On the Use of Genetic Algorithms for Solving the RWA Problem Employing the Maximum Quantity of Edge Disjoint Paths

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ABSTRACT

In this paper, the routing and wavelength assignment problem in all optical networks is considered. A solution to the RWA problem is proposed through a Genetic Algorithm (GA) based approach to search for the most suitable set of paths from many possible ones. We use GAs to solve this problem by introducing a new fitness function based on the mean value of occurrence of the common edges between the different genes of a single chromosome. In addition, we further improve performance and particularly execution times by considering the maximum quantity of edge disjoint paths (EDPs) to initialize the population with some *indigo* chromosomes. These EDPs are pre-computed and inserted in the GA-RWA problem. The proposed approach has been evaluated on the NSF network topology and compared with other similar schemes.

1. INTRODUCTION

Introducing optical transparency in the optical layer on one hand leads to a dynamic, flexible optical layer with the possibility to add extra "intelligence". On the other hand, transparency reduces the ability of the digital electronics layer to interact with the optical layer. Thus, optical transparency has an impact on network design, either by adapting the size of WDM transparent domains in order to neglect physical impact on Quality of Transmission, or by introducing physical considerations in the network and wavelength planning process. The problem of setting up lightpaths by routing and assigning a wavelength to each connection is called *routing and wavelength assignment* (RWA) problem [1],[2]. The RWA problem belongs to the category of NP-complete problems, that is, the computational time would increase exponentially with the problem size. Thus, a wide range of optimization methods and heuristics have been proposed to solve various optical network optimization problems. Integer linear programming was employed for example in [2]. Their high complexity, however requires intensive computational efforts and therefore other novel heuristic algorithms such as Tabu-search, [3], simulated annealing, [4],[5] and genetic algorithms, [6]-[9]. Genetic algorithms are stochastic search optimization methods that are widely used in combinatorial optimization and parameter tuning applications. They have been used for solving the plain single objective RWA problem, [7], for optimizing amplifier placement, [8] as well for multicasting sessions, [9]. In this paper, a new approach of using GA for solving the RWA problem is proposed. First, two new cost metrics, the average (μ) and the variance (σ) of the occurrence of the common edges are introduced in the chromosome fitness function, to improve GAs performance and secondly the maximum quantity of edge disjoint path is used to initialize population. The latter further improve performance and execution times.

2. GENETIC ALGORITHMS

Genetic Algorithms (GAs) is a class of search strategies based on the mechanism of biological evolution. GA tries to emulate a phenomenon observed in nature: survival of the fittest. Usually each solution is represented using a gene, and all solutions, all genes form an individual chromosome. The latter mate to each other to create outcrossings, until a good individual of the problem is found. GAs do not guarantee that an optimal solution can be found, since it a stochastic process. The main steps for executing a GA algorithm are:

***Initialization**:* During that phase, a random set of individual chromosomes (also called initial population) is initialized with random values. A unique cost metric is assigned to all, to identify their fitness. This function depends on the problem to be solved and also determine the fitness of each individual.

***Crossover**:* During that phase, individual chromosomes are crossovered (mate) with a specified probability, to produce the next generation individuals. After crossover a new era of additional individual is created in the total population. The cost of each is calculated again and the worst performing ones are discarded. Usually, an upper bound in the number of individuals is maintained (population), and when this is reached all the rest are not considered for next generation crossovers.

***Mutation**:* During that step a single gene is modified. This is done to avoid loops around a local, but not global optimal solution. This is necessary since GAs, as a stochastic search engines, may be trapped around sub-optimal solution during random crossovers between the best performing individuals.

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2.1 Genetic Algorithms for solving the RWA problem

***Problem Definition*:** Given a set of source-destination pairs minimize the number of wavelengths needed to support the given set of lightpaths.

In the case of GA-RWA, each gene in an individual chromosome represents one of the k-shortest paths for a specific source-destination pair. Each chromosome consists of n genes, where n is the number of all source-destination pairs and constitute a solution to the RWA problem. Figure 1a shows an example for k=3. The genes that constitute an individual correspond to the following source-destination *(s,d)* pairs: *{(1,2), (2,4), (3,1), (3,5)}* Each gene binary denotes a certain routing path. If the best chromosome is the one below the new graph is shown in Figure 1b and thus the minimum number of wavelengths is two. The nodes in Figure 1b correspond to the genes of the solution, while the edges to the common links of that solution.

Let *G(V, E)* denote a simple graph that models the network, where V is the vertex set and E is the edge set. The demand set D is a set of pairs $\{(s_1, d_1), (s_2, d_2) \ldots, (s_k, d_k)\}$, where $s_i, d_i \in V$, and $i = 1,\ldots,k$, where, k is the total number of requests for connections, s_i is the source and d_i the destination of that request. For each request i, a separate wavelength and lightpath must assigned, denoted here as λ_i and $L_i \subseteq E$, in the sense that the edges of the lightpath belong in E. To this end, each individual in the genetic algorithm, can be represented as $L_i, \in \{1\ldots k\}$.. The aim of the RWA problem is to minimize $\max\{\lambda_i\}$, under the condition $L_i \cap L_j = \varnothing\ \forall\, i, j$.

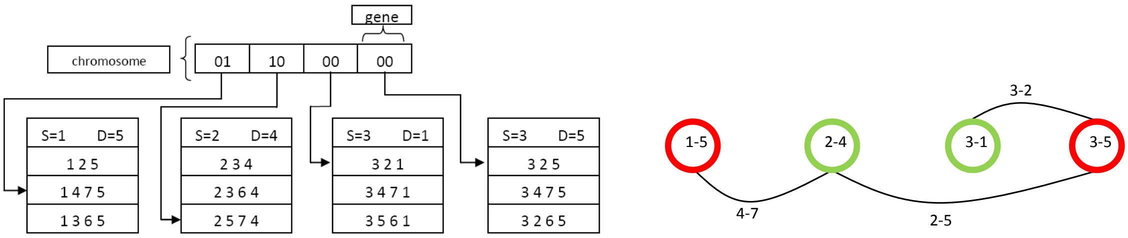

Figure 1: (a) Example of the individual (chromosome) structure with four genes, each pointing to a candidate routing path. (b) Illustrative solution displaying the common edges of the genes (s-d pairs). For example gene 1-5 and gene 2-4 have in common edge 4-7.

For solving the GA-based RWA algorithm, a fitness cost is assigned to the chromosome, that must represent the number of the common edges of each L_i. This value monotonically increases with the chromosome fitness cost. Thus, if $E(L_i)$ are the edges for the $\{s_i, d_i\}$ pair, then the set that contains the common elements of $E(L_i)$ with all the $E(L_{j \neq i})$ is represented as $\varepsilon_i \cap \{E(L_i)\}$. In [7], an exponentially cost was used as follows: $\sum_{\forall i \in \cap\{\mathbf{E}(\mathbf{L}_i)\}} V^{F_i}$.

However, summing the exponential costs does not reveal the true fitness of the individual, since a highly repeated link can significantly increase the cost of a path that may result in discarding a good candidate solution. Thus, genetic algorithms may not reach the global optimum. To this end, we have introduced two innovative features. First, we introduce two new cost metrics, the average (μ) and the variance (σ) and then we make use of the maximum number of edge disjoint paths as in [10].

Fitness function: What is important is the repeatability of each edge of L_i in the lightpaths and thus we may assign to each gene of the chromosome *Ch* a cost c_i which equals the number of ε_i. A simple fitness function could be the mean number of the costs of each gene, $F(Ch) = V^{\mu(cLi)}\, \forall \varepsilon_i$.

For example, to find $F(Ch)$ of the chromosome depicted in Figure 1, we need to examine each gene and calculate its $c_{i,}$ cost for $i = 1\ldots4$. The first gene has two common edges with the second gene (edges (4,7) and (7,5)) thus $c_1 = 2$, the second gene has two common edges with the first gene (edges (4,7) and (7,5)) and one common edge with the forth gene (edge (2,5)) thus $c_2 = 3$, the third gene has one common edge with the fourth gene (edge (3,2)) thus $c_3 = 1$ and finally the forth gene has one common edge with the second gene (edge(2,5)) and one common edge with the third gene (edge (3,2)) thus $c_4 = 2$. To this end, the cost of this solution, assuming that $V = \{1, 2, 3, 4,5, 6, 7\}$, is: $F(Ch) = V^{\mu(c_i)} = 7^{\frac{2+3+1+2}{4}} = 49$.

Crossover: A n -point crossover is used for a chromosome. This mechanism is adopted so that if a path is assigned to a particular *(s, d)* pair, during crossover the identity of the path is maintained in entirety. The individuals for crossover are chosen on the conventional Roulette Wheel selection scheme where the Fitness is assigned by interpolating between the best individual (whose Fitness function is least) to the worst individual (whose Fitness function is largest) according to a simple monotonic function which maps it to the Roulette wheel as in [7]. After crossover an additional individual is generated and included in the population. If the population is of size v, then the first v individuals maintained based on their fitness, while the rest are discarded.

Mutation: A random uniform mutation with a probability of $p_m = \frac{1}{k}$ is used, where k is the length of a chromosome. In mutation the created chromosome replaces itself regardless of the fitness function. The individual with the worst Fitness function is selected for mutation. This is done with the idea to produce a fitter individual from a bad individual in the population.

In the following Table 1, we summarize results (maximum number of wavelengths) considering the NSF network topology for different fitness functions and for different number of source-destination pairs. The initial and maximum population size chosen was 50 and 100 respectively, while the number of iterations (epochs) 1000.

Table 1. Maximum number of wavelengths for different fitness functions considering the NSF network topology with 14 nodes and 21 edges.

SD pairs, k	$\sigma(c_i)$	$\mu(c_i)$	$V^{\mu(c_i)}$	$\sum V^{(c_i)}$
20, *k*=3	5	4	4	6
40, *k*=3	9	9	7	9
80, *k*=2	17	15	14	23
120, *k*=2	23	22	20	26
150, *k*=2	28	27	25	30
182, *k*=2	34	34	30	37

From Table 1, it is clear that considering the mean or variance of common edges occurrence yields significantly better results. We have further improved performance of the proposed GA-RWA by making use of the maximum quantity of edge disjoint paths (EDPs) instead of all possible alternate routing paths per (s_i, d_i).

Maximum quantity of EDPs: In order to find a set of edge disjoint paths for effective wavelength assignment, the maximal flow problem from a source *s* to a destination *d* in a given graph *G*, is solved, where any edge is undirected and all capacities are equal to one. The mechanism that searches the maximum flow is based on the Ford–Fulkerson algorithm with complexity *O(E*f)*, where *E* is the number of edges in the graph and *f* is the maximum flow in the graph. The maximum possible edge disjoint paths for each *(s, d)* pair is denoted by the *cardinality* of the *edge cut set* between *s* and *d.* At this end a set of all the EDPs per *s-d* pair is created and stored for the specific physical topology.

Considering a given traffic matrix (set of *(s, d)* pairs) the set of the pre-computed set of EDPs is fetched and the paths with commons edges are then discarded. What remains is the maximum disjoint paths of the topology for a given set of *(s, d)* pairs and which are used as input to the genetic algorithm, with the difference that the genes that these paths correspond to, do not crossover or mute. They remain un-changeable since they potential constitute optimal solutions. Figure 2 graphically shows such an individual, called *indigo* chromosome.

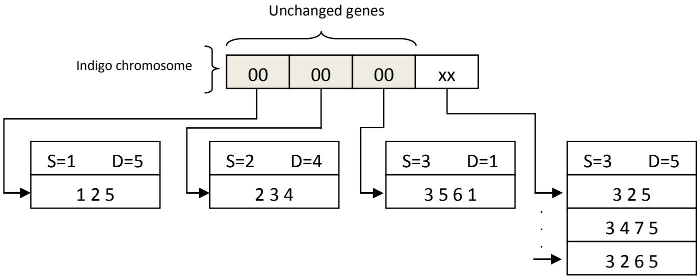

Figure 2. Example of an indigo chromosome structure with three un-changeable genes.

The use of the maximum quantity of edge disjoint path to initialize the population in the GA-RWA problem is of paramount importance, since they force GAs to search around an optimal solution of a subset of paths rather than blindly searching into all initial population. In addition, the use of EDPs is further advantageous when multiple flows per *(s, d)* pair are considered [10]. In order to investigate this, we have performed simulation experiments, with even a smaller initial population size and compare both the number of wavelengths, as well as the number of iterations needed to reach the same result with and without employing the pre-computed EDPs. Table 2 and Table 3 summarize our findings using the $V^{\mu(c_i)}$ fitness function, while Table 4 reports the mean execution time of an epoch that was different for different numbers of *(s, d)* pairs. Simulations were carried out using Matlab environment on a 3 GHz Pentium-4 PC. Table 2 compares the number of epochs needed to reach the same number of wavelengths when employing the conventional k-shortest path as well as the max-EDPs, while Table 3 shows the optimal number of wavelengths needed for different (*s-d)* pairs, when employing the max-EDPs into GA-RWA. The simulation experiments were again carried out over the NSF network topology with an initial and maximum population size of 25 and 75 respectively, and with $k = 2$. From Table 2 and 2, it can be seen that the use EDPs significantly improve execution times, while an overall better solution is reached.

3. CONCLUSIONS

In this paper, a new approach for using GA for solving the RWA problem in optical networks is presented. The proposed GA-RWA algorithm uses some new fitness functions to improve performance and further use the maximum quantity of edge disjoint paths, which are computed in advance, to initialize the population set. This forces the GA to search around a (possible) global optimal solution of at least a subset of routing paths. The evaluation results have shown that this approach improves overall performance in terms of both computational time and number of wavelengths.

Table 2. Number of epochs needed to reach the same number of wavelengths when employing the conventional k-shortest path and the max-EDPs into GA-RWA.

GA-RWA with		*k* shortest paths	max-EDPs
SD pairs	λ	Epochs	epochs
40	7	155	1
80	14	353	199
150	25	727	441
182	30	624	463
40x2	15	221	23
80x2	29	309	199

Table 3. Number of wavelengths calculated using the max-EDPs into the GA-RWA.

SD pairs	λ	epochs
40	6	507
80	14	441
150	25	837
182	29	749
40x2	12	793
80x2	27	485

Table 4. Mean time for an epoch.

SD pairs	Mean time of an epoch (msec)
40	5
80	15
120	31
150	47
182	71

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