Solving the Knapsack Problem with a Simple Genetic Algorithm

Posted on March 12, 2017

Contributed by: Eugen Stripling, Seppe vanden Broucke, Bart Baesens

This article first appeared in Data Science Briefings, the DataMiningApps newsletter. Subscribe now for free if you want to be the first to receive our feature articles, or follow us @DataMiningApps. Do you also wish to contribute to Data Science Briefings? Shoot us an e-mail over at briefings@dataminingapps.com and let's get in touch!

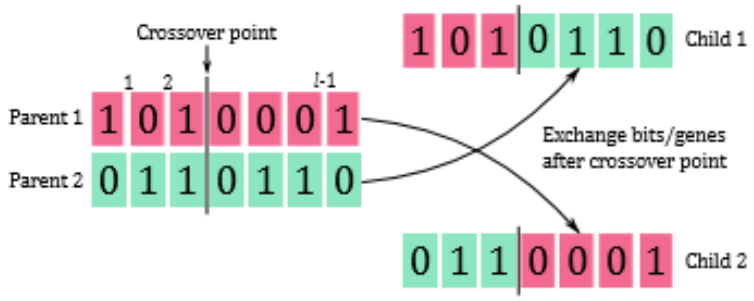
The *knapsack problem* is popular in the research field of constrained and combinatorial optimization with the aim of selecting items into the knapsack to attain maximum profit while simultaneously not exceeding the knapsack's capacity. We explain how a simple genetic algorithm (SGA) can be utilized to solve the knapsack problem and outline the similarities to the feature selection problem that frequently occurs in the context of the construction of an analytical model.

Genetic algorithms (GAs) are stochastic search algorithms that mimic the biological process of evolution enabling thereby users to solve complex optimization problems [1, 2]. They operate based on a population of chromosomes, where a chromosome represents a candidate solution. *Genetic operators* allow the population to evolve over time and to converge to the optimal solution. In the spirit of "*survival of the fittest*," GAs are naturally designed to solve maximization problems in which chromosomes with high fitness are

more likely to survive and the objective function is termed fitness function. The fitness function is a mathematical expression that evaluates the "quality" of a chromosome and steers the evolutionary search toward high fitness regions in the given search space. Note that the search space is usually a multi-dimensional space that consists of all candidate solutions. Two appealing properties of GAs are that they require no derivatives of the objective function and they are capable of performing global optimization. The former is in particular useful in situations in which, for example, no derivatives of the objective function exist and hence conventional techniques like gradient decent methods can–because of their very nature–not be applied. Given an unlimited amount of search time, GAs are able to find the *global optimum* in the search space. That is because they are less likely to get trapped in a local maximum due to their intrinsic stochastic mechanisms.

A SGA is probably the best known GA design, where chromosomes are represented as a binary string like '1010001'. The zeros and ones are the *genes* of a binary chromosome, and their meaning depends on the problem one tries to solve. To apply a SGA to a given optimization problem, an initial population of binary strings is first created in a random manner, subsequently the quality of each chromosome is evaluated using the fitness function. Based on the fitness values, a selection is done in such a way that high fitness chromosomes have a higher probability of being selected into the mating pool than low fitness chromosomes. The *mating pool* represents the foundation for breeding new candidate solutions. Chromosomes selected into the mating pools are also called parents [2].

Once the mating pool is created, a crossover is performed in order to exchange gene material between parents, which in turn creates new chromosomes, also called *offspring* or *children*. In SGAs, *single-point crossover* is a popular genetic operator that often used to perform the crossover for binary-encoded chromosomes (Figure 1). That is, with a probability pc, two parents are randomly selected from the mating pool, as well as a single *crossover point* between 1 and *l*−1 is randomly determined, where *l* is the length of the chromosome [2]. The children are then created by exchanging the genes of the parents after the crossover point.



Recent Posts

- Web Picks (week of 28 January 2025)
- Credit Limits as Risk Adjusted Customer Lifetime Value
- Hierarchical forecasting: end-to-end or post-hoc?
- Web Picks (week of 7 January 2025)
- Web Picks (week of 2 December 2024)

Archives

- February 2025
- January 2025
- November 2024
- October 2024
- September 2024
- August 2024
- July 2024
- June 2024
- June 2023
- May 2023
- March 2023
- February 2023
- January 2023
- December 2022
- November 2022
- October 2022
- September 2022
- November 2021
- July 2021
- March 2021
- February 2021
- October 2020
- August 2020
- June 2020
- May 2020
- April 2020
- March 2020

Figure 1: Single-point crossover, adapted from [2].

Next, mutation is applied to introduce a higher diversity into the population. The induced randomness of this genetic operator is useful because it helps to explore the search space and enables the SGA to escape local optima. A common operator is the *bit-flip mutation* (Figure 2). Similar to crossover, a chromosome is randomly selected with probability p_m from the processed mating pool. The selected chromosome can either be a parent or a child. Then, a gene j of the selected chromosome is randomly picked and its value is flipped over, i.e., 0 becomes 1 and 1 becomes 0 [2]. A *mutant* is then a genetically modified chromosome as a result of the mutation operator. Thus, the mating pool now consists of parents (chromosomes that have been selected but neither undergo crossover nor mutation), children (new chromosomes resulting from crossing parents), and mutants (new chromosomes resulting from mutating parents or children). In the SGA implementation that we are going to use, p_c and p_m are by default set to 0.8 and 0.1, respectively. Thus, the lion's share of the processed mating pool are likely children. In the next step, the fitness of children and mutants is evaluated.

Figure 2: Bit-flip mutation [2].

After having applied the genetic operators, the population is updated to the next generation, and the SGAs converges to the (global) maximum one generation at a time. The update is conducted as follows: the mating pool obtained in the previous step is in principle the next generation. However, often SGAs utilize a mechanism called *elitism* which ensures that a certain proportion of the fittest chromosomes of the current population survives to the next generation. In other words, chromosomes with the lowest fitness in the mating pool are substituted with the fittest chromosomes of the current population. Once having done this, the mating pool becomes the next population, and the algorithm iterates. The advantage of elitism is that it increases the selective pressure among the chromosomes that compete for survival across generations and helps to maintain a high quality fitness level in the population, as well as keeping track of the best solution obtained so far. The steps outlined above are carried out repeatedly until a predefined number of maximum generations is reached or—commonly also applied—the best fitness function value has not improved for a predetermined number of generations. If a termination criterion is met,

- February 2020
- January 2020
- December 2019
- November 2019
- October 2019
- September 2019
- August 2019
- June 2019
- May 2019
- April 2019
- March 2019
- December 2018
- November 2018
- October 2018
- September 2018
- August 2018
- July 2018
- June 2018
- May 2018
- April 2018
- March 2018
- February 2018
- January 2018
- December 2017
- November 2017
- October 2017
- September 2017
- August 2017
- July 2017
- June 2017
- May 2017
- April 2017
- March 2017
- February 2017
- January 2017
- December 2016
- November 2016
- October 2016
- September 2016
- August 2016
- July 2016
- June 2016
- May 2016
- April 2016
- March 2016
- February 2016
- January 2016
- December 2015

the SGA returns the fittest population member, which represents the final solution.

Given its zero-one encoding scheme, SGAs are naturally applicable to solve the knapsack problem. The knapsack problem aims to maximize the total profit for a selection of items, each with a profit p_i and a weight w_i, from a given item set of size n, while simultaneously preventing the violation of the constraint that the total weight of selected items exceeds the knapsack's capacity W.

Let $f(\cdot)$ represent the fitness function and $\mathbf{x} = (x_1,\ldots,x_n)$ be a binary vector, indicating selected items, i.e., $x_i = 1$ if the i^{th} item is selected into the knapsack, and $x_i = 0$ otherwise (note that this example, as well as the following mathematical formulations and code, have been adapted from [2, 3]). The knapsack problem can be formally described as follows [2]:

$$\text{maximize}\,\{f(\mathbf{x})\} = \text{maximize}\left\{\sum_{i=1}^{n} x_i p_i\right\}$$

$$\text{subject to} \quad \sum_{i=1}^{n} x_i w_i \leq W$$

$$x_i \in \{0,1\},\ i = 1,2,\ldots,n$$

where we seek to find $\mathbf{x}^* = \text{argmax}\{f(\mathbf{x})\}$ which represents the final solution, revealing which items to select for maximum profit under the capacity constraint. To illustrate the knapsack problem, we consider the data from [2, p. 271] with $n = 7$ and $W = 9$:

Item	1	2	3	4	5	6	7
p_i	6	5	8	9	6	7	3
w_i	2	3	6	7	5	9	4
$r_i = p_i/w_i$	3	1.67	1.33	1.29	1.2	.78	.75

Intuitively, it makes sense to select items with low weight and high profit for the knapsack. To facilitate the picking, we can compute the ratio r_i of profit to weight for each item. When proceeding in a greedy fashion, we first pick the item with the highest r_i, then the second highest, and so on, until the constraint is met. According to this method, the solution consists of the items {1,2,7}, yielding a total profit of $\Sigma^7_{i=1}\, x_i p_i = 14$ and a total weight of $\Sigma^7_{i=1}\, x_i w_i = 9$. Let us now consider how we can use a

- November 2015
- October 2015
- September 2015
- August 2015
- July 2015
- June 2015
- May 2015

SGA to solve this knapsack problem, by executing the following R code:

```
library(GA) # Version 3.0.1

# Define data
p <- c(6, 5, 8, 9, 6, 7, 3) # Profits
w <- c(2, 3, 6, 7, 5, 9, 4) # Weights
W <- 9 # Knapsack 's capacity
n <- length(p) # Number of items

# Define fitness function
knapsack <- function(x) {
  f <- sum(x * p)
  penalty <- sum(w) * abs(sum(x * w) - W)
  f - penalty
}

# Run SGA
SGA <- ga(type="binary",
  fitness=knapsack ,
  nBits=n,
  maxiter=100, # Maximum number of generations
  run=200,     # Stop if the best-so-far fitness
               # hasn't improved for 'run' generati
  popSize=100,
  seed=101)

x.star <- SGA@solution # Final solution: c(1, 0, 0,
sum(x.star)     # Total number of selected items: 2
sum(x.star * p) # Total profit of selected items: 1
sum(x.star * w) # Total weight of selected items: 9
```

The solution found by the SGA is $\mathbf{x}^* = (1,0,0,1,0,0,0)$, meaning that, under the knapsack's capacity constraint of $W = 9$, the optimal solution is to pick the items {1,4} which yields a total profit of $f(\mathbf{x}^*) = 15$. Thus, with the SGA solution we obtain a higher profit than with the greedy approach, although the total weight of selected items is in both cases equal to 9. The reason for the inferiority of the greedy approach is that it performs a local optimization in which the final solution depends on the choices made along the way, and thus got trapped in a local optimum. On the other hand, the SGA only evaluates the fitness of solutions once they are completely constructed. This ultimately allows the SGA to avoid getting trapped in a local optimum and, given enough search time, performs a global optimization.

In this example, we use a brute-force approach to find $\mathbf{x}^*$, and although it is sufficient for this simple example, note that the algorithmic design can further be modified to run more efficiently in finding the global solution. That is, the presented setup does not check whether a newly created solution is also feasible (i.e., not violating the capacity constraint). In order to do so, one could implement an additional mechanism that “repairs” infeasible solutions before fitness evaluation [2, 3]. However, as pointed out by Scrucca [3], the repairing step is unlikely to be computationally very efficient.

The knapsack problem might appear very theoretical, but in fact has diverse practical applications, e.g., in cargo loading, project selection, assembly line balancing, and so on [2]. This problem, however, has also striking similarities with the feature selection task in a data modeling context. That is, the knapsack problem can be parsed into a feature selection problem where the ones and zeros in $\mathbf{x}$ represent the inclusion or exclusion of a feature in the model, n is the number of features, the fitness function might consist of the model performance such as the negative Akaike information criterion (AIC) or the negative Bayesian information criterion (BIC), and the constraint on the knapsack’s capacity is—for simplicity—disabled (i.e., $W = \infty$). Note that lower values of AIC or BIC typically indicate better model performance. This is why these values would need to be multiplied with minus one in order to formulate a maximization problem. Once this has been set up, the $\mathbf{x}^*$ found by the SGA would then indicate the important features. Again, the major advantage of using SGA is that they optimize globally, revealing the optimal set of features that should be included in the analytical model to get the globally best model performance. Compare this, for example, to a stepwise regression model, which includes or excludes features at each step in a greedy fashion—similarly, as illustrated in the simple knapsack problem above. Thus, it is likely that such a greedy procedure gets trapped in a local optimum, especially if the number of features is large.

In conclusion, GAs are powerful meta-algorithms inspired by natural selection that can be used for solving complex optimization problems. Here, we only discussed the application to one instance of constrained optimization: the knapsack problem. In a simple example, we demonstrated that the SGA solution yields a higher total profit than the greedy approach, where both solutions exhibit the same total weight at the capacity limit. Last but not least, we briefly outlined how the knapsack problem can be adapted to a feature selection problem in which a SGA can be utilized to find the globally best set of features.

References

1. E. Eiben and J. E. Smith, *Introduction to Evolutionary Computing*. SpringerVerlag, 2003.
2. Yu and M. Gen, *Introduction to Evolutionary Algorithms*, ser. Decision Engineering. Springer, 2010.
3. Scrucca, “GA: A package for genetic algorithms in R,” *Journal of Statistical Software*, vol. 53, no. 4, pp. 1–37, 2013.

‹ Web Picks (week of 13 February 2017)

What is the betweenness in social network analytics and how can it be used for fraud detection? ›