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Competing edge networks

Mark Parsons*, Peter Grindrod 1

School of Mathematics and Physical Sciences, University of Reading, Whiteknights, PO Box 220, Reading, RG6 6AX, United Kingdom

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ABSTRACT

We introduce a model for a pair of nonlinear evolving networks, defined over a common set of vertices, subject to edgewise competition. Each network may grow new edges spontaneously or through triad closure. Both networks inhibit the other's growth and encourage the other's demise. These nonlinear stochastic competition equations yield to a mean field analysis resulting in a nonlinear deterministic system. There may be multiple equilibria; and bifurcations of different types are shown to occur within a reduced parameter space. This situation models competitive communication networks such as BlackBerry Messenger displacing SMS; or instant messaging displacing emails.

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1. Introduction

In this Letter we consider an extension of modelling nonlinear evolving edge networks introduced in [8], specifically by introducing a competing aspect to multiple networks' dynamics. For simplicity we shall consider two different types of edges, henceforth referred to as *Red* and *Blue* edges, acting upon the same group of nodes, where each edge type has its own discrete time dynamics, and series of adjacency matrices detailing its evolution. Since these edge types act upon the same group of nodes, they may be superimposed onto a single graph, providing the different edge types are clearly differentiated. The work presented in this Letter considers such a network where the different edge types are competing with one another, that is they negatively impact each other's growth. The specifics of our chosen model are outlined in Section 2.

Whilst the extension of tradition network theory from a stochastic to a dynamic setting has recently earned much attention [1,3,4,11,9,12,13], the notion of competing networks remains largely unexplored. Competing networks can however be observed in many technological fields, for example one might consider a group of BlackBerry owners: the networks of BlackBerry Messenger usage and SMS texting amongst this group are seen to be competing with one another due to their similar functions. Here we see the BlackBerry Messenger network partially displaces the SMS network as users switch their method of communication, leading to a fall in SMS usage [2]. It should also be noted that

this competition is not driven by financial motives, instead users are choosing to switch due to mutual convenience. Public and social communication poses challenges to both commercial interests (mass customer industries such as telecommunications, retail, consumer goods, marketing, advertising and new media) and public interests (security, defence policy and opinion formation). Accordingly it is very timely to consider how one type of communication platform may displace another.

Such competing technologies are typically emergent, with one network, Red, boasting superior features (and hence its edge density will grow more rapidly) whereas the other, Blue, possessing a higher userbase (and hence has a higher initial edge density). We are interested in the equilibrium positions obtained by both networks (henceforth referred to as the system), and in Section 3 we introduce a mean field approximation of our system, to aid in locating these equilibria. We conclude that it is unlikely both networks would reach a high equilibrium position, since that would imply individual's node-node relations use both methods of communication, and instead argue that each other's presence negatively impacts each network. Section 4 shows that this causes either one network to be eliminated or both networks find a compromise at low edge density values, and we examine all possible equilibrium positions for the system, together with conditions for their existence.

Finally, in Section 5, we make observations concerning the system's equilibria in the case of highly asymmetric competition.

2. Competing edge dynamics

First we introduce some terminology to define our competing evolving networks.

^{*} Corresponding author. Tel.: +44 118 931 8996.

E-mail addresses: m.c.parsons@pgr.reading.ac.uk (M. Parsons),
p.grindrod@reading.ac.uk (P. Grindrod).

¹ Tel.: +44 118 931 8994.

Following [8,7,10] we define an evolving network, over discrete time steps indexed by $k=1,2,\ldots$, via a sequence of adjacency matrices, say $\{A_k\}$. We shall assume that all edges are undirected and we do not allow any edges connecting a vertex with itself. Thus all of our adjacency matrices lie in the set S_n of binary, symmetric, $n \times n$ matrices having zeros along their main diagonals. We assume the evolving network dynamic is first order in time: at the (k+1)th time step each edge in A_{k+1} will have a birth or death rate that is conditional on A_k . However no new vertices will enter, nor shall any existing vertices be permanently removed from the evolving network. At each time step the evolving network is thus a random network conditional on the evolving network at the previous time step, with a probability distribution $P(A_{k+1}|A_k)$, defined as A_{k+1} ranges over S_n .

We shall assume that presence of each edge in A_{k+1} is determined independently of all other edges. This means that it is sufficient to specify the conditional expectation that each edge is present, given by

$$\langle A_{k+1}|A_k\rangle = \sum_{A_{k+1}\in S_n} A_{k+1} P(A_{k+1}|A_k),$$

rather than dealing with full probability distribution. In fact for such edge-independent conditional random networks we may write

$$\begin{split} P(A_{k+1}|A_k) &= \prod_{i < j} (\langle A_{k+1}|A_k \rangle)_{ij}^{(A_{k+1})_{ij}} (1 - (\langle A_{k+1}|A_k \rangle)_{ij})^{1 - (A_{k+1})_{ij}}, \end{split}$$

demonstrating their equivalence.

Notice that since distinct edges may be conditionally dependent on some of the same information, it is possible for their appearance to be highly correlated over time, despite their independence.

Let the sequence $\{A_k\}$ within S_n denote a Red evolving network defined over a set of n vertices. Similarly let the sequence $\{B_k\}$ within S_n denote a Blue evolving network defined over the same set of n vertices. Then, extending the above ideas, we will assume that both evolving networks have a first order edge-independent dynamic such that each network at each time step is a random network conditionally dependent upon both networks at the previous time step. Then such a competitive dynamic is completely determined by matrix equations of the form

$$\langle A_{k+1}|A_k, B_k\rangle = A_k \circ \left(\mathbf{1} - \Omega_A(A_k, B_k)\right)$$

$$+ (\mathbf{1} - A_k) \circ \Lambda_A(A_k, B_k),$$

$$\langle B_{k+1}|A_k, B_k\rangle = B_k \circ \left(\mathbf{1} - \Omega_B(A_k, B_k)\right)$$

$$+ (\mathbf{1} - A_k) \circ \Lambda_B(A_k, B_k).$$

Here **1** denotes the adjacency matrix for the n-vertex clique (all ones except for the main diagonal); \circ denotes the elementwise (Hadamard) matrix product; $\Lambda_A(A_k, B_k)$ and $\Lambda_B(A_k, B_k)$ denote matrices of conditional edge birth probabilities ($P(\text{edge}_{ij} \in A_{k+1}|\text{edge}_{ij} \notin A_k) \in [0,1]$); and $\Omega_A(A_k, B_k)$ and $\Omega_B(A_k, B_k)$ denote matrices of conditional edge death probabilities ($P(\text{edge}_{ij} \notin A_{k+1}|\text{edge}_{ij} \in A_k) \in [0,1]$).

Now let us be more specific. We define our networks' individual edge birth rates to be based upon a triangulation mechanism [8] (where friends of friends are more likely to become friends, called triadic closure [5]),² and also containing some antagonistic terms. We shall increase the probability of an existing Red edge dying if

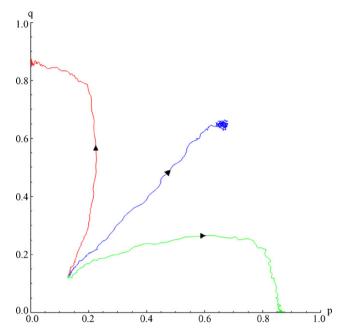


Fig. 1. Three separate simulations of competing networks, modelled according to (1) and (2). In each case the edge densities of the competing networks are plotted against one another at each timestep. Notice that each simulation is performed with the same network parameter values and initial matrix pair, however evolve towards distinct network positions.

a Blue edge is also present between those two vertices, and vice versa. We shall also decrease the probability of a Red edge being born if a Blue edge is already present between those two vertices, and vice versa. Thus we consider

$$\langle A_{k+1}|A_k, B_k\rangle = A_k \circ \left(\mathbf{1}(1 - \omega_A) - \mu_A B_k\right) + (\mathbf{1} - A_k) \circ \left(\delta_A + \epsilon_A A_k^2 - \gamma_A B_k\right), \tag{1}$$

$$\langle B_{k+1}|A_k, B_k\rangle = B_k \circ \left(\mathbf{1}(1 - \omega_B) - \mu_B A_k\right) + (\mathbf{1} - B_k) \circ \left(\delta_B + \epsilon_B B_k^2 - \gamma_B A_k\right), \tag{2}$$

where $\omega_A, \omega_B, \delta_A, \delta_B, \epsilon_A, \epsilon_B, \mu_A, \mu_B, \gamma_A$ and γ_B are all real constants in (0, 1).

Notice that since both A_{k+1} and B_{k+1} are dependent upon A_k and B_k , there is therefore no 'first/late mover advantage' [6] for the Red or Blue network.

Fig. 1 shows the evolution of various synthetic networks in terms of the edge density for the Red and Blue networks, where each simulation starts from the same initial pair of matrices, A_1 and B_1 . Their evolution is modelled according to (1) and (2), with n=39, and the same parameter values for both Red and Blue networks: $\omega=1/25$, $\epsilon=1/110$, $\mu=1/17$, $\delta=1/600$ and $\gamma=1/600$. Notice that multiple apparently stable equilibria exist and that they are reachable from the same initial network pair at the first time step. This highlights the significance of identifying these equilibria for a given network, and motivates the analysis in the next section.

3. Mean field approximation

In order to identify and analyse the long term equilibria, we take the mean field approximation introduced in [8]. Symmetry of the dynamics implies there are no preferred vertices or edges (all edges satisfy the same rules since the birth and death rates have no explicit edge dependencies), so we assume that we may write $\langle A_k \rangle \approx p_k \mathbf{1}$ and similarly $\langle B_k \rangle \approx q_k \mathbf{1}$ where p_k and q_k represent the edge densities of the Red and Blue networks at the kth time step; and hence that these networks are approximated by Erdos–Renyi random graphs. Then the mean field approximation for the

² These are networks that strive to achieve triadic closure where the edge dynamics between two vertices depends, amongst other values, on their current number of neighbours in common.

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