

A Two-Population Based Evolutionary Approach for Optimizing Routing, Modulation and Spectrum Assignments (RMSA) in O-OFDM Networks

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Abstract—We propose a novel two-population genetic algorithm (MPGA) to optimize the routing, modulation and spectrum assignments (RMSA) in optical orthogonal frequency-division multiplexing (O-OFDM) networks. The proposed MPGA makes two populations evolve in parallel with different selection and mutation strategies, and incorporates a migration operation to exchange individuals between them. Performance evaluations show that the MPGA outperforms several existing algorithms.

Index Terms—Multi-population genetic algorithm (MPGA), routing, modulation and spectrum assignment (RMSA), optical orthogonal frequency-division multiplexing (O-OFDM).

I. INTRODUCTION

NOWADAYS, optical orthogonal frequency-division multiplexing (O-OFDM) [1] has attracted intensive research interests due to its elastic nature of bandwidth allocation (i.e. granularity at a few GHz). As it transmits high-speed data over a few narrow-band subcarrier frequency slots, this technology has the flexibility of choosing modulation formats based on the transmission distance [2]. When planning a network that employs O-OFDM, operators need to come up with an efficient routing, modulation and spectrum assignment (RMSA) scheme that can serve all traffic demands with the minimum number of subcarrier frequency slots [3]. To solve this problem, previous works have proposed several integer linear programming (ILP) models [4], and heuristic algorithms [3-6]. However, as the complexity of the network planning scales rapidly with the network size and the volume of lightpath requests, these algorithms can become less effective.

In this letter, we propose a two-population genetic algorithm (MPGA) that can solve the RMSA problem for large-scale networks with high efficiency. The proposed MPGA makes two populations evolve in parallel, applies different selection and mutation strategies to them, and incorporates a migration operation to exchange individuals between them. Simulations show that the MPGA outperforms several existing algorithms by providing more efficient network planning results within reasonable computation time. To further investigate the performance of the MPGA, we design a single-population genetic algorithm (SPGA) as the reference. The comparative study shows that the MPGA has superior algorithm robustness.

II. MULTI-POPULATION GENETIC ALGORITHM FOR RMSA

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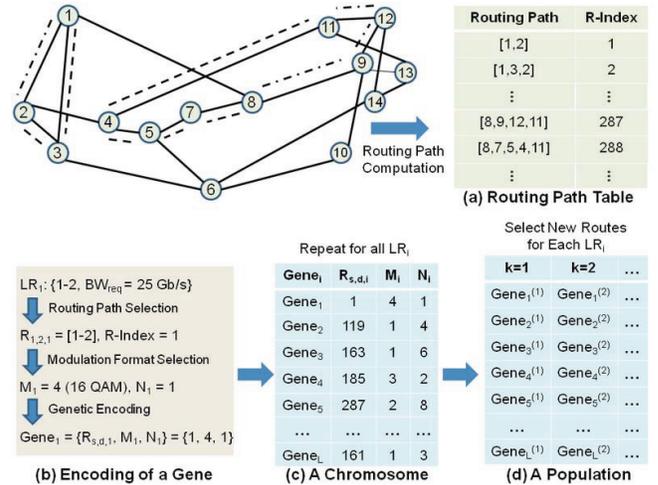


Fig. 1. Proposed genetic encoding scheme for the RMSA problem.

Genetic algorithm (GA) is a search heuristic that mimics the process of natural evolution [7]. In GA, each feasible solution is represented with a group of genes, which is known as an individual chromosome. A SPGA makes all individuals evolve together in a common population, while our proposed MPGA divides the individuals into two populations and makes them evolve in parallel with different selection and mutation strategies. By doing so, we try to solve the famous dilemma of GA: *How to make tradeoff between search performance and algorithm robustness?* The MPGA utilizes a *Coarse-Exploring Population (C-POP)* to increase genetic diversity, while the other *Fine-Tuning Population (F-POP)* is designed to prevent chromosomal disruption. During parallel evolution, these two populations can exchange their individuals by using the migration operation.

We apply this MPGA-based optimization to solve the planning of large-scale O-OFDM networks, where the traffic matrix or the lightpath requests are known a priori. The physical network topology is $G(V, E)$, where V is the node set and E is the fiber link set. For a lightpath request LR_i from node s to d , $s, d \in V$, we assign N_i contiguous slots with a modulation of M_i bits per symbol to satisfy the requested bandwidth. In this work, we assume that M_i can be 1, 2, 3, 4 for BPSK, QPSK, 8 QAM and 16 QAM, respectively, and the selection of M_i solely relies on the routing path length of LR_i . *Algorithm 1* describes the logic flow of our proposed MPGA for RMSA, where $P^{(j)}$ is the j -th population, P is the combined population ($P = P^{(1)} \cup P^{(2)}$), $PSize_j$ is the size of the j -th population, $RSet_{s,d}$ is the set of feasible routing paths between s and d , $R_{s,d,i}^{(k)}$ ($R_{s,d,i}^{(k)} \in RSet_{s,d}$) is the k -th individual's routing path for the i -th lightpath request LR_i that is from s to d .

Algorithm 1 Two-Population Genetic Algorithm for RMSA

Output: Best RMSA solution S_{best}

{Phase I: Construct Initial Populations}

- 1: **for** all populations $P^{(j)} (j = 1, 2)$ **do**
- 2: **while** $k \leq PSize_j$ **do**
- 3: **for** all lightpath requests LR_i **do**
- 4: select $R_{s,d,i}^{(k)}$ randomly from $RSet_{s,d}$;
- 5: compute $M_i^{(k)}$ and $N_i^{(k)}$ based on $R_{s,d,i}^{(k)}$ and LR_i ;
- 6: construct $Gene_i^{(k)} = \{R_{s,d,i}^{(k)}, M_i^{(k)}, N_i^{(k)}\}$;
- 7: $Individual[k] \leftarrow Gene_i^{(k)}$;
- 8: **end for**
- 9: $P^{(j)} \leftarrow Individual[k]$;
- 10: $k = k + 1$;
- 11: **end while**
- 12: $P \leftarrow P^{(j)}$;
- 13: **end for**

{Phase II: Multi-Population Evolution}

- 14: **while** MPGA has not converged **do**
- 15: **for** all populations $P^{(j)} (j = 1, 2)$ **do**
- 16: evaluate individuals in $P^{(j)}$;
- 17: $S_{best} \leftarrow$ the fittest one in $P^{(j)}$;
- 18: evolve $P^{(j)}$ for one generation;
- 19: **end for**
- 20: **if** migration is necessary **then**
- 21: $P = P^{(1)} \cup P^{(2)}$;
- 22: $\{P, P^{(1)}, P^{(2)}\} = Migrate(P)$;
- 23: **end if**
- 24: evaluate the degree of diversity D_P for $P^{(1)}$ (F-POP);
- 25: **end while**

A. Genetic Encoding

Fig. 1 illustrates the genetic encoding scheme that represents a feasible RMSA of a lightpath request LR_i as a gene, combines the genes for all lightpath requests as an individual chromosome (i.e. feasible network planning), and groups different chromosomes into a population. For each s - d pair in $G(V, E)$, all feasible routing paths are pre-determined with a Link-Disjoint Path Search (LDPS) algorithm [8]. Each LR_i 's RMSA starts from randomly selecting a feasible routing path for its s - d pair, and then determines M_i based on the distance of the path. We assume that a frequency slot is 12.5 GHz, and set the transmission reach for BPSK, QPSK, 8 QAM, and 16 QAM signals in it as 10000 km, 5000 km, 2500 km, and 1250 km, respectively, based on the experimental results in [2,9]. Then, we use M_i and the request bandwidth to calculate N_i . After accommodating all L lightpath requests, we form a chromosome that contains L genes. When we select different routing paths for some/all of the genes, a different chromosome can be formed.

B. Spectrum Assignment and Fitness Evaluation

For each individual k , we perform spectrum assignments in a gene-by-gene way with a descending order based on $|R_{s,d,i}^{(k)}|$ firstly and then $N_i^{(k)}$. The assignments are done with the *First-Fit* scheme under the spectrum continuity and non-overlapping constraints, and they conclude the RMSA with a

feasible network planning solution. We can then evaluate this solution (i.e. individual k) with the fitness function as:

$$F_k = \max\{f(e)\}, \forall e \in E \quad (1)$$

where, $f(\cdot)$ is the function to return the index of the last used slot on a link e in $G(V, E)$. A smaller fitness F_k reflects a more efficient RMSA, as we can allocate a smaller number of frequency slots per fiber link to satisfy the same traffic demands. Consequently, the fittest individual (i.e. the best network planning solution) should be the one that has the smallest fitness in a generation.

C. Genetic Operations

Based on the individuals' fitness, we select parents out for crossover. The truncation selection [7] first sorts the individuals according to their fitness and then selects certain proportion of the fittest individuals. The tournament selection [10] involves running several tournaments among a fixed number of individuals that are randomly chosen from the population. The winner of each tournament (i.e. the fittest individual in the group) is selected. As the truncation selection usually preserves individuals that are already fit better than tournament selection, we apply truncation and tournament selections to F-POP and C-POP, respectively.

Then, in both C-POP and F-POP, the selected parents crossover to produce children using a multi-point operation on the gene-level [7]. Specifically, the selected parents are first sorted from the fittest to less fit, and then we take pairs in a descending order to crossover. In the crossover, the number of genes that are exchanged between the parents is fixed according to a preset crossover rate, but the actual exchange locations in the chromosome are randomly selected. For each population, we then select certain numbers of fittest individuals from the chromosome pools made by the parents and children as the next generation, and keep their population sizes constant.

The individuals in C-POP and F-POP go through mutation afterwards. The mutation first makes an individual determine whether each of its genes needs to be mutated according to a preset mutation rate. Then, the genes that are selected for mutation changes its routing path $R_{s,d,i}^{(k)}$ randomly, and its $M_i^{(k)}$ and $N_i^{(k)}$ are then recalculated. To facilitate genetic diversity, the mutation rate of C-POP is higher than that of the F-POP. To update its fitness, we redo spectrum assignments for each individual when the crossover and mutation are done. The migration is performed every a few generations to exchange certain fittest individuals in the C-POP with the least-fit ones in the F-POP. To quantify the MPGA's convergence performance, we define the degree of diversity of F-POP as:

$$D_P = \frac{2}{PSize_1(PSize_1 - 1)} \sum_{k_1=1}^{PSize_1-1} \sum_{k_2=k_1+1}^{PSize_1} \frac{d(k_1, k_2)}{L} \quad (2)$$

where $d(k_1, k_2)$ returns the number of different genes between individuals k_1 and k_2 , and L is the number of genes in an individual. Since F-POP is used to tune the solutions finely without chromosomal disruption, it actually provides the final optimization result for the MPGA. When the D_P of F-POP

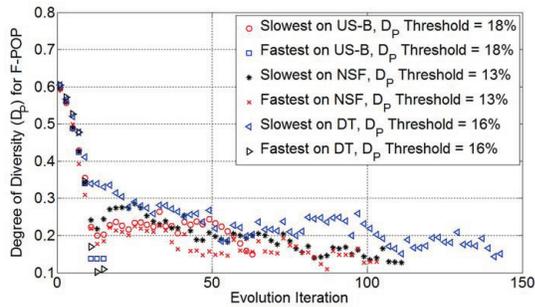


Fig. 2. Convergence performance of the MPGA as the degree of diversity D_P vs. the evolution iteration.

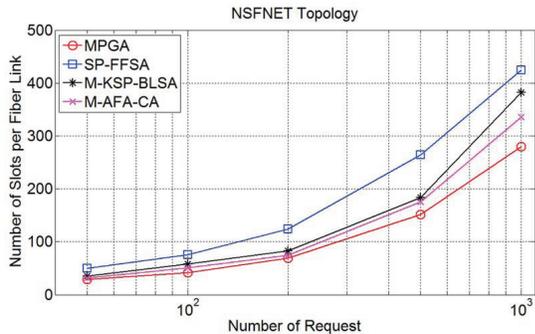


Fig. 3. Number of frequency slots per fiber link obtained by different RMSA algorithms in the NSFNET topology.

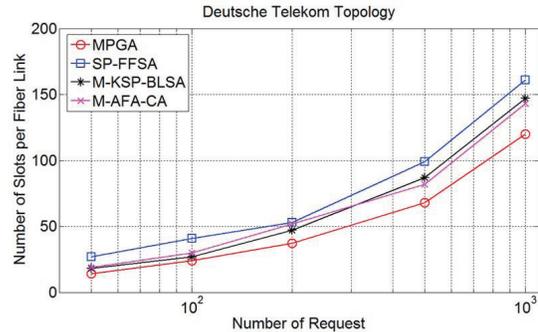


Fig. 4. Number of frequency slots per fiber link obtained by different RMSA algorithms in the Deutsche Telekom topology.

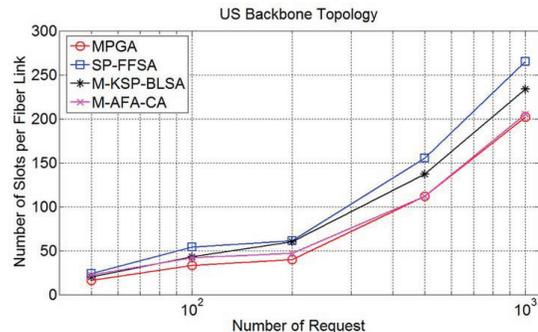


Fig. 5. Number of frequency slots per fiber link obtained by different RMSA algorithms in the US Backbone topology.

has converged, it means that the fitness of the best individual in both F-POP and C-POP cannot be improved even with the periodic migration. Therefore, we can claim the MPGA has converged if D_P has been lower than a pre-set threshold for 5 generations or more [7].

For the demonstration of the output stability of the proposed MPGA, we design a SPGA as the reference algorithm. The SPGA's population size is $PSize_1 + PSize_2$, and we use tournament selection for it. The principles of the mutation and crossover are the same as those in the MPGA, but with different mutation and crossover rates.

III. SIMULATION RESULTS

We evaluate the proposed MPGA with simulations using three mesh topologies, 14-node Deutsche Telekom (DT) [11], 14-node NSFNET (NSF) [12], and 28-node US Backbone (US-B) [13]. The range of lightpath requests' bandwidth is 10 - 100 Gb/s, and the populations of F-POP and C-POP are both 30. Both the $s-d$ pair and the bandwidth of a lightpath request are randomly selected, and all requests are served in the simulations. Fig. 2 shows the results on D_P from simulations using the three topologies and 1000 requests. We run 10 simulations for each topology and plot the fastest and slowest convergence cases. It can be seen that for all of the three topologies, the MPGA converges within 145 generations. Note that D_P converges to slightly different values for different topologies, and that's why the thresholds are not the same. We determine the threshold of D_P for the topologies by running the simulations with a large number of generations (e.g. 500), monitoring the trend of D_P and then choosing a reasonable

value [7]. For the fastest and slowest cases, the MPGA outputs best fitness as 209 and 207, 117 and 115, and 277 and 270, for US-B, DT, and NSF topologies, respectively.

Fig. 3-5 show the performance comparisons of the MPGA to three algorithms, the Shortest Path and First Fit Spectrum Assignment (SP-FFSA) [3], the Modified K-Shortest Paths and Balanced Load Spectrum Assignment (M-KSP-BLSA) [5], and the Modified Adaptive Frequency Assignment and Collision Avoidance (M-AFA-CA) [6]. Note that both KSP-BLSA and AFA-CA are for Routing and Spectrum Assignment (RSA) only, and are not originally designed for RMSA. As RMSA has to consider adaptive modulation-level assignment and the number of slots required by a request can vary for different routing paths [3], it is fundamentally more complicated than RSA [4]. To conduct fair comparisons, we modify both KSP-BLSA and AFA-CA and make them suitable for RMSA. Traffic cases with 50 - 1000 requests are simulated in the three topologies using these algorithms. It can be seen that the MPGA always achieves the best RMSA that requires the smallest number of frequency slots per link to support the same traffic load. Compared to the SP-FFSA, M-KSP-BLSA, and M-AFA-CA, the MPGA can reduce the frequency slots up to 45%, 28% and 16%, respectively. Note that for the US Backbone topology, when there are 500 and 1000 requests, the results from the MPGA and M-AFA-CA are comparable. For the 500- and 1000-request cases, we also generate 8 different request sets and solve them with the MPGA, SP-FFSA, M-KSP-BLSA and M-AFA-CA in the NSF topology. Table I shows the simulation results. We also compare the

TABLE I
NUMBER OF SLOTS PER LINK IN NSFNET FROM DIFFERENT RMSA ALGORITHMS WITH DIFFERENT SETS OF REQUESTS

		Set-1	Set-2	Set-3	Set-4	Set-5	Set-6	Set-7	Set-8
500 Requests	MPGA	159	153	155	154	167	158	158	164
	SP-FFSA	263	283	261	241	276	252	258	270
	M-KSP-BLSA	193	202	186	188	180	209	200	221
	M-AFA-CA	176	172	189	171	178	175	173	180
1000 Requests	MPGA	269	276	287	280	279	284	289	278
	SP-FFSA	476	437	477	490	447	459	488	502
	M-KSP-BLSA	340	329	383	355	355	380	368	342
	M-AFA-CA	298	303	330	311	335	336	336	323

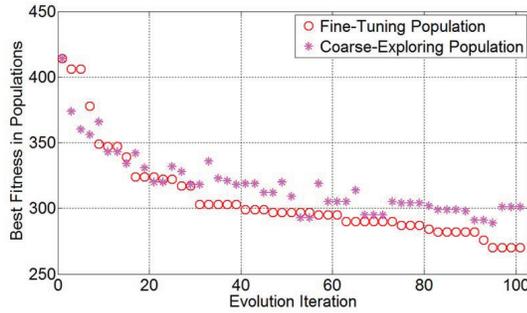


Fig. 6. Evolutions of F-POP and C-POP for 1000 requests in NSF.

TABLE II
NUMBER OF SLOTS PER LINK IN NSFNET FROM DIFFERENT RMSA ALGORITHMS WITH 400 Gb/s - 1 Tb/s REQUESTS

# of Requests	MPGA	SP-FFSA	M-KSP-BLSA	M-AFA-CA
20	106	190	168	170
40	198	400	248	268
60	207	430	327	295
80	281	532	395	449

performance of the RMSA algorithms when the bandwidth of the lightpath requests is large (400 Gb/s - 1 Tb/s), and Table II shows the simulation results.

Fig. 6 shows the evolutions of the F-POP and C-POP for a 1000-request case in the NSF topology. The F-POP evolves in a more stable way, and the migration expedites the evolution of the F-POP at generations 17, 31, 63 and etc. The performance of the proposed MPGA is also compared to a SPGA with 60 individuals. For each scenario, 10 simulations are executed to serve 1000 requests in the three topologies. Table III shows the results. The proposed MPGA achieves better performance on the output stability, or for different runs, the values of the best fitness from it have smaller variances.

IV. CONCLUSIONS

We proposed a novel MPGA to optimize RMSA in O-OFDM networks. The propose algorithm outperformed several existing algorithms by providing more efficient RMSA for the network planning. Simulations showed that the algorithm could converge within 145 generations even for complicated network planning problems that needed to serve 1000 requests in large-scale mesh topologies. We also verified that the MPGA has better output stability than a SPGA with the same population size.

TABLE III
PERFORMANCE COMPARISONS OF SPGA AND MPGA

		SPGA			MPGA		
		DT	NSF	US-B	DT	NSF	US-B
Best Fitness	Max	128	283	213	115	277	209
	Min	120	264	201	111	265	204
	Mean	122.9	274.1	207.2	113.2	271.5	207.2
	Var	7.88	50.54	11.73	2.84	15.16	2.18

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