Lab 1 732A75

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About Data

We have 27 measure of Nutrient levels which were measured in a 3 ounce portion of various foods.

Name is the name of the item. **Energy** is the number of calories. **Protein** is the amount of protein in grams. **Fat** is the amount of fat in grams. **Calcium** is the amount of calcium in milligrams. **Iron** is the amount of iron in milligrams.

	tion: food					
No.	1: Name	2: Energy	3: Protein	4: Fat	5: Calcium	6: Iron
	String	Numeric	Numeric	Numeric	Numeric	Numeric
1	Braised beef	340.0	20.0	28.0	9.0	2.6
2	Hamburger	245.0	21.0	17.0	9.0	2.7
3	Roast beef	420.0	15.0	39.0	7.0	2.0
4	Beefsteak	375.0	19.0	32.0	9.0	2.6
5	Canned beef	180.0	22.0	10.0	17.0	3.7
6	Broiled chicken	115.0	20.0	3.0	8.0	1.4
7	Canned chicken	170.0	25.0	7.0	12.0	1.5
8	Beef heart	160.0	26.0	5.0	14.0	5.9
9	Roast lamb leg	265.0	20.0	20.0	9.0	2.6
10	Roast lamb shoulder	300.0	18.0	25.0	9.0	2.3
11	Smoked ham	340.0	20.0	28.0	9.0	2.5
12	Pork roast	340.0	19.0	29.0	9.0	2.5
13	Pork simmered	355.0	19.0	30.0	9.0	2.4
14	Beef tongue	205.0	18.0	14.0	7.0	2.5
15	Veal cutlet	185.0	23.0	9.0	9.0	2.7
16	Baked bluefish	135.0	22.0	4.0	25.0	0.6
17	Raw clams	70.0	11.0	1.0	82.0	6.0
18	Canned clams	45.0	7.0	1.0	74.0	5.4
19	Canned crabmeat	90.0	14.0	2.0	38.0	0.8
20	Fried haddock	135.0	16.0	5.0	15.0	0.5
21	Broiled mackerel	200.0	19.0	13.0	5.0	1.0
22	Canned mackerel	155.0	16.0	9.0	157.0	1.8
23	Fried perch	195.0	16.0	11.0	14.0	1.3
24	Canned salmon	120.0	17.0	5.0	159.0	0.7
25	Canned sardines	180.0	22.0	9.0	367.0	2.5
26	Canned tuna	170.0	25.0	7.0	7.0	1.2
27	Canned shrimp	110.0	23.0	1.0	98.0	2.6

Question 1 : SimpleKmeans

1.1: Choose a set of attributes for clustering and give a motivation.

Kmeans algorithm is directly not applicable to the categorical variable as sample space for categorical data is discrete, and thus Euclidean distance function on such space does not provide meaningful results.

Since Name attribute is discrete; thus, we will ignore it while considering remaining continuous numerical values based features; namely Energy, Protein, Fat, Calcium, and Iron.

1.2: Experiment with at least two different numbers of clusters, e.g. 2 and 5, but with the same seed value 10.

Obtained Result at seed value 10

When Number of cluster(K) = 2 with seed 10

=== 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: food

Instances: 27

Attributes: 6 Energy Protein Fat Calcium Iron

Ignored: Name

Test mode: evaluate on training data

Clustering model (full training set)

kMeans

Number of iterations: 2

Within cluster sum of squared errors: 5.069321339929419

Initial starting points (random):

Cluster 0: 340,20,28,9,2.6 Cluster 1: 170,25,7,12,1.5

Missing values globally replaced with mean/mode

Final cluster centroids:

		Cluster#		
Attribute	Full Data	0	1	
	(27.0)	(9.0)	(18.0)	
Energy	207.4074	331.1111	145.5556	
Protein	19	19	19	
Fat	13.4815	27.5556	6.4444	
Calcium	43.963	8.7778	61.5556	
Iron	2.3815	2.4667	2.3389	

Time taken to build model (full training data): 0 seconds

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

Clustered Instances

0 9 (33%) 1 18 (67%)

When Number of cluster(K) = 5 with seed 10

=== 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 5 -A "weka.core.EuclideanDistance -R first-last" -I 500 -num-slots 1 -S 10

Relation: food

Instances: 27

Attributes: 6 Energy Protein Fat Calcium Iron

Ignored: Name

Test mode: evaluate on training data

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

kMeans

Number of iterations: 4

Within cluster sum of squared errors: 2.750432407251998

Initial starting points (random):

Cluster 0: 340,20,28,9,2.6 Cluster 1: 170,25,7,12,1.5 Cluster 2: 90,14,2,38,0.8 Cluster 3: 180,22,9,367,2.5 Cluster 4: 300,18,25,9,2.3

Missing values globally replaced with mean/mode

Final cluster centroids:

		Cluster#				
Attribute	Full Data (27.0)	0 (7.0)	1 (8.0)	2 (6.0)	3 (1.0)	4 (5.0)
Energy	207.4074	352.8571	153.125	102.5	180	222
Protein	19	18.5714	23.25	13.5	22	18.8
Fat	13.4815	30.1429	5.75	3.8333	9	15
Calcium	43.963	8.7143	23.75	87.5	367	8.8
Iron	2.3815	2.4143	2.45	2.5333	2.5	2.02

Time taken to build model (full training data): 0 seconds

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

Clustered Instances

0 7 (26%) 1 8 (30%) 2 6 (22%) 3 1 (4%) 4 5 (19%)

1.3: Then try with a different seed value, i.e. different initial cluster centers. Compare the results with the previous results. Explain what the seed value controls.

Changing seed value to 15 and recalculating.

At k=2 with seed at 15

=== 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 15

Relation: food Instances: 27 Attributes: 6 Energy Protein Fat Calcium Iron Ignored: Name Test mode: evaluate on training data

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

Number of iterations: 4

Within cluster sum of squared errors: 5.082974846131301

Initial starting points (random):

Cluster 0: 375,19,32,9,2.6 Cluster 1: 355,19,30,9,2.4

Missing values globally replaced with mean/mode

Final cluster centroids:

		Cluster#		
Attribute	Full Data	0	1	
	(27.0)	(8.0)	(19.0)	
Energy	207.4074	341.875	150.7895	
Protein	19	18.75	19.1053	
Fat	13.4815	28.875	7	
Calcium	43.963	8.75	58.7895	
Iron	2.3815	2.4375	2.3579	

Time taken to build model (full training data): 0 seconds

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

Clustered Instances

0 8 (30%) 1 19 (70%)

At k = 5 with seed at 15

=== 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 5 -A "weka.core.EuclideanDistance -R first-last" -I 500 -num-slots 1 -S 15 Relation: food Instances: 27 Attributes: 6 Energy Protein Fat Calcium Iron Ignored: Name Test mode: evaluate on training data

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

kMeans

=====

Number of iterations: 6

Within cluster sum of squared errors: 3.4159629151204487

Initial starting points (random):

Cluster 0: 375,19,32,9,2.6 Cluster 1: 355,19,30,9,2.4 Cluster 2: 205,18,14,7,2.5 Cluster 3: 110,23,1,98,2.6 Cluster 4: 340,20,28,9,2.6

Missing values globally replaced with mean/mode

Final cluster centroids:

		Cluster#				
Attribute	Full Data	0	1	2	3	4
	(27.0)	(1.0)	(6.0)	(6.0)	(9.0)	(5.0)
Energy	207.4074	420	341.6667	102.5	156.1111	222
Protein	19	15	19.1667	13.5	23.1111	18.8
Fat	13.4815	39	28.6667	3.8333	6.1111	15
Calcium	43.963	7	9	87.5	61.8889	8.8
Iron	2.3815	2	2.4833	2.5333	2.4556	2.02

Time taken to build model (full training data): 0 seconds

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

Clustered Instances

0 1 (4%) 1 6 (22%) 2 6 (22%) 3 9 (33%) 4 5 (19%)

Impact of changed seed value

The seed value is used to randomly generate the initial k number of means, which are used as initial centroids of clusters, and initial clustering is done using them.

While checking the impact of seed, it can be seen that in the case of k=5, with different seed values of 10 and 15, it take more iterations before classifying and along with increased in sum of square error(SSE).

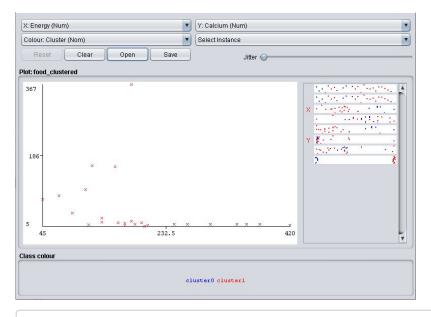
Table of Comparison with Number of Cluster set to 5

Table of Comparison with Number of Cluster set to 2

1.4: Do you think the clusters are "good" clusters? (Are all of its members "similar" to each other? Are members from different clusters dissimilar?)

When k=2 regardless of seed value, it can be seen that classification is majorly done in two variables, namely Energy and Calcium, while reaming are just randomly assigned to clusters based on centroid mean.

When k=5, it can be seen that clusters majorly formed between 3 Variable Energy, Fat and Calcium yet no clear information can be derived from it thus these many clusters for such small dataset do not provide much of information in order to make a decision thus cannot be considered an as good cluster.



Cluster when k=2 between Energy and Calcium

1.5: What does each cluster represent? Choose one of the results. Make up labels (words or phrases in English) which characterize each cluster

When K=2 and seed is 10, we could consider the division of data into based on centroid namely as Cluster-0 as **High Energy - Low Calcium** which is marked with blue colour and Cluster-1 as **Low Energy - High Calcium** the cluster which is marked with green colour.

	Instance_number \$	Name \$	Energy \$	Protein \$	Fat \$	Calcium \$	Iron \$	Cluster \$
1	0	Braised beef	340	20	28	9	2.6	cluster0
2	1	Hamburger	245	21	17	9	2.7	cluster0
3	2	Roast beef	420	15	39	7	2	cluster0
4	3	Beefsteak	375	19	32	9	2.6	cluster0
5	4	Canned beef	180	22	10	17	3.7	cluster1
6	5	Broiled chicken	115	20	3	8	1.4	cluster l
7	6	Canned chicken	170	25	7	12	1.5	cluster1
8	7	Beefheart	160	26	5	14	5.9	cluster1
9	8	Roast lamb leg	265	20	20	9	2.6	cluster0
10	9	Roast lamb shoulder	300	18	25	9	2.3	cluster0
11	10	Smoked ham	340	20	28	9	2.5	cluster0
12	11	Pork roast	340	19	29	9	2.5	cluster0
13	12	Pork simmered	355	19	30	9	2.4	cluster0
14	13	Beef tongue	205	18	14	7	2.5	cluster 1
15	14	Veal cutlet	185	23	9	9	2.7	cluster 1
16	15	Baked bluefish	135	22	4	25	0.6	cluster 1
17	16	Raw clams	70	11	1	82	6	cluster 1
18	17	Canned clams	45	7	1	74	5.4	cluster 1
19	18	Canned crabmeat	90	14	2	38	8.0	cluster 1
20	19	Fried haddock	135	16			0.5	cluster l
21	20	Broiled mackerel	200	19	13	5	1	cluster l
22	21	Canned mackerel	155	16	9	157	1.8	cluster 1
23	22	Fried perch	195	16	11	14	1.3	cluster l
24	23	Canned salmon	120	17	5	159	0.7	cluster l
25	24	Canned sardines	180	22	9	367	2.5	cluster1
26	25	Canned tuna	170	25	7	7	1.2	cluster1
27	26	Canned shrimp	110	23	1	98	2.6	cluster l

Question 2 : MakeDensityBasedClusters

Use the SimpleKMeans clusterer which gave the result you haven chosen in 5 Experiment with at least two different standard deviations. Compare the results.

We are using SimpleKMeans with 2 clusters and seed as 10 to make DensityBased Cluster with a different value of standard deviations. Over here, we have change minimal standard deviation, which allows us to set a minimum threshold for standard deviation applied to the normal distribution of features in all dimensions.

Case: When minStdDev = 100

=== Run information ===

Scheme: weka.clusterers.MakeDensityBasedClusterer -M 100.0 -W 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: food

Instances: 27

Attributes: 6 Energy Protein Fat Calcium Iron

Ignored: Name

Test mode: evaluate on training data

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

MakeDensityBasedClusterer:

Wrapped clusterer:

kMeans

Number of iterations: 2

Within cluster sum of squared errors: 5.069321339929419

Initial starting points (random):

Cluster 0: 340,20,28,9,2.6 Cluster 1: 170,25,7,12,1.5

Missing values globally replaced with mean/mode

Final cluster centroids:

		Cluster#		
Attribute	Full Data	0	1 (18.0)	
	(27.0)	(9.0)		
Energy	207.4074	331.1111	145.5556	
Protein	19	19	19	
Fat	13.4815	27.5556	6.4444	
Calcium	43.963	8.7778	61.5556	
Iron	2.3815	2.4667	2.3389	

Fitted estimators (with ML estimates of variance):

Cluster: O Prior probability: 0.3448

Attribute: Energy

Normal Distribution. Mean = 331.1111 StdDev = 101.2078

Attribute: Protein

Normal Distribution. Mean = 19 StdDev = 100

Attribute: Fat

Normal Distribution. Mean = 27.5556 StdDev = 100

Attribute: Calcium

Normal Distribution. Mean = 8.7778 StdDev = 100

Attribute: Iron

Normal Distribution. Mean = 2.4667 StdDev = 100

Cluster: 1 Prior probability: 0.6552

Attribute: Energy

Normal Distribution. Mean = 145.5556 StdDev = 101.2078

Attribute: Protein

Normal Distribution. Mean = 19 StdDev = 100

Attribute: Fat

Normal Distribution. Mean = 6.4444 StdDev = 100

Attribute: Calcium

Normal Distribution. Mean = 61.5556 StdDev = 100

Attribute: Iron

Normal Distribution. Mean = 2.3389 StdDev = 100

```
Time taken to build model (full training data): 0 seconds

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

Clustered Instances

0 7 ( 26%)
1 20 ( 74%)

Log likelihood: -28.45138
```

Case: When minStdDev = 0.001

=== Run information ===

Scheme: weka.clusterers.MakeDensityBasedClusterer -M 0.001 -W 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: food

Instances: 27

Attributes: 6 Energy Protein Fat Calcium Iron

Ignored: Name

Test mode: evaluate on training data

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

MakeDensityBasedClusterer:

Wrapped clusterer:

kMeans

Number of iterations: 2

Within cluster sum of squared errors: 5.069321339929419

Initial starting points (random):

Cluster 0: 340,20,28,9,2.6 Cluster 1: 170,25,7,12,1.5

Missing values globally replaced with mean/mode

Final cluster centroids:

		Cluster#		
Attribute	Full Data	0	1 (18.0)	
	(27.0)	(9.0)		
	.=======			
Energy	207.4074	331.1111	145.5556	
Protein	19	19	19	
Fat	13.4815	27.5556	6.4444	
Calcium	43.963	8.7778	61.5556	
Iron	2.3815	2.4667	2.3389	

Fitted estimators (with ML estimates of variance):

Cluster: O Prior probability: 0.3448

Attribute: Energy

Normal Distribution. Mean = 331.1111 StdDev = 50.9781

Attribute: Protein

Normal Distribution. Mean = 19 StdDev = 1.633

Attribute: Fat

Normal Distribution. Mean = 27.5556 StdDev = 6.0939

Attribute: Calcium

Normal Distribution. Mean = 8.7778 StdDev = 0.6285

Attribute: Iron

Normal Distribution. Mean = 2.4667 StdDev = 0.2

Cluster: 1 Prior probability: 0.6552

Attribute: Energy

Normal Distribution. Mean = 145.5556 StdDev = 44.9348

Attribute: Protein

Normal Distribution. Mean = 19 StdDev = 4.9777

Attribute: Fat

Normal Distribution. Mean = 6.4444 StdDev = 3.9892

Attribute: Calcium

Normal Distribution. Mean = 61.5556 StdDev = 88.6962

Attribute: Iron

Normal Distribution. Mean = 2.3389 StdDev = 1.749

Time taken to build model (full training data) : 0 seconds

```
=== Model and evaluation on training set ===
Clustered Instances

0 10 ( 37%)
1 17 ( 63%)
```

Log likelihood: -16.97883

As we can see, when the standard deviation changes from 0.001 to 100 variation in cluster increase. Thus when density-based clustering is applied cluster which was part of Cluster 0 were moved into Cluster 1, as now because of changed variation density reachable point changed and thus new clusters with different numbers were obtained.