# CS-415: Computational Biology: Project 1a

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#### **ACM Reference Format:**

#### 1 INTRODUCTION

Currently in class, we have developed a simple genetic algorithm framework to:

- (1) Generate individuals
- (2) Give the randomly generated individuals a genome
- (3) Measure the individuals fitness
- (4) Mutate the individuals genome
- (5) Insert individuals in populations which consist of numerous individuals.
- (6) Pick the most fit individuals from the population for reproduction

Within this report, I will propose a couple experiments that I will be performing on this genetic algorithm framework and how I will be interpreting and visualizing the data gathered.

### **2 EXPERIMENT PROPOSITIONS:**

In this report, I propose performing the following experiments on the Genetic Algorithm Framework:

- (1) I will increase the rate of mutation of individuals and see how this effects populations of various size magnitudes. For example, an individual mutation rate of 20% with varying population sizes of 50, 100, 200, 500, etc. Observe if increasing the population of individuals with a higher mutation rate would lead to a majority of mutated individuals.
- (2) The next experiment that I will perform will be changing the fitness calculation algorithm. I will construct a slightly more biologically accurate fitness algorithm that will calculate the number of triplet "T" occurrences within an individuals genome. Without replacement, so it will not count duplicate triplets. I will then see how this affects the average fitness of populations of various sizes.

## 3 PROPOSED DATA VISUALIZATION:

My proposed method of data visualization for the outcomes of these experiments is in the form of a scatter plot. I'm going to try and use either a graphing software like Desmos or a python Graphing package like matplotlib. An example of the scatterplot is listed below.

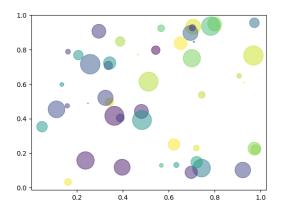


Figure 1: Example Scatter Plot Generated From Experiment Findings

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