

CSCI-B 565 DATA MINING

Homework 2

Afternoon Class

Computer Science Core

Fall

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All the work herein is solely mine.

1 Solutions to Theoretical aspects of k -Means

1. k -Means Convergence

- (a) No, The given k -means algorithm does not converge.
- (b) Convergence of k -means depend lot of factors like distribution of data,nature of convexity of the data etc. So, it is imperative that this new formal parameter needed should not depend on the data. One good option is to use the number of Iterations as an formal parameter to stop the algorithm.
- (c) There is no direct way of deciding the actual value of of iterations. This directly depends on the nature of data, hence no silver bullet algorithm is possible for finding the data. Usually, a good approach is to run k -means with multiple times and decide the trade-off between more iterations and accuracy.

2. Problems in Initialization of k -Means

- (a) If random points are used for initialization, there is a possibility that the output of the algorithm is different with every run.
- (b) The Randomized points generated for the multiple centroids might be near. Hence we have to handle additional overhead of defining closeness of one centroid to other and managing these scenarios are necessary.
- (c) The Centroids can overlap with each other, Hence care should be taken that no two centroids should have same starting attributes
- (d) If the randomly generated centroid is local minima of a non-convex space, there is a challenge that the centroid never changes throughout the iterations.

3. Run time of k -Means

The run time of the algorithm depends on following factors

- (a) Data : Larger the data, more time it takes to process the data
 - (b) Number of centroids, Higher the centroids : Higher the computation
 - (c) Number of Features of Dataset
 - (d) Number of iterations n
4. Can be skipped as instructed.
5. Indicators of representative measures
- (a) Median is a good measure of the representation. This is more robust against using mean, as mean is affected even by a small outlier. Hence Median of those values would provide more robustness and less influential to the potential outliers.
 - (b) Mode of the distribution is also one possible representative.
6. Closer Centroids
- (a) During the k -Means algorithm, it might happen that two centroids can come "near" to each other. This distorts the boundary line of the algorithm. Hence to overcome this we can define two new parameters minimum cluster distance c_d and reassign method m_d . The cluster distance would be the minimum distance after which we can classify that two clusters are too close to each other, the minimum threshold. And the method would be how do we re-assign these centroids after we determine it is too close.
 - (b) With the new parameters, the signature of the k means would be (data Δ , distance $d : \Delta^2 \rightarrow \mathbb{R}_{\geq 0}$, centroid number k , threshold τ , iterations n , minimum cluster distance m_d , cluster reassign method m_d)
 - (c) This reassign method can be reassigning random points inside that cluster, taking two farthest points from the cluster centres, or sometimes merge these two centroids to one another. This cannot be defined ubiquitous and should be considered on case by case basis.
7. (a) Solution for e: 1, since x and $x \cup y$ are not equal
- (b) Solution for f: 0. This is a form of DeMorgan's theorem, hence both x and y are equal
- (a) $d(x, y) = \frac{3}{5}$
 - (b) $d(x \cap y, \{a, b\}) = 0$
 - (c) $d(x, x \cup y) = \frac{1}{5}$
 - (d) $d(\neg(x \cap y), \neg x \cup \neg y) = 0$
8. (a) $d(x, y) = 3$
- (b) $d(\text{concat}(\mathbf{x}, \mathbf{x}), \text{concat}(\mathbf{x}, \mathbf{y})) = 3$
- (c) From above two solutions, hamming distance is concerned with only the difference of the bits and not on the length of the bits.
- (d) $d(\mathbf{N_orth}, \mathbf{nort_h}) = 5$ First 5 character are different in both strings.
- (e) $d(\text{upper}(\text{space}(\mathbf{N_orth})), \text{upper}(\text{space}(\mathbf{nort_h}))) = 0$ Removing case and converting all character to upper case will render both the characters to be same, hence zero distance.
- (f) $d(\mathbf{north}, \mathbf{south}) = 3$ 1, 3 and 4 characters are different.
- (g) The problem of string distances
- i. Distance $d(\text{string1}, \text{string2}) = \text{Levenshtein distance}(\text{lookup}(\text{String1}), \text{lookup}(\text{String2}))$
This distance function consists of two single functions. A fast look up table which can resolve any string to its normalized string ie (walk, walking etc to walk) and Levenshtein distance function to find distance between these normalized strings. Levenshtein distance is already a known metric for finding string distances.

This lookup table for normalization can be either driven by the manual dictionary approach or an computer-aided approach. It interesting thing is that in the paper "A Comparison of String Metrics for Matching Names and Records", William W. Cohen, Pradeep Ravikumar and Stephen E. Fienberg discusses possibilities of Supervised and Unsupervised learning algorithms to build these hash tables.

- ii. Another simpler approach is to append trailing zeroes to make the length of both the strings equal, convert all strings to upper cases and calculate the first character. If they are equal, then distance function value is 1 else 0.

9.

$$c(x) = \begin{cases} 1, & \text{if concat(set } x \text{) is equal to string } x \\ 0, & \text{otherwise} \end{cases} \quad (1)$$

$$d(\mathbf{x}, \mathbf{y}) = c(x) - c(y) \quad (2)$$

Prove the above defined function is a distance metric

Consider an example, three data points $((c, a, t), cat), ((b, a, t), bat), ((p, a, t), pat)$

$d(((c, a, t), cat), ((c, a, t), cat)) = 1 - 1 = 0$ coincidence axiom

$d(((c, a, t), cat), ((b, a, t), bat))) = d(((b, a, t), bat)), ((c, a, t), cat)) = 1 - 1 = 0$ symmetry axiom

$d(((c, a, t), cat), ((p, a, t), pat))) \leq d(((c, a, t), cat), ((b, a, t), bat))) + d(((b, a, t), bat)), ((p, a, t), pat)))$

$0 \leq 0 + 0$ Triangle Inequality axiom

Hence this proposed distance function

2 Application of K Means to Medical Data

```
library(rpart)
library(rpart.plot)
library(rattle)
library(entropy)
#Load the data into R
setwd("C:/Users/Ganesh/Google_Drive/Courses/CSCI_B_565/Homework/Homework_2")
del<-read.csv(file = "breast-cancer-wisconsin.data", header = FALSE, na.strings = "?")
head(del)
colnames(del)<-c("SCN", "Clump.Thickness", "Cell.Size", "Cell.Shape", "M.Adhesion", "SECS",
                "B.Nuclei", "B.Chromatin", "N.Nucleoli", "Mitoses", "class")
#Filter complete cases
delstar<-del[complete.cases(del),]
#Filter missing data
delm<-del[!complete.cases(del),]
write.csv(delstar, "bcData.csv", row.names = FALSE)
```

- (a) (a) Considering there are 699 observations and each observations has to pay \$ 5000, the total cost comes to be about \$ 3,495,000.

- (b) Considering there are 241 Malignant Tumors, with each masectomies about \$ 55,000 the total cost would be \$ 1,32,55,000.

2. Ignoring SCN, the dataset has 10 more attributes

3. (a) There are 16 observations with missing values. Only 16 Missing values are there and all of them are Bare Nuclei data.

- (b) Following SCNs have missing data

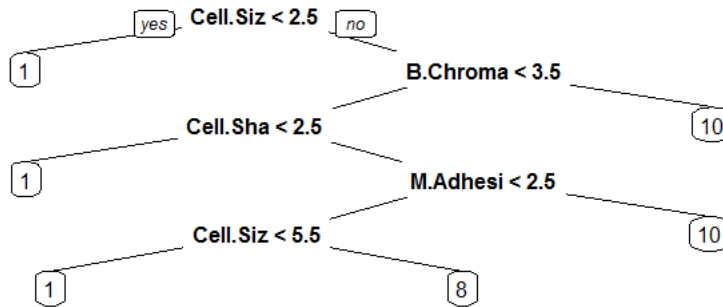
```
delm[,1]
[1] 1057013 1096800 1183246 1184840 1193683 1197510 1241232 169356 432809 563649
[11] 606140 61634 704168 733639 1238464 1057067
```

- (c) If we were to re-examine everyone, the cost would be \$ 5,000 for 16 persons, \$ 80,000.
- (d) Cleaning the data : The snippet is shown above
- (e) Replacing the missing data:
- This is a reverse machine learning problem on the data set itself. We can assume the complete data as the train data, model the decision tree and test in on the missing data to identify the missing values.

```
#Train a Decision Tree for finding B.Nuclei missing values
fit<-rpart(B.Nuclei~Clump.Thickness+Cell.Shape+Cell.Size+M.Adhesion+SECS+
           B.Nuclei+B.Chromatin+N.Nucleoli+Mitoses, data=delstar, method = "class")
prp(fit)
nas<-predict(fit, newdata=delm, type = "class")
delmstar<-delm
delmstar$B.Nuclei<-as.numeric(as.character(nas))

#Train a decision tree to predict the class from other values
fit1<-rpart(class~Clump.Thickness+Cell.Shape+Cell.Size+M.Adhesion+SECS+
            B.Nuclei+B.Chromatin+N.Nucleoli+Mitoses+B.Nuclei, data=delstar, method = "class")
prp(fit1)
```

The resulting Decision tree is as follows,



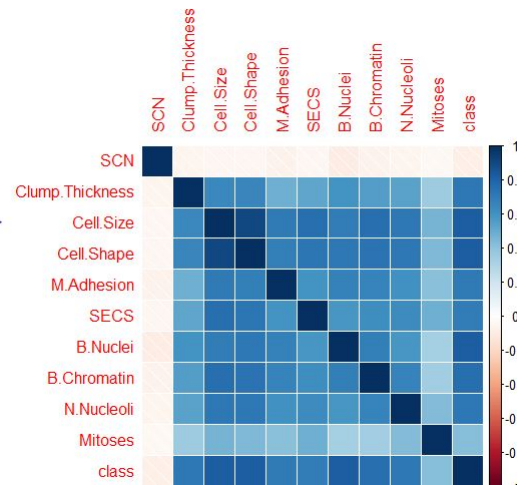
This model was used to predict the missing values and the missing values are as follows,

```
delmstar[,c(1,7)]
      SCN B.Nuclei
24  1057013      1
41  1096800     10
140 1183246      1
146 1184840      1
159 1193683      1
165 1197510      1
236 1241232      1
250  169356      1
276  432809      1
293  563649     10
295  606140      1
298   61634      1
316  704168     10
322  733639      1
412 1238464      1
618 1057067      1
```

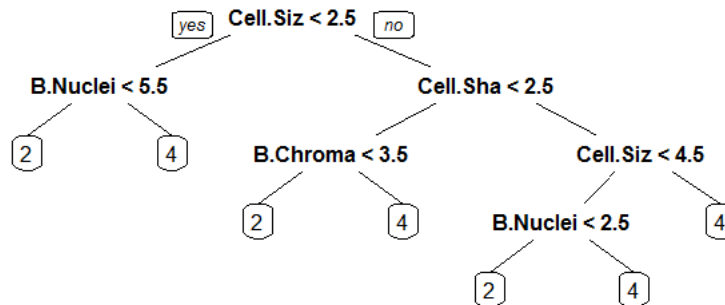
Answers to the exercises:

(a) Significance of the missing data

- i. Yes, the amount of missing data is significant. From the training data, a correlation matrix was devised which indicates clearly that the B.Nuclei, of which there were missing data has good correlation to the predicted value.



Moreover a decision tree was built over the test data to predict the class, it is seen that several node decisions were taken based on the values of B.Nuclei. Incase if this data is absent, this would lead to increase in entropy at the root level before leaves and the eventual uncertainty of how to split this node.



- (b) When the tuples are removed because of the missing values, this requires that all these subjects then undergo biopsies again. This would increase the cost. Whereas keeping the tuples with missing values and replacing the old values, we include these tuples to further analysis, and now only 3 people of the missing values require masectomy. Thus this approach reduces both cost and morbidity.

4. (a) *#Function for Variance*

```

data.variance <- function(dataframe, attributelist){
  names<-colnames(dataframe)
  toPrintnames=c()
  toPrintVal=c()
  for(i in attributelist){
    variance<-var(dataframe[,i])
    toPrintnames=c(toPrintnames,names[i])
    toPrintVal=c(toPrintVal,variance)
  }
  printdf<-as.data.frame(cbind(toPrintnames,toPrintVal))
}

```

```

    colnames(printdf)<-c("label", "variance")
    print(printdf)
}
data.variance(delstar, c(2:10))

```

The Output of the above code is as follows,

```

data.variance(delstar, c(2:10))
      label      variance
1 Clump.Thickness 7.95669441784777
2      Cell.Size 9.39511298695165
3      Cell.Shape 8.93161530766027
4      M.Adhesion 8.20571654293848
5          SECS 4.94210894664302
6      B.Nuclei 13.2776950060755
7  B.Chromatin 6.00101329738131
8   N.Nucleoli 9.31877219271542
9      Mitoses 3.00215969738475

```

It is clearly seen that B.Nuclei has the highest variance

(b) Entropy:

```

#Function for Entropy
data.entropy <- function(dataframe, attributelist){
  names<-colnames(dataframe)
  toPrintnames=c()
  toPrintVal=c()
  for(i in attributelist){
    entropy_d<-entropy(dataframe[, i], unit="log2")
    toPrintnames=c(toPrintnames, names[i])
    toPrintVal=c(toPrintVal, entropy_d)
  }
  printdf<-as.data.frame(cbind(toPrintnames, toPrintVal))
  colnames(printdf)<-c("label", "Entropy")
  print(printdf)
}
data.entropy(delstar, c(2:10))

```

The output is,

```

data.entropy(delstar, c(2:10))
      label      Entropy
1 Clump.Thickness 9.12010690808455
2      Cell.Size 8.83190208479647
3      Cell.Shape 8.87057622257544
4      M.Adhesion 8.82394225367755
5          SECS 9.13824665773771
6      B.Nuclei 8.73895611645067
7  B.Chromatin 9.08497909039174
8   N.Nucleoli 8.76060529737097
9      Mitoses 8.93412908252063

```

As with the previous question, B.Nuclei has the least entropy.

(c) For KL distance, the package entropy is used. This has functions to empirically calculate the frequency of the two datasets and then performs KL divergence over that probability function.

```

#Calculate KL Distance
calculateKL <- function(dataframe,col1,col2){
  output<-matrix(0,nrow=length(col1),ncol = length(col1))
  for (i in 1:length(col1)){
    for(j in 1:length(col1)){
      #print(i)
      k1<-freqs(dataframe[,i])
      k2<-freqs(dataframe[,j])
      kl<-KL.empirical(k1,k2,unit = "log2")
      output[i,j]<-kl
    }
  }
  print(output)
}
delkl<-delstar[,2:10]
col<-1:9
calculateKL(delkl,col,col)

```

The KL Distance Values are as follows,

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	0.00	0.35	0.33	0.46	0.26	0.48	0.30	0.48	0.43
[2,]	0.33	0.00	0.09	0.30	0.23	0.34	0.24	0.32	0.53
[3,]	0.31	0.09	0.00	0.32	0.24	0.33	0.25	0.33	0.53
[4,]	0.45	0.28	0.30	0.00	0.33	0.38	0.32	0.44	0.56
[5,]	0.28	0.24	0.24	0.35	0.00	0.43	0.23	0.36	0.35
[6,]	0.44	0.30	0.29	0.39	0.40	0.00	0.34	0.50	0.68
[7,]	0.30	0.25	0.25	0.31	0.21	0.38	0.00	0.36	0.45
[8,]	0.45	0.27	0.28	0.43	0.34	0.47	0.33	0.00	0.59
[9,]	0.49	0.48	0.50	0.55	0.35	0.68	0.48	0.54	0.00

5. K Means Implementation for the medical dataset.

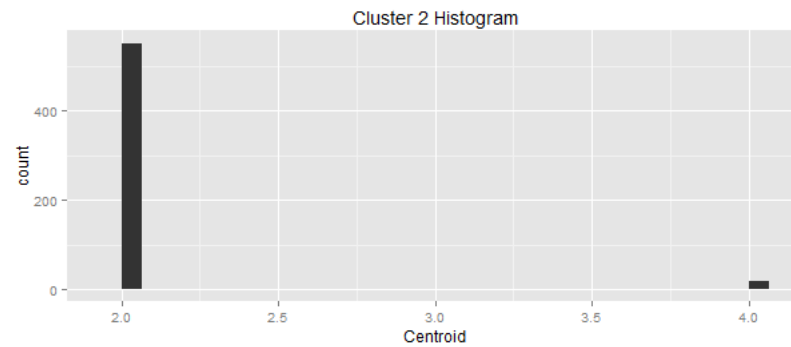
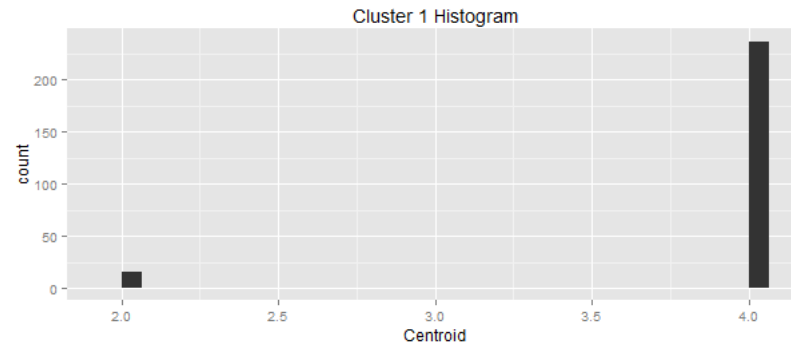
(a) K-Means was implemented with java for this exercise. The entire solution has following stages.

- i. Preprocessing : R and R studio are used for preprocessing. The missing values are removed in R and exported as CSV.
- ii. DataStructure Framework: EJML, Efficient Java Matrix Library is an open source library for extending matrix data structures to java. This supports loading of CSV files directly as matrix, perform advanced operations like matrix, SVD, and calculate distances. However for the purpose of this assignment, they are just used as data structures and this assignment uses no advanced operation required of these data structures.
- iii. Data munging for EJML : EJML reads data only as matrix and requires space separation instead of comma separated values. Hence these steps are done manually to replace comma with a space and replace first line with number of rows, columns and the data type. Following is a sneak peak of the file used for this assignment.

```

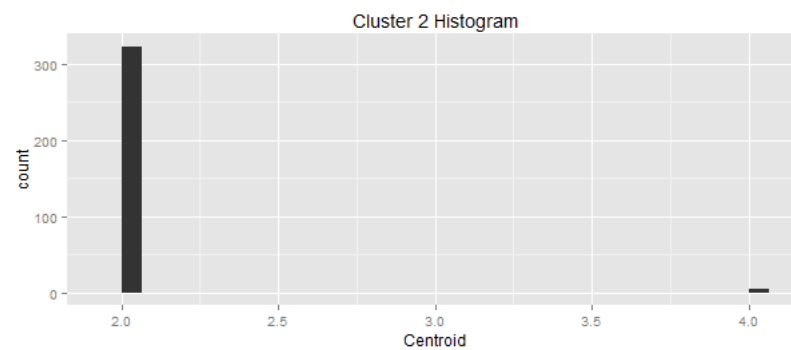
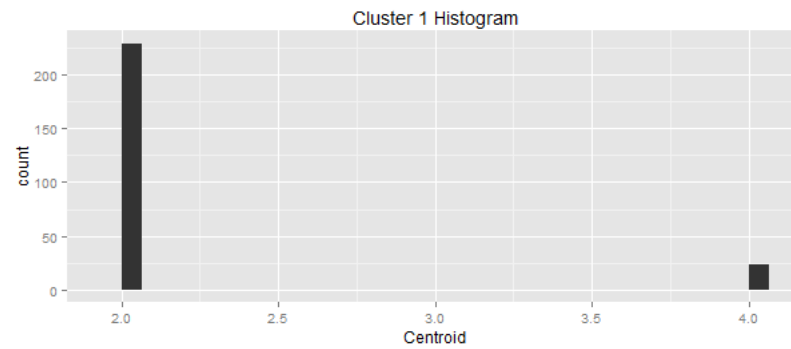
683 11 real
1000025 5 1 1 1 2 1 3 1 1 2
1002945 5 4 4 5 7 10 3 2 1 2
1015425 3 1 1 1 2 2 3 1 1 2
1016277 6 8 8 1 3 4 3 7 1 2
1017023 4 1 1 3 2 1 3 1 1 2
1017122 8 10 10 8 7 10 9 7 1 4

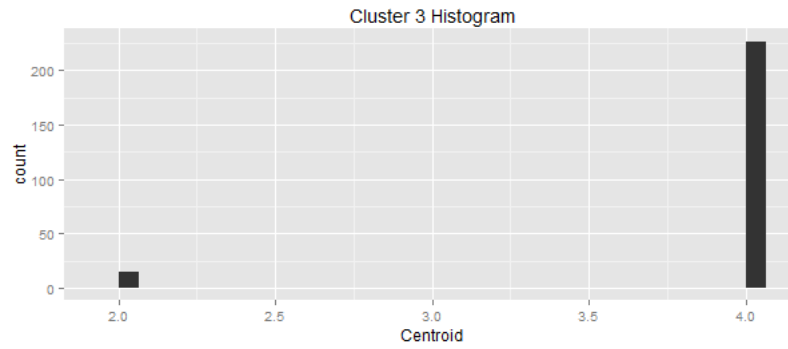
```

It can be clearly seen that class 2 is dominant in cluster 2 and class 4 is dominant in cluster 1.

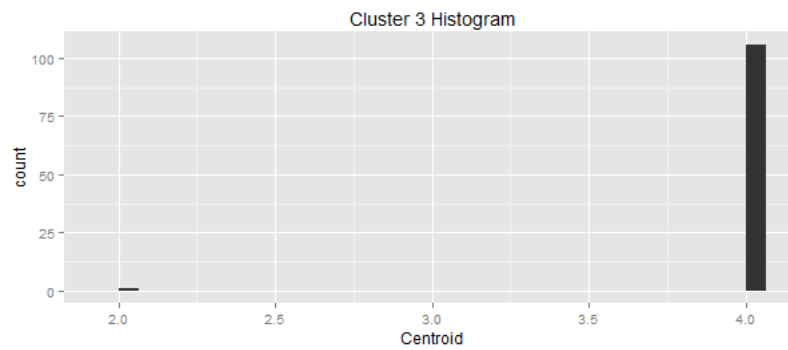
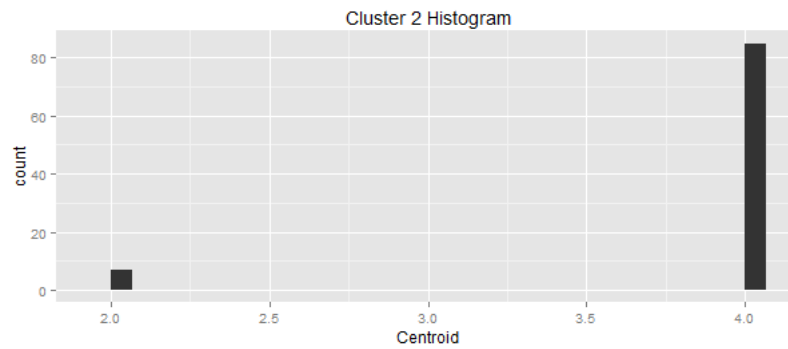
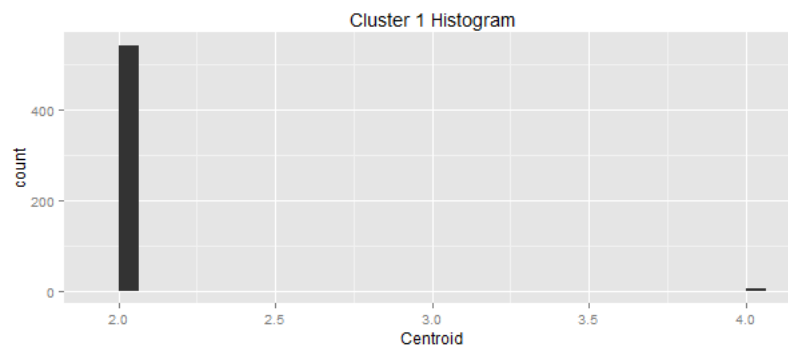
ii. Consider Test Data Set 2: Now instead of two Three centroids are calculated.

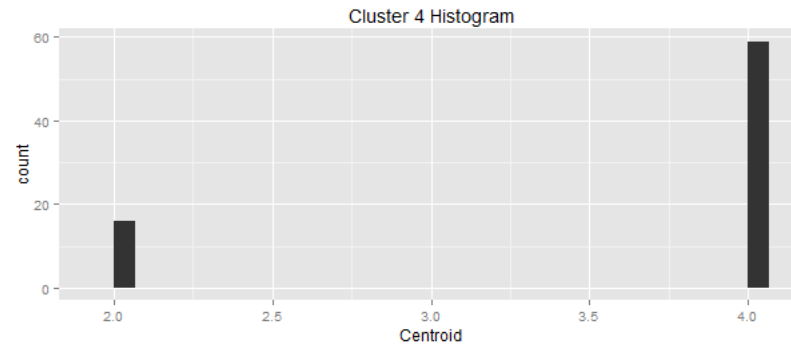




It can be seen that there are two clusters in which attribute 2 is dominant and the third has attribute 4 dominant.

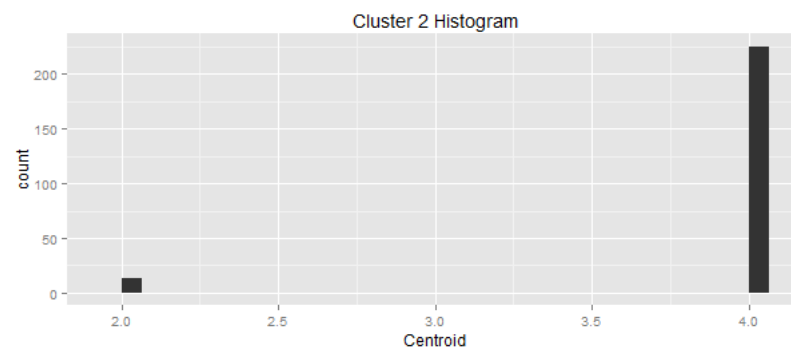
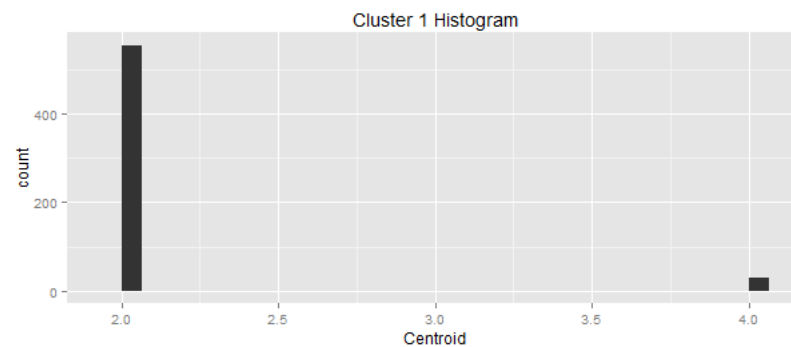
iii. Consider Test Data Set 3 : Consider 4 centroids:





It can be seen that there are three clusters in which attribute 4 is dominant, whereas in the other cluster attribute 2 is dominant.

- iv. Hence by intuition, as number of centroid increases the attributes are distributed across the centroids and this is not desired. Hence the best choice at this point is two centroids.
- v. Now, changing the feature set, intuitively columns which have higher variance has richer data and might contribute significantly to the predicted value than other attributes. Choosing columns which have top 5 variance, following is the histogram results.



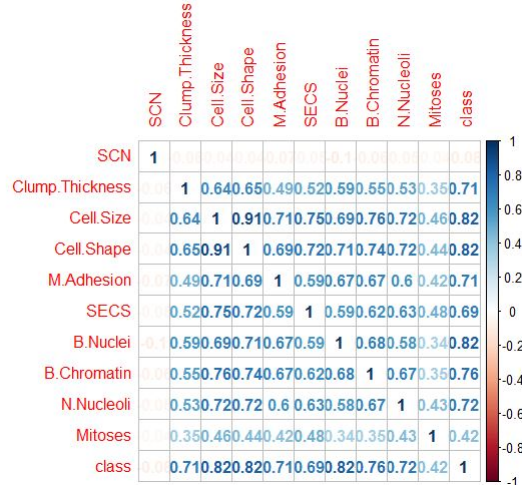
```
data.variance(dclstar,c(2:10))
      label      variance
1 Clump.Thickness 7.95669441784777
2      Cell.Size 9.39511298695165
3      Cell.Shape 8.93161530766027
4      M.Adhesion 8.20571654293848
5          SECS 4.94210894664302
6      B.Nuclei 13.2776950060755
7 B.Chromatin 6.00101329738131
```

8 N.Nucleoli 9.31877219271542
9 Mitoses 3.00215969738475

On Investigation, there were 551 correct and 31 wrong items classified in cluster 1. Cluster 2 had 225 correct items and 13 wrong items.

Hence $PPV = \frac{(551+225)}{((551+225)+(13+31))} = 0.9463$.

- vi. Comparing this to test data 1, which considered all features for calculation of centroid, $PPV = \frac{(225+554)}{(225+554)+(16+19)} = 0.9570025..$ Thus even after reducing half the attributes, there was only a marginal degradation of performance. Hence attributes 2,3,4,6,8 in the above table are good representations of the data. Coincidentally the covariance matrix also infers the same relation.



6. Crossfold validations: The data set is divided to 10 parts and K-mean was run on all these clusters. Then misplaced data points and correctly identified points are counted and summarized as follows.

	C1		C2		
TestSet	T	F	T	F	PPV
1	40	5	31	2	0.9103
2	53	3	26	1	0.9518
3	46	3	24	1	0.9459
4	37	5	50	7	0.8788
5	33	3	36	1	0.9452
6	58	1	15	0	0.9865
7	75	2	15	0	0.9783
8	73	0	11	0	1
9	51	1	23	0	0.9867
10	69	1	13	1	0.9762
					9.5596

The Average ppv was found to be 95.59. V fold validation offers more robustness than the single iteration k means. Surprisingly it was found that there were duplicates in SCN, however for the purpose of this analysis, they were considered as separate sets. Hence there might spike in few bins in the above table.

Both cross validation and normal k means give a ppv around 95, ie 95 percent of the items are classified correctly.