Lab 1 - 732A75 - Clustering Algorithms

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1. SimpleKmeans

Apply "SimpleKMeans" to your data. In Weka euclidian distance is implemented in SimpleKmeans. You can set the number of clusters and seed of a random algorithm for generating initial cluster centers. Experiment with the algorithm as follows:

1.

Choose a set of attributes for clustering and give a motivation. (Hint: always ignore attribute "name". Why does the name attribute need to be ignored?)

```
Number of iterations: 6
Within cluster sum of squared errors: 5.9104334390998226
Missing values globally replaced with mean/mode
Cluster centroids:
```

		Cluster#	
Attribute	Full Data	0	1
	(27)	(11)	(16)
Energy	207.4074	122.7273	265.625
Protein	19	16.7273	20.5625
Fat	13.4815	4.6364	19.5625
Calcium	43.963	94.2727	9.375
Iron	2.3815	2.1455	2.5438

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

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

Clustered Instances

0 11 (41%)
1 16 (59%)
```

The attributes for the simpleKmeans clustering algorithm we choose are 2 clusters, with seed = 1. Two clusters is the minimum that we can choose, and it is a good start to see what happens if we simply want to divide the data into two groups. For the seed we started with 1, just so we can easily compare to other seeds. The output is depicted in the image.

The name attribute needs to be ignored because it is a string with labels, which is already a categorization of different groups.

2.

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

```
Number of iterations: 2
Within cluster sum of squared errors: 5.069321339929419
Missing values globally replaced with mean/mode
```

Cluster centroids:

		Cluster#	
Attribute	Full Data	0	1
	(27)	(9)	(18)
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) : 0.01 seconds

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

Clustered Instances

9 (33%)

18 (67%)

Number of iterations: 4 Within cluster sum of squared errors: 2.750432407251998 Missing values globally replaced with mean/mode

Cluster centroids:

		Cluster#				
Attribute	Full Data	0	1	2	3	4
	(27)	(7)	(8)	(6)	(1)	(5)
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) : 0.01 seconds

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

Clustered Instances

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

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.

Number of iterations: 4 Within cluster sum of squared errors: 5.082974846131301 Missing values globally replaced with mean/mode

Cluster centroids:

		Cluster#	
Attribute	Full Data	0	1
	(27)	(19)	(8)
Energy	207.4074	150.7895	341.875
Protein	19	19.1053	18.75
Fat	13.4815	7	28.875
Calcium	43.963	58.7895	8.75
Iron	2.3815	2.3579	2.4375

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

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

Clustered Instances

19 (70%) 8 (30%)

Number of iterations: 10 Within cluster sum of squared errors: 3.413323983598554 Missing values globally replaced with mean/mode

Cluster centroids:

		Cluster.				
Attribute	Full Data	0	1	2	3	4
	(27)	(11)	(6)	(3)	(1)	(6)
Energy	207.4074	159.5455	341.6667	238.3333	420	110
Protein	19	21.5455	19.1667	19.6667	15	14.5
Fat	13.4815	6.8182	28.6667	17	39	4.5
Calcium	43.963	20.3636	9	8.3333	7	146.1667
Iron	2.3815	2.0364	2.4833	2.6	2	2.8667

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

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

Clustered Instances

11 (41%) 6 (22%)

The seed value controls for different initial centroids. Different initial centroids could lead to different clustering outcomes.

4.

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

5.

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

2. MakeDensityBasedClusters

Now with MakeDensityBasedClusters, SimpleKMeans is turned into a density-based clusterer. You can set the minimum standard deviation for normal density calculation. Experiment with the algorithm as the follows:

1.

Use the SimpleKMeans clusterer which gave the result you haven chosen in 5).

Number of iterations: 10 Within cluster sum of squared errors: 3.413323983598554 Missing values globally replaced with mean/mode

Cluster centroids:

		Cluster#				
Attribute	Full Data	0	1	2	3	4
	(27)	(11)	(6)	(3)	(1)	(6)
Energy	207.4074	159.5455	341.6667	238.3333	420	110
Protein	19	21.5455	19.1667	19.6667	15	14.5
Fat	13.4815	6.8182	28.6667	17	39	4.5
Calcium	43.963	20.3636	9	8.3333	7	146.1667
Iron	2.3815	2.0364	2.4833	2.6	2	2.8667

Clustered Instances

0 10 (37%) 1 6 (22%) 2 3 (11%) 3 1 (4%)

Log likelihood: -18.1147

7 (26%)

2.

Experiment with at least two different standard deviations. Compare the results. (Hint: Increasing the standard deviation to higher values will make the differences in different runs more obvious and thus it will be easier to conclude what the parameter does)

Number of iterations: 10 Within cluster sum of squared errors: 3.413323983598554 Missing values globally replaced with mean/mode

Cluster centroids:

		Cluster#				
Attribute	Full Data	0	1	2	3	4
	(27)	(11)	(6)	(3)	(1)	(6)
Energy	207.4074	159.5455	341.6667	238.3333	420	110
Protein	19	21.5455	19.1667	19.6667	15	14.5
Fat	13.4815	6.8182	28.6667	17	39	4.5
Calcium	43.963	20.3636	9	8.3333	7	146.1667
Iron	2.3815	2.0364	2.4833	2.6	2	2.8667

Clustered Instances

0 10 (37%) 1 6 (22%) 2 3 (11%) 3 1 (4%) 4 7 (26%)

Log likelihood: -18.33321