



# Scale-free properties of information flux networks in genetic algorithms

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## ABSTRACT

In this study, we present empirical analysis of statistical properties of mating networks in genetic algorithms (GAs). Under the framework of GAs, we study a class of interaction network model—information flux network (IFN), which describes the information flow among generations during evolution process. The IFNs are found to be scale-free when the selection operator uses a preferential strategy rather than a random. The topology structure of IFN is remarkably affected by operations used in genetic algorithms. The experimental results suggest that the scaling exponent of the power-law degree distribution is shown to decrease when crossover rate increases, but increase when mutation rate increases, and the reason may be that high crossover rate leads to more edges that are shared between nodes and high mutation rate leads to many individuals in a generation possessing low fitness. The magnitude of the out-degree exponent is always more than the in-degree exponent for the systems tested. These results may provide a new viewpoint with which to view GAs and guide the dissemination process of genetic information throughout a population.

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## 1. Introduction

A recent surge of research has focused on modeling and analyzing interactions in complex systems through establishing networks. The interaction networks of numerous natural populations have been found to be heterogeneous (i.e., few nodes in the interaction network have most of connections). Of particular interest are scale-free networks [1], a class of highly heterogeneous graphs, which have been shown to be quite ubiquitous in systems involving contacts between individuals, such as email networks [2], the Internet [3], sexual contacts [4], and mobile communication [5]. Scale-free topologies exhibit a power-law distribution of vertex connectivity, such that the probability a given vertex has  $k$  connections is governed by the relationship  $P(k) \propto k^{-\gamma}$ , where  $\gamma$  is referred to as the scaling exponent [6]. Accordingly, there has been an interest in studying dynamical processes on scale-free topologies. Examples include the dynamics of infectious disease in epidemiological models [7,8], information cascades in binary decision models [9], the emergence of cooperative behavior in evolutionary games [10,11], and evolutionary optimization [12,13]. Scale-free networks, which also influence information flux for the existing of hubs, are prone to the spreading and the persistence of infections whatever spreading rate the epidemic agents possess [8].

In particular, analysis of the structural properties of spatial interaction networks (the network of a realized movement of people, freight or information between an origin and a destination) in evolving artificial populations has also received attention in the evolutionary algorithm. In Ref. [14], a mating network was introduced, which described reproductive interactions that occur in a Steady State Genetic Algorithm (SSGA) population. The mating network showed scale-free characteristics if

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the fitness is actively being improved and population has not yet converged, or there is at least some selection pressure. In addition, the effect of small-world (a type of mathematical graph in which most nodes are not neighbors of one another, but most nodes can be reached from every other by a small number of hops or steps) and scale-free population structures on the dynamics of evolutionary algorithms have also been examined, focusing primarily on the structural characteristics of the network of potential mating interactions (i.e. the population structure, the topological properties of inter-individual interaction networks) [15–17]. The evolutionary dynamics of populations evolving on scale-free imposed spatial topologies have been explored in the context of evolutionary game theory [15]. The evolutionary dynamics of populations evolving on both small-world and scale-free imposed spatial topologies have been investigated with genetic algorithms [16]. Moreover there was some research to assess the structural characteristics of the emergent mating topologies (EMTs: the topology of actual mating interactions that emerge when a population evolves on a given imposed spatial topology (IST)) of a generational GA on a variety of ISTs: regular graphs, small-world graphs, and scale-free graphs [17], in which the EMTs from both scale-free and regular ISTs with sufficient selection pressure were found to be scale-free.

The GA mentioned in the last paragraph is a search heuristic that mimics the process of natural evolution. This heuristic is routinely used to generate useful solutions to optimization and search problems. Genetic algorithms belong to the larger class of evolutionary algorithms (EA), which generate solutions to optimization problems using techniques inspired by natural evolution, such as inheritance, mutation, selection, and crossover [18]. Their application to physical problems has been recently studied by many research groups, for example the group of Ard Louis in self-assembling and gene regulatory systems [19,20]. In Ref. [19], the authors investigated the evolutionary dynamics of an idealized model for the robust self-assembly of two-dimensional structures called polyominoes. The relationship between the model's rule set and its resulting self-assembled structure can be viewed as a genotype–phenotype map and incorporated into a genetic algorithm. In Ref. [20], the effect of scale-free and Erdős-Rényi topologies on the interplay between evolvability and robustness of model gene regulatory networks is investigated with Boolean threshold dynamics. Genetic algorithms have been also used in science and engineering as adaptive algorithms for solving practical problems and as computational models of natural evolutionary systems [21].

There is a strong connection between the function of a system and its network structure (i.e. small-world property, heavy-tailed degree distributions, and clustering). Understanding the structure of the EMT may provide more direct insights regarding the adaptability of a population and the rate at which genetic information disseminates throughout a population. However, the EMT studied in Ref. [17] only incorporated genetic information of recombinant and ignored not only the edge multiplicity, but also the information flux between the parents and offspring. Similarly, mating network in Ref. [14] also lacked in considering the mutation operations of individuals in GA. Since these networks partially captured the information flow, it is necessary to rebuild a new model to involve all the operations in the algorithm, which could well describe the whole information flux through a population.

We propose a new EMT of genetic algorithm, called information flux network (IFN), which is constructed to depict the dissemination of genetic information in GA. In Section 2, we explain the modeling method of IFN in detail, whose connections represent interactions among the individuals during all generations. Then we test a classical function and establish the IFN in Section 3. In the next two sections, we construct a series of experiments on the structure of IFN based on different settings of parameters in GA, and discuss the influence of the operations of GA on the scaling exponent of IFN. We finish with our conclusions, presenting new contributions to understanding the search process of genetic algorithm and some work in future.

## 2. Methods

### 2.1. Framework of genetic algorithms

Before modeling, it is necessary to give a brief overview of genetic algorithm. Genetic algorithms (GAs) are general purpose search algorithms developed by Holland [18] with roots in work by Bledsoe [22], Fogel et al. [23] and others [21]. Loosely motivated by the example of population genetics, genetic search is population based and proceeds from generation to generation. The criterion of “the survival of the fittest” provides evolutionary pressure for populations to develop increasingly fit individuals. The basic mechanism of a GA consists of (i) evaluation of individual fitness and selection to form a gene pool and (ii) recombination and mutation.

Individuals (chromosomes) are typically fixed length strings (e.g. binary, real number, etc.). They are selected to the gene pool in proportion to some monotonic function of their relative fitness (determined by the objective function). Then next generation results from mutation and crossover between two individuals. Mutation consists of flipping a subset of the bits of an individual, according to some mutation rate. The simplest implementation of crossover selects two “parents” from the pool and after choosing the same random positions within each parent string, exchanges their tails. Crossover is typically performed with some probability (the crossover rate), and parents are otherwise cloned. The resulting “offspring” form the subsequent population (see Fig. 1).

### 2.2. Modeling of IFN

In general, good models of complex networks can catch the key and main characteristics of the problem. With this purpose, we simplify the generation mechanism of IFN in order to capture the essential topological structure. As mentioned

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