A Constructive Genetic Algorithm For The Generalised Assignment Problem

Luiz A. N. Lorena

LAC/INPE- Instituto Nacional de Pesquisas Espaciais

Caixa Postal 515

12201-970 - São José dos Campos – SP, Brazil

lorena@lac.inpe.br

Marcelo G. Narciso

Embrapa Informática Agropecuária

Av. Dr. André tosello, s/n, Unicamp

13083-970 – Campinas - SP, Brazil

narciso@cnptia.embrapa.br

J.E. Beasley

The Management School, Imperial College

London SW7 2AZ, England

j.beasley@ic.ac.uk

Abstract

We present in this paper an application of the *Constructive Genetic Algorithm (CGA)* to the *Generalised Assignment Problem (GAP).* The *GAP* can be described as a problem of assigning *n* items to *m* knapsacks, *n>m*, such that each item is assigned to exactly one knapsack, but with capacity constraints on the knapsacks. The *CGA* has a number of new features compared to a traditional *genetic algorithm.* These include a dynamic population size and the possibility of using heuristics. In our application of *CGA* to *GAP* we use a binary representation and an assignment heuristic which allocates items to knapsacks. Computational tests are presented using large publically available instances taken from the literature.

1. Introduction

In this paper we consider an important combinatorial optimisation problem, the *Generalised Assignment Problem (GAP)*. This is the problem of assigning at minimum cost n items to m knapsacks ($n>m$), such that each item is assigned to exactly one knapsack subject to capacity constraints on the knapsacks.

Many real life applications can be formulated as a *GAP*, e.g. resource scheduling, the allocation of memory space in a computer, the design of a communication network with capacity constraints at each network node, assigning software development tasks to programmers, assigning jobs to computers in a network, vehicle routing problems, and others [1,4,6,7].

GAP is NP-hard [16]. A number of algorithms in the literature are exact tree search algorithms [15,18], and there are also a number of heuristics for the problem [4,8,11,12,14-16].

Genetic Algorithms (GA) have become popular in recent years as effective heuristics for NP-hard combinatorial optimisation problems such as the *GAP*. Today there are many variations on the general *GA* theme but all such variations can be classified generically as **population heuristics** [3], that is as heuristics which progressively evolve a population of solutions. Such heuristics are in marked contrast to other approaches, such as tabu search and simulated annealing, that operate on just a single solution. We shall assume throughout this paper some familiarity on the part of the reader with genetic algorithms.

Holland [10] originated *GA's*. For application to optimisation problems the first step in a *GA* is the definition of a representation – some way of encoding a solution to the problem under consideration, typically into a binary bit string. For example, if there are 7 binary (zero-one) variables in an optimisation problem then solutions can be represented as 0100010, 1100110, 1010101, etc – all of which are 7 digit binary bit strings. Solutions are evaluated though use of a *fitness function* and the fitness value associated with a solution indicates "how good" the solution is in terms of the original optimisation problem that is being considered.

Suppose now that, although we are sure of certain variable values in a solution, we are unsure of others. For example 101#1#1 represents the situation where we are sure of variable values for all except the fourth and sixth variables, unsure variable values being conventionally represented by #. 101#1#1 is an example of a **schema**. Clearly the schema:

101#1#1

comprises four solutions, namely:

1010101
1010111
1011101
1011111

formed by enumerating all combinations of possible values for each # in 101#1#1.

Holland put forward the *building block* hypothesis (schemata formation and conservation) as a theoretical basis for the *GA* mechanism. In this view avoiding disruption of good schemata is the basis for the good behaviour of a *GA*. One major difficulty with the building block hypothesis however is that schemata are only evaluated

indirectly, via evaluation of specific solutions. This raises two problems:

1. a schema with v #'s has 2^v solutions (replace each # by zero or one) and inevitably, for computational reasons, we typically only gain limited information about the schema by examination of a limited number of the 2^v possible solutions
2. a solution with v decided variables is a member of 2^v-1 schemata (replace each decided variable by # or not) and so when using an evaluated solution we are attempting to use information about many schemata.

In this paper we use the word **structure** as a generic term to cover both solutions and schemata.

The *Constructive Genetic Algorithm (CGA)* [9,13,17] was proposed recently as an alternative to the traditional *GA* approach. One of the objectives of a *CGA* is the direct evaluation of schemata. In this paper we present a CGA for the GAP.

This paper is organised as follow. Application of the *CGA* to the *GAP* is presented in Section 2. In a *CGA* the original problem is regarded as a bi-objective optimisation problem that drives the evolutionary search for well adapted structures. The relevant aspects of our *CGA* for the *GAP* are explained: structure representation, the evolution process, selection, recombination and mutation, and *CGA* pseudo-code is presented. Section 3 presents computational tests using large publically available instances from the literature, providing insights into *CGA* performance.

2. CGA for the GAP

2.1 GAP formulation

The *GAP* is best described using knapsack problems [15]. Given n items and m knapsacks, with p_{ij} as the cost associated with assigning item j to knapsack i, w_{ij} as the weight of assigning item j to knapsack i, and c_i as the capacity of knapsack i, assign each item j to exactly one knapsack i, not exceeding knapsack capacities. Defining x_{ij}=1 if item j is assigned to knapsack i, =0 otherwise, the *GAP* can be formulated as:

$$\text{minimise} \quad \sum_{i=1}^{m} \sum_{j=1}^{n} p_{ij}x_{ij} \qquad \text{\{minimise total cost\}}$$

$$\text{subject to:} \quad \sum_{j=1}^{n} w_{ij}x_{ij} \pounds c_i \qquad i \hat{I} M = \{1,\ldots,m\} \qquad \text{\{respect knapsack capacities\}}$$

$$\sum_{i=1}^{m} x_{ij} = 1 \qquad j \hat{I} N = \{1,\ldots,n\} \qquad \text{\{all items assigned\}}$$

$$x_{ij} \hat{I} \{0,1\} \qquad " i \hat{I} M ," j \hat{I} N$$

In order to apply the *CGA* to the *GAP* we will view the problem as a bi-objective optimisation problem. Whilst in other evolutionary algorithms the evaluation of individuals is based on a single function (the fitness function), in a *CGA* this process relies on two functions. We first describe the structure representation.

2.2 Structure representation

For structure representation we used a sequence of n characters, where n is the number of items. This n character representation contains just three symbols:

1 - to indicate that the item is a seed item and has been assigned to a knapsack
0 - to indicate that the item is a non-seed item which will be assigned to a

knapsack by a heuristic
- to indicate that the item is temporarily out of the problem (an undecided item).

Seed items are initially assigned to the *m* knapsacks, exactly one per knapsack, so there are always precisely *m* 1's in each structure.

For example, considering a problem with *n*=7 items and *m*=3 knapsacks, we could have a structure *S* = (#1#01#1), where the 3 seed items are: item number 2 assigned to knapsack 1, item number 5 assigned to knapsack 2, and item number 7 assigned to knapsack 3. Item 4 has the label 0 and will be assigned to one of the knapsacks according to an assignment heuristic. Items 1, 3 and 6 have the label # and are temporarily not being considered. As *S* contains #'s it is a schema. By contrast the structure *S* =(0100101) is not a schema but a solution.

The following assignment heuristic is used to translate any structure *S* into a solution to the underlying *GAP*.

Assignment Heuristic - AH

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1 – Assign the m items with label 1 to the m knapsacks, and update the knapsack capacities accordingly

2 – Assigning the other n-m items to the knapsacks (labels 0 and #)
- *2.1 – Solve the m knapsack problems separately exactly*
- *2.2 – Update the knapsack capacities for the items assigned to exactly one knapsack*
- *2.3 – Resolve the m knapsack problems separately exactly for the remaining items*
- *2.4 – Update the knapsack capacities for the items assigned to exactly one knapsack*
- *2.5 – For each item j remaining, assign it to knapsack i* corresponding to the smallest* w_{i^*j}
- *2.6 – If the solution obtained is not feasible for the GAP, restart the assignment of the n-m items (the m seed items were already assigned in step 1), assigning (if possible) item j to knapsack i* corresponding to the smallest* w_{i^*j} *for which capacities are not violated*

3 – If the solution is feasible for the GAP improve the solution with the second part of MMTH (see [14])

4 – Discard from knapsacks any items with label # in S

2.3 The bi-objective problem

Let C be the set of all 3^n structures that can be generated by the *0-1-#* representation we have adopted, and consider two functions f and g, defined as $f:C \to \Re_+$ and $g:C \to \Re_+$ such that $g(S) \geq f(S)\ \forall S \in C$. We define the double fitness evaluation of a structure due to functions f and g as *fg-fitness.*

For the *GAP* the function g represents the cost of items assigned to knapsacks after application of the assignment heuristic *AH*. Letting $C_i(S)_{AH}$ represent the items assigned to knapsack i after application of *AH* to structure S we have $g(S) = \sum_{i=1}^{m} \sum_{j \in C_i(S)_{AH}} p_{ij}$. Note here that from step 4 in *AH* above any item j assigned a label # in S is not assigned to any knapsack at the end of *AH* and so is not included in $g(S)$.

For the *GAP* the function f represents the cost of items assigned to knapsacks after taking the solution produced by *AH* and moving a single item between knapsacks. To define f the following *MAH* heuristic is applied to S, producing an additional move of one item between two knapsacks:

Modified Assignment Heuristic – MAH

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1. Apply *AH* to S
2. Over all the items in knapsacks presenting label 0 in S let j^* be the item with the most costly assignment (ties broken arbitrarily)
3. Let i^* be the knapsack corresponding to the least cost assignment of item j^* (ties broken arbitrarily)
4. Assign (move) item j^* to knapsack i^*

Letting $C_i(S)_{MAH}$ represent the items assigned to knapsack i after application of *MAH* to

structure *S* we have $f(S) = \sum_{i=1}^{m} \sum_{j \in C_i(S)_{MAH}} p_{ij}$. Clearly we have that *g(S)* ³ *f(S)*. The difference *g(S)* - *f(S)* ≥ 0 can be interpreted as the cost of a wrong assignment if the resulting *GAP* solution is feasible. Considering our representation, *fg-fitness* values increase as the number of # labels decrease and therefore structures with few # labels have higher *fg-fitness.*

In our *CGA* for the *GAP fg-fitness* plays two roles:

- ***interval minimisation*** we would like to search for a $S \in C$ that minimises *g(S)* - *f(S)*, since obviously a good quality solution to the *GAP* cannot be improved by moving a single item between knapsacks.
- ***g maximisation*** we would like to search for a $S \in C$ that maximises *g(S)*, since we need to increase cost to ensure feasibility. A structure that has very few items assigned to knapsacks, e.g. because it is a schema in which most items are labelled #, will have low cost, but will not be a feasible solution to the *GAP*. This objective can be viewed as encouraging the process to move from schemata to solutions.

Hence our *CGA* implicitly considers the following *Bi-objective Optimisation Problem (BOP)*:

minimise *g(S)* - *f(S)*

maximise *g(S)*

subject to: *g(S)* ³ *f(S)* $\forall S$

$S \in C$

2.4 The evolution process

The *BOP* defined above is not directly considered as the set *X* is not completely known. Instead we consider an evolution process to attain the objectives (*interval minimisation* and *g maximisation*) of the *BOP*.

At the beginning of the process, two *expected values* are given to these objectives:

- for the *g maximisation* objective we use a value $g_{max} > \max_{S \in X} g(S)$ that is an upper bound on the objective value
- for the *interval minimisation* objective we use a value dg_{max}, obtained from g_{max} using a real number $0 < d \leq 1$.

The evolution process proceeds using an adaptive rejection threshold, which considers both objectives. Given a parameter $a \geq 0$ a structure *S* is discarded from the population if:

$$g(S) - f(S) \geq dg_{max} - a d[g_{max} - g(S)] \qquad (1)$$

The right-hand side of equation *(1)* is the threshold for structure removal from the population and is composed of the expected value dg_{max} associated with interval minimisation and the measure $[g_{max} - g(S)]$, which is the difference between g_{max} and $g(S)$ evaluations. For $a=0$ equation *(1)* is equivalent to comparing the interval length associated with *S* against the expected length dg_{max}. When $a > 0$, structures containing a high number of # labels (i.e. structures which are schemata) have a higher probability of being discarded as, in general, they have higher differences $[g_{max} - g(S)]$ since g_{max} is fixed and $g(S)$ is smaller for schemata than for solutions.

In our approach the value of the *evolution parameter* a is related to time in the evolution process. As initially good schemata need to be preserved for recombination a starts from zero and then slowly increases (in steps of e) from generation to generation. The population at evolution time a, denoted by P_a, is dynamic in size according to the value of the adaptive parameter a. The population can shrink to zero during the evolution process (extinction).

Rearranging equation *(1)* a structure *S* should be discarded from the population if

$$d(S) = \frac{dg_{\max} - [g(S) - f(S)]}{d[g_{\max} - g(S)]} \leq a$$

A key computational point here is that $d(S)$ (which we refer to as the **rank** of a structure) is fixed in value at the time the structure is created. The evolution parameter a on the other hand does increase over time. Hence we need only compute the rank $d(S)$ of a structure once and then continually compare it against the changing evolution parameter in deciding whether to discard the structure or not. Obviously the larger the rank the longer a structure will exist in the population, since a structure is only discarded once a becomes large enough to satisfy $d(S) \leq a$.

2.5 Selection and recombination

Selection of individuals can be made in several ways. *CGA* has been tested with a number of optimisation problems and in all cases an appropriate approach is that the population is kept ordered using a key value that involves for each structure its *fg-fitness* and its

proximity to a feasible solution. Then, several times in a generation, two structures are randomly selected, one from among the best part of the population and the other from the whole population, and these are recombined to form (one or more) new structures (see Lorena and Furtado [13]).

The manner of recombination depends on the problem and the way the structure represents a solution. The main goal of recombination is population diversification. Structures representing feasible solutions can be generated not only by recombination, but also by complementation of a selected schema. The best results found with the *CGA* approach use mutation over structures that represent feasible solutions for the problem (see Lorena and Furtado [13]).

In our *CGA* for the *GAP* the population is ordered in increasing value of $\Delta(S) = \frac{1 + d(S)}{n - n_{\#}(S)}$, where $d(S) = \frac{g(S) - f(S)}{g(S)}$ and $n_{\#}(S)$ is the number of # labels in S. Structures with small $n_{\#}(S)$ and/or with small $d(S)$ appear in first order positions.

The method used for selecting structures for recombination takes one structure from the *n* first positions in the ordered population (*base*) and the second structure from the whole population (*guide*). Before recombination the first structure is changed to generate a structure representing a solution, i.e. all #'s are replaced by 0's. This complete structure suffers mutation and is compared to the best solution found so far (which is kept throughout the process).

Recombination merges information from both selected structures, but preserves the number of 1 labels (number of knapsacks) in the new generated structure.

Recombination

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if $S_{base}(j) = S_{guide}(j)$ *then* $S_{new}(j) \neg S_{base}(j)$

if $S_{guide}(j) = \#$ *then* $S_{new}(j) \neg S_{base}(j)$

if $S_{base}(j) = \#$ *and* $S_{guide}(j) = 0$ *then* $S_{new}(j) \neg 0$

if $S_{base}(j) = \#$ *or* 0 *and* $S_{guide}(j) = 1$ *then*

$S_{new}(j) \neg 1$ *and* $S_{new}(i) \neg 0$ *for some* $S_{new}(i) = 1$

if $S_{base}(j) = 1$ *and* $S_{guide}(j) = 0$ *then*

$S_{new}(j) \neg 0$ *and* $S_{new}(i) \neg 1$ *for some* $S_{new}(i) = 0$

At each generation, exactly *n* new structures are created by recombination. If a new structure does not represent a feasible solution, then it is inserted into the population; otherwise it suffers mutation and is compared to the best solution found so far. The following pseudo-code describes the mutation process.

Mutation

For each position *j* with label 1 ***do***
    For each position *k* with label 0 ***do***
        Interchange the labels on positions *j* and *k* generating an offspring S_{new} *;*
                {offspring generation}
        Interchange the labels on positions *j* and *k ; {return to the original S}*
    End_for
End_for

The mutation process was limited to considering just ten new structures to avoid excessive computation time.

At each generation, after new structure insertion, the population is scanned to remove all

structures S satisfying the condition $d(S) \leq a$. As described earlier in this paper, the evolution parameter a is initially set to zero and slowly increased at each generation.

2.6 CGA pseudo-code

The pseudo-code for our *CGA* [13] is:

Constructive Genetic Algorithm - CGA

a := 0	*{initialise a}*
e := 0.01	*{step value for time advance}*
Initialise P_a	*{initial population}*
Evaluate P_a	*{compute fg-fitness}*
For all $S \in P_a$ *compute* $d(S)$	*{rank computation}*
While (not stopping condition) *do*	
Discard from the population P_a all $S \in P_a$ *satisfying* $d(S) \leq a$	*{evolution test}*
$a := a + e$	*{increment a}*
Produce P_a from P_{a-e}	*{generate new population}*
Evaluate P_a	*{compute fg-fitness}*
For all *new* $S \in P_a$ *compute* $d(S)$	*{rank computation}*
End_while	

As the evolution parameter a increases, the population size initially increases and then start to decrease until eventually the population becomes empty. Two stopping conditions are considered: stop when the population is empty, or when a pre-defined generation limit is reached.

To compute the upper bound g_{max}, at the very beginning of the process, a structure S representing a solution (i.e. containing no #'s) is randomly generated and g_{max} set equal to $g(S)$. For all the computational results presented in this paper an initial population was randomly created comprising structures with exactly m (number of knapsacks) label 1's and $n/5$ label 0's with the remainder of the structure being # labels.

3. Results

In this section we outline the *CGA* performance on the *GAP*. The *CGA* was coded in *C* and run on a *SUN ULTRA SERVER 2, 200 MHz* machine.

A set of large-scale instances were solved of dimensions, $m \times n$, (5×100), (5×200), (10×100), (10×200), (20×100) and (20×200), from OR-Library [2]. These comprise 24 instances of different sizes and types. Referring to *Table 1* the problems in classes *A, B* and *C* present increasingly constrained knapsacks. Class *D* comprises more difficult correlated problems.

Table 1 presents the *CGA* results (best feasible solution found over ten replications of *CGA*) compared with the best known solutions reported in [5]. The *CGA* parameters are set to:

d = 0.15
e = 0.1 for 0 £ a £ 1
e = 0.01 for a > 1
stopping condition: maximum number of generations = 150 or the population is empty

For problems in class A the best known solutions are optimal so the algorithm was terminated when those solutions were found.

The *CGA* solutions reported in *Table 1* are very close to the best known solutions, obtained in the *GA* implementation of Chu and Beasley [5] who ran their *GA* until 500000 distinct solutions were found. It can be conjectured that the computational effort involved in our *CGA* is small compared to their *GA*. The computer times are not directly comparable as their *GA* was run on a different machine.

Table 1: Computational results

Problem	*Best known solution*	*CGA solution*	*Number of generations*	*CGA times (seconds)*
A 5´100	1698	***best***	51	253
A 5´200	3235	***best***	1	502
A 10´100	1360	***best***	87	308
A 10´200	2623	***best***	72	930
A 20´100	1158	***best***	1	350
A 20´200	2339	***best***	19	860
B 5´100	1843	***best***	150	302
B 5´200	3553	3601	150	432
B 10´100	1407	1410	150	165
B 10´200	2831	***best***	150	949
B 20´100	1166	***best***	150	474
B 20´200	2340	2347	150	683
C 5´100	1931	1941	150	195
C 5´200	3458	3460	150	405
C 10´100	1403	1423	150	203
C 10´200	2814	2815	150	498
C 20´100	1244	***best***	150	479
C 20´200	2397	***best***	150	1059
D 5´100	6373	6479	150	259
D 5´200	12796	12823	150	1253
D 10´100	6379	6390	150	497
D 10´200	12601	12634	150	1321
D 20´100	6269	6280	150	974
D 20´200	12452	12471	150	2158

best means that the CGA solution was the same as the best known solution

4. Conclusions

In this paper we have presented an application of the constructive genetic algorithm to the generalised assignment problem. Computational results were promising as compared to a previous genetic algorithm approach presented in the literature.

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