Neutral Network Assortativity Shapes Whether Selective Pressure Promotes or Hinders Robustness

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***Abstract*—Due to the friendship paradox, the average robustness of the single mutation neighbours (μ_n) of genotypes on a neutral network is larger than the average robustness of the genotypes (μ_g). Random walks on neutral networks have an average degree equal to μ_n and, intuitively, we expect that evolution will not converge on populations whose average degree is considerably lower than this. This paper argues that a population achieving an average robustness higher than μ_n is facilitated by nodes of degree higher than μ_n being mutationally biased towards other nodes of degree higher than μ_n. Thus, we present the hypothesis that, for biologically realistic degree distributions, assortativity allows selection to increase robustness above μ_n. Furthermore, although counterexamples do exist, it is argued that it is highly plausible that in the majority of cases in which selection increases robustness above μ_n, that the neutral network is assortative. These arguments are reinforced by simulations of evolution on randomly generated Erdős-Renyi and power-law networks. Elucidating the role of assortativity provides valuable insight into the mechanisms by which robustness evolves as well as the conditions under which it will do so. Moreover, it demonstrates the large influence that higher-order mutational biases can have on evolutionary dynamics.**

I. INTRODUCTION

Mutational bias is emerging as a pertinent topic in the study of both digital and natural evolution. This is due to the fact that biases in the mutational neighbourhoods of genotypes enable two critical features of evolutionarily successful organisms: *evolvability* [1] and *mutational robustness* [2].

The existence of such biases is fundamentally linked to the manner in which genetic information is translated into phenotypes. In Evolutionary Computing (EC) this is termed the representation problem and concerns itself with the issue of how to represent and adapt (mutate and recombine) genotypes in order that a broad range of complex solutions can be represented by relatively simple genotype encodings [3]. The choice of representation and associated operators has been found to have a profound impact on both the evolution of viable solutions as well as other aspects of the evolutionary dynamics [3], [4], [5]. A plethora of representations have been proposed for a variety of task domains [6]. These range from the simple one-to-one encoding of the genetic algorithm [7] to developmental encodings which map a small genotype space onto a subset of a substantially larger phenotype space [8].

Similarly, in nature, genetic information defining the form and function of an organism is stored within its genotype, however, the developmental process which translates this information into phenotypes (the G → P map) is not well understood [9]. Yet, it has become clear that the G → P map is neither one-to-one nor linear [10]. In many organisms and *Ribonucleic acid* (RNA) folding [11], it has been found that many genotypes can code for a single phenotype and that genetic change resulting from mutation is not proportional to phenotypic change [9], [2], [12].

These features of the G → P map allow for the phenotypes encoded for by a genotype's mutational neighbours to be a non-uniform sampling of the encoded phenotypes in the entire genotype space, that is biased. This opens up the possibility that this sampling is in some way advantageous [13], [12], [14], [15], [16] and this has been interpreted as increasing evolvability [1], [17], [18]. Furthermore, it has been demonstrated that robots evolving in fluctuating environments with many-to-one encodings are able to evolve mutational biases that improve their rate of adaptation to environmental changes [19], [20], [21].

As many genotypes can code for one phenotype, it is possible that some number of a genotype's mutational neighbors code for the same phenotype as it does, thus affording the genotype a degree of mutational robustness [2], [22]. It has been found that a variety of organisms, as well as RNA folding, have a substantial degree of mutational robustness [23]. This robustness has been shown to play an important role in facilitating evolvability by allowing for greater genetic variation within a population [24] as well as access to a larger region of the genotype space [2]. Moreover, it has been demonstrated that evolvability facilitating rapid adaptation to environmental change is concomitant with robustness, as both are dependent on mutational biases [25].

The importance of robustness begs the question of how it evolved and whether selection favors its emergence. Under the assumptions that the population is evolving on a fitness plateau and that non-identical offspring are non-viable, it is easy to see the selective advantage that robustness confers. Robust genotypes have a greater probability of producing viable offspring which will go on to reproduce. This is a selective advantage which is not conferred by fitness, leading Bullock to label it *effective fitness* [26].

A useful tool in the study of robustness is the neutral

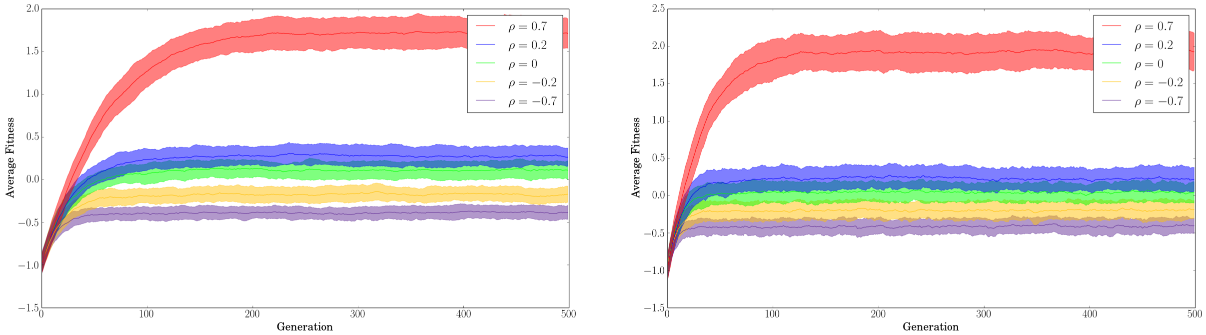

Fig. 1. Plots of the difference between the average robustness of the population and the network's average robustness of mutational neighbors (μ_n) over evolutionary time for the various values of the assortativity coefficient (ρ). These results are concerning evolution on the 100 Erdős-Renyi networks rewired to have each of the specified values of ρ and the plots are of the average over these 100 runs. The standard deviation is represented by the shaded region around each line. The figure on the left displays these results for networks with $10N$ edges and the figure on the right concerns those with $20N$ edges.

network, that is networks whose nodes are the genotypes of a given fitness where edges connect nodes who differ by a single mutation. Topological features of neutral networks have been used to study the evolution of robustness with great effect. Van Nimwegen et. al. [23] along with Wilke [27] studied the equilibrium distribution of infinite populations evolving asexually and demonstrated that the population's average robustness (μ_g) is equal to the network's spectral radius.

Despite this result's insight, the spectral radius is an opaque network measure, which cannot easily be related to other relevant metrics such as the degree distribution and degree-degree correlation. Moreover, it does little to elucidate the underlying mechanics of the evolution of robustness, such as higher order mutational biases and the extent to which selection has increased robustness.

Although robustness itself represents a type of mutational bias, one can question the existence and role of higher order mutational biases, that is biases towards biases. Indeed, mutations on the neutral network, that is mutations that lead to viable genotypes, are biased towards higher degree nodes due to the friendship paradox [28]. This effect is named after the phenomenon where in social networks the average number of friends of friends is higher than the average number of friends. Moreover, this effect is present in all networks, where the average number of neighbors of neighbors is higher than the average number of neighbors of nodes in the network. The cause of this paradox is that sampling the degrees of neighbors is equivalent to sampling the degrees of nodes at the end of edges, which is biased towards higher degree nodes. Using notation applicable to neutral networks, the relationship between these two averages can be expressed as: [28]

$$\mu_n = \mu_g + \frac{\sigma_g^2}{\mu_g} \tag{1}$$

where μ_g is the average degree (robustness) of genotypes on the neutral network, σ_g^2 is the variance of these degrees and μ_n is the average degree of single mutation neighbors. An implication of this result, as demonstrated by van Nimwegen et. al. [23], is that random walks on neutral networks result in an average neutrality equal to μ_n.

Intuitively, we would not expect populations to converge on an average level of robustness substantially lower than what a random walk would provide. Moreover, it gives us a benchmark with which to conclude that selection has increased or decreased robustness. Various authors, including van Nimwegen et. al. [23] and Wilke [27] have demonstrated increases in the robustness of populations of various modelled organisms over time. However, they have compared the resultant level of robustness with the network genotype average (μ_g) as opposed to the neighbor average (μ_n). Furthermore, these authors do not examine the circumstances under which selection would be unable to increase robustness, or could even decrease it.

Although robust genotypes have a selective advantage in that they produce more viable offspring, if these offspring themselves are not robust it is difficult to see how the population could converge on this lineage. Therefore, the selection of robustness is facilitated by the existence of highly robust nodes whose offspring are also highly robust. This sort of higher order mutational bias is provided by network assortativity, that is, correlation in the degrees of the nodes at the end of edges [29]. Thus, the central hypothesis of this paper is that, for biologically realistic degree distributions, assortativity allows selection to increase robustness above μ_n. Furthermore, although counterexamples do exist, it is argued that it is highly plausible that in the majority of cases in which selection increases robustness above μ_n, that the neutral network is assortative.

Experiments are presented in which randomly generated Erdős-Renyi networks were subjected to a rewiring algorithm to make them assortative or disassortative. It was found that evolution on assortative, unassortative and disassortative networks caused populations to achieve an average robustness higher than, equal to and slightly less than μ_n, respectively. Finally, experiments are presented in which populations are evolved on non-rewired power-law networks, which tended to

Parameter	Value
number of nodes (N)	1000
number of edges	$[10N, 20N]$

TABLE I
PARAMETERS FOR THE ERDŐS-RENYI NETWORKS

Parameter	Value
Population size (M)	1000
Parents selected per generation (P)	1000
Assumed genome length (L)	200
Recombination	None

TABLE II
EVOLUTIONARY ALGORITHM PARAMETERS

be disassortative. In a few instances it was found that disassortative networks were capable of producing populations with average robustness substantially higher than μ_n. A discussion is presented explaining this counterexample as being due to the outsized effect of extremely high degree nodes and biases towards their progeny being identical.

II. METHODS

A. Random Network Generation

Networks were randomly generated using the graph-tool [30] software library and the metropolis-hastings algorithm [29] implemented therein. All networks were checked for connectedness and disconnected networks were discarded, as the above mentioned results of van Nimwegen et. al. [23] only apply to connected networks and the analysis for non-connected networks is substantially more complicated.

Networks were generated to either conform to the Erdős-Renyi model [32], or to have a power-law degree distribution. The relevant parameters for the Erdős-Renyi networks are presented in table I. In the power-law networks the degrees were distributed according to $p_k \ (k-2)^{-\gamma}$ where p_k and k are the degree probability and degree, respectively. Here k was limited to the range $[3, 500]$, where the lower bound was chosen to increase the proportion of produced networks which were connected and the upper bound was chosen for computational reasons. As with the Erdős-Renyi networks, the number of nodes in the network (N) was chosen to be 1000.

B. Assortative rewiring

The expected assortativity value (ρ) for the Erdős-Renyi networks is 0 [29]. In order to both increase and decrease the assortativity the rewiring algorithm of van Miegham et. al. [33], was used. This algorithm operates by iteratively picking two edges at random and observing the degrees of the four nodes at their endpoints. If the goal is to increase assortativity, the two nodes with the highest degrees are connected by an edge and, likewise, the lowest degree nodes are also connected. Moreover, the original two edges are removed from the network. Similarly, if the goal is to decrease assortativity, the maximum degree node is connected to the minimum degree node and the remaining two nodes are also connected. Clearly, rewiring does not take place if the desired connectivity arrangement between the four nodes was already present. This iterative process is repeated until the desired value of ρ is achieved.

C. Evolutionary Model

A population of M individuals were initialized by assigning them each a random node on the network. Each generation P parents were selected randomly from the population to produce offspring. With a probability d/L an offspring is produced at a node neighboring the parent, where d is the parent's degree and L is the assumed genome length and therefore the total number of possible mutations. These dynamics are based on the assumption that genotypes which fall off the neutral network are completely non-viable. Moreover, they are equivalent to those studied by van Nimwegen et. al. [23] and and Wilke [27] with off network fitness (σ) equal to 0 and a variable mutation rate (μ) equal to $P \langle d \rangle / L$, where $\langle d \rangle$ is the average degree of genotypes in the population. A full list of evolutionary parameters is listed in table II.

III. EXPERIMENTS AND RESULTS

In order to ascertain the influence of assortativity on the evolution of robustness on neutral networks, networks were randomly generated so as to conform to the Erdős-Renyi model. This model was chosen as it represents a uniform sampling of networks with a given number of nodes and edges [32], thus giving our results broad relevence. For each of the seven values of ρ, $[-0.7, -0.2, 0, 0.2, 0.7]$, 100 networks were generated, using the techniques and parameters specified in section . Each of these networks were rewired so as to attain their given assortativity value ρ. Following this, the evolution of a population was simulated as specified in the section II-C. Moreover, this was done for both of the two tested numbers of network edges.

The difference between the average robustness of the population and μ_n is plotted in figure 1. We can see here that populations evolving on unassortative networks attain a level of robustness equal to μ_n, that those evolving on assortative networks attain higher robustness and that those evolving on disassortative networks attain a lower value. These results support our hypothesis that the evolution of robustness higher than μ_n is facilitated by assortative neutral networks.

In addition, an average of the degree-degree distributions of the generated networks is plotted in figure 2. This plot elucidates the manner in which, in assortative networks, the higher degree nodes have a mutational bias towards other high degree nodes.

Although the results presented in figure 2 indicate that, for the majority of networks, robustness will only increase above μ_n in the event that the network is assortative, it is reasonable that there may be exceptions to this trend. As assortativity is a global property of the network, it was concluded that networks which have nodes which deviate substantially from the average in some way would be a promising place to look. Power-law

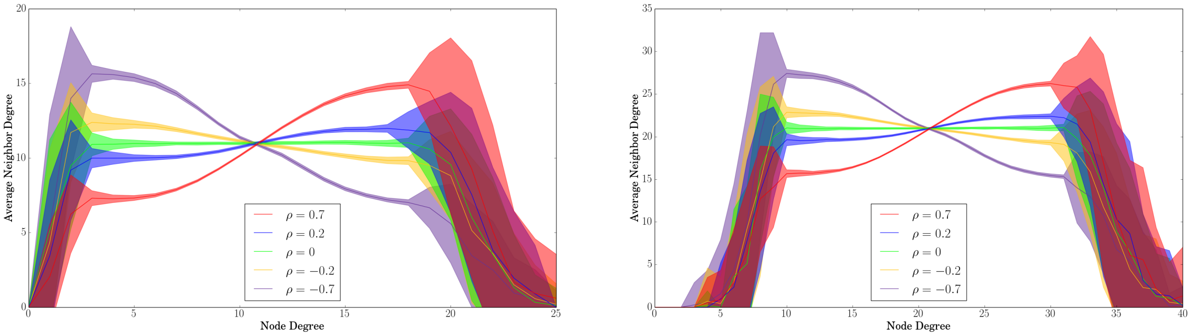

Fig. 2. Plots of the degree-degree distributions of the Erdős-Renyi networks used in the experiments for each of the various values of the assortativity coefficient (ρ). These plots are the average over the 100 networks generated and rewired for each value of (ρ) with the standard deviation being represented by the shaded regions. The figure on the left displays these results for networks with $10N$ edges and the figure on the right concerns those with $20N$ edges.

(scale free) networks can contain nodes with degrees orders of magnitude larger than the network average.

Due to these arguments, power law networks were generated as specified in the methods section. However, these networks were not rewired, as it was found that producing a significant change in their assortativity was prohibitively computationally expensive. We generated 100 such networks for each value of γ and the chosen values as well as the resultant average values of ρ and μ are shown in table III.

Figure 3 contains plots of the difference between the average robustness of the population and μ_n. Lower values of γ caused populations to converge on an average robustness less than μ_n. However, the highest value of γ tested, 2.5, on average caused populations to have a mean robustness equal to μ_n. Further analysis of these results revealed that, 77 of the 100 generated networks caused their population to achieve a mean robustness greater than μ_n. The largest difference between the mean robustness and μ_n was a value of 3.6, on a network where $\mu_n = 7.7$ and $\rho = -0.02$.

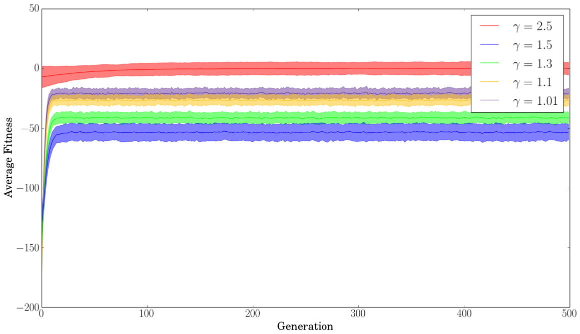

Fig. 3. Plots of the difference between the average robustness of the population and the network's average robustness of mutational neighbors (μ_n) over evolutionary time when evolution occurred on the power-law networks. The plots are the averages over the runs on each of the 100 networks generated for each value of $gamma$. The standard deviation is represented by the shaded region around each line.

γ	ρ	μ_n
1.01	-0.55 (0.03)	245 (8)
1.1	-0.62 (0.03)	229 (7)
1.3	-0.65 (0.02)	185 (6)
1.5	-0.61 (0.05)	150 (12)
2.5	-0.05 (0.03)	11 (9)

TABLE III
THE VALUES OF ρ AND μ_n FOR THE POWER-LAW NETWORKS, AVERAGED OVER THE 100 GENERATED NETWORKS FOR EACH VALUE OF γ. STANDARD DEVIATIONS ARE SHOWN IN BRACKETS.

IV. DISCUSSION

Due to the fact that the average robustness of genotypes found by following a mutation is higher than the average across all genotypes on the network, the bar with which to judge the efficacy of selection is raised. Although a population might achieve a mean level of robustness greater than the average in the network, if the population's average robustness is lower than the average achieved by a random walk on the network then we conclude that selection has hindered, rather than helped, the evolution of robustness.

With this in mind, it is of interest to note that in the disassortatively rewired Erdős-Renyi networks, the resultant robustness of the population was lower than μ_n. The addition of selection decreased the robustness below that achievable by a random sampling of mutations.

This paper set out to demonstrate the importance of assortativity in the evolution of robustness by indicating not only that the assortativity of a network is positively correlated with its ability to produce robust populations but also that the bulk of networks which increase robustness above μ_n are likely to be assortative. The fact that the disassortatively and unassortatively rewired Erdős-Renyi networks, as well as the lower exponent power-law networks yielded robustnesses lower than μ_n supports this argument. Moreover, even though a majority of the networks with the highest exponent did beget high robustness, the average across all runs was roughly equal to μ_n. Thus, in the bulk case, selection raising robustness requires the higher order mutational bias provided by assortativity.

Nevertheless, it is appropriate to query the mechanisms by which unassortative and disassortative networks can engender the selection of robustness. Analysis of the populations evolved on these networks showed that they contained multiple copies of rare, extremely high-degree nodes. Moreover, due to the high exponent, these nodes mainly connect to very low degree nodes, of degrees three and four in our experiments. Thus, we hypothesize that the population has converged around these very high degree nodes and that these node's offspring either produce offspring identical to the high degree nodes, or produce low degree nodes who's progeny soon get excluded from the population.

This hypothesis conforms to this paper's core argumentation behind the importance of assortativity in the evolution of robustness, namely, that in order for selection to encourage the emergence of robustness, the nodes who's offspring selection favors (those that are more robust) must produce lineages that are biased towards high robustness.

V. CONCLUSION AND FUTURE WORK

As argued in the introduction, biases in genotype space are not only of great consequence in evolutionary dynamics, but are also emerging as pertinent topic of study within theoretical biology and artificial life. However, very little attention has been paid towards higher order biases, that is biases towards biases. This paper has explored this topic by investigating mutational biases towards robustness. It has done so from the starting point of the bias present in all neutral networks, implied by the friendship paradox. It further demonstrated that, although there are some exceptions, the evolution of robustness higher than provided by this base bias requires the neutral network to be assortative, as this biases high degree nodes to other high degree nodes. This provides valuable insight into the mechanics by which robustness evolves, delineating the roles which selection and higher order mutational biases play as well as the relationships between them.

Two main avenues of future work are being considered at present. The first is to gain a quantitative understanding of the proportion of those networks which allow for the evolution of high robustness that are assortative, unassortative and disassortative. The second is to attempt to achieve a broader framework than simple degree-degree assortativity as an explanation for the selection of high robustness. Promising avenues of research include local assortativity [34], which could be used in the description of networks with certain extremal nodes which dominate evolutionary dynamics, and long-range degree correlations [35], which could be used to analyse cases in which biases towards robustness in an organisms progeny is not present in the first generation.

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