

# Stat 243 Final Project

Titouan Jehl, Junyuan Gao, Jeffrey Kwarsick, Ming Qiu

December 15, 2017

## 1 Final Project Location

Our Genetic Algorithm (GA) Package is located on Ming Qiu's github. The account name is **carslawbroccli**.

## 2 Skeleton of the Genetic Algorithm

To implement the genetic algorithm, we chose to break the algorithm into independent blocks so each of us could work separately. To realize those standalone blocks we first consider two parts that are separable the initialization and the loop. Initialisation should create the first generation from the data provided by the user and the number of individual per generation. On the other hand the loop can still be broken into subblocks. We decided to implement 5 methods:

- a 'training' method that takes as input a candidate with his information, data, a model to fit and fitness function. This method fits the model on the data with respect to the candidate genetic information. It then outputs the fitness value of this candidate. This method dealing with only one candidate as a time, it enables us to later parallelize the update of a generation by running this method on different cores.
- a 'select\_parent' method that takes as input the vector of fitness values of the candidate of the current generation as well as all the way to select the parents - with/without replacement, tournament, etc. This method selects pairs of parents with respect to the fitness values of the candidate. It returns a list of pairs of parents that will breed to create the next generation
- a 'breeding' method that takes as input the pairs of parents, and the input needed to chose the breeding technique (number of crossover points etc.). This methods create the candidates of the next generation. This method does not implement the mutation. Note that this method could have been split in a smaller block on which we could have parallelize a loop. The output of this method is the binary dataframe representing the genetic information of the next generation
- a 'mutation' method that takes as input the new generation and the rate of mutation to modify the genetic information randomly and output the new generation post mutations

- a ‘get\_model’ method that returns for a given candidate the model that has been fitted on it

Each of these methods are completely stand alone and can be tested without the rest of the method. However, provided the right comments to standardize the input and the output so assembling the blocks doesn’t raise errors, this skeleton enables the team to separately implement the algorithm efficiently

### 3 Collaborator Contributions

Below are the individual contributions made by each collaborator for this project. In addition to these contributions, we reviewed each other’s contributions and worked to streamline the code and make the overall algorithm more efficient.

#### 3.1 Titouan Jehl’s Contribution

Titouan designed the skeleton. We first discussed during a meeting the global algorithm and then we tried to design stand alone blocks. Once the standalone blocks were decided, I coded the skeleton of the ‘utils.R’ file so the whole group could be on the same page about the data type of the inputs and outputs. To do so I adopted the Google style of comment for each method. This example gives a good understanding of the information of each comment:

---

```
"""Fetches rows from a Bigtable.
```

```
Retrieves rows pertaining to the given keys from the Table instance
represented by big_table. Silly things may happen if
other_silly_variable is not None.
```

```
Args:
```

```
big_table: An open Bigtable Table instance.
```

```
keys: A sequence of strings representing the key of each table row
to fetch.
```

```
other_silly_variable: Another optional variable, that has a much
longer name than the other args, and which does nothing.
```

```
Returns:
```

```
A dict mapping keys to the corresponding table row data
fetched. Each row is represented as a tuple of strings. For
example:
```

```
{ 'Serak ': ( 'Rigel VII ', 'Preparer ' ),
  'Zim ': ( 'Irk ', 'Invader ' ),
  'Lrrr ': ( 'Omicron Persei 8 ', 'Emperor ' ) }
```

```
If a key from the keys argument is missing from the dictionary,
then that row was not found in the table.
```

*Raises :*

*IOError: An error occurred accessing the bigtable.Table object.*  
” ” ”

---

### 3.2 Jeffrey Kwarsick’s Contribution

Jeffrey Kwarsick worked on the *select\_parents()* function. Jeffrey was also responsible for building the package and making sure all of the proper documentation on each function and for running the package as a whole were present.

### 3.3 Junyuan Gao’s Contribution

Junyuan Gao worked on the formal testing for the completed algorithm, checking to ensure that proper inputs for each function in our algorithm were able to handle improper inputs. He also worked on writing the breeding function as well as the *get\_model* function

### 3.4 Ming Qiu’s Contribution

Ming Qiu worked on the *select.R* function that handles the iterations for the genetic algorithm as well as the *training* function.

## 4 Testing

We conducted testing on all of the inputs for all functions in our package and confirmed that if an invalid input was entered, that the code would properly handle the error and not execute. In addition to testing all of the outputs, all the functions were also tested independently. Below is an itemized list of how each function within our algorithm was tested.

- **training**

- The algorithm works with both *lm()* and *glm()*.

- That the algorithm works with both AIC and BIC for fitness functions.

- That the output vector of the *training* function is non-zero and correctly outputs all fitness values for candidate chromosomes.

- **select\_parents**

- The function produces correct length of parent pairs for breeding

- That each call of *select\_parents()* produces a different set of parent pairs for breeding.

- If either selection mechanism is called, the same number of parent pairs (based on the number of input parents) is the same.

- **breed**

That the output is a data frame of the correct (P x c) dimension

Everytime repeated crossover and mutation will produce different new generations

That the generation gap can only be between (0,1]

- **get\_model**

output is the same class as the training method

- **select** – integration test of the function, checking all inputs

Lastly, we conducted testing of the algorithm as a whole by generating some fake data within R and then using our package to fit the data. This is located in the *test-training.R* file.