**A quantum-inspired genetic algorithm comparision with genetic algorithm for k-means clustering**

**Abstract**

In this paper we want to compare two diffrent algorithms for k-means clustering, first is Quantum Inspired Genetic Algorithm that we will implement it from Quantom Inspired genetic article, and second is a simple genetic algorithm from another article.

**Contents**

* Introduction
* Quantum-inspired genetic algorithm for k-means clustering implementation
* Genetic algorithm for k-means clustering implementation
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* Conclusion

**Introduction**

Clustering plays an important role in many unsupervised learning areas, such as pattern recognition, data mining and knowledge discovery. Clustering problem can be summarized as: Given n points in Rd space and an integer k, find a set of k points, called centroids, such that the sum of the distances of each of the n points to its nearest centroid is minimized. Generally speaking, conventional clustering algorithms can be grouped into two main categories, namely hierarchical clustering algorithms and partitional clustering algorithms. A hierarchical clustering algorithm outputs a dendrogram, which is a tree structure showing a sequence of clusterings with each clustering being a partition of the dataset. Unlike the hierarchical clustering algorithm, the partitional clustering algorithms partition the data set into a number of clusters, and the output is only a single partition of the data set. The majority of partitional clustering algorithms obtain the partition through the maximization or minimization of some criterion functions. Recent researches show that the partitional clustering algorithms are well suited for clustering a large dataset due to their relatively low computational requirements. And the time complexity of the partitional algorithms is almost **linear**, which makes them widely used. Among the partitional clustering algorithms, the most famous one is **k-means clustering**. K-means clustering algorithm first randomly generates k initial cluster centroids. After several iterations of the algorithm, data can be classified into certain clusters by the criterion function, which makes the data close to each other in the same cluster and widely separated among clusters. However, the traditional k-means clustering algorithm has two drawbacks. The one is that the number of clusters has to be known in advance, and the other is that the clustering result is sensitive to the selection of initial cluster centroids and this may lead the algorithm converge to the local optima. Different datasets have different number of clusters, which is difficult to known beforehand, and the initial cluster centroids are selected randomly, which will make the algorithm converge to the different local optima. Therefore, a lot of research efforts have been conducted on mitigating the two drawbacks of the conventional k-means clustering algorithm. The **genetic algorithm** (GA) is one of the methods to avoid local optima and discover good initial centroids that lead to superior partitions under k-means.

in this paper we implemented two diffrent genetic algorithm for k-means algorithm :

**A Quantum-inspired genetic algorithm for k-means Clustering**

**Genetic Algorithm for k-means Clustering**

k-means clustering method selects randomly k patterns from the dataset D which is of size n, as initial cluster centers.  
These initial centers are also called seed-points. Let M(0) = {M(0) 1 ,M(0)2 , . . . ,M(0)k } be the set of initial seed points.  
Remaining (n-k) patterns are assigned to their nearest cluster centers.  
New centroid (mean) of each cluster is computed. Each pattern X є D is again assigned to the nearest hub and new centers are again found. This process is iterated until all centers (means) remain unchanged in two successive iterations.  
The time multifaceted nature of the k-means technique is O (nkt), where n is the quantity of examples in the dataset, k is the quantity of groups and t is the quantity of emphases till the convergence.

**Input:**  
k: the digit of clusters,  
A: data set of n size.  
**Output:**  
An arrangement of k clusters.  
**Routine:**

1. Selection of k items from A (initial cluster centroid)
2. Repeat until no changeK-Means Clustering & Application of Genetic Algorithm in K-Means Clustering  
   2.1 Each item is allocated to the closest cluster to its nearest. (Distance of each item is calculated from selected cluster centroid using sum of squared error)  
   2.2 Recalculate new cluster centroids
3. Display the final generated clusters.

**Quantum-inspired genetic algorithm for k-means clustering implementation**

In [1]:

**def** download\_progress\_hook(count, blockSize, totalSize):

"""A hook to report the progress of a download. This is mostly intended for users with

slow internet connections. Reports every 5% change in download progress."""

**global** last\_percent\_reported

percent **=** int(count **\*** blockSize **\*** 100 **/** totalSize)

**if** last\_percent\_reported **!=** percent:

**if** percent **%** 5 **==** 0:

sys**.**stdout**.**write("%s%%" **%** percent)

sys**.**stdout**.**flush()

**else**:

sys**.**stdout**.**write(".")

sys**.**stdout**.**flush()

last\_percent\_reported **=** percent

**def** read\_df(filename, expected\_bytes**=None**, force**=False**):

"""Download a file if not present, and make sure it's the right size."""

dest\_filename **=** os**.**path**.**join(data\_root, filename)

dir **=** dest\_filename[:dest\_filename**.**rfind('/')]

**if** **not** os**.**path**.**exists(dir):

os**.**makedirs(dir)

**if** force **or** **not** os**.**path**.**exists(dest\_filename):

print('Attempting to download:', filename)

filename, \_ **=** urlretrieve(root\_url **+** filename, dest\_filename, reporthook**=**download\_progress\_hook)

print('\nDownload Complete!')

**return** np**.**array(pd**.**read\_csv(filename, header**=None**))

*# read\_df(spectf\_test)*

*# iris\_addr = 'iris/iris.data'*

*# wine\_addr = 'wine/wine.data'*

*# glass\_addr = 'glass/glass.data'*

*# spectf\_train = 'spect/SPECTF.train'*

*# spectf\_test = 'spect/SPECTF.train'*

In [2]:

**def** sda(num,clusterMembersNum**=**100) :

"This function will generate random datasets : sda1,sda2,sda3"

seed **=** 0

np**.**random**.**seed(seed)

dataset **=** **None**

**if** num **==** 1 :

"generating sda1 according to its table in essay"

dataset **=** np**.**concatenate([np**.**random**.**uniform(0,20,(clusterMembersNum,2)),

np**.**random**.**uniform(40,60,(clusterMembersNum,2)),

np**.**random**.**uniform(80,100,(clusterMembersNum,2))])

**elif** num **==** 2 :

"generating sda2 according to its table in essay"

dataset **=** np**.**concatenate([np**.**random**.**uniform(0,20,(clusterMembersNum,2)),

np**.**random**.**uniform(40,60,(clusterMembersNum,2)),

np**.**random**.**uniform(80,100,(clusterMembersNum,2)),

np**.**array([[np**.**random**.**uniform(0,20),np**.**random**.**uniform(80,100)] **for** i **in** range(clusterMembersNum)])])

**else** :

"generating sda3 according to its table in essay"

dataset **=** np**.**concatenate([np**.**random**.**uniform(0,20,(clusterMembersNum,2)),

np**.**random**.**uniform(40,60,(clusterMembersNum,2)),

np**.**random**.**uniform(80,100,(clusterMembersNum,2)),

np**.**array([[np**.**random**.**uniform(80,100),np**.**random**.**uniform(0,20)] **for** i **in** range(clusterMembersNum)]),

np**.**array([[np**.**random**.**uniform(0,20),np**.**random**.**uniform(180,200)] **for** i **in** range(clusterMembersNum)]),

np**.**array([[np**.**random**.**uniform(180,200),np**.**random**.**uniform(0,20)] **for** i **in** range(clusterMembersNum)]),

np**.**array([[np**.**random**.**uniform(180,200),np**.**random**.**uniform(80,100)] **for** i **in** range(clusterMembersNum)]),

np**.**array([[np**.**random**.**uniform(180,200),np**.**random**.**uniform(180,200)] **for** i **in** range(clusterMembersNum)])])

**return** np**.**array(dataset)

In [15]:

**def** minmax(data):

normData **=** data

data **=** data**.**astype(float)

normData **=** normData**.**astype(float)

**for** i **in** range(0, data**.**shape[1]):

tmp **=** data**.**iloc[:, i]

*# max of each column*

maxElement **=** np**.**amax(tmp)

*# min of each column*

minElement **=** np**.**amin(tmp)

*# norm\_dat.shape[0] : size of row*

**for** j **in** range(0, normData**.**shape[0]):

normData[i][j] **=** float(

data[i][j] **-** minElement) **/** (maxElement **-** minElement)

normData**.**to\_csv('result/norm\_data.csv', index**=None**, header**=None**)

**return** normData

In [27]:

minmax(pd**.**DataFrame(read\_df(iris\_addr)[:,:**-**1]))

Out[27]:

|  | **0** | **1** | **2** | **3** |
| --- | --- | --- | --- | --- |
| **0** | 0.222222 | 0.625000 | 0.067797 | 0.041667 |
| **1** | 0.166667 | 0.416667 | 0.067797 | 0.041667 |
| **2** | 0.111111 | 0.500000 | 0.050847 | 0.041667 |
| **3** | 0.083333 | 0.458333 | 0.084746 | 0.041667 |
| **4** | 0.194444 | 0.666667 | 0.067797 | 0.041667 |
| **5** | 0.305556 | 0.791667 | 0.118644 | 0.125000 |
| **6** | 0.083333 | 0.583333 | 0.067797 | 0.083333 |
| **7** | 0.194444 | 0.583333 | 0.084746 | 0.041667 |
| **8** | 0.027778 | 0.375000 | 0.067797 | 0.041667 |
| **9** | 0.166667 | 0.458333 | 0.084746 | 0.000000 |
| **10** | 0.305556 | 0.708333 | 0.084746 | 0.041667 |
| **11** | 0.138889 | 0.583333 | 0.101695 | 0.041667 |
| **12** | 0.138889 | 0.416667 | 0.067797 | 0.000000 |
| **13** | 0.000000 | 0.416667 | 0.016949 | 0.000000 |
| **14** | 0.416667 | 0.833333 | 0.033898 | 0.041667 |
| **15** | 0.388889 | 1.000000 | 0.084746 | 0.125000 |
| **16** | 0.305556 | 0.791667 | 0.050847 | 0.125000 |
| **17** | 0.222222 | 0.625000 | 0.067797 | 0.083333 |
| **18** | 0.388889 | 0.750000 | 0.118644 | 0.083333 |
| **19** | 0.222222 | 0.750000 | 0.084746 | 0.083333 |
| **20** | 0.305556 | 0.583333 | 0.118644 | 0.041667 |
| **21** | 0.222222 | 0.708333 | 0.084746 | 0.125000 |
| **22** | 0.083333 | 0.666667 | 0.000000 | 0.041667 |
| **23** | 0.222222 | 0.541667 | 0.118644 | 0.166667 |
| **24** | 0.138889 | 0.583333 | 0.152542 | 0.041667 |
| **25** | 0.194444 | 0.416667 | 0.101695 | 0.041667 |
| **26** | 0.194444 | 0.583333 | 0.101695 | 0.125000 |
| **27** | 0.250000 | 0.625000 | 0.084746 | 0.041667 |
| **28** | 0.250000 | 0.583333 | 0.067797 | 0.041667 |
| **29** | 0.111111 | 0.500000 | 0.101695 | 0.041667 |
| **...** | ... | ... | ... | ... |
| **120** | 0.722222 | 0.500000 | 0.796610 | 0.916667 |
| **121** | 0.361111 | 0.333333 | 0.661017 | 0.791667 |
| **122** | 0.944444 | 0.333333 | 0.966102 | 0.791667 |
| **123** | 0.555556 | 0.291667 | 0.661017 | 0.708333 |
| **124** | 0.666667 | 0.541667 | 0.796610 | 0.833333 |
| **125** | 0.805556 | 0.500000 | 0.847458 | 0.708333 |
| **126** | 0.527778 | 0.333333 | 0.644068 | 0.708333 |
| **127** | 0.500000 | 0.416667 | 0.661017 | 0.708333 |
| **128** | 0.583333 | 0.333333 | 0.779661 | 0.833333 |
| **129** | 0.805556 | 0.416667 | 0.813559 | 0.625000 |
| **130** | 0.861111 | 0.333333 | 0.864407 | 0.750000 |
| **131** | 1.000000 | 0.750000 | 0.915254 | 0.791667 |
| **132** | 0.583333 | 0.333333 | 0.779661 | 0.875000 |
| **133** | 0.555556 | 0.333333 | 0.694915 | 0.583333 |
| **134** | 0.500000 | 0.250000 | 0.779661 | 0.541667 |
| **135** | 0.944444 | 0.416667 | 0.864407 | 0.916667 |
| **136** | 0.555556 | 0.583333 | 0.779661 | 0.958333 |
| **137** | 0.583333 | 0.458333 | 0.762712 | 0.708333 |
| **138** | 0.472222 | 0.416667 | 0.644068 | 0.708333 |
| **139** | 0.722222 | 0.458333 | 0.745763 | 0.833333 |
| **140** | 0.666667 | 0.458333 | 0.779661 | 0.958333 |
| **141** | 0.722222 | 0.458333 | 0.694915 | 0.916667 |
| **142** | 0.416667 | 0.291667 | 0.694915 | 0.750000 |
| **143** | 0.694444 | 0.500000 | 0.830508 | 0.916667 |
| **144** | 0.666667 | 0.541667 | 0.796610 | 1.000000 |
| **145** | 0.666667 | 0.416667 | 0.711864 | 0.916667 |
| **146** | 0.555556 | 0.208333 | 0.677966 | 0.750000 |
| **147** | 0.611111 | 0.416667 | 0.711864 | 0.791667 |
| **148** | 0.527778 | 0.583333 | 0.745763 | 0.916667 |
| **149** | 0.444444 | 0.416667 | 0.694915 | 0.708333 |

150 rows × 4 columns

The overall flowchart of KMQGA :

First we import libraries, we will needed in future :

In [3]:

**from** \_\_future\_\_ **import** print\_function

**import** matplotlib.pyplot **as** plt

**from** sklearn.cluster **import** KMeans

**import** numpy **as** np

**import** pandas **as** pd

**import** os

**import** sys

**import** random

**import** copy

**import** math

**from** six.moves.urllib.request **import** urlretrieve

*# from six.moves import cPickle as pickle*

**%matplotlib** inline

In [4]:

X **=** np**.**array([[1, 2], [1, 4], [1, 0],

[4, 2], [4, 4], [4, 0]])

kmeans **=** KMeans(n\_clusters**=**6, random\_state**=**0)**.**fit(X)

kmeans**.**cluster\_centers\_

*# kmeans.predict([[0, 0], [4, 4]])*

Out[4]:

array([[ 4., 4.],

[ 1., 0.],

[ 4., 0.],

[ 1., 4.],

[ 1., 2.],

[ 4., 2.]])

Initalizing constants, we are needed in future :

In [5]:

*# Data loading params*

data\_root **=** ''

root\_url **=** 'https://archive.ics.uci.edu/ml/machine-learning-databases/'

iris\_addr **=** 'iris/iris.data'

wine\_addr **=** 'wine/wine.data'

glass\_addr **=** 'glass/glass.data'

spectf\_train **=** 'spect/SPECTF.train'

spectf\_test **=** 'spect/SPECTF.test'

last\_percent\_reported **=** **None** *# needed for showing progress in download*

*# seed initialization*

seed **=** 0

random**.**seed(seed)

np**.**random**.**seed(seed)

*# color map for data visualization*

LABEL\_COLOR\_MAP **=** {

0 : 'r',

1 : '#006266',

2 : 'g',

3 : 'B',

4 : 'c' ,

5 : 'm' ,

6 : 'y' ,

7 : '#C4E538'

}

*# Quantum genetic algorithm essay params*

pop\_size **=** 100

N\_max **=** (100,300)

n\_max **=** 15

m\_max **=** 25

pc **=** 0.9

pm **=** 0.01

pcc **=** (1 **-** pc) **\*** random**.**random() **+** pc

pmm **=** (2**\***pm **-** pm) **\*** random**.**random() **+** pm

This class will provide us with function, we will be needed in future :

In [6]:

**class** ToolBox :

@staticmethod

**def** translate(value, leftMin, leftMax, rightMin, rightMax):

"""this function will map value from range(leftMin,leftMax)

to range(rightMin,rightMax)"""

*# Figure out how 'wide' each range is*

leftSpan **=** leftMax **-** leftMin

rightSpan **=** rightMax **-** rightMin

*# Convert the left range into a 0-1 range (float)*

valueScaled **=** float(value **-** leftMin) **/** float(leftSpan)

value **=** int(rightMin **+** (valueScaled **\*** rightSpan))

**if** value **==** rightMax :

value **=** rightMax **-** 1

*# Convert the 0-1 range into a value in the right range.*

**return** value

@staticmethod

**def** euclideanDistance(x,y):

"return euclidean distance between x and y"

e **=** 0

**for** i,j **in** zip(x,y):

e **+=** (i **-** j)**\*\***2

**return** np**.**sqrt(e)

**Qbit Implementation**

In [7]:

**class** Qbit :

**def** \_\_init\_\_(self) :

self**.**a **=** random**.**random()

self**.**b **=** np**.**sqrt(1 **-** self**.**a**\*\***2)

self**.**bit **=** **None**

**def** \_\_str\_\_(self) :

**return** '({}, {})'**.**format(self**.**a,self**.**b)

**def** mutate(self) :

self**.**a,self**.**b **=** self**.**b,self**.**a

**def** toBit(self) :

"transform qbit to zero or one"

**if** random**.**random() **<** self**.**a**\*\***2 :

self**.**bit **=** 0

**else** :

self**.**bit **=** 1

**return** self**.**bit

**def** rotate(self,bi,isGreater) :

dt **=** 0

sign **=** 0

ri **=** self**.**bit

positive **=** self**.**a **\*** self**.**b **>** 0

aZero **=** **not** self**.**a

bZero **=** **not** self**.**b

*# initializing angle and sign of rotation*

**if**(isGreater) :

**if** **not** ri **and** bi :

dt **=** np**.**pi **\*** .05

**if** aZero :

sign **=** 1

**elif** bZero :

sign **=** 0

**elif** positive :

sign **=** **-**1

**else** :

sign **=** 1

**elif** ri **and** **not** bi :

dt **=** np**.**pi **\*** .025

**if** aZero :

sign **=** 0

**elif** bZero :

sign **=** 1

**elif** positive :

sign **=** 1

**else** :

sign **=** **-**1

**elif** ri **and** bi :

dt **=** np**.**pi **\*** .025

**if** aZero :

sign **=** 0

**elif** bZero :

sign **=** 1

**elif** positive :

sign **=** 1

**else** :

sign **=** **-**1

**else** :

**if** ri **and** **not** bi :

dt **=** np**.**pi **\*** .01

**if** aZero :

sign **=** 1

**elif** bZero :

sign **=** 0

**elif** positive :

sign **=** **-**1

**else** :

sign **=** 1

**elif** ri **and** bi :

dt **=** np**.**pi **\*** .005

**if** aZero :

sign **=** 0

**elif** bZero :

sign **=** 1

**elif** positive :

sign **=** 1

**else** :

sign **=** **-**1

t **=** sign **\*** dt

self**.**a,self**.**b **=** np**.**dot(

np**.**array([[np**.**cos(t),**-**np**.**sin(t)],[np**.**sin(t),np**.**cos(t)]]),np**.**array([self**.**a,self**.**b])

)

**Pattern Implementation**

In [8]:

**class** Pattern :

**def** \_\_init\_\_(self,size) :

self**.**size **=** size

self**.**clusterMembers **=** **None**

self**.**centroid **=** **None**

self**.**id **=** np**.**array([])

**for** \_ **in** range(size) :

self**.**id **=** np**.**append(self**.**id,Qbit())

self**.**real **=** **None**

**def** \_\_str\_\_(self) :

**return** '({})'**.**format(self**.**real)

**def** toReal(self,maxValue) :

"transform pattern to real number which is centroid position"

self**.**real **=** 0

**for** i,qbit **in** enumerate(self**.**id) :

self**.**real **+=** qbit**.**toBit()**\***np**.**power(2,self**.**size **-** i **-** 1)

self**.**real **=** ToolBox**.**translate(

self**.**real,0,

np**.**power(2,len(self**.**id))**-**1,

0,maxValue) *# fit generated number to length of the dataset*

**return** self**.**real

**def** rotate(self,b,isGreater) :

"rotate each qbit"

**for** i,qbit **in** enumerate(self**.**id) :

qbit**.**rotate(b**.**id[i],isGreater)

**def** mutate(self,pos) :

"will mutate the qbit in position {pos} in pattern"

self**.**id[pos]**.**mutate()

**Chromosome Implementation**

In [9]:

**class** Chromosome :

**def** \_\_init\_\_(self,cSize,iSize) :

self**.**size **=** cSize

self**.**iSize **=** iSize

self**.**fitness **=** float('-inf')

self**.**r **=** np**.**array([])

**if** (cSize **==** 0) :

print(cSize)

print('hi babe')

**for** \_ **in** range(cSize) :

self**.**r **=** np**.**append(self**.**r,Pattern(iSize))

**def** \_\_str\_\_(self) :

**return** str([p**.**real **for** p **in** self**.**r])

**def** \_\_len\_\_(self) :

**return** self**.**iSize **\*** self**.**size

**def** toReal(self,dpSize,dataset) :

"transforming each pattern to real number"

**for** p **in** self**.**r :

p**.**toReal(dpSize)

isEqualReal **=** **True**

**while** isEqualReal :

isEqualReal **=** **False**

*#check if there is two pattern with same real number*

**for** p **in** self**.**r :

**for** p2 **in** self**.**r :

**if** p **!=** p2 :

**while** np**.**min([i **==** j **for** i,j **in** zip(dataset[p**.**real],dataset[p2**.**real])]) :

isEqualReal **=** **True**

p**.**toReal(dpSize)

**def** rotate(self,b,isGreater) :

**for** i,pattern **in** enumerate(self**.**r) :

pattern**.**rotate(b**.**r[i],isGreater)

**def** mutate(self) :

"generating a random number and change a and b in position of rnd in chromosome"

rnd **=** np**.**random**.**randint(0,self**.**\_\_len\_\_())

pos **=** self**.**patternPos(rnd)

self**.**r[pos[0]]**.**mutate(pos[1])

**def** computeFitness(self,dataset) :

self**.**toReal(len(dataset),dataset)

*# self.\_kMeansClustering(dataset)*

self**.**\_alocateCluster(dataset)

self**.**\_calculateCentroid(dataset)

s **=** [np**.**mean([ToolBox**.**euclideanDistance(pattern**.**centroid, member) \

**for** member **in** dataset[pattern**.**clusterMembers]]) **for** pattern **in** self**.**r]

self**.**fitness **=** 1**/**np**.**mean([np**.**max([(s[i] **+** s[j])**/**ToolBox**.**euclideanDistance(pattern**.**centroid,pattern2**.**centroid) \

**for** j,pattern2 **in** enumerate(self**.**r) **if** i **!=** j]) **for** i,pattern **in** enumerate(self**.**r)])

**return** self**.**fitness

**def** \_kMeansClustering(self,dataset) :

kmeans **=** KMeans(n\_clusters**=**self**.**size,init**=**np**.**array([dataset[pattern**.**real] **for** pattern **in** self**.**r]),n\_init**=**1)**.**fit(dataset)

*# kmeans = KMeans(n\_clusters=self.size).fit(dataset)*

"Alocating data points to each cluster via their euclidean distance"

**for** i,pattern **in** enumerate(self**.**r) :

self**.**r[i]**.**clusterMembers **=** np**.**array([])**.**astype(int)

**for** i,label **in** enumerate(kmeans**.**labels\_) :

self**.**r[label]**.**clusterMembers **=** np**.**append(self**.**r[label]**.**clusterMembers,i)

"Calculate each centroid point via mean of every cluster member"

self**.**\_calculateCentroid(dataset)

*# for i,pattern in enumerate(self.r):*

*# # calculating centroid for every cluster*

*# self.r[i].centroid = kmeans.cluster\_centers\_[i]*

**def** \_alocateCluster(self,dataset) :

"Alocating data points to each cluster via their euclidean distance"

**for** i,centroid **in** enumerate(self**.**r) :

self**.**r[i]**.**clusterMembers **=** np**.**array([])**.**astype(int)

**for** i,data **in** enumerate(dataset):

minDist **=** float('inf')

minCentroidIndex **=** **-**1

**for** j,centroid **in** enumerate(self**.**r) :

dist **=** ToolBox**.**euclideanDistance(dataset[i],dataset[centroid**.**real])

**if** dist **<** minDist :

minCentroidIndex **=** j

minDist **=** dist

self**.**r[minCentroidIndex]**.**clusterMembers **=** np**.**append(self**.**r[minCentroidIndex]**.**clusterMembers,i)

**def** \_calculateCentroid(self,dataset) :

"Calculate each centroid point via mean of every cluster member"

**for** pattern **in** self**.**r:

*# calculating centroid for every cluster*

**if** len(pattern**.**clusterMembers) **==** 0 :

print(pattern**.**clusterMembers)

pattern**.**centroid **=** np**.**mean(dataset[pattern**.**clusterMembers],axis**=**0)

**def** patternPos(self,qbitPos) :

"""calculating the position of the qbit in pattern

return (patternPos,qbitInPatternPos)"""

**if** qbitPos **>=** self**.**\_\_len\_\_() :

print('warning ' **+** str(qbitPos))

print(int(np**.**floor(qbitPos**/**self**.**iSize)),int(qbitPos **%** self**.**iSize))

**return** (int(np**.**floor(qbitPos**/**self**.**iSize)),int(qbitPos **%** self**.**iSize))

**Population Implementation**

In [10]:

**class** Population :

**def** \_\_init\_\_(self,pSize,cSize,iSize) :

self**.**size **=** pSize

self**.**cSize **=** cSize

self**.**iSize **=** iSize

self**.**bestChromosomeIndex **=** **None**

self**.**p **=** np**.**array([])

**for** \_ **in** range(pSize) :

self**.**p **=** np**.**append(self**.**p,Chromosome(cSize,iSize))

**def** toReal(self) :

**for** c **in** self**.**p :

c**.**toReal()

**def** rotate(self,bestChoromosome) :

**for** chromosome **in** self**.**p :

*# checking if the length of the chromosomes are the same as th*

**if** len(chromosome) **>** len(bestChoromosome) :

chrom **=** Chromosome(int(np**.**ceil(len(bestChoromosome)**/**self**.**iSize)),self**.**iSize)

**for** i **in** range(len(chrom)) :

chromPatternPos **=** chrom**.**patternPos(i)

chrom**.**r[chromPatternPos[0]]**.**id[chromPatternPos[1]] **=** chromosome**.**r[chromPatternPos[0]]**.**id[chromPatternPos[1]]

chromosome **=** chrom

**elif** len(chromosome) **<** len(bestChoromosome) :

chrom **=** Chromosome(int(np**.**ceil(len(bestChoromosome)**/**self**.**iSize)),self**.**iSize)

**for** i **in** range(len(chromosome)) :

chromPatternPos **=** chrom**.**patternPos(i)

chrom**.**r[chromPatternPos[0]]**.**id[chromPatternPos[1]] **=** chromosome**.**r[chromPatternPos[0]]**.**id[chromPatternPos[1]]

chromosome **=** chrom

chromosome**.**rotate(bestChoromosome,bestChoromosome**.**fitness **>** chromosome**.**fitness)

**def** mutate(self,prob) :

**for** chromosome **in** self**.**p :

rnd **=** random**.**random()

**if** rnd **<** prob :

chromosome**.**mutate()

**def** computeFitness(self,dataset) :

maxFit **=** float('-inf')

**for** i,chromosome **in** enumerate(self**.**p) :

chromosome**.**computeFitness(dataset)

**if** chromosome**.**fitness **>** maxFit :

maxFit **=** chromosome**.**fitness

self**.**bestChromosomeIndex **=** i

**return** maxFit

**def** eliteSelection(self,population) :

maxFit **=** np**.**max([ch**.**fitness **for** ch **in** population**.**p])

**if** self**.**p[self**.**bestChromosomeIndex]**.**fitness **>** maxFit :

**for** ch **in** sorted(self**.**p, key**=lambda** x: x**.**fitness) :

**if** ch**.**fitness **>** maxFit :

population**.**p[np**.**random**.**randint(0,self**.**size)] **=** copy**.**deepcopy(ch)

**return** population

**def** selection(self) :

population **=** Population(self**.**size,self**.**cSize,self**.**iSize)

*# Roulette selection*

**for** i **in** range(self**.**size) :

population**.**p[i] **=** copy**.**deepcopy(self**.**roulette())

*# Elite selection*

maxFit **=** np**.**max([ch**.**fitness **for** ch **in** population**.**p])

**if** self**.**p[self**.**bestChromosomeIndex]**.**fitness **>** maxFit :

**for** ch **in** sorted(self**.**p, key**=lambda** x: x**.**fitness) :

**if** ch**.**fitness **>** maxFit :

population**.**p[np**.**random**.**randint(0,self**.**size)] **=** copy**.**deepcopy(ch)

**return** population

**def** roulette(self) :

sumFit **=** np**.**sum([ch**.**fitness **for** ch **in** self**.**p])

pick **=** random**.**uniform(0, sumFit)

current **=** 0

**for** chromosome **in** self**.**p:

current **+=** chromosome**.**fitness

**if** current **>** pick:

**return** chromosome

**def** catastrophe(self,bestChromosome) :

self**.**\_\_init\_\_(self**.**size,self**.**cSize,self**.**iSize)

self**.**p[0] **=** copy**.**deepcopy(bestChromosome)

**def** crossover(self,prob,method**=**'first',dataset**=None**) :

population **=** Population(self**.**size,self**.**cSize,self**.**iSize)

**for** i **in** range(int(self**.**size**/**2)) :

self**.**\_mating(prob,population,i,method)

**if** method **==** 'first' :

population**.**computeFitness(dataset)

**return** self**.**eliteSelection(population)

**else** :

**return** population

**def** \_mating(self,prob,population,j,method**=**'first') :

firstPoint **=** 0

secondPoint **=** 0

isDiffrentParent **=** **False**

**if** method **==** 'first' :

parent1 **=** copy**.**deepcopy(self**.**roulette())

parent2 **=** copy**.**deepcopy(self**.**roulette())

**else** :

parent1 **=** copy**.**deepcopy(self**.**p[np**.**random**.**randint(0,self**.**size)])

parent2 **=** copy**.**deepcopy(self**.**p[np**.**random**.**randint(0,self**.**size)])

*# finding the standard points for crossover*

**if** random**.**random() **<=** prob:

isStandardPoint **=** **False**

**while** (**not** isStandardPoint) :

firstPoint **=** np**.**random**.**randint(0,len(parent1))

secondPoint **=** np**.**random**.**randint(0,len(parent2))

firstChildLen **=** (firstPoint **+** len(parent2) **-** secondPoint)

secondChildLen **=** (len(parent1) **-** firstPoint **+** secondPoint)

isStandardPoint **=** (firstChildLen **%** self**.**iSize **==** 0) **and** (firstChildLen**/**self**.**iSize **>** 1) **and** \

(secondChildLen **%** self**.**iSize **==** 0) **and** (secondChildLen**/**self**.**iSize **>** 1)

*# 2 point crossover*

firstChildLen **=** firstPoint **+** len(parent2) **-** secondPoint

secondChildLen **=** len(parent1) **-** firstPoint **+** secondPoint

child1 **=** Chromosome(int(np**.**ceil(firstChildLen**/**self**.**iSize)),self**.**iSize)

child2 **=** Chromosome(int(np**.**ceil(secondChildLen**/**self**.**iSize)),self**.**iSize)

**for** i **in** range(firstChildLen) :

childPatternPos **=** child1**.**patternPos(i)

**if** i **<** firstPoint :

parentPatternPos **=** parent1**.**patternPos(i)

child1**.**r[childPatternPos[0]]**.**id[childPatternPos[1]] **=** parent1**.**r[parentPatternPos[0]]**.**id[parentPatternPos[1]]

**else** :

parentPatternPos **=** parent2**.**patternPos(secondPoint **+** (i **-** firstPoint))

child1**.**r[childPatternPos[0]]**.**id[childPatternPos[1]] **=** parent2**.**r[parentPatternPos[0]]**.**id[parentPatternPos[1]]

**for** i **in** range(secondChildLen) :

childPatternPos **=** child2**.**patternPos(i)

**if** i **<** secondPoint :

parentPatternPos **=** parent2**.**patternPos(i)

child2**.**r[childPatternPos[0]]**.**id[childPatternPos[1]] **=** parent2**.**r[parentPatternPos[0]]**.**id[parentPatternPos[1]]

**else** :

parentPatternPos **=** parent1**.**patternPos(firstPoint **+** (i **-** secondPoint))

child2**.**r[childPatternPos[0]]**.**id[childPatternPos[1]] **=** parent1**.**r[parentPatternPos[0]]**.**id[parentPatternPos[1]]

population**.**p[2**\***j] **=** copy**.**deepcopy(child2)

population**.**p[2**\***j**+**1] **=** copy**.**deepcopy(child1)

**Algorithm Implementation**

In [11]:

**def** quantumGeneticAlgorithm(dataset,popSize,pcc,pc,pm,pmm,preCriterion,catCriterion,iterNum,initPatternNum **=** **None**) :

"main method, we will implement algorithm in it"

bestFitArr **=** np**.**array([])

bestFitCentArr **=** np**.**array([])

bestChromosome **=** **None**

bestSameIter **=** 0

bestFitness **=** float('-inf')

populations **=** np**.**full((iterNum),**None**)

*# randomly choosing initial pattern number in a chromosome in range(2,np.sqrt(N) + 1)*

**if** initPatternNum :

initialPatternNum **=** initPatternNum

**else** :

initialPatternNum **=** random**.**randint(2,np**.**floor(np**.**sqrt(len(dataset)) **+** 1))

PatternSize **=** int(np**.**ceil(np**.**log2(len(dataset))))

populations[0] **=** Population(popSize,initialPatternNum,PatternSize)

bestFit **=** populations[0]**.**computeFitness(dataset)

bestFitArr **=** np**.**append(bestFitArr,bestFit)

bestFitCentArr **=** np**.**append(bestFitCentArr,len(populations[0]**.**p[populations[0]**.**bestChromosomeIndex]**.**r))

**if** bestFit **>** bestFitness :

bestChromosome **=** copy**.**deepcopy(populations[0]**.**p[populations[0]**.**bestChromosomeIndex])

bestFitness **=** bestFit

bestSameIter **=** 0

**else** :

bestSameIter **+=** 1

**for** generation **in** range(1,iterNum) :

print('--------------------generation : {} ------------------'**.**format(generation))

print('best fitness : {}'**.**format(bestFit))

print('best chromosome cluster numbers : {}'**.**format(len(bestChromosome**.**r)))

print('best chrom fit : {}'**.**format(bestFitness))

print('best chrom cluster numbers : {}'**.**format(len(bestChromosome**.**r)))

**if** bestSameIter **<** preCriterion :

populations[generation **-** 1] **=** populations[generation **-** 1]**.**selection()

*# populations[generation - 1] = populations[generation - 1].crossover(pc,'second',dataset)*

populations[generation **-** 1]**.**mutate(pm)

bestFit **=** populations[generation **-** 1]**.**computeFitness(dataset)

**if** bestFit **>** bestFitness :

bestChromosome **=** copy**.**deepcopy(populations[generation **-** 1]**.**p[populations[generation **-** 1]**.**bestChromosomeIndex])

bestFitness **=** bestFit

bestSameIter **=** 0

**if** bestSameIter **<** catCriterion :

populations[generation **-** 1]**.**rotate(bestChromosome)

**else** :

populations[generation **-** 1]**.**catastrophe(bestChromosome)

bestSameIter **=** 0

**else** :

populations[generation **-** 1] **=** populations[generation **-** 1]**.**selection()

*# populations[generation - 1] = populations[generation - 1].crossover(pcc,'second',dataset)*

populations[generation **-** 1]**.**mutate(pmm)

bestFit **=** populations[generation **-** 1]**.**computeFitness(dataset)

**if** bestFit **>** bestFitness :

bestChromosome **=** copy**.**deepcopy(populations[generation **-** 1]**.**p[populations[generation **-** 1]**.**bestChromosomeIndex])

bestFitness **=** bestFit

bestSameIter **=** 0

**if** bestSameIter **<** catCriterion :

populations[generation **-** 1]**.**rotate(bestChromosome)

**else** :

populations[generation **-** 1]**.**catastrophe(bestChromosome)

bestSameIter **=** 0

populations[generation] **=** populations[generation **-** 1]

bestFit **=** populations[generation]**.**computeFitness(dataset)

bestFitCentArr **=** np**.**append(bestFitCentArr,len(populations[generation]**.**p[populations[generation]**.**bestChromosomeIndex]**.**r))

bestFitArr **=** np**.**append(bestFitArr,bestFit)

**if** bestFit **>** bestFitness :

bestChromosome **=** copy**.**deepcopy(populations[generation]**.**p[populations[generation]**.**bestChromosomeIndex])

bestFitness **=** bestFit

bestSameIter **=** 0

**else** :

bestSameIter **+=** 1

**return** bestFitArr,bestChromosome

**Rotation Table**

In [12]:

**def** colorMapGenerator(clusters,dataset) :

"this color will assign color to each data point in dataset"

c **=** np**.**full((len(dataset)),**None**)

**for** i,cluster **in** enumerate(clusters) :

c[cluster**.**clusterMembers] **=** LABEL\_COLOR\_MAP[i]

**return** c

**Running KMQGA on first simulated dataset**

In [34]:

sda1 **=** sda(1)

sda1\_response **=** quantumGeneticAlgorithm(sda1,pop\_size,pcc,pc,pm,pmm,n\_max,m\_max,10)

--------------------generation : 1 ------------------

best fitness : 1.5145969217728323

best chromosome cluster numbers : 15

best chrom fit : 1.5145969217728323

best chrom cluster numbers : 15

--------------------generation : 2 ------------------

best fitness : 3.6262594323898645

best chromosome cluster numbers : 3

best chrom fit : 3.6262594323898645

best chrom cluster numbers : 3

--------------------generation : 3 ------------------

best fitness : 3.6262594323898645

best chromosome cluster numbers : 3

best chrom fit : 3.6262594323898645

best chrom cluster numbers : 3

--------------------generation : 4 ------------------

best fitness : 3.6262594323898645

best chromosome cluster numbers : 3

best chrom fit : 3.6262594323898645

best chrom cluster numbers : 3

--------------------generation : 5 ------------------

best fitness : 3.6262594323898645

best chromosome cluster numbers : 3

best chrom fit : 3.6262594323898645

best chrom cluster numbers : 3

--------------------generation : 6 ------------------

best fitness : 3.6262594323898645

best chromosome cluster numbers : 3

best chrom fit : 3.6262594323898645

best chrom cluster numbers : 3

--------------------generation : 7 ------------------

best fitness : 3.6262594323898645

best chromosome cluster numbers : 3

best chrom fit : 3.6262594323898645

best chrom cluster numbers : 3

--------------------generation : 8 ------------------

best fitness : 3.6262594323898645

best chromosome cluster numbers : 3

best chrom fit : 3.6262594323898645

best chrom cluster numbers : 3

--------------------generation : 9 ------------------

best fitness : 3.6262594323898645

best chromosome cluster numbers : 3

best chrom fit : 3.6262594323898645

best chrom cluster numbers : 3

In [ ]:

plt**.**plot(list(range(10)),sda1\_response[0])

plt**.**ylabel('fitness value')

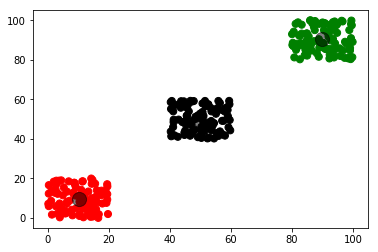
plt**.**xlabel('iteration number')

In [142]:

plt**.**scatter(sda1[:, 0], sda1[:, 1],c**=**colorMapGenerator(sda1\_response[1]**.**r,sda1), s**=**50, cmap**=**'viridis')

centers **=** np**.**array([pattern**.**centroid **for** pattern **in** sda1\_response[1]**.**r])

plt**.**scatter(centers[:,0], centers[:, 1], c**=**'black', s**=**200, alpha**=**0.5);



as u see it found all of the clusters correctly.

**Running KMQGA on second simulated dataset**

In [143]:

sda2 **=** sda(2)

sda2\_response **=** quantumGeneticAlgorithm(sda2,pop\_size,pcc,pc,pm,pmm,n\_max,m\_max,10)

--------------------generation : 1 ------------------

generation : 1.889294252033498

generation : 3

--------------------generation : 2 ------------------

generation : 3.636934372001022

generation : 4

--------------------generation : 3 ------------------

generation : 3.636934372001022

generation : 4

--------------------generation : 4 ------------------

generation : 3.636934372001022

generation : 4

--------------------generation : 5 ------------------

generation : 3.636934372001022

generation : 4

--------------------generation : 6 ------------------

generation : 3.636934372001022

generation : 4

--------------------generation : 7 ------------------

generation : 3.636934372001022

generation : 4

--------------------generation : 8 ------------------

generation : 3.636934372001022

generation : 4

--------------------generation : 9 ------------------

generation : 3.636934372001022

generation : 4

In [146]:

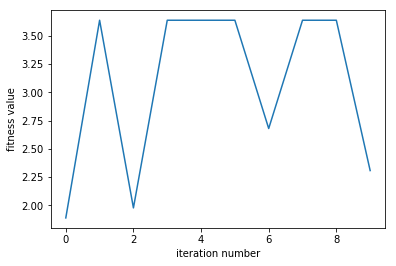
plt**.**plot(list(range(10)),sda2\_response[0])

plt**.**ylabel('fitness value')

plt**.**xlabel('iteration number')

Out[146]:

Text(0.5,0,'iteration number')



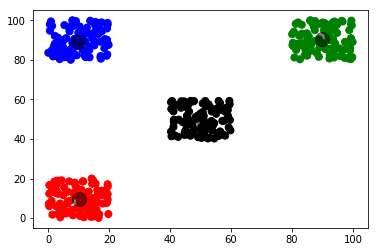
as u see KMQGA is so non-deterministic and it can't converge to anything slowly , its fitness value quickly changed in every generation.

In [147]:

plt**.**scatter(sda2[:, 0], sda2[:, 1],c**=**colorMapGenerator(sda2\_response[1]**.**r,sda2), s**=**50, cmap**=**'viridis')

centers **=** np**.**array([pattern**.**centroid **for** pattern **in** sda2\_response[1]**.**r])

plt**.**scatter(centers[:,0], centers[:, 1], c**=**'black', s**=**200, alpha**=**0.5);



**Running KMQGA on Third simulated dataset**

In [38]:

sda3 **=** sda(3)

sda3\_response **=** quantumGeneticAlgorithm(sda3,pop\_size,pcc,pc,pm,pmm,n\_max,m\_max,N\_max[1])

--------------------generation : 1 ------------------

best fitness : 1.4901137088578937

best chromosome cluster numbers : 25

best chrom fit : 1.4901137088578937

best chrom cluster numbers : 25

--------------------generation : 2 ------------------

best fitness : 2.791091186894506

best chromosome cluster numbers : 5

best chrom fit : 2.873763028350168

best chrom cluster numbers : 5

--------------------generation : 3 ------------------

best fitness : 2.0512788216643156

best chromosome cluster numbers : 5

best chrom fit : 2.873763028350168

best chrom cluster numbers : 5

--------------------generation : 4 ------------------

best fitness : 2.873763028350168

best chromosome cluster numbers : 5

best chrom fit : 2.873763028350168

best chrom cluster numbers : 5

--------------------generation : 5 ------------------

best fitness : 2.905951014003348

best chromosome cluster numbers : 7

best chrom fit : 2.905951014003348

best chrom cluster numbers : 7

--------------------generation : 6 ------------------

best fitness : 2.4208677006350188

best chromosome cluster numbers : 7

best chrom fit : 2.905951014003348

best chrom cluster numbers : 7

--------------------generation : 7 ------------------

best fitness : 2.1241087214597294

best chromosome cluster numbers : 7

best chrom fit : 2.905951014003348

best chrom cluster numbers : 7

--------------------generation : 8 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 9 ------------------

best fitness : 2.420867700635018

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 10 ------------------

best fitness : 2.873763028350168

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 11 ------------------

best fitness : 2.873763028350168

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 12 ------------------

best fitness : 2.873763028350168

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 13 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 14 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 15 ------------------

best fitness : 2.905951014003348

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 16 ------------------

best fitness : 2.905951014003348

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 17 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 18 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354652

best chrom cluster numbers : 8

--------------------generation : 19 ------------------

best fitness : 4.501955748354653

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 20 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 21 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 22 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 23 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 24 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 25 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 26 ------------------

best fitness : 4.501955748354653

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 27 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 28 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 29 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 30 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 31 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 32 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 33 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 34 ------------------

best fitness : 4.501955748354653

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 35 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 36 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 37 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 38 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 39 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 40 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 41 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 42 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 43 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 44 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 45 ------------------

best fitness : 1.9069221947754862

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 46 ------------------

best fitness : 1.8637868595707743

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 47 ------------------

best fitness : 2.9059510140033487

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 48 ------------------

best fitness : 2.6489553527462673

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 49 ------------------

best fitness : 2.8737630283501683

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 50 ------------------

best fitness : 2.8737630283501683

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 51 ------------------

best fitness : 2.9059510140033487

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 52 ------------------

best fitness : 2.8737630283501683

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 53 ------------------

best fitness : 2.8737630283501683

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 54 ------------------

best fitness : 2.9059510140033487

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 55 ------------------

best fitness : 4.501955748354652

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

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best fitness : 2.9059510140033487

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

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best fitness : 4.501955748354652

best chromosome cluster numbers : 8

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best chromosome cluster numbers : 8

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--------------------generation : 59 ------------------

best fitness : 2.8737630283501683

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

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best fitness : 2.9059510140033487

best chromosome cluster numbers : 8

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best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

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best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

--------------------generation : 67 ------------------

best fitness : 2.905951014003348

best chromosome cluster numbers : 8

best chrom fit : 4.501955748354653

best chrom cluster numbers : 8

**---------------------------------------------------------------------------**

**KeyboardInterrupt** Traceback (most recent call last)

**<ipython-input-38-5945ebd7a7ee>** in <module>**()**

1 sda3 **=** sda**(3)**

**----> 2** sda3\_response **=** quantumGeneticAlgorithm**(**sda3**,**pop\_size**,**pcc**,**pc**,**pm**,**pmm**,**n\_max**,**m\_max**,**N\_max**[1])**

**<ipython-input-32-71e65796cfc8>** in quantumGeneticAlgorithm**(dataset, popSize, pcc, pc, pm, pmm, preCriterion, catCriterion, iterNum, initPatternNum)**

47 populations**[**generation **-** **1]** **=** populations**[**generation **-** **1].**crossover**(**pcc**,'second',**dataset**)**

48 populations**[**generation **-** **1].**mutate**(**pmm**)**

**---> 49** bestFit **=** populations**[**generation **-** **1].**computeFitness**(**dataset**)**

50 **if** bestFit **>** bestFitness **:**

51 bestChromosome **=** copy**.**deepcopy**(**populations**[**generation **-** **1].**p**[**populations**[**generation **-** **1].**bestChromosomeIndex**])**

**<ipython-input-31-9721c50bff2a>** in computeFitness**(self, dataset)**

40 maxFit **=** float**('-inf')**

41 **for** i**,**chromosome **in** enumerate**(**self**.**p**)** **:**

**---> 42** chromosome**.**computeFitness**(**dataset**)**

43 **if** chromosome**.**fitness **>** maxFit **:**

44 maxFit **=** chromosome**.**fitness

**<ipython-input-30-829fb8346d51>** in computeFitness**(self, dataset)**

44 **def** computeFitness**(**self**,**dataset**)** **:**

45 self**.**toReal**(**len**(**dataset**),**dataset**)**

**---> 46** self**.**\_kMeansClustering**(**dataset**)**

47 **# self.\_alocateCluster(dataset)**

48 **# self.\_calculateCentroid(dataset)**

**<ipython-input-30-829fb8346d51>** in \_kMeansClustering**(self, dataset)**

60

61 **for** i**,**label **in** enumerate**(**kmeans**.**labels\_**)** **:**

**---> 62** self**.**r**[**label**].**clusterMembers **=** np**.**append**(**self**.**r**[**label**].**clusterMembers**,**i**)**

63

64 **"Calculate each centroid point via mean of every cluster member"**

**C:\Program Files (x86)\Microsoft Visual Studio\Shared\Anaconda3\_64\envs\deeplearning\lib\site-packages\numpy\lib\function\_base.py** in append**(arr, values, axis)**

5164 values **=** ravel**(**values**)**

5165 axis **=** arr**.**ndim**-1**

**-> 5166 return** concatenate**((**arr**,** values**),** axis**=**axis**)**

**KeyboardInterrupt**:

In [155]:

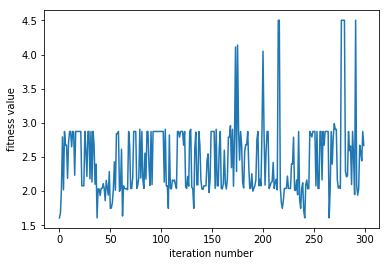
plt**.**plot(list(range(N\_max[1])),sda3\_response[0])

plt**.**ylabel('fitness value')

plt**.**xlabel('iteration number')

Out[155]:

Text(0.5,0,'iteration number')

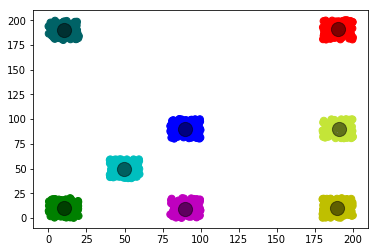


In [170]:

plt**.**scatter(sda3[:, 0], sda3[:, 1],c**=**colorMapGenerator(sda3\_response[1]**.**r,sda3), s**=**50, cmap**=**'red')

centers **=** np**.**array([pattern**.**centroid **for** pattern **in** sda3\_response[1]**.**r])

plt**.**scatter(centers[:,0], centers[:, 1], c**=**'black', s**=**200, alpha**=**0.5);



In [ ]:

iris\_dataset **=** read\_df(iris\_addr)[:,:**-**1]**.**astype(float)

iris\_response **=** quantumGeneticAlgorithm(iris\_dataset,pop\_size,pcc,pc,pm,pmm,n\_max,m\_max,N\_max[1],3)

--------------------generation : 1 ------------------

best fitness : 1.7632131963588025

best chromosome cluster numbers : 3

best chrom fit : 1.7632131963588025

best chrom cluster numbers : 3

--------------------generation : 2 ------------------

best fitness : 1.7295533527886473

best chromosome cluster numbers : 3

best chrom fit : 1.7632131963588025

best chrom cluster numbers : 3

--------------------generation : 3 ------------------

best fitness : 2.09291642626602

best chromosome cluster numbers : 3

best chrom fit : 2.09291642626602

best chrom cluster numbers : 3

--------------------generation : 4 ------------------

best fitness : 2.09291642626602

best chromosome cluster numbers : 3

best chrom fit : 2.09291642626602

best chrom cluster numbers : 3

--------------------generation : 5 ------------------

best fitness : 2.09291642626602

best chromosome cluster numbers : 3

best chrom fit : 2.09291642626602

best chrom cluster numbers : 3

--------------------generation : 6 ------------------

best fitness : 1.7628004643388027

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--------------------generation : 7 ------------------

best fitness : 1.7715082013081347

best chromosome cluster numbers : 3

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--------------------generation : 8 ------------------

best fitness : 1.8139540177343123

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best chrom cluster numbers : 3

--------------------generation : 9 ------------------

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best chromosome cluster numbers : 3

best chrom fit : 2.09291642626602

best chrom cluster numbers : 3

--------------------generation : 10 ------------------

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best chromosome cluster numbers : 3

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--------------------generation : 11 ------------------

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--------------------generation : 16 ------------------

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best fitness : 1.7870774635083644

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best fitness : 1.7715082013081347

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--------------------generation : 20 ------------------

best fitness : 1.797255293500889

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--------------------generation : 21 ------------------

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--------------------generation : 89 ------------------

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--------------------generation : 94 ------------------

best fitness : 1.752593866403893

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best fitness : 1.8780448017176326

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--------------------generation : 106 ------------------

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--------------------generation : 108 ------------------

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--------------------generation : 109 ------------------

best fitness : 1.6659042761400151

best chromosome cluster numbers : 3

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--------------------generation : 110 ------------------

best fitness : 1.6526012702105426

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--------------------generation : 118 ------------------

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--------------------generation : 119 ------------------

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--------------------generation : 120 ------------------

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best chrom cluster numbers : 3

--------------------generation : 281 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 282 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 283 ------------------

best fitness : 1.9228339292959287

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 284 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 285 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 286 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 287 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 288 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 289 ------------------

best fitness : 2.1695978389962987

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 290 ------------------

best fitness : 2.1695978389962987

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 291 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 292 ------------------

best fitness : 1.7819926800713044

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 293 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 294 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 295 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 296 ------------------

best fitness : 1.8609833931591282

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 297 ------------------

best fitness : 1.701080322967199

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 298 ------------------

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best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

--------------------generation : 299 ------------------

best fitness : 2.1239802789975797

best chromosome cluster numbers : 3

best chrom fit : 2.6521336945525813

best chrom cluster numbers : 3

In [123]:

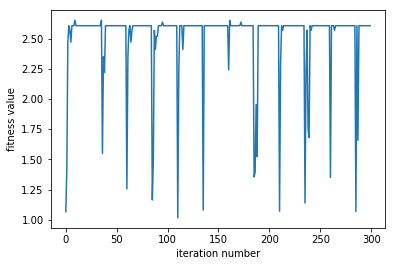
plt**.**plot(list(range(300)),iris\_response[0])

plt**.**ylabel('fitness value')

plt**.**xlabel('iteration number')

Out[123]:

Text(0.5,0,'iteration number')



In [ ]:

wine\_dataset **=** read\_df(wine\_addr)[:,1:]

*# wine\_dataset.shape*

*# X = np.array([[1, 2], [1, 4], [1, 0],*

*# [4, 2], [4, 4], [4, 0]])*

*# kmeans = KMeans(n\_clusters=3,init=np.array([wine\_dataset[1],wine\_dataset[10],wine\_dataset[80]]),n\_init=1).fit(wine\_dataset)*

*# kmeans.cluster\_centers\_*

wine\_response **=** quantumGeneticAlgorithm(wine\_dataset,pop\_size,pcc,pc,pm,pmm,n\_max,m\_max,N\_max[1],3)

--------------------generation : 1 ------------------

best fitness : 1.9506533175483063

best chromosome cluster numbers : 3

best chrom fit : 1.9506533175483063

best chrom cluster numbers : 3

--------------------generation : 2 ------------------

best fitness : 2.0527095262396475

best chromosome cluster numbers : 3

best chrom fit : 2.1164623801686417

best chrom cluster numbers : 3

--------------------generation : 3 ------------------

best fitness : 2.243888888069059

best chromosome cluster numbers : 3

best chrom fit : 2.243888888069059

best chrom cluster numbers : 3

--------------------generation : 4 ------------------

best fitness : 2.4548855382997057

best chromosome cluster numbers : 3

best chrom fit : 2.4548855382997057

best chrom cluster numbers : 3

--------------------generation : 5 ------------------

best fitness : 2.1922064002255395

best chromosome cluster numbers : 3

best chrom fit : 2.4548855382997057

best chrom cluster numbers : 3

--------------------generation : 6 ------------------

best fitness : 1.9462549799811946

best chromosome cluster numbers : 3

best chrom fit : 2.4548855382997057

best chrom cluster numbers : 3

--------------------generation : 7 ------------------

best fitness : 1.9409880996515287

best chromosome cluster numbers : 3

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best chrom cluster numbers : 3

--------------------generation : 8 ------------------

best fitness : 1.9495648265409058

best chromosome cluster numbers : 3

best chrom fit : 2.4548855382997057

best chrom cluster numbers : 3

--------------------generation : 9 ------------------

best fitness : 1.9395654732538483

best chromosome cluster numbers : 3

best chrom fit : 2.4548855382997057

best chrom cluster numbers : 3

--------------------generation : 10 ------------------

best fitness : 1.9981348162746437

best chromosome cluster numbers : 3

best chrom fit : 2.4548855382997057

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--------------------generation : 11 ------------------

best fitness : 1.960158256644605

best chromosome cluster numbers : 3

best chrom fit : 2.4548855382997057

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--------------------generation : 12 ------------------

best fitness : 1.9981348162746437

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--------------------generation : 13 ------------------

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--------------------generation : 14 ------------------

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--------------------generation : 15 ------------------

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--------------------generation : 16 ------------------

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--------------------generation : 18 ------------------

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--------------------generation : 19 ------------------

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--------------------generation : 20 ------------------

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--------------------generation : 21 ------------------

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--------------------generation : 22 ------------------

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--------------------generation : 23 ------------------

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--------------------generation : 24 ------------------

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--------------------generation : 25 ------------------

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--------------------generation : 26 ------------------

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--------------------generation : 27 ------------------

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--------------------generation : 28 ------------------

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best chrom fit : 2.573191206406723

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--------------------generation : 29 ------------------

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--------------------generation : 30 ------------------

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--------------------generation : 33 ------------------

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--------------------generation : 50 ------------------

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--------------------generation : 54 ------------------

best fitness : 2.551294183862262

best chromosome cluster numbers : 3

best chrom fit : 2.727221839692173

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--------------------generation : 55 ------------------

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--------------------generation : 94 ------------------

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--------------------generation : 95 ------------------

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best chromosome cluster numbers : 3

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--------------------generation : 96 ------------------

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--------------------generation : 110 ------------------

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--------------------generation : 116 ------------------

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--------------------generation : 118 ------------------

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--------------------generation : 122 ------------------

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--------------------generation : 124 ------------------

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--------------------generation : 125 ------------------

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best chrom cluster numbers : 3

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--------------------generation : 131 ------------------

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best chrom fit : 2.8209190774111272

best chrom cluster numbers : 3

--------------------generation : 132 ------------------

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best chromosome cluster numbers : 3

best chrom fit : 3.245267990484283

best chrom cluster numbers : 3

In [28]:

wine\_dataset **=** read\_df(wine\_addr)[:,1:]

wine\_dataset**.**shape

*# X = np.array([[1, 2], [1, 4], [1, 0],*

*# [4, 2], [4, 4], [4, 0]])*

kmeans **=** KMeans(n\_clusters**=**3,init**=**np**.**array([wine\_dataset[1],wine\_dataset[10],wine\_dataset[80]]),n\_init**=**1)**.**fit(wine\_dataset)

In [22]:

centers **=** np**.**array([pattern**.**centroid **for** pattern **in** wine\_response[1]**.**r])

centers**.**shape

Out[22]:

(2, 13)

In [94]:

plt**.**plot(list(range(N\_max[1])),wine\_response[0])

plt**.**ylabel('fitness value')

plt**.**xlabel('iteration number')

Out[94]:

<matplotlib.text.Text at 0x18e92ef3a58>

In [14]:

glass\_dataset **=** read\_df(glass\_addr)

glass\_dataset

*# glass\_response = quantumGeneticAlgorithm(glass\_dataset,pop\_size,pcc,pc,pm,pmm,n\_max,m\_max,N\_max[1],2)*

Out[14]:

array([[ 1. , 1.52101, 13.64 , ..., 0. , 0. ,

1. ],

[ 2. , 1.51761, 13.89 , ..., 0. , 0. ,

1. ],

[ 3. , 1.51618, 13.53 , ..., 0. , 0. ,

1. ],

...,

[212. , 1.52065, 14.36 , ..., 1.64 , 0. ,

7. ],

[213. , 1.51651, 14.38 , ..., 1.57 , 0. ,

7. ],

[214. , 1.51711, 14.23 , ..., 1.67 , 0. ,

7. ]])

In [ ]:

centers **=** np**.**array([pattern**.**centroid **for** pattern **in** glass\_response[1]**.**r])

centers**.**shape

In [100]:

plt**.**plot(list(range(N\_max[1])),glass\_response[0])

plt**.**ylabel('fitness value')

plt**.**xlabel('iteration number')

Out[100]:

<matplotlib.text.Text at 0x18eadaeddd8>

In [40]:

spectf\_dataset **=** read\_df(spectf\_train)[:,1:]

spectf\_response **=** quantumGeneticAlgorithm(spectf\_dataset,pop\_size,pcc,pc,pm,pmm,n\_max,m\_max,N\_max[1],2)

--------------------generation : 1 ------------------

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best chromosome cluster numbers : 2

best chrom fit : 0.8629255753038232

best chrom cluster numbers : 2

--------------------generation : 2 ------------------

best fitness : 4.070396086588954

best chromosome cluster numbers : 2

best chrom fit : 4.070396086588954

best chrom cluster numbers : 2

--------------------generation : 3 ------------------

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best chrom cluster numbers : 2

In [29]:

**def** three\_point\_bruteforce(dataset) :

bestFit **=** float('-inf')

bestI **=** 0

bestJ **=** 1

bestZ **=** 2

**for** first **in** range(dataset**.**shape[0]) :

**for** second **in** range(first,dataset**.**shape[0]) :

**if** equality(dataset[first],dataset[second]) :

**continue**

**for** third **in** range(second,dataset**.**shape[0]) :

**if** equality(dataset[first],dataset[third]) :

**continue**

**if** equality(dataset[second],dataset[third]) :

**continue**

fitness **=** calFitThird(dataset,first,second,third)

**if** fitness **>** bestFit :

bestFit **=** fitness

bestI **=** first

bestJ **=** second

bestZ **=** third

**if**((first **+** second **+** third) **%** 300 **==** 0) :

print(bestFit)

print('------------------------------------')

print(bestFit)

**return** bestFit,bestI,bestJ,bestZ

**def** calFitThird(dataset,first,second,third) :

clusterMembers **=** np**.**array([**None**,**None**,**None**])

**for** i,pattern **in** enumerate(clusterMembers) :

clusterMembers[i] **=** np**.**array([])**.**astype(int)

**for** i,data **in** enumerate(dataset):

minDist **=** float('inf')

minCentroidIndex **=** **-**1

**for** j,centroid **in** enumerate([first,second,third]) :

dist **=** ToolBox**.**euclideanDistance(dataset[i],dataset[centroid])

**if** dist **<** minDist :

minCentroidIndex **=** j

minDist **=** dist

clusterMembers[minCentroidIndex] **=** np**.**append(clusterMembers[minCentroidIndex],i)

"Calculate each centroid point via mean of every cluster member"

centroids **=** np**.**array([**None**,**None**,**None**])

**for** i,cm **in** enumerate(clusterMembers):

*# calculating centroid for every cluster*

**if** len(cm) **==** 0 :

print(cm)

centroids[i] **=** np**.**mean(dataset[cm],axis**=**0)

s **=** [np**.**mean([ToolBox**.**euclideanDistance(pattern, member) \

**for** member **in** dataset[clusterMembers[i]]]) **for** i,pattern **in** enumerate(centroids)]

fitness **=** 1**/**np**.**mean([np**.**max([(s[i] **+** s[j])**/**ToolBox**.**euclideanDistance(pattern,pattern2) \

**for** j,pattern2 **in** enumerate(centroids) **if** i **!=** j]) **for** i,pattern **in** enumerate(centroids)])

**return** fitness

**def** two\_point\_bruteforce(dataset) :

bestFit **=** float('-inf')

bestI **=** 0

bestJ **=** 1

**for** first **in** range(dataset**.**shape[0]) :

**for** second **in** range(first,dataset**.**shape[0]) :

**if** equality(dataset[first],dataset[second]) :

**continue**

fitness **=** calFit\_2(dataset,first,second)

**if** fitness **>** bestFit :

bestFit **=** fitness

bestI **=** first

bestJ **=** second

**if**((first **+** second) **%** 100 **==** 0) :

print(bestFit)

**return** bestFit,bestI,bestJ

**def** calFit(dataset,first,second) :

kmeans **=** KMeans(n\_clusters**=**2,init**=**np**.**array([dataset[pattern] **for** pattern **in** [first,second]]),n\_init**=**1)**.**fit(dataset)

clusterMembers **=** np**.**array([**None**,**None**])

**for** i,pattern **in** enumerate(clusterMembers) :

clusterMembers[i] **=** np**.**array([])**.**astype(int)

**for** i,label **in** enumerate(kmeans**.**labels\_) :

clusterMembers[label] **=** np**.**append(clusterMembers[label],i)

"Calculate each centroid point via mean of every cluster member"

centroids **=** np**.**array([**None**,**None**])

**for** i,cm **in** enumerate(clusterMembers):

*# calculating centroid for every cluster*

**if** len(cm) **==** 0 :

print(cm)

centroids[i] **=** np**.**mean(dataset[cm],axis**=**0)

s **=** [np**.**mean([ToolBox**.**euclideanDistance(pattern, member) \

**for** member **in** dataset[clusterMembers[i]]]) **for** i,pattern **in** enumerate(centroids)]

fitness **=** 1**/**np**.**mean([np**.**max([(s[i] **+** s[j])**/**ToolBox**.**euclideanDistance(pattern,pattern2) \

**for** j,pattern2 **in** enumerate(centroids) **if** i **!=** j]) **for** i,pattern **in** enumerate(centroids)])

**return** fitness

**def** calFit\_2(dataset,first,second) :

*# kmeans = KMeans(n\_clusters=2,init=np.array([dataset[pattern] for pattern in [first,second]]),n\_init=1).fit(dataset)*

clusterMembers **=** np**.**array([**None**,**None**])

**for** i,pattern **in** enumerate(clusterMembers) :

clusterMembers[i] **=** np**.**array([])**.**astype(int)

**for** i,data **in** enumerate(dataset):

minDist **=** float('inf')

minCentroidIndex **=** **-**1

**for** j,centroid **in** enumerate([first,second]) :

dist **=** ToolBox**.**euclideanDistance(dataset[i],dataset[centroid])

**if** dist **<** minDist :

minCentroidIndex **=** j

minDist **=** dist

clusterMembers[minCentroidIndex] **=** np**.**append(clusterMembers[minCentroidIndex],i)

*# print(clusterMembers)*

"Calculate each centroid point via mean of every cluster member"

centroids **=** np**.**array([**None**,**None**])

**for** i,cm **in** enumerate(clusterMembers):

*# calculating centroid for every cluster*

**if** len(cm) **==** 0 :

print(cm)

centroids[i] **=** np**.**mean(dataset[cm],axis**=**0)

s **=** [np**.**mean([ToolBox**.**euclideanDistance(pattern, member) \

**for** member **in** dataset[clusterMembers[i]]]) **for** i,pattern **in** enumerate(centroids)]

fitness **=** 1**/**np**.**mean([np**.**max([(s[i] **+** s[j])**/**ToolBox**.**euclideanDistance(pattern,pattern2) \

**for** j,pattern2 **in** enumerate(centroids) **if** i **!=** j]) **for** i,pattern **in** enumerate(centroids)])

**return** fitness

**def** equality(firstDp,secondDp) :

**if** (len(firstDp) **!=** len(secondDp)) :

print("Error Length of array ")

**return** **None**

**for** i **in** range(len(firstDp)) :

**if** firstDp[i] **!=** secondDp[i] :

**return** **False**

**return** **True**

In [17]:

spectf\_dataset **=** read\_df(spectf\_train)[:,1:]

*# fitness,bestI,bestJ = two\_point\_bruteforce(spectf\_dataset)*

spectf\_dataset**.**shape

Out[17]:

(80, 44)

In [ ]:

wine\_dataset **=** read\_df(wine\_addr)[:,1:]

fitness,bestI,bestJ,bestZ **=** three\_point\_bruteforce(np**.**array(minmax(pd**.**DataFrame(wine\_dataset))))

wine\_dataset**.**shape

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In [30]:

iris\_dataset **=** read\_df(iris\_addr)[:,:**-**1]**.**astype(float)

fitness,bestI,bestJ,bestZ **=** three\_point\_bruteforce(np**.**array(minmax(pd**.**DataFrame(read\_df(iris\_addr)[:,:**-**1]))))

iris\_dataset**.**shapeb

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Out[30]:

(150, 4)

In [31]:

glass\_dataset **=** read\_df(glass\_addr)[:,1:**-**1]

fitness,bestI,bestJ **=** two\_point\_bruteforce(np**.**array(minmax(pd**.**DataFrame(glass\_dataset))))

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In [27]:

print(fitness)

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In [58]:

glass\_dataset **=** read\_df(glass\_addr)[:,1:]

fitness,bestI,bestJ **=** two\_point\_bruteforce(np**.**array(minmax(pd**.**DataFrame(glass\_dataset))))

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