ICS 674 Mini Project: Random Genetic String Matcher (A Slight Biological Approach)

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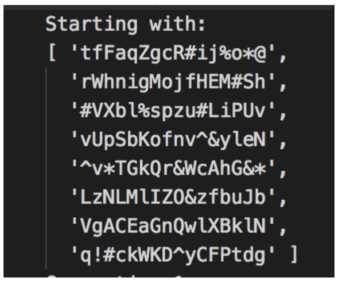
1 Introduction

As an introduction to genetic algorithms, I made basic genetic string matcher where the main idea is that given a random initial population of strings, the algorithm will generate a fixed population of random strings. The algorithm has a target string that one of the random strings must reach or else the application will not terminate, this may cause issues in performance depending on the run. The mutation function is random in the sense that there is a 50/50 chance that when the function is mutating, there is also a chance that nothing happens or a mutation does occur. The same can be said about the crossover function as well where there is a 50/50 chance a crossover may occur. The competition in the algorithm is basic in that the competition is for the population to compete with it's next nearing neighbor. The main factors that change the rate and time is the length of strings, the size of the population, and the chance for mutations and recombinations to occur.



```
Starting with:
[ 'tfFaqZgcR#ij%o*@',
  'rWhnigMojfHEM#Sh',
  '#VXbl%spzu#LiPUv',
  'vUpSbKofnv^&yleN',
  '^v*TGkQr&WcAhG&*',
  'LzNLMlIZO&zfbuJb',
  'VgACEaGnQwlXBklN',
  'q!#ckWKD^yCFPtdg' ]
```

(1.1)

The above is an example of the random strings from which my initial population came from before evolution. From these strings, I create a an N amount population that mutates into a new generation that works to get closer and closer to the target string that I set it too.

1.1 Tools Used

The tools I used for this project was Node Javascript and a node package called “geneticalgorithm” which provided a slight template for the algorithm that may be written. The developer has the following responsibilties when it comes to actual implementation of the algorithm:

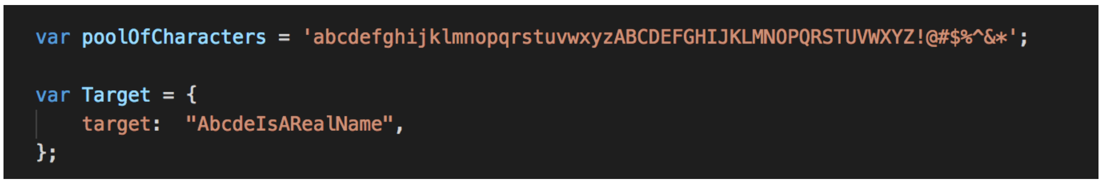
- Implementing the fitness function
- Implementing the mutation function
- Implementing the crossover function
- Implementing the phenotype(s) to evolve
- Implementing how you get the metrics for scores
- Implementing the control over the output of the algorithm
- (Optionally) Implementing a Competition Function

2 Details of Project

In this section, I will explain the details of the project such as defining the search space, objective function, variation operators, and selection function. Algorithm-wise there is alot based on randomness which determines how the generations may occur therefore no two runs of the evolution are exactly the same, however the amount of generations is roughly in the same ballpark of $+/-$ 50 generations. However adding randomness and probability into mutations and crossover chances do indeed add even more variations into the mix and the amount of generation may grow exponentially which does cause performance issues from time to time.

2.1 Search Space

The search space for the algorithm varied depending on the length of the target string that I decided I want the program to converge on. The possible pool of characters is shown below and there are a total of 60 possible characters to choose from for the string, therefore depending on the lenghth of the string, we would have search space of size $60^{targetStringLength}$.



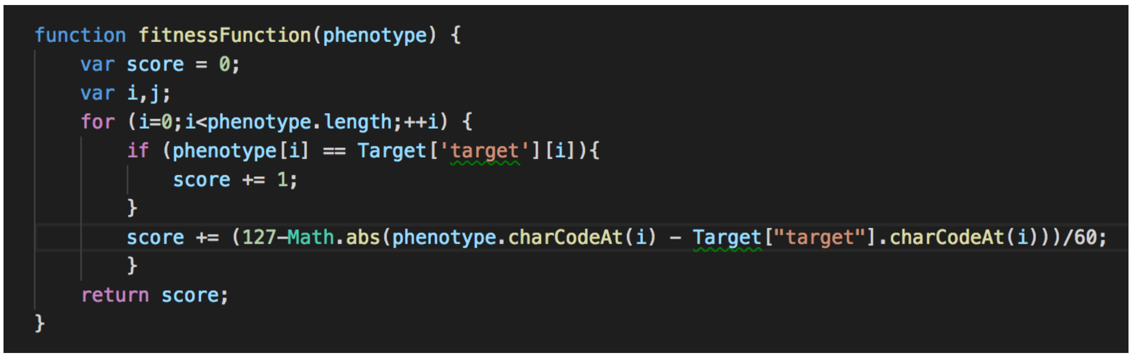
```
var poolOfCharacters = 'abcdefghijklmnopqrstuvwxyzABCDEFGHIJKLMNOPQRSTUVWXYZ!@#$%^&*';

var Target = {
    target:  "AbcdeIsARealName",
};
```

(2.1)

Based on the example above, the target string “AbcdeIsARealName” is of length 16 and therefore the search space is 60^{16} or the size of roughly 2.82×10^{28}.

2.2 Objective/Fitness Function

The Objective function is a simple function that compares the inputted string and compares character for character to the target string. The objective function then inputs a plus one score if the same index of each string is the same character. In the case the characters the two compared indexes are not the same, we use ASCII code values and increment the fitness by the code value divided by 60 to represent that the index was getting warmer and warmer to the target string.



```
function fitnessFunction(phenotype) {
    var score = 0;
    var i,j;
    for (i=0;i<phenotype.length;++i) {
        if (phenotype[i] == Target['target'][i]){
            score += 1;
        }
        score += (127-Math.abs(phenotype.charCodeAt(i) - Target["target"].charCodeAt(i)))/60;
        }
    return score;
}
```

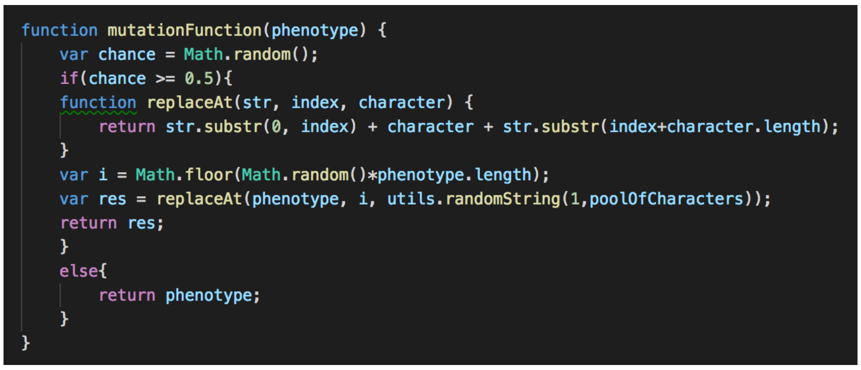
(2.2)

2.3 Variation Functions

The variation function we have are a crossover function and a mutation function. Each of them add a random chance probability that the occurance of a silent mutation and the actual may occur. This will be further elaborated on when the selection functions are explained in the next section of this paper.

2.3.1 Mutation Function

The mutation function is simple in that it will first have a 50% chance of the mutation actually surfacing, hence a possible silent mutation. When the mutation does actually occur, what it will do is replace a random character in the string with a character from the gene pool and return the mutant string. When the mutation does not occur, the function will just return initial string.

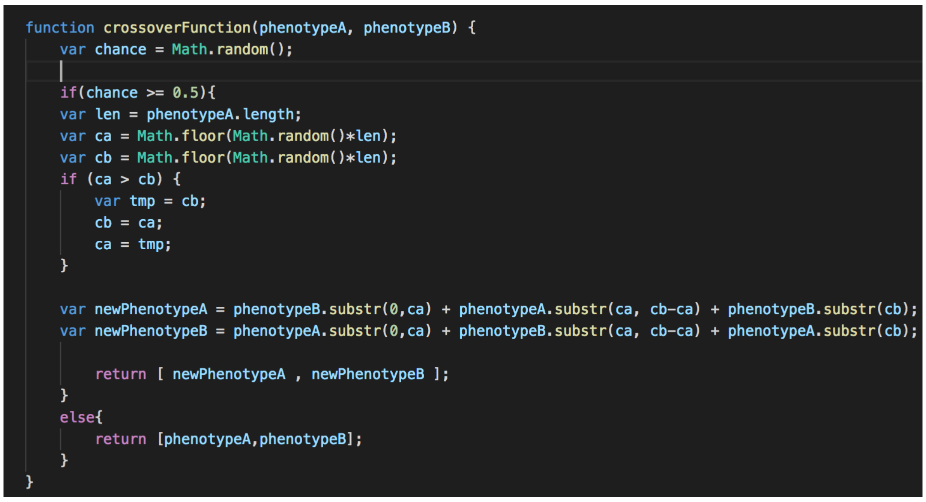


```
function mutationFunction(phenotype) {
    var chance = Math.random();
    if(chance >= 0.5){
    function replaceAt(str, index, character) {
        return str.substr(0, index) + character + str.substr(index+character.length);
    }
    var i = Math.floor(Math.random()*phenotype.length);
    var res = replaceAt(phenotype, i, utils.randomString(1,poolOfCharacters));
    return res;
    }
    else{
        return phenotype;
    }
}
```

(2.3)

2.3.2 Crossover Function

The crossover function is straightfoward with the added probability that even if there is a chance of crossover due to proximity, the crossover itself may not occur. On the chance that a crossover occur's, the function will generate two random length/index values that will serve to decide the substrings of a random length in the same indices that the function will swap to produce two new strings. This serves a mimic of two-point crossover.

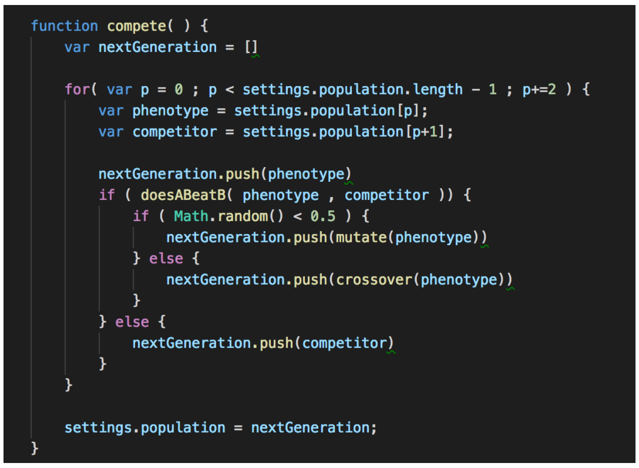


```
function crossoverFunction(phenotypeA, phenotypeB) {
    var chance = Math.random();

    if(chance >= 0.5){
    var len = phenotypeA.length;
    var ca = Math.floor(Math.random()*len);
    var cb = Math.floor(Math.random()*len);
    if (ca > cb) {
        var tmp = cb;
        cb = ca;
        ca = tmp;
    }

    var newPhenotypeA = phenotypeB.substr(0,ca) + phenotypeA.substr(ca, cb-ca) + phenotypeB.substr(cb);
    var newPhenotypeB = phenotypeA.substr(0,ca) + phenotypeB.substr(ca, cb-ca) + phenotypeA.substr(cb);

        return [ newPhenotypeA , newPhenotypeB ];
    }
    else{
        return [phenotypeA,phenotypeB];
    }
}
```

(2.4)

2.4 Selection Operator

The selection operators are straightforward competition algorithms and was done in two different manners. The underlying mechanic however is that when two neighboring strings are compared, the one with the larger fitness score is the one who wins. To explain in more detail, lets label the two competing strings as original and neighbor, if the winner is the neighbor, they will take the spot of the original in the next generation. However if the original wins, they undergo a chance for either mutation or crossover to enhance it even further in the next generation.

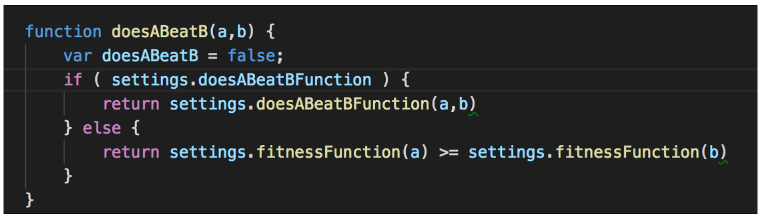


```
function compete( ) {
    var nextGeneration = []

    for( var p = 0 ; p < settings.population.length - 1 ; p+=2 ) {
        var phenotype = settings.population[p];
        var competitor = settings.population[p+1];

        nextGeneration.push(phenotype)
        if ( doesABeatB( phenotype , competitor )) {
            if ( Math.random() < 0.5 ) {
                nextGeneration.push(mutate(phenotype))
            } else {
                nextGeneration.push(crossover(phenotype))
            }
        } else {
            nextGeneration.push(competitor)
        }
    }

    settings.population = nextGeneration;
}
```

(2.5)

2.4.1 Disease and No Disease

Below we see the simple competition where we can rely on no outside factors detering the string from evolving and the only threat they have is each other. Hence we can see the underlying idea of just returning the function with the better fitness score.

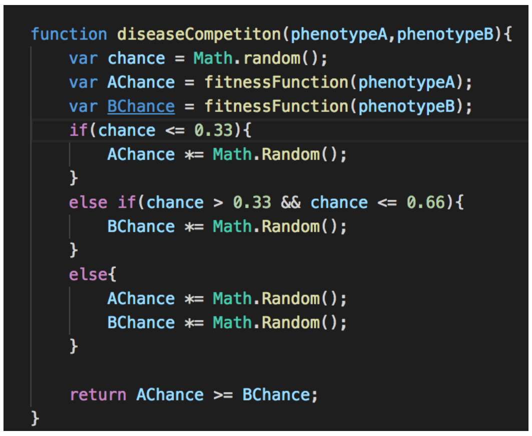


```
function doesABeatB(a,b) {
    var doesABeatB = false;
    if ( settings.doesABeatBFunction ) {
        return settings.doesABeatBFunction(a,b)
    } else {
        return settings.fitnessFunction(a) >= settings.fitnessFunction(b)
    }
}
```

(2.6)

On this end however we find that the competition method that can be used is changed in that we now have a random factor of disease can have an impact of reducing the score of the fitness of strings. From this function we can now emulate the following scenarios:

- Dominate strings have the chance of dying off and further increasing the amount of generations needed
- Weaker strings dominate stronger strings
- Both strings catch disease and only one of them survives

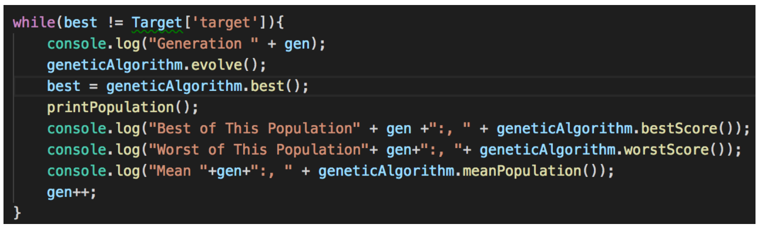


```
function diseaseCompetiton(phenotypeA,phenotypeB){
    var chance = Math.random();
    var AChance = fitnessFunction(phenotypeA);
    var BChance = fitnessFunction(phenotypeB);
    if(chance <= 0.33){
        AChance *= Math.Random();
    }
    else if(chance > 0.33 && chance <= 0.66){
        BChance *= Math.Random();
    }
    else{
        AChance *= Math.Random();
        BChance *= Math.Random();
    }

    return AChance >= BChance;
}
```

(2.7)

2.5 Termination

The termination is very straightforward in that the evolution and algorithm will keep on going until a single string of a generated population evolves into the target string.



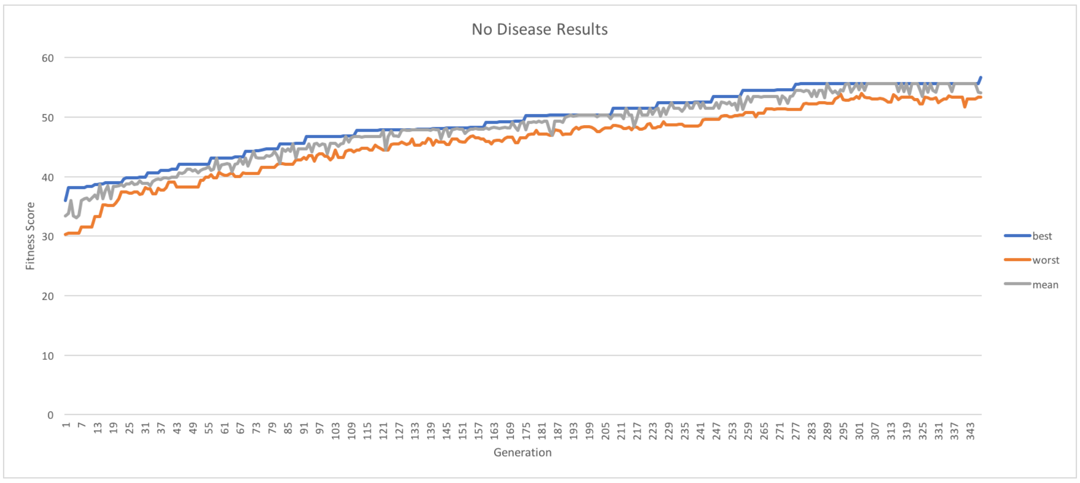
```
while(best != Target['target']){
    console.log("Generation " + gen);
    geneticAlgorithm.evolve();
    best = geneticAlgorithm.best();
    printPopulation();
    console.log("Best of This Population" + gen +":, " + geneticAlgorithm.bestScore());
    console.log("Worst of This Population"+ gen+":, "+ geneticAlgorithm.worstScore());
    console.log("Mean "+gen+":, " + geneticAlgorithm.meanPopulation());
    gen++;
}
```

(2.8)

3 Resulting Data

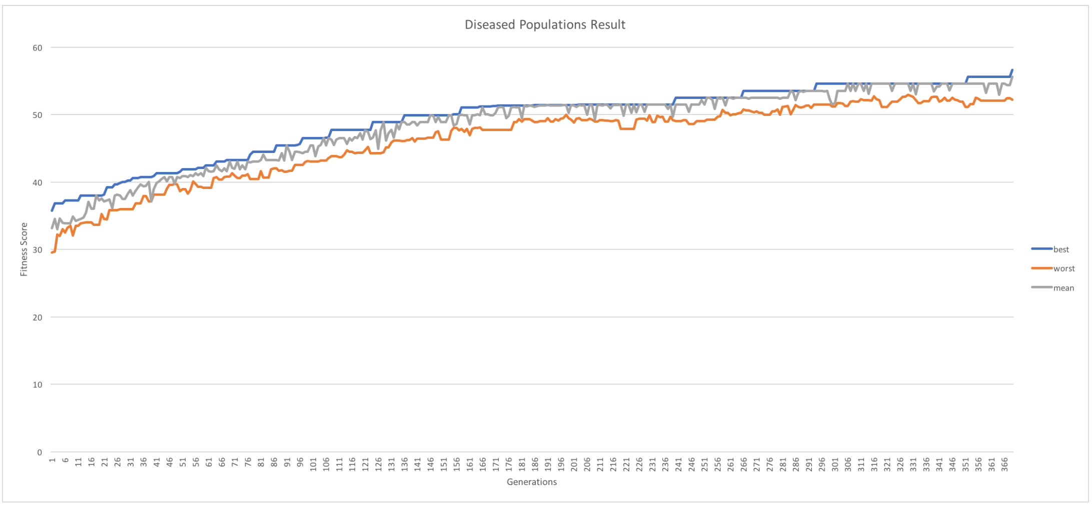
This section covers the resulting data and will cover the trajectory of populations of two instances of runs. These two differ in that the competition/selection function are marginally different in an attempt to spice up the evolution. The end result as we see below is that trajectory path wise they share similar trends, but one takes more generations to reach the target string compared to the other. The obvious behavior saying that the disease did stall the evolution more in some degree.

3.1 No Disease Data



(3.1)

3.2 Disease Data



(3.2)

4 CONCLUSION

In conclusion to the study, the idea was to see how trying to replicate basic genetics behavior and adding pools of possibilities through additional probability would have an effect on the overall growth and evolution. While there is a strong amount of randomness, it seeks to emulate from a biological standpoint what can occur when running this algorithm. So depending on the setting, throwing more and more randomness does have an obvious effect on the bounds of generation steps, but to reliably measure it is the challenging part.