Analysis of Properties of Recombination Operators Proposed for the Node-Depth Encoding

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ABSTRACT

The node-depth encoding is a representation for evolutionary algorithms applied to tree problems. Its represents trees by storing the nodes and their depth in a proper ordered list. The original formulation of the node-depth encoding has only mutation operators as the search mechanism. Although it is computationally efficient, the exclusive use of mutation restricts the exploration of the search space and the algorithm convergence. Then, this work proposes two specific recombination operators to improve the convergence of the algorithm using the node-depth encoding representation. These operators are based on recombination operators for permutation representations. Analysis of the proposed recombination operators have shown that both operators have a bias towards stars and high heritability.

Categories and Subject Descriptors

I.2.8 [**Artificial Intelligence**]: Problem Solving, Control Methods, and Search—*Graph and tree search strategies*

General Terms

Algorithms

Keywords

Genetic Algorithms, Representations, Performance Analysis

1. INTRODUCTION

Node-depth encoding is a representation for evolutionary algorithms (EAs) applied to network design problems [4]. This encoding is based on the relation node-depth in a rooted tree. Also, the node-depth encoding genotypes always produces a valid phenotype. In order to produce new solutions from previous ones, the node-depth encoding uses only mutation operators, i.e., no recombination operator is available in the literature. These operators produce only new feasible solutions. This encoding has been applied with EAs to several network design problems with good performance in computational time and solution [2, 4].

Nevertheless, the literature has shown that EAs with recombination and mutation operators can be more efficient on some complex problems [1]. Recombination operators are important as source of diversity in the offspring produced. Another important issue is that recombination and mutation operators complement each other.

In order to improve the node-depth encoding rate of convergence, this paper proposes two recombination operators based on reproductive mechanism for permutation problems. This type of problem was chosen as inspiration because their representation has similar characteristics with the node-depth encoding. In this kind of problems recombination operators must to preserve the order of the genes and also avoid repeat genes.

For a proper use of representations and their operators, it is important to have an adequate understanding of properties of the representations, like heritability and bias [3]. The heritability measures whether the new solutions produces by recombination operators of an encoding are similar to their parents. The bias of a representation describes whether either the genotype-phenotype mapping or the evolutionary search operators like mutation or recombination prefer a specific type of solution and thus, leads a population towards this direction. Previously work already tested the node-depth encoding and its mutation operators for the important property bias [2].

The purpose of this paper is to present the recombination operators for the node-depth encoding representation and investigate the bias and the heritability of the proposed operators for the encoding. The results are the proposal of two recombination operators NOX, based on Order Crossover (OX), and NPBX, based on Position-Based Crossover (PBX). The properties analysis shows that for small graphs both recombination operators have a bias towards stars.

2. THE NODE-DEPTH ENCODING

The node-depth encoding (NDE) [4] is based on storing the nodes and their depth in an ordered list. For a tree of size n, the nodes v_i ($i \in \{1, \ldots, n\}$) and their corresponding depths d_i are listed in an array as pairs (v_i, d_i). The order of the nodes in the array is important since an encoding/decoding algorithm traverses this array from the first to the last position, determining the edges that compose the tree. A depth-first search (DFS) can be used to encoding a tree by starting from a root node v_1 with depth $d_1 = 0$.

3. RECOMBINATION OPERATORS

Recombination operators are the reproductive mechanism in which subsets of genes from two or more parents are cloned and reassembled to create a new offspring. This operation plays an important role introducing more diversity in the population in the beginning of the evolutionary process [1]. Recombination and mutation operators complement each other, and they have achieved important results when they are used together.

In order to improve the performance of NDE for problems represented by complete graphs, this paper proposes two recombination

operators NOX and NPBX based on recombination operators for permutation problems OX and PBX respectively.

3.0.1   NDE Order Crossover - NOX

NOX recombination operator is based on OX operator for permutation representations. As in OX, in NOX we select two crossover points at random, and we mark the nodes in the genes from the segment between the points in the other parent. The main differences between OX and NOX are:

1. In NOX, the two first positions have fixed values to the depth: $d_1 = 0$ and $d_2 = 1$;

2. In NOX, the remain positions of the offspring, after copy the segment between the crossover points, are filled from the first positions of the other parent and the offspring, instead of start after the second crossover point. This change avoid produce offsprings with different node root.

Algorithm 3.1 presents the pseudocode of NOX for NDE genotypes.

Algorithm 3.1 - NOX Pseudocode.

//Let be P_1 and P_2 the NDE of the parents.
//Let be O_1 and O_2 the NDE of the offspring.
//A_1 and A_2 arrays to mark the nodes.
(1) Choose two crossover points at random. These points define a segment;
(2) Mark in $A_2(A_1)$ the nodes in the segment between the crossover points in $P_1(P_2)$;
(3) Fill the genes into $O_1(O_2)$ with the genes from $P_2(P_1)$, avoiding the marked nodes, until the first crossover point in $O_1(O_2)$. If needfull correct the depth of the node;
(4) Fill the segment between the crossover points into $O_1(O_2)$ with the genes in the same positions from $P_1(P_2)$. If needfull correct the depth of the node;
(5) Fill the remains genes into $O_1(O_2)$, with the genes from $P_2(P_1)$, from the last used position in step (3). If needfull correct the depth of the node;

In order to guarantee only feasible NDE genotypes, when the procedure is copying the genes can be needfull to apply a depth correction. It happens when the difference between d_i and d_{i-1} is bigger than 1 ($d_i - d_{i-1} > 1$). In this case we make $d_i = d_{i-1} + 1$.

3.0.2   NDE Position Based Crossover - NPBX

NPBX recombination operator is based on PBX operator for permutation representations. As in PBX, in NPBX we select a set of positions at random and mark them into the other parent. As in NOX que main difference between PBX and NPBX are that the two first genes have fixed values to the depth: $d_1 = 0$ and $d_2 = 1$.

Algorithm 3.2 presents the pseudocode of NPBX for NDE genotypes.

Algorithm 3.2 - NPBX Pseudocode.

//Let be P_1 and P_2 the NDE of the parents.
//Let be O_1 and O_2 the NDE of the offspring.
//A_1 and A_2 arrays to mark the nodes.
(1) Choose a set of positions of $P_1(P_2)$ at random;
(2) Mark in $A_2(A_1)$ the nodes in the genes of the set of positions of $P_1(P_2)$ selected in Step(1);
(3) Fill the genes into $O_1(O_2)$ that correspond to the set of positions with the genes in the same position from $P_1(P_2)$. Fill the remain genes with the genes from $P_2(P_1)$ avoiding the marked nodes. Keep the depths of the two first positions fixed and if needfull correct the depth of the node;

As in NOX, in order to guarantee only feasible NDE genotypes, the same depths correction must to be applied in NPBX, in the same conditions.

4.   PROPERTIES ANALYSIS

In order to evaluate the behavior of NOX and NPBX in relation of the properties, empirical tests were performed. For these tests were used four Euclidean Graphs size for the Steiner tree problem with $n = 10, 20, 40$ and 80, with 5 instances for each size, available on OR-Library[1]. The evolutionary algorithm uses the NDE, its mutation operators, no selection method, and Prüfer numbers to create the initial population of, because it is an unbiased representation [3]. Each instance was tested 10 times with 1,000 individual in the population. The results shows that both recombination operators present a bias towards stars. Also, we obtain that they have a high hereditability with low number of non-parental edges. In the worst case, around $20\%(15/79)$ of the edges, in the offspring, are non-parental edges.

5.   CONCLUSIONS

This paper proposes two recombination operators for the NDE: NOX and NPBX. This operators are based on permutation recombination operators, OX and PBX, respectively. In addiction, we analyze NOX and NPBX with the properties to representations and operators heritability and bias. The analysis shows that both operators has a high heritability, specially to graphs with a bigger number of nodes. Both operators, also, present a bias towards stars with no mutation operation.

Acknowledgments

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