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On the use of Multi-Objective Optimization Algorithms for solving the Impairment Aware-RWA problem

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Abstract— In future transparent optical networks, it is important to consider the impact of physical impairments in the routing and wavelengths assignment process, to achieve efficient connection provisioning. In this paper, we use classical multi-objective optimization (MOO) strategies and particularly genetic algorithms to jointly solve the impairment aware RWA (IA-RWA) problem. Fiber impairments are indirectly considered through the insertion of the path length and the number of common hops in the optimization process. It is shown that blocking is greatly improved, while the obtained solutions truly converge towards the Pareto front that constitutes the set of global optimum solutions. We have evaluated our findings, using an Q estimator tool, that calculates the signal quality of each path analytically.

***Index Terms*— RWA, Genetic Algorithm, All-Optical Networks, Multi Objective Optimization.**

I. 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 electronic 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]. 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, as for example integer linear programming, [1]. Their high complexity, however requires intensive computational efforts and therefore other novel heuristic algorithms such as Tabu-search, [2], simulated annealing, [3] and genetic algorithms, [4], [5] have been used.

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, [4], for optimizing amplifier placement, as well for multicasting sessions [5]. When however, fiber impairments are considered, most of these studies consider the QoT problem separately from the RWA problem [6]. If Q factor is greater than the requested quality, connection is accepted, or otherwise is dropped and a new candidate path is calculated. Another approach is to incorporate impairments into the cost function of the RWA problem. However, a cost function that considers both linear and nonlinear is still an open issue. Therefore, other metrics have been used, including the average measured Q, [8] or the noise variance [7]. In any case, accurate Q-path estimations is a heavy computational task and even in the static RWA problem, with offline processing, it requires calculations for all combinations of the *k*–shortest paths for all source-destination pairs.

In this paper, we use classical multi-objective optimization (MOO) strategies to jointly solve the impairment aware RWA (IA-RWA) problem. Solving the joint IA-RWA problem is quite complex as it requires optimizers that instead of providing a single optimal solution, yield a set of optimal solutions. When however, IA-RWA is considered as a multi-objective optimization problem, a global optimal solution should be searched among the set of all feasible solutions. That global solution comprises the set of all routing paths per source-destination pair. Which combination of the individual paths yields the best performing solution is part of the optimization process. In this paper, we make use of Genetic algorithms for optimizing multiple objective functions relevant to fiber impairments. The rest of the paper is organized as follows. Section II presents the concept of multi-objective optimization (MOO) and how it can be used for solving the IA-RWA problem. Section III presents results on the use of genetic algorithm for multi objective approximations, while Section IV concludes the paper.

II. MULTI-OBJECTIVE OPTIMIZATION ALGORITHMS

A typical multi-objective optimization problem (MOOP) presents a set of compromised solutions, usually referred to as the *tradeoff surface*, or the set of *Pareto-optimal* or *non-dominated* optimal solutions. These solutions are optimal in

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the sense that no other solutions in the search space are superior to them when all objectives of the problem are considered. The goal of a MOOP is to find as many Pareto-optimal solutions as possible, and reveal the tradeoffs that exist among the different objectives. A multi-objective optimization problem can be formulated as:

minimize $F(x) = (f_1(x), f_2(x), \ldots, f_z(x))$

subject to $H(x)=0$ and $G(x)\geq 0$, $x \in$ X,

involving $z \geq 2$ different objective functions $f_i : R^n \rightarrow R$ to be minimized (or maximized). Note that if f_i is to be maximized, it is equivalent to minimizing ($-f_i$). In the abovementioned formulation, X is the solution search space, while functions $H(x)$ and $G(x)$ are the constraints in the model. Fig. 1 illustrates a multi-objective optimization problem with dominant and non-dominant (Pareto Front) solutions across a search space X and a vector fitness function F that maps solutions in X to objective vectors made up of two component "costs" f_1 and f_2. In the example of Fig. 1, these costs have to be minimized. The filled points are objective vectors that are non-dominated and comprise the Pareto front. The solutions corresponding to these points are Pareto optimal.

The dominance relation between two objective vectors $F^1=F(x_1)=$ $(f_1(x_1), f_2(x_1), \ldots, f_z(x_1))$ and $F^2=F(x_2)=$ $(f_1(x_2), f_2(x_2), \ldots, f_z(x_2))$ is denoted by operand $\prec$. We say that F^1 dominates F^2 or $F^1 \prec F^2$ if for all objective costs f_i the inequality $f_i(x_1)<f_i(x_2)$ holds, assuming that f_i is minimized [9]. With respect to Fig. 1, the relation between the three objective vectors A, B, and C, is $A \prec B \prec C$.

There two directions to follow in order to solve a MOOP. The first one is to convert the multi-objective problem to a single objective one and solve it. Such methods being used are the weighted sum, the ε-constraint, Benson and min-max. All of these methods try to find the optimal Pareto front using different approximation techniques. The second strategy is to make use of multi-objective optimization algorithms (meta-heuristics). Meta-heuristics like genetic algorithms or other evolutionary, ant colony, mimetic, Tabu search, and simulated annealing algorithm are difficult to apply. This is because; determining a single fitness function to include all fiber impairments yields the same problem of how to combine optimization objectives.

A. Considering IA-RWA as a Multi-Objective Optimization Problem

A major difference, when considering the IA-RWA problem as an optimization problem is that the set of all feasible solutions is being searched to find the best performing one. The search process tries to optimize some objective parameters that are related to fiber impairments. Here, we have considered impairments of different nature, and by determining the main reason these effects occur, we derived relevant optimization functions. In particular, we have considered amplified spontaneous emission noise (ASE), polarization mode dispersion (PMD), crosstalk (XT), filter concatenation (FC), cross-phase modulation (XPM) and four-wave mixing (FWM) fiber impairments and analyze how they affect signal quality. We have developed an analytical Q estimator software tool that models the abovementioned phenomenon given a network topology (transmission span, link lengths etc), as follows: ASE noise variance for a cascade of N amplifiers is described by [6]:

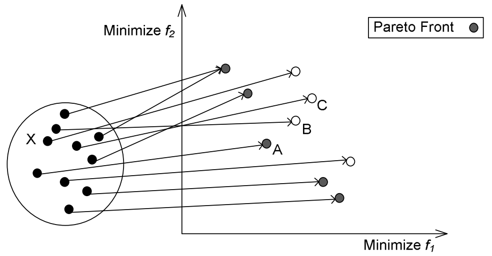

Fig. 1: An illustration of a multi-objective optimization problem across a search space X

$$\sigma^2_{ASE} = 4R^2_\lambda b_i P_{avg}(N,\lambda_i) P_{ASE}(N,\lambda_i) B_e / B_o \quad \text{, Eq. 1}$$

where b_i is zero or two if i=0 or i=1, R_λ the responsivity of the receiver (1.25A/W), P_{avg} the average signal power in channel λ_i, P_{ASE} is the power in an optical bandwidth B_0 and B_e the electrical bandwidth of the receiver. The ASE noise variance is used to calculate the Q factor degradation due to ASE. The penalty induced by the PMD is modelled using [10]:

$$Q_{PMD} = 10.2 B^2 D_{PMD} L \text{ in dB,} \quad \text{Eq. 2}$$

where D_{PMD} is the fiber dispersion parameter, L is the length of the transmission fiber and B is the signal bit rate. The noise variance of crosstalk is described by [6]:

$$\sigma^2_{XT} = 2\xi_{pol} R^2_\lambda b(i) P_{ave} P_{XT} \quad \text{, Eq. 3}$$

where ξ_{pol} is the polarization mismatch factor between the signal and the crosstalk light waves and P_{XT} expresses the amount of energy that interferes in neighboring channels.

The effect of the filter concatenation as the light passes through a number of optical components, such as multiplexers and demultiplexers, is approximated using third-order Butterworth filter transfer functions. The equation describing a complex third-order Butterworth filter is given as:

$$H(f) = \frac{1}{\prod_{k=1}^{3}[\frac{if}{f_{3dB}} - \exp\left(\frac{i\pi}{2}\left(1+\frac{2k-1}{3}\right)\right)]} \quad \text{, Eq. 4}$$

The analytical expression for the noise-variance due to FWM is described by [10]:

$$\sigma^2_{FWM} = 2K^2 P_s \left\{ \frac{1}{8}\sum_{I} P_{pqr} + \frac{1}{4}\sum_{II} P_{pqs} + \frac{1}{4}\sum_{III} P_{ppr} \right\} \quad \text{, Eq.5}$$

where P_s is the peak power of the selected channel s, P_{pqr} is the power of a single FWM component generated from the combination of channels p, q and r that satisfy the condition $p+q-r=s$, $K=ne/hf$, n is the quantum efficiency of the detector, e is the electron charge, h is Planck's constant, and f is the channel frequency. We have also investigated the impact of XPM on the performance of a single link considering the analytical model in [11], properly modified to match the specific link architecture. The XPM induced intensity modulation (IM) frequency response is used to obtain an analytic expression for the XPM noise-like variance given by [12]:

$$\sigma^2_{XPM} = \bar{P}(0)^2 \sum_{k=1,k\neq i}^{N} \frac{1}{2\pi} \int_{-\infty}^{\infty} \left|H^{IM}_{XPM,ik}(\omega,L)\right|^2 . \left|H_{opt.filter}(\omega)\right|^2 .PSD_k(\omega) d\omega \quad \text{, Eq. 6}$$

, where $\overline{P}(0)$ is the average channel power, $H_{XPM,ik}(\omega)$ the transfer function due to XPM, $H_{opt.filter}(\omega)$ the transfer function
optical filter at the receiver and $PSD_k(\omega)$ is the power spectral density of channel k.

In total, we have categorized the physical impairments according to the network parameters that mainly affect them. First, ASE depends on the number of EDFAs of the path, which in turn depends mainly on the length of the path. PMD also depends on the length of the path. Other impairments, such as XT and FC, have a significant effect when signals go through common OXC. So, the length of a path and the number of common hops among the paths are important parameters that affect the QoT of an RWA solution. These approximations have been used for optimizing IA-RWA solution, while the Q estimator software tool was used to verify results.

III. GENETIC ALGORITHMS FOR SOLVING THE MULTI-OBJECTIVE, IMPAIRMENT AWARE RWA.

Genetic Algorithms (GAs) is a class of search strategies based on the mechanism of biological evolution. 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 out-crossings, until a good individual for the problem is found. GAs do not guarantee that an optimal solution can be found, since it is 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 randomly. Each individual is assigned with a cost metric, in order to identify it's fitness according to a fitness function.

***Crossover**:* During that phase, individual chromosomes are crossovered (mate) with a specified probability, to produce the next generation individuals. The cost of each individual 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 rests 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.

Let $G(V,E)$ denote a simple graph that models the network, where V denotes the set of nodes (assumed not to be equipped with wavelength conversion capabilities), and E denotes the set of point-to-point single-fiber links. Each fiber link $l \in E$ is able to support W distinct wavelengths. Let also Λ be a given traffic matrix of nonnegative integers, where Λ_{sd} denotes the number of connections that have to be established from source node s to destination node d. There may be multiple connection requests for a given source-destination pair (s,d). The way the Genetic Algorithm works is described next. For each source-destination pair (s,d), we calculate k-shortest length paths. The set of candidate paths for source-destination pair (s,d) is denoted as P_{sd}. Let Ch represent an *individual chromosome*. In the proposed Genetic Algorithm (GA-RWA), each *gene* in an individual chromosome represents one of the k-shortest paths for a specific source-destination pair (s,d). Thus, each individual chromosome consists of $\sum_{(s,d)pairs} \Lambda_{sd}$ genes, which corresponds to the routes that would serve the connection requests.

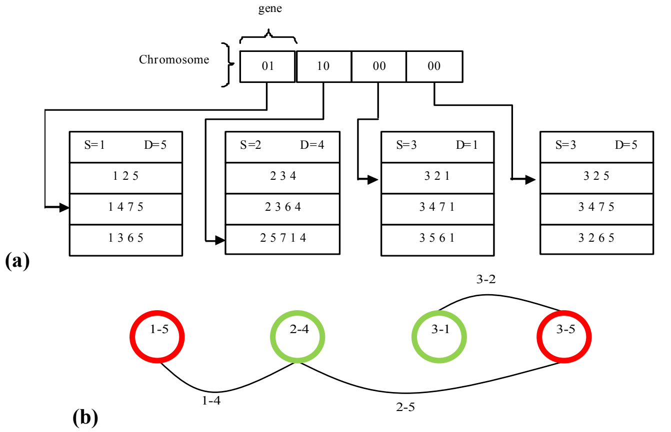

Fig. 2: (a) Example of the individual (chromosome) structure with four genes and k=3. Each gene corresponds to a path for a source destination pair (s,d). (b) Common edge graph of the genes. The gene that corresponds to pair (1,5) and the gene that corresponds to pair (2,4) have in common link 1-4.

In the RWA problem we want to find for each source destination pair (s,d), a lightpath (p,w), that consists of a path $p \in P_{sd}$ and a wavelength w. The distinct wavelength assignment constraint that has to be satisfied states that for two requests i and j, $i \neq j$, for which the same wavelength is used ($w_i = w_j$) there cannot exist a link that belongs to both paths p_i and p_j used to route these requests. The aim of the RWA problem is to minimize W, under the distinct wavelength assignment constraint.

Fig.2 (a) shows an example of chromosome encoding. It corresponds to a network consisting of V *nodes* $V=\{1,2,3,4,5,6,7\}$, where the source-destination (s,d) pairs $\{(1,5), (2,4), (3,1), (3,5)\}$ have to be served. Three (k=3) different paths for each (s,d) pair have been pre-calculated. The genes that constitute an individual chromosome are represented with a binary number. The binary number of each gene denotes a certain path of the k-shortest paths of that particular source-destination pair. Assuming that this chromosome is the best one (that is, is the final solution obtained by the GA), the common edge graph of the paths that comprise is shown in Fig.2 (b). The nodes in Fig.2 (b) correspond to the genes of the solution, while an edge exits between the nodes if the genes of the node have at least one common link. Subsequently, coloring is applied on the nodes of the common edge graph, for determining the number of wavelengths, (in Fig.2(b) two wavelengths are required).

Having this common edge graph in mind, we define the objective of the GA algorithm so as to yield a graph that can be colored with the smallest number of wavelengths. We denote by F_l the cost of a link l, and we assume that is equal to the number of paths that cross link l. In the GA proposed in [4], the *fitness* of a chromosome Ch is given by $F(Ch) = \sum_{l \in E} N^{F_l}$, where $N=|V|$ is the number of nodes in the network. However, summing the exponential costs of the links does not reveal the true fitness of the chromosome Ch, since a link that is utilized by many paths in the chromosome can significantly increase the cost of a path. Thus, GA may discard a good candidate solution and not reach the global optimum. To avoid this, we define a cost for each gene of the

TABLE I. Maximum number of wavelengths for different fitness functions considering the DT network topology with 14 nodes and 21 edges.

sd* pairs, *k	$\sigma(c_{sd})$	$\mu(c_{sd})$	$N^{\mu(c_{sd})}$	$\sum N^{c_{sd}}$
20, *k*=3	4	3	3	4
40, *k*=3	4	4	4	5
80, *k*=2	9	9	8	10
120, *k*=2	14	15	13	16
150, *k*=2	17	18	16	20
182, *k*=2	22	23	20	25

chromosome and examine three different fitness functions *F*(.) for the chromosomes. These fitness functions are based on the average $\mu(.)$ and the variance $\sigma(.)$ of the cost values of the genes that comprise the chromosome. In addition, we have further improved the performance of the proposed GA-RWA by using a better set of candidate paths as input to the GA. In particular, we take into account the maximum number of edge disjoint paths (EDPs) as in [13], in order initialize the population with some *indigo* chromosomes. In what follows, we describe the most salient features of the proposed genetic algorithm:

Fitness function: To obtain a graph that can be colored with a small number of wavelengths it is important to avoid the repeatability of the links in the paths (genes) that comprise the chromosome. Thus, in our formulation we assign to each gene (*s*,*d*) of the chromosome *Ch* the following cost $c_{sd}=\sum_{l\in p}F_l$, $p\in P_{sd}$ and $p\in Ch$.

We then define the following three fitness functions of the chromosome *Ch*:

i) $F(Ch)=\sigma(c_{sd})$, ii) $F(Ch)=\mu(c_{sd})$, iii) $F(Ch)=N^{\mu(c_{sd})}$,

where $\mu(.)$ and $\sigma(.)$ are the average and the variance of the cost values that comprise *Ch*. For example, to find the cost $F(Ch)=N^{\mu(c_{sd})}$ of the chromosome *Ch* depicted in Fig.2(a), we need to examine each gene and calculate its cost c_{sd}. The first gene that corresponds to source-destination pair (1,5) has one common edges with the second gene (namely, edge (1-4)), and thus $c_{1,5}=1$; the second gene (2,4) has one common edges with the first gene (edges (1-4)) and one common edge with the fourth gene (edge (2-5)), and thus $c_{2,4}=2$; the third gene (3,1) has one common edge with the fourth gene (edge (3-2)), and thus $c_{3,1}$=1; finally, the fourth gene (3,5) has one common edge with the second gene (edge(2-5)) and one common edge with the third gene (edge (3-2)), and thus $c_{3,5}$=2. Since in the given topology *N*=7, the cost of this solution is:

$$F(Ch)=N^{\mu(c_{sd})}=7^{\frac{1+2+1+2}{4}}=18{,}52\ .$$

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 [4]. 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.

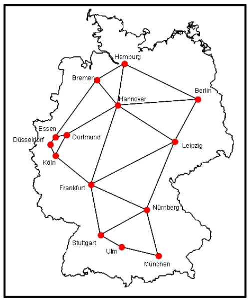

Fig. 3: DTAG/T-Systems National Core Network

Mutation: A random uniform mutation is used with a probability of $1/\sum_{(s,d)\,pairs}\Lambda_{sd}$. 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 TABLE I, we summarize results (maximum number of wavelengths) considering the DT network topology shown in Fig.3 for different fitness functions and for different number of source-destination pairs. The initial and maximum population chosen was 50 and 75 respectively, while the number of iterations (epochs) was set to1000.

Population initialization: Instead of using the k-shortest paths, we make use of the maximum quantity of edge disjoint paths (*max-EDPs*) to initialize the population in the GA-RWA problem. The use of *max-EDPs* 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. In this case, a set of all the EDPs per s-d pair is created and stored for the specific physical topology as in [13].

When 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 unchangeable since they potential constitute optimal solutions. Fig.4 graphically shows such an individual, called *indigo* chromosome. The evaluation results have shown that the max EDPs approach improves overall performance in terms of both computational time and number of wavelengths. TABLE II and III compares GA performance, when the *k-shortest paths* or *max-EDPs* are used to initialize population. In particular TABLE II summarizes the number of epochs needed to reach the same number of wavelengths, while TABLE III the corresponding max number of wavelengths needed.

A. Considering fiber impairment in the optimization process

Driven by the observations in section II, we assign to each chromosome an objective vector function *F* with entries being different scalar objective functions based on the path length and the number of common hops of the paths that comprise the chromosome. To this end, we form a classical multi-objective optimization problem. By minimizing path length

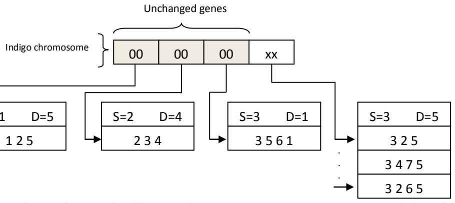

Fig. 5: Example of an indigo chromosome structure with three unchangeable genes.

TABLE II. 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.

SD pairs	*W*	*k* shortest paths Epochs	max-EDPs Epochs
40	4	50	1
80	9	102	1
150	16	332	61
182	20	496	91
80x2(multi flows)	16	992	1

TABLE III. Number of wavelengths calculated using the max-EDPs into the GA-RWA.

SD pairs	*W*	Epochs
40	4	1
80	8	259
150	15	161
182	18	414
80x2(multi flows)	15	138

and number of common hops, we aim at obtaining a solution that consists of lightpaths that have acceptable QoT. A Multi-objective Genetic Algorithm (MOGA) approach was used for solving the joint problem, considering also the fiber impairments in the RWA problem, leveraging on the GA concept described above. We have additionally defined for each gene (*s*,*d*) a length-cost $d_{sd}= d_p$, where d_p is the length of the selected path $p\in P_{sd}$ and $p\in Ch$. Further, given a chromosome *Ch*, we also defined F_n as the number of paths in that chromosome that utilize node $n\in V$. Thus, we can assign to each gene (*s*,*d*) a cost that reflects the number of common hops between the selected path for that (*s*,*d*) pair and all the other selected paths that comprise the chromosome:

$$h_{sd} = \sum_{n\in p} F_n,\ p\in P_{sd} \text{ and } p\in Ch$$

Objective Vectors: Based on the above formulation, we assign to a chromosome *Ch* the following objective vector: $F(Ch) = \{f_1(Ch), f_2(Ch), f_3(Ch)\}$, where: $f_1(Ch) = N^{\mu(d_{sd})}$, $f_2(Ch) = N^{\mu(h_{sd})}$, $f_3(Ch) = N^{\mu(c_{sd})}$ are the length, common hops and link utilization costs respectively. In the above equations, $\mu(.)$ denotes the average of the corresponding cost values of the genes in the chromosome.

We have evaluated the proposed MOGA scheme for solving the IA-RWA problem using again the DT network topology. We have examined the blocking performance of the single objective genetic algorithm (SOGA) , that optimizes the utilization of wavelengths, a multi-objective genetic algorithm (MOGA1) that optimizes only the impairment-related cost functions f_1 (path length) and f_2 (common hops), and finally a multi-objective genetic algorithm (MOGA2) that also includes the link utilization in the optimization process, and thus optimize all the three objective described above. The parameters of the simulations are summarized in TABLE IV. It must be noted here that the number of wavelengths are placed on the ITU grid with the stringent requirement to be adjacent. Fig. 5 displays the corresponding blocking probabilities. Tags in Fig.5 denote the min number of wavelengths calculated. From Fig.5, it is clear that the proposed MOGA significantly decrease blocking and thus optimize RWA against impairments. It also results in an increase in the number of min wavelengths required, primarily because the more wavelengths are available; the more efficient assignment of wavelength is achieved, thus decreasing for example XPM or FWM effect in the most congested paths or links. The min number of wavelengths is decreased again, when link utilization is inserted in the optimization process and thus the MOGA tries to both optimize impairments and minimize wavelengths used. Indeed from Fig.5, it can be seen that the number of wavelengths used decrease and for loads higher than 80 requests (see MOGA2 curve) actually match that of plain RWA case (SOGA curve). The slightly increase in blocking is the inevitable effect of wavelength suspension.

TABLE IV. Simulation Parameters

Genetic Algorithm k	2	Q-threshold	11,6
Initial population	50	Po	-4dbm
Max population	75	EDFA NF	6db
Epochs (for Single Objective)	300	Span	50Km
Channel Spacing	100GHz		

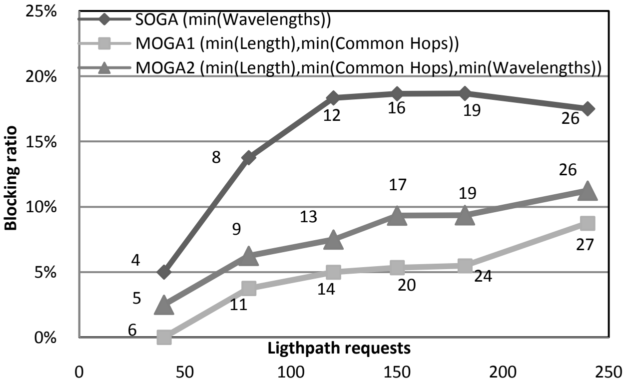

Fig. 4: Blocking probability versus load (number of active sd pairs). The tags next to the points indicate the corresponding number of wavelengths.

B. Algorithm Convergence

A question that rises is how and if the proposed MOGAs converge over time. In most real search problems, the location of the actual Pareto-front is, by definition, unknown, and the identification of a “best value” of some criterion does not necessarily mean global convergence. Most of the MOEAs (Multi-Objective Evolutionary Algorithms) available in the literature, achieve diversity and equivalent solutions through some diversity preserving mechanism. However, convergence efficiency and speed is not considered. Any explicit diversity preserving method needs prior knowledge of many parameters and the efficacy of such a mechanism depends on a successful fine tuning of these parameters. In this work, we have used Kumar’s proposal [14] to gain knowledge of the propagation of the solution front through successive generations of the population. This can serve as a cue for convergence and reveal the rate of propagation towards the Pareto-front. The basic concept of *Pareto Converge Genetic Algorithm* (PCGA) is that the individuals are compared against the total population

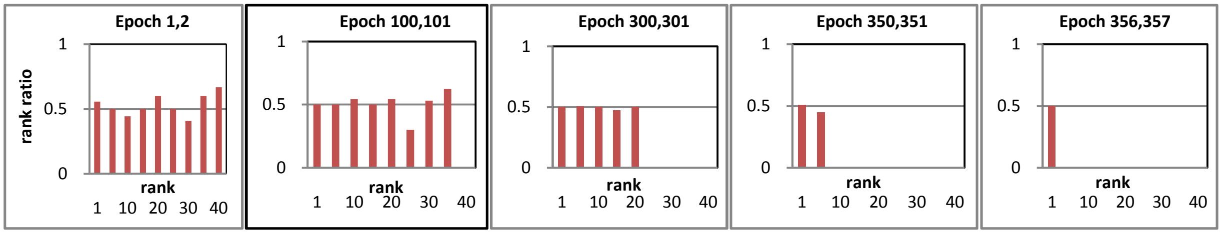

Fig. 6: Intra-population ranking histogram displaying the ratio of a certain rank of genes between two successive generations.

set according to tied Pareto-ranking and the population is selectively moved towards convergence by discarding the weakest individuals in each evolution. For this, we make use of the domination relation (see Section II).

In our studies we have examined intra and inter ranking histograms to verify if the MOGA has converged and at which epoch. The first is the ratio of a given rank in the current population to that of the combined and re-ranked population of the current and the preceding epoch. We are interested to demonstrate the shift of the set of non-dominated solutions between epochs, hence the rationing of rank entries. The second histogram, combines and re-ranks different output solutions (potentially optimal Pareto solutions) in order to demonstrate, whether the solution obtained is close (or not) to the *true* Pareto-front. It can be the case, that no evolutionary gain is achieved beyond a certain number of final solutions(generations). An example of such verification is shown in Fig.6 that displays the intra-population ranking histogram for a load of 40 ligthpath requests. It can be seen that the optimization process converge at epoch 357 (mean execution time 5msec/epoch). Beyond 357 epochs, all next generations consist of only non-dominated chromosomes, which is a cue that optimization has converged to an optimal solution.

Fig.7 displays the corresponding inter-rank histogram (blue), between two merged optimal solutions. It is clear that the fetched solution is not “close” to the Pareto front since some individuals have been degenerated and are now dominated by some others (rank 5, 10 and 35). Clearly, this is due to the limited search space and therefore, we have experimented with larger populations (red, green and purple histograms in Fig.7). As expected, better results were obtained by increasing the initial population size as well as the maximum population limit, since the algorithm searches in a wider set of solutions, but with a cost in the computational time. From Fig.7, it can be seen that total convergence (rank ratio=1) is reach, in the case of having an initial and maximum population of 500 and 1000 respectively. This is of paramount importance, since being on or even close to the true Pareto front, is a true indication of the genetic algorithms reliability, which are combinatorial optimization and parameter tuning algorithms.

IV. CONCLUSIONS

In this paper we have examined the use of multi-objective optimization algorithms and particular genetic algorithms to jointly solve the impairment aware RWA (IA-RWA) problem. We have used the number of common hops and end-to-end path length as the objective functions to be minimized. It has been shown that when these functions are used, impairments are indirectly but satisfactory considered, significantly improving blocking ratio. In addition, we have shown that the proposed MOGA truly converge towards an Pareto-optimal solution, when a sufficient large population size is considered.

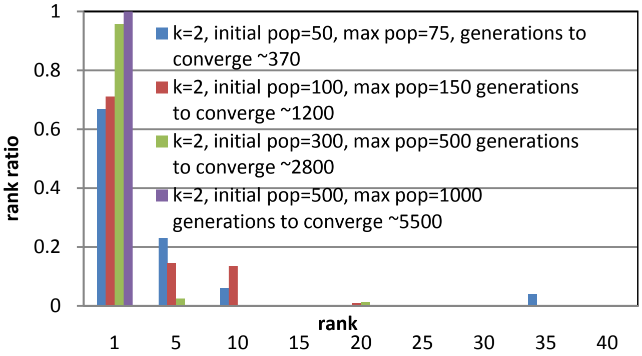

Fig. 7: Inter rank histogram of two merged optimal solutions on several experiments with different parameters

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