Multi-objective optimization of the Multiple Traveling Salesmen Problem Using a Non-dominated Sorting Genetic Algorithm (NSGA-II)

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*Abstract*— **The multi-objective multiple traveling salesmen problem (MOMTSP) is a rather popular multi-objective combinatorial optimization problem (MOCOP) with many real-world application. The non-dominated sorting genetic algorithm NSGA-II is a fast, elitist genetic algorithm, and has been used to solve the problem and other similar MOCOPs in literature. This project report details the implementation of the NSGA-II algorithm to solve two different formulations of the MOMTSP- one, to minimize the difference between the longest and shortest individual tour lengths, and the other, to minimize the sum of the difference between the average tour time and time taken for each individual tour, both in addition to minimizing the total traveled distance. Four crossover operators, a small range of mutation probabilities, and three population sizes were tested to find the best combination of values among them for both cases. Additionally, the implementation showed better or comparable performance when compared against the benchmark and results in literature. The obtained experimental results are detailed in this report.**

1. INTRODUCTION

Solutions to multi-objective optimization problems (MOOPs) often find applications in the real world [], as many real world problems often have multiple conflicting objectives. A few of the domains that benefit from research into such solutions are resource management [], manufacturing [], network coverage [], and various other domains []. A popular example of such problems is the multi-objective multiple traveling salesmen problem (MOMTSP), first studied by Frederickson, Hecht, and Kim [] in 1978.

The MOMTSP, which is NP-Hard, can be briefly formulated as minimizing the total distance travelled and balancing the workload for *m* salesmen visiting *n* cities exactly once, with each salesman originally departing and finally returning to a common origin city or ‘depot’. A particular modern application of the problem that comes to mind would be in the deployment of multiple drones to achieve certain goals (e.g. delivery of packages) at certain locations and return. Due to limitations on battery life, there is a need to ensure all deployed drones are active for similar times so the coverage of locations can be maximized and all drones allowed to return before the end of their battery life. In addition, many other multi-objective combinatorial optimization problems (MOCOPs) like the vehicle routing problem [] and job shop scheduling problem [] can be transformed into the MOMTSP and solved, which allows the MOMTSP to act as an adequate test problem for MOCOP solvers.

Evolutionary algorithms have been at the forefront of heuristic algorithms for solving MOCOPs and MOOPs for over a decade [], with the non-dominated sorting genetic algorithm NSGA-II, proposed by Deb [] in 2002, being the most cited and used algorithm in literature for solving problems in this class []. Some salient points which make this algorithm so popular are that it incorporates an explicit diversity preservation mechanism, as well as implicit elitism [] to retain the best solutions across generations. Due to the mentioned advantages, proven effectiveness [] as well as the open availability of the NSGA-II [], the algorithm has been used as a sort of gold standard for comparing other (novel) algorithms [], especially since similarly (or more) efficient tools used in industry are inaccessible.

However, the NSGA-II when used with conventional crossover operators devised for permutation-based problems like the Partially Mapped Crossover (PMX) has been noted to converge prematurely []. Although there is a lack of studies as to why this is the case, it may be intuitively attributed to two reasons: first, a lack of evolvability when using the mentioned operators, as the ‘good’ subsequences or arrangement of genes are not preserved during inheritance; and secondly, because in later generations, the population of solutions may lack in diversity [].

On the other hand, studies [] have noted that modifications to the NSGA-II, in terms of specialized genetic operators, replacing or supplementing the diversity preservation mechanism, or hybridizing with other algorithms [] can allow the resultant algorithm to be just as good if not better than the benchmark algorithms for the considered problem domain.

In this project, the main objective is to implement the NSGA-II algorithm to solve the MOMTSP and test a number of crossover operators (PMX, CX, OX, HGAX), and effects of varying population size and mutation probabilities on instances from TSPLIB.

Running with the drone application mentioned earlier, two different objective functions were considered separately in addition to minimizing the total distance traveled— *first*, minimizing the difference between the longest and shortest individual tours, which would be representative of the ideal case where all salesmen (or drones) deployed travel at the same speed and without any delays between cities; and the *second*, minimizing the difference of the total travel times of each salesman with the average travel time, assuming that each traversal between two cities *i* and *j* is done at a random speed between a given range. The former formulation has benchmarks for certain instances from TSPLIB in literature obtained using the brute force CPLEX [], while the latter does not. Either ways, the effectiveness of the implementation can be observed by comparing the final range of total traveled distances obtained with the benchmarks as well as from [] and [], both of which have tested either of the two cases.

The main deliverable for the project is the software written for the implementation in Python, submitted alongside the report and also made available in a public access GitHub repository. The repository contains functions to implement the NSGA-II as well as the various crossover operators mentioned, four mutation operators, and a selection operator; and also the main code to solve the MOMTSP (both variations) for both random instances and select instances (eil51, berlin52, eil76, and rat99) from TSPLIB, which are also included as text files.

The project report beyond this introduction is structured as follows: first, the relevant background information needed for the project, such as terms related to multi-objective optimization and the NSGA-II algorithms are introduced along with the mathematical formulation(s) of the MOMTSP; the next section briefly mentions related work on NSGA-II as well as its (and other GA) application to variations of the MTSP with specially mentioned proposed solutions to the above discussed issues with EAs; thirdly, the implementation of the algorithm and genetic operators is detailed along with the design of the experiments to test the implementation; and lastly, the obtained results are discussed, with some critical analysis connecting the results to the broader issues in EAs and their usage in solving MOCOPs.

2. BACKGROUND

***2.1. Pareto-Optimality and Dominance***

In multi-objective problems, it is required to find an optima for every one of the objectives, and thus, for conflicting objectives, it becomes impossible to find a singular optimal solution. Instead, the goal of solving the problem is to determine an optimal pareto front, which is the set of optimal solutions to the problem (Pareto-Optimal Solutions or POS), from which appropriate trade-offs can be considered to choose a suboptimal solution.

The pareto-optimal front is composed of solutions that “dominate” all other solutions but not each other. Here, a solution, say X, is said to dominate another, say Y, if X evaluates to better than Y for at least one objective function, and equal to Y for the rest of the objective functions. Graphically, this can be seen in Figure 1, where the round solutions dominate the square ones for two objectives (obj1 and obj 2). Thus, the round solutions constitute the optimal pareto front.

More generally, a pareto front (alternatively pareto frontier) consists of solutions that do not dominate each other. This is the concept of non-dominance which is exploited in the NSGA and NSGA-II.

***2.2. Multiple Traveling Salesmen Problem***

As described earlier, the MTSP involves *m* salesmen visiting *n* cities exactly once. While there are multiple variations that arise from this point, such as multiple origin cities, different origin and final destination cities, and so on, the problem considered is of the conventional closed circuit with all salesmen originating and finally returning to the same depot, called the SD-MTSP.

Considering the problem in graph form, it can be represented by the undirected graph with *V* being the set of vertices representing cities and *A* being the set of arcs between the cities. There is an associated distance matrix C of dimensions , with each element being the distance between *i* and *j*. Each salesman , travels from city *i* to city *j* and is an indicator of whether *k* travelled the arc between *i* and *j* (if yes,=1; else,=0).The set of constraints on the tours can then be mathematically described as:

|  |  |
| --- | --- |
|  | (1) |
|  | (2) |
|  | (3) |
|  | (4) |
|  | (5) |

where ‘0’ is taken to be the depot city.

Constraints (1) and (2) limit the traversal of each arc to just one time across all salesmen; constraints (3) and (4) ensure all salesmen start and end their tours at the depot; and lastly, constraint (5) is to ensure that no sub-tours excluding the depot are created.

The first combination of objectives is to minimize the total distance travelled by all salesmen and the difference between the longest and shortest tours, which can be represented by the equations (6) and (7) respectively:

|  |  |
| --- | --- |
|  | (6) |

and,

|  |  |
| --- | --- |
|  | (7) |

where,

The second combination of objectives is (6) and also minimizing the differences of the travel times of each salesman with the average, represented by (8). The

|  |  |
| --- | --- |
|  | (8) |

where,

and,

The first combination, i.e., is a well-known SD-MTSP called the MinMax SD-MTSP, while the second is a much lesser known combination without much depth of study in literature.

***2.3. NSGA-II***

The Non-dominated Sorting Genetic Algorithm was proposed by Deb and Agarwal [] in 2002 as an improvement to the older NSGA, with the addition of elitism. The basic principle behind the titular fast sorting mechanism is the concept of ‘non-dominance,’ or simply that the solutions in a population be ranked based on their level of non-dominance.

In the algorithm, the solutions which are not dominated by any other solutions are ranked first, with solutions that are dominated by a single other solution being ranked second. Naturally, solutions having the same rank constitute a pareto frontier, and thus, each solution only needs to be compared once with all other solutions in the population, which is the mechanism exploited by the algorithm to speedily sort the solution population and determine elite solutions.

There are two main methods in the NSGA-II: fast non-dominated sorting, and crowding distance assignment, of which the former is described above. The crowding distance of a solution, as described by the authors, is the sum of the differences between each objective function evaluation of the nearest neighbors of the solution. The nearest neighbors are solutions such that they ‘box’ in the solution. Thus for a bi-objective problem, the crowding distance of a solution would be the perimeter of the cuboid formed if the function values of its nearest neighbors were plotted on diagonally opposite vertices.

According to the algorithm, the less crowded solutions, i.e., ones that are farther away from any other would be relatively unique and thus worth preserving more than more crowded solutions in the same non-dominance level. Thus the algorithm discriminates between the solutions first on the basis of non-dominance level, and second (if the solutions are on same rank), on the basis of crowding distance. This is the diversity preservation mechanism in the algorithm.

While the crowding distance operator acts as a comparison function for the binary tournament selection of parents, it also acts as a way to sort the solutions of the same non-dominance level. In the algorithm, the offspring population is combined with the parent population after recombination and mutation, and the next generation (same size as parent population) is chosen from the best of this combined population, first sorting by non-dominance level, and if there is a front that will have leftover solutions after cutting off the rest, enough solutions in that front are chosen starting from the least crowded.

The steps of the algorithm are: *1)* Initial population formation (size=*N*); *2)* Selection of parents for next generation by binary crowded tournament; *3)* Recombination and mutation to form an offspring population of size *N*; *4)* Parents and offspring are clumped together in a population of size *2N* from which the top *N* solutions are selected via non-dominated sorting and comparison of crowding distance (elitism); and, *5)* The steps *2*-*5* are repeated until a satisfactory number of iterations or until there is no to little change in the pareto-front (convergence).

3. RELATED WORK

Both the MTSP and NSGA-II (and other GAs), separately and in combination, have been extensively studied in literature. In this section, *first*, an overview of EAs and other solvers for MOOPs and MOCOPs is provided; *secondly*, some significant papers on the MTSP and other recent novel methods of solving the problem are reported; and *thirdly*, papers that describe the modification, improvement and/or direct implementation of the NSGA-II, both generally and in solving variations of the MTSP are described.

Verma, Pant, and Snasel. Kumar, Gopal and Kumar. Von Lucken, Baran, and Brizuela. De Buck et al. Toffolo and Benini. Hassanat et al.

Wang, Fand, Li and Jin. Yousefikhoshbakht, Didehvar, and Rahmati. Pang, Li, Dai, and Yu.

Shuang, Yunfeng and Kai. Alves and Lopes. Bolanos, Echeverry, and Escobar. Yokoyama and Sato. D’Souza, Sekaran and Kandasamy. Wang et al. (water).

4. METHODOLOGY

***4.1. Design***

*4.1.1. Chromosome Representation*

The encoding of the information such that the crossover operations lead to new solutions in the search space effectively is a major consideration in the design of GAs. Two chromosome representations were considered in the project: a two-string chromosome as shown in Fig. [], and a single-string chromosome as shown in Fig. []. The former had a real-number string consisting of a permutation of the city IDs, and another string denoting which salesman is assigned to the city. The two strings encoded the information about the tours jointly, with each city ID and its counterpart salesman ID in the second string forming a single gene. The second method involved appending a shorter string containing breakpoints to a permutation string (of the city IDs). The breakpoints demarcated each salesman’s individual tours.

While the two-string method worked for all cases, it had the distinct disadvantage of creating a perpetual link between each city and a salesman, which was carried over during the crossover operations, limiting the effectiveness of finding new solutions in the search space. The second was far better at the task, and performed better for all cases, with the optimal pareto fronts obtained always dominating the ones obtained using the first method. Hence, the single-string with breakpoints representation was adopted for the rest of the project.

*4.1.2. Crossover Operators*

As mentioned in previous sections, the crossover operators considered in the project are Partially Mapped Crossover, Cyclic Crossover, Ordered Crossover and Hierarchical Crossover.

The PMX algorithm involves selecting two random breakpoints on a parent chromosome, and exchanging the respective sections contained within the breakpoints between each of the two parents. After the exchange, the resultant offspring are minimally adjusted such that each city appears once in the string, as is required for permutation-based operators. A distinct disadvantage of the operator is that sometimes the children turn out to be exactly the same as the parents, which decreases the effectiveness of the algorithm. In addition, this operation leads to breaking up of at least two, but usually more linkages (arrangement of cities).

In CX,

In OX,

The hierarchical crossover method was adopted from [], where the authors called it HGA crossover, and has three variations by itself. The general concept, shown in Fig. [], is to first choose a city *k* and add it to an empty list *A*. The city adjacent to *k* (to the right of, unless *k* is at the last position, in which case it is to the left of) in the two parents are compared to see which of them is closer to *k* (as in Euclidean distance). *k* is then deleted from each parent and the closer city is chosen as the next *k*, and appended to *A*. The above steps are repeated until the parents are empty, with the list *A* containing the permutation part of the first child. One of the breakpoint parts of the two parents is copied to the child, thus fully forming the first child. For the second child, the permutation parts of the parents are decoded, adding 0 at the beginning of each individual sub-tour as shown in Fig. []. The steps of forming the first child are followed to get the list *A*, from which any zeroes are removed. To the resultant permutation of cities, randomized breakpoints (*m-1*) are added to form the second child.

*4.1.3. Mutation Operators*

Four mutation operators were considered in the project— Insert mutation, Swap mutation, Invert mutation, and Scramble mutation. All four were used, with each having equal probability of being chosen.

Insert mutation involves selecting a random gene in the chromosome and a location to insert. The selected gene is then removed from its current location and placed at selected location. Swap mutation simply swaps the genes at two random locations in the chromosome. Invert mutation involves selection of a range (two breakpoints) of genes and inverting the order of their placement. Lastly, Scramble mutation involves, similar to Inversion, selection of a range and scrambling the genes’ positions.

Each of the mutation operators involves breaking apart linkages in the chromosome, which is effective in producing mutations for permutation-based problems, and especially problems like TSP, where the order is doubly important.

*4.1.4. Overall Algorithm*

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***4.2. Implementation***

The program to run the algorithm and solve the MOMTSP was written in Python 3 and run on an Intel Core i7-7700HQ CPU (Windows 10 OS). The code was written from scratch, with the rare references to existing code on GitHub, marked clearly in the appended code.

***4.3.Experiment Design***

There were three questions involved in the design of the solver that were interesting enough to design the experiments around: How important is the population size to the performance of the NSGA-II, and does this importance change for different crossover operators? Which crossover operator(s) and mutation probability allow the NSGA-II to converge properly when solving the problems (comparing performance)? How does the implementation, considering the best parameters, compare against solutions in literature and the benchmark, if such exists? To answer the questions, three separate experiments were designed:

The first, to gauge the importance of the population size, involved checking the obtained optimal pareto front after 1000 iterations of the algorithm, for each crossover operator, keeping the mutation probability at 0.05.

Second, with the population size decided from the first experiment, vary the crossover operators and mutation probability values {0.01,0.05,0.08} to select best combination of crossover and mutation.

Lastly, with the parameters decided from the previous two experiments, solve the eil51 [], berlin52 [], eil76 [], and rat99 [] instances from TSPLIB for MinMax SD-MTSP, i.e., ; and the pr76 [] instance for . For the eil51 and berlin52 instances, the number of iterations was set to 1500, while for the other instance, it was set to 2500. The former set of results (for the was compared with the benchmark values presented in [] obtained using the CPLEX method as well as the implementations in [] and []; and the latter compared with the lone implementation in [].

5. RESULTS

The results from running the experiments detailed in the previous section are shown and inferenced from in this section, which as such is split into two parts— the first detailing the results of the parametric experiments, and the second presenting how well the implementation performed against the benchmark and/or results from literature.

***5.1. Parametric tests***

The parameters considered for this half of the experiments are the type of crossover operator, mutation probability, and population size. Note that as the obtained pareto fronts are irregular and very different from one another, it is not meaningful to have a metric quantifying how much better one parametric combination is over another. Rather, the results are discussed more subjectively and in the relative terms “slightly”, “moderately”, and “significantly”. More than the level of difference is the observation of which objective function axis the pareto front(s) is oriented towards, and the degree to which that is the case. Such observations provide insight into which objective was emphasized by the combination, which could then be used to hybridize or tune a GA for future problems.

*5.1.1. min (F1,F2)*

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*5.1.2. min (F1,F3)*

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***5.2. Benchmark and literature comparison***

*5.2.1. min (F1,F2)*

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*5.2.2. min (F1,F3)*

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***5.3. Further discussion***

While the implementation was successful at getting solutions in the neighborhood of the benchmark most of the time, there is a need for a more focused and in-depth parametric study of NSGA-II (with HX) being used to solve the MTSP. This may allow some hitherto unknown relationships between the parameters to come to light, besides being able to see if selecting better parameters could vastly affect the performance of the solver. From the limited experiments done in this project, such a thing could not be identified beyond the fact that changes in the parameters had little to no effect on the program with HX operator and there was some perceivable effect with the other operators. However, [] shows that such studies are not meaningless and could result in improvements.

In the NSGA-II, the crowding distance is sometimes believed to be an insufficient diversity preservation method []. By replacing the mechanism with other diversity preservation methods such as a neighborhood attractor schema [], it may be possible to find out if that is the reason why the program, in all runs with PMX, CX, and to a lesser extent OX, converged prematurely. If that is disproven, then it can be finally concluded that the three crossover operators were after all, unsuitable for the problem, and not due to the failings of the NSGA-II. This is one of the things that could not be done due to lack of time in this project.

On the other hand, a commentary on GAs [] remarks that checking if the envisioned crossover operator is suitable for the problem at hand is probably the more important question to ask rather than if a GA is suitable for the problem. The author states that the crossover operator is the only mechanism in the GA that “by chance bring(s) together good ingredients of a solution to produce something better because they co-occur.” Thus, regardless of the algorithm, the blame for poor performance can be placed on the crossover operators. Indeed, when comparing the HX to the other operators used in the project, it is clear that HX manages to overcome all (if any) other factors to have a performance comparable to the benchmark.

As an aside, while discussing why a particular GA worked or failed, it has to be acknowledged that although GAs are widespread in their use, their effectiveness at somehow identifying characteristics and exploring the search space to find a somewhat optimal solution is mysterious at best. In addition, even when GAs are shown to work for some problem, having a number of runs and combining the results from them to get at the possibly most optimal pareto front is necessary to mitigate the randomness of GAs. This was rather acutely observed in the project, and as such the results shown in this report and appended are some of the best obtained, and not repeatable. It is possible to use a seed and an update mechanism to make the whole program pseudo-random as it were, but that would mean achieving a set of god results would be dependent on what seed is chosen, which seems untenable. It may be better to leave things to chance, which is the basis of GAs.

While the implementation proved that the MinMax SD-MTSP can be optimized satisfactorily using the NSGA-II, the problem itself is a bit simple to be of direct use in the real world. Again considering the drone application, there are at least two possible additional constraints— maximum flying time of each drone, certain locations to be visited compulsorily as recharging spots, of which the first is necessary. Adding such constraints to the implementation would necessitate a reworking of quite a few of the functions, and a re-tuning of the entire algorithm. On the other hand, modern SAT/SMT solvers are much easier to use when considering ease of adding or changing constraints. Indeed, as the complexity of the constraints grows and to meet changing demands, GAs are probably not the best solvers to use.

6. CONCLUSION

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REFERENCES

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