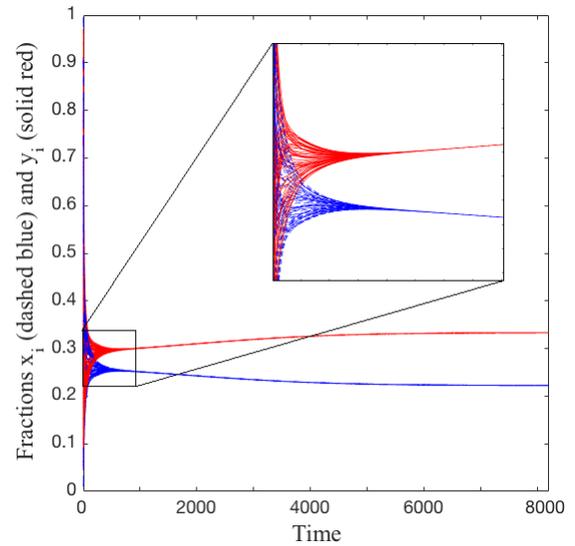

Fig. 6. Dynamics on the regular networked Buckminster dome.

a mathematical model of the dynamics of this networked system and provided a description of the equilibrium. We also provided a sufficient condition for stability of this equilibrium in terms of a lower bound on the cross-inhibitory signals. Finally we looked at a related model, inspired by a diffusion model on susceptible and infected agents.

For future research we will investigate the case where the system parameters are different for each group. We also wish to provide a necessary condition on the stability of the equilibrium of a regular and unweighted graph. Finally, we would like to investigate stability of a weighted network that is not necessarily regular.

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