Genetic Algorithm-R Package Final Report

David Chen, Qi Chen, Emily Suter and Xinyi(Cindy) Zhang

December 13, 2017

Abstract

Genetic Algorithm (GA) is a search-based optimization technique based on the principles of Genetics and Natural Selection. It is frequently used to find optimal or near-optimal solutions to difficult problems which otherwise would take a lifetime to solve. In this report, we will first introduce how we set up the genetic algorithm and the main steps. We then describe the testing procedure carried out. In section 3, we include the results from the example we have taken to apply our GA algorithm. Contributions of each team member is collected in the last part, section 4.

1 Introduction to Our Genetic Algorithm

Our package is comprised of 4 major functions: *select()*, *regress()*, *mate()*, and *evolve()*.

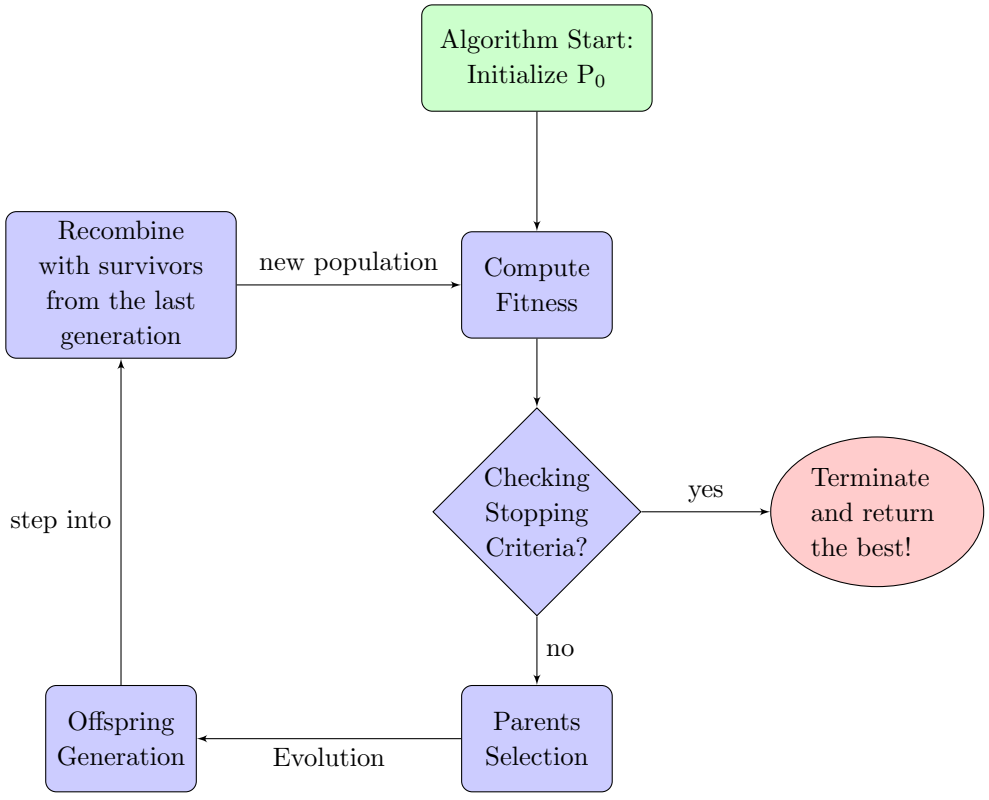
select() is the main, exported function which takes in all user arguments and wraps all other functions. *select()* also loops over generations, checks stopping criteria, and creates the output list object with 4 components: *optimum*, *fitPlot*, *fitStats*, and *GA*. *optimum* contains the names of the selected variables, the fitness value achieved, and the regression object. *fitPlot* is a ggplot of the mean, median, and maximum fitness per generation and is generated from the table in *fitStats*. *GA* contains the elite subset of genotypes and all fitness values for each generation.

regress() calculates the fitness of the regresssion model using a particular group of covariates and returns fitness metric as a single number to be maximized. In our GA implementation, *regress()* is called in an apply loop to operate over the entire genotype poulation and return a vector of fitness values.

mate() selects parents using one of 4 selection methods: tournament selection, linear ranking selection, exponential ranking selection, or roulette wheel selection. Each method is defined as a sub-function which is then called by *mate()*. The output is a genotype population of parents to be passed into *evolve()*.

evolve() performs crossing-over of genotypes and mutates single alleles by calling subfunctions *singlecrossover()*, *multiplecrossover()*, and *mutate()*. It returns a population of altered genotypes to be combined with elite survivors to produce the next generation.

To better introduce our genetic algorithm, the following Figure 1 diagrams the workflow



2 Testing

We have tested the input and output format for each individual functions in our GA algorithm. To test the function select() as a whole, we also test the following parts:

1. Ability to find max fitness using lm/glm and AIC/BIC on a manufactured dataset. Table comparing brute forced optima and optima found via select()

2. Ability to distinguish between variables via strength of correlation. The optimal set of covariates recommended by our function will likely include variables only weakly correlated and likely by chance. The user is provided with the regression model and can, by evaluating the coefficients, establish a threshold under which to exclude variables as spurious correlations.

To investigate whether our GA algorithm can attain the same optimum as global search for all possible genotypes, we create another dataset to test this. How data generated is presented as follows:

Consider number of variables $p = 5$, and we generate covariates $X = (X_1, \cdots, X_5)^{\mathrm{T}}$ from different distributions, where $X_1 \sim N(0, 25)$, $X_2 \sim \mathrm{Unif}(0, 1)$, $X_3 \sim \mathrm{Poisson}(1)$, $X_4 \sim \exp(2)$, $X_5 \sim \mathrm{Gamma}(10, 1)$. The responses Y are generated by simply averaging X_1 and X_3, i.e. $Y = \frac{X_1+X_3}{2}$. Apart from finding optimal genotype via Genetic Algorithm, we also compute all the fitness values for all 32 genotypes to see what the exact global optimum is and thus the "best" genotype. Since the reponse Y is only related to variables X_1 and X_3, we hope that both the global search approach and the GA algorithm can only select these two features but not others. Additionally, we also hope that the results returned by these two methods are consistent. Comparison results are presented below in Table 1.

Table 1: Comparison of optimal fitness values with respect to global search and GA algorithm

Table 2: Global Search

	AIC	BIC
lm	19963.50	19945.41
glm	20175.50	20160.68

Table 3: GA Algorithm

	AIC	BIC
lm	19963.50	19945.41
glm	20175.50	20160.68

One can see from the results in Table 1 that for each combination of fitted model and fitness criteria, the GA algorithm and global search method give exactly the same results. In other words, our GA algorithm does find the global maximum fitness value, i.e global minimum value for AIC or BIC.

Next, we present the genotypes returned by both global search and GA algorithm in Table 4.

Table 4: Comparison of optimal fitness values with respect to global search and GA algorithm

Table 5: Global Search

	AIC	BIC
lm	11100	10100
glm	10100	10100

Table 6: GA Algorithm

	AIC	BIC
lm	11100	10100
glm	10100	10100

In summary, our GA algorithm can find the global optima, results of which are consistent with that from global search.

3 Application

In this section, we considered two applications of our genetic algorithm, one on the dataset generated from a linear regression model, which aims to evaluate whether the designed algorithm can successfully select those important features, given known relevant variables combined with some noise terms. Another application is based on the baseball data collected from the textbook "Computational Statistics" Givens and Hoeting (2013). Details will be illustrated as follows.

3.1 Application on Data Generated from Linear Regression Model

In this section, we will first introduce how we generate the covariates and responses for evaluating our genetic algorithm on feature selection. We first generate covariates from the multivariate normal distribution $N_p(\mathbf{0}, \Sigma_x)$, where the (j, j') Σ_x satisfies

$$\Sigma_{x(j,j')} = 0.5^{|j-j'|}, \text{ for } 1 \leq j, j' \leq p.$$

Setting sample size $n = 300$ and feature dimension $p = 20$, we then fit the linear regression model

$$Y = X\beta,$$

where $\beta = (\beta_1, \cdots, \beta_6)^{\mathrm{T}}$ is generated from univariate normal distribution $N(3, 25)$. Moreover, we add some noise $\epsilon = (\epsilon_1, \cdots, \epsilon_n)$ to the covariates generated as above. ϵ_i, for $1 \leq i \leq n$, is generated from $N_{10}(\mathbf{0}, \Sigma_x)$, which has the same parameter setting as X except the dimension. We then combine X and the noise terms together. The resulting covariates matrix is given by

$$\tilde{X} = (X|\epsilon).$$

Apply our genetic algorithm to fit a linear model regressing $Y \in \mathbb{R}^n$ on $\tilde{X} \in \mathbb{R}^{n \times 30}$. Given 20 relevant covariates and 10 noise terms, the designed GA algorithm gives the following results for feature selection

$$\text{genotype} = (0, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 1, 1, 1, 1, 1, 1, 0, 1, 1, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1).$$

One can see that our GA algorithm can select most of the relevant variables, but will also include some irrelevant noise terms denoted in red.

3.2 Application on Baseball Data

We next test our genetic algorithm on a real data set to demonstrate the ability to select and optimal variable subset. A data set of baseball player statistics and salary numbers was obtained via the website for Givens and Hoeting (2013).

The data set contains 27 different statistics (such as hits and on-base percentage) for 337 players in the 1991 baseball season. Additionally, the data set contains the salaries for the same 337 players in the 1992 season. We used our genetic algorithm to select player statistic(s) that most influence that players salary in the following year.

We tested our algoritms performance on combinations of different fitness criteria (AIC, BIC) and selection method (tournament, exponential ranking, linear ranking, roulette wheel). All other input parameters were held constant at maxGen = 500, minGen = 50, population = 500, pMutate = 0.1, crossParams = c(0.8, 1), and eliteRate = 0.1. The fitness values are shown in Table 7.

Table 7: Maximum Fitness Value

Selection Method	LM, AIC	LM, BIC	GLM, AIC	GLM, BIC
Tournament	5376.012	5409.318	5375.850	5412.395
Linear	5376.354	5409.318	5375.850	5409.318
Exponential	5378.926	5414.315	5379.316	5422.321
Roulette	5376.365	5417.421	5376.353	5417.723

In this simulation, the minimum (i.e., best) fitness value was produced using GLM as the model, AIC as the fitness criteria, and tournament or linear ranking as the selection method. Generally, the difference between AIC and BIC was greater than the variance across selection methods.

The exponential ranking selection method converged the fastest, followed by tournament selection, as shown in Table 8.

Table 8: Iterations to Reach Maximum Fitness Value

Selection Method	LM, AIC	LM, BIC	GLM, AIC	GLM, BIC
Tournament	64	69	62	63
Linear	75	96	80	88
Exponential	53	52	53	53
Roulette	84	85	94	111

In general, the top genotype returned when using BIC fitness criteria had fewer variables than those using AIC. This makes sense since BIC has a greater penalty for higher numbers of variables: with AIC, the penalty is $2p$, whereas with BIC the penalty is $ln(n)p$.

The number of variables returned in the best genotype of each combination is shown in Table 9.

Table 9: Number of Variables in Best Genotype

Selection Method	LM, AIC	LM, BIC	GLM, AIC	GLM, BIC
Tournament	10	6	12	6
Linear	10	7	15	6
Exponential	11	7	16	8
Roulette	14	7	14	7

Regardless of method, model, or criteria, Strength of Schedule (*sos*), Runs Batted In (*rbis*), Free Agency (*freeagent*), and Arbitration (*arbitration*) are all included in the top genotypes. Free Agency and Arbitration had very high regression coefficients, hovering around 1300 and 850, respectively; conversely, the coefficients of RBIs and SOS were much lower, about 25 and -12. We hypothesize that this is because a player that becomes a free agent and gets signed to a new team will likely negotiate a large salary contract with their new team; players that enter free agency and don't get signed aren't included in this data set.

4 Group Member Contributions

David Chen:

Qi Chen:

Emily Suter:

Xinyi(Cindy) Zhang:

References

Anupriya Shukla, H. M. P. and Mehrotra, D. (2015). Comparative review of selection techniques in genetic algorithm .

Givens, G. H. and Hoeting, J. A. (2013). *Computational Statistics*. Wiley.