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Reduction of Search Space by Applying Controlled Genetic Operators for Weight Constrained Shortest Path Problem

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***Abstract*—**The weight constrained shortest path problem (WCSPP) is one of most several known basic problems in combinatorial optimization. Because of its importance in many areas of applications such as computer science, engineering and operations research, many researchers have extensively studied the WCSPP. This paper mainly concentrates on the reduction of total search space for finding WCSP using some existing Genetic Algorithm (GA). For this purpose, some controlled schemes of genetic operators are adopted on list chromosome representation. This approach gives a near optimum solution with smaller elapsed generation than classical GA technique. From further analysis on the matter, a new generalized schema theorem is also developed from the philosophy of Holland's theorem.

***Keywords*—**Genetic Algorithm, Evolutionary Optimization, Multi Objective Optimization, Non-linear Schema Theorem, WCSPP.

I. Introduction

WEIGHT constrained shortest path problem (WCSPP) is a superset of the shortest path problem. WCSPP has an extra characteristic that deals with some multi-objective constraints. WCSPP is defined by the following input and output requirements [1], Input: n node undirected graph $G = (V,E)$ for each edge $(v_i,v_j) \in E$, it has a positive integer length $l(v_i,v_j)$ and a positive integer weight $w(v_i,v_j)$; specified node $\{s,t\} \subseteq V$ and positive integer K and L. Output: Is there any path p from s to t in G, $p = \{s, v_0, v_1 \ldots. v_k, t\}$ that has both total weight at most W that is, $w(p) < K$ and total length at most L that is, $l(p) < L$. WCSPP is not an NP-Hard problem if it has same weights around each weight and same length. In this case, there exist many efficient algorithms that can take over the problem.

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II. Overview of Methods in the Literature

Methods appearing in the literature that apply to the WCSPP can be divided into those based on k shortest paths, node labeling methods derived from dynamic programming equations, Lagrangean relaxation, and approximation algorithms, although some work combines these approaches. Preprocessing can also be important. It was observed early that k shortest path methods could solve the WCSPP, paths are generated in increasing order of cost, and the method stopped as soon as a weight feasible path is found. Handler and Zang [2] implement the k shortest path method of Yen [3], and compare it with their Lagrangean relaxation approach. A number of early papers gave dynamic programming formulations, for example Joksch [4] and Lawler [5]. A variety of algorithms based on these dynamic programming formulations, all used some kind of node labeling approach, have been developed since. Examples are the methods of Aneja et al [6], Desrosiers, Pelletier and Soumis, Desrochers and Soumis [7] and more recently Jaumard, Semet and Vovor. Another attempt with integer programming approach is also extensively studied by Dumitrescu and Boland [8]. However, so far it is known, this is the first attempt to solve the WCSPP using GA. Due to lack of sufficient reference; controlled GA approach is only compared with classical GA approach, other than previously devised non-heuristic techniques.

III. Problem Specification for Classical GA based Technique

In the case of classical GA, the encoding scheme is done using vector chromosome. Each chromosome defines a path in the graph G. Each gene corresponds to the vertices along the path. The representation should not contain information beyond that needed to represent a solution to the problem. Whichever representation to choose, operators should be picked in such way that are appropriate for the concerning representation. So the main problems to consider: 1. Constraints for chromosome representation, 2.Approximation of chromosome length and 3. Devise operators to avoid those

solutions that are out of feasibility.

IV. Problem in Fixed Length Chromosome

For the solution of WCSPP, or similar problems, such as TSP [9]-[11], Maximal length path [9] etc. many types of representation are proposed [9]. They are Adjacency representation, Ordinal Representation, Path representation and Matrix representation. From the detailed study, these early proposed representation suffers from below noted problems in finding solution to the WCSPP,

1) If an optimal path length is smaller than the chromosome length, the occurrence of repeating genes is not possible to avoid.
2) If an optimal path length is smaller than the chromosome length, the occurrence of partial path or premature-cycle [9] is not possible to avoid.
3) In order to avoid these anomalies, some extra repair algorithm [9] must be applied.

V. Floyd-Warshall's Algorithm to Approximate the Chromosome Length

Some detailed studies have revealed that if the dimension of the chromosome is just equal to the dimension of the optimal shortest path, the GA can escape from the occurrence of repeating and premature cycle. So in this case the objective would be to predict the length of the optimal solution or the path length of the shortest weight constrained path. So, for a given a graph $G = (V, E)$, if a WCSP is to be found using GA with vector chromosome (path representation) and if the length of the chromosome is l and path length of the optimal WCSP is smaller then l, then there must be an occurrence of repetition or premature cycle. This proposition can be proved easily, suppose, the optimal solution has the chromosome of length l_o and the vector chromosome has the fixed length of l_f. Here, the case that we have to consider is $l_f > l_o$ and excess of length is $\delta l = l_f - l_o$. When crossover and other genetic operators are applied, somehow it must be filled δl spaces with random vertices. So, when an optimal solution is reached, δl spaces will be filled by a series of same vertices and thus repeated path must occur in the solution. So, for the prediction of the most optimal chromosome length, the possible length of the chromosome should be found out somehow. This can be done by Floyd – Warshall's algorithm [10]. Floyd – Warshall's algorithm find the length of a shortest path $d(v_i,v_j)$ (the length of the shortest path between v_i and v_j) in a graph G, where, $G = (V, E)$, $V = \{v_0, v_1, v_2, \ldots. v_k\}$ and weights $w(v_i,v_j)$ with $w(v_i,v_j) = \infty$ if $(v_i,v_j) \notin E$. If $s = v_0$ and $t = v_k$ then we can set up chromosome length as $d(v_i.v_j)$ when $w(v_i,v_j) = 1$ for all $(v_i,v_j) \in E$. However, this leads to the aforementioned anomalies. To overcome this limitation vector representation will not be used.

VI. Variable Length Chromosome Definition

It becomes apparent that, list chromosome representation is most feasible way to explain each solution exactly. However in classical GA, first population is chosen randomly. This will results into many invalid tours in the graph. In the long run huge generation elapse is required to obtain the result. The objective of this thesis work is to minimize the iteration. So this approach is not wise to start with. Here a controlled genetic operation is applied to create each initial individual chromosome so that each of them represents a valid tour. In this context list chromosome representation is suitable for WCSPP. Though, it still suffers from some anomalies, such as blocked path creation.

VII. Creation of Initial Population

The initial population is created in a list chromosome and each node is chosen randomly so that every chromosome defines a valid tour. The overall process becomes clear form the below algorithm, Here, the problem will find a path from start point s to destination t. The algorithm, *CONTROLLED_CHROMOSOMECREATION* describes the creation of chromosome for initial population (population at time t is $p(t)$). Fig. 1 describes the proper illustration for *CONTROLLED_CHROMOSOMECREATION.*

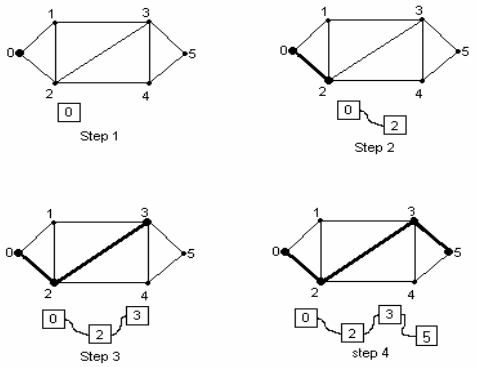

Fig. 1 Creation of an individual

Procedure *CONTROLLED_CHROMOSOMECREATION*
Begin
  $i := 0$
  Take first gene, $u_i := s$
  While $(u_i \neq t)$
  Begin
    $K := \{\varnothing\}$
    $j := 0$
    While $(j \leq |V|)$
    Begin
      if $((u_i,v_j) \in E)$
      apply $v_j \in K$
      $j := j+1$
    End
    if $(K \neq \{\varnothing\})$
    Choose randomly any v_k *from K*
    $i := i + 1$
    Add to next gene $u_i := v_k$
  End
End
Here, $I_0 = (s, u_1, u_2 \ldots u_k, t)$ *the first individual in p(t).*
I_0 *defines a valid path from s to t.*

VIII. Creation of Blocked Path

The technique that is used here for chromosome creation still suffers from some anomalies. This problem is the creation of chromosome defining partial valid tour or blocked path. The creation scenario of such kind of individual is given in Fig. 2. The creation of blocked path may lead to an invalid tour. However, this concern raises the possibility of discarding or preserving the blocked path in the initial population. However a blocked path may contain useful information for an optimal solution. So, in this experiment, blocked path chromosome is preserved in the initial population.

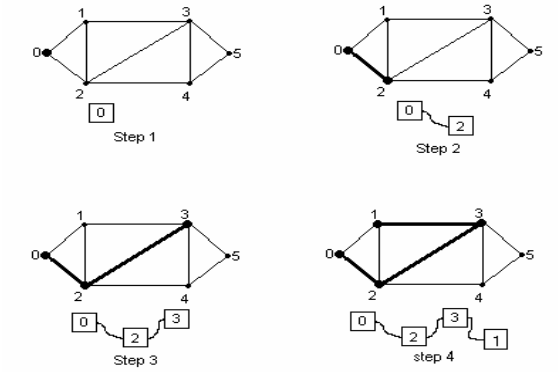

Fig. 2 Creation of blocked path

IX. Controlling the Crossover

Here, the crossover technique is adopted in such a way that each offspring created from a pair of parent will define a valid tour. So, for this purpose the crossover point is chosen in a controlled manner. The overall process is described in the following algorithm *CONTROLLED_CROSSOVER*. Fig. 3 describes the proper illustration of the algorithm *CONTROLLED_CROSSOVER.*

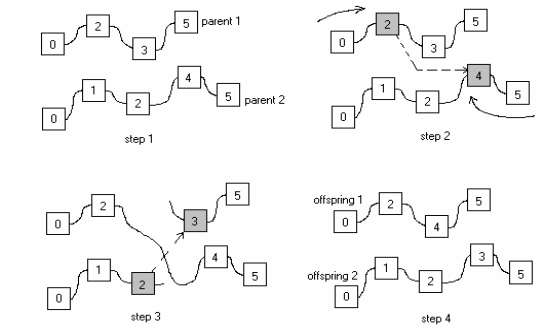

Fig. 3 *CONTROLLED_CROSSOVER* in operation

Procedure *CONTROLLED_CROSSOVER*
Begin
Take two parents $I_i = \{s, u^i_1, u^i_2 \ldots u^i_k, t\}$ *and* $I_j = \{s, u^j_1, u^j_2 \ldots u^j_k, t\}$ *randomly.*
From I_i*, randomly chose a gene* u^i_x*, the direction of choosing is forward (from s to t)*
From I_j*, at inverse direction (from t to s), chose a gene* u^j_x
if($(u^i_x, u^j_x) \in E$ *and* $\{u^i_{x-1}, u^i_{x+1}\} \not\subset \{u^j_{x+1}, u^j_{x+2} \ldots t\}$ *)*
The crossover point is u^i_x *and* u^j_x*.*
Now Apply crossover and create new offspring I^o_1
Obviously, $(u^i_{x-1}, u^i_x) \in E$, $(u^i_x, u^i_{x+1}) \in E$ *and* $\{u^j_{x+1}, u^j_{x+2} \ldots t\} \subseteq I_j$.
else
Crossover failed

If $((u^i_{x+1}, u^j_{x-1}) \in E)$
Another crossover point is u^i_{x+1} *and* u^j_{x-1}
Now Apply crossover and create another offspring I^o_2.
else
Crossover failed
Include I^o_1 *and* I^o_2 *to new population p(t+1). Preserve* I_i *and* I_j *to old population p(t)*
End

If the condition, $(u^i_{x+1}, u^j_{x-1}) \in E$, is not satisfied, creation of I^o_2 will not occur since it is an invalid tour. So, after this genetic operation, offspring are $I^o_1 = \{s, u^i_1, u^i_2 \ldots u^i_{x-1}, u^i_x, u^j_x, u^j_{x+1} \ldots u^j_{k-1}, u^j_k, t\}$ and $I^o_2 = \{s, u^j_1, u^j_2 \ldots u^j_{x-2}, u^j_{x-1}, u^i_{x+1}, u^i_{x+2} \ldots u^i_{k-1}, u^i_{k-1}, t\}$. Where parents are, $I_i = \{s, u^i_1, u^i_2 \ldots u^i_{x-1}\, u^i_x, u^i_{x+1} \ldots u^i_{k-1}, u^i_k, t\}$ and $I_j = \{s, u^j_1, u^j_2 \ldots u^j_{x-1}\, u^j_x, u^j_{x+1} \ldots u^j_{k-1}, u^j_k, t\}$.

X. Controlling the Mutation

Like all other genetic optimization, mutation is also applied to find the optimal solution. However, in this experiment, the mutation technique is also done in controlled manner. The overall step is described in *CONTROLLED_MUTATION*; a path *p* is described by the chromosome, $I = \{s, u_0, u_1 \ldots u_{i-1}, u_i, u_{i+1} \ldots t\}$. Fig. 4 describes the proper illustrations for *CONTROLLED_MUTATION.*

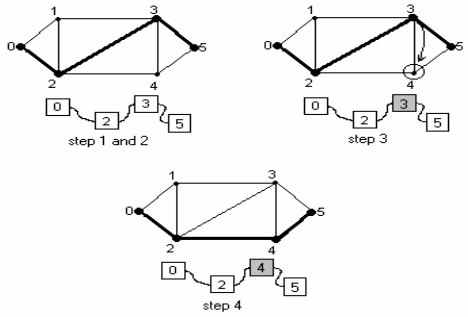

Fig. 4 *CONTROLLED_MUTATION* in operation

Procedure *CONTROLLED_MUTATION*
Begin
Take a chromosome I_i *randomly.*
Choose a gene u_i *from* I_i *randomly.*
Take $V_M := \{\varnothing\}$
While (all vertex u_k*, adjacent to* u_i *are checked)*
Begin
Take any vertex, u_k
If $((u_k, u_{i-1}) \in E$ *and* $\{u_k, u_{i+1}\} \in E)$
apply $u_k \in V_M$
End
If($V_M \neq \{\varnothing\}$ *)*
Randomly choose any u_j *from* V_M.
Replace u_i *with* u_j.

else
Mutation failed
End

XI. Feasibility of New Search Technique

The main feasibility issue behind this new approach is to minimize the search space. In the consequence, an optimal solution may be obtained by smaller generation than conventional technique. The approximation of the search space can be deduced by easy mathematics. If the graph $G = (V, E)$ has $|V|$ number of vertices, let $|V| = n$ and the length of the list chromosome may span from 0 to $n - 2$. So, first 0 space of gene can be filled with n vertices in ${}^nP_0$ ways, 1 space of gene can be filled with n vertices in ${}^nP_1$ ways, 2 space of gene can be filled with n vertices in ${}^nP_2$ ways and in the same way, $n - 2$ space of gene can be filled with n vertices in ${}^nP_{n-2}$ ways. So total search space,

$$S_n = {}^nP_1 + {}^nP_2 + {}^nP_3 + \ldots + {}^nP_{n-2}$$
$$= n!/2! + n!/3! + \ldots + n!/(n-2)! + n!/(n-1)! + n!/n!$$
$$= n!\,(1 + 1/2! + 1/3! + \ldots + 1/n!) - n!$$

For general case, if the graph is very large, this can be assumed that n is also very large. So, $S_n = n!(e - 1)$ In this case the graph is completely connected. However if the graph were not completely connected, the search space would change a little. Now, in new scheme, if the graph is not completely connected, the search space becomes,

$$S_k = ({}^nP_0 - k_1) + ({}^nP_1 - k_2) + \ldots + ({}^nP_{n-2} - k_n)$$
$$= ({}^nP_0 + {}^nP_1 + \ldots + {}^nP_{n-2}) - (k_1 + k_2 + \ldots + k_n)$$
$$= n!(e - 1) - K = S_n - K$$

So, obviously $S_k < S_n$. Total number of search space is reduced. Here $k_1, k_2 \ldots k_n$ represents permutation by invalid tour. K equals to the grand total of all invalid tours in the graph. So, this mathematical deduction proves that the search space is reduced if the controlled scheme of genetic operation is adopted.

XII. Measuring Fitness

The fitness each chromosome should be measured in terms of both weight $w(I_i)$ and length $l(I_i)$. So this multi-objective optimization problem [9] is solved in classical way. There are some classical methods for multi-objective optimization. This includes a method of objective weighting [9], where multiple objective functions f_i are combined into one overall objective function F. Another approach (method of distance functions) combines objective functions into one on the of demand level vector y as in (1).

$$F(x) = \left(\sum_{i=1}^{k} \left| f_i(x) - y_i \right|^r\right)^{1/r} \quad (1)$$

Where, (usually) r = 2 (Euclidian Metric). In the case of WCSPP, $F(I)$, (i.e. overall fitness of individual I), is defined by (2).

$$F(I) = [(w(I) - W)^2 + (l(I) - L)^2]^{1/2} \quad (2)$$

TABLE I
Comparative Analysis

Example Graphs	Total Number of Nodes	K	L	Generation Elapsed		% Reduction
				Controlled Genetic Operator	Classical GA	
GRAPH-1	10	13	17	150	500	70
GRAPH-2	21	18	11	1600	5000	68
GRAPH-3	35	17	12	2200	6800	67
GRAPH-4	28	7	8	2000	5800	62
GRAPH-5	8	17	8	100	320	69
GRAPH-6	5	12	6	100	300	70
GRAPH-7	97	20	19	4000	13000	69
GRAPH-8	56	13	11	3500	10540	66
GRAPH-9	89	6	13	3800	11400	67
GRAPH-10	6	14	17	100	300	70

Percentage Reduction means the reduction of generation's elapse for GA with Controlled Genetic operations. K and L refer to maximum weight and maximum length for each of the graphs respectively.

Here, $w(I)$ and $l(I)$ is $w(p)$ and $l(p)$ respectively. Since, all Pareto-optimal solutions [1], [11], [12] might be of some interest; ideally, the system will report back the set of all Pareto-optimal points in future experiments.

XIII. Experimental Results

The experiments are done on 10 graphs that are generated randomly. In every case $l(e)$ *and* $w(e)$ does not exceed 20. Here in each experiment, $p_c = 0.8$ and $p_m = 0.15$. The first entry in each edge is the weight and next entry is the length. That is, in every case, $(w(e),l(e))$. Table 1 represents the comparative analysis of controlled genetic operation with classical genetic operations. In every case population size is 200. From this data, it becomes clear that using controlled genetic operations; generations elapse is reduced up to 70% approximately. That is, the convergence speed is increased to 3 times more than classical genetic algorithm approach. An instance of randomly generated graph, GRAPH – 2 is illustrated in Fig. 5. The starting node s is 0 and ending node t is 20. For example, curve plot of Generation vs. best individual fitness and Generation vs. Average fitness are also given in Fig.6 and Fig.7 respectively.

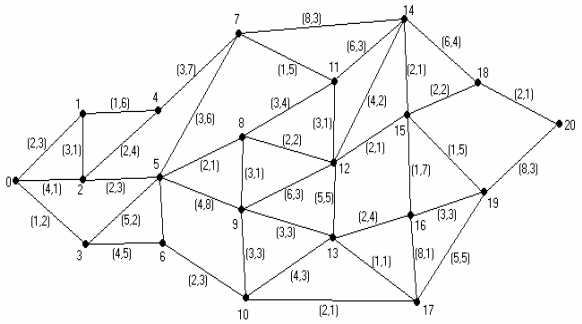

Fig. 5 GRAPH – 2

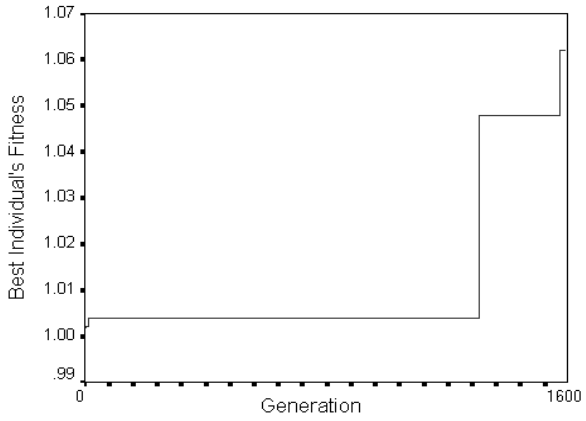

Fig. 6 Best Individual's fitness vs. Generation (for GRAPH-2)

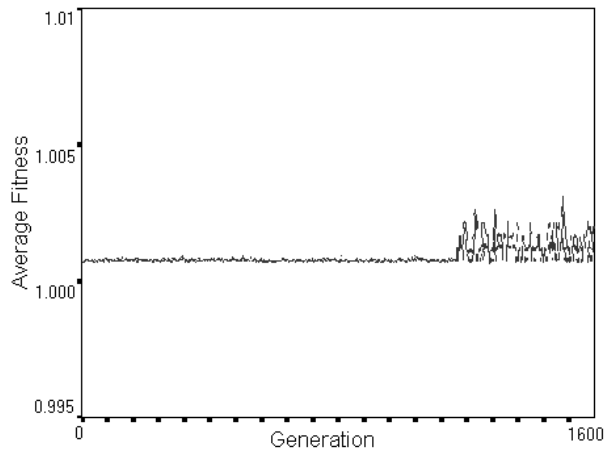

Fig. 7 Average fitness vs. Generation (for GRAPH-2)

XIV. Non-Linear Schema Theroem for WCSPP

Generally Holland's schema theorem [11] is designed for binary vector chromosome [9]. However, chromosome can be designed in many ways. Most general case is the graph representation of binary chromosome. The nonlinear schema theorem [13] for this type of cases is extensively discussed by W.A. Greene [13]. In the same way, schema theorem for WCSPP can be deduced easily from that idea. We need a notion analogous to a schema's defining length. We have assumed there is a notion of distance between two nodes in graph G. If B is some subset of G-nodes, define the *diameter* of B to be the maximum distance between any two nodes in B. Since graph G is finite, the diameter of any G-subset, including G itself, is a well-defined (finite) positive real number. Given a schema H, define its *relative diameter*

$$rel\Delta(H) = \Delta fixed(H)/\Delta(G) \quad (3)$$

Where, *fixed (H)* is the set of fixed nodes in H. Note that in the original Holland scenario, when L bits are arranged in a linear sequence, the relative diameter of a schema H is δ(H)/L – 1. The non linear schema equation [13] is defined as

$$m[\mu(H)/\mu(P)][1 - p_c\, rel(\Delta H)](1 - p_m)^{order(H)} \quad (4)$$

where terms are identical to Holland's theorem except $rel\Delta(H)$. However in the case of WCSPP, the chromosome is variable length and every individual's length in each generation is changed after every genetic operation. So some modification is still required at this context. During the whole iteration crossover and mutation may occur in three ways, these are, 1. Crossover occurs but not mutation, 2. Mutation occurs but not crossover and 3. Mutation and crossover both occurs. Mutation and crossover are independent event. So the total probability P is, $P = p_m + p_c + p_m.p_c$ If the length of i^{th} individual is L_i then after each genetic operation, the change in length is δL ($0<\delta L<L_i$). So finally length of each individual after every genetic operation is, $L_i \pm P\delta L$. Now transforming L_i and δL to the notion analogous to graph, $rel(\Delta H)$ can be rewritten as, $rel(\Delta H) = \delta(H)/(L_i \pm P\delta L)$. Now equation (4) can be written as

$$m \cdot \left(\frac{\mu(H)}{\mu(P)}\right) \cdot \left(1 - p_c \frac{\delta(H)}{(L_i \pm P\delta L)}\right) \cdot (1 - p_m)^{order(H)} \quad (5)$$

$\delta(H)$ is the short defining length [9],[11] of schema [9],[11] H. As long as the genetic iteration occurs, the length term $(L_i \pm P\delta L)$ converges to the length of the fittest chromosome.

XV. Conclusion and Future Exploration

In this paper, we have proposed a computationally fast method to find WCSP in a graph. Our next target is to simultaneously find Multiple Pareto-optimal solutions in a population. A GA is unique optimization algorithm in solving multi-objective optimization problems in this respect. In one implementation, non-domination concept [12] will be used next time with all objective functions to determine a fitness measure for each solution. Thereafter, the GA operators described here will be used as usual. On a number of multi objective optimization problems, this non-dominated sorting GA [12] has been able to find multiple Pareto-optimal solutions in one single run.

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