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In search of efficient network structures: The needle in the haystack

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La recherche de réseaux efficaces : l'aiguille dans la botte de foin

Résumé

La modélisation de la formation de réseaux a récemment fait l'objet d'un intérêt croissant en économie. Un des aspects importants relevés dans la littérature est l'efficacité des réseaux. Malheureusement, dès que les fonctions de gain ne sont pas élémentaires, la recherche des réseaux efficaces s'avère être un problème analytique difficile, ainsi que une tâche informatique très lourde, même pour le cas où le nombre d'agents est faible. Dans cet article, nous explorons la possibilité d'utiliser les algorithmes génétiques (AG) pour identifier les formes efficaces de réseaux dans la mesure où ces algorithmes ont démontré leur capacité à résoudre des problèmes d'optimisation complexes. La robustesse de leur capacité à prédire les réseaux efficaces est testée sur deux modèles simples introduits par Jackson et Wolinski (1996), modèles pour lesquels les réseaux efficaces sont analytiquement connus pour l'ensemble de l'espace des paramètres. Nous démontrons aussi que cette approche permet d'obtenir des résultats exploratoires dans le modèle de connexion linéaire spatialisé de Johnson et Gilles (2000), modèle dans lequel l'allocation efficace des connexions bilatérales est guidée par des forces contradictoires qui favorisent soit une structure centralisée autour d'un agent, soit des réseaux uniquement localement connectés.

Mots-clés : Réseaux; Efficience; Algorithmes génétiques

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Abstract

The modelling of networks formation has recently become the object of an increasing interest in economics. One of the important issues raised in this literature is the one of networks efficiency. Nevertheless, for non trivial payoff functions, searching for efficient network structures turns out to be a very difficult analytical problem as well as a huge computational task, even for a relatively small number of agents. In this paper, we explore the possibility of using genetic algorithms (GA) techniques for identifying efficient network structures, because the GA have proved their power as a tool for solving complex optimization problems. The robustness of this method in predicting optimal network structures is tested on two simple stylized models introduced by Jackson and Wolinski (1996), for which the efficient networks are known over the whole state space of parameters values. We also show that this approach can provide new exploratory results for the linear-spatialized connections model of Johnson and Gilles (2000), in which the efficient allocation of bilateral connections is driven by contradictory forces that push either for a centralized structure around a coordinating agent, or for only locally and evenly distributed connections.

Key words: Networks; Efficiency; Genetic Algorithms

JEL : D85; C61

In search of efficient network structures: The needle in the haystack

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Abstract

The modeling of networks formation has recently become the object of an increasing interest in economics. One of the important issues raised in this literature is the one of networks efficiency. Nevertheless, for non trivial payoff functions, searching for efficient network structures turns out to be a very difficult analytical problem as well as a huge computational task, even for a relatively small number of agents. In this paper, we explore the possibility of using genetic algorithms (GA) techniques for identifying efficient network structures, because the GA have proved their power as a tool for solving complex optimization problems. The robustness of this method in predicting optimal network structures is tested on two simple stylized models introduced by Jackson and Wolinski (1996), for which the efficient networks are known over the whole state space of parameters values. We also show that this approach can provide new exploratory results for the linear-spatialized connections model of Johnson and Gilles (2000), in which the efficient allocation of bilateral connections is driven by contradictory forces that push either for a centralized structure around a coordinating agent, or for only locally and evenly distributed connections.

Keywords: Networks, Efficiency, Genetic Algorithms

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1 Introduction

Modelling networks has recently become the object of an increasing interest in economics and other social sciences. Indeed, in many situations, not only local interactions but the whole network structure matter for determining individual and collective outcomes of various activities. A large set of examples includes, among others, networks of firms' board members, scientific collaboration networks, friendship networks for information exchange on job opportunities, buyers sellers networks, or co-invention networks. Two main questions are central in the economic approach (Jackson, 2004). Which networks are likely to form when agents choose their connections in order to maximize given individual payoffs structures? How efficient are networks that emerge from self-interested agents' choices, that is, how individual incentives for links formation affect social welfare?

A first stylized economic model that tackles those two questions is the *coauthor model*, introduced by Jackson and Wolinski (1996) (hereafter **JW96**). It considers the simple strategies of researchers in accepting (or refusing) to spend time in bilateral collaborations with peers for writing papers. Agents aim to efficiently allocate their time on bilateral research projects. The simple specification of the individual payoffs in these models allows the authors to obtain systematic analytical results on graphs efficiency and partial results on networks stability. In a second stylized model, called the *connections model*, also introduced by JW96, links represent relationships (for example, friendships) between individuals. The latter benefit from their direct and costly connections and also from indirect connections, through the relational network of their partners. Thus, agents try to maximize the value generated from direct and indirect connections taking into account the cost of direct connections, and avoiding superfluous links. Nevertheless, the efficient and stable network structures in these two models are very simple (complete network, empty network, complete star, disconnected pairs) and have little in common with real social or economic networks.

More recently, Johnson and Gilles (2000) (hereafter **JG00**) and Carayol and Roux (2004, 2006) propose spatialized variations of the connections model. They assume that agents are located at equidistant intervals respectively on a linear and on a circular world and assume that link formation costs increase with spatial distance. Such models generate emerging networks that are much complex and which tend to correspond more to the empirically observed social networks¹. Nevertheless, it becomes then difficult to compute both analytically and numerically the efficient network structures². It is only for specific values of the parameters that efficient networks are known. Therefore, one can not systematically appreciate to what extent emerging networks are efficient and whether they are structurally different from the optimal networks. This constitutes an issue that may be faced by many network formation models.

In this paper, we propose a technique intended to solve this problem. As a matter of fact, the connection structure of any network can be expressed as an ordered sequence of binary elements (a vector of bits). The value function maps each of such sequences onto the value space. The search for efficient networks can hence be seen as an optimization problem on the space of such sequences *i.e.*

¹In particular, Carayol and Roux (2006) obtain, in a dynamic setting and for a wide set of parameters, networks that exhibit the Small World properties (i.e. highly clustered connection structures and short average path length).

²Even for a relatively small numbers of players, the number of possible networks becomes very large. JG00 observe that the number of possible networks for n agents is $\sum_{k=1}^{c(n,2)} c(c(n,2), k) + 1$ where, for every $k \leq n$, $c(n, k) := n! / (k!(n-k)!)$. For example, when $n = 8$, the number of possible networks exceeds 250 million.

the space of all possible networks. We propose here to use a tool well designed for solving optimization problems of such kind, namely *Genetic Algorithms*. Therefore, the first aim of the present study is to develop and to test this method. GA performance is assessed on the two stylized simple models (the connections model and the coauthor model) introduced by JW96, for which analytical results on network efficiency cover the whole state space of the parameters values, as well as on the *linear spatialized connection model* of JG00 for which benchmark efficient networks are available (using analytical or numerical techniques) for some regions of the parameters values.

The second aim of the paper is to provide the first explorative use of the GA optimization tool to determine efficient networks when no benchmark is readily available. Therefore, we intend to show that this new approach is effectively useful in the exploration of the efficient structures in models of networks formation for which we can not systematically rely on analytical results. The linear spatialized connections model of JG00 is a rather good candidate, essentially for two main reasons. Firstly, since the efficient network structures are known for some subsets of the parameter space of this model, it is possible to benchmark the capacity of the GA approach to correctly find efficient networks in this very model. The second reason is related to the economic analysis. This model exhibits simultaneously positive externalities to link formation that decay geometrically with social distance, and link formation costs that increase linearly with the spatial distance. Efficiency in this model is thus driven by two contradictory forces. On the one hand, cost minimization strongly favours the sole formation of local connections. On the other hand, the maximization of externalities pleads for network coordination around some central and highly connected agent (thus even to distant agents through costly connections). The exploratory analysis we propose provides new results that highlight the circumstances under which the networks should be either only locally connected, or centrally structured around a key player who may be complemented by some local stars.

The article is structured as follows. The next section begins with some basic definitions on graphs and efficiency. Section 3 presents the three stylized models developed in JW96 and JG00 and efficient network configurations in these models. Section 4 introduces the Genetic Algorithms. The performance of the GA in determining network efficiency in the stylized models are presented and discussed in Section 5. Exploratory results for the spatialized connections model of JG00 are given in Section 6. The last section briefly concludes.

2 Background notions and definitions

In this section, we introduce the notation and the basic notions for studying networks efficiency. We limit our attention to the case of non-directed graphs, where bonds are symmetric and built on mutual consent, as it occurs in many real social networks. We begin with some basic notations for networks in this context. Then, we present the notions of network value and efficiency.

2.1 Basic notions on graphs

We consider a fixed and finite set of n agents, $N = \{1, 2, \dots, n\}$ with $n \geq 3$. Let i and j be two members of this set. Agents are represented by the nodes of a non-directed graph, which's edges represent the links between them. The graph constitutes the relational network between the agents. A link between two distinct agents i and $j \in N$ is denoted ij . A graph g is a list of unordered

pairs of connected and distinct agents. Formally, $\{ij\} \in g$ means that the link ij exists in g . We define the complete graph $g^N = \{ij \mid i, j \in N\}$ as the set of all subsets of N of size 2, where all players are connected to all others. Let $g \subseteq g^N$ be an arbitrary collection of links on N . We define $G = \{g \subseteq g^N\}$ as the finite set of all possible graphs between the n agents.

Then for any g , we define $N(g) = \{i \mid \exists j : ij \in g\}$, the set of agents who have at least one link in the network g . We also define $N_i(g)$ as the set of neighbors agent i has, that is: $N_i(g) = \{j \mid ij \in g\}$. The cardinal of that set $\eta_i(g) = \#N_i(g)$ is called the *degree* of node i . The total number of links in the graph g is $\eta(g) = \#g = \frac{1}{2} \sum_{i \in N} \eta_i(g)$, while the average number of neighbors is given by $\bar{\eta}(g) = 2\eta(g)/n$.

A *path* connecting i to j in a non empty graph $g \in G$, is a sequence of edges between distinct agents such that $\{i_1i_2, i_2i_3, \dots, i_{k-1}i_k\} \subset g$ where $i_1 = i$, $i_k = j$. The length of a path is the number of edges it contains. Let $i \longleftrightarrow_g j$ be the set of paths connecting i and j on the graph g . The set of *shortest paths* between i and j on g noted $i \xleftrightarrow{g} j$ is such that $\forall k \in i \xleftrightarrow{g} j$, we have $k \in i \longleftrightarrow_g j$ and $\#k = \min_{h \in i \longleftrightarrow_g j} \#h$. We define the *geodesic distance* between two agents i and j as the number of links of the shortest path between them: $d(i, j) = d_g(i, j) = \#k$, with $k \in i \xleftrightarrow{g} j$. When there is no path between i and j , their geodesic distance is conventionally infinite: $d(i, j) = \infty$. A graph $g \subseteq g^N$ is said to be *connected* if there exists a path between any two vertices of g .

Two other typical graphs can be introduced here. The *empty graph*, denoted g^\emptyset , is such that it does not contain any links. A non empty graph $g \in G$ is a (complete) *star*, denoted g^\star , if there exists $i \in N$ such that if $jk \in g^\star$, then either $j = i$ or $k = i$. Agent i is called the center of the star. Notice that there are n possible stars, since every node can be the star center.

2.2 Networks value and efficiency

The payoffs that individuals naturally obtain from their position in the network result from the difference between the benefits derived from this position and the costs borne to maintain it. Let $\pi_i(g)$ be the net individual payoff that the agent i receives from maintaining his position in the network g , with $\pi_i : \{g \mid g \subseteq g^N\} \rightarrow \mathfrak{R}$.

We consider the strongest notion of efficiency which is preferred in the economics of networks literature since the pioneering work of JW96. Let the network social value $\pi(\cdot)$ be computed by simply summing individual payoffs³. The total value of a graph g , with $\pi(\emptyset) = 0$ is given by:

$$\pi(g) = \sum_{i \in N} \pi_i(g) \tag{1}$$

A network is then said to be efficient since it maximizes this sum. The formal definition follows.

Definition 1 *A network $g \subseteq g^N$ is said to be efficient if it maximizes the value function $\pi(g)$ on the set of all possible graphs $\{g \mid g \subseteq g^N\}$ i.e. $\pi(g) \geq \pi(g')$ for all $g' \subseteq g^N$.*

It should be noticed that several networks can lead to the same maximal total value. For example, if we consider strictly homogenous agents, any isomorphic graph of an efficient network is also efficient.

We will use this definition of efficiency (Definition 1) in this paper.

³One can also consider that the social value of a network could be reallocated among the individuals of the network, for example, through taxes or subsidies, in order to take into account their investment in this network (for example, in the case of a star, the center of this network supports important costs for direct connections and thus could be compensated for this). For much more details on the question of allocation rules, see Jackson (2004).

3 Networks efficiency in stylized models of network formation

In this section, we present three stylized models of network formation (the two first models were introduced by JW96 while the third was proposed by JG00) and predictions regarding network efficiency.

3.1 The coauthor model

The coauthor model intends to represent the simple strategies of researchers in accepting (or refusing) to spend time in bilateral collaborations, with peers, for writing articles. Agents aim to efficiently allocate their time on bilateral research projects. The amount of time that an agent can spend on a project is inversely related to the number of projects he is involved in. Therefore, indirect connections produce negative effects on agents' productivity: an additional collaboration generates a negative externality on actual coauthors. In the initial model there is no explicit cost for direct connections. In the version presented here we introduce such costs as in Carayol and Roux (2004). Formally, the net profit received by any agent i at period t , is given by the following equation:

$$\pi_i(g) = \sum_{j \in N_i(g)} \left(\frac{1}{\eta_i(g)} + \frac{1}{\eta_j(g)} + \frac{1}{\eta_i(g)\eta_j(g)} - c \right) \quad (2)$$

when $\eta_i(g) \neq 0$, and it is assumed that $\pi_i(g) = 0$ otherwise.

Recall that $\eta_i(g)$ is the number of agents directly connected to i (i 's coauthors). As a consequence, each agent i benefits from any of his coauthors j by the fraction of his time (or efforts normalized to unity) he spends working with him $1/\eta_i(g)$, and by the fraction of time j spends to write a paper with i , $1/\eta_j(g)$. The term $1/\eta_i(g)\eta_j(g)$ accounts for some increased productivity for agents who spend a high share of their time working together. We consider here that the agent also bears a unitary cost c to sustain each of his direct connections.

The predictions regarding network efficiency in this model are the following.

Proposition 1 (extension of the Proposition4 in JW96). *Assume that n is even.*

(i) *If $c < 3$, the unique efficient network in the coauthor model is a graph consisting of $n/2$ separate pairs.*

(ii) *If $c > 3$, the unique efficient network is the empty network g^\emptyset .*

The proofs when $c = 0$ are given by JW96. When $0 < c < 3$, it can be easily shown that $n(3 - c)$ is the maximal total value obtained in this model ($n(3 - c)$ is the value of $n/2$ separate pairs corresponding to: $\forall i, j \in N, \eta_i(g) = \eta_j(g) = \eta_i(g)\eta_j(g) = 1$). When $c > 3$, any connected pair of such network generates a negative value, and any non empty network (including any network composed of a given number of separate pairs) has a negative value. Therefore, the empty network which generates a null value becomes the only efficient network.

3.2 The connections model

In the connections model, links represent individuals' relationships. One can think of those links as the support of communications that produce informational benefits in terms of job opportunities or innovative ideas. In such a context, agents benefit also from indirect connections, through the

relational network of their partners. Nevertheless, the communication is not perfect: the positive externality deteriorates with the relational distance between indirectly connected agents. Formally, there is a decay parameter which stands for the quality of information flows through each bilateral connection. Moreover, individuals' direct connections involve also some costs in this model. As a consequence, agents try to maximize the value generated from direct and indirect connections, avoiding superfluous connections. It follows that in this model nobody wants to be the center of a star because it is too costly, but everybody wants to be connected to a star.

The net profit received by any agent i , is given by the following simple expression:

$$\pi_i(g) = \sum_{j \in N \setminus i} \delta^{d(i,j)} - \sum_{j:ij \in g_t} c_{ij} \quad (3)$$

where $d(i, j)$ is the geodesic distance between i and j . $\delta \in]0; 1[$ is the decay parameter and $\delta^{d(i,j)}$ gives the payoffs resulting from the (direct or indirect) connection between i and j . It is a decreasing function of the geodesic distance since δ is less than unity. If there is no path between i and j , then $d(i, j) = \infty$ and thus $\delta^{d(i,j)} = 0$. Finally, c_{ij} is the cost born by i to maintain a direct connection with j . For simplicity, JW96 assume that $c_{ij} = c$ a positive parameter.

The predictions of this model regarding efficient networks are summarized in the following proposition and in Figure 1.

Proposition 2 (JW96, Proposition 1). *The unique efficient network in the connections model is:*

- (i) the empty network g^0 if $c > \delta + \frac{n-2}{2}\delta^2$, (border C_1 in Figure 1);
- (ii) the star g^* if $\delta - \delta^2 < c < \delta + \frac{n-2}{2}\delta^2$;
- (iii) the complete graph g^N if $c < \delta - \delta^2$, (border C_2 in Figure 1).

Proofs can be found in JW96.

3.3 The linear spatialized connections model

We now turn to a spatialized variant of the connections model that has been introduced by JG00. Agents are arranged on a line, according to their index and at unitary intervals so that the geographic distance between i and j is defined as $l(i, j) \equiv |i - j|$. Moreover, relying on Debreu's (1969) hypothesis according to which closely located players incur lower costs to establish communications, payoffs linearly decrease with geographic distance. Formally, the net profit received by any agent i is still given by the standard connections model (equation 3), but where c_{ij} is now differently computed. It is proportional to the geographic distance separating i and j ($c_{ij} \propto l(i, j)$). Moreover, as a normalization device, and in order to account for an inverse relation between the costs and the size of the population, JG00 implicitly assume that, for all n , the costliest possible connection always costs unity: $\max_{i,j \in N} c_{ij} \equiv 1$. In the linear metric we have $\max_{i,j \in N} l(i, j) = l(1, n) = n - 1$ and these assumptions logically imply that

$$c_{ij} = l(i, j) / (n - 1). \quad (4)$$

The analytical predictions regarding network efficiency in this model are summed up in the following proposition.

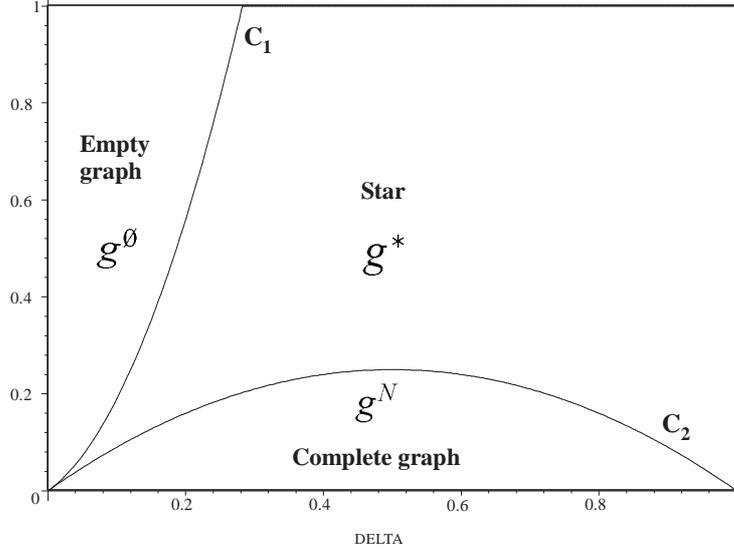


Figure 1: Efficient graphs in the connections model depending on δ and c

Proposition 3 (JG00, Theorem 1).

- (i) If $\frac{1}{n-1} > \delta + \frac{1}{n-1} \sum_{k=2}^{n-1} (n-k) \delta^k$, the unique efficient network is the empty network g^\emptyset .
- (ii) If $\delta < \frac{1}{n-1} < \delta + \frac{1}{n-1} \sum_{k=2}^{n-1} (n-k) \delta^k$, the unique efficient network is the chain g° .

Proofs can be found in JG00. A chain g° corresponds to a network where all agents are connected to their immediate geographic neighbors: $\forall i, j \in N, ij \in g^\circ$ iff $l(i, j) = 1$.

Since this proposition concerns very limited regions of the values of δ , JG00 propose to numerically explore all possible networks. However, the number of possible networks rapidly becomes very large with n (see footnote 1) and therefore this technique rapidly meets computational boundaries. Therefore JG00 restrain themselves to computing efficient networks when $n \leq 7$. Their numerical predictions (see Figure 5 in JG00) are synthesized in Table 1⁴. The network structures mentioned in this table are defined as follows⁵: $g^1 = \{12, 23, 24, 34, 45\}$, $g^A = \{12, 23, 34, 35, 45, 56\}$, $g^B = \{12, 13, 23, 34, 35, 45, 56\}$, $g^C = \{13, 23, 34, 35, 45, 46\}$, $g^D = \{13, 23, 34, 35, 56\}$, $g^E = \{12, 23, 24, 34, 45, 46, 56, 67\}$, $g^F = \{12, 13, 23, 34, 35, 45, 56, 57, 67\}$, $g^G = \{12, 13, 23, 24, 34, 45, 46, 47, 56, 67\}$, $g^H = \{12, 24, 34, 45, 46, 67\}$, $g^{**} = \{14, 24, 34, 45, 46, 47\}$.

g^{**} is a complete star network of 7 agents with the agent in the middle of the line (agent 4) being the center of the star.

⁴JG00 also have some results for $n = 3$ and 4 which we do not investigate and thus do not report here.

⁵These structures should be considered as encompassing the mirror network obtained by switching identities of all agents $i \in N$ to $N + 1 - i$.

| $n = 5$ | | $n = 6$ | | $n = 7$ | |
|------------------|---------------|------------------|---------------|------------------|---------------|
| δ | g | δ | g | δ | g |
| [0, 0.2149] | g^\emptyset | [0, 0.1726] | g^\emptyset | [0, 0.1464] | g^\emptyset |
| [0.2150, 0.4287] | g° | [0.1727, 0.3141] | g° | [0.1465, 0.2467] | g° |
| [0.4288, 0.8128] | g^1 | [0.3142, 0.3375] | g^A | [0.2468, 0.3480] | g^E |
| [0.8129, 1) | g° | [0.3376, 0.7236] | g^B | [0.3481, 0.4299] | g^F |
| | | [0.7237, 0.8788] | g^C | [0.4300, 0.7886] | g^G |
| | | [0.8789, 0.9306] | g^D | [0.7887, 0.8811] | g^{**} |
| | | [0.9307, 1) | g° | [0.8812, 0.9030] | ? |
| | | | | [0.9031, 0.9694] | g^H |
| | | | | [0.9695, 1) | g° |

Table 1: Numerical computations of efficient networks by JG00 for $n = 5, 6, 7$ and the possible values of δ . The sign ? refers to an uncharacterized situation.

4 Searching for efficient networks: an approach using Genetic Algorithms

Searching for efficient network structures is in general a difficult analytical task. But, once the payoff structure is well defined in relation with the connection structure, one is tempted to explore this question using more heuristic strategies. As a matter of fact, the connection structure of the network can be expressed as a matrix of bits (1 for connection or 0 for absence of connection) and the payoff structure can assign a value to each of such matrices. The search for efficient networks can hence be seen as an optimization problem in the connection-matrix space, *i.e.* the space of all possible networks. This optimization problem yields analytical solutions only for simple payoff structures. We examine here a numerical tool for optimization: genetic algorithms (**GA**) that have proved their efficacy in optimization problems where the potential solutions can be represented as binary strings. Our networks can effectively be quite easily represented as binary strings.

4.1 Representing networks as binary strings

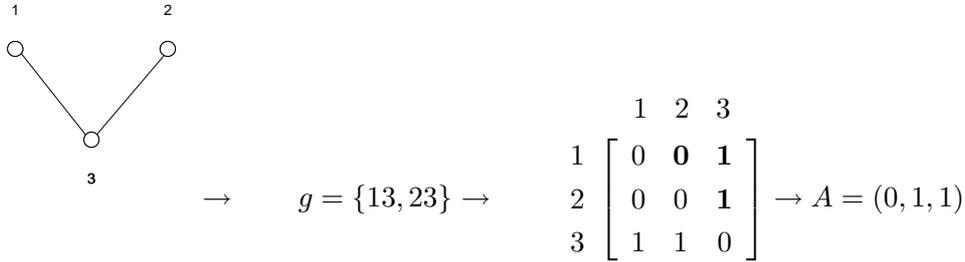
Our problem is to find the networks g which maximize social value π as given by the equation 1 over the set of all possible networks G . In order to use the GA for this optimization problem, we need to represent our networks as binary strings (sequences of bits – 1 or 0).

Consider first that any network with n agents (whether directed or not, eventually with self-connections) can, without loss of generality, be represented by a connection matrix of size $n \times n$ of binary elements. Given that all networks consider here are undirected (i is connected to j *iff* j is also connected to i) and that self-connections are excluded, the upper triangular part of this connection matrix, excluding the diagonal, provides complete information on the network structure. As a consequence, the vector composed by all the connection *bits* of this upper triangular part in some conventionally chosen order sums up the network structure. Thus for a network of n agents, this vector is a binary string of *length* $L = (n^2 - n) / 2$.

In a genetic algorithm, undirected networks can hence be formally represented as *chromosomes*

defined as sequences of binary elements: $A = (a_1, a_2, \dots, a_L)$ with $a_i \in \{0, 1\}, \forall i \in \{1, 2, \dots, L\}$.

In the example below with $n = 3$ agents, the undirected network $g = \{13, 23\}$ is fully characterized by the chromosome $A = (0, 1, 1)$, the length of which is $L = (3^2 - 3) / 2 = 3$.



Once we represent it, we can compute the value of a connection matrix (its *fitness*) using the equation 1 and utilize the Genetic Algorithms to search for matrices with the highest value.

4.2 Genetic Algorithms: How do they work?

Genetic algorithms (**GA**) are numerical optimization techniques developed by John Holland (*see* for example Holland (2001), which has initially been published in 1975). GA transpose to other problems the strategies that the biological evolution has successfully used for *exploring* complex fitness landscapes. The search for an optimum by a GA corresponds to the evolution of a population of candidate solutions through *selection*, *crossover* (combination) and *mutation* (random experiments). The GA have been used for solving a very large set of problems directly, or indirectly as a component of a classifier system. Goldberg (1991) gives quite an exhaustive account of the characteristics of the GA and of their applications (for a more recent survey in French, *see* Vallée and Yıldızoğlu (2004)). For applications of the GA as a learning algorithm, *see* Yıldızoğlu (2002).

```

procedure evolution program
begin
  t ← 0
  (1) initialize P(t)
  (2) evaluate P(t)
  while (not termination-condition) do
  begin
    t ← t + 1
    (3) select P(t) from P(t - 1)
    (4) alter P(t)
    (5) evaluate P(t)
  end
end

```

Figure 2: The structure of an evolutionary program (Michalewicz, 1996)

The *canonical genetic algorithm* makes evolve a population of binary strings (chromosomes composed of 1 and 0). The size of the population m is given. It is the source of one of the strengths of the

GA: implicit parallelism (the exploration of the solution space using several candidates in parallel). The population of chromosomes at step t (a generation) is denoted $P(t) = \{A_j\}_t$ with $\#P(t) = m$, and $\forall t = 1, 2 \dots T$ with T the given total number of generations. Notice that T is the other source of the strengths of the GA. The algorithm (randomly) generates an initial population $P(0)$ of candidate chromosomes which are evaluated at each period using the fitness (value) function. They are used for composing a new population at the next period $P(t+1)$. Figure 2 gives the general structure of an evolutionary algorithm and the GA are part of this family.

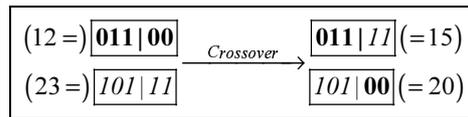


Figure 3: A simple example of crossover operation

Each chromosome has a probability of being **selected** that is increasing in its fitness. The members included in the new population are recombined using a **crossover** mechanism (see Figure 3). The crossover operation introduces controlled innovations in the population since it combines the candidates already selected in order to invent new candidates with a potentially better fitness. Moreover, the **mutation** operator randomly modifies the candidates and introduces some random experimenting in order to more extensively explore the state space and escape local optima. Typically, the probability of mutation is rather low in comparison with the probability of crossover because otherwise the disruption introduced by excessive mutations can destruct the hill-climbing capacity of the population. Finally, an **elitism** operator can be used which ensures that the best individual of a population will be carried to the next generation. The Figure 4 gives a deliberately trivial example of optimization for illustrative purposes.

| <i>Population at date t</i> | <i>Fitness: f(x)=x²</i> | <i>Expected number: f(x)/Mean_t</i> | <i>Effective number proportionally drawn</i> | <i>New population</i> |
|-----------------------------------|------------------------------------|---|--|-----------------------|
| 1) 00011 (=3) | 1) 9 | 1) 0.0 | 1) 0 | 1) 10111 (=23) |
| 2) 01100 (=12) | 2) 144 | 2) 0.6 | 2) 1 | 2) 01100 (=12) |
| 3) 10111 (=23) | 3) 529 | 3) 2.4 | 3) 2 | 3) 10111 (=23) |
| | Mean _t =227 | Sum=3 | Sum=3 | |
| <i>Crossover (3)-(2) at bit 3</i> | | | | |
| 1) 10111 (=23) | | | | |
| 2) 01111 (=15) | | | | |
| 3) 10100 (=20) | | | | |
| <i>Mutation (1)</i> | | | | |
| 1) 11111 (=31*) | | | | |
| 2) 01111 (=15) | | | | |
| 3) 10100 (=20) | | | | |
| <i>Population at date t+1</i> | | | | |
| 1) 11111 (=31) | | | | |
| 2) 01111 (=15) | | | | |
| 3) 10100 (=20) | | | | |

Simple application of GAs to optimisation of the function $f(x)=x^2$ over the interval 0-31. Integers are coded with five bits binary code: 00001=1, 11111=31. The example uses an initially random population of 3 members and the GA constructs a new population through selective reproduction, combination (crossover) and random experiments (mutation). In this schematic example, the GA attains the optimum (31) in one period. For each string, the crossover, its position and the partner, as well as mutation position are chosen randomly. The mutation bit simply switches its value: 0->1 or 1->0. **This process is controlled by: population size, bit-string size, probability of crossover and probability of mutation.**

Figure 4: A simple example of genetic algorithm

In our approach, each mutation corresponds either to the creation of a new link in the network or to the deletion of an existing link. The impact of the crossover is more dramatic: it combines subnets belonging to two different networks in order to connect them, and create two new networks

in the population (in replacement of their parents). Our results show below that these two operations, combined with selection and elitism, provide a very effective way of finding efficient network structures.

4.3 Genetic Algorithms: Why do they work?

The apparent simplicity of the GA should not lead us to underestimate their power. Even if their mechanisms are mainly heuristic, analytical results concerning this power have been established in the literature, under the heading of the *schemata theorem* that shows that the strength of the GA comes from its capacity to make evolve *schemata* in a direction that increases the average fitness of the population (Chapter 6, Holland, 2001).

A *schemata* is a general template that can correspond to a large class of different chromosomes. The schemata is constructed using an alphabet slightly different from the one used for coding specific chromosomes: the initial alphabet $\{0, 1\}$ is completed by a third letter $\{*\}$ that is also called the *don't care* symbol and that can replace indifferently the other two letters. Hence the schemata $0*0$ can cover both the chromosomes 000 and 010 . The schemata is a tool for representing the general structure of the chromosome classes (depending on the positions covered by the *don't care* symbol). We can for example distinguish between abstract schemata with many $*$ letters (like $**1**$) and specific ones (like 00100 or 11111 that are both covered by the preceding schemata). As a consequence, the schemata corresponds to the tool that should be used for characterizing the structure of the population because a schemata can correspond to several chromosomes in the population. *The schemata theorem* is based on the observation that the real object of the evolutionary operators (selection, crossover and mutation) is the schemata.

The *selection operator* implies that each schemata in the population will diffuse with a speed that is equal to the ratio of the average fitness of the schemata to the average fitness in the population (Holland, 2001). Moreover this diffusion takes place in parallel for all schemata in the population (if the length of the chromosomes is L and the size of the population is m , there is up to $m2^L$ schemata in the population) and this establishes the implicit parallelism of the GA. As a consequence, the selection operator gives an exponentially increasing space to the schemata with a fitness that is higher than the average fitness in the population and, symmetrically, an exponentially decreasing space to the schemata below the average. Without any novelty, the first kind of schemata end up by dominating the population and the latter becomes homogenous quite quickly. But, nothing assures that this population contains optimal solutions.

Novelty is necessary for exploring the state space and the genetic operators (*crossover* and *mutation*) are necessary for introducing novelty. If we define the *order* of the schemata as the number of specific bits and the *defining length* of the schemata as the distance between the two outmost specific bits⁶, the schemata theorem establishes that schemata of low order with a small defining length and above the average fitness will diffuse quickly in the population. The schemata theorem is the major results behind the GA but, complementary specific results have been more recently established using approaches based on quantitative genetics or Markov chains (see Mitchell (1996), chapter 4, for a presentation of the theoretical foundations of GA and Dawid (1999)).

⁶For the schemata $1*0*1$, the order is 3 and the defining distance is $5 - 1 = 4$.

5 Robustness assessment of the GA for computing efficient networks

We test whether the GA is a robust tool for finding out the optimal social network structures. To this end, we use the GA to determine the optimal network structures in configurations for which analytical results do exist.

The Java *JGAP*⁷ library is used to implement the GA based on binary chromosomes. The GA that we use is *elitist* and its probability of crossover and mutation are both computed by *JGAP*⁸. The relevance of the GA as a search algorithm for efficient networks is tested in the two stylized models presented in Section 3: the coauthor model, the connections model and the linear spatialized connection model.

For each model, we execute a fixed number of simulations (*NSIM*) in order to reasonably cover the parameter space (possible configurations are explored using Monte Carlo procedures for randomly drawing all significant parameters). For each of the *NSIM* configurations, the GA is run a given number of generations in order to obtain the final candidate network (the efficient network predicted by the GA). We confront this network structure with the one that is analytically determined. Randomly drawn configurations (values between 50 and 500) of the parameters of the GA (*m* the number of chromosomes in the population and *T* the number of generations) were tried so as to assess their impact on the performance of the GA. Their impact is only reported in the connections model since they do not affect significantly the GA performance for the two other models.

5.1 In the coauthor model

We use here GA for computing the optimal network type in the coauthor model of JW96, extended in Carayol and Roux (2004), as presented in Section 3. We run 500 simulations using these specifications and with even $n \in [6, 20]$, and $c \in [0, 4]$. The results of the simulations are given in Figure 5. These results are perfectly in accordance with the Proposition 1. We consequently get a rate of success of 100% with the GA. Figure 6 gives some examples of the optimal networks found by the GA.

Proposition 4 *The GA is always able to find efficient networks in the coauthor model (with even n such that $5 < n \leq 20$ and with $c \in [0, 4]$).*

5.2 In the connections model

As we have seen in Section 3, the connections model admits three different types of efficient networks: the empty graph (g^\emptyset), the complete graph (g^N) and the star (g^*), depending on the parameters values (c , δ and n).

As a first step, we compute 1,000 uniform independent random draws of the model parameters (the number of agents n and the payoffs parameters c and δ), in predefined value spaces ($5 \leq n < 20$; $c, \delta \in]0, 1[$). For each combination, we compute the efficient network according to the Proposition 2. We then compare the prediction of the GA with the theoretical efficient network in order to check the robustness of the GA method.

⁷<http://jgap.sourceforge.net/>

⁸Probability of crossover is 0.5 and the probability of mutation is 1/15.

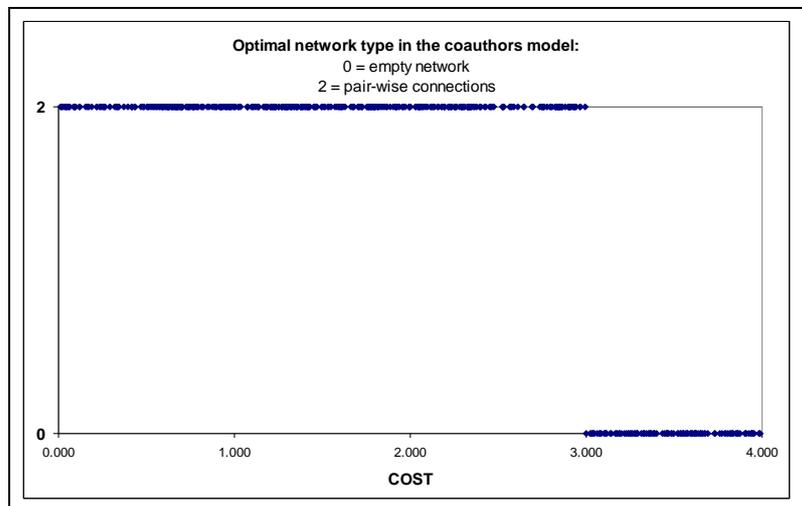


Figure 5: Optimal networks in the coauthor model

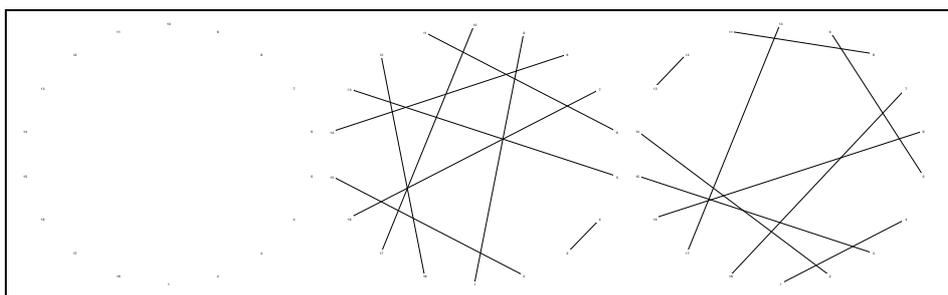


Figure 6: Typical efficient networks obtained for the coauthor model: the empty network when $c > 3$ and dissociated pairs when $c < 3$.

Table 2 provides the share of correct predictions of the GA for different values of n and for the different optimal network structures (that should be predicted). The results are summarized in the following propositions.

Proposition 5 *In the connections model, both when g^\emptyset or g^N is the efficient structure, the GA remarkably finds them whatever n (with $5 \leq n < 20$). It is only when g^* is the efficient network and n increases that the GA might provide some incorrect estimations of the efficient networks.*

For example, when $n = 12$, the GA is deceived in 3% of the cases corresponding to a star as the optimal network.

Proposition 6 *The probability that the GA provides a correct prediction of the connections model globally decreases with the number of agents n , whereas it increases with the number of chromosomes m and with the number of generations T .*

Indeed, errors are partly due to an inefficient GA characterized by too few chromosomes or too few generations. Nevertheless, we cannot establish a monotonic relationship between these two dimensions of the GA and its effectiveness. We just empirically observe a region of best effectiveness around 300 for the number of chromosomes and the number of generations. We hence use this value in the next point that we explore.

| Efficient network # of agents | g^* | g^\emptyset | g^N |
|----------------------------------|-------|---------------|-------|
| 5 | 1 | 1 | 1 |
| 6 | 1 | 1 | 1 |
| 7 | 1 | 1 | 1 |
| 8 | 1 | 1 | 1 |
| 9 | 0.98 | 1 | 1 |
| 10 | 1 | 1 | 1 |
| 11 | 1 | 1 | 1 |
| 12 | 0.97 | 1 | 1 |
| 13 | 0.87 | 1 | 1 |
| 14 | 0.97 | 1 | 1 |
| 15 | 0.87 | 1 | 1 |
| 16 | 0.76 | 1 | 1 |
| 17 | 0.67 | 1 | 1 |
| 18 | 0.76 | 1 | 1 |
| 19 | 0.71 | 1 | 1 |
| Average | 0.90 | 1 | 1 |

Table 2: Proportion of correctly predicted efficient networks depending on the number of agents and the efficient network

In order to explore more in detail these deceiving cases, we run 500 simulation experiments exclusively dedicated to the randomly drawn cases for which the star (g^*) is the optimal network.

As explained above, the GA is used from this point on with $m = T = 300$. These experiments are reported in Table 3. We observe therein that when $n < 12$, the GA offers only correct predictions. When $n \geq 12$ the GA is not always able to find the correct graph shape (g^*). The probability of error, conditional to $20 > n \geq 12$, is 0.126. The non linearity of the network value state space leads the GA to stabilize on local maxima. Nevertheless, even when deceived, the GA finds networks that have an average social value equal to 98.66% the social value of g^* .

| # of agents | Share of good predictions | # of observations |
|-------------|---------------------------|-------------------|
| 5 | 1 | 25 |
| 6 | 1 | 29 |
| 7 | 1 | 31 |
| 8 | 1 | 31 |
| 9 | 1 | 30 |
| 10 | 1 | 36 |
| 11 | 1 | 32 |
| 12 | 0.94 | 35 |
| 13 | 0.93 | 27 |
| 14 | 0.95 | 39 |
| 15 | 0.90 | 41 |
| 16 | 0.82 | 33 |
| 17 | 0.69 | 39 |
| 18 | 0.92 | 37 |
| 19 | 0.86 | 35 |
| Average | 0.90 | 500 |

Table 3: Proportion of correctly predicted g^* configurations with $m = T = 300$

In order to better understand the nature of the deceptive configuration, we address the following question: are mistaken predictions uniformly distributed over the state space (c, δ) for which stars are optimal networks ? The Figure 7 represents all experiments performed for which the star is the optimal network in the (c, δ) space, in accordance with the analytical predictions summed up in Figure 1. The black dots on this figure represent the experiments for which the GA fails. If we compare the position of these dots on the graph with the borders in Figure 7, it clearly appears that the mistakes are not uniformly distributed, but located close to the borders (C_1 and C_2) of the regions where optimal networks are different. Given that the crossover and mutation operators explore the state-space in a discontinuous manner, they make the GA jump from one side of the border to the other, making very difficult the finding of the optimal graph. Everywhere else, the GA is efficient in finding the efficient star network.

Proposition 7 *When g^* is the optimal network of the connections model, the GA may fail to systematically find it when c and δ take values close from those that generate different optimal networks. In these cases, the predicted networks still have an average social value equal to nearly 99% the social value of g^* .*

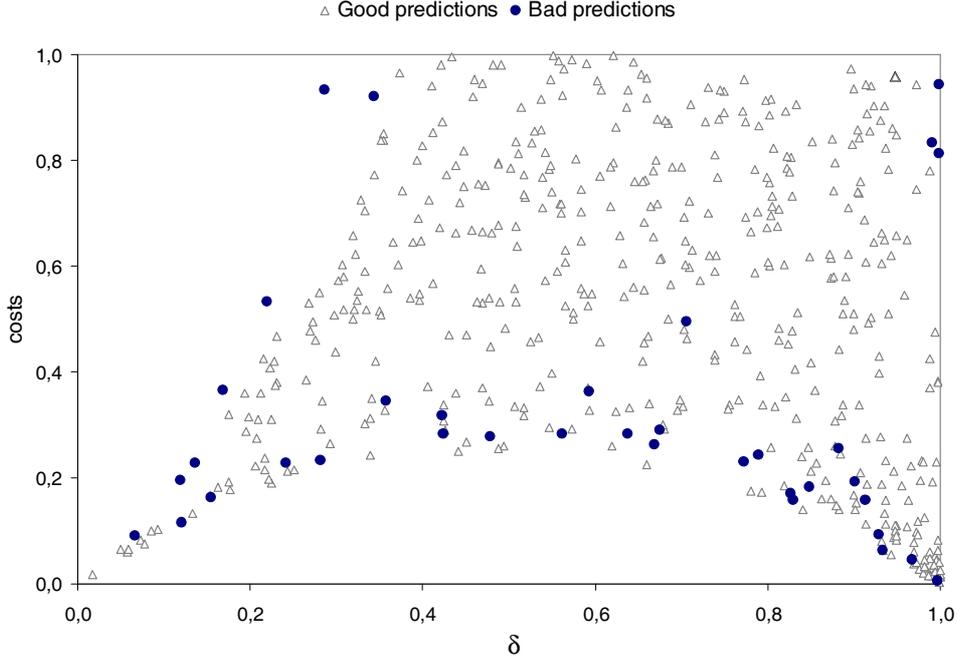


Figure 7: Experiments when the g^* network is efficient.

One may finally wonder about the structure of the inefficient networks that are found by the GA. A systematic analysis of the structural properties of inefficient networks leads to the following threefold conclusion. First, all inefficient networks which correspond to points in the space (c, δ) close to the frontier between the two regions where the empty graph and the star networks are efficient⁹, are empty networks. Secondly, when δ is close to one and c is also very high, the GA finds networks that are structurally very similar to the star network, with one or two agents being connected to an agent who is not the center of the network. Such typical network is reproduced in left graph of Figure 8. The social value generated by such a typical network is very close to the one of the star network since, when δ is close to 1, direct and indirect connections generate nearly the same value. Finally, when the experiment corresponds to a couple (c, δ) which is close to the frontier with the region where the complete network is efficient¹⁰, two types of inefficient networks appear to be selected. Two typical networks are reproduced in the central and the right graphs of Figure 8. The first one is composed of two main (non complete) stars connected with nearly all other agents who are never directly connected the one to the other (there are eventually some other smaller stars in the network). The second one appears to be a structural mix between the former network and a random graph.

5.3 In the linear spatialized connections model

We now confront the networks predicted by the GA to both the analytical results in Proposition 3 and numerical computations summarized in Table 1. Again, the GA was ran 1,000 times using random integer values of n such that $5 \leq n < 20$ and with random values of $\delta \in]0, 1[$. We first

⁹Given by $c = \delta + \frac{n-2}{2}\delta^2$.

¹⁰Given by $c = \delta - \delta^2$.

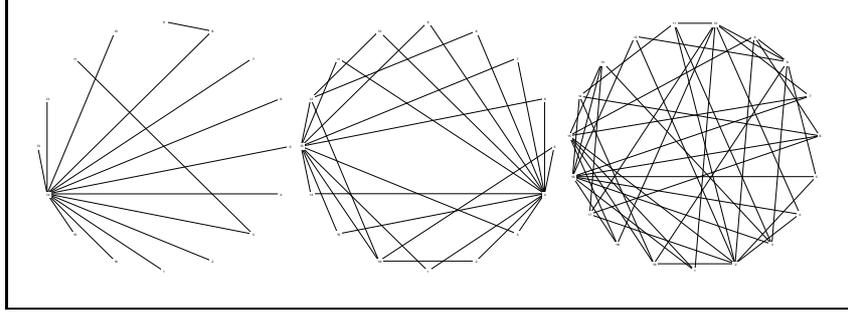


Figure 8: Some typical inefficient networks found by the GA at the internal frontiers of the region where g^* is the efficient network

find that the GA correctly finds all but one efficient networks among the runs that correspond to configurations covered by Proposition 3¹¹.

Among the runs which are covered by the numerical computations of JG00 (when $n = 5, 6$ or 7 ; 185 runs), all their predictions are confirmed by the GA, with the following exceptions (see Figure 9):

- g^C is not found by the GA, which instead selects $g^{C'} = g^C - 46 + 56$. Simple computations confirmed that indeed $\forall \delta \in]0, 1[, \pi(g^{C'}) > \pi(g^C)$.
- g^G is not found by the GA, which instead selects $g^{G'} = g^G - 13 + 14$. Simple computations confirm that $\pi(g^{G'}) > \pi(g^G)$ for all $\delta \in]0.277, 0.936[$, a region which includes the one indicated by JG00 as corresponding to g^G as the efficient network (see Table 1).
- g^D is not found by the GA, which instead selects $g^{D'} = g^D - 13 + 12$. Simple computations confirm that $\pi(g^{D'}) > \pi(g^D)$ when $\delta > 0.919$, region in which our randomly drawn values of δ are comprised. Of course, our results do not imply that g^D is not the efficient network when $\delta \in [0.8789, 0.919]$.
- $g^{2*} = \{13, 23, 34, 35, 45, 56, 57\}$, a network constituted by two interlocked local stars (see Figure 9), is found for $n = 7$ and $\delta \in [0.835, 0.907]$. In this region of δ , g^{2*} dominates g^{**} and g^H , and it must be chosen even when the efficient network remains unspecified in JG00 (region marked by an ?)¹².

Proposition 8 *In the linear spatialized connection model, the GA computations nearly always correspond to the predictions of Proposition 3 and corroborate the predictions of JG00. When the networks generated by the GA are different than the networks found by JG00, their social surplus is greater.*

6 Efficient networks in the linear spatialized connections model

We now turn to the use of the GA technique to perform the first fully exploratory analysis of the efficient networks in the linear spatialized connection model of JG00. The question we would like

¹¹For instance, when $n = 10$, Proposition 3 yields that if $\delta < 0.10114$, the empty network is the unique efficient network, and if $0.10114 < \delta < 0.11111$, the chain network is the only efficient network.

¹² g^{**} is found as the most efficient network when $\delta \in [0.789, 0.810]$, and g^H is also efficient when $\delta \in [0.924, 0.969]$.

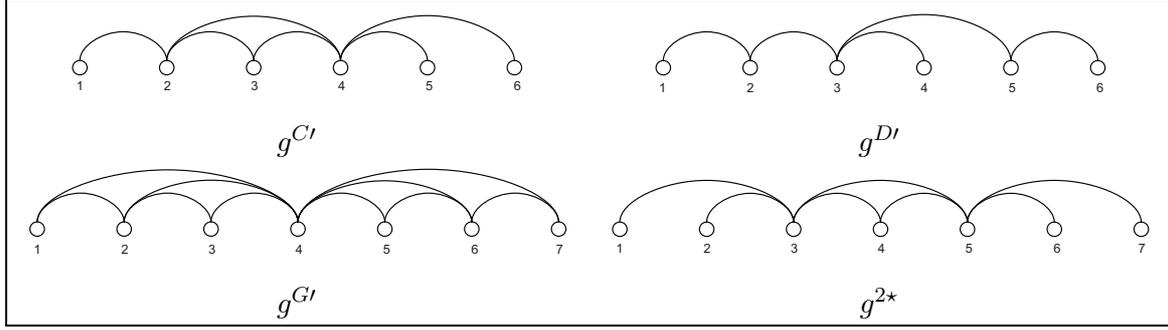


Figure 9: Original networks found by the GA as efficient for specific values of δ

to address here is related to the issue of the optimal creation of inter-individual connections and their distribution among agents. Since the model exhibits positive externalities that deteriorate geometrically with relational distance and bond costs that increase with linear exogenous distance, we especially wonder to what extent the efficient networks need to be organized around central agents or need to be locally connected. To put it differently, should the network be structured with one agent in the middle who mediates the externalities between all others in a similar fashion as g^{**} or even as $g^{G'}$? Should the network rather be locally coordinated with small stars in more peripheral positions as in g^{2*} ? Should instead connections be only locally formed and thus more equally distributed among agents? Should these various forms coexist in some extent? The answers to these questions of course strongly depend on the decay parameter δ which determines the extent to which the network is conducive to positive externalities.

We are willing to address these questions synthetically for different sizes of the population. Therefore, we propose to rely on the following four simple indicators, to be computed for each GA efficient network, that grasp most of the structural attributes we are interested in:

$$\Delta(g) = \frac{1}{n} \sum_{i \in N} \frac{\eta_i(g)}{(n-1)}, \quad (5)$$

$$\Gamma(g) = \frac{1}{(n-1)} \max_{i \in N} \eta_i(g), \quad (6)$$

$$\Omega(g) = \frac{1}{(n-1)} \text{second max}_{i \in N} \eta_i(g), \quad (7)$$

$$\Phi(g) = \frac{1}{(n-1)} \sum_{ij \in g} l(i, j). \quad (8)$$

$\Delta(g)$ gives the average number of links per agent relative to the maximum number of links any agent can sustain: $(n-1)^{13}$. $\Gamma(g)$ gives the size of the largest neighborhood on network g again scaled by the size of the largest possible neighborhood in a population of n agents. $\Omega(g)$ gives the size of the second largest neighborhood on g , again scaled by $(n-1)$. Lastly, $\Phi(g)$ is the average geographic distance in the network g , scaled by the maximum geographic distance when there are n agents positioned in our linear world, that is the distance between the two agents located at the far ends of the line: $(n-1)$. All indicators are positive and they can not exceed the unity.

¹³It is equal to twice the *density* of the network as it is usually referred to in the literature on social networks. This density is equal to $\eta(g)/(n(n-1))$.

Let us now explain how the simultaneous analysis of the four indexes provides synthetical information on the structuration of networks. A high value for $\Gamma(g)$ and simultaneously a much lower value for both $\Omega(g)$ and $\Delta(g)$ indicate a structuration of the connections around a central agent. On the contrary, if the network is not globally structured around one central agent, and if the two most connected agents have a similar number of neighbors, then typically $\Gamma(g) \approx \Omega(g)$. If, in addition $\Omega(g) \gg \Delta(g)$, then one can conclude that there are several (at least two) stars in the network. Otherwise, if $\Omega(g) \approx \Delta(g)$, then agents are quite equal in the size of their neighborhoods. Lastly, if $\Phi(g)$ is low, then it can be inferred that connections are mainly established in the geographical neighborhoods.

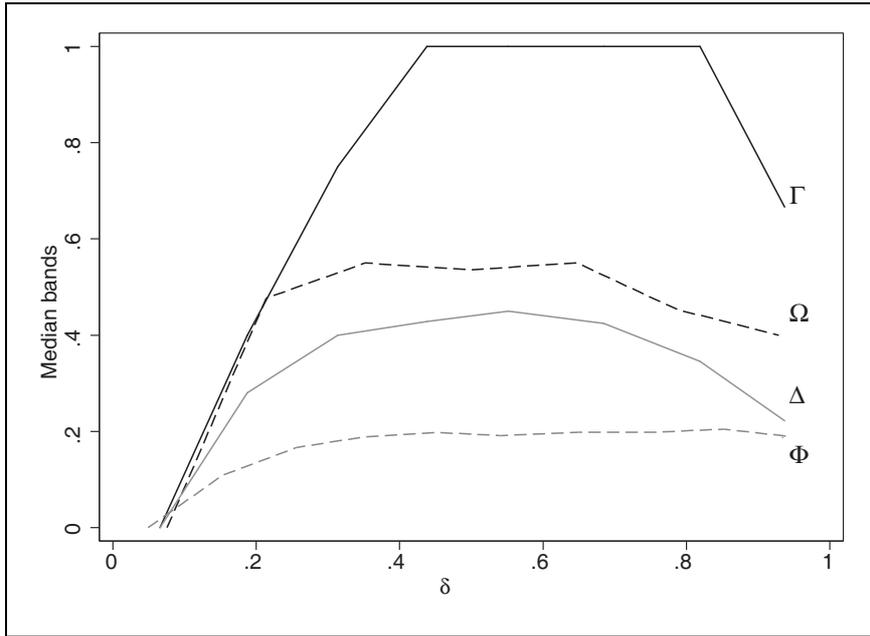


Figure 10: Median band values of Γ , Ω , Δ and Φ computed for 1000 GA-efficient networks with random integer values of n between 5 and 19 (inclusive) and with random values of $\delta \in]0, 1[$

We draw in Figure 10 the median bands of these indicators. Let us examine how do efficient networks structures evolve with δ . When δ increases from 0 to 0.2, we observe that $\Gamma(g) \approx \Omega(g) \approx \Delta(g)$ and, simultaneously, that $\Phi(g)$ remains low. That indicates that no star has been formed and connections are mainly local. In this region, $\Phi(g)$ increases with δ because the density of efficient networks increases: once connections at distance one are all formed then local density increases by establishing connections at distance two and so on so forth. When δ increases from 0.2 up to 0.45, $\Gamma(g)$ increases up to unity which means that then one agent at least is connected to all others. In the meantime, $\Omega(g)$ increases slowly to reach about 0.5. Both indexes remain on a plateau between $\delta \approx 0.45$ and $\delta \approx 0.65$. In this region, one observes only a slight difference between $\Omega(g)$ and $\Delta(g)$. In the meantime $\Phi(g)$ remains below 0.2 (in other words, the average geographic distance between any two connected agents is on average equal to twenty percent of the distance between the far ends). All this indicates that networks are mediated by a central agent who displays positive externalities in the population. There are no significant secondary stars but a strong local density. It is only when $\delta \gtrsim 0.55$ that the network density (grasped through $\Delta(g)$) begins to decrease. Simultaneously, $\Phi(g)$

continues to increase. This indicates that the centrality of the star is reinforced because some local connections have become inefficient and are not formed anymore. When $\delta \approx 0.85$, the density of the central agent sharply decreases while the density of the second most connected agent decreases less sharply. The need for global centralization is much reduced and a small window for more local centralization appears (in a similar fashion as g^{2*}).

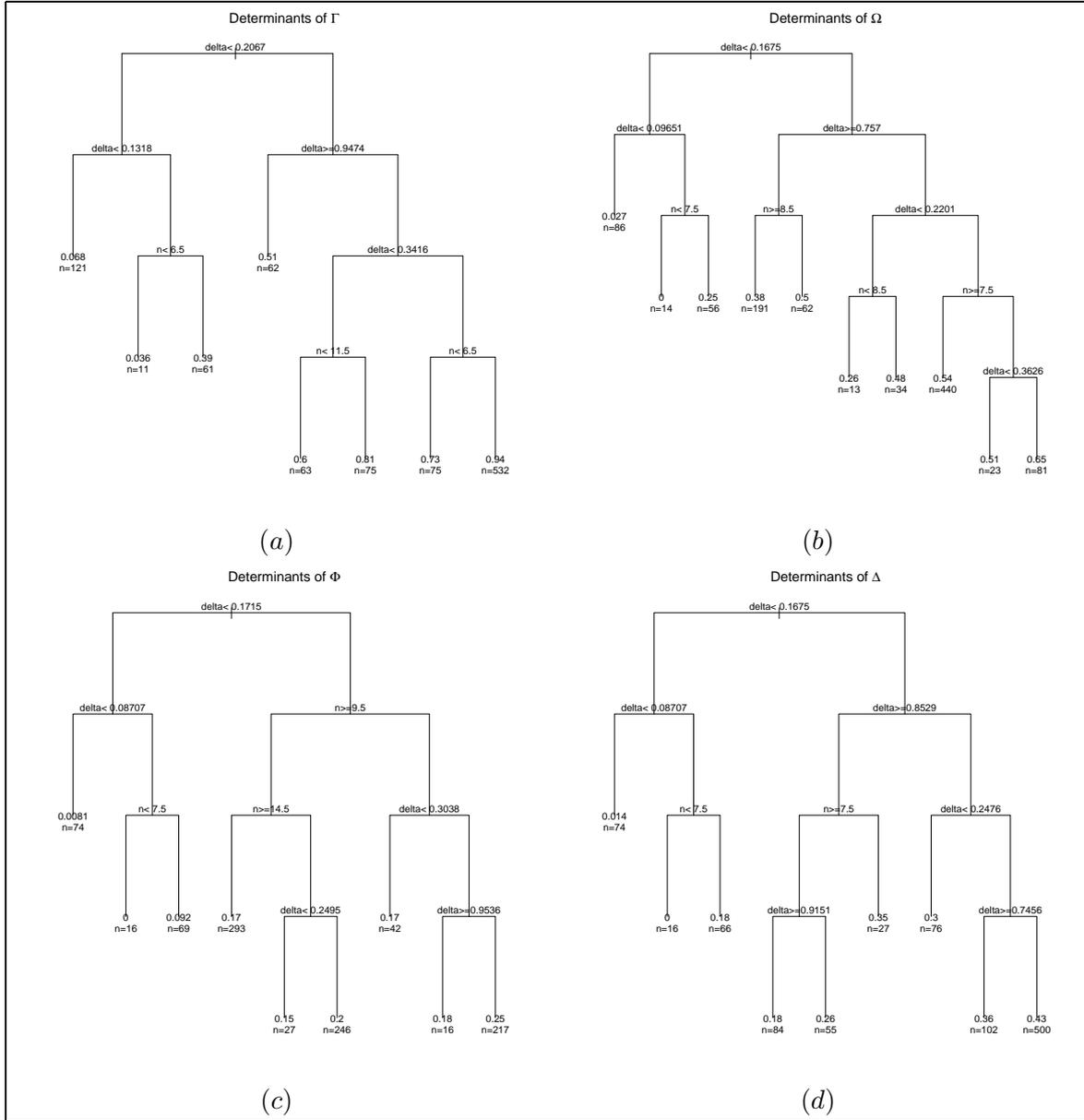


Figure 11: Distributions of Δ, Γ, Φ and Ω

In order to verify that our structural inferences based on the medians are fully consistent with the raw data, we also rely on regression trees (Venables and Ripley [1999], chapter 10). A regression tree establishes a hierarchy between independent variables using their contributions to the overall fit (R^2) of the regression for a given dependent variable. More exactly, it splits the set of observations in sub-classes characterized by their value in terms of their contribution to the explained variance. Regression trees are very flexible in the sense that they do not specify any functional relation between the explained and the explaining variables. The tree gives a hierarchical sequence of conditions on the

values of the explaining variables. The stronger the explanatory role of a condition in the classification of the observed cases, the higher its status on the tree. For each condition, the left branch gives the cases for which the condition is true and the right branch gives the cases that are compatible with the complementary condition. Regression trees can hence be used for obtaining a finer and more robust picture of the influence of δ on the indicators Γ, Δ, Φ and Ω . We also introduce n as an explanatory variable. At the final end of each branch, the numbers respectively give the expected value of the indicator under the conditions corresponding to this branch and the number of observations that correspond to these conditions¹⁴.

The regression trees, given in Figure 11, firstly confirm that δ is the main factor explaining efficient network structures whereas n plays a more minor role on the indexes (n does not appear in the highest branches of the trees)¹⁵. This was expected since the indexes were precisely designed to avoid important effects of population size. Secondly, the detailed study of the impact of δ on efficient networks structure tend to confirm our initial results. Indeed, δ plays non linearly on Γ, Ω , and Δ which first increase reach a max and then decrease. More precisely, we observe that the maximal expected value of Γ, Ω , and Δ (prior meeting any branching condition on n) are observed respectively when $\delta \in [0.3416, 0.9474[$ (see Tree (a)), when $\delta \in [0.2201, 0.757[$ (see Tree (b)), and when $\delta \in [0.2476, 0.8529[$ (see Tree (d)). As expected also, larger values of Φ are obtained when δ is greater.

Our results lead us to interpret the structure of efficient networks as resulting (for each δ) from two interrelated trade-offs that are simultaneously operated by the maximization of social returns. The first relates to the creation of links, while the second corresponds to their allocation among agents. These two phenomena exhibit similar non linear patterns as δ increases. As regards the first trade-off, when δ remains below 0.55, networks become denser with δ because both the social returns to the formation of connections increase with δ and the difference between the social returns to more direct connections and more indirect connections tend to increase (thus favoring the formation of “overlapping” connections). On the contrary, when $\delta \gtrsim 0.55$, though the gross returns to link formation still increase, the number of links tends to decrease with δ because the social returns to more indirect connections tend to become equal to those of more direct connections. Thus “overlapping” bonds tend to become redundant and efficient networks are less and less dense.

The second trade-off, which deals with the distribution of links among agents, is in fact equivalent to the issue of network centralization vs. local connectivity. It is when δ takes intermediary values that the social returns to centralization are the greatest. Indeed, a central agent (connected to all others) allows all other agents to gain at least δ^2 from all the agents with whom they are not directly connected. When δ is low, the gross social returns to connections are low and remain below the costs of distant connections. When δ is very high (close to unity), though the gross social returns of direct connections are large, indirect connections obtained through cheap local links tend to provide similar

¹⁴The reader should notice that the variable n at the end of the branches of the trees has a different signification from in the rest of the article: It only corresponds to the number of cases. Unfortunately, this is a default notation in R-project and it cannot be customized.

¹⁵If n plays a (secondary) role on the global structuration of efficient networks, it appears to intervene around the threshold of $n = 7$, a value which often intervenes in the third level ramifications of the trees (cf. Figure 11). This tends to indicate that the cases studied by JG00 might be quite specific since they correspond to $n \leq 7$.

social returns because the spillovers do not much depend on social distance any more. Then, when either δ is low or high, local connections of lower cost are preferably selected against costly distant ones which are necessary to centralization.

The simultaneity of the two trade-offs makes that when efficient networks have a central agent (when δ is intermediate), they are also much denser, especially in local areas. However, there is a slight shift between the two trade-offs as δ varies, which produces specific network structures for certain values of δ . When $\delta \approx 0.2$, the need for centralization is still not there while efficient networks are already quite dense. Efficient networks are then strongly only locally connected. When $\delta \approx 0.85$, efficient networks have a low connectivity while the need for centralization is still strong. This configuration gives a small window for local stars to appear.

Proposition 9 *In the linear spatialized connections model, when the decay of externalities is either very low (δ close to 0) or very high (δ close to 1), networks should be only locally connected and no central agent is needed. In intermediate cases, efficient networks are both centrally structured around some coordinating agent and locally connected. On the borders between these three configurations, the efficient networks are either only locally connected without any central coordination (when $\delta \approx 0.2$) or coordinated by local stars (when $\delta \approx 0.85$).*

7 Conclusions

One critical problem faced by economists interested in networks formation is the complete characterization of the efficient networks for non trivial individual payoffs functions. We test in this paper the relevance and the performances of an original method, namely the genetic algorithms (GA), for computing such efficient network structures. In order to assess the efficacy of this technique, we compute GA-efficient networks in models for which benchmark results are available. Our results show that the GA are a powerful tool for network optimization. More precisely, in the coauthor model of JW96, the GA is able to find the optimal structures in all simulations. In the connections model of JW96, the GA finds again the efficient network structures but it can be deceived on the borders between the areas corresponding to two distinct optimal structure (between empty network and the star, as well as between the complete network and the star). In the interior of these areas, the GA perfectly determines the relevant optimal network structure. In the linear spatialized connections model of JG00, the GA performs almost perfectly when analytical results are available and are more efficient than the numerical techniques employed by JG00 for a limited number of agents.

Then, an explorative use of the GA for computing efficient networks in the linear spatialized connections model allows us to discuss the issue of the efficient structuration of networks. We find that, depending on the parameter tuning the decay of positive externalities through connections, networks should be structured quite differently. When the decay is either very low or very high, networks should be only locally connected and no central agent is needed. When externalities are low, the social returns to distant connections can not compensate their high costs. When externalities are very high, centralization becomes not socially desirable anymore since social distance becomes ineffective on externalities. In between, networks should be both centrally structured around some coordinating agent and locally connected. Therefore, centralization and local structuration are mostly found to be complementary rather than exclusive. Nevertheless, it should be noticed that efficient networks

have very different shape when δ shifts from 0.2 to 0.4. Indeed, they shift from local connectivity with all agents having the same number of connections and without any central coordination, to the emergence of a star agent connected to all others while the connectivity of the others remain nearly constant.

The GA technique may be further employed for exploring the optimal network structures in other models for which analytical or even computational results on efficient structures can not be provided. Another obvious application is to systematically compare the structural properties of the emergent and of the efficient networks (for an exploration see Carayol, Roux and Yıldızoğlu, 2007).

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