A RANDOM-KEYS GENETIC ALGORITHM FOR ROUTING AND WAVELENGTH ASSIGNMENT

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ABSTRACT. We propose a simple, robust and efficient genetic algorithm for the problem of routing and wavelength assignment (RWA) in WDM optical networks. The algorithm extends the best heuristic in the literature (Skorin-Kapov, 2007) by embedding it into an evolutionary framework. Experimental results show that, on average, the genetic algorithm improves the performance of a multi-start variant of the Skorin-Kapov heuristic by 24.3%.

1. INTRODUCTION

The problem of routing and wavelength assignment (RWA) in WDM optical networks consists in routing a set of connections (called lightpaths) and assigning a wavelength to each of them, such that connections whose paths share a common link in the network are assigned to different wavelengths. Two lightpaths may use the same wavelength, provided they do not share any common link. We consider the min-RWA offline variant, in which all connection requirements are known beforehand and no wavelength conversion is possible. The objective is to minimize the number of wavelengths used for routing all connections. There are different heuristics for min-RWA. Some approaches decompose the problem into two subproblems: the routing subproblem and the wavelength assignment subproblem [2], while others tackle the two subproblems simultaneously [3]. The most recent heuristic, `BFD-RWA` [3], is an extension of the best fit heuristic for the bin packing problem. When used within a multi-start procedure, `BFD-RWA` obtains, to date, the best results in the literature for min-RWA. Furthermore, `BFD-RWA` was the first heuristic in the literature to be able to solve large instances with up to 100 nodes and 9900 connections.

2. SOLUTION APPROACH

The genetic algorithm (GA) proposed in this paper is based on the work of Bean [1]. The chromosomes are vectors of real numbers (called random keys) in the range $[0, 1]$. There is one random key associated with each connection. The decoding is made in two steps. First, the connections are sorted by the (hop-count) values of the shortest paths between their endnodes plus the value of their random keys. Then, the resulting permutation is used as input to the `BFD-RWA` heuristic. The number of wavelengths found by `BFD-RWA`

TABLE 1. Experimental results

Name	Nodes	Degree	P_l	BFD–RWA	GA-V1	GA-V2	GA-V3	GA-V4	GA-V5	GA-V6
Rand1	100	0.4	0.2	117.98	2.9%	3.7%	0.7%	10.4%	9.9%	10.6%
Rand2	100	0.3	0.4	2913.41	15.3%	32.9%	22.3%	19.0%	10.1%	22.4%
Rand3	100	0.3	0.6	1307.43	7.7%	9.0%	5.3%	1.8%	12.8%	4.3%
Rand4	100	0.4	0.6	233.63	3.4%	2.9%	-2.9%	15.1%	-3.5%	-0.6%
Rand5	100	0.5	0.6	2262.67	10.8%	35.9%	24.5%	15.1%	45.4%	34.8%
Rand6	100	0.3	0.8	632.4	11.9%	18.6%	14.5%	4.9%	13.7%	0.1%
Rand7	100	0.4	0.8	194.13	31.9%	27.8%	26.8%	12.3%	13.5%	16.5%
Rand8	100	0.4	0.8	981.13	36.3%	60.3%	18.0%	20.6%	13.7%	19.8%
Rand9	100	0.4	1.0	238.26	6.6%	12.2%	1.1%	32.0%	23.9%	18.6%
Rand10	100	0.5	1.0	754.73	22.7%	24.8%	29.1%	15.1%	25.5%	23.2%
Rand11	100	0.5	1.0	1330.43	59.7%	83.0%	53.5%	53.4%	57.8%	47.9%
Grid1	10×10	0.4	0.2	329.61	-17.0%	-15.6%	-16.0%	-9.6%	-2.2%	1.8%
Grid2	6×17	0.4	0.4	388.78	-4.1%	20.6%	1.9%	12.4%	19.4%	5.2%
Grid3	10×10	0.4	0.6	1282.32	11.0%	6.2%	4.5%	9.4%	10.3%	7.6%
Grid4	4×25	0.4	0.8	739.87	30.9%	37.6%	27.8%	32.8%	15.6%	20.9%
Grid5	5×20	0.4	0.8	145.63	23.0%	29.8%	15.4%	11.6%	9.1%	14.7%
Grid6	6×17	0.4	0.8	422.77	43.9%	37.8%	41.0%	30.2%	35.7%	33.0%
Grid7	8×13	0.4	0.8	604.92	6.3%	30.9%	18.2%	9.3%	27.2%	1.5%
Grid8	5×20	0.4	1.0	3181.5	-1.4%	3.5%	11.9%	-2.2%	-6.0%	-11.3%
				Average:	15.9%	24.3%	15.7%	15.5%	17.5%	14.3%

with the given permutation is used as the fitness of the chromosome. The random keys are randomly generated in the initial population. The population is partitioned into three sets *A*, *B*, and *C*. The best solutions are kept in *A*, the worst ones in *C*, and the others in *B*. The sizes of sets *A*, *B*, and *C* are parameters that must be tuned. At each new generation, the chromosomes in *A* are copied to the new population, those in *C* are replaced by new randomly generated chromosomes, and the ones in *B* are replaced by crossover. The GA learns the relationship between the random keys and the good solutions, converging to better solutions faster than the multi-start BFD-RWA.

3. NUMERICAL RESULTS

The experiments were performed on an SGI Altix 3700 Supercluster running RedHat Advanced Server with SGI ProPack (32 1.5-GHz Itanium-2 processors). Each run was limited to a single processor. The first set of instances was randomly generated as in [3], with 100 nodes and average degrees of edges varying from 0.03 to 0.05. The second set of instances was based on $n \times m$ grids embedded on the torus. Each node is connected to the nearest four nodes. The value of n ranges from 4 to 10 and that of m is adjusted in a manner that each instance has approximately 100 nodes. The probability P_l of the

existence of a lightpath between any two nodes ranges from 0.2 to 1. The instances have up to 9900 connections.

Six versions of the GA were evaluated, with variations in the population size and the number of chromosomes in sets A and C. Versions `GA-V1`, `GA-V2`, and `GA-V3` have their population size equal to τ. The latter is equal to 2τ for versions `GA-V4`, `GA-V5`, and `GA-V6`, where τ is the number of nodes in the network. $|C| = 2|A| = 0.2\tau$ for `GA-V1` and `GA-V4`, $|A| = 5|C| = 0.25\tau$ for `GA-V2` and `GA-V5`. For the other versions, $|A| = |C| = 0.15\tau$.

The multi-start `BFD-RWA` and the GA were applied 200 times to each instance with different seeds. The algorithms stop whenever a solution with cost better than or equal to a given target is found. The target is equal to the value of the best known solution for each instance. The computational results are presented in Table 1. The first column displays the name of the instance. The three next columns give the number of vertices, the average edge degree of the vertices, and the probability of the existence of a lightpath between two vertices. The fifth column displays the average time `BFD-RWA` took to find a solution as good as the target. The average times to reach the target for the six versions of the GA are given in the last columns, as a percent deviation of `BFD-RWA` times.

4. CONCLUDING REMARKS

We proposed a simple, robust and efficient genetic algorithm for min-RWA. It extends the best heuristic in the literature by embedding it into an evolutionary framework. The experimental results showed that `GA-V2` provides the best choice of parameters. It improved the performance of the multi-start `BFD-RWA` by 24.3% on average. Among the 19 instances tested, the latter was faster than `GA-V2` on only one instance. Furthermore, the results showed that the adjustment of the parameters is not crucial, since all versions converged to good solutions at least 14% faster than the multi-start `BFD-RWA`.

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