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TE IT	Roll number : 8669
Expt. number : 6	Date of implementation: 10/05/2021
Aim : To analyze and evaluate the performance of different clustering algorithms using WEKA (data mining tool)	
Related Course outcome : CO3 Upon completion of this course students will be able to evaluate the performance of different data mining algorithms using latest tools	

Theory : WEKA contains "clusterers" for finding groups of similar instances in a dataset. The clustering schemes available in WEKA are k-means, Cobwebs, DBSCAN, OPTICS. Clusters can be visualized and compared to true clusters. Evaluation is based on log likelihood if clustering scheme produces a probability distribution.In 'preprocess' window click on 'open file...' button to select data file.

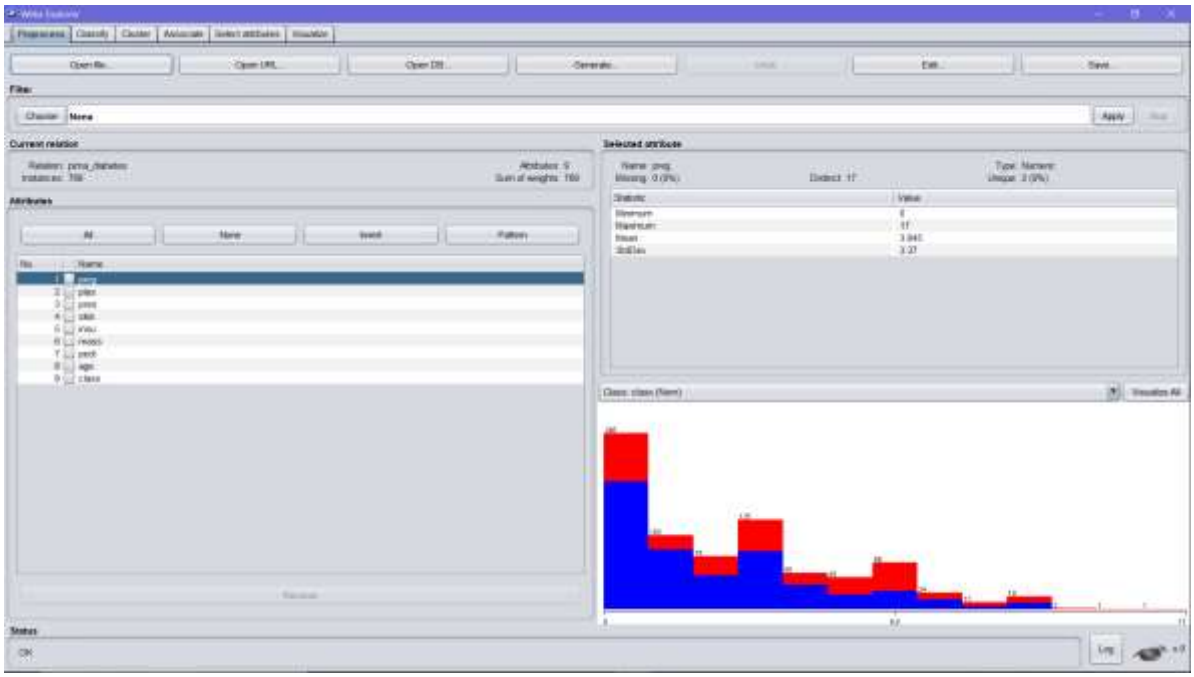
Choosing Clustering scheme : In the 'clusterer' box click on 'choose' button. In pull-down menu select WEKA → Clusteres, and select the cluster scheme 'simple K means'. Some implementations of K -means only allow numerical values for attributes ; therefore we do not need to use a filter.

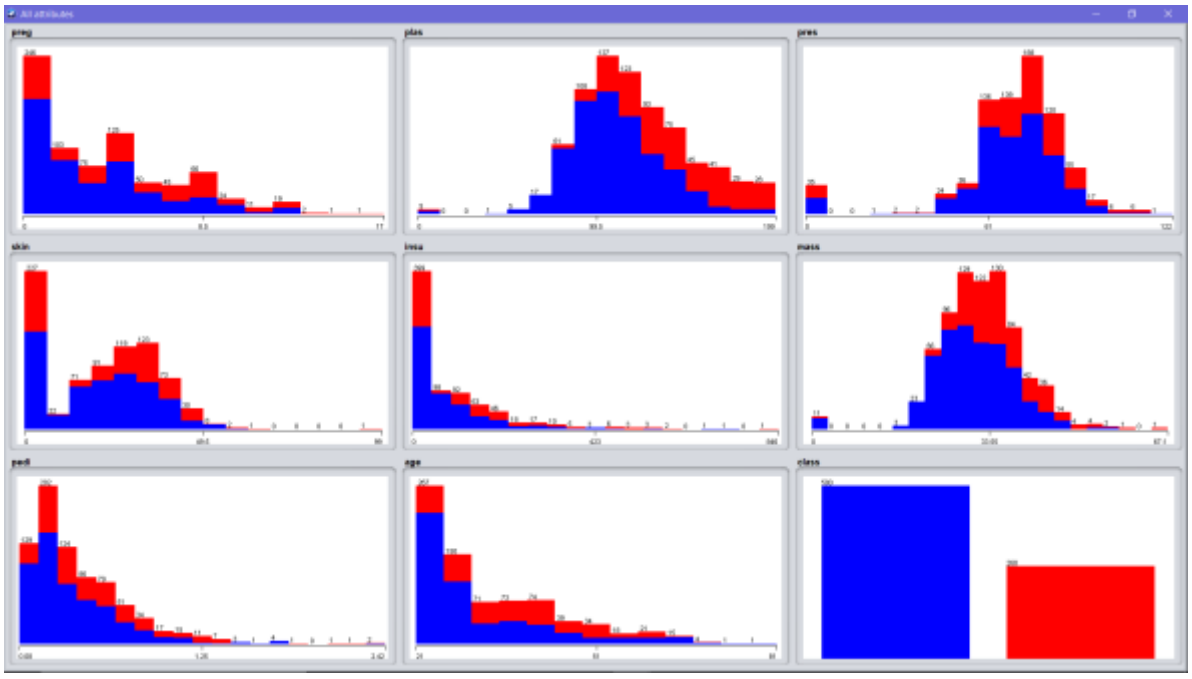
Once the clustering algorithm is chosen, right click on algorithm, 'weak.gui.GenericObjectEditor' comes up to the screen. Set the value in 'numclusters' box to number of clusters required. The seed value is used in generating a random number, which is used for making the initial assignments of instances to clusters. Before we run the clustering algorithm, we need to select 'cluster mode'. Click on 'Classes to cluster evaluation' radio-button in 'Cluster mode' box. Click the start button to run the program. When training set is complete, the 'Cluster' output area on the right panel of 'Cluster' window is filled with text describing the results of training and testing. A new entry appears in the 'Result list' box on the left of the result. Run information gives the information about : the clustering scheme used, the relation name, the number of instances, number of attributes. The clustering model shows the centroid of each cluster and statistics on the number and percentage of instances assigned to different clusters. Cluster centroid is the mean vector of each cluster so each dimension value and centroid represents mean value for that dimension in the cluster. Thus centroids can be used to characterize the cluster.

Another way of representation of results of clustering is through visualization. Right click on the entry in the 'Result list' and select ' Visualize cluster assignments' in the pull-down window. This brings up Weka clusterer visualize window. This window displays clusters in different colors for better visibility.

The other density based clustering methods such as DBSCAN and OPTICS are also analyzed and compared.

Dataset:





1. **Clustering K-means**
   - Use training set

=== Run information ===

Scheme: weka.clusterers.SimpleKMeans -init 0 -max-candidates 100 -periodic-pruning 10000 -min-density 2.0 -t1 -1.25 -t2 -1.0 -N 2 -A "weka.core.EuclideanDistance -R first-last" -I 500 -num-slots 1 -S 10
Relation: pima_diabetes
Instances: 768
Attributes: 9
preg
plas
pres
skin
insu
mass
pedi
age
class
Test mode: evaluate on training data

=== Clustering model (full training set) ===

kMeans
======

Number of iterations: 4
Within cluster sum of squared errors: 149.5177664581119

Initial starting points (random):

Cluster 0: 1,126,56,29,152,28.7,0.801,21,tested_negative
Cluster 1: 8,95,72,0,0,36.8,0.485,57,tested_negative

Missing values globally replaced with mean/mode

Final cluster centroids:

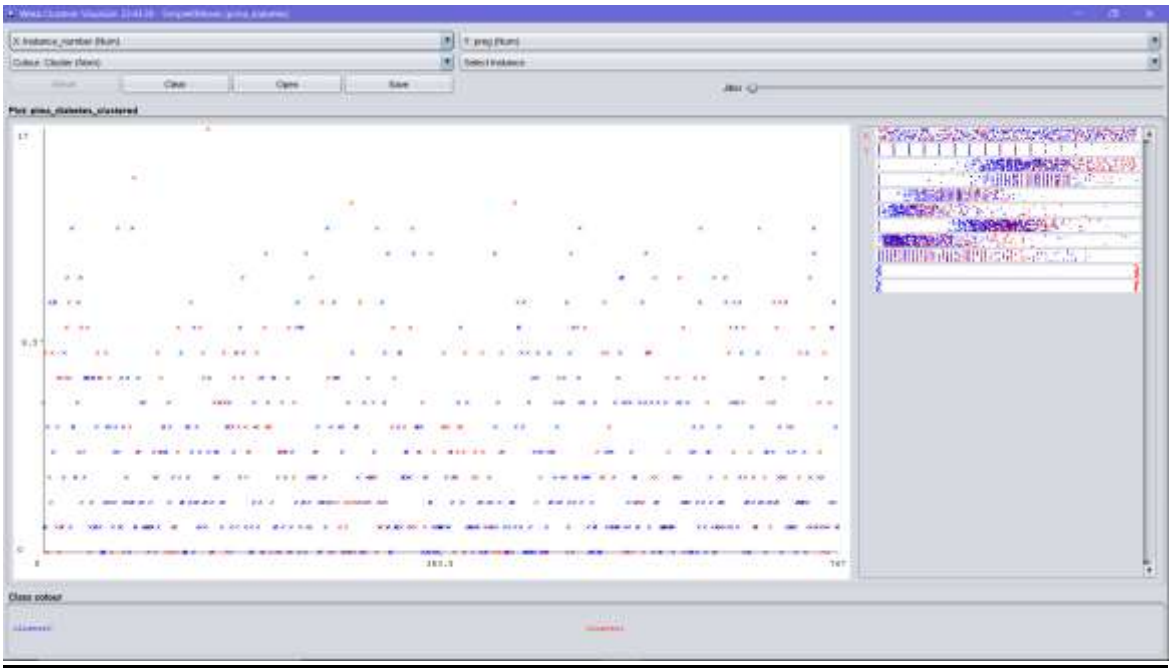
	Cluster#		
Attribute	Full Data	0	1
	(768.0)	(500.0)	(268.0)
preg	3.8451	3.298	4.8657
plas	120.8945	109.98	141.2575
pres	69.1055	68.184	70.8246
skin	20.5365	19.664	22.1642
insu	79.7995	68.792	100.3358
mass	31.9926	30.3042	35.1425
pedi	0.4719	0.4297	0.5505
age	33.2409	31.19	37.0672
class	tested_negative	tested_negative	tested_positive

Time taken to build model (full training data) : 0.03 seconds

=== Model and evaluation on training set ===

Clustered Instances

0 500 (65%)
1 268 (35%)



- Percentage split

=== Run information ===

Scheme: weka.clusterers.SimpleKMeans -init 0 -max-candidates 100 -periodic-pruning 10000 -min-density 2.0 -t1 -1.25 -t2 -1.0 -N 2 -A "weka.core.EuclideanDistance -R first-last" -I 500 -num-slots 1 -S 10
Relation: pima_diabetes
Instances: 768
Attributes: 9
preg
plas
pres
skin
insu
mass
pedi
age
class
Test mode: split 66% train, remainder test

=== Clustering model (full training set) ===

kMeans
======

Number of iterations: 4
Within cluster sum of squared errors: 149.5177664581119

Initial starting points (random):

Cluster 0: 1,126,56,29,152,28.7,0.801,21,tested_negative
Cluster 1: 8,95,72,0,0,36.8,0.485,57,tested_negative

Missing values globally replaced with mean/mode

Final cluster centroids:

		Cluster#	
Attribute	Full Data	0	1
	(768.0)	(500.0)	(268.0)
preg	3.8451	3.298	4.8657
plas	120.8945	109.98	141.2575
pres	69.1055	68.184	70.8246
skin	20.5365	19.664	22.1642
insu	79.7995	68.792	100.3358
mass	31.9926	30.3042	35.1425
pedi	0.4719	0.4297	0.5505
age	33.2409	31.19	37.0672
class	tested_negative	tested_negative	tested_positive

Time taken to build model (full training data) : 0.02 seconds

=== Model and evaluation on test split ===

kMeans
======

Number of iterations: 2
Within cluster sum of squared errors: 115.21146310581545

Initial starting points (random):

Cluster 0: 10,148,84,48,237,37.6,1.001,51,tested_positive
Cluster 1: 6,154,74,32,193,29.3,0.839,39,tested_negative

Missing values globally replaced with mean/mode

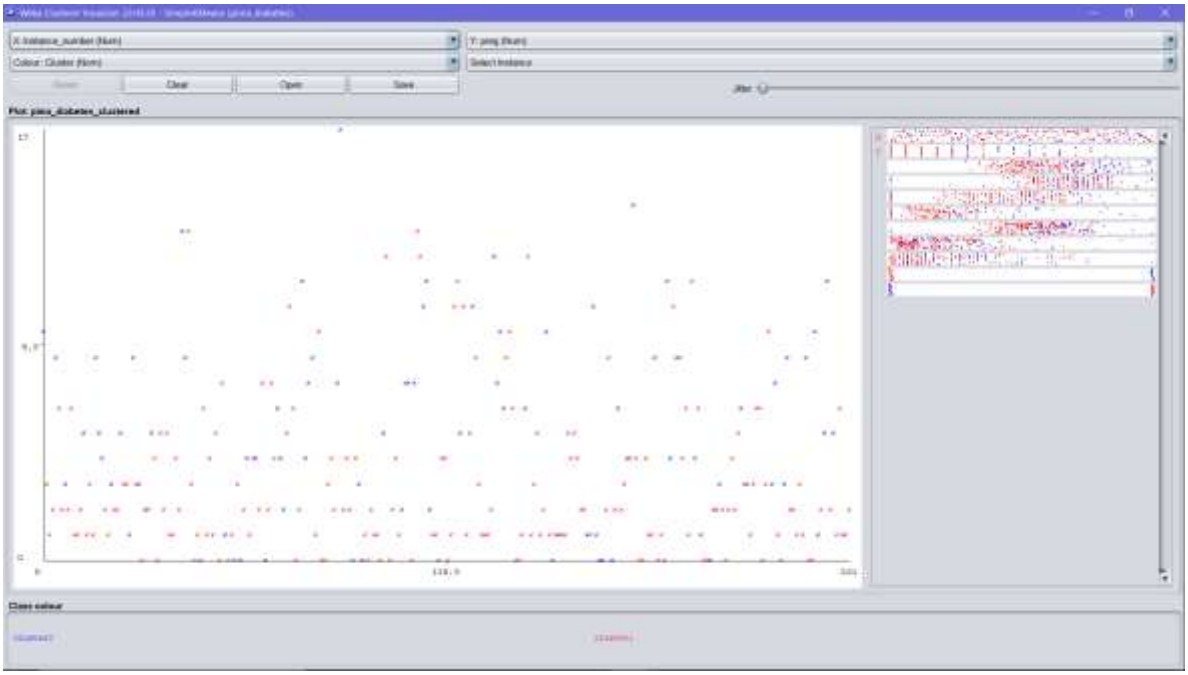
Final cluster centroids:

	Cluster#		
Attribute	Full Data	0	1
	(506.0)	(184.0)	(322.0)
preg	3.919	4.7826	3.4255
plas	121.164	139.3967	110.7453
pres	69.1779	70.8587	68.2174
skin	19.9486	21.962	18.7981
insu	78.585	90.0217	72.0497
mass	32.0275	35.2766	30.1708
pedi	0.4798	0.5516	0.4388
age	33.7925	37.4674	31.6925
class	tested_negative	tested_positive	tested_negative

Time taken to build model (percentage split) : 0.01 seconds

Clustered Instances

0 84 (32%)
1 178 (68%)



- Classes to clusters evaluation

=== Run information ===

Scheme: weka.clusterers.SimpleKMeans -init 0 -max-candidates 100 -periodic-pruning 10000 -min-density 2.0 -t1 -1.25 -t2 -1.0 -N 2 -A "weka.core.EuclideanDistance -R first-last" -I 500 -num-slots 1 -S 10
Relation: pima_diabetes
Instances: 768
Attributes: 9
preg
plas
pres
skin
insu
mass
pedi
age
Ignored:
class
Test mode: Classes to clusters evaluation on training data

=== Clustering model (full training set) ===

kMeans
======

Number of iterations: 7
Within cluster sum of squared errors: 121.2579017999101

Initial starting points (random):

Cluster 0: 1,126,56,29,152,28.7,0.801,21
Cluster 1: 8,95,72,0,0,36.8,0.485,57

Missing values globally replaced with mean/mode

Final cluster centroids:

	Cluster#		
Attribute	Full Data	0	1
	(768.0)	(515.0)	(253.0)
preg	3.8451	2.0835	7.4308
plas	120.8945	115.3282	132.2253
pres	69.1055	65.9903	75.4466
skin	20.5365	21.8194	17.9249
insu	79.7995	85.0194	69.1739
mass	31.9926	31.7751	32.4352
pedi	0.4719	0.4708	0.4741
age	33.2409	26.7728	46.4071

Time taken to build model (full training data) : 0.01 seconds

=== Model and evaluation on training set ===

Clustered Instances

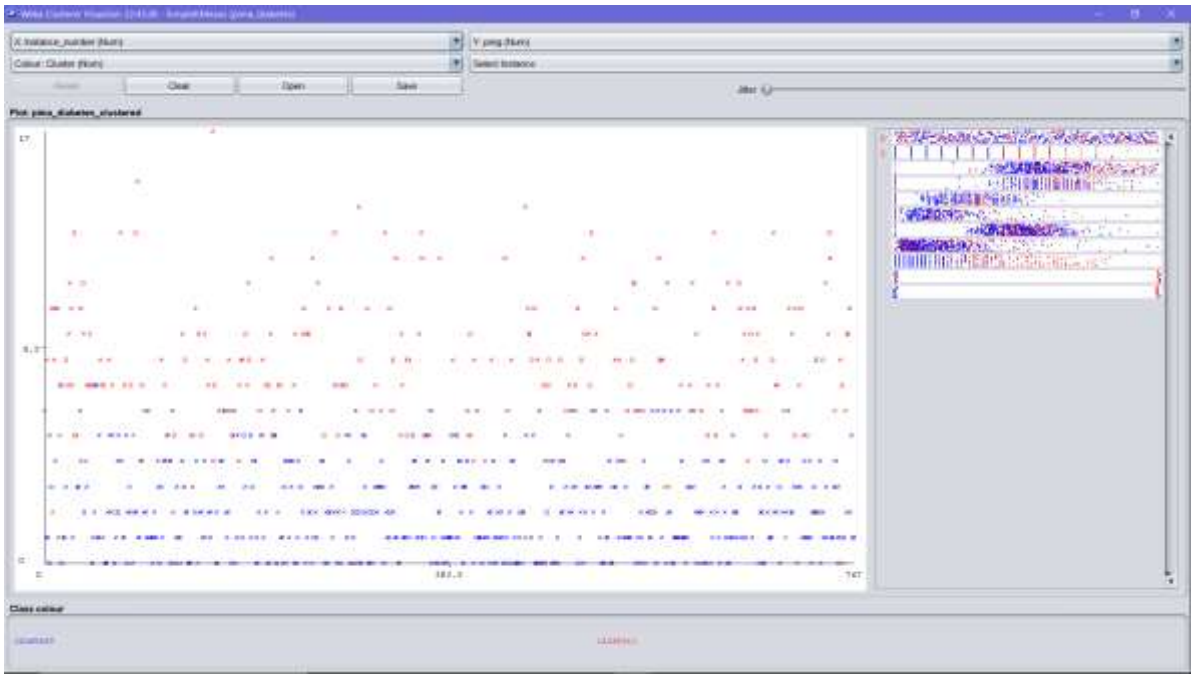
0 515 (67%)
1 253 (33%)

Class attribute: class
Classes to Clusters:

0 1 <-- assigned to cluster
380 120 | tested_negative
135 133 | tested_positive

Cluster 0 <-- tested_negative
Cluster 1 <-- tested_positive

Incorrectly clustered instances : 255.0 33.2031 %



2. DB Scan

- Use training set

=== Run information ===

Scheme: weka.clusterers.DBSCAN -E 0.9 -M 6 -A "weka.core.EuclideanDistance -R first-last"
Relation: pima_diabetes
Instances: 768
Attributes: 9
preg
plas
pres
skin
insu
mass
pedi
age
class
Test mode: evaluate on training data

=== Clustering model (full training set) ===

DBSCAN clustering results
==========

Clustered DataObjects: 768
Number of attributes: 9
Epsilon: 0.9; minPoints: 6
Distance-type:
Number of generated clusters: 2
Elapsed time: .14

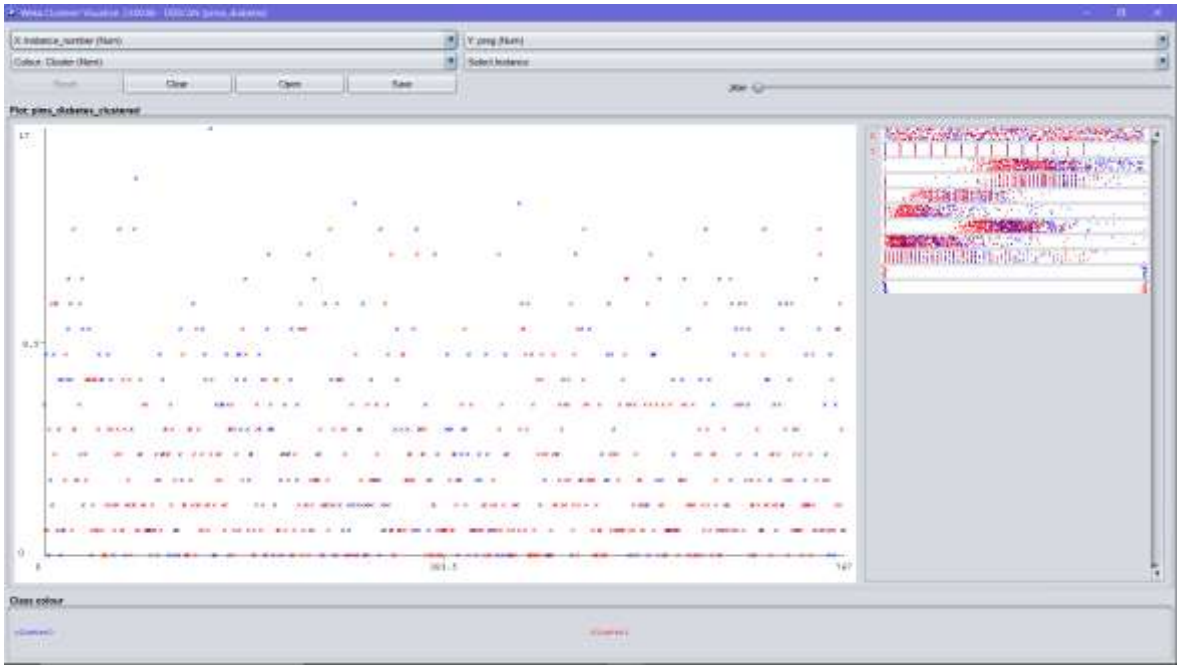
(0.) 6,148,72,35,0,33.6,0.627,50,tested_positive --> 0
(1.) 1,85,66,29,0,26.6,0.351,31,tested_negative --> 1
(2.) 8,183,64,0,0,23.3,0.672,32,tested_positive --> 0
(3.) 1,89,66,23,94,28.1,0.167,21,tested_negative --> 1
(4.) 0,137,40,35,168,43.1,2.288,33,tested_positive --> 0
(5.) 5,116,74,0,0,25.6,0.201,30,tested_negative --> 1
(6.) 3,78,50,32,88,31,0.248,26,tested_positive --> 0
.
.
.
(761.) 9,170,74,31,0,44,0.403,43,tested_positive --> 0
(762.) 9,89,62,0,0,22.5,0.142,33,tested_negative --> 1
(763.) 10,101,76,48,180,32.9,0.171,63,tested_negative --> 1
(764.) 2,122,70,27,0,36.8,0.34,27,tested_negative --> 1
(765.) 5,121,72,23,112,26.2,0.245,30,tested_negative --> 1
(766.) 1,126,60,0,0,30.1,0.349,47,tested_positive --> 0
(767.) 1,93,70,31,0,30.4,0.315,23,tested_negative --> 1

Time taken to build model (full training data) : 0.14 seconds

=== Model and evaluation on training set ===

Clustered Instances

0 268 (35%)
1 500 (65%)



- Percentage split

=== Run information ===

Scheme: weka.clusterers.DBSCAN -E 0.9 -M 6 -A "weka.core.EuclideanDistance -R first-last"
Relation: pima_diabetes
Instances: 768
Attributes: 9
preg
plas
pres
skin
insu
mass
pedi
age
class
Test mode: split 66% train, remainder test

=== Clustering model (full training set) ===

DBSCAN clustering results
==========

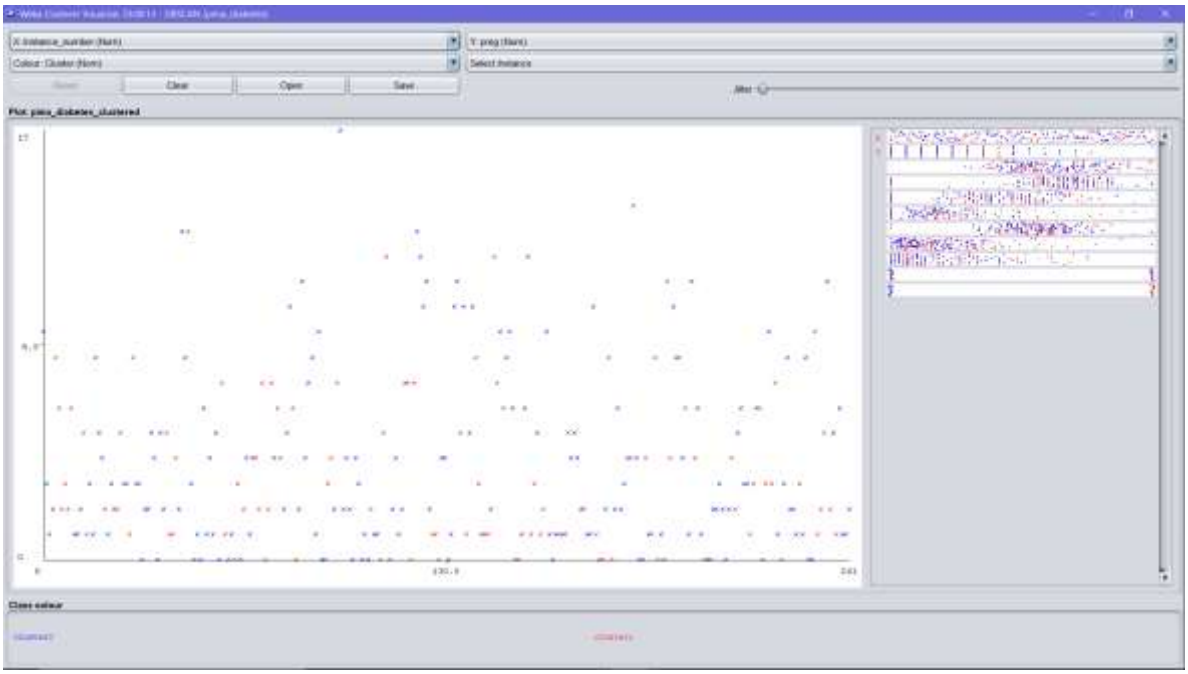
Clustered DataObjects: 768
Number of attributes: 9
Epsilon: 0.9; minPoints: 6
Distance-type:
Number of generated clusters: 2
Elapsed time: .09

(0.) 6,148,72,35,0,33.6,0.627,50,tested_positive --> 0
(1.) 1,85,66,29,0,26.6,0.351,31,tested_negative --> 1
(2.) 8,183,64,0,0,23.3,0.672,32,tested_positive --> 0
(3.) 1,89,66,23,94,28.1,0.167,21,tested_negative --> 1
(4.) 0,137,40,35,168,43.1,2.288,33,tested_positive --> 0
(5.) 5,116,74,0,0,25.6,0.201,30,tested_negative --> 1
.
.
.
(500.) 1,124,60,32,0,35.8,0.514,21,tested_negative --> 0
(501.) 2,197,70,99,0,34.7,0.575,62,tested_positive --> 1
(502.) 0,151,90,46,0,42.1,0.371,21,tested_positive --> 1
(503.) 7,178,84,0,0,39.9,0.331,41,tested_positive --> 1
(504.) 2,83,65,28,66,36.8,0.629,24,tested_negative --> 0
(505.) 3,99,62,19,74,21.8,0.279,26,tested_negative --> 0

Time taken to build model (percentage split) : 0.07 seconds

Clustered Instances

0 164 (63%)
1 98 (37%)



- Classes to clusters evaluation

=== Run information ===

Scheme: weka.clusterers.DBSCAN -E 0.9 -M 6 -A "weka.core.EuclideanDistance -R first-last"
Relation: pima_diabetes
Instances: 768
Attributes: 9
preg
plas
pres
skin
insu
mass
pedi
age
Ignored:
class
Test mode: Classes to clusters evaluation on training data

=== Clustering model (full training set) ===

DBSCAN clustering results
==========

Clustered DataObjects: 768
Number of attributes: 8
Epsilon: 0.9; minPoints: 6
Distance-type:
Number of generated clusters: 1
Elapsed time: .1

(0.) 6,148,72,35,0,33.6,0.627,50 --> 0
(1.) 1,85,66,29,0,26.6,0.351,31 --> 0
(2.) 8,183,64,0,0,23.3,0.672,32 --> 0
(3.) 1,89,66,23,94,28.1,0.167,21 --> 0
(4.) 0,137,40,35,168,43.1,2.288,33 --> 0
(5.) 5,116,74,0,0,25.6,0.201,30 --> 0
.
.
.
(762.) 9,89,62,0,0,22.5,0.142,33 --> 0
(763.) 10,101,76,48,180,32.9,0.171,63 --> 0
(764.) 2,122,70,27,0,36.8,0.34,27 --> 0
(765.) 5,121,72,23,112,26.2,0.245,30 --> 0
(766.) 1,126,60,0,0,30.1,0.349,47 --> 0
(767.) 1,93,70,31,0,30.4,0.315,23 --> 0

Time taken to build model (full training data) : 0.1 seconds

=== Model and evaluation on training set ===

Clustered Instances

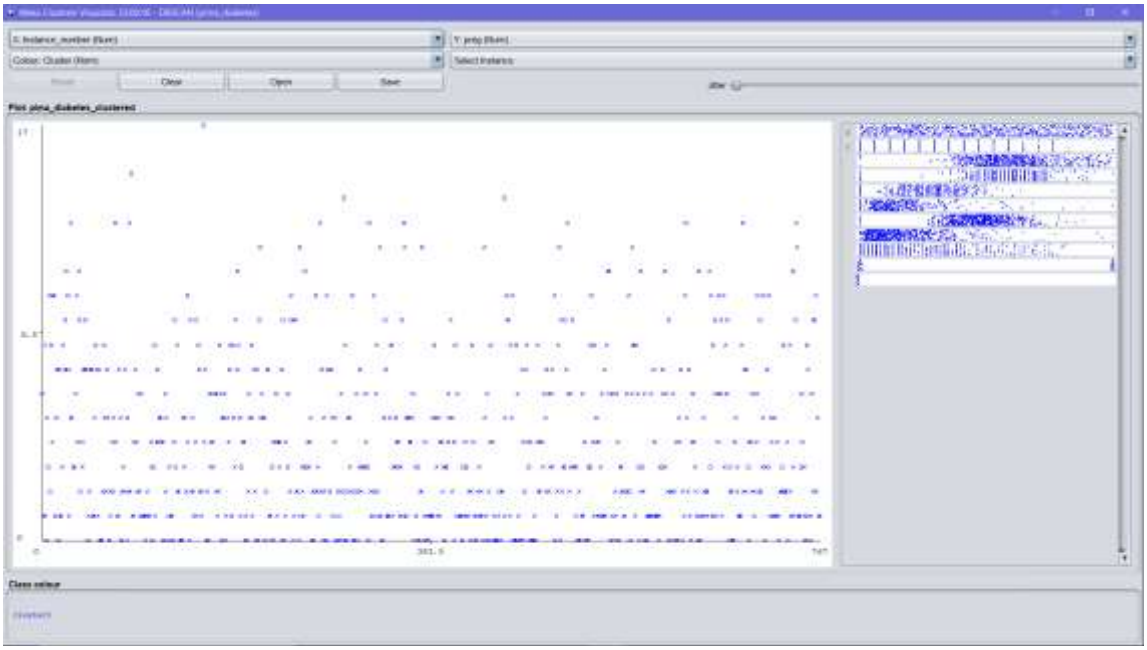
0 768 (100%)

Class attribute: class
Classes to Clusters:

0 <-- assigned to cluster
500 | tested_negative
268 | tested_positive

Cluster 0 <-- tested_negative

Incorrectly clustered instances : 268.0 34.8958 %



3. OPTICS

- Use training set

=== Run information ===

Scheme: weka.clusterers.OPTICS -E 0.9 -M 6 -A "weka.core.EuclideanDistance -R first-last" -db-output .
Relation: pima_diabetes
Instances: 768
Attributes: 9
preg
plas
pres
skin
insu
mass
pedi
age
class
Test mode: evaluate on training data

=== Clustering model (full training set) ===

OPTICS clustering results
==========

Clustered DataObjects: 768
Number of attributes: 9
Epsilon: 0.9; minPoints: 6
Write results to file: no
Distance-type:
Number of generated clusters: 0
Elapsed time: .19

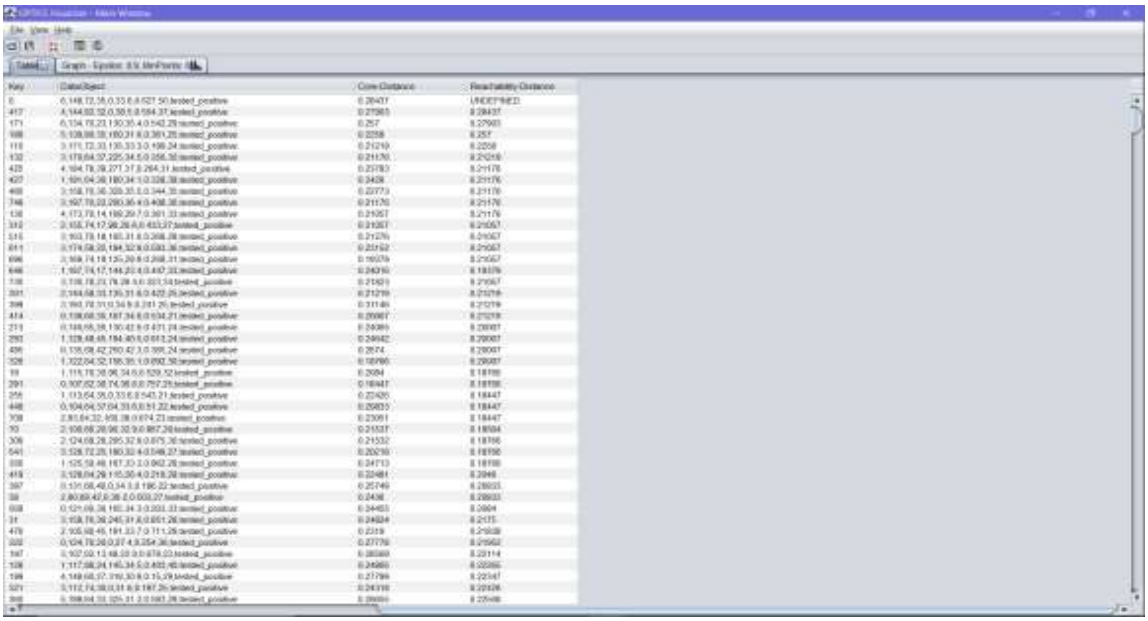
(0.) 6,148,72,35,0,33.6,0.627,50,tested_posit --> c_dist: 0.284 r_dist: UNDEFINED
(417.) 4,144,82,32,0,38.5,0.554,37,tested_posit --> c_dist: 0.279 r_dist: 0.284
(171.) 6,134,70,23,130,35.4,0.542,29,tested_pos --> c_dist: 0.257 r_dist: 0.279
(189.) 5,139,80,35,160,31.6,0.361,25,tested_pos --> c_dist: 0.226 r_dist: 0.257
(110.) 3,171,72,33,135,33.3,0.199,24,tested_pos --> c_dist: 0.212 r_dist: 0.226
(132.) 3,170,64,37,225,34.5,0.356,30,tested_pos --> c_dist: 0.212 r_dist: 0.212
(425.) 4,184,78,39,277,37,0.264,31,tested_posit --> c_dist: 0.238 r_dist: 0.212
.
.
.
(622.) 6,183,94,0,0,40.8,1.461,45,tested_negati --> c_dist: 0.535 r_dist: 0.445
(744.) 13,153,88,37,140,40.6,1.174,39,tested_ne --> c_dist: 0.487 r_dist: 0.445
(487.) 0,173,78,32,265,46.5,1.159,58,tested_neg --> c_dist: 0.58 r_dist: 0.447
(58.) 0,146,82,0,0,40.5,1.781,44,tested_negati --> c_dist: 0.545 r_dist: 0.494
(453.) 2,119,0,0,0,19.6,0.832,72,tested_negativ --> c_dist: 0.632 r_dist: 0.499

(228.) 4,197,70,39,744,36.7,2.329,31,tested_neg --> c_dist: 0.88 r_dist: 0.776

Time taken to build model (full training data) : 0.39 seconds

=== Model and evaluation on training set ===

Clustered Instances
Unclustered instances : 768



- Percentage split

  === Run information ===

  Scheme: weka.clusterers.OPTICS -E 0.9 -M 6 -A "weka.core.EuclideanDistance -R first-last" -db-output .
  Relation: pima_diabetes
  Instances: 768
  Attributes: 9
  preg
  plas
  pres
  skin
  insu
  mass
  pedi
  age
  class
  Test mode: split 66% train, remainder test

  === Clustering model (full training set) ===

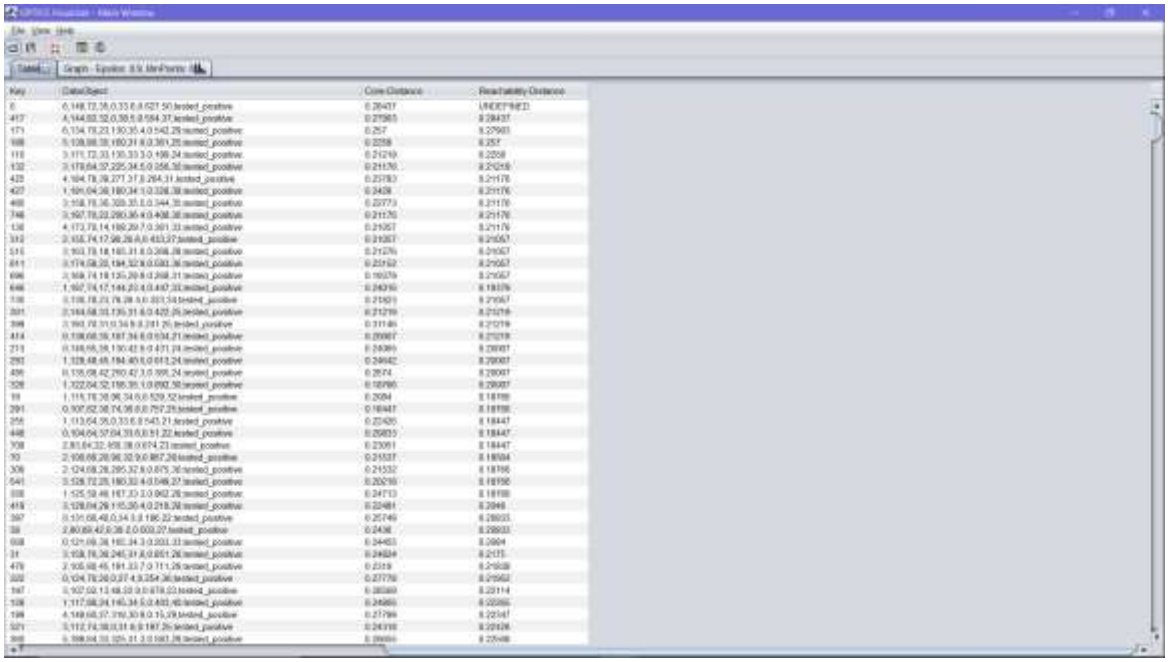
  OPTICS clustering results
  ==========

  Clustered DataObjects: 768
  Number of attributes: 9
  Epsilon: 0.9; minPoints: 6
  Write results to file: no
  Distance-type:
  Number of generated clusters: 0
  Elapsed time: .14

  (0.) 6,148,72,35,0,33.6,0.627,50,tested_posit --> c_dist: 0.284 r_dist: UNDEFINED
  (417.) 4,144,82,32,0,38.5,0.554,37,tested_posit --> c_dist: 0.279 r_dist: 0.284
  (171.) 6,134,70,23,130,35.4,0.542,29,tested_pos --> c_dist: 0.257 r_dist: 0.279
  (189.) 5,139,80,35,160,31.6,0.361,25,tested_pos --> c_dist: 0.226 r_dist: 0.257
  (110.) 3,171,72,33,135,33.3,0.199,24,tested_pos --> c_dist: 0.212 r_dist: 0.226
  (132.) 3,170,64,37,225,34.5,0.356,30,tested_pos --> c_dist: 0.212 r_dist: 0.212
  (425.) 4,184,78,39,277,37,0.264,31,tested_posit --> c_dist: 0.238 r_dist: 0.212
  .
  .
  .
  (74.) 0,137,40,35,168,43.1,2.288,33,tested_pos --> c_dist: 0.649 r_dist: 0.537
  (4.) 6,0,68,41,0,39,0.727,41,tested_positive --> c_dist: 0.588 r_dist: 0.549
  (175.) 0,180,78,63,14,59.4,2.42,25,tested_posit --> c_dist: 0.752 r_dist: 0.559
  (397.) 1,189,60,23,846,30.1,0.398,59,tested_pos --> c_dist: 0.861 r_dist: 0.561
  (146.) 13,129,0,30,0,39.9,0.569,44,tested_posit --> c_dist: 0.665 r_dist: 0.565
  (469.) 11,135,0,0,0,52.3,0.578,40,tested_positi --> c_dist: 0.658 r_dist: 0.62
  (501.) 2,197,70,99,0,34.7,0.575,62,tested_posit --> c_dist: 0.823 r_dist: 0.745

Time taken to build model (percentage split) : 0.29 seconds

Clustered Instances
Unclustered instances : 262



- Classes to clusters evaluation

=== Run information ===

Scheme: weka.clusterers.OPTICS -E 0.9 -M 6 -A "weka.core.EuclideanDistance -R first-last" -db-output .
Relation: pima_diabetes
Instances: 768
Attributes: 9
preg
plas
pres
skin
insu
mass
pedi
age
Ignored:
class
Test mode: Classes to clusters evaluation on training data

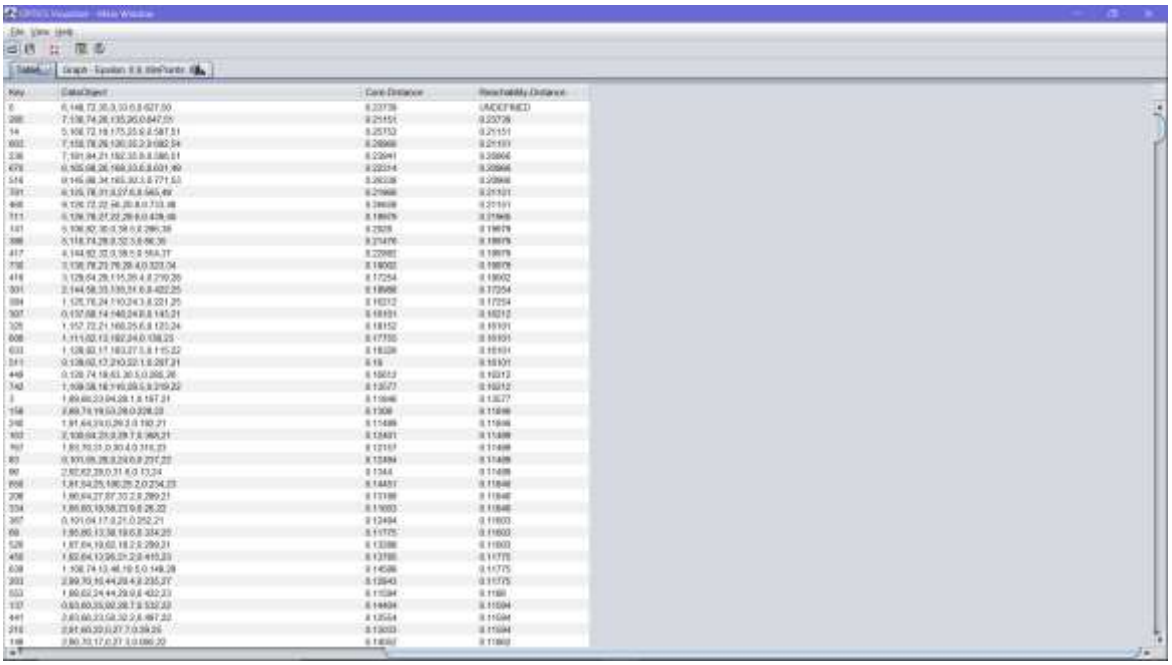
=== Clustering model (full training set) ===

OPTICS clustering results
==========

Clustered DataObjects: 768
Number of attributes: 8
Epsilon: 0.9; minPoints: 6
Write results to file: no
Distance-type:
Number of generated clusters: 0
Elapsed time: .14

(0.) 6,148,72,35,0,33.6,0.627,50 --> c_dist: 0.237 r_dist: UNDEFINED
(285.) 7,136,74,26,135,26,0.647,51 --> c_dist: 0.212 r_dist: 0.237
(14.) 5,166,72,19,175,25.8,0.587,51 --> c_dist: 0.258 r_dist: 0.212
(603.) 7,150,78,29,126,35.2,0.692,54 --> c_dist: 0.21 r_dist: 0.212
(236.) 7,181,84,21,192,35.9,0.586,51 --> c_dist: 0.239 r_dist: 0.21
(670.) 6,165,68,26,168,33.6,0.631,49 --> c_dist: 0.223 r_dist: 0.21
(516.) 9,145,88,34,165,30.3,0.771,53 --> c_dist: 0.263 r_dist: 0.21
.
.
.
(4.) 0,137,40,35,168,43.1,2.288,33 --> c_dist: 0.53 r_dist: 0.459
(357.) 13,129,0,30,0,39.9,0.569,44 --> c_dist: 0.552 r_dist: 0.479
(13.) 1,189,60,23,846,30.1,0.398,59 --> c_dist: 0.703 r_dist: 0.481
(453.) 2,119,0,0,0,19.6,0.832,72 --> c_dist: 0.632 r_dist: 0.499
(228.) 4,197,70,39,744,36.7,2.329,31 --> c_dist: 0.776 r_dist: 0.588
(579.) 2,197,70,99,0,34.7,0.575,62 --> c_dist: 0.771 r_dist: 0.646

Time taken to build model (full training data) : 0.25 seconds



Post-lab Questions:

1. What is an outlier?

Ans:

a. In statistics, an outlier is a data point that differs significantly from other observations.
b. An outlier may be due to variability in the measurement or it may indicate experimental error; the latter are sometimes excluded from the data set. An outlier can cause serious problems in statistical analyses.
c. Sometimes outliers might be errors that we want to exclude or an anomaly that we don't want to include in our analysis.
d. But at other times it can reveal insights into special cases in our data that we may not otherwise notice.
e. Outliers can be of two types: Univariate and Multivariate.
f. Univariate outliers are outliers in a 1 dimensional space.
g. Multivariate outliers are outliers in an n-dimensional space.
h. Most common causes of outliers on a data set:
    - Data entry errors (human errors)
    - Measurement errors (instrument errors)
    - Experimental errors (data extraction or experiment planning/executing errors)
    - Intentional (dummy outliers made to test detection methods)
    - Data processing errors (data manipulation or data set unintended mutations)
    - Sampling errors (extracting or mixing data from wrong or various sources)
    - Natural (not an error, novelties in data)

2. Give any method to detect an outlier.

Ans:

a. Most commonly used method to detect outliers is visualization.
b. We use various visualization methods, like Box-plot, Histogram, Scatter Plot
c. Use capping methods. Any value which out of range of 5th and 95th percentile can be considered as outlier 3.Data points, three or more standard deviation away from mean are considered outlier
d. d.Outlier detection is merely a special case of the examination of data for influential datapoint sanditals depends on the business understanding
e. Bivariate and multivariate outliers are typically measured using either an index of influence or leverage, or distance. Some of the most popular methods for outlier detection are:
   Z-Score or Extreme Value Analysis (parametric)
   Probabilistic and Statistical Modeling (parametric)
   Linear Regression Models (PCA, LMS)
   Proximity Based Models(non-parametric)
   Information Theory Models
   High Dimensional Outlier Detection Methods (high dimensional sparse data)
   Z-Score
   a. The z-score or standard score of an observation is a metric that indicates how many standard deviations a data point is from the sample's mean, assuming a gaussian distribution. This makes z-score a parametric method. Very frequently data points are not to described by a gaussian distribution, this problem can be solved by applying transformations to data i.e.: scaling it.
   b. SomePython libraries likeSciPy and Sci-kit Learn have easy to use functions and classes for easy implementation along with Pandas andNumPy.

c. After making the appropriate transformations to the selected feature space of the dataset, the z-score of any data point can be calculated with the following expression: Z = x - μ / sigma
d. When computing the z-score for each sample on the dataset a threshold must be specified.Some Good Thumbrule' thresholds can be: 2.5, 3, 3.5 or more standard deviations.
e. By ‘tagging’ or removing the data points that lay beyond a given threshold We are classifying data into outliers and not outliers
f. Z-scoreisasimple, yet powerful method to get rid of outliers in data if are dealing with parametric distributions in a low dimensional feature space