RESEARCH ARTICLE

Prisoner's Dilemma and Clusters on Small-World Networks

XAVIER THIBERT-PLANTE* AND LAEL PARROTT

Complex Systems Laboratory, Département de Géographie, Université de Montréal, CP 6128, Succursale Centre-ville, Montréal, Québec, Canada H3C 3J7

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The structure of interaction plays an important role in the outcome of evolutionary games. This study investigates the evolution of stochastic strategies of the prisoner's dilemma played on structures ranging from lattices to small world networks. Strategies and payoffs are analyzed as a function of the network characteristics of the node they are playing on. Nodes with lattice-like neighborhoods tend to perform better than the nodes modified during the rewiring process of the construction of the small-world network. © 2007 Wiley Periodicals, Inc. Complexity 12: 22–36, 2007

Key Words: small-world networks; prisoner's dilemma; clusters

1. INTRODUCTION

mall-world network structure commonly emerges in complex systems [1]. In this study, we explore the effect of this topology on the evolution of cooperative behavior with an individual based approach, using a model in which each node of the network is a strategy in the iterated prisoner's dilemma game.

Small-world networks [1] are playgrounds to study complex systems. They merge a strong local dynamics with large-scale interactions. They are between regular grids and random networks, sharing their small characteristic path

Correspondence to: Lael Parrott (e-mail: lael.parrott@ umontreal.ca)

*Present address: Redpath Museum and Department of Biology, McGill University, 859 Sherbrooke Street West, Montréal, Québec, Canada H3A 2K6. length with random graphs and their high degree of clustering with regular lattices. They are associated with the concept of six degrees of separation: there is a path connecting any two randomly chosen people in the world with five intermediates or less in the acquaintance network. They are also associated with synchronized dynamics, the result of fast diffusion in a densely connected environment [2]. The small-world network topology is a good model to represent various emergent networks like the power grid of the western United States, the neural network of Caenorhabditis elegans, collaboration graphs of film actors and scientists, and the process of propagation of infectious disease [1,3]. Following the method of [1], we can build a small-world network with only small modifications to a regular grid. For a grid G = (V, E) with *n* nodes V = $\{v_1, v_2, ..., v_n\}$ and *m* undirected edges $E = \{e_1, e_2, ..., e_m\}$ linking two nodes $e_k = (v_i, v_j)$. For each $e_k \in E$ there is a small probability (ρ) that one of the nodes associated with it, say v_i , will be replaced by a random one v_{rand} , where $(v_{rand}, v_j) \notin E$.







The prisoner's dilemma has become the standard paradigm for studying the evolution of cooperation among selfish individuals [4]. It is a simple two-player game where each player is confronted with a choice: to cooperate or not with the opponent. If both players cooperate they are rewarded by R points each; if both defect, they are punished by P points each. If one cooperates while the other defects, the cooperator gets the sucker tax (S) and the defector gets T points for the temptation to defect. By definition in the prisoner's dilemma, T > R > P > S and 2R > T [5]. Thus when two opponents meet for a single confrontation it is always better to defect: each gets at least the same amount of points as his opponent T > S or P = P. The possibility of cooperation emerges for rational players if they can meet again with a nonzero probability; this scenario is called the iterated prisoner's dilemma (IPD). The IPD also includes the case where the number of encounters is finite and known between two players, but we do not consider this case in this study. In the IPD, the better strategy is not trivial anymore, and cooperation among players can emerge. The IPD has been used to model the evolution of cooperation in populations of fish (sticklebacks) [6], vampire bats [7], and primates [8, 9]. Even if the rules of the game are simple, the dynamics generated by different strategies in different environments (how players meet each other, the numerical values of the payoff) is complex.

Tit-For-Tat is a classical strategy in the iterated prisoner's dilemma: it cooperates on the first move and then does what the opponent did during the previous move. This strategy won the two numerical tournaments organized by Axelrod [5] where people (academic and non academic) were invited to submit strategies of the IPD game. Tit-For-Tat is not the final state, a generous variation, Generous Tit-for-Tat (GTFT), which cooperates one time out of three after the opponent defects, performs well in a noisy environment (when misperception and misimplementation of decisions are probable, i.e., for stochastic strategies) [10]. TFT and GTFT are reactive strategies; they make their decisions as a function of the opponent's previous move; other types of strategies include general strategies that base their decision on their previous reward and memoryless strategies that take nothing into account when making a decision. Pavlov, a general strategy, outperforms Tif-for-Tat [11]. Pavlov keeps the same decision



Boxplots of simulation characteristics as a function of the rewiring probability for reactive strategies. Fifty percent of the simulations fall within the vertical box. The median is represented by the horizontal line inside the box. (A) mean score, (B) position of the emergent score, (C) Γ_{tot} of the emergent score, (D) position of the emergent ρ , (E) Γ_{tot} of the emergent ρ , (F) position of the emergent q, and (G) Γ_{tot} of the emergent q.

(cooperate or defect) as long as it pays (reward is *T* or *R*) and switches otherwise.

The model can be extended to a spatial version where the game is played on an $n \times n$ chessboard. In this case, each player occupies a square on the chessboard and the game is played between nearest neighbors. At the end of each game, each player adopts the best scoring strategy in its neighborhood for the next game. The introduction of space changes the dynamics of the game: coexistence of some strategies becomes possible and the best strategies in the spatial context are not the same for the same parameters in the nonspatial version. Simple strategies of the prisoner's dilemma that always cooperate (ALLC) and always defect (ALLD) create beautiful fractals when they coexist [12]. GTFT is more generous in a spatial environment; it cooperates twice as often when the opponent defects [13].

The discovery that space can have important effects on the dynamics of the model has led to a series of studies exploring the role of population structure on the emergence of cooperation in the prisoner's dilemma. The difference between structured populations (grid configuration as per a chessboard) and random networks, where all players have the same number of neighbors, for general stochastic strategies of the IPD is that the average score is higher in spatially structured populations because the grid allows clusters of cooperators to emerge and stabilize the population [14]. Clustered neighborhoods and persistent random networks can also allow cooperation to emerge with reactive stochastic strategies [15]. Clusters therefore have an important impact on the dynamics of the game.

The role of clusters on the dynamics of small-world networks was first explored by Watts and Strogatz [1] with their study of the region between structured and random populations. They showed in the context where the population is only composed of fully cooperative (ALLC) or fully defective (ALLD) strategies that the fraction of cooperators decreases as the amount of randomness introduced in the graph (ρ) increases. These observations were confirmed in [16], where they looked at the fractions of ALLC and ALLD that emerge under different values of *T* (temptation of defection) and ρ (rewiring probability). They found that the fraction of ALLC decreases when ρ or *T* increases. The score, in particular the



temptation to defect (*T*), was shown to have a major effect on the fraction of ALLC for different values of ρ .

To investigate the role of hubs in complex networks, an "influential node" was added to a small-world networks of ALLC and ALLD [17]. The "influential node" is a node, taken at random in the network, to which additional directed links are added. These links have an effect on a large fraction of the population, but not the inverse. This type of node creates an instability in the system, having a great effect when it switches strategy from ALLC to ALLD. When the influential node flips to noncooperation, the fraction of cooperators in the population decreases significantly [17]. This shows that in addition to the network structure, the characteristics of a single node can affect the dynamics of the whole system.

In this study, the evolution of stochastic strategies in the prisoner's dilemma played on small-world networks will be analyzed to identify the effect of the randomness (ρ) and individual node characteristics (clustering coefficient, sum of euclidean distances) on the dynamics of each node (strategies and score).

Although previous studies have concentrated on macroscopic characteristics of networks and associated them to the average score or the presence or absence of certain







strategies in the population, in this study, we monitor the whole population in a steady state to see the influence of the characteristics of each individual node (clustering coefficient and sum of euclidean distance) on the model. We look at the score (phenotype) given by different stochastic strategies [genotypes: (p) and (p,q)] as a function of each node characteristic for small-world networks with different degrees of randomness (ρ) . We observe a marked difference in behaviors between nodes that remain in the highly clustered grid configuration and those that are randomly rewired, suggesting that small-world structure does not affect the dynamics of all nodes in a network uniformly.

2. THE MODEL

In this study we used a 32×32 grid with periodic boundary conditions to explore the role of the structure of the network on the dynamics of the population. The initial network is the standard grid with a Moore neighborhood (the neighbors of a node are all nodes accessible by the king's move on a chessboard); every node is also linked to itself. We then modify the network with the rewiring process of [1] for different probabilities ($\rho = \{0, 0.01, 0.02, ..., 0.12\}$). The network structure is constant during a given simulation.

Every node on the graph has a stochastic strategy of the prisoner's dilemma game. Two different types of strategies are studied here: strategies without memory and reactive



Time evolution of a representative simulation with reactive strategies at $\rho = 0.1$. (A) Evolution of the overall population mean score compared with the emergent score. (B) Evolution of the overall population mean p compared with the emergent p. (C) Evolution of the overall population mean q compared with the emergent q. (D) Evolution of the fraction of the population in the emergent score. (E) Evolution of the population in the emergent p. (F) Evolution of the population in the emergent q.

strategies. The strategy without memory is a number (p) that represents the probability of cooperation at every moment. The reactive strategies are represented by two numbers: the first (p) represents the probability of cooperation after the opponent cooperates; the second (q) represents the probability of cooperation after the opponent defects. To avoid error-free strategies, the probability of cooperation is exclusively between 0 and 1, such that every probability (p or q) is restricted to $(\epsilon, 1 - \epsilon)$, where $\epsilon > 0$ is small. We use the same payoff function as [5]: (S, P, R, T) = (0, 1, 3, 5). Each simulation is initialized with a population in which all p and q are uniformly distributed random numbers between zero and one exclusively.

The genotype is the strategy of a node (p) or (p,q), and the phenotype is the genotype's average score per decision (payoff) resulting from confrontations with all the strategies in its neighborhood.

Every round, each strategy effectively plays an infinite number of iterations against all the strategies that are linked to it (its neighbors). After the end of each round, every

TABLE 1

Similarity Between Grid and Non-Grid Configurations

	Without memory			Reactive		
	Grid vs. nongrid	Grid vs. grid	Two time steps	Grid vs. nongrid	Grid vs. grid	Two time steps
Score	1%	31%	14%	2%	29%	14%
р	20%	80%	53%	12%	76%	48%
q	_	—	—	40%	87%	71%

The average fraction of time after the transient period that the two PDFs are the same with a Kolmogorov-Smirnov test with an interval of confidence of 95%. The grid-grid comparison is between two successive time steps of the nodes that are still in a grid configuration in a simulation. These are the cumulative results for all simulations.



Neighborhood of a node in a standard grid configuration. The nodes linked by a dashed line with node *i* are in its Moore neighborhood. Neighbors to the north, south, east, and west are 1 unit of distance from node *i* and the other neighbors are at a distance of $\sqrt{2}$ units. The solid lines are the links between the neighbors of node *i*.

node adopts the strategy in its neighborhood that obtained the best average score per decision. This update is done simultaneously over the whole network.

To avoid convergence and mitigate the effects of the initial conditions, there is a small probability of mutation (0.002 per gene: p and q) that is constant during the simulation. The mutation operation changes the value of the gene to a random number on the range (ϵ , $1 - \epsilon$) and is performed after the nodes are updated.

Simulations were run for 1000 iterations (round) and 30 replicates were done for each simulation. Although the system usually takes about 20 iterations to reach the steady state, all the analyses are done with the last 900 iterations to fully eliminate the transient period at the beginning of each simulation.

3. RESULTS

3.1. Analysis of Phenotypes

The overall mean score (sum of all scores per decision divided by the number of nodes) decreases as the rewiring probability (ρ) increases for both reactive and memoryless strategies [Figs. 1(A) and 2(A)] as [1], [3], and [16] observed, suggesting that cooperation decreases in small-world networks. However, a study of the frequency distribution of scores clearly shows that distribution is not normal [Figs. 3(A) and 4(A)]; the mean score is neither the median, nor the first moment. In all simulations, a prominent bin containing a large fraction of the population is present in the histogram. This bin is never equivalent to the mean score and, unlike the mean score, its position remains stable throughout a simulation [Figs. 5(A) and 6(A)]. We call this bin the "emergent score." The mean score varies in synchronization with the the fraction of the population in the emergent score because the mean score is highly influenced by the fraction of the population in the emergent score [Figs. 5(C) and 6(D)].

The position of the emergent score as a function of the rewiring probability (ρ) is constant over all simulations and represents random behavior (50% cooperate, 50% defect) versus random behavior for memoryless strategies [Fig. 1(B)] and mutual cooperation for reactive strategies [Fig. 2(B)]. As the rewiring probability (ρ) increases, the total fraction of the population over a simulation in the emergent score [$\Gamma_{tot}(score)$] decreases [Figs. 1(C) and 2(C)] for both types of simulations. The transition from a grid to a small-world network does not affect the position of the emergent score, but changes its accessibility.

Is the introduction of randomness in the network creating different classes of node? Some nodes after the rewiring remain in a grid configuration: no links that are related to the node have been added, removed, or modified, and the neighbors are still connected together after the rewiring process. We compared the score probability distribution function (PDF) between two successive time steps for the whole PDF and for nodes in the grid configuration only and between grid and nongrid configurations for the same time step. We used a Kolmogorov-Smirnov test for this purpose. Because this is a dynamic process, we do not expect a full confirmation that every PDF is from the same distribution. The Kolmogorov-Smirnov test with 5% error shows that the PDF of the nodes in the grid configuration is more similar than the PDF of the whole population. The comparison between grid and nongrid configurations is accepted only rarely. Table 1 shows the results in more detail. The dynamics of the phenotypic evolution is thus different for different network characteristics of the node.

We quantify the difference between nodes in the grid configuration and modified nodes to study the impact of these quantities on the performance (score) of nodes. In general, the performance of cooperators is enhanced in clusters because they are more likely to face other cooperators [14]. We look at two quantitative variables associated with network structure and the cluster phenomena: the individual clustering coefficient and the sum of distances, to investigate their relationship with the score.

The individual clustering coefficient (CC_i) is a measure of the correlation in the neighborhood of a node. When its value is high, neighbors of a node are linked together. It varies from 0 to 1, where 0 means no neighbors of a node are linked together and 1 means all neighbors of a node are linked together. The clustering coefficient (CC_i) of v_i is

$$CC_i = 2 \frac{|(v_j, v_k)|}{n(n-1)},$$
 (1)

where $|(v_j, v_k)|$ is the number of links present in the set of all edges in the network (E), v_j , v_k are nodes in the neighborhood of v_i , n is the number of nodes present in the neighborhood of v_i , and [n(n - 1)/2] is the total number of links possible between the neighbors of v_i . This equation holds for undirected edges [3]. The nodes in the grid configuration have eight neighbors, that have 12 links between them (Fig. 7), giving a clustering coefficient of

$$CC_i = 2\frac{12}{56} = \frac{3}{7}.$$
 (2)

2D histograms of the score (*y* axis) and CC_i (*x* axis) contain all normalized score histograms in the vertical for every CC_i . Frequency is indicated on a gray scale, with darker values for higher frequencies [Figs. 8(A) and 9(A)]. The horizontal darkest line of the 2D histogram is the emergent score. The position of the emergent score remains the same for all CC_i [Figs. 8(A) and 9(A) for representative simulation results]. $\Gamma(score)$ is the frequency of the 2D histogram at the emergent score; here $\Gamma(score)$ is a function of CC_i . $\Gamma(score)$ changes as a function of CC_i , [Figs. 8(C) and 9(D) for representative simulations results]. As the CC_i increases $\Gamma(score)$ increases, but it is not a linear or a simple polynomial function [Figs. 8(C) and 9(D)]. We used a linear robust fit to determine the sign of the slope of the $\Gamma(score)$ as a function of the CC_i . The sign of the slope confirms the tendency of the increasing Γ (*score*) as a function of increasing *CC_i*; more extensive tests for all simulations and all ρ show that this trend is universal. In general the mean score of nodes with high CC_i will be higher, not because they score high values, but because they score well more often. For lower values of CC_i there is more noise in the values [Figs. 8(C) and 9(D)]. The increased noise



Phenotypic and genotypic variation as a function of the quantitative network characteristics (CC_i and SoD) for a representative simulation for memoryless strategies at $\rho = 0.1$. In (A), (B), (E), and (F) are 2D histograms with the network characteristic (CC_i or SoD) in x and the score or ρ in y. Frequency of the y-value is indicated on a gray color scale, with darker values for higher frequencies. The 2D histogram is normalized for the network characteristic (the sum of all values in a vertical line is one), so comparaison between network characteristics is possible. Not all CC_i and SoD are represented, giving some vertical white areas. The dark horizontal line represents the emergent score or ρ . In (C), (D), (G) and (H) Γ of the emergent score or ρ is shown as a function of the CC_i and SoD.





Phenotypic and genotypic variation as a function of the quantitative network characteristics (CC_i and SoD) for a representative simulation for reactive strategies at $\rho = 0.1$. In (A), (B), (C), (G), (H) and (I) are 2D histograms with the network characteristic (CC_i or SoD) in x and the score, p or q in y. Frequency of the y-value is indicated on a gray color scale, with darker values for higher frequencies. The 2D histogram is normalized for the network characteristic (the sum of all values in a vertical line is one), so comparaison between network characteristics is possible. Not all CC_i and SoD are represented, giving some vertical white areas. The dark horizontal line represents the emergent score, p or q. In (D), (F), (J), (K), and (L) Γ of the emergent score, p or q is shown as a function of the CC_i and SoD.

for highly modified nodes (low CC_i), is due to the smaller amount of nodes who have the same characteristics: one point on the graph can be the behavior of a single node, because there are no other nodes who share this network characteristic.

Another way of characterizing a node is by studying its geographic location relative to its neighbors. When the network is a modification of a grid, the initial Cartesian position (before the rewiring process) of the node is used to characterize the geometric distance between the node and its neighbors. The sum of the geometric distance between a node and all its neighbors is called the Sum of Distances (hereafter SoD). In the grid configuration, the sum over all neighbors is $SoD = (4 \times 1) + (4 \times 2^{1/2})$ for each node (Fig. 7). If there is one more link from this node node to another 5 units further, the

SoD will become $SoD = 5 + (4 \times 1) + (4 \times 2^{1/2})$. In general as the SoD increase, the CC_i decreases for a node.

The position of the emergent score is the same for all SoD, but the Γ (*score*) decreases while the SoD increases, the tendency is shown for representative simulations [Figs. 8(E, G) and 9(G, J)]. Thus, nodes with geographically close neighbors score well more often than nodes with geographically far neighbors. The relation between the SoD and Γ (*score*) is also neither linear, nor a simple polynomial, but by evaluating the sign of the slope with the same fitting function as for the *CC_i* the signs shows that this trend is universal. For SoD larger than the radius of the initial grid (radius \approx 24) there is more noise in the results [Figs. 8(G) and 9(J)]. In addition, nodes with SoD bigger than the radius of the grid must have more than one rewired links, and therefore



The mean fraction of time a node switches on and off the emergent score or p and its associated standard deviation for one representative simulation of memoryless strategies. The fraction of time a node (A) in the emergent score switches as a function of the CC_i , (B) in the emergent p switches as a function of the CC_i , (C) in the emergent score switches as a function of the SoD, and (D) in the emergent p switches as a function of the SoD.

a small CC_i , which diminishes the local influence and correlation.

3.2. Analysis of Genotypes

The same analyses were also done for the genotypes: (p) for memoryless strategies and (p,q) for reactive strategies. The frequency distribution of p and q shows that the distributions are not normal, and there is a prominent bin containing a large fraction of the population for every p and q; these bins will be called the emergent p and emergent q, respectively [Figs. 3(B) and 4(B, C)]. For the purpose of simplification, we use the term emergent genotype to designate both emergent p and emergent q without distinction if nothing else is stated. For memoryless strategies the emergent genotype is called emergent p, for reactive strategies, there are two emergent genotypes: emergent p and emergent q.

Emergent genotypes are different from the mean genotypes and are more stable in time [Figs. 5(B) and 6(B, C)]. There is a synchronization in the variation of the mean

genotype and the fraction of the population in the emergent genotype(s) [Figs. 5(D) and 6(E, F)], because the mean genotype(s) are influenced by the fraction of the population in the emergent genotype. The emergent *p* for memoryless strategies is around p = 50%, which represents a coin flipping strategy (50% cooperate, 50% defect; Fig. 1(D)). For the reactive strategies the emergent p is more cooperative and is close to 1 [Figure 2(D)], and the reaction to defection by the opponent, emergent q, is around q = 50% [Figure 2(F)]. As the rewiring probability (ρ) increases, the fraction of the population in emergent p ($\Gamma(p)$, same definition as $\Gamma(score)$, but transposed to p) decreases for memoryless strategies [Figure 1(E)] and reactive strategies [Figure 2(E)]. An interesting feature of *p* is the emergence of other emergent genotypes in both memoryless and reactive strategies, so when a node is not in the emergent p, it is probably in an other emergent p and not necessarily in the noisy region around the emergent p [Figs. 3(B) and 4(B)]. In opposition, the q value is adopted by almost all the population (40–80%; Figure 2 (G)], and there is no other emergent q [Figure 4(C)].



The mean fraction of time a node switches on and off the emergent score, p or q and its associated standard deviation for one representative simulation of reactive strategies. The fraction of time a node (A) in the emergent score switches as a function of the CC_i , (B) in the emergent p switches as a function of the CC_i , (C) in the emergent q switches as a function of the CC_i , (C) in the emergent q switches as a function of the CC_i , (D) in the emergent p switches as a function of the SoD, (E) in the emergent p switches as a function of the SoD, and (F) in the emergent p switches as a function of the SoD.

There is a difference again if the node is in a "grid configuration" or not. Because the neighbors do not affect the genotype during a round, the Kolmogorov-Smirnov test between the grid configuration and nongrid configuration are more often accepted (Table 1). There is more similarity again in the grid vs. grid comparison than the whole PDF for two time steps, and the grid versus nongrid is accepted less often. There is thus a difference in the dynamics of the genotype for different network characteristics of a node.

The value of CC_i for nodes also has an effect on $\Gamma(p)$ and $\Gamma(q)$ [Figs. 8(B) and 9(B, C)]. For high CC_i , nodes are less often in the emergent p and q. As CC_i increases, $\Gamma(p)$ and $\Gamma(q)$ decreases [Figs. 8(D) and 9(E)]; this trend is universal for all ρ . For q a large fraction of the population adopts the emergent q [Figure 2(G)]. As the CC_i increases, $\Gamma(q)$ decreases [Figure 9(F)], but it remains high (40%). This tendency is present for all ρ . Nodes with high *CC_i* tend to be more often in the emergent genotype.

As the SoD increases, $\Gamma(p)$ increases [Figs. 8(F, H) and 9(H, K)]. The increasing tendency is confirmed for all ρ . For emergent q, the same tendency is observed for all simulations, but at another range of values, in fact $\Gamma(q)$ is higher than the $\Gamma(p)$ [Fig. 9(I, L)]. Nodes with low SoD tend to be in the emergent genotype more often.

3.3. Strategy Switching

Nodes falling into the emergent score/genotype do not stay there forever; they switch on and off the emergent score/genotype. The fraction of time a node switches in and out of the score/genotype is an indirect measure of how long it can keep the emergent score/genotype. There is no clear tendency between the fraction of time a node switches on



Spatial configuration of the network at one time step for representative simulations with memoryless strategies for various rewiring probabilities (ρ). Nodes in black are part of the emergent score (top row) or emergent p (bottom row).

and off the emergent score and the network characteristics CC_i and SoD, because the score of a strategy is determined by its own genotype and the genotype of all its neighbors [Figures 10(A, C) and 11(A, D)]. There are more factors that influence the fraction of time a node switches on and off the emergent score than for the fraction of time a node switches on and off the emergent genotype. In contrast, a node will switch its behavior only if a neighbor performs better than it (we neglect the mutation that occurs only rarely). As the CC_i increases, the fraction of time nodes switch on and off the emergent genotype(s) decreases [Figures 10(B) and 11(B, C)]. In opposition, as the SoD increases the fraction of time, they switch increases [Figs. 10(D) and 11(E, F)]. More extensive tests for all simulations and all ρ show that this trend is universal. Rewired nodes are thus more likely than nodes in the grid to switch on and off the emergent genotype. For low CC_i and high SoD there is more noise in the results.

3.4. Spatial Analysis

To visualize the system, we plot the nodes in their initial Cartesian positions, not as a function of their links after the rewiring process. Because small-world networks maintain strong local interactions, this "relaxed network" is a good 2D representation of the network (Figs. 12 and 13).

The fraction of the population in the emergent score/genotype at a given time can be calculated as the total area occupied by the emergent score/genotype. On the "relaxed network," we can measure the perimeter associated with the area. We consider all nodes as one unit squares, so the

perimeter of a node is four units (north, south, east, and west). Only edges between a node in the emergent score/genotype and one outside it count in the calculation of the perimeter of the emergent area.

As seen before, as the rewiring probability (ρ) increases the fraction of the population in the emergent score/genotype decreases. In other terms, the area of nodes in the emergent score/genotype decreases. In Figures 12 and 13 we see more and more fragmentation as ρ increases. To measure this fragmentation, we used the perimeter over area ratio of the nodes in the emergent score/genotype. The plot of the total perimeter over the total area at each time step for nodes in the emergent score/genotype increases as the rewiring probability (ρ) increases (Figs. 14 and 15). There are still identifiable clusters in the small-world network, because a strong local correlation remains. As ρ increases the mean perimeter of nodes in the relaxed network increases, because the clusters are more fragmented.

4. DISCUSSION AND CONCLUSION

The mean performance of the population decreases with the rewiring probability (ρ), but this apparent change in overall performance is not caused by a drift of the whole population to another state. In fact, fraction of the population in the emergent score is decreasing while the ρ is increasing. Although the rewiring affects only a small fraction of the population, macroscopic measures like the mean score are affected.





Nodes with different network characteristics behave differently. Nodes that keep their original grid configuration usually perform well more often than those that are highly modified (low CC_i and high SoD), even if highly modified nodes are more often in the emergent genotype(s). Highly modified nodes are more often in the emergent genotype(s) because they switch on and off of it more often: they are less able to stay in the emergent genotype(s) and perform well enough to stay there.

Explanation of decreased overall cooperation requires more than a simple study of the presence or absence of clusters in a network [14, 15] and of nodes in or out of clusters. There are different levels of clustering that can be quantified by the CC_i and SoD. The CC_i is a good measure for highly correlated clusters (a lot of neighbors from a node are neighbors together). For networks containing nodes with low CC_i , like a von Neumann grid (neighbors of a node are the four closest nodes: north, south, east, and west) for which $CC_i = 0$ for all nodes, this measure is not useful. Even after the rewiring process, in which CC_i usually decreases, here CC_i is already at the lower bound. In contrast, the SoD is still a good measure for low and even zero CC_i , because SoD will not be zero unless the node is isolated. This measure, which considers spatial proximity on a network, is thus a very useful method of characterizing the local structure of less-connected networks.

Every node in the network tries to maximize its score. To acheive this, a node adopts the most effective strategy it is in contact with. The optimal strategy of a node might depend on its network characteristic. Because all nodes do not have the same network characteristics, there are multiple optimization processes running at the same time and interacting with each other. The interactions cause interference, because they share information about potentially different problems and try to use this information on another problem. The group with the largest number of members contains the nodes in the grid configuration, so there is more information in the network about how to optimize nodes in a grid configuration. Members of other groups will use this information and fail to improve their score with it, so they switch strategies more often.

The presence of rewired nodes creates instabilities on the network; they keep changing strategy over and over, so their neighbors have a hard time adapting their strategies as a function of this highly variable neighbor. These instabilities





create more fragmentation in the network, because rewired nodes have neighbors in different regions of the grid who are influenced by their changing strategies, such that these instabilities have an effect on noncontiguous regions of the grid.

If there is less cooperation in a small-world network than on a grid, why would small-world structure emerge in social cooperation networks such as networks of scientists? In this study we use the mean score per decision to compare nodes and update their strategies as a function of it. In the real world it is the cumulative score of an individual that matters, not the mean score per decision. Because rewired nodes are more likely to have more neighbors, they have more oportunities to score and thus increase their cumulative score. Another dilemma arises: is it better to have more neighbors and score below the emergent score or to have the standard number of neighbors and score the emergent score, which is usually one of the best scores achieved in the population, more often? We speculate that it's better to have more neighbors. The prisoner's dilemma can be viewed as a cost and benefit situation.

FIGURE 15



The mean and standard deviation of the ratio of the perimeter of *i* the emergent zone (the black in Figure 13) over the area of the emergent zone for each time step for simulations with memoryless strategies as a function of the rewiring probability (ρ). The ratio for (A) the emergent score, (B) the emergent *p*, and (C) the emergent *q*.

Cooperators pay the cost *c* and the opponents get the benefit b, defectors do not pay the cost. If two nodes cooperate, they each pay the cost c and gets the benefits b; if both defect, nobody pays the cost, so there is no benefit; if one cooperates while the other defects, the cooperator pays the cost while the defector gets the benefit *b*. If b > c > 0 the prisoner's dilemma equality is respected [18]. In real networks, there is a limit to the number of neighbors that a node can have because there is a cost to create and maintain a cooperative link. In collaboration networks of scientists, the limited amount of time available is probably the main limitation for the maintenance and the expansion of the network. On the other hand, geographical proximity promote cooperation between scientists [19]; even if communication tools facilitate long distance cooperation [20], those technologies increase group separation between academic economists [21]. Physical distance still play an important role in this particular network.

In summary, the migration from a regular grid to a smallworld network does not modify the strategies that are present. As the rewiring probability increases, $\Gamma(\text{score/genotype})$ decreases, revealing that the fraction of the population in the emergent score/genotype decreases. Because the emergent score is usually one of the best, if not the best, score that is acheived in the population, if $\Gamma(\text{score})$ decreases, the overall mean score of the population decreases as ρ increases. Highly modified nodes will switch strategies more often, creating instabilities and fragmentation on the network.

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