

Fall 2020: CSCI 4588/5588 Programming
Assignment #1B”.

“Name: Tharani Maaneeivaannan
ID:2575198

Solution to Genetic Algorithm

Program:

```
import os
import random
import operator
import matplotlib.pyplot as plt
from textwrap import wrap

class GeneticAlgorithm:
    def __init__(self):
        """
        1. Initialize the Population
        """
        self.newPopulationList = []

    """
    This module generates the Chromosome Orientation/structure in Random for the
    given sequence
    Input: [gene1,gene2,...,gene_N]
    Output: [(gene1, (X1, Y1)), (gene2, (X2, Y2)), ..., (gene_N, (Xn, Yn))]
    """
    def chromosomeOrientation(self,sequence):
        #Assigning the first value of binary sequence to (0,0) position initially
        currentPosition=(0,0)
        chromosome=[(sequence[0],currentPosition)]
        #Creating a dictionary to store assigned coordinates
        assignedCoordinates={currentPosition}
        for gene in sequence[1:]:
            allOptions=[]
            validOptions=[]
            # Adding the right direction option
            allOptions.append((currentPosition[0]+1,currentPosition[1]))
            # Adding the left direction option
            allOptions.append((currentPosition[0]-1,currentPosition[1]))
            # Adding the Up direction option
            allOptions.append((currentPosition[0],currentPosition[1]+1))
            # Adding the Down direction option
            allOptions.append((currentPosition[0],currentPosition[1]-1))

            # filtering valid options from allOptions
            for axis in allOptions:
                if axis not in assignedCoordinates:
                    validOptions.append(axis)
```

```

        # Select one Valid position in random and assign the gene as it's position and move forward with the orientation
        forwardPosition = random.choice(validOptions)
        chromosome.append((gene, forwardPosition))
        assignedCoordinates.add(forwardPosition)
        currentPosition = forwardPosition
    return chromosome
"""
Given a chromosome this function calculates and returns the fitness value
"""
def calculateFitness(self, chromosome):
    chromosome_dict={}
    fitness=0
    for indexposition, chromosomedata in enumerate(chromosome):
        chromosome_dict[chromosomedata[1]]=(indexposition, chromosomedata[0])

    for key, _ in chromosome_dict.items():
        #get the fitness value if there is a topological neighbour in right
        fitness = fitness + self.individualFitness(key, (key[0]+1, key[1]), chromosome_dict)
        #get the fitness value if there is a topological neighbour in left
        fitness = fitness + self.individualFitness(key, (key[0]-1, key[1]), chromosome_dict)
        #get the fitness value if there is a topological neighbour in up
        fitness = fitness + self.individualFitness(key, (key[0], key[1]+1), chromosome_dict)
        #get the fitness value if there is a topological neighbour in down
        fitness = fitness + self.individualFitness(key, (key[0], key[1]-1), chromosome_dict)
    return fitness
"""
This function returns the individual fitness at a selected axis by comparing the topological neighbours
"""
def individualFitness(self, baseAxis, neighbourAxis, chromosome_dict):
    #if the neighbouraxis is part of the chromosome orientation
    if neighbourAxis in chromosome_dict:
        baseGene=chromosome_dict[baseAxis]
        # print(baseGene)
        neighbourGene=chromosome_dict[neighbourAxis]
        # print(neighbourGene)
        # checking the topological neighbours in ascending order and eliminating the covalent bonded neighbours
        if (baseGene[0]<neighbourGene[0]) and (abs(baseGene[0]-neighbourGene[0])>1):

```

```

        if baseGene[1]=='h' and neighbourGene[1]=='h':
            return 1
    return 0

def rouletteWheelSelection(self,population):
    max=0
    current=0
    for i in population:
        max+=i[1]
    selection=random.randint(0,max)
    for i in population:
        current+=i[1]
        if current>selection:
            return i[0]

def crossover(self,selectedChromosomes,crossoverPosition):
    chromosome1 = selectedChromosomes[0]
    chromosome2 = selectedChromosomes[1]
    # print(chromosome1,chromosome2,crossoverPosition)
    partOfChromosome1=chromosome1[:crossoverPosition+1]
    partOfChromosome2=chromosome2[crossoverPosition+1:]
    partOfChromosome1Axes={i[1] for i in partOfChromosome1}

    #Detecting Previous Direction
    prevDir = None

    Ax = [0,0,0]
    Ay = [0,0,0]

    if chromosome1[crossoverPosition][1][1]==chromosome1[crossoverPosition-1][1][1]:
        if (chromosome1[crossoverPosition-1][1][0] - chromosome1[crossoverPosition][1][0]) == 1:
            prevDir = 'RIGHT'
        else:
            prevDir = 'LEFT'
    else:
        if (chromosome1[crossoverPosition-1][1][1] - chromosome1[crossoverPosition][1][1]) == 1:
            prevDir = 'UP'
        else:
            prevDir = 'DOWN'

    if prevDir == 'RIGHT':
        Ax = [-1,0,0]

```

```

        Ay = [0,1,-1]

    elif prevDir == 'LEFT':
        Ax = [1,0,0]
        Ay = [0,1,-1]

    elif prevDir == 'UP':
        Ax = [1,-1,0]
        Ay = [0,0,-1]
    elif prevDir == 'DOWN':
        Ax = [1,-1,0]
        Ay = [0,0,1]

    # performing three crossovers based on the direction of the first chromosome
    for itr in range(3):
        crossoverList = partOfChromosome2
        crossover_Xdir = chromosome1[crossoverPosition][1][0]+Ax[itr] - chromosome2[crossoverPosition+1][1][0]
        crossover_Ydir = chromosome1[crossoverPosition][1][1]+Ay[itr] - chromosome2[crossoverPosition+1][1][1]

        crossoverList[0] = (crossoverList[0][0],(chromosome1[crossoverPosition][1][0]+Ax[itr],chromosome1[crossoverPosition][1][1]+Ay[itr]))

        for j in range(len(crossoverList)-1):
            crossoverList[j+1] = (chromosome2[crossoverPosition+j+2][0],(chromosome2[crossoverPosition+j+2][1][0]+ crossover_Xdir ,chromosome2[crossoverPosition+j+2][1][1]+ crossover_Ydir))

        crossover_Axes = {a[1] for a in crossoverList}

        if not self.collision(partOfChromosome1Axes,crossover_Axes):
            return partOfChromosome1 + crossoverList

    elif itr == 2:
        return None

def collision(self,axes1,axes2):
    for axis in axes2:
        if axis in axes1:
            return True
    return False

def mutate(self,chromosome):

```

```

    # print(chromosome)
    # Selecting the random index by omitting 1st and last positions.
    # This index will be used for mutation
    randomIndexInChromosome = random.randint(1,len(chromosome)-2)
    # print(randomIndexInChromosome)

    selectedGeneAxis = chromosome[randomIndexInChromosome][1]

    # First Part will remain constant
    firstPart = chromosome[:randomIndexInChromosome+1]
    possibleCollisionAxes = {i[1] for i in firstPart}

    #Second part will be rotated and joined
    secondPart = chromosome[randomIndexInChromosome+1:]

    #90 Degree Rotation
    rotated=[(value,(axis[1]+selectedGeneAxis[0]-
selectedGeneAxis[1],selectedGeneAxis[0]+selectedGeneAxis[1]-
axis[0])) for value,axis in secondPart]
    rotatedAxes={i[1] for i in rotated}
    if (not(self.collision(possibleCollisionAxes,rotatedAxes))):
        # print("90 Rotated")
        return firstPart+rotated

    #180 Degree Rotation
    rotated=[(value,(2*selectedGeneAxis[0]-axis[0],2*selectedGeneAxis[1]-
axis[1])) for value,axis in secondPart]
    rotatedAxes={i[1] for i in rotated}
    if (not(self.collision(possibleCollisionAxes,rotatedAxes))):
        # print("180 rotated")
        return firstPart+rotated

    #270 Degree Rotation
    rotated=[(value,(selectedGeneAxis[0]+selectedGeneAxis[1]-
axis[1],axis[0]+selectedGeneAxis[1]-
selectedGeneAxis[0])) for value,axis in secondPart]
    rotatedAxes={i[1] for i in rotated}
    if (not(self.collision(possibleCollisionAxes,rotatedAxes))):
        # print("270 Rotated")
        return firstPart+rotated

    # If all rotations failed
    return None

def plotFigure(self,chromosome,filename,sequence,bestfitness,maxFitness):

```

```

x = [x[1][0] for x in chromosome]
y = [y[1][1] for y in chromosome]
x0 = [x[1][0] for x in chromosome if x[0]=='h' ]
x1 = [x[1][0] for x in chromosome if x[0]=='p' ]
y0 = [y[1][1] for y in chromosome if y[0]=='h' ]
y1 = [y[1][1] for y in chromosome if y[0]=='p' ]
plt.figure(figsize=(10,8))
plt.title("\n".join(wrap("Sequence: '%s', Best Fitness: %d, Max_Fitness:
%d"%(sequence,bestfitness,maxFitness))))
plt.plot(x,y,linewidth=3.0)
hmarker = dict(color='0',marker='o',markersize=10,linewidth=0,label='h')
plt.plot(x0,y0,**hmarker)
pmarker = dict(color='0',marker='o',markersize=10,fillstyle='none',linewi
dth=0,label='p')
plt.plot(x1,y1,**pmarker)
plt.grid(True)
# plt.show()
plt.legend(loc="best")
plt.savefig('figure-%s'%(str(filename)))
plt.close()

def GA_Main(self,proteinList,sIdx):
    sequence=proteinList[0]
    maxFitness=proteinList[1]
    # print(sequence)
    # print(fitness)
    chromosomeList = []
    populationList = []
    elitePopulation = []
    crossoverPopulation = []
    randomPopulation = []
    topFitnessList = []

    generation = 0
    # binarySequence=self.getBinarySequence(sequence)

    while (len(chromosomeList)<300):
        try:
            chromosomeList.append(self.chromosomeOrientation(list(sequence)))
            # When there is situation of collision while forming chromosome randoml
            # mly, IndexError occurs
            # I catch the exception and drop that structure
        except IndexError:
            # print("No Valid Options to select")
            continue

```

```

    """
    2. Compute Fitness of Population for all Chromosome Ci
    """
    for chromosome in chromosomelist:
        populationList.append((chromosome, self.calculateFitness(chromosome)))
)

    # print(self.populationList[0],len(self.populationList))
    """
    3. Sort the Population in descending order based on their fitness
    """
    populationListSorted = sorted(populationList,key=operator.itemgetter(1),reverse=True)
    # print(*populationListSorted,sep='\n')
    #currentGenerationPopulation =
    """
    4. Examine: C1/Progress or Max_gen, Exit Condition
    """
    while generation < 80000:
        print("Generation Number %d"%(generation))
        if generation > 0:
            currentGenerationPopulationSorted = sorted(self.newPopulationList,
key=operator.itemgetter(1),reverse=True)
            self.newPopulationList = []
        else:
            currentGenerationPopulationSorted = populationListSorted

        topFitness = currentGenerationPopulationSorted[0][1]
        topFitnessList.append(topFitness)
        print("Top_Fitness: %d"%(topFitness))
        """
        Breaking conditions defined below
        """
        # break if the program reached 80000 generations
        if generation>80000:
            break
        # break the program if the maximum fitness is attained
        if topFitness == maxFitness:
            self.plotFigure(currentGenerationPopulationSorted[0][0],sIdx,sequence,topFitness,maxFitness)
            break
        # break the program if there is no progress in the fitness value after 100 iterations,
        # if the last 30 top fitness is same exit the program
        if len(topFitnessList)>100:
            if len(set(topFitnessList[-30:]))==1:

```



```

        print("No Progress - So Breaking")
        self.plotFigure(currentGenerationPopulationSorted[0][0],sIdx,
sequence,topFitness,maxFitness)
        break

    """
    5. Taken 5% of Elite and form a New Population
    """

    elitePopulation = currentGenerationPopulationSorted[:15]
    self.newPopulationList = self.newPopulationList + elitePopulation
    # print("After Elite : %d"%(len(self.newPopulationList)))
    """

    6. 80% crossover chromosomes and fill the New Population
    """

    beforeCrossoverPopulation = currentGenerationPopulationSorted[15:255]
    crossoverResultList = []
    while (len(crossoverResultList)<240):
        try:
            selectedChromosomes=[]
            for _ in range(2):
                selectedChromosomes.append(self.rouletteWheelSelection(beforeCrossoverPopulation))
                crossoverResult=self.crossover(selectedChromosomes,random.randint(2,len(selectedChromosomes[0])-2))
                if not (crossoverResult==None):
                    crossoverResultList.append(crossoverResult)
            except:
                # print(e)
                continue

        for xover in crossoverResultList:
            crossoverPopulation.append((xover,self.calculateFitness(xover)))
        # print(crossoverPopulation)
        crossoverPopulationSorted = sorted(crossoverPopulation,key=operator.itemgetter(1),reverse=True)
        # print(self.crossoverPopulation)
        self.newPopulationList = self.newPopulationList + crossoverPopulationSorted

        # print("After Crossover : %d"%(len(self.newPopulationList)))
    """

    7. Fillup Pop2 randomly
    """

    randomPopulation = []
    forRandomPopulation = crossoverPopulationSorted + currentGenerationPopulationSorted[255:]

```

```

        for _ in range(30):
            selectedIndex = random.randint(0,len(forRandomPopulation)-1)
            randomPopulation.append(forRandomPopulation[selectedIndex])
        self.newPopulationList = self.newPopulationList + randomPopulation
        # print("After Random : %d"%(len(self.newPopulationList)))
        """

    8. Mutate the 5% of the Non elite chromosome in the
    population1 and fill it in Pop2
    """

    mutationPopulation = []
    while len(mutationPopulation)<15:
        selectedChromosomeIndex = random.randint(15,len(currentGeneration
PopulationSorted)-1)
        selectedChromosometoMutate = currentGenerationPopulationSorted[se
lectedChromosomeIndex]
        # print(selectedPopulationForMutation[selectedChromosomeIndex])
        mutationResult = self.mutate(selectedChromosometoMutate[0])
        # print(mutationResult)
        if not (mutationResult == None):
            mutationPopulation.append((mutationResult,self.calculateFitne
ss(mutationResult)))

    self.newPopulationList = self.newPopulationList + mutationPopulation
    # print("After Mutation : %d"%(len(self.newPopulationList)))
    """

    9.Increase Generation and Goto Step2
    """

    # self.newPopulationList = elitePopulation + randomPopulation
    # print(currentGenerationPopulation[:30],sep='\n')
    # print(len(self.newPopulationList))
    elitePopulation = []
    crossoverPopulation = []
    randomPopulation = []
    generation += 1

def main():
    with open("Input.txt") as f:
        content = f.readlines()
    seqValues = []
    fitnessValues = []
    contents = [x.strip() for x in content]
    for line in contents:
        if len(line)>0:

```

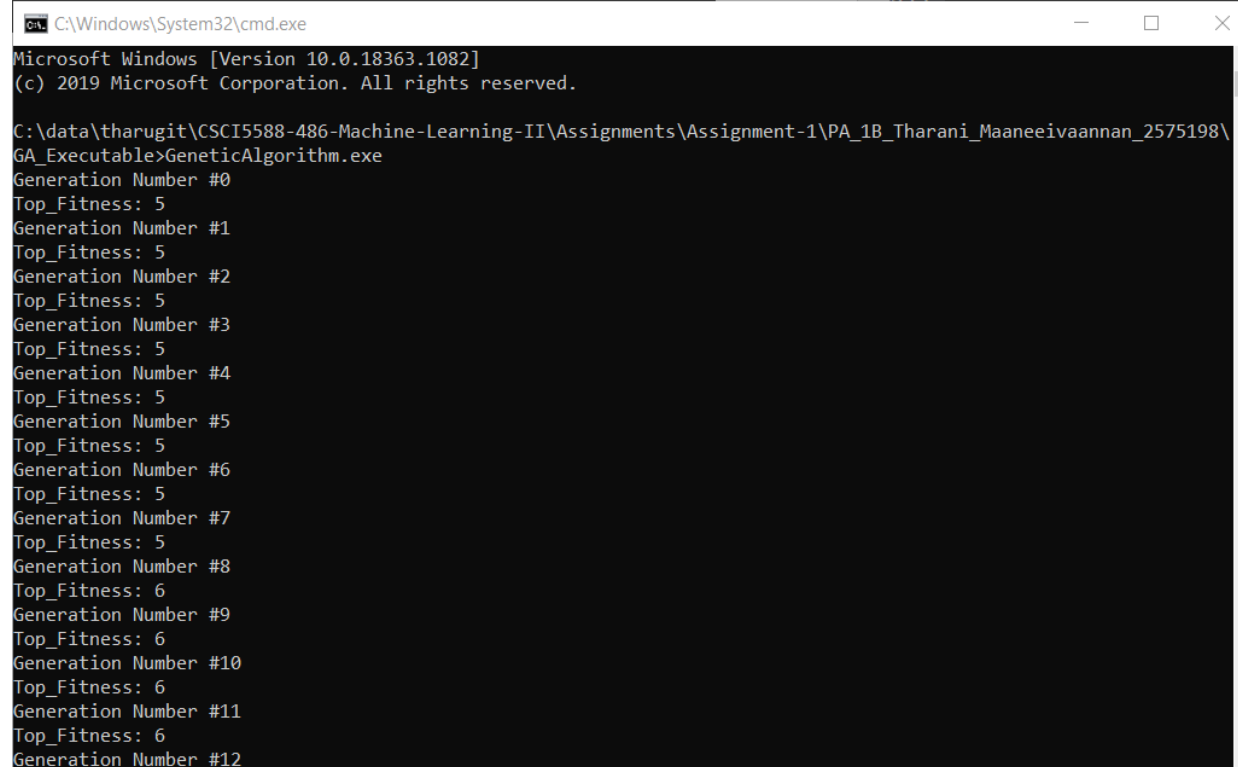
```

        if "Comment" in line:
            continue
        if "Seq" in line:
            seqValues.append(line.replace("Seq = ", ""))
        if "Fitness =" in line:
            fitnessValues.append(abs(int(line.replace("Fitness = ", ""))))
    proteinList = list(zip(seqValues,fitnessValues))
    for idx,value in enumerate(proteinList):
        GeneticAlgorithm().GA_Main(value,idx)

if __name__ == '__main__':
    main()

```

Output:



```

C:\Windows\System32\cmd.exe
Microsoft Windows [Version 10.0.18363.1082]
(c) 2019 Microsoft Corporation. All rights reserved.

C:\data\tharugit\CSCI5588-486-Machine-Learning-II\Assignments\Assignment-1\PA_1B_Tharani_Maaneivaannan_2575198\
GA_Executable>GeneticAlgorithm.exe
Generation Number #0
Top_Fitness: 5
Generation Number #1
Top_Fitness: 5
Generation Number #2
Top_Fitness: 5
Generation Number #3
Top_Fitness: 5
Generation Number #4
Top_Fitness: 5
Generation Number #5
Top_Fitness: 5
Generation Number #6
Top_Fitness: 5
Generation Number #7
Top_Fitness: 5
Generation Number #8
Top_Fitness: 6
Generation Number #9
Top_Fitness: 6
Generation Number #10
Top_Fitness: 6
Generation Number #11
Top_Fitness: 6
Generation Number #12

```

PA_1B_Th... > GA_Executable		Search GA_Executable		
Name	Date	Type	Size	Tags
lib	9/19/2020 1:04 AM	File folder		
figure-0.png	9/19/2020 1:13 AM	PNG File	30 KB	
figure-1.png	9/19/2020 1:13 AM	PNG File	37 KB	
figure-2.png	9/19/2020 1:13 AM	PNG File	36 KB	
figure-3.png	9/19/2020 1:13 AM	PNG File	36 KB	
figure-4.png	9/19/2020 1:13 AM	PNG File	32 KB	
figure-5.png	9/19/2020 1:13 AM	PNG File	28 KB	
figure-6.png	9/19/2020 1:13 AM	PNG File	32 KB	
figure-7.png	9/19/2020 1:14 AM	PNG File	30 KB	
figure-8.png	9/19/2020 1:14 AM	PNG File	29 KB	
figure-9.png	9/19/2020 1:14 AM	PNG File	35 KB	
figure-10.png	9/19/2020 1:14 AM	PNG File	29 KB	
figure-11.png	9/19/2020 1:14 AM	PNG File	37 KB	
figure-12.png	9/19/2020 1:14 AM	PNG File	31 KB	
figure-13.png	9/19/2020 1:14 AM	PNG File	37 KB	
GeneticAlgorithm.e...	9/8/2020 11:29 PM	Application	16 KB	
Input.txt	9/19/2020 12:53 AM	Text Document	1 KB	
python37.dll	12/23/2018 9:21 PM	Application extens...	3,554 KB	

Protein sequence figures will be generated in the same folder