

A genetic algorithm for maximizing the accepted demands in routing and wavelength assignment in optical networks

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Abstract

Given a set of lightpath requests, the problem of routing and wavelength assignment (RWA) in optical networks consists in routing a subset of these requests and assigning a wavelength to each of them, such that two lightpaths that share a common link are assigned to different wavelengths. There are many variants of this problem in the literature. We focus in the variant in which the objective is to maximize the number of requests that may be accepted, given a limited set of available wavelengths. This problem is called max-RWA and it is of practical and theoretical interest, because algorithms for this variant can be extended to other problems that arise from the design of optical networks. In this paper, we propose a biased random-key genetic algorithm for max-RWA. Computational experiments showed that for the largest instances in the literature where only upper bounds to the value of the optimal solutions are known, the average optimality gap of the best of the proposed biased random-key genetic algorithm is smaller than 4%.

1 Introduction

In optical networks, the information is transmitted as optical signals through optical fibers. *Wavelength Division Multiplexing* (WDM) allows the more efficient use of the capacity of the optical fibers. An all-optical point-to-point connection between two nodes is called a *lightpath*. Each lightpath is characterized by its route and by the wavelength with which it is multiplexed. Two lightpaths may use the same wavelength, provided they do not share any common fiber.

Given the physical topology of an optical network and a set of lightpaths defining a logical topology in this network, the problem of *Routing and Wavelength Assignment* (RWA) in WDM optical networks consists in routing the set of lightpaths and assigning a wavelength to each of them, such that lightpaths whose routes share a common fiber are assigned to different wavelengths. We consider the max-RWA variant, in which the set of lightpath requests are known beforehand and no wavelength conversion is available. Let $G = (V, A)$ be a directed graph representing the physical network topology, where V is the set of the nodes and A represents the fiber connections between the nodes. Let also R be the set of lightpaths requests, each one defined by a source and a destination node in V . There can be more than one lightpath request between two nodes, since the traffic between a pair of nodes can be larger than that supported by a single lightpath. We denote by Λ the set of available wavelengths.

As the size of optical networks increase, exact algorithms become inefficient to solve large problems. In this paper, we propose a random-key genetic algorithm to efficiently solve large, real-life size instances of max-RWA. Computational experiments showed that the average optimality gap obtained with this heuristic are smaller than 4% for classic instances in the literature.

2 Biased random-key genetic algorithm

Genetic algorithms with random keys, or random-key genetic algorithms (RKGA), were first introduced by Bean [1]. Solutions are represented as vectors of randomly generated real numbers called keys. A deterministic algorithm, called a decoder, takes as input a solution vector and associates with it a feasible solution. Two parents are selected at random from the entire population to implement the cross-over operation in the implementation of a RKGA. Parents are allowed to be selected for mating more than once in a given generation.

A biased random-key genetic algorithm (BRKGA) differs from a RKGA in the way parents are selected for crossover, see [3] for a review. In a BRKGA, each element is generated combining one element selected at random from the elite solutions in the current population, while the other is a non-elite solution. Selection is biased, since one parent is always an elite individual. The development and application of a BRKGA to max-RWA was motivated by successful applications to other network optimization problems, such as other variants of routing and wavelength assignment [4, 6–8] and routing in OSPF networks [2].

The biased random-key genetic algorithm for max-RWA evolves a population of chromosomes that consists of vectors of real numbers (called keys). Each solution is represented by an $|R|$ -vector, in which each component is a real number in the range $[0, 1]$ associated with a lightpath request in R . Each solution represented by a chromosome is decoded by a decoding heuristic that receives the vector of keys and builds a feasible solution for max-RWA.

The minimum length (min-length) of a lightpath is defined as the number of hops in the route with the smallest number of arcs between its endnodes. The decoding heuristic consists of two steps. First, the lightpaths are sorted in non-decreasing order of their min-lengths. Therefore, the relative order between lightpaths with the same min-length value is defined by their keys. The resulting order is used in the second step as the vector $\Pi = \pi(1), \dots, \pi(|R|)$ by the decoding heuristic. We notice that the larger is the minimum length of a lightpath, the larger is the number of arcs used by its shortest route, and the harder will be to route it. Therefore, the decoding heuristic will first consider the lightpaths with the smallest minimum lengths, as a strategy to accept a higher number of lightpaths. Since there might be several lightpath with the same minimum length, ties are broken in favor of that with minimum key.

Next, a graph $G_k = (V, A_k)$ is created for each wavelength $k \in \Lambda$, where V is the set of nodes and A_k is the set of arcs in which a lightpath multiplexed with wavelength k can be routed. Initially, $A_k = A$. Every time a lightpath is assigned to a new route and a wavelength k , the arcs in this route are removed from G_k to avoid that other lightpaths multiplexed with wavelength k use them. For each lightpath $j \in R$, the decoding heuristic computes the shortest path $P(j, G_k)$ between its endnodes in each copy G_k , with $k = 1, \dots, |\Lambda|$, and sets $P(j, G_k) = \emptyset$ if there is no such a path.

Let $k^* = \operatorname{argmin}_{k \in \Lambda} \{\text{length}(P(j, G_k))\}$, where $\text{length}(P(j, G_k))$ denotes the number of arcs in $P(j, G_k)$, with $\text{length}(P(j, G_k)) = \infty$ if $P(j, G_k) = \emptyset$. If $P(j, G_{k^*}) \neq \emptyset$, then lightpath j is accepted, assigned to wavelength k^* , and routed using the arcs in $P(j, G_{k^*})$. All these arcs are removed from G_{k^*} to avoid that other lightpaths use them. Otherwise, lightpath j is not accepted because it cannot be routed in any of the copies of G and the procedure moves to the next lightpath following the order defined by permutation Π , until all of them are considered. The number of lightpaths accepted by this heuristic will be used as the fitness of the chromosome.

We use the parametrized uniform crossover scheme proposed in [9] to combine two parent solutions and produce an offspring. In this scheme, the offspring inherits each of its keys from the best fit of the two parents with probability 0.7 and from the least fit parent with probability 0.3. This genetic algorithm does not make use of the standard mutation operator. Instead, the concept of mutants is used: a fixed number of mutant solutions are introduced in the population in each generation, randomly generated in the same way as in the initial population.

The keys associated to each lightpath request are randomly generated in the initial population. At each generation, the population is partitioned into two sets: *TOP* and *REST*. Consequently, the size of the population is $|TOP| + |REST|$. Subset *TOP* contains the best solutions in the population. Subset *REST* is formed by two disjoint subsets: *MID* and *BOT*, with subset *BOT* being formed by the worst

elements on the current population. The chromosomes in *TOP* are simply copied to the population of the next generation. The elements in *BOT* are replaced by newly created mutants that are placed in the new set *BOT*. The remaining elements of the new population are obtained by crossover with one parent randomly chosen from *TOP* and the other from *REST*. Therefore, $|MID| = |REST - BOT|$ offspring solutions are created. In our implementation, the population size was set to $|TOP| + |MID| + |BOT| = |V|$, with the sizes of sets *TOP*, *REST*, and *BOT* set to $0.25 \times |V|$, $0.7 \times |V|$, and $0.05 \times |V|$, respectively, as suggested by Noronha et al. [7].

3 Computational experiments

In order to evaluate if BRKGA efficiently identifies the relationships between keys and good solutions and converges to near-optimal solutions, we compared its performance with that of a multi-start (MS) procedure that uses the same decoding heuristic as BRKGA. Each iteration of the multi-start procedure applies the same decoding heuristic, but starting from a randomly generated vector of keys. Therefore, nothing is learned from one iteration of MS to the next. We have considered 72 instances in the experiments, divided in three test sets of 24 instances. They are built from 24 networks and consider three different numbers of wavelengths for each network.

Each of the heuristics BRKGA and MS was given ten minutes of computation time and stopped thereafter. Ten runs of each heuristic have been performed for each instance. The average optimality gap (with respect to the upper bounds reported in [5]) observed for BRKGA was only 3.56%, while that for MS was 5.04%.

Figure 1(a) illustrates the evolution of the solution population along 200 generations of BRKGA for one execution of one of the tested instances. It shows that the biased random-keys genetic algorithm is able to continuously evolve the solution population and to improve the best solution value. Figure 1(b) illustrates for the same instance how the best solutions found by BRKGA and by the multi-start procedure evolve along the six first seconds of processing time. It shows that the biased random-key genetic algorithm systematically finds better solutions faster than the other algorithm. The best solution obtained by BRKGA is better than that found by multi-start at any time along the run whose results are displayed in these figures.

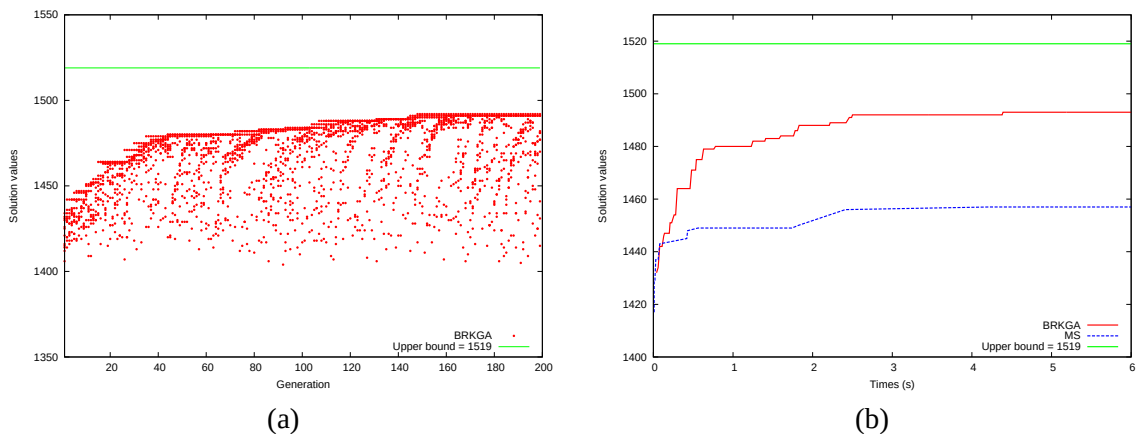


Figure 1: (a) Population evolution: the value of the best solution found by BRKGA after 4.42 seconds (200 generations) is 1492, while the best solution value after 10 minutes of running time is 1502. (b) Evolution of the best solutions found by BRKGA and MS along the six first seconds of processing time: the best solution value obtained by BRKGA is 1493, while that found by MS is only 1457.

4 Conclusions

We proposed a biased random-key genetic algorithm to for the max-RWA problem. Computational experiments show that the biased random-key genetic algorithm BRKGA is very effective and has found near-optimal solutions whose average optimality gap was at most 10.53% over all 72 test instances. The average optimality gap within each test set never exceeded 4% and the overall average gap amounted to only 3.56%. Detailed results are reported in the full version of this paper.

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