

# Mating Networks in Steady State Genetic Algorithms are Scale Free

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## 1. INTRODUCTION

In this paper, we investigate *mating network* interactions in a genetic algorithm (GA). We approach this study using a computational method from the study of complex systems: the analysis of networks interactions and network topology among basic components. Why should we study evolutionary algorithms (EAs) in this way? First, this approach is feasible and easily implemented. EAs are simulations of evolutionary processes and as such they can readily produce any data required to perform virtually any data-driven analysis of their behavior; much in the same way that large genomic and proteomic databases are fueling systems biology research. Second, this approach can serve as a unifying framework for studying evolutionary systems, both natural and computational. The data needed for this type of analysis is independent of the implementation and of the particular flavor of the evolutionary system.

Results from complex systems research indicate that most biological networks are scale-free [3, 4, 5] and that, in fact, scale-free networks are pervasive in many natural and engineered systems. Examples of such systems include protein interactions, social networks, the world-wide web, and—most relevant for our case—the web of human sexual contacts. In scale free networks, the probability,  $P(k)$ , that a node is adjacent to  $k$  other nodes decays according to the power law distribution, given by  $P(k) \propto k^{-\gamma}$ . The power law distribution is not affected by natural scaling [3]. Also, approximation of the Erdos-Renyi (ER) model is not realistic for various complex networks specifically because random graphs do not reflect two important features; preferential attachment and the clustered structure [3],[1]. The structure of scale free networks result in two key properties: error tolerance and vulnerability to focused attacks [2].

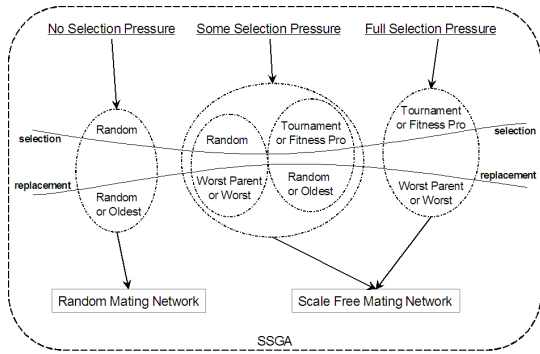
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## 2. MATING NETWORKS

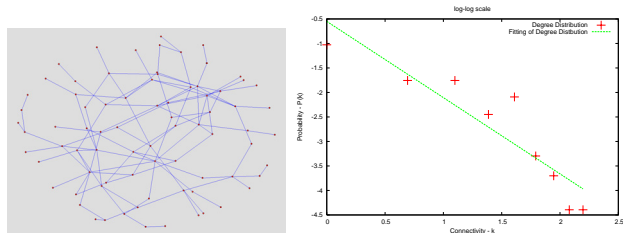
Our work introduces the idea of a *mating network* in a steady state GA (SSGA). We define a mating network to be the network of reproductive interactions that occur in an SSGA population. The individuals from a population are the network nodes. Two nodes are connected by an edge if these nodes represent individuals that have jointly contributed genetic material towards a single offspring—have mated—during the course of the evolutionary process. We choose to study mating networks because understanding genetic information flow—schema propagation—in evolving populations is fundamental for the analysis of the evolutionary algorithms. Mating networks partially capture this information flow by providing information on how parental genetic information recombines to form new individuals. We investigate the complexity of the mating networks for various commonly used selection methods. We do so by examining the distributions of their node connectivity or vertex degree distributions. Initial studies suggest that the mating network of an SSGA may possess similar characteristics as the scale free networks found in many complex systems. GA selection methods favor fitter individuals; the probability of being selected to be a parent is directly or indirectly related to an individual's fitness value. This property is essentially the same as the preferential attachment property of scale free networks.

## 3. EXPERIMENTAL STUDY

For our experiments, we use a steady state GA in order to maintain a single population to which individuals are added and removed throughout a GA run. Using SSGA allows us to record a single, dynamically changing mating network. We used a fixed population size of 100 individuals with a random initial population. The SSGA then iterates through an evaluate-select-reproduce-replace cycle until the stopping condition is satisfied. The selection and replacement policies defines the level of selection pressure. We have conducted our experiments on two different fitness functions with three different selection methods and four different parent replacement policies. The fitness functions we have chosen are the classical 128 bit OneMax (OM) problem and 16x8 bit Royal Road (RR) problem. We conduct our experiments on fitness proportional selection, tournament selection, and random selection. Fitness proportional selection and tournament selection are well known and widely used selection methods in the GA community. Random selection is included to set a baseline for the stochastic process of natural selection. The parent replacement policies we have selected are replace the



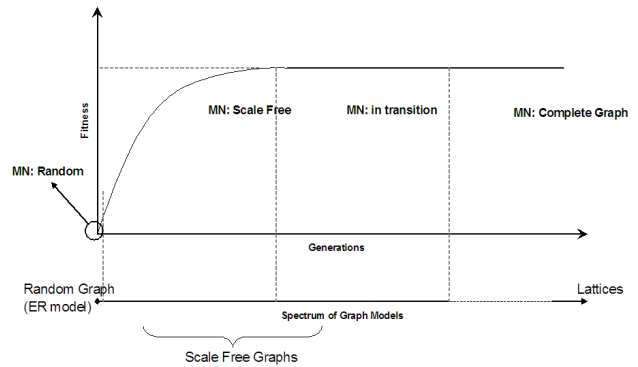
**Figure 1:** While the mating network when there is no selection pressure is random, it is scale free when there is at least some selection pressure.



**Figure 2:** Full selection pressure: (left) Mating network, (right) Degree distribution, log-log scale

worst individual (Worst), replace a random individual (Random), replace the worst parent of the kid (Worst Parent), and replace the oldest individual (Oldest).

Our goal is to conduct experiments that investigate three levels of selection pressure in an SSGA; none at all, some, and full. Figure 1 illustrates what constitutes each of these categories. All selection and replacement combinations in each category of selection pressure produced similar characteristics, so we will only analyze one combination for each category. The fitness functions OM and RR do not appear to change the resulting output. The mating network under *no selection pressure* is generated by an SSGA with random selection and random replacement on OM. The final network graph is mostly unconnected and does not have a dominant giant component. As result, the vertex degree distributions for this graph can only be analyzed by looking at the components individually. These components appear to be random graphs following a Poisson distribution. The mating network under *some selection pressure* is generated using tournament selection and oldest replacement on OM. Although the final network graph still includes some small components which are not connected to the giant component, the giant component itself is large enough for analysis and it is scale free and follows a power law distribution. The mating network under *full selection pressure* is generated using tournament selection and worst replacement on OM. Figure 2 shows the plot of its vertex degree distribution just after convergence. Under full selection, the emergent mating network is clearly scale free and follows a power law distribution. While both *full selection pressure* and *some selection pressure* appear to generate scale free mating net-



**Figure 3:** Life cycle of SSGA: mating networks over generations resemble the spectrum of graph models

works, the number of edges in the *full selection pressure* networks is always higher than the number of edges in *some selection pressure* networks. This difference suggests that an increase in selection pressure makes the network more connected. We also observe that, interestingly, the SSGA life cycle resembles the spectrum of graph models as shown in figure 3. The mating network in an SSGA begins as a random graph because of the random population initialization. Over multiple reproductive iterations, the randomness in the mating network decreases and it becomes scale free. After the convergence of the population, the mating network tends to become more connected and becomes a lattice (complete graph) in the long run.

## 4. CONCLUSIONS

Under the assumption that we are using a steady state GA on the OneMax or RR functions, our experiments show that GA mating networks are scale free as shown in figure 1 if; (i) the fitness is actively being improved (evolutionary process is still active) and population has not yet converged, (ii) there is at least some selection pressure. We also offer experimental evidence on the resemblance of the GA life cycle with the spectrum of graph models. We believe that these initial results are encouraging because they show that there is a correlation between indirect data-driven observation and analysis and the actual state of the evolutionary process.

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