Ninjas' Revenge: the secret genetic technique

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Abstract

This is a great project and therefore it has a concise abstract.
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1. Problem statement and goals

One of the most popular problems studied in constrained combinatorial optimization is the knapsack problem. Given a finite set of objects with associated weights and values, the objective is to maximize the value of a collection formed by these items without exceeding a predefined weight limit.

The knapsack problem has diverse practical applications which makes it particularly interesting. For example, it has been applied to production and inventory management Ziegler (1982), financial models Mathur et al. (1983) and queueing operations in computer systems Gerla and Kleinrock (1977) or manufacturing Bitran and Tirupati (1989).

There are several variations to the knapsack problem. We could consider there are multiple copies of each item or take into consideration their volume in addition to their weight. However, we will focus on the simplest case, the one dimensional 0-1 knapsack problem, where the only constraint is the weight and the number of copies of each item is limited to 1.

Although the premise might look simple on the surface, this is actually an NP-hard problem. Thus, there is no known algorithm that achieves optimal solutions in polynomial time for all cases of this problem. Still, a sufficiently good solution can be found quickly by resorting to heuristics methods. The one that we will explore is an effective and commonly used metaheuristic known as genetic algorithm.

Genetic algorithms (GAs) belong to the family of techniques known as evolutionary algorithms. They draw inspiration from natural selection and genetic processes to provide solutions to complex optimization problems and model evolutionary systems.

The main process can be described as an evolutionary cycle. They first initialise a population of chromosomes, which represent candidate solutions. Some of these individuals will

be drawn from the population by means of a selection mechanism and compared according to their fitness. In the reproduction phase, the genetic material of the best individuals will be combined to form offspring. Also, some values of the offspring's chromosomes will be mutated. Finally, a replacement strategy is set to generate the next generation population. This process is repeated for a number of generations or until some convergence criterion is met.

We can describe formally the 0-1 knapsack problem as follows: given a set of n items and a *knapsack* with

$$p_j = \text{profit of item } j,$$
$$w_j = \text{weight of item } j$$
$$c = \text{capacity of the knapsack},$$

select a subset of items so as to

$$\text{maximize } z = \sum_{j=1}^{n} p_j x_j$$
$$\text{subject to } \sum_{j=1}^{n} w_j x_j < c,$$

where
$$x_j = \begin{cases} 1 & \text{if item } j \text{ is selected;} \\ 0 & \text{otherwise} \end{cases}, \qquad j \in N = \{1, ..., n\}$$

A solution to the knapsack problem can be represented as a sequence of binary values $[x_1, x_2, ..., x_n]$. We will apply GAs to eighteen different cases, each of them specified by a file containing a value for n and c in the first line and values for p_j and w_j in subsequent lines for each object x_j.

The goal of this project is to find the optimal solution to each of the eighteen knapsack problems proposed by applying GAs. To this end, we will have to choose and implement suitable mechanisms in each of the phases of the evolutionary cycle. The description of these methods, as well as the reasons for their election, are detailed in Section 3.

2. Previous work

This is a very important part, because it puts your work in context.

3. The CI methods

When applying genetic algorithms to a problem, there are several aspects to consider, each one with its own methods. In this section, we define the different methods used in our implementation for each one of these aspects.

3.1. Population initialization

For the initialization of the population, we have used a random initialization approach, which has been traditionally used in GAs for its simplicity and efficiency. However, we introduced an initialization range parameter in order to give the algorithm better chances of finding the optimal solution in case we know where this solution should be. This initialization range in conjunction with the possibility of sorting the input items by their value/weight rate can highly improve the algorithm performance.

3.2. Fitness function and selection

To be able to assess how well an individual (i.e. possible solution) fits our objective we must first define the fitness function. For our particular problem, we defined the following fitness function:

$$F(x) = \begin{cases} -\infty & if \ x \bullet w > c \\ x \bullet v & otherwise \end{cases}$$

, where x is the bitstring representing the individual, w is the list of item weights, v is the list of item values and c is the knapsack capacity.

Once we have the fitness function we are able to proceed to the selection step. We decided to implement the tournament and elitism selection methods for our algorithm. Particularly, we use a fixed value of $k = 2$ for both tournament and elitism. We decided to use tournament selection instead of other methods such as standard roulette wheel or rank selection because of its simplicity and because seems to outperform the other approaches Razali et al. (2011). On the other hand, elitism was implemented because of its usage in the tournament selection method.

3.3. Crossover and mutation

Several crossover techniques can be applied in GAs such as one-point, 2-point, multi-point (with more than two cut points) and uniform crossovers. In this work, we have implemented the one-point, 2-point and uniform crossovers. The reason behind this choice is the simplicity of these techniques and their good performance, especially the 2-point crossover Hasançebi and Erbatur (2000); DeJong and Spears (1990); Adeli and Cheng (1993).

For the mutation step, we implemented a simple bit-flip where a random number of genes between 1 and the size of the chromosome are flipped. In addition, we set the mutation probability to 0.5 since lower values made the algorithm get stuck in local minimums more frequently.

3.4. Replacement strategy

The final step of the GA is the replacement strategy used to obtain the new generation. In our case, we used elitism to replace the worst individuals of the current population. With this strategy, in some cases could happen that the old generation is entirely replaced. In addition to the elitism, we also decided to remove repeated individuals before applying

the replacement. This decision was made to ensure that the diversity of the population is maintained. Additionally, we defined an extra case that does not use elitism. This is when there is no good solution (i.e. the fitness value is $-\infty$) neither in the parents nor the offspring. In this case, we decided to obtain the new generation by selecting, randomly, half of the individuals from μ and the other half from λ.

4. Results and Discussion

Sol	#items	Best value	Best value found	Time without sort (s)	Best found	Time with sort (s)	Best found
1	4	19	19	0.0378	4/4	0.0375	4/4
2	19	12248	12248	2.445	4/4	0.430	4/4
3	30	99798	99798	34.501	0/3	24.437	2/3
4	40	99924	99924	4.382	3/3	0.674	3/3
5	45	23974	23974	117.021	1/3	2.102	3/3
6	50	142156	142156	247.373	0/3	76.890	1/3
7	50	5345	5345	73.624	3/3	18.885	3/3
8	60	99837	99837	12.803	3/3	34.425	3/3
9	100	99837	99837	94.960	0/3	109.723	1/3
10	100	1333930	1333930	321.234	0/2	23.198	2/2
11	100	10892	10892	322.240	1/2	128.105	1/2
12	200	100236	100236	49.784	2/2	24.183	2/2
13	200	1103604	1103604	632.185	0/2	512.575	1/2
14	300	1688692	1688692	417.575	0/2	196.617	1/2
15	400	3967180	3967180	216.064	0/2	258.675	1/2
16	500	54939	54939	614.917	0/2	191.009	1/2
17	1000	109899	109894				
18	10000	1099893	1099132				

Table 1: Results for each problem file.

5. Strengths and weaknesses

After seeing the results obtained from our GA implementation we have detected some strengths and weaknesses in it.

Starting with its strengths, we have seen how the algorithm can find the optimal solution in a reasonable amount of time in most cases. This is a very good result since we usually would expect to obtain sub-optimal results. Also, we noticed that the algorithm is able to find multiple optimal solutions for some of the problems. Being able to find several optimal solutions to one problem opens the possibility to introducing new factors when deciding which one best suits us. This can be considered a strength compared to the standard exhaustive search algorithm since the latter is only able to find one possible solution. Another strong point of our solution is its simplicity since it does not require complex functions or procedures to achieve good results. We consider that this makes the algorithm easy to understand and extensible to other problems that can be represented as bitstrings.

Following with its weaknesses, we have seen how the algorithm struggles when the size of the problem increases dramatically (e.g. 1000 or 10000 items). In these cases, we observed how the exhaustive search outperformed our algorithm in terms of solution quality and time complexity since it could find the optimal solution in less time. Also, for some problems, we observed how successive executions performed considerably different when looking at the execution time and the solution obtained. From this, we infer that the GA is highly dependent on the initialization of the initial population.

6. Conclusions and future work

The genetic algorithm implemented has proven to be a good heuristic for generating approximate solutions of the unidimensional 0-1 knapsack problem. The results achieved were optimal or near-optimal in the eighteen scenarios studied despite the imposition of stopping criteria.

We noted how the performance of the system improves drastically when the data is preprocessed in a suitable way. Having a good understanding of the problem representation and the internal mechanisms in a GA is essential for this preliminary step.

Another aspect that determines the performance of the system is, of course, the strategies implemented in each phase of the evolutionary cycle. We counted with several methods to choose from at each step which makes these systems very flexible and adaptable. This along with a proper selection of parameters allowed us to tailor the algorithm to the problem.

There are ways to further optimize the developed method. As we mentioned earlier, GAs are highly sensitive to the population seeding technique. The random initialization of the population can generate individuals with poor fitness, which increases the time needed to achieve optimality. Instead, we could resort to better seeding techniques such as Sorted Population Yugay et al. (2008), which creates a large initial population, sorts it in ascending order according to their fitness and chooses a percentage of individuals that have above average fitness. This and other initialization techniques like Nearest Neighbour or Gene Bank are described and compared in Hassanat et al. (2018).

As we have seen in Section 5, one of the main weaknesses of our algorithm is that its execution time increases dramatically with the problem size. One way to slightly improve this issue could be to parallelize the reproduction process. In this way, we could randomly split the population into multiple batches and then perform the reproduction step simultaneously for each batch. With this, we only would need to wait for the slowest batch to finish and then join all the resulting offspring together to perform the replacement step.

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