EE449

Homework 2 – Evolutionary Algorithms

Due: 23:55, 22/05/2022

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Sec1

Table of Contents

1. Experimental Results

1.1 Number of Individuals

After first 1000th generation, results are:

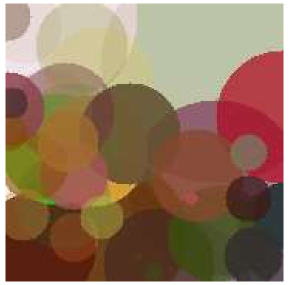


Figure 1: Result at 1000th generation (# of individuals = 5)

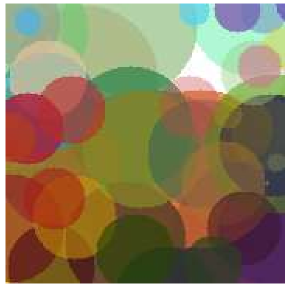


Figure 2: Result at 1000th generation (# of individuals = 10)

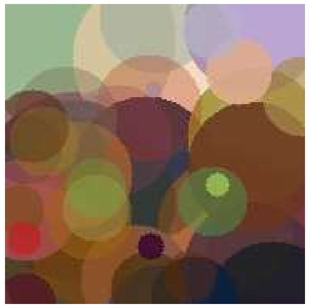


Figure 3: Result at 1000th generation (# of individuals = 20)

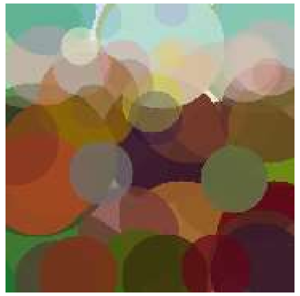


Figure 4: Result at 1000th generation (# of individuals = 50)

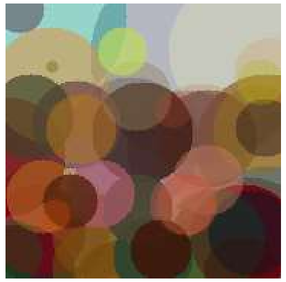


Figure 5: Result at 1000th generation (# of individuals = 75)

In figures below, as you can go from left upper corner to right bottom corner, number of generations is increased by 1000.

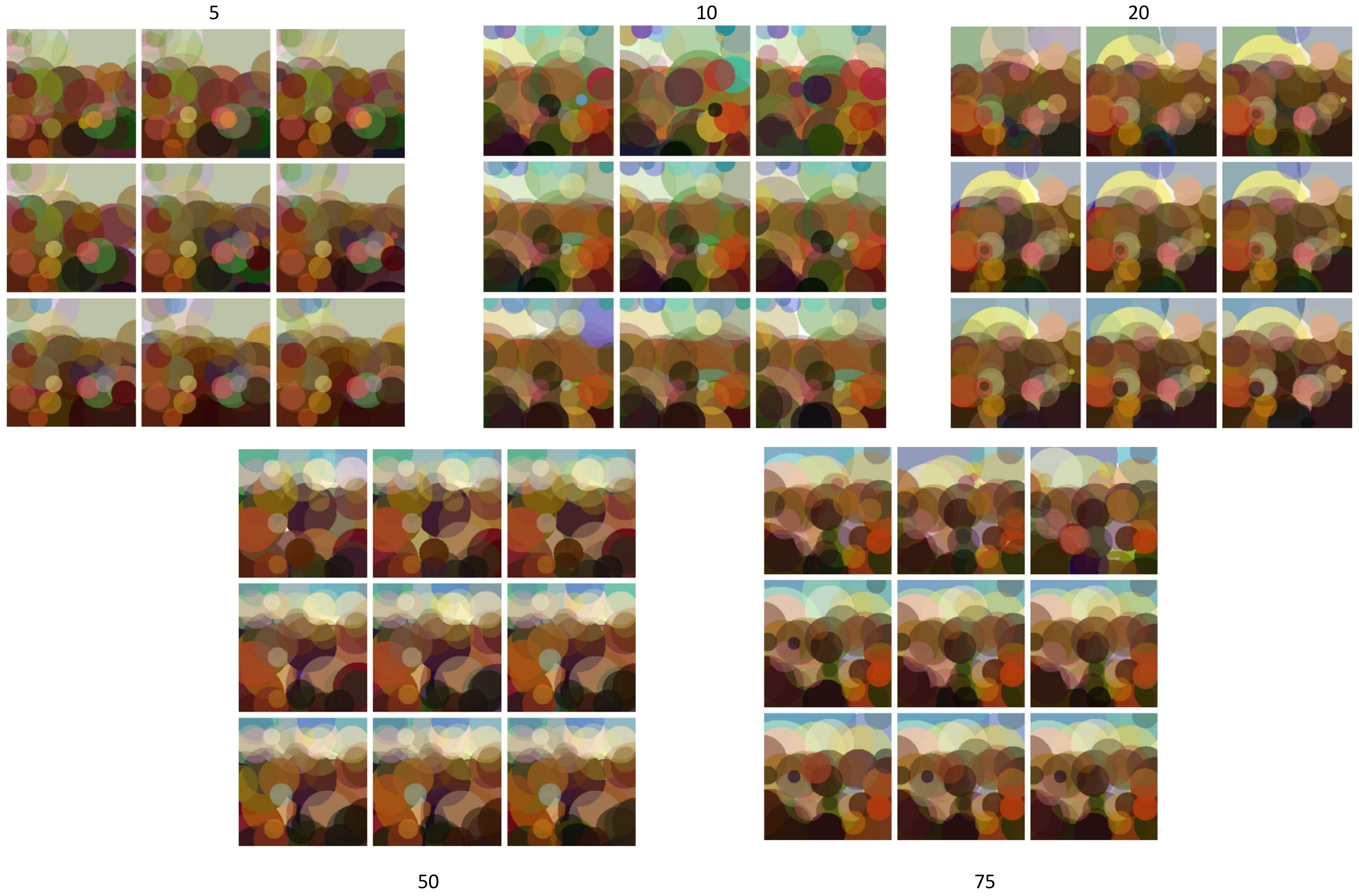


Figure 6: Result at each 1000th generation with having different individual numbers

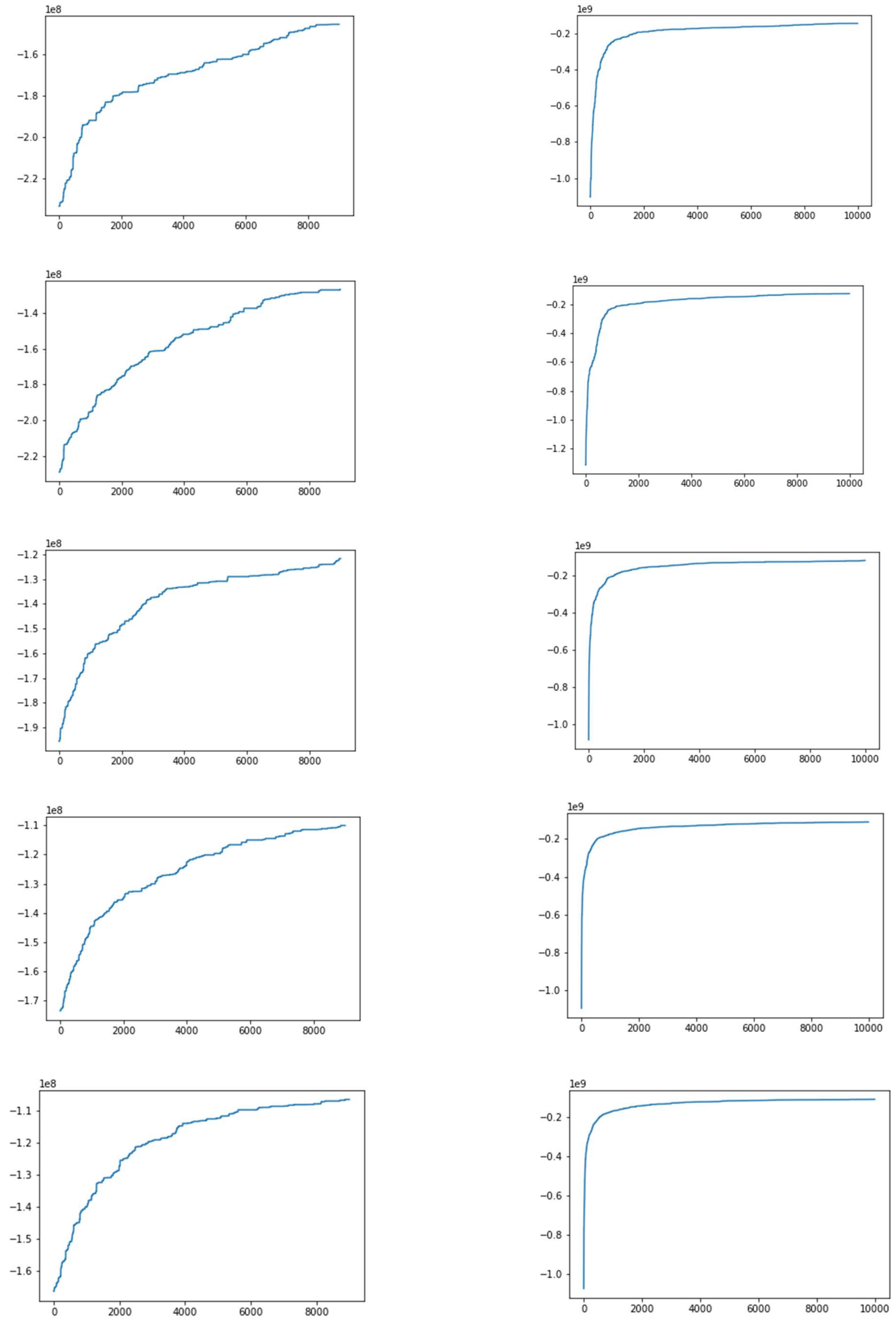


Figure 7: Fitness Values at each iteration taken for different number of individuals (left = 1000-10000, right=1-10000)

(Since there is a default case, I used same results for that case (num_of_indv=20))

(from upper to bottom, it is in descending order)

1.2 Number of Genes

After first 1000th generation, results are:

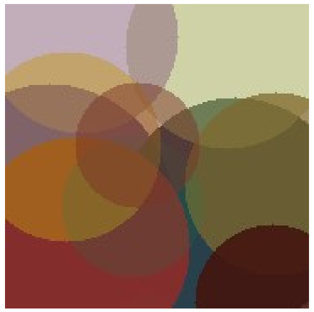


Figure 8: Result at 1000th generation (# of genes = 10)

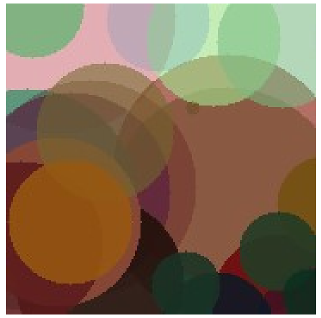


Figure 9: Result at 1000th generation (# of genes = 25)

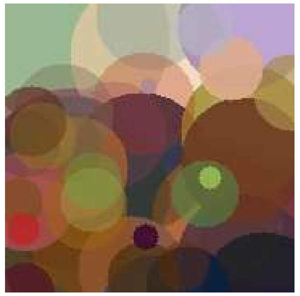


Figure 10: Result at 1000th generation (# of genes = 50)

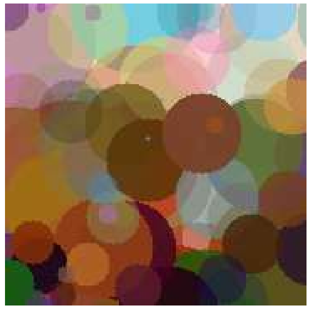


Figure 11: Result at 1000th generation (# of genes = 100)

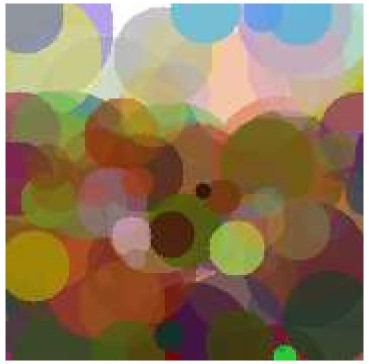


Figure 12: Result at 1000th generation (# of genes = 150)

In figures below, as you can go from left upper corner to right bottom corner, number of generations is increased by 1000.

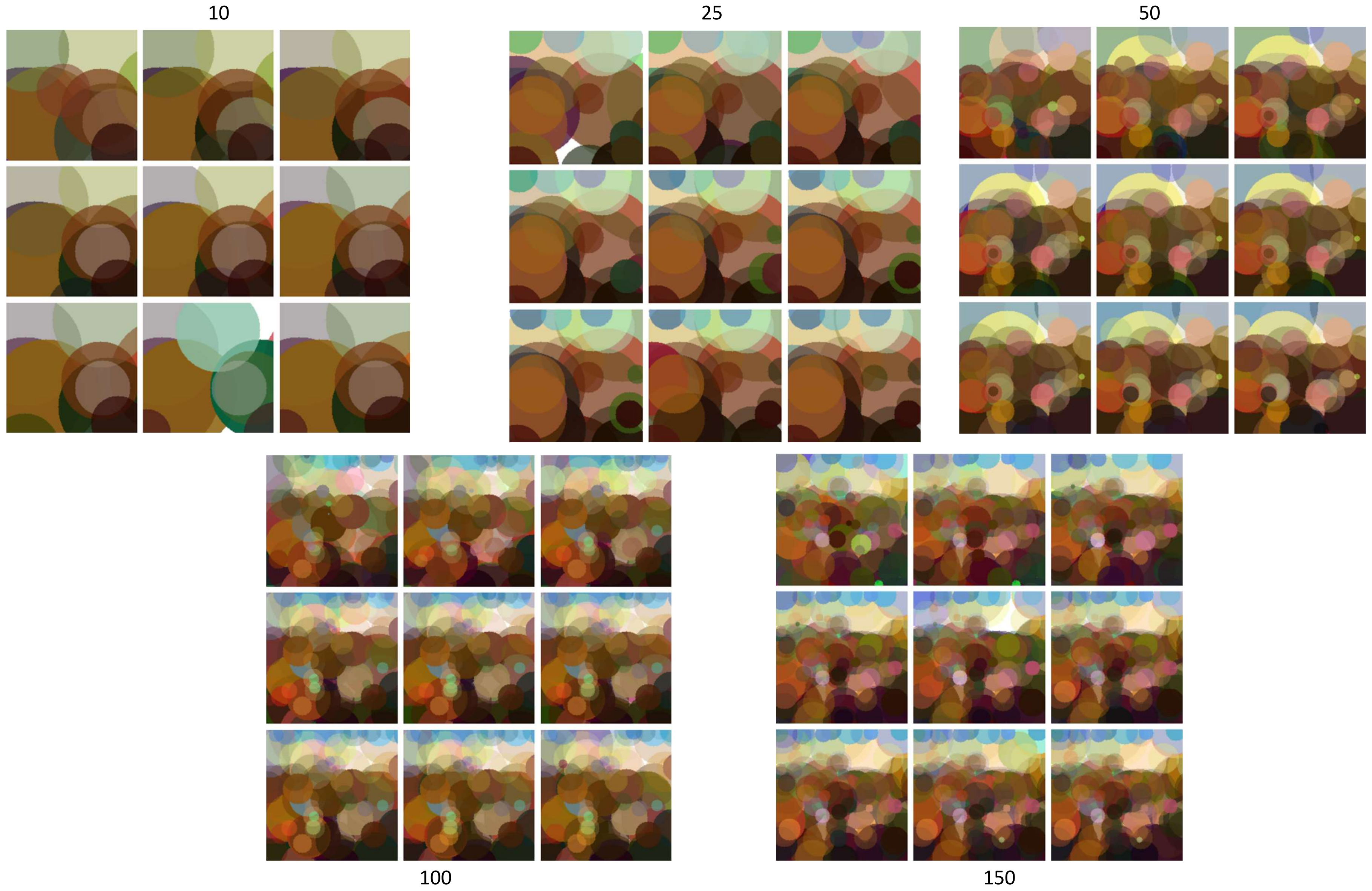


Figure 13: Result at each 1000th generation with having different number of genes

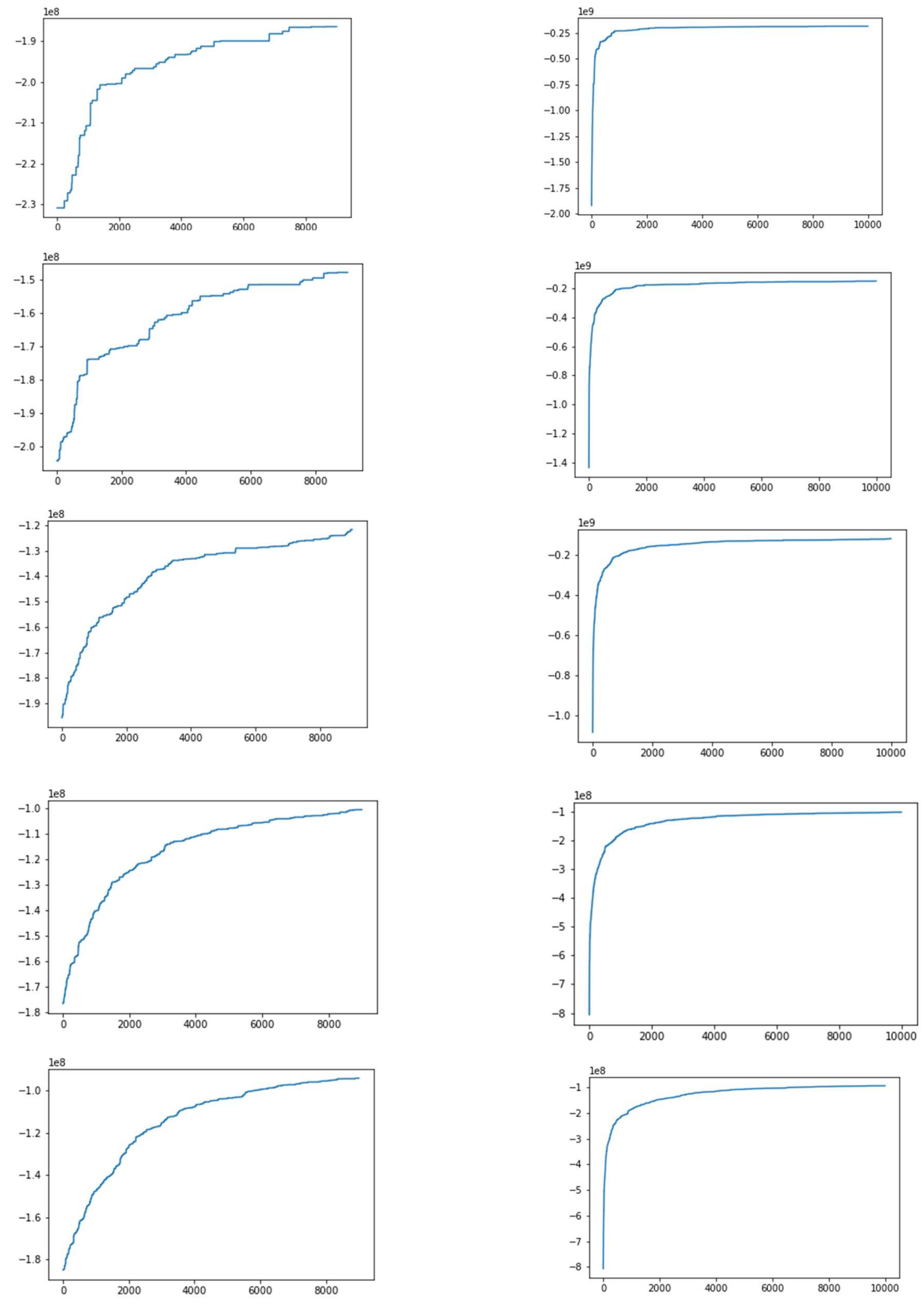


Figure 14: Fitness Values at each iteration taken for different number of genes (left = 1000-10000, right=1-10000)

(Since there is a default case, I used same results for that case (num_of_genes=50),from upper to bottom it is in descending order of the parameter)

1.3 Tournament Size

After first 1000th generation, results are:

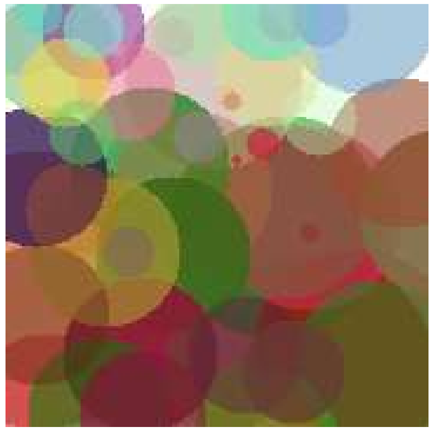


Figure 15: Result at 1000th generation (size of tournament= 2)

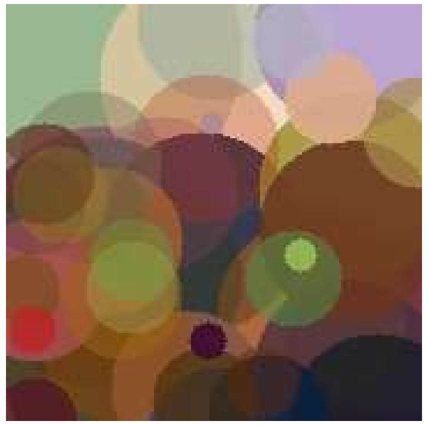


Figure 16: Result at 1000th generation (size of tournament = 5)

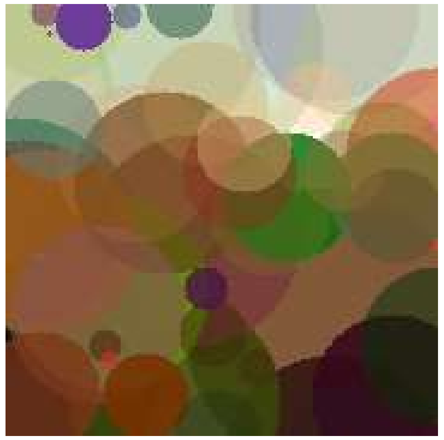


Figure 17: Result at 1000th generation (size of tournament =10)

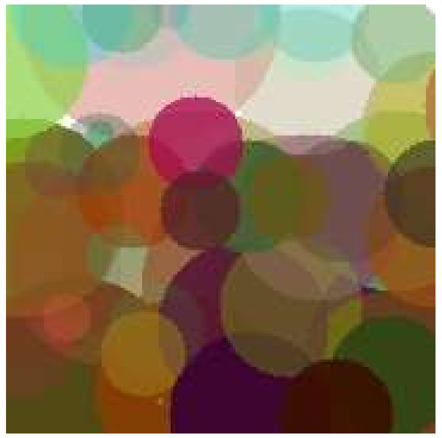


Figure 18: Result at 1000th generation (size of tournament = 20)

In figures below, as you can go from left upper corner to right bottom corner, number of generations is increased by 1000.

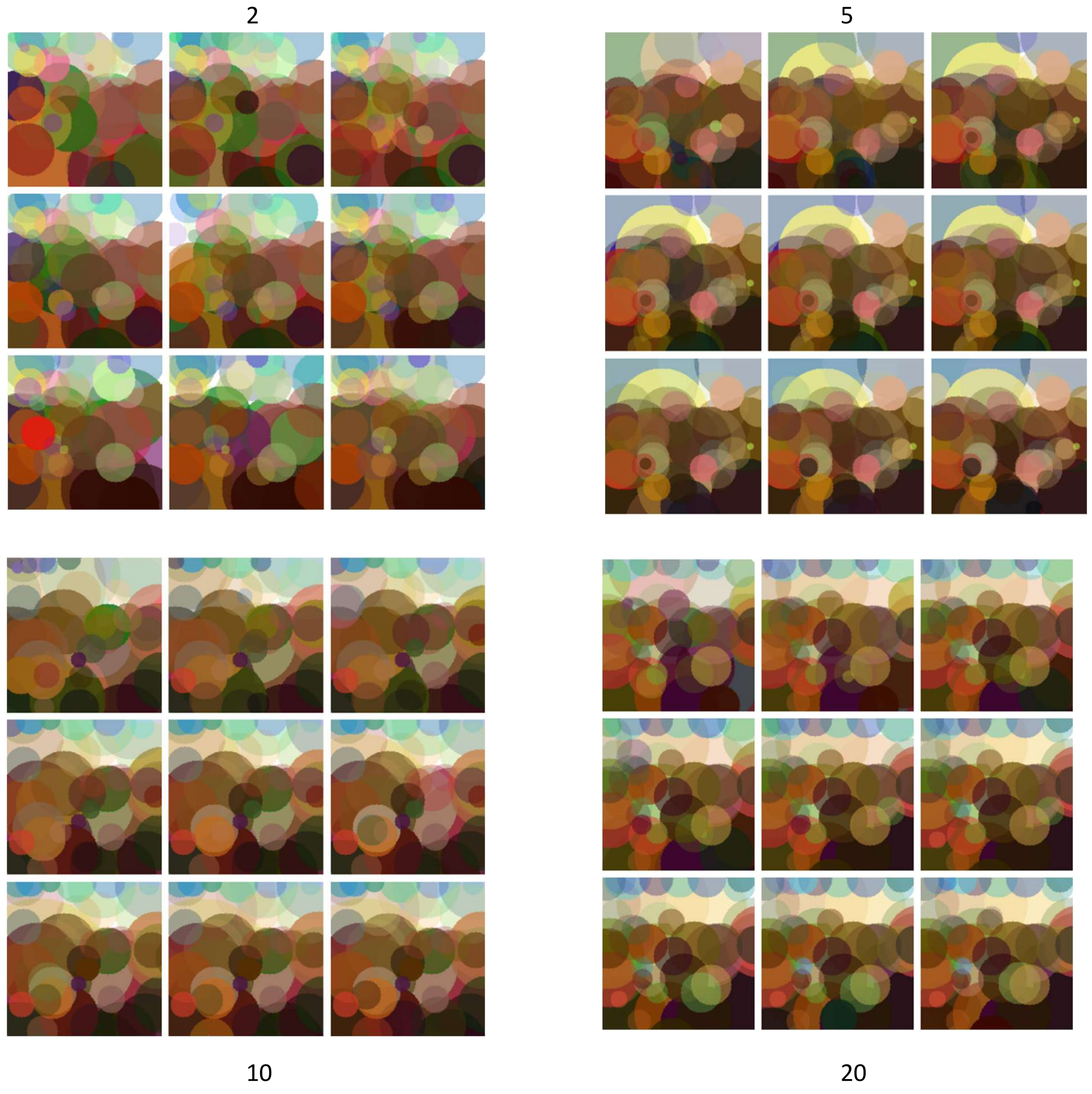


Figure 19: Result at each 1000th generation with having different number of sizes of tournament

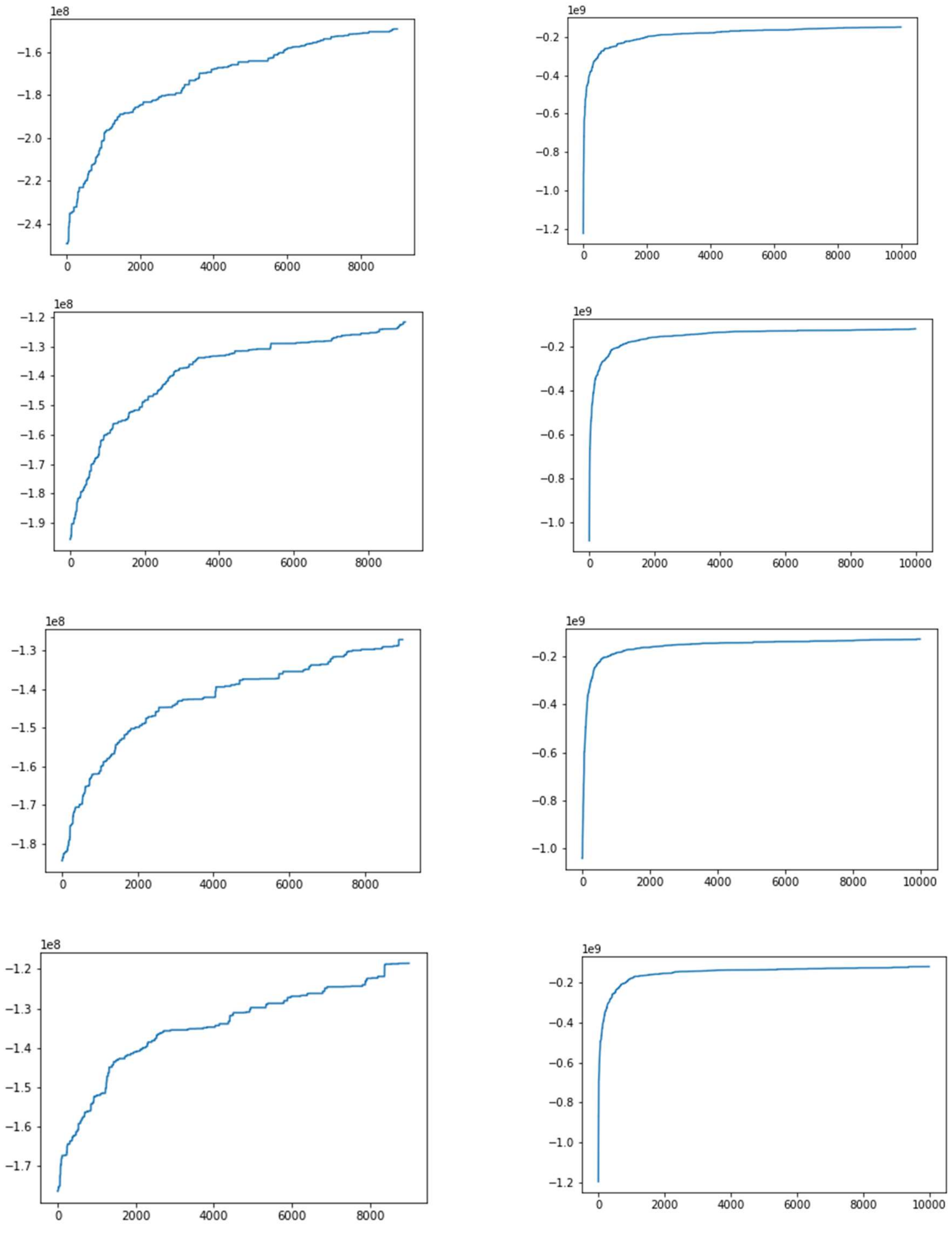


Figure 20: Fitness Values at each iteration taken for different number of sizes of tournament (left = 1000-10000, right=1-10000)

(Since there is a default case, I used same results for that case (sizes of tournament =5), (from upper to bottom, it is in descending order of the parameter)

1.4 Frac Elites

After first 1000th generation, results are:

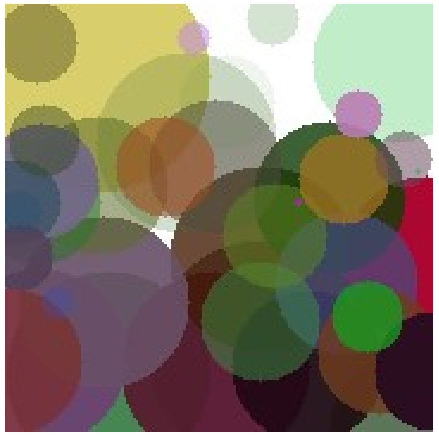


Figure 21: Result at 1000th generation (fraction of elites = 0.05)

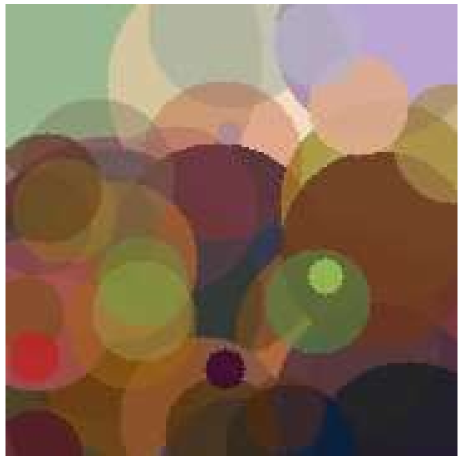


Figure 22: Result at 1000th generation (fraction of elites = 0.2)

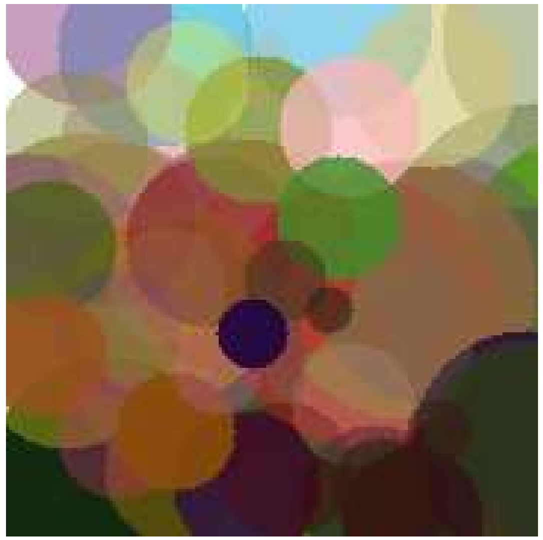
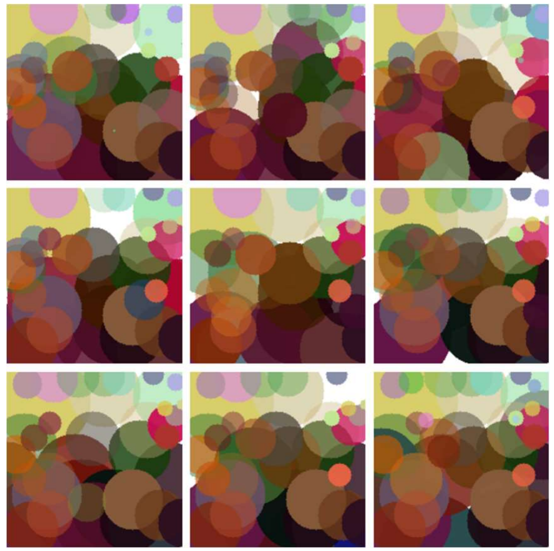


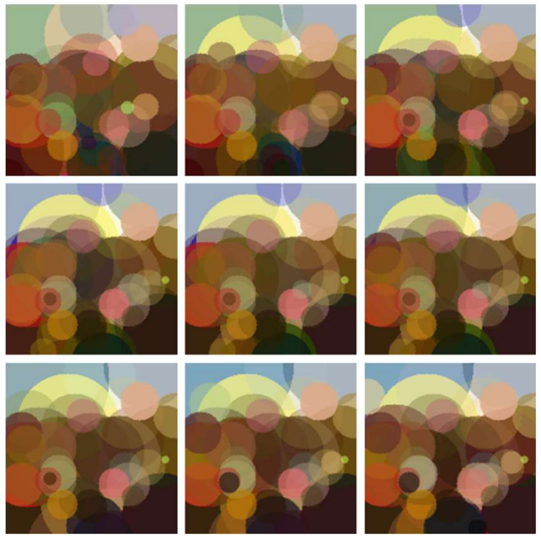
Figure 23: Result at 1000th generation (fraction of elites = 0.4)

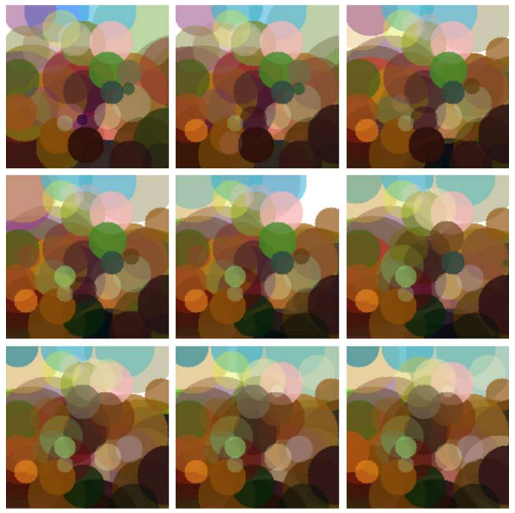
In figures below, as you can go from left upper corner to right bottom corner, number of generations is increased by 1000.

0.05



0.2





0.4

Figure 24: Result at each 1000th generation with having different number of fractions of elites

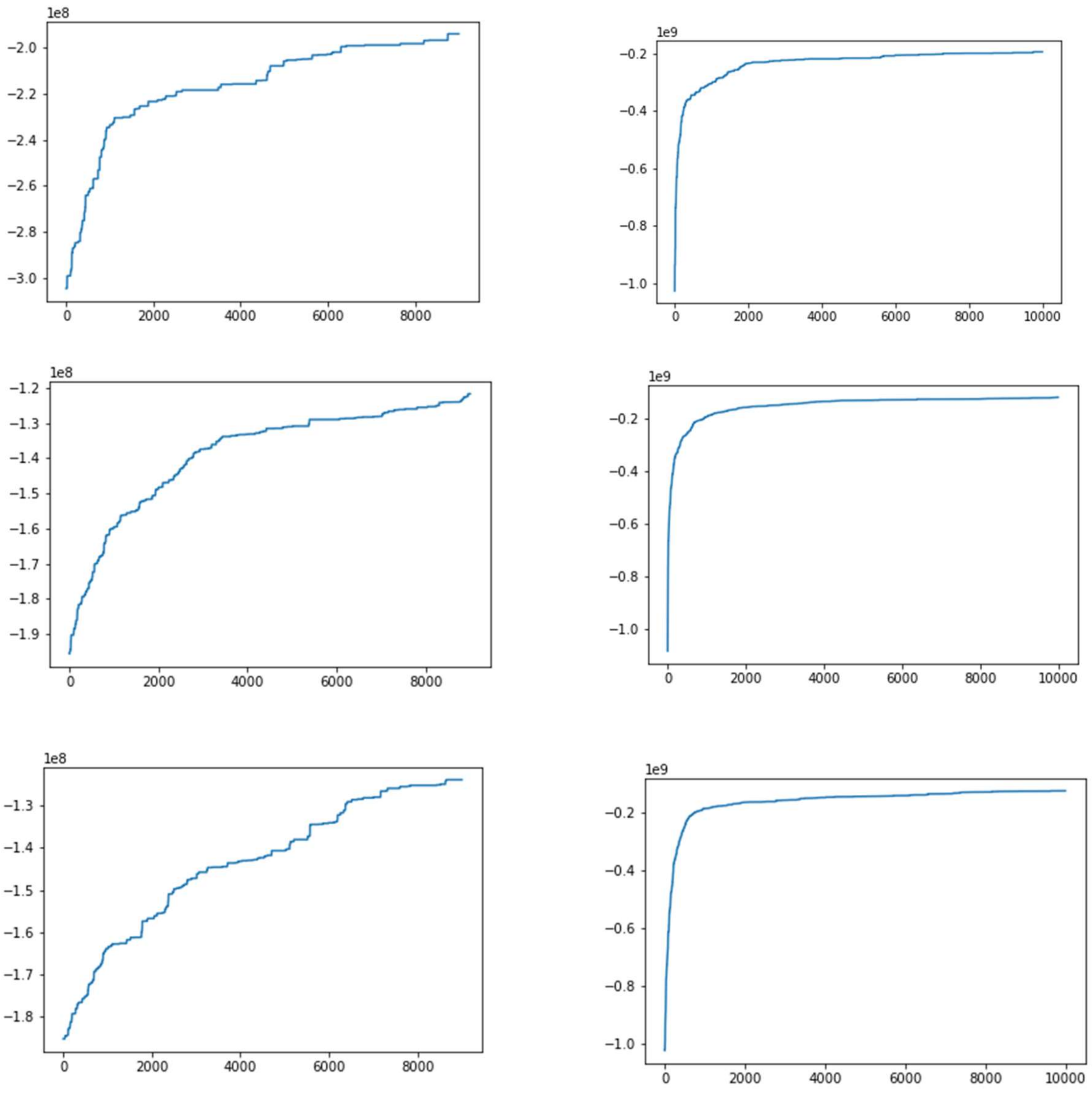


Figure 25: Fitness Values at each iteration taken for different number of fractions of elites (left = 1000-10000, right=1-10000)

(Since there is a default case, I used same results for that case (fractions of elites =0.2) (from upper to bottom, it is in descending order)

1.5 Frac Parents

After first 1000th generation, results are:

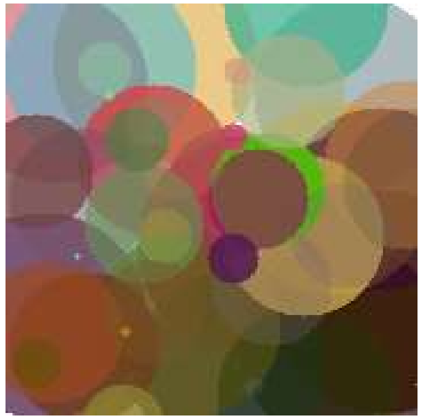


Figure 26: Result at 1000th generation (fraction of parents= 0.2)

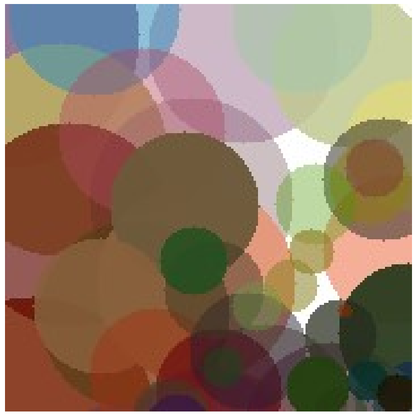


Figure 27: Result at 1000th generation (fraction of parents = 0.4)

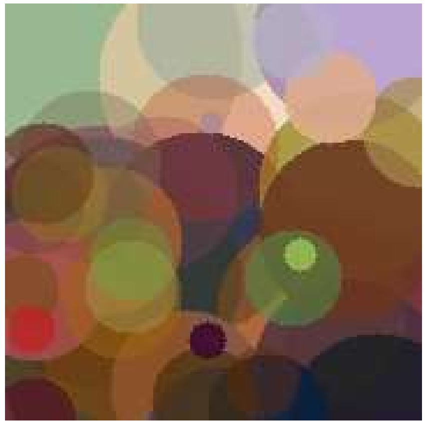


Figure 28: Result at 1000th generation (fraction of parents =0.6)

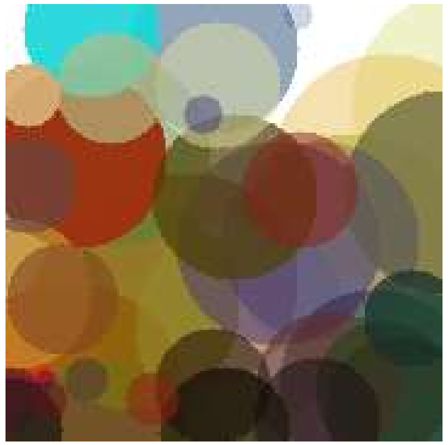


Figure 29: Result at 1000th generation (fraction of parents = 0.8)

In figures below, as you can go from left upper corner to right bottom corner, number of generations is increased by 1000.

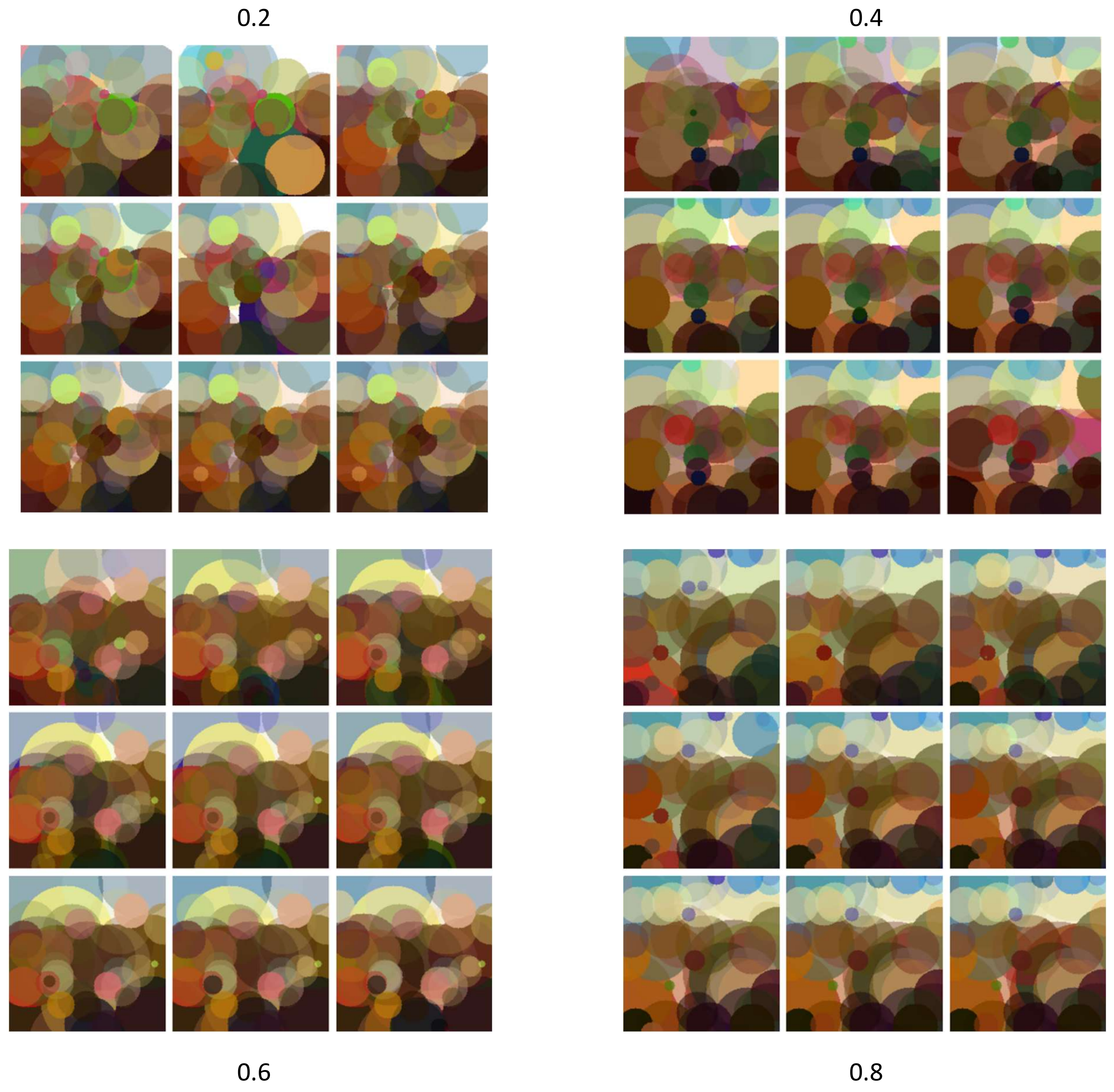


Figure 30: Result at each 1000th generation with having different number of fraction of parents

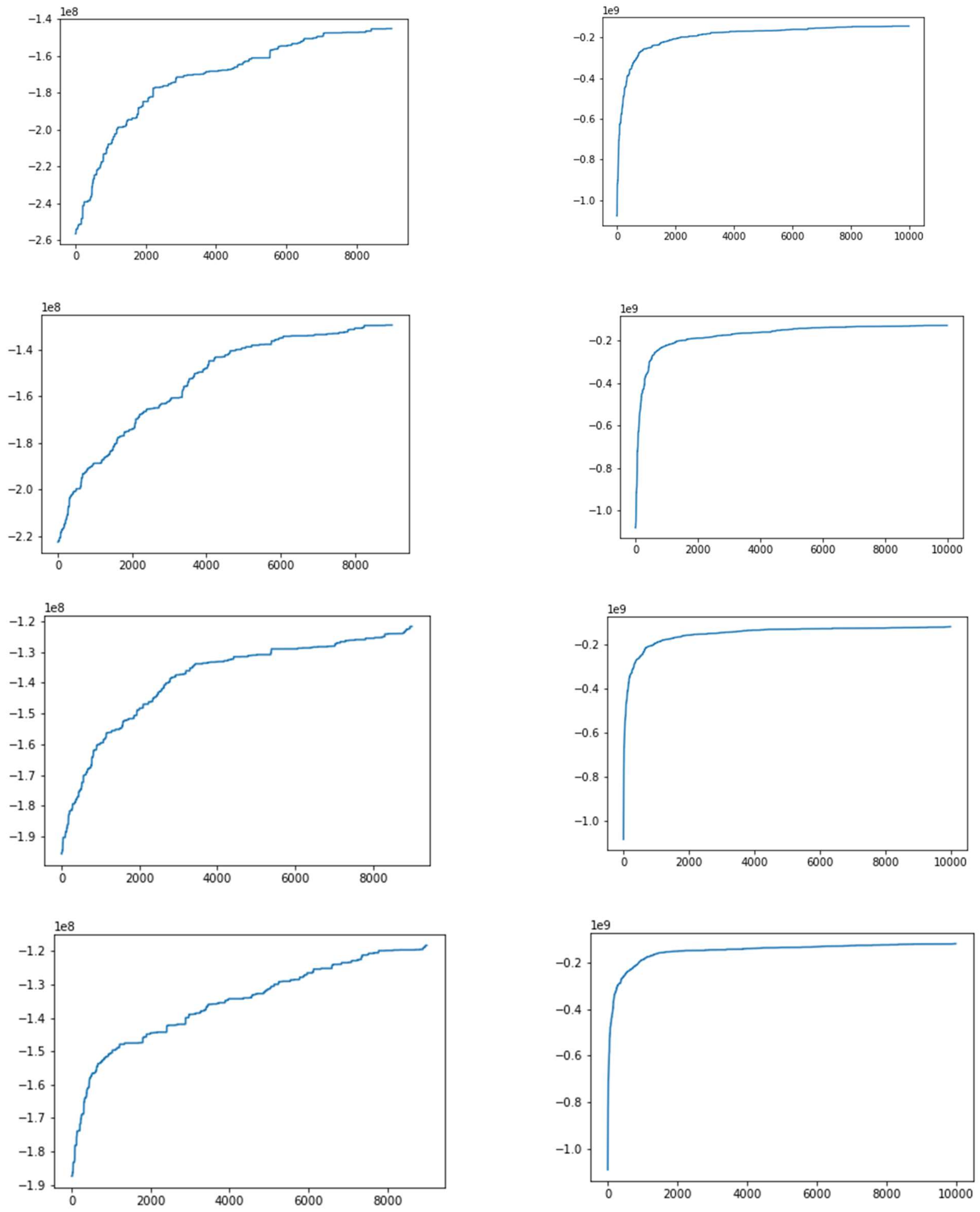


Figure 31: Fitness Values at each iteration taken for different number of fraction of parents (left = 1000-10000, right=1-10000)

(Since there is a default case, I used same results for that case (fraction of parents =0.6) (from upper to bottom, it is in descending order.)

1.6 Mutation Probability

After first 1000th generation, results are:

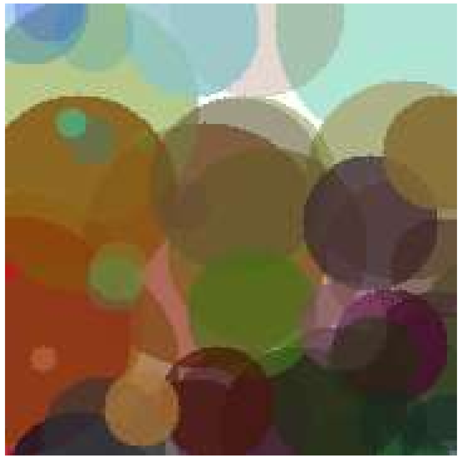


Figure 32: Result at 1000th generation (mutation probability= 0.1)

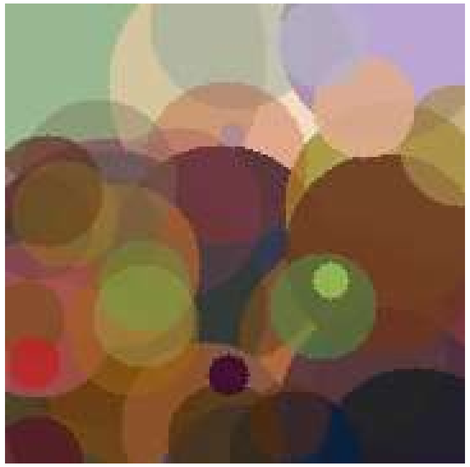


Figure 33: Result at 1000th generation (mutation probability= 0.2)

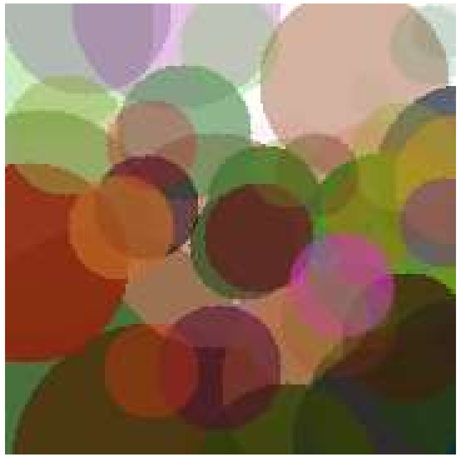


Figure 34: Result at 1000th generation (mutation probability =0.5)

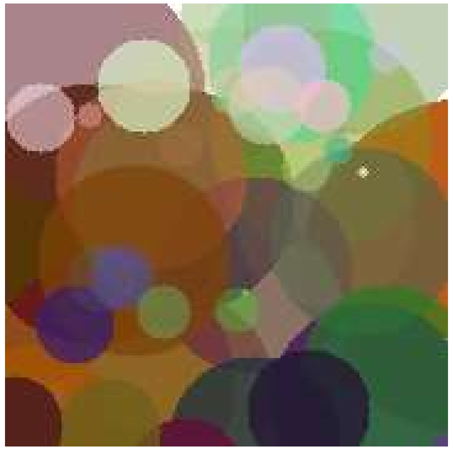


Figure 35: Result at 1000th generation (mutation probability = 0.8)

In figures below, as you can go from left upper corner to right bottom corner, number of generations is increased by 1000.

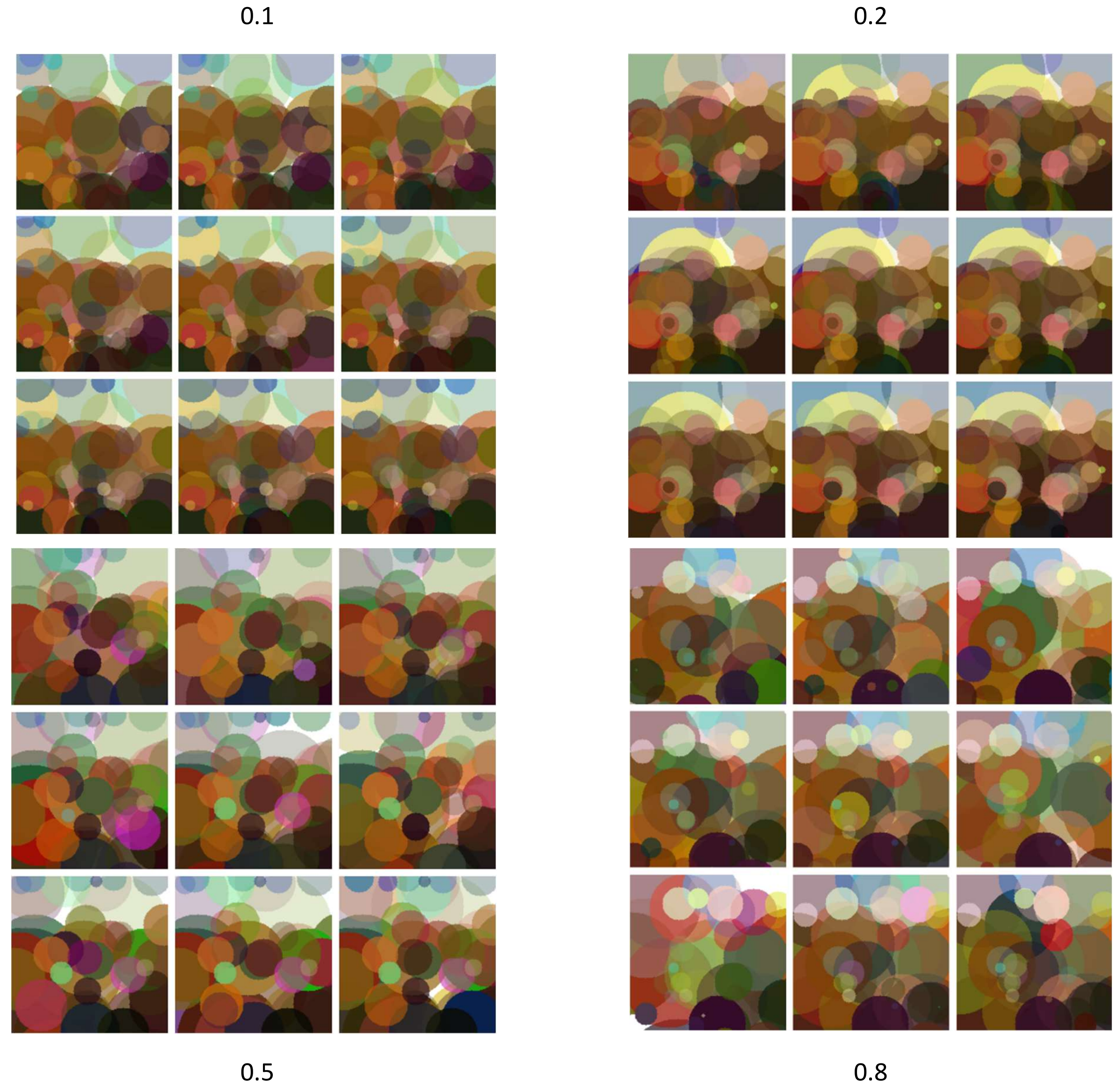


Figure 36: Result at each 1000th generation with having different number of mutation probabilities

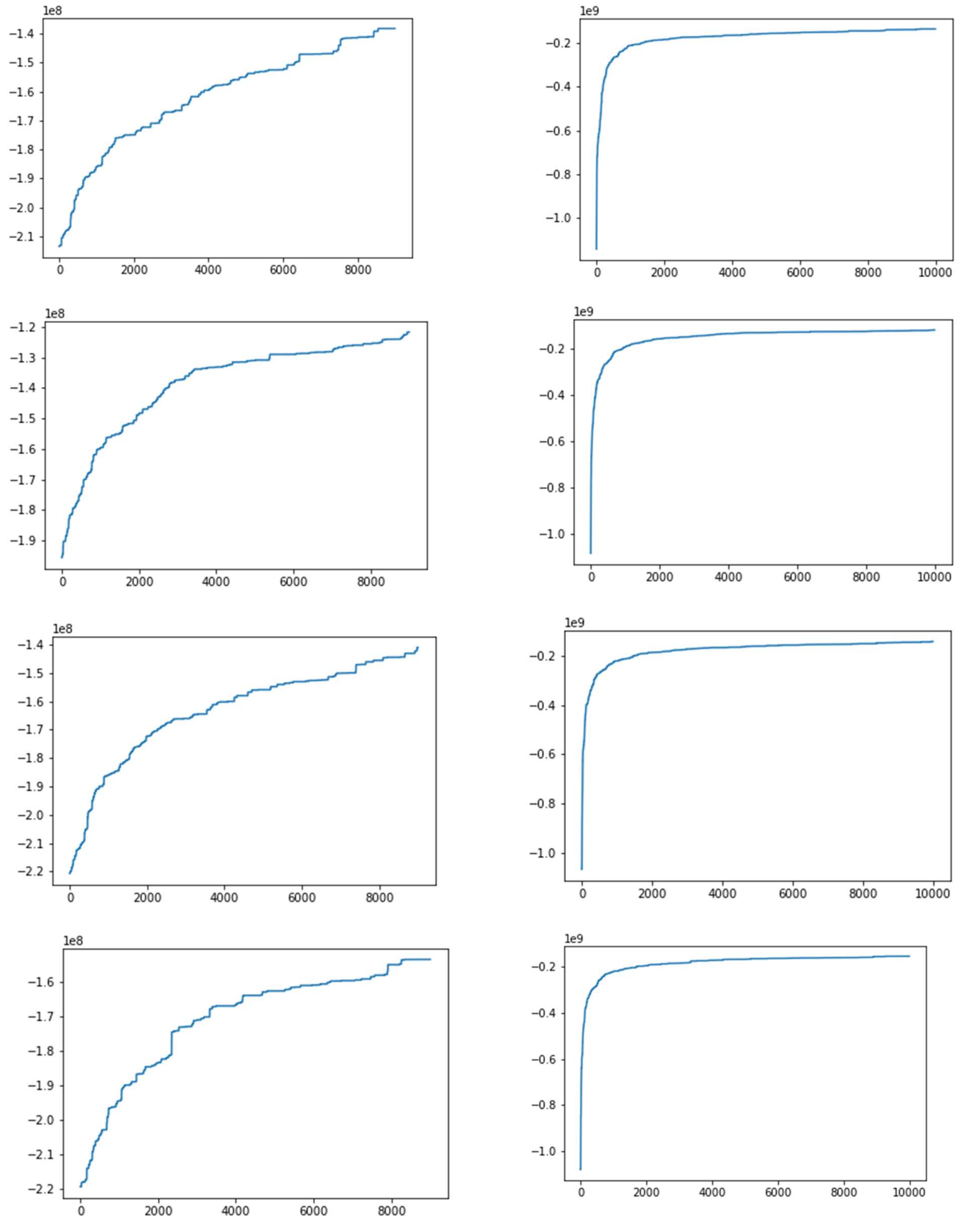


Figure 37: Fitness Values at each iteration taken for different number of mutation probabilities (left = 1000-10000, right=1-10000)

(Since there is a default case, I used same results for that case (mutation probabilities =0.2) (from upper to bottom, it is in descending order))

1.7 Mutation Guide

After first 1000th generation, results are:

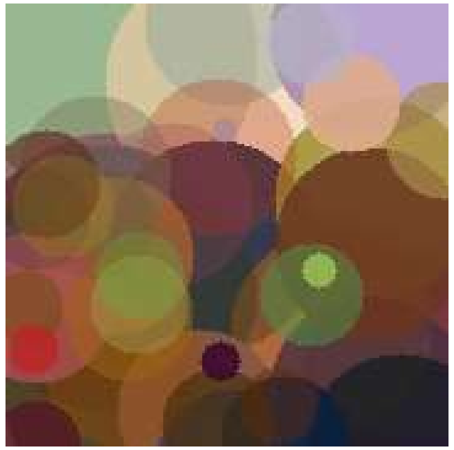


Figure 38: Result at 1000th generation (mutation guide = “guided”)

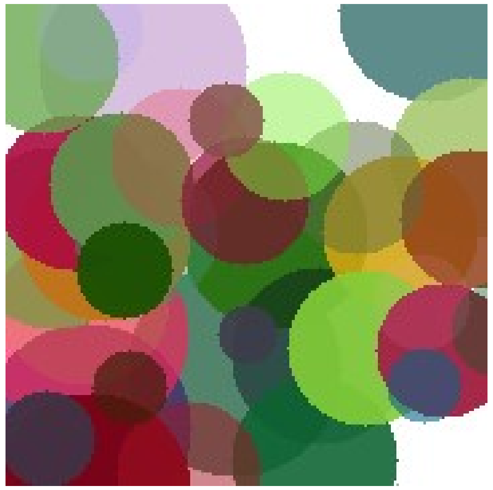
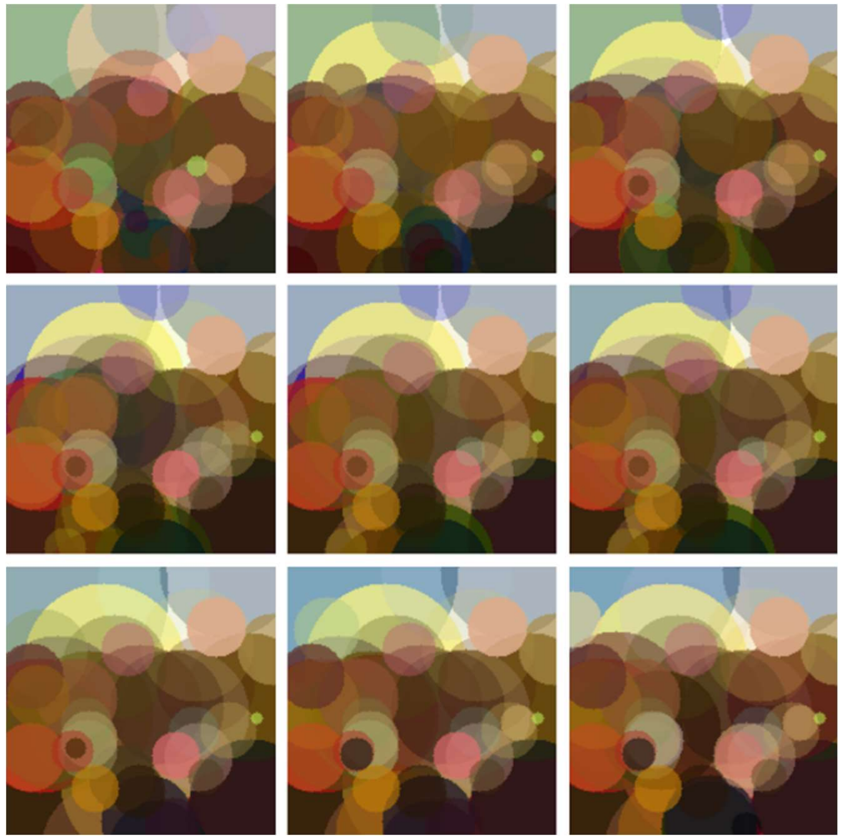
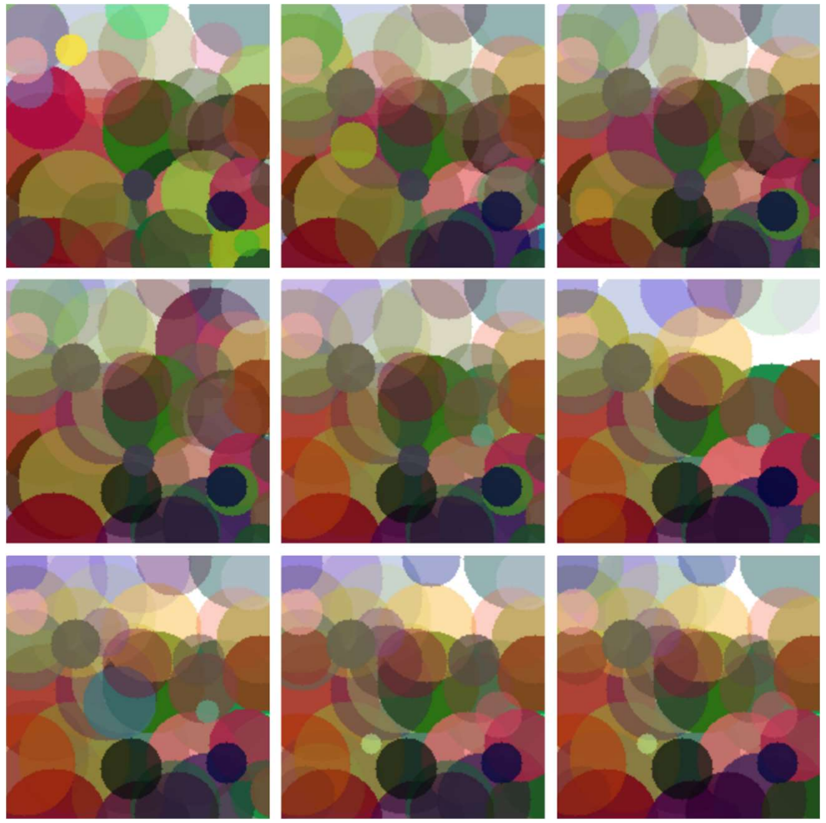


Figure 39: Result at 1000th generation (mutation guide = “unguided”))

In figures below, as you can go from left upper corner to right bottom corner, number of generations is increased by 1000



“Guided”



“Unguided”

Figure 40: Result at each 1000th generation with having different types of mutation

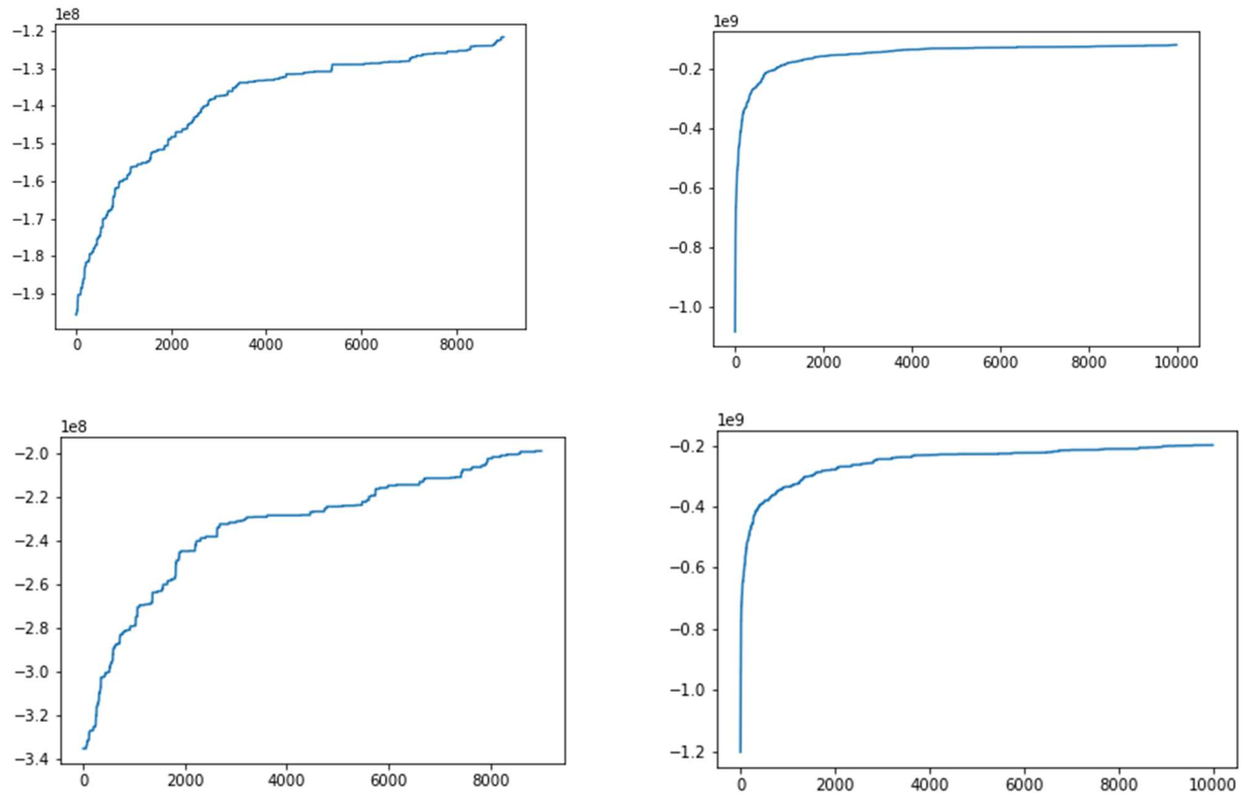


Figure 41: Fitness Values at each iteration taken for different types of mutation (left = 1000-10000, right=1-10000)

(Since there is a default case, I used same results for that case (mutation guide =”guided”), upper=guided, lower=unguided)

2. Discussions

My three suggestions can be listed as follows:

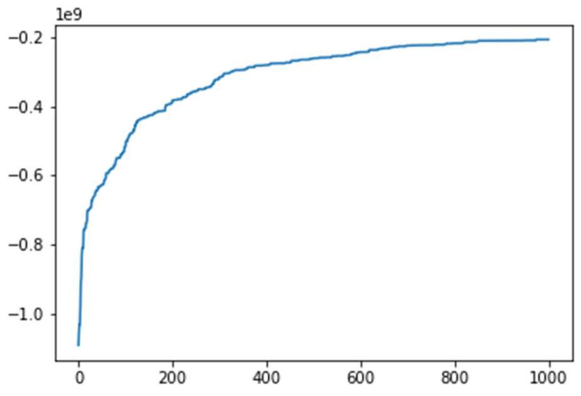
- Suggestion #1: Changeable mutation probabilities
- Suggestion #2: Changeable fraction of elites/parents
- Suggestion #3: Better Mutation Method

Before mentioning one by one, the first two ones have same point. They are all trying to do maximize power by adapting selection intensity. At the begging of training, we want to get diverse individuals. However, at the middle point of training, our aim is to decrease diversity. These diversity amount can be adjusted by mutation probabilities, fraction of elites/parents, or mutation type (which is not mentioned here).

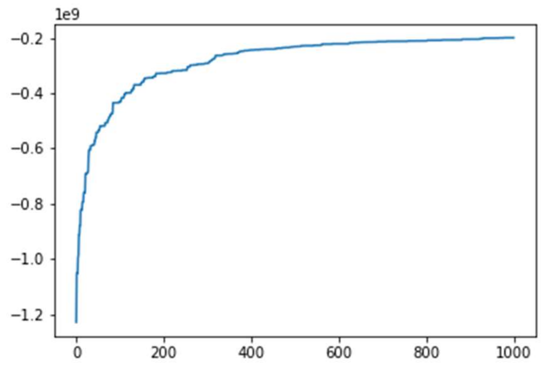
Also, since they are all independent from each other, we can apply them in one train to get perfect result of convergence time.

2.1. Changeable Mutation Probabilities

As we mentioned above, mutation probability will provide us a way to adjust selection intensity. To get better result, we are going to adjust mutation probability high as possible at the beginning so that we will have larger diversity. As the number of iteration increases, we are going to decrease this probability. This will result in smaller convergence time. The results are shown below:



Mut_prob = 0.2



Mut_prob= Changed as time passes

Figure 42: Fitness value vs iteration number with different two mutation probability method

As figure 42 states, at the iteration 600, adaptive version of mutation probability convergences; however, for constant mutation probability, it convergences at the iteration 900. Although they are both converging at the same fitness value. As you can guess, it is hard to compare from their plotting, since they converged at the iteration of 1000.

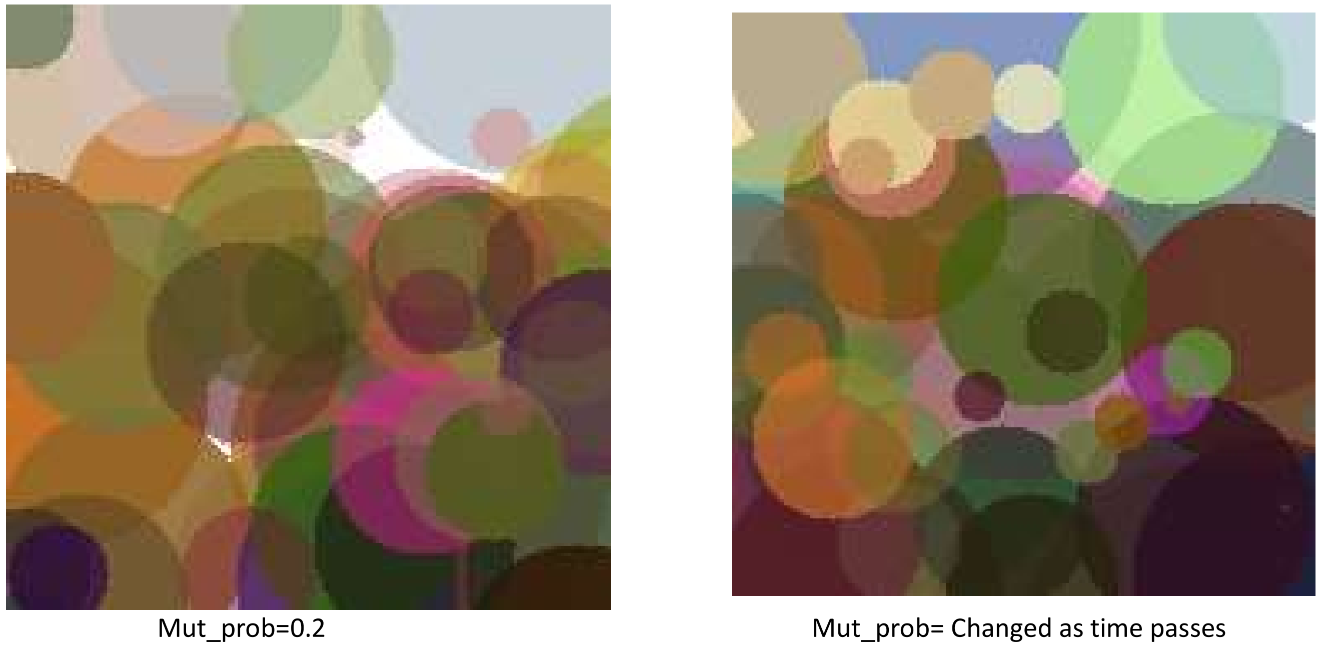
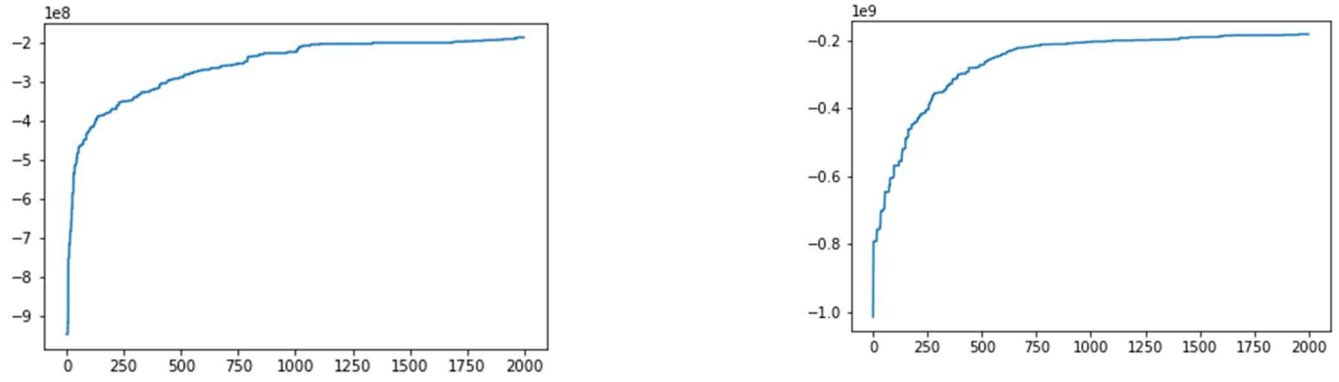


Figure 43: Results at iteration number of 1000 with different two mutation probability method

2.2. Changeable Fraction of Elites/Parents

As we mentioned above, fraction of elites(parents) will provide us a way to adjust selection intensity. To get better result, we are going to adjust fraction of elites(parents) low(high) as possible at the beginning so that we will have larger diversity. In other words, we are encouraging individuals to join tournament at the beginning rather than being a warrior in tournament. As the number of iteration increases, we are going to increase(decrease) this fraction. This will result in smaller convergence time. The results are shown below:

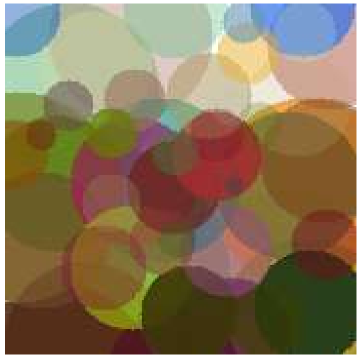


Fractions = Constant

Fractions = Changed as time passes

Figure 44: Fitness value vs iteration number with different two fractions method

Note: While training with my suggestion-2 converges at the iteration of 800, normal training results in convergence time of 1000th iteration although there are converges same point.


Fractions = Constant

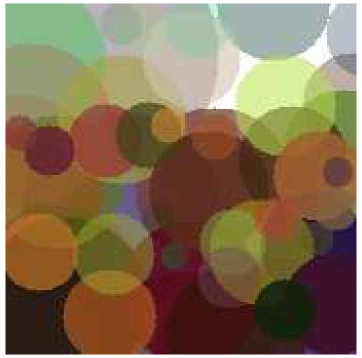
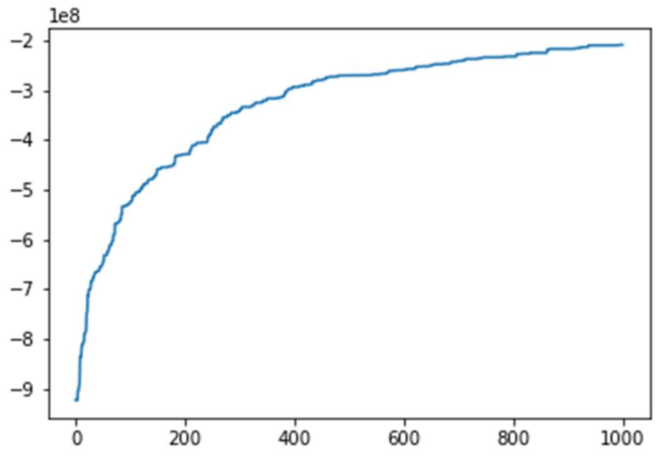
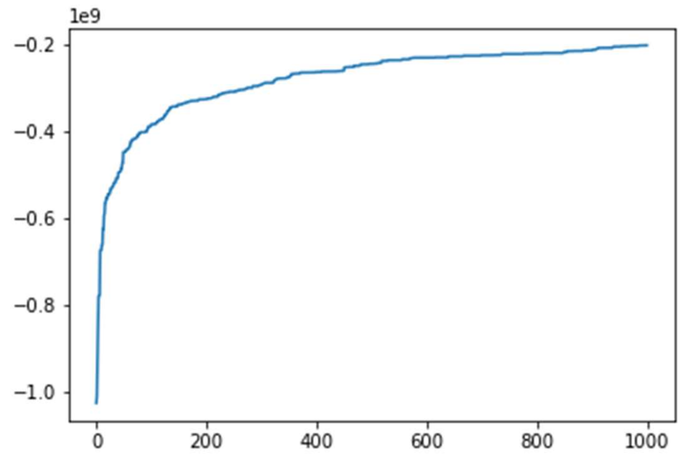

Fractions = Changed as time passes

Figure 45: Results at iteration number of 1000 with different two fractions method

2.3. Better Mutation Method

Mutation is done without considering any decrease in fitness value so we can say that do mutation until mutated one has better fitness value than previous (unmutated) one. However, this will create a slower mutation loop especially when it gets higher fitness value. Therefore, it can be done in a very small interval and at the beginning. As another application, this method can be applied with a very tiny probably (might be 0.0001).



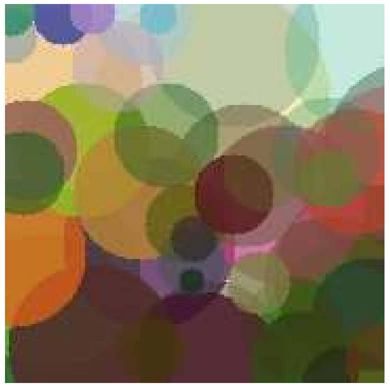


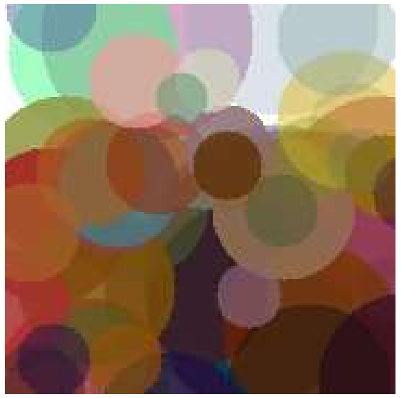
Mutation = Normal

Mutation = At the beginning, Forced mutation

Figure 46: Fitness value vs iteration number with different two mutation method

Note: As figure 46 states, at the beginning there is a huge difference between fitness values.





Mutation = Normal

Mutation = At the beginning, Forced mutation

Figure 47: Fitness value vs iteration number with different two mutation method

```
#Importing necessary libraries
import cv2
from random import randint
from random import random
from random import uniform
from copy import deepcopy
import numpy as np
import matplotlib.pyplot as plt

#Initialize variables with an input image
input_path='inputs/example.png'
im = cv2.imread(input_path)
width,height,_ = im.shape
# Reference to :https://note.nkmk.me/en/python-opencv-pillow-image-size/
print("Widht is ", width)
print("Height is ",height)

#Gene Class
#-----------------------------------------------------------------------------------------
----------------
class gene:
    def __init__(self,ID):
        #Constructor Method
        while True:
            #random intialize of radius x and y
            self.r=randint(1,40)
            self.x= int(1.5 * width * random())#int function is used
            self.y= int(1.5 * height * random())#otherwise cirlce function is giving me
an error
            if self.intersects() == True:#If intersects does not validate, break the loop
                break
            #If it does not intersect with our graph, then randomize again
        #Directly randomize values
        self.red=randint(0,255)
        self.blue=randint(0,255)
        self.green=randint(0,255)
        self.alpha=random()
        self.ID = ID


    def intersects(self): #This method is checking whether circle is intersecting with
graph or not
        if(self.x < width and self.y < height):
            return True#Inside the image
        elif(self.x < width and self.y -height < self.r):
            return True#Upper region of image
        elif(self.y < height and self.x -width < self.r):
            return True#Right region of image
        else:#At the right upper corner

            hipo = (self.x-width)* (self.x-width) +(self.y-height) *(self.y-height)
            # If it is intersects with right upper corner
            if(hipo < self.r*self.r ):
                return True
            else:
                return False
    #Apply mutation on the gene
    def mutate(self,ref):
        if ref =="G":#Guided
            #Took the original values
            radii=self.r
            xii=self.x
            yii=self.y
            while True:
                offset=randint(-10,10)#Randomize offset value
                if(radii+offset > 0): #If it does not go to out of region, then assign
offset
                    self.r= radii+offset    #Assign
                    break
                #If it goes out of region, then randomize offset value again
            while True:
                self.x=randint(max(0,int(xii-width/4)),int(xii+width/4))#Randomize x value
                self.y=randint(max(0,int(yii-width/4)),int(yii+width/4))#Randomize yvalue
                if self.intersects() == True:#If it does not go to out of region, then
```

```
assign these values
                    break
                #If it does not go to out of region, then randomize again
            while True:
                offset=randint(-64,64)#Randomize offset value
                if ((self.red+offset > -1) and(self.red+offset < 256)):#If it does not go
to out of definition boundaries, then assign offset
                    self.red= self.red+offset   #Assign
                    break
                #If it goes out of  definition boundaries, then randomize offset value
again
            while True:
                offset=randint(-64,64)#Randomize offset value
                if ((self.blue+offset > -1) and(self.blue+offset < 256)):#If it does not
go to out of definition boundaries, then assign offset
                    self.blue= self.blue+offset   #Assign
                    break
                #If it goes out of  definition boundaries, then randomize offset value
again
            while True:
                offset=randint(-64,64)#Randomize offset value
                if ((self.green+offset > -1) and(self.green+offset < 256)):#If it does
not go to out of definition boundaries, then assign offset
                    self.green= self.green+offset   #Assign
                    break
                #If it goes out of  definition boundaries, then randomize offset value
again
            while True:
                #Reference to:
                #https://www.geeksforgeeks.org/python-number-uniform-method/
                offset=uniform(-0.25,0.25)#Randomize offset value
                if ((self.alpha+offset >= 0) and(self.alpha+offset <= 1)):#If it does not
go to out of definition boundaries, then assign offset
                    self.alpha= self.alpha+offset   #Assign
                    break
                #If it goes out of  definition boundaries, then randomize offset value
again
        else: #Unguided
            #Apply same randomize with __init__ method
            while True:
                self.r=randint(1,40)
                self.x= int(1.5 * width * random())#int function is used
                self.y= int(1.5 * height * random())#otherwise cirlce function is giving
me an error
                if self.intersects() == True:
                    break
            self.red=randint(0,255)
            self.blue=randint(0,255)
            self.green=randint(0,255)
            self.alpha=random()

#------------------------------------------------------------------------------------------
------------
#Individual Class
class indv:
    def __init__(self,ID=-1,num_genes=50):
        #Constructor Method
        self.ID=ID
        self.num_genes=num_genes
        #Create empty list for choromosomes
        self.chromosome = list()
        for i in range(1,num_genes+1):
            bi=gene(i)#create temp gene for chromosome
            self.chromosome.append(bi)

    def evaulation(self):
        #Reference to:
#https://www.techiedelight.com/sort-list-of-objects-python/#:~:text=A%20simple%20solution%2
0is%20to,only%20arguments%3A%20key%20and%20reverse.
        self.chromosome.sort(key=lambda x: x.r, reverse=True)

        #Reference to:
        #https://www.geeksforgeeks.org/create-a-white-image-using-numpy-in-python/
        image = np.full((width, height, 3),255, dtype = np.uint8)
        for i in self.chromosome:
            #overlay <- image
            #Avoid shallow copy issues, assign it with deep copy
            #Reference to :
            #https://docs.python.org/3/library/copy.html
            overlay=deepcopy(image)

            # Draw the circle on overlay.
            # Reference to:
            # https://www.geeksforgeeks.org/python-opencv-cv2-circle-method/
            # Center coordinates
            center_coordinates = (i.x, i.y)
            # Radius of circle
            radius = i.r
            # color in BGR
            color = (i.blue, i.green, i.red)
            # Line thickness of -1 px
            thickness = -1
            cv2.circle(overlay, center_coordinates, radius, color, thickness)

            # image <- overlay x alpha + image x (1-alpha)
            # Reference to:
            # https://www.educba.com/opencv-addweighted/
            cv2.addWeighted(overlay, i.alpha, image, (1-i.alpha), 0.0,image)

        #Calculating fitness of INDV
        diff=np.subtract(np.array(im, dtype=np.int64), np.array(image, dtype=np.int64))
        self.fitness = np.sum(-1*np.power(diff, 2))
        if self.fitness >0:
            print("ERROR-----------------------------------------------------------")
            #Undesired situtation
            #Code should not be entered this region

    def takeImage(self):#This method will be called when a image is reqiured
        #Reference to:
#https://www.techiedelight.com/sort-list-of-objects-python/#:~:text=A%20simple%20solution%2
0is%20to,only%20arguments%3A%20key%20and%20reverse.
        self.chromosome.sort(key=lambda x: x.r, reverse=True)

        #Reference to:
        #https://www.geeksforgeeks.org/create-a-white-image-using-numpy-in-python/
        image = np.full((width, height, 3),255, dtype = np.uint8)
        for i in self.chromosome:
            #overlay <- image
            #Avoid shallow copy issues, assign it with deep copy
            #Reference to :
            #https://docs.python.org/3/library/copy.html
            overlay=deepcopy(image)

            # Draw the circle on overlay.
            # Reference to:
            # https://www.geeksforgeeks.org/python-opencv-cv2-circle-method/
            # Center coordinates
            center_coordinates = (i.x, i.y)
            # Radius of circle
            radius = i.r
            # color in BGR
            color = (i.blue, i.green, i.red)
            # Line thickness of -1 px
            thickness = -1
            cv2.circle(overlay, center_coordinates, radius, color, thickness)

            # image <- overlay x alpha + image x (1-alpha)
            # Reference to:
            # https://www.educba.com/opencv-addweighted/
            cv2.addWeighted(overlay, i.alpha, image, (1-i.alpha), 0.0,image)
        return image

    def mutation(self,prob,guide):
        while(random()<prob):#Do it with a given probablity
            #mutate random gene in the chromosome
            genMutated= randint(0,self.num_genes-1)
            if(guide=="guided"):#guided
                self.chromosome[genMutated].mutate("G")

            else:#unguided
                self.chromosome[genMutated].mutate("U")

#-------------------------------------------------------------------------------------------
-------------
#Population Class
class popu:
    def
__init__(self,ID,num_idv,num_genes,num_iteration,frac_elites,frac_parents,tm_size,mutation_
prob,mutation_guide):
        #Constructor method for population
        self.mutation_prob=mutation_prob
        self.mutation_guide=mutation_guide
        self.num_iteration=num_iteration
        self.frac_elites=frac_elites
        self.frac_parents=frac_parents
        self.ID=ID
        self.num_idv=num_idv
        self.num_genes=num_genes
        self.tm_size=tm_size
        #Clear individual lists
        self.indvs = list()
        for i in range(0,num_idv):
            bi=indv(i,num_genes)#Temp Indv to add to population
            self.indvs.append(bi)
            #Create individual

    def evaluation(self):#This method is our main method to train, it will train our
model and record all necessary information
        print(f"Evaloation{self.ID} is started...")#Informative printing
        number=0
        #Clear all necessary lists
        self.allfitness=list()#This will hold all fitness values corresponds to population
        self.parents=list()#Parents will hold the individuals who will have children
        self.children=list()#Children will hold the individuals who is created with
crossover
        self.elites=list()#Elites will hold the individuals who can go to next generation
directly
        for i in range(1,self.num_iteration+1):
            #----------------------------------------SUGGESTION
            # #--------------------------------------TO SEE MY SUGG1 UNCOMMMENT THIS SIDE
            # if(self.ID==27):
            #     if (i<300):
            #         self.mutation_prob=0.8
            #     elif(i<400):
            #         self.mutation_prob=0.5
            #     elif(i<600):
            #         self.mutation_prob=0.2
            #     else:
            #         self.mutation_prob=0.1
            # #--------------------------------------TO SEE MY SUGG2 UNCOMMMENT THIS SIDE
            # if(self.ID==29):
            #     if (i<500):
            #         self.frac_elites=0.05
            #         self.frac_parents=0.8
            #     elif(i<750):
            #         self.frac_elites=0.2
            #         self.frac_parents=0.6
            #     else:
            #         self.frac_elites=0.4
            #         self.frac_parents=0.4

            #-------------------------------------------------------------------------


            #Calculate fitness value for each individual in the generation
            for j in self.indvs:
                j.evaulation()

            #Calculate number of elites and parents
            self.num_elites=int(self.frac_elites * self.num_idv)
            self.num_parent=int(self.frac_parents * self.num_idv)


            #if it is even number add 1
            if self.num_parent % 2 == 1:
                self.num_parent = self.num_parent + 1

            #Sort the individuals according to their fitness values
            #Reference to:

#https://www.techiedelight.com/sort-list-of-objects-python/#:~:text=A%20simple%20solution%2
0is%20to,only%20arguments%3A%20key%20and%20reverse.
            self.indvs.sort(key=lambda x: x.fitness, reverse=True)

            #Choosing elites list
            #Clear at the beggining
            self.elites.clear()
            for z in range(self.num_elites):
                #Since we sorted the indvs (.:Fitness Values)
                #The first z ones will be z amount individual with highest fitness
                #Avoid shallow copy issues, assign it with deep copy
                #Reference to :
                #https://docs.python.org/3/library/copy.html
                self.elites.append(deepcopy(self.indvs[z]))

            #Start Tournament
            #Since we want to get num_parents amount of parents, and every tournament
will give us one winner
            #we should do tournament num_parents times.
            for _ in range(self.num_parent):
                self.parents.append(self.tournament())
            #Tournament is finished -----------
            #Record the best fitness
            self.allfitness.append(self.elites[0].fitness)

            #Remove elites from individuals
            for _ in range(self.num_elites):
                self.indvs.pop(0)


            #Crossover Starts
            #Clear the children lists
            self.children.clear()
            #Call the crossover method
            self.crossover()
            #Crossover Finishes --------------

            #Mutation Starts
            self.mutation(i)
            #Mutation finishes ---------------

            #Print informative message
            if i% 200 == 0:
                print(f"Iteration {i}")
                print(self.elites[0].fitness)
            #Record the image for each 1000th generation
            if i% 1000 ==0:
                #Self.ID is our population ID
                print("Population ID is ",self.ID)
                #Record each image for differnet folder locaion
                if self.ID in [0,1,2,3,4]:

cv2.imwrite("Output/NUM_OF_INDV/Res_NI_"+str(self.num_idv)+"_I_"+str(number)+".png",self.in
dvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [5,6,7,8,9]:

cv2.imwrite("Output/NUM_OF_GENES/Res_NG_"+str(self.num_genes)+"_I_"+str(number)+".png",self
.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [10,11,12,13]:

cv2.imwrite("Output/TM_SIZE/Res_TS_"+str(self.tm_size)+"_I_"+str(number)+".png",self.indvs[
0].takeImage())
```

```
                    print("TOOK IMAGE")
                if self.ID in [14,15,16]:

cv2.imwrite("Output/FRAC_ELITE/Res_FE_"+str(self.frac_elites)+"_I_"+str(number)+".png",self
.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [17,18,19,20]:

cv2.imwrite("Output/FRAC_PARENT/Res_FP_"+str(self.frac_parents)+"_I_"+str(number)+".png",se
lf.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [21,22,23,24]:

cv2.imwrite("Output/MUT_PROB/Res_MP_"+str(self.mutation_prob)+"_I_"+str(number)+".png",self
.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [25,26]:

cv2.imwrite("Output/MUT_GUI/Res_MG_"+str(self.mutation_guide)+"_I_"+str(number)+".png",self
.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [27]:

cv2.imwrite("Output/SUGG_1/Res_updated_I_"+str(number)+".png",self.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [28]:

cv2.imwrite("Output/SUGG_1/Res_old_I_"+str(number)+".png",self.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [29]:

cv2.imwrite("Output/SUGG_2/Res_updated_I_"+str(number)+".png",self.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [30]:

cv2.imwrite("Output/SUGG_2/Res_old_I_"+str(number)+".png",self.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [31]:

cv2.imwrite("Output/SUGG_3/Res_updated_I_"+str(number)+".png",self.indvs[0].takeImage())
                    print("TOOK IMAGE")
                if self.ID in [32]:

cv2.imwrite("Output/SUGG_3/Res_old_I_"+str(number)+".png",self.indvs[0].takeImage())
                    print("TOOK IMAGE")
                number+=1
        print(f"Evaloation{self.ID} is ended...")
        #Reference to:

#https://chartio.com/resources/tutorials/how-to-save-a-plot-to-a-file-using-matplotlib/
        plt.figure()
        plt.plot(self.allfitness[999:])#Print the fitness values from 1000-10000
        #Record each image for differnet folder locaion
        if self.ID in [0,1,2,3,4]:
            plt.savefig("Output/NUM_OF_INDV/Res_Fitness1000_NI_"+str(self.num_idv)+".png")
        if self.ID in [5,6,7,8,9]:

plt.savefig("Output/NUM_OF_GENES/Res_Fitness1000_NG_"+str(self.num_genes)+".png")
        if self.ID in [10,11,12,13]:
            plt.savefig("Output/TM_SIZE/Res_Fitness1000_TS_"+str(self.tm_size)+".png")
        if self.ID in [14,15,16]:

plt.savefig("Output/FRAC_ELITE/Res_Fitness1000_FE_"+str(self.frac_elites)+".png")
        if self.ID in [17,18,19,20]:

plt.savefig("Output/FRAC_PARENT/Res_Fitness1000_FP_"+str(self.frac_parents)+".png")
        if self.ID in [21,22,23,24]:

plt.savefig("Output/MUT_PROB/Res_Fitness1000_MP_"+str(self.mutation_prob)+".png")
        if self.ID in [25,26]:

plt.savefig("Output/MUT_GUI/Res_Fitness1000_MG_"+str(self.mutation_guide)+".png")
        if self.ID in [27]:
            plt.savefig("Output/SUGG_1/Res_Fitness1000_updated.png")
        if self.ID in [28]:
            plt.savefig("Output/SUGG_1/Res_Fitness1000_old.png")
        if self.ID in [29]:
            plt.savefig("Output/SUGG_2/Res_Fitness1000_updated.png")
        if self.ID in [30]:
            plt.savefig("Output/SUGG_2/Res_Fitness1000_old.png")
        if self.ID in [31]:
            plt.savefig("Output/SUGG_3/Res_Fitness1000_updated.png")
        if self.ID in [32]:
            plt.savefig("Output/SUGG_3/Res_Fitness1000_old.png")
        plt.figure()
        plt.plot(self.allfitness[:])#Print the fitness values from 1-10000
        #Record each image for differnet folder locaion
        if self.ID in [0,1,2,3,4]:
            plt.savefig("Output/NUM_OF_INDV/Res_FitnessAll_NI_"+str(self.num_idv)+".png")
        if self.ID in [5,6,7,8,9]:

plt.savefig("Output/NUM_OF_GENES/Res_FitnessAll_NG_"+str(self.num_genes)+".png")
        if self.ID in [10,11,12,13]:
            plt.savefig("Output/TM_SIZE/Res_FitnessAll_TS_"+str(self.tm_size)+".png")
        if self.ID in [14,15,16]:

plt.savefig("Output/FRAC_ELITE/Res_FitnessAll_FE_"+str(self.frac_elites)+".png")
        if self.ID in [17,18,19,20]:

plt.savefig("Output/FRAC_PARENT/Res_FitnessAll_FP_"+str(self.frac_parents)+".png")
        if self.ID in [21,22,23,24]:

plt.savefig("Output/MUT_PROB/Res_FitnessAll_MP_"+str(self.mutation_prob)+".png")
        if self.ID in [25,26]:

plt.savefig("Output/MUT_GUI/Res_FitnessAll_MG_"+str(self.mutation_guide)+".png")
        if self.ID in [27]:
            plt.savefig("Output/SUGG_1/Res_FitnessAll_updated.png")
        if self.ID in [28]:
            plt.savefig("Output/SUGG_1/Res_FitnessAll_old.png")
        if self.ID in [29]:
            plt.savefig("Output/SUGG_2/Res_FitnessAll_updated.png")
        if self.ID in [30]:
            plt.savefig("Output/SUGG_2/Res_FitnessAll_old.png")
        if self.ID in [31]:
            plt.savefig("Output/SUGG_3/Res_FitnessAll_updated.png")
        if self.ID in [32]:
            plt.savefig("Output/SUGG_3/Res_FitnessAll_old.png")

    #Mutation method is to mutate population
    def mutation(self,ind=0):
        #Create indvs list for who are applied to mutation
        #Children and other individuals(we excluded elites already )
        mutationTeam=self.children + self.indvs
        for i_indv in mutationTeam:
            #---------------------------------------------------SUGGESTION 3
            #----------------------------------------------FORCED MUTATION
            if(self.ID==31 and (ind > 0) and (ind<5)):#At the beggingign ,it isforced
                i_indv.evaulation()#Calculate fitness value
                prevFitness=i_indv.fitness#Hold the previous fitness value
                i_indv.mutation(self.mutation_prob,self.mutation_guide)#Mutate
                i_indv.evaulation()#Evalute again
                afterFitness=i_indv.fitness
                while True:
                      if(afterFitness > prevFitness):#If there is a upgrade on fitness,
                          #Finish the mutation
                          break
                      else:
                          #If not,
                          #Mutate again untill there is a upgrade on fitness
                          i_indv.mutation(self.mutation_prob,self.mutation_guide)
                          i_indv.evaulation()
                          afterFitness=i_indv.fitness
            #---------------------------------------------------SUGGESTION 3  ENDS
            else:
            #----------------------------------------------DIRECT MUTATION
                i_indv.mutation(self.mutation_prob,self.mutation_guide)
        #Assign new generation list to indvs
        #Avoid shallow copy issues, assign it with deep copy
        #Reference to :
        #https://docs.python.org/3/library/copy.html
        self.indvs=deepcopy( self.children +self.elites + self.indvs)
    #Crossover method
    #This will update children list with newly created
        #individuals crossovering parents
    def crossover(self):
        for _ in range(0,self.num_parent,2):#Iterate the amount of parents divided by two
                                            #Since each children has two parents
            father=self.parents.pop(randint(0,len(self.parents)-1))#Randomly assign father
            mother=self.parents.pop(randint(0,len(self.parents)-1))#Randomly assign mother
            childrenA=indv(father.ID,self.num_genes)#Create new children
            childrenB=indv(mother.ID,self.num_genes)#Create new children
            #For each gen, randomize a number between 0 and 1
            # if it is smaller than 0.5
            #father will give the gene to children
            #if not
            #mother will give the gene to children
            for i in range(0,self.num_genes):
                res=uniform(0,1)
                if res<0.5:
                    childrenA.chromosome[i]=father.chromosome[i]
                    childrenB.chromosome[i]=mother.chromosome[i]
                else:
                    childrenA.chromosome[i]=mother.chromosome[i]
                    childrenB.chromosome[i]=father.chromosome[i]
            #Update the children list to
            self.children.append(childrenA)
            self.children.append(childrenB)
    #Tourname method will give us a winner
    def tournament(self):
        #Randomly choose one of them
        #Assign it as temporary winner
        bestInd=randint(0,len(self.indvs)-1)
        bestFitness=self.indvs[bestInd].fitness

        #Since we initialize with a random assignment
        #One of the warrior is decided
        #Therefore, we should iterate tm_size - 1 times
        for _ in range(self.tm_size-1):
            #Randomly choose one of them as a warrior
            currentInd=randint(0,len(self.indvs)-1)
            #Take the warrior's fitness value
            currentFitness=self.indvs[currentInd].fitness
            #Compare it with the best one
            if(currentFitness > bestFitness):
                #If the iterated warrior wins
                #Label him as best
                bestFitness=currentFitness
                bestInd=currentInd
        #end of for loop
        #Winner is decided
        #Temporary indv to be added to parent since it is the winner.
        temp=self.indvs[bestInd]
        self.indvs.pop(bestInd)#Delete the winner from current generation
        return temp#Return it so that parents will be updated correctly

#Hyperparameters----------------------------------
num_of_indv=[5,10,20,50,75]
num_of_genes=[10,25,50,100,150]
tm_sizes=[2,5,10,20]
frac_elites=[0.05,0.2,0.4]
frac_parents=[0.2,0.4,0.6,0.8]
mut_probs=[0.1,0.2,0.5,0.8]
mut_gui=["guided","unguided"]
num_generation=10000
#num_generation = 2000 #------------------------------------------UNCOMMENT TO SEE MY
SUGGESTION 2-3 IN A FASTER WAY


#What do you want??
#Choose one of them and uncomment to see the results
#Do not organize folder tree so that recording can be done!!!!
```

```
#-------------------------NUM OF INDV------------------------------------------------
# tempPop
=popu(0,num_of_indv[0],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop.evaluation()
# tempPop1
=popu(1,num_of_indv[1],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop1.evaluation()
# tempPop2
=popu(2,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop2.evaluation()
# tempPop3
=popu(3,num_of_indv[3],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop3.evaluation()
# tempPop4
=popu(4,num_of_indv[4],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop4.evaluation()
# playsound("cak.mp3")
#-------------------------NUM OF GENES------------------------------------------------
# tempPop
=popu(5,num_of_indv[2],num_of_genes[0],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop.evaluation()
# tempPop1
=popu(6,num_of_indv[2],num_of_genes[1],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop1.evaluation()
# # tempPop2
=popu(7,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# # tempPop2.evaluation() SAME WITH DEFAULT CASE
# tempPop3
=popu(8,num_of_indv[2],num_of_genes[3],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop3.evaluation()
# tempPop4
=popu(9,num_of_indv[2],num_of_genes[4],num_generation,frac_elites[1],frac_parents[2],tm_siz
es[1],mut_probs[1],mut_gui[0])
# tempPop4.evaluation()

# #-------------------------TM SIZE------------------------------------------------
# tempPop
=popu(10,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[0],mut_probs[1],mut_gui[0])
# tempPop.evaluation()
# # tempPop1
=popu(11,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# # tempPop1.evaluation() SAME WITH DEFAULT CASE
# tempPop2
=popu(12,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[2],mut_probs[1],mut_gui[0])
# tempPop2.evaluation()
# tempPop3
=popu(13,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[3],mut_probs[1],mut_gui[0])
# tempPop3.evaluation()

# #-------------------------FRAC ELITE------------------------------------------------
# tempPop
=popu(14,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[0],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# tempPop.evaluation()
# # tempPop1
=popu(15,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# # tempPop1.evaluation() SAME WITH DEFAULT CASE
# tempPop2
=popu(16,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[2],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
```

```
# tempPop2.evaluation()


# #-------------------------FRAC PARENTS-------------------------------------------------
# tempPop
=popu(17,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[0],tm_si
zes[1],mut_probs[1],mut_gui[0])
# tempPop.evaluation()
# tempPop1
=popu(18,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[1],tm_si
zes[1],mut_probs[1],mut_gui[0])
# tempPop1.evaluation()
# # tempPop2
=popu(19,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# # tempPop2.evaluation() SAME WITH DEFAULT CASE
# tempPop3
=popu(20,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[3],tm_si
zes[1],mut_probs[1],mut_gui[0])
# tempPop3.evaluation()

# #-------------------------MUT PROB-------------------------------------------------
# tempPop
=popu(21,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[0],mut_gui[0])
# tempPop.evaluation()
# # tempPop1
=popu(22,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# # tempPop1.evaluation() SAME WITH DEFAULT CASE
# tempPop2
=popu(23,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[2],mut_gui[0])
# tempPop2.evaluation()
# tempPop3
=popu(24,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[3],mut_gui[0])
# tempPop3.evaluation()

# #-------------------------MUT GUIDE-------------------------------------------------
# tempPop
=popu(25,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# tempPop.evaluation()   SAME WITH DEFAULT CASE
# tempPop4
=popu(26,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[1])
# tempPop4.evaluation()


# #-------------------------SUG 1-------------------------------------------------
# tempPop1
=popu(27,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# tempPop1.evaluation()
# tempPop2
=popu(28,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# tempPop2.evaluation()

#-------------------------SUG 2-------------------------------------------------
# tempPop2
=popu(29,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
# tempPop2.evaluation()
#
tempPop3=popu(30,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[
2],tm_sizes[1],mut_probs[1],mut_gui[0])
# tempPop3.evaluation()

#-------------------------SUG 3-------------------------------------------------
# tempPop2
=popu(31,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[2],tm_si
zes[1],mut_probs[1],mut_gui[0])
```

```
# tempPop2.evaluation()
#
tempPop3=popu(32,num_of_indv[2],num_of_genes[2],num_generation,frac_elites[1],frac_parents[
2],tm_sizes[1],mut_probs[1],mut_gui[0])
# tempPop3.evaluation()
```