

# Hacettepe University

BBM 203 Software Laboratory I

## **ASSIGNMENT 3**

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#### 1-Problem Definition

GA is inspired by the notion of survival of the fittest, a theory driven from biological evolution. GA makes use of a population which is composed of individuals, also called chromosome, to solve both constrained and unconstrained optimization problem. GA is an iterative algorithm and, at every step, it employs generic operators involving selection, crossover, and mutation to evolve new, hopefully better, individuals that represent the solution toward the problem at hand. The quality of each evolved chromosome is evaluated through a given fitness function.

At the end of the evolutionary process, it returns the best solution found for the problem.

#### 2-Methods and solution

**Readingfile:** I read the data in the input file with realloc. I have defined them all with a function that returns this data as char array (string).

**Instalization of Linked List:** Before creating the Linked list, I separated the data in the population string line by line. Then I turned this data into a matrix. I sent this matrix to the function with the node I named head. I created the list by connecting the head nodes.

**Selection :** I chose to run both pairs one by one in Selection.

**Crossover:** I applied the crossover command one by one for each chromosome 2 and repeated it for each line. I did down the selection index. Then I made the right crossover index by finding the nodes I found elsewhere.

I used a for loop to swap the selected indexes and crossover genes between the selected ones.

**Mutation :** Since all chromosomes are already selected in the mutation function by selection, I have reversed all the genes in the given index.

**Fitness:** I sent the head because the fitness function is a kind of binary representation. From the beginning, I collected each gene with the result returned from the power function I created.

**Best chromosome :** I kept the best chromosome in a different node. If it comes to a better chromosome, I've updated it. If not, the population continued to remain the head of the first row.

**Sorting:** I compared the sorting function according to the fitness presentation of the given nodes. I made the swap operation and renewed the linked list.

### 3-Functions implementation

```
#include <stdio.h>
#include <stdlib.h>
#include <string.h>
struct Node{
 int data;
 struct Node*right ,*down,*up;
struct Node* newNode(int d){ ...
int power(int base, int exponent) { ...
int fitnesscalculate(struct Node* head,int maxgen){ ...
void swap(struct Node *node1, struct Node *node2){ ...
void sort(struct Node **recordsHead,int maxgen){ ...
int bestchromosome(struct Node* head,int gensize){ ...
struct Node* CopyList(struct Node* head){ ...
void display(struct Node* head,int probsize,int gensize) { ...
int intswap(int *a,int *b){ ...
int xover(struct Node* head, int select1, int select2, int xover1,
                             int xover2,int popsize,int maxgen){
int runMutate(struct Node* head,int mutindex){ ...
struct Node* AddLL(int **arr, int m, int n){ ...
int** CreateLL(char * population, int gensize,int row,int column){ ...
int runcommand(struct Node* head, char *selectbyselect,
                             char *xoverline,int popsize,int maxgen){ ...
int command(struct Node* head, char * xover, char * selection,
                     char * Mutate,int probsize,int gensize,int popsize){ ...
char *readingfile(FILE *f){ ...
int main(int argc, char *argv[]){
```

#### **REFERENCES**

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