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A new crossover mechanism for genetic algorithms with variable-length chromosomes for path optimization problems

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ABSTRACT

Genetic Algorithm (GA) has found wide application in path optimization problem. In many fields such as navigating system, oil transportation, paths between the starting node and the termination node often have distinct number of relay-nodes, which leads to the corresponding chromosomes would have different length. We refer to chromosomes with non-consistent lengths as the variable-length chromosomes. This paper first investigated GAs with variable-length chromosomes widely used and found that Same Point (SP) crossover is the most popular crossover mechanism. Then, a new crossover mechanism called Same Adjacency (SA) is proposed for GA with variable-length chromosomes for path optimization problem, which outperforms GA with SP by a better search capability as the mathematical analysis shows. The simulation study indicates that GAs with our crossover operators could obtain a better solution, as compared to GAs with SP, while still being able to converge fast in different networks with varied sizes.

1. Introduction

As a biological evolution inspired method, genetic algorithms (GAs) were firstly proposed in 1975 (Holland, 1992). GA represents the solution space as a collection of individuals named chromosomes. At each iteration chromosomes compete with each other through a quality measure called fitness. Furthermore, GA iteratively generates new chromosomes by two operators called the crossover operator and the mutation operator respectively. Various path optimization problems in science and engineering fields such as flexible manufacturing systems, Traveling Salesman Problem (TSP), can often be effectively solved by GAs. An important feature of these combinatorial optimization problems is that the number of nodes or states contained in each solution is consistent. Hence, the resulting GA using a string $(v_0, v_1, v_2, \ldots, v_L)$ as the chromosome to represent a solution has uniform length chromosomes. Here, the gene $v_i (i = 1, 2, \ldots, L)$ denotes one node or one state. A lot of crossover operators of this kind GA have been proposed since its first introduction, e.g., the partially-mapped (PMX) crossover proposed by Goldberg and Lingle (Goldberg & Lingle, 1985), the order crossover (OX) proposed by Davis (Davis, 1985) and the cycle crossover (CX) introduced by Oliver (Oliver, Smith, & Holland, 1987).

However, there are also some path optimization problems such as communication path problems, to which GAs with varied length chromosome are effectively applied. For instance, in communication fields, paths between the starting node and the termination node often have distinct number of relay-nodes and the corresponding chromosomes would have different length. We refer to chromosomes with non-consistent lengths as variable-length chromosomes (Ahn & Ramakrishna, 2002). GAs with variable-length chromosomes have various applications in intelligent decisions and systems such as Personal navigating system (Maruyama, Shibata, Murata, Yasumoto, & Ito, 2004), Transportation system (Ojha, Das, Mondal, & Maiti, 2010). Abbaspour (Abbaspour & Samadzadegan, 2011) used GA with variable-length chromosomes to solve the tour planning problem, in which both single-point and two-point crossovers are used. Mendes (Mendes, Gonçalves, & Resende, 2009) presented a genetic algorithm for Resource Constrained Project Scheduling; Yaghini (Yaghini, Momeni, Sarmadi, Seyedabadi, & Khoshraftar, 2015) proposed a GA with variable-length chromosomes to solve a fuzzy railroad blocking model for Iranian railways; Lee (Lee & Kim, 2016) adopted GA with variable-length chromosomes for robot to find a feasible path that proceeds from a starting point to a destination point without intersecting any obstacles in the given environment. Alajlan et al. (Alajlan, Koubaa, Chaari, Bennaceur, & Ammar, 2013) also adopted GA with variable-length chromosomes in path planning for mobile robots,

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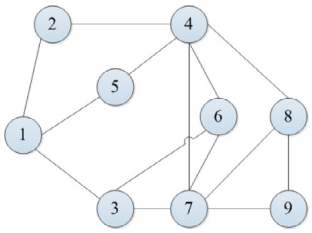

Fig. 1. A network topology.

and they proposed a GA for efficiently finding an optimal path in regulating mobile robots.

Even though GAs with variable-length chromosomes have been widely applied in many fields, the study of GAs with variable-length chromosomes is still far from being satisfactory. Munemoto (Munetomo, Takai, & Sato, 1998) proposed a practically feasible algorithm in 1998, which employed variable-length chromosomes for encoding the problem. Munemoto presented a classic crossover mechanism called same point (SP) crossover which contains two cross operators: one-point and two-point crossovers. The crossover operation exchanges partial chromosomes (partial routes) after the crossing sites (see Section 2.2). Here, crossing sites (points) are the loci where identical genes in the both chosen chromosomes are found. To our best knowledge, almost all later GAs (Alajlan et al., 2013; Chung & Xu, 2010; Lee & Kim, 2016; Leela, Thanulekshmi, & Selvakumar, 2011; Shi, Sagduyu, & Li, 2014; Yaghini et al., 2015) with variable-length chromosomes inherit this mechanism. It should be noted that (Alajlan et al., 2013) proposed a modified crossover operator, but it also used the same point as the cross loci.

Our purpose is to study the crossover mechanism for GA with variable-length chromosomes for path optimization problems and a new crossover mechanism called Same Adjacency (SA) crossover is proposed. This paper is organized as follows. Section 2 provides a review of SP crossover. The proposed crossover mechanism is analyzed from a theoretical perspective in Section 3. Section 4 presents a detailed implementation of the GAs with our crossover mechanism. Section 5 evaluates various aspect of our algorithm. Some conclusions are given in Section 6.

2. Review of SP crossover

2.1. Variable-length chromosomes

Variable-length chromosomes are especially attractive to problems that can be abstracted as a connected graph. Given a set consisting of labeled objects as Fig. 1, the goal is to find a path with a minimal or a maximal volume under a specific sense. Many practical problems can be abstracted as graphs of this kind, such as bandwidth-intensive communication, transportation optimization.

In Fig. 1, we want to find paths between the starting node 1 and the termination node 9. Consider two paths, path $1:1-2-4-6-7-9$, and path $2:1-3-7-8-9$. There exist some useful approaches to represent chromosomes for connected graphs. Some representation methods include the adjacency representation, the ordinal representation and the path representation. Path representation is the most natural and intuitive method since it just uses a path as the chromosome directly. For convenience, we use path representation to represent the above paths. It is clear that the length of two chromosomes are different: the chromosome 1: (1, 2, 4, 6, 7, 9), has six genes, while chromosome 2: (1, 3, 7, 8, 9) has five genes.

2.2. Same point crossover

In this classic scheme, two chromosomes chosen for crossover should have at least one common gene (node) except the starting node and the termination node. Suppose that there are two chromosomes: $P=(v_0,v_1,\ldots,v_i,\ldots,v_L)$, $P'=(v'_0,v'_1,\ldots,v'_j,\ldots,v'_K)$, the SP crossover mechanism contains two crossover opertators: one-point crossover and two-point crossover. One-point crossover can be described as follows. If P and P' have common nodes (we would do nothing if there is no common node), then we randomly choose one, say $v_i=v'_j$, and exchange all nodes after v_i and v'_j (see Fig. 2). For the above example in Section 2.1, chromosome 1 and 2 would crossover at node 7. Unlike one-point crossover, the two-point crossover operator should find two identical genes and exchange gene fragments between these two point.

3. New crossover mechanism for GA with variable-Length chromosomes

3.1. Same adjacency crossover

It has been known that when trying to do SP crossover on a population, two chosen chromosomes need to find at least one common gene except the starting node and the termination node. Hence, to obtain crossover points between two chromosomes, each node in one chromosome must be comparable to every node of the other in SP crossover. Therefore, a list of crossover points are generated with respect to the same gene contained in two chromosomes. Indeed, on the one hand, it is not likely that common genes between two selected chromosomes always exist, while on the other hand, if the crosspoint is too near the starting node or the termination node, then the generated offspring would be less different from the parent. Suppose that $P=(v_0,v_1,v_2,\ldots,v_{L-1},v_L)$ and $P'=(v'_0,v'_1,v'_2,\ldots,v'_{K-1},v'_K)$ are two chromosomes, and $v_0=v'_0$ is the start node, $v_L=v'_K$ is the termination node. Then it would do nothing since crossing at $v_1=v'_1$ or $v_{L-1}=v_{K-1}$ would yield new offspring identical to parent. We would like a new crossover mechanism to smoothly increase crossover points for parent chromosomes, thus yielding more diverse offspring to extend the searching abilities to the optimal solution.

We proposed a new crossover mechanism called Same Adjacency (SA) crossover. In SA crossover, we do not compare each single node but two neighboring nodes instead. Given a connected graph: $G=(V,E)$, for $v\in\mathbf{V}, N(v)=\{v'\in\mathbf{V}|(v,v')\in\mathbf{E}\}$ denotes the set of nodes connected to v. Consider two paths: chromosome $1{:}P=(v_0,v_1,\ldots,v_{i-1},v_i,\ldots,v_L)$ and chromosome 2: $P'=(v'_0,v'_1,\ldots,v'_{j-1},v'_j,\ldots,v'_K)$. For (v_{i-1},v_i) in chromosome 1 and (v'_{j-1},v'_j) in chromosome 2, if $v_i\in\mathbf{N}(\mathbf{v'_{j-1}})$ and $v'_j\in\mathbf{N}(\mathbf{v_{i-1}})$ (as shown in Fig. 3), then (v_{i-1},v'_{j-1}) can be taken as the crosspoint pair. The crossing way shown in Fig. 4 is analogous to SP crossover introduced before, that is, two chromosomes exchange gene frag-

Fig. 2. Same point (SP) crossover.