Question - 3

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0.1 Approach - 1

A. Using R, load the /public/bmort/R/wheat.csv data set into a data frame. Are there any missing values? Perform any necessary data imputation on the data set.

```
In [64]: df = read.csv("/public/bmort/R/wheat.csv")
```

```
In [65]: dim(df)
```

1. 200 2. 8

```
In [66]: head(df, 5)
```

A data.frame: 5 Œ 8

area <dbl>	perimeter <dbl>	compactness <dbl>	length <dbl>	width <dbl>	asymmetry <dbl>	groove <dbl>	type <fct>
15.26	14.84	0.8710	5.763	3.312	2.221	5.220	A
14.88	14.57	0.8811	5.554	3.333	1.018	4.956	A
14.29	14.09	0.9050	5.291	3.337	2.699	4.825	A
13.84	13.94	0.8955	5.324	3.379	2.259	4.805	A
16.14	14.99	0.9034	5.658	3.562	1.355	5.175	A

```
In [67]: print(ncol(df))
         print(nrow(df))
```

```
[1] 8
[1] 200
```

```
In [68]: # count the missing values by column wise
         print("Count of missing values by column wise")
         sapply(df, function(x) sum(is.na(x)))
```

```
[1] "Count of missing values by column wise"
```

area 0 **perimeter** 0 **compactness** 0 **length** 0 **width** 1 **asymmetry** 0 **groove** 0 **type** 0
Width column has 1 missing value

```
In [69]: # finding mode value

         find_mode <- function(x) {
           u <- unique(x)
           tab <- tabulate(match(x, u))
           u[tab == max(tab)]
         }

         mode_val = find_mode(df$width)
```

```
In [70]: # replacing null value with mode value

         # which(is.na(df$width))
         df$width[8] = mode_val
```

```
In [71]: sapply(df, function(x) sum(is.na(x)))
```

area 0 **perimeter** 0 **compactness** 0 **length** 0 **width** 0 **asymmetry** 0 **groove** 0 **type** 0

B. Produce a table of summary statistics on the data set. How do the ranges of the values in the columns compare? Does each column of data have similar magnitudes and ranges? Are there any outliers?

```
In [72]: summary(df)
```

```
      area          perimeter      compactness         length
 Min.   :10.59   Min.   :12.41   Min.   :0.8081   Min.   :4.899
 1st Qu.:12.38   1st Qu.:13.47   1st Qu.:0.8583   1st Qu.:5.257
 Median :14.40   Median :14.38   Median :0.8745   Median :5.534
 Mean   :14.94   Mean   :14.60   Mean   :0.8721   Mean   :5.639
 3rd Qu.:17.41   3rd Qu.:15.78   3rd Qu.:0.8879   3rd Qu.:6.009
 Max.   :21.18   Max.   :17.25   Max.   :0.9183   Max.   :6.675
     width         asymmetry          groove       type
 Min.   :2.642   Min.   :0.7651   Min.   :4.519   A:68
 1st Qu.:2.965   1st Qu.:2.4935   1st Qu.:5.043   B:69
 Median :3.244   Median :3.5915   Median :5.226   C:63
 Mean   :3.272   Mean   :3.6627   Mean   :5.414
 3rd Qu.:3.564   3rd Qu.:4.7043   3rd Qu.:5.879
 Max.   :4.033   Max.   :8.4560   Max.   :6.550
```

0.2 Each column of data have a different magnitude and range so let's normalize it

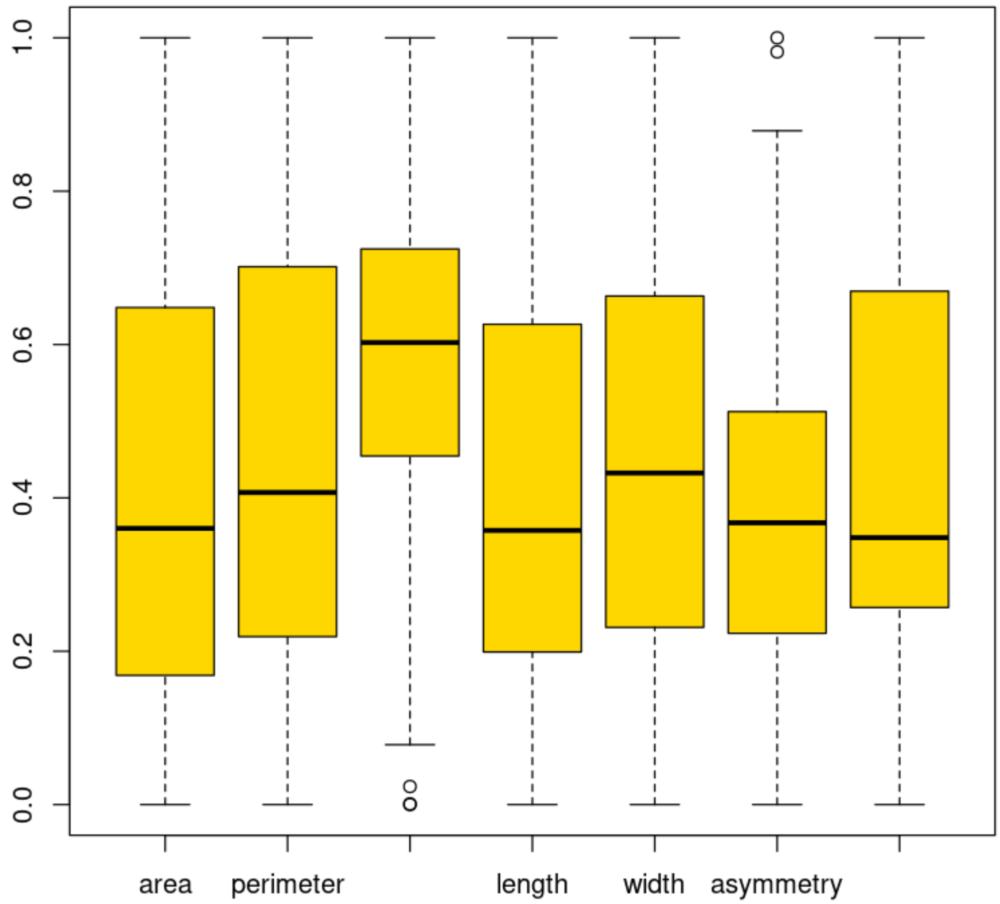
```
In [73]: # normalize data

         normalize <- function(x) {
         return ((x - min(x)) / (max(x) - min(x)))
         }
```

In [74]:
```
df$area = normalize(df$area)
df$perimeter = normalize(df$perimeter)
df$length = normalize(df$length)
df$width = normalize(df$width)
df$asymmetry = normalize(df$asymmetry)
df$groove = normalize(df$groove)
df$compactness = normalize(df$compactness)
```

In [76]:
```
summary(df)
```

```
      area          perimeter       compactness          length
 Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
 1st Qu.:0.1688   1st Qu.:0.2190   1st Qu.:0.4555   1st Qu.:0.2017
 Median :0.3602   Median :0.4070   Median :0.6025   Median :0.3575
 Mean   :0.4112   Mean   :0.4524   Mean   :0.5804   Mean   :0.4164
 3rd Qu.:0.6438   3rd Qu.:0.6968   3rd Qu.:0.7244   3rd Qu.:0.6249
 Max.   :1.0000   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
     width          asymmetry          groove        type
 Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   A:68
 1st Qu.:0.2324   1st Qu.:0.2247   1st Qu.:0.2578   B:69
 Median :0.4324   Median :0.3675   Median :0.3481   C:63
 Mean   :0.4528   Mean   :0.3768   Mean   :0.4408
 3rd Qu.:0.6627   3rd Qu.:0.5122   3rd Qu.:0.6696
 Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
```

In [83]:
```
out = df[1:7]
boxplot(out, col='gold')
```



0.2.1 Compactness column and groove column have outliers

In [17]:
```
# # replacing outlier values with NaN values

# # Outlier Calculation

# ##Function to calculate outliers

# # FindOutliers <- function(data) {
# #   lowerq = quantile(data)[2]
# #   upperq = quantile(data)[4]
# #   iqr = upperq - lowerq #Or use IQR(data)
# #   # we identify extreme outliers
```

```
# #   extreme.threshold.upper = (iqr * 3) + upperq
# #   extreme.threshold.lower = lowerq - (iqr * 3)
# #   result <- which(data > extreme.threshold.upper | data < extreme.threshold.lower
# # }

# FindOutliers <- function(data) {
#   lowerq = quantile(data)[2]
#   upperq = quantile(data)[4]
#   iqr = upperq - lowerq #Or use IQR(data)
#   # we identify extreme outliers
#   extreme.threshold.upper = (iqr * 3) + upperq
#   extreme.threshold.lower = lowerq - (iqr * 3)
#   result <- which(data > extreme.threshold.upper | data < extreme.threshold.lower)
#   length(result)
# }
# apply(out, 2, FindOutliers)
```

In [18]:
```
# Replacing outlier values with NaN values

for (x in c('compactness','asymmetry'))
{
  value = df[,x][df[,x] %in% boxplot.stats(df[,x])$out]
  df[,x][df[,x] %in% value] = NA
}
```

In [19]:
```
#Checking whether the outliers in the above defined columns are replaced by NULL or n

print(sum(is.na(df$compactness)))
print(sum(is.na(df$asymmetry)))
```

```
[1] 3
[1] 2
```

In [20]:
```
sapply(df, function(x) sum(is.na(x)))
```

area 0 **perimeter** 0 **compactness** 3 **length** 0 **width** 0 **asymmetry** 2 **groove** 0 **type** 0

In [21]:
```
# # finding mode value

# find_mode <- function(x) {
#   u <- unique(x)
#   tab <- tabulate(match(x, u))
#   u[tab == max(tab)]
# }

# mode_val = find_mode(df$compactness)
```

In [22]:
```
# # replacing null value with mode value in compactness column
```

```
# index = which(is.na(df$compactness))
# print(index)

# for (i in index)
# {
#     df$compactness[i] = mode_val
# }
# # df$width[8] = mode_val
```

In [23]:
```
# # replacing null value with mode value in asymmetry column

# index = which(is.na(df$asymmetry))
# index

# for (i in index)
# {
#     df$asymmetry[i] = mode_val
# }
```

In [24]:
```
# sapply(df, function(x) sum(is.na(x)))
```

In [25]:
```
# now let's remove the rows that has null values

#Removing the null values

library(tidyr)
df = drop_na(df)
as.data.frame(colSums(is.na(df)))
# sapply(df, function(x) sum(is.na(x)))
```

A data.frame: 8 Œ 1

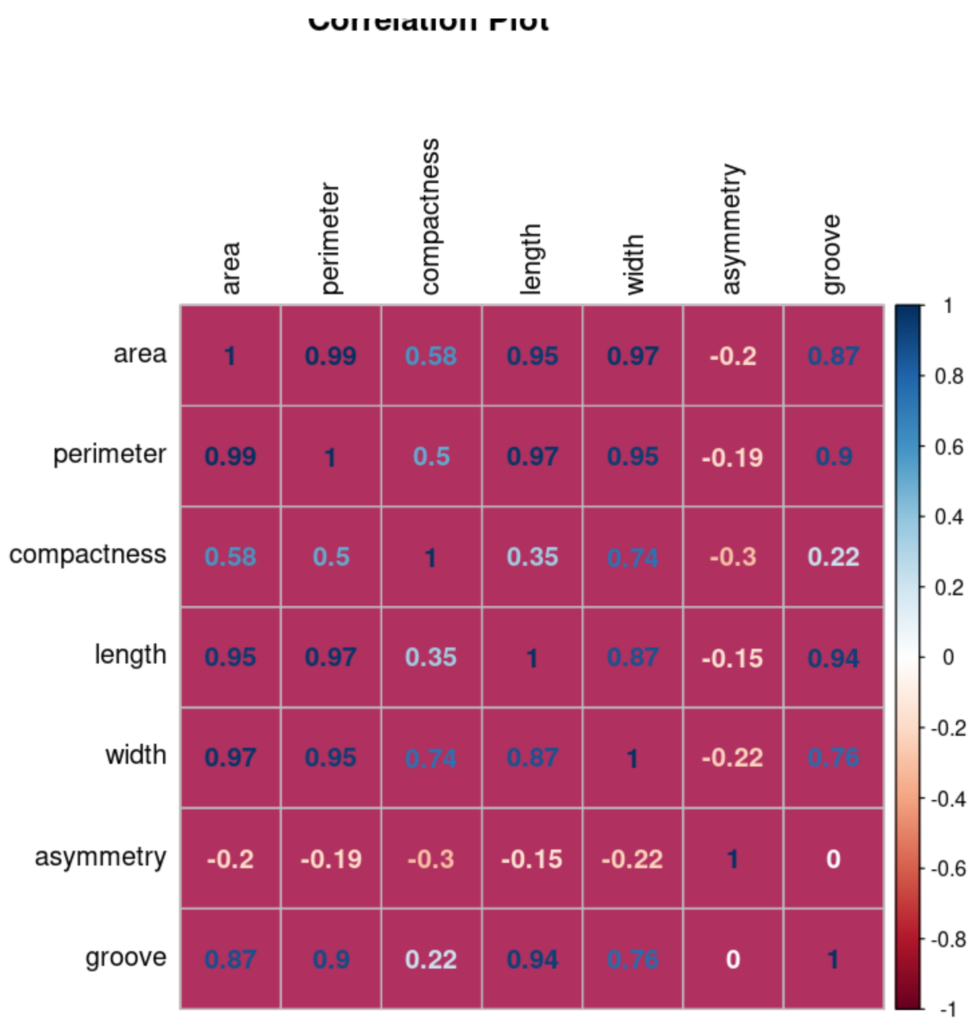
	colSums(is.na(df)) <dbl>
area	0
perimeter	0
compactness	0
length	0
width	0
asymmetry	0
groove	0
type	0

0.3 All Outliers have been removed

C. Using the corrplot library's corrplot() function, generate a plot showing the correlations between the numerical data in the data set. Show the command used to generate the plot and include the plot in your output.

In [26]:
```
library(corrplot)
relation = cor(out)
corrplot(relation, title='Correlation Plot', bg='maroon', method='number', tl.col='bla
```

```
corrplot 0.84 loaded
```



D. Partition the beans data set so that 80% will be used for training and 20% will be used for testing your machine learning model. You can do the partition manually at random or use the createDataPartition() function in R's caret library.

```
In [8]: library(caret)
```

```
Loading required package: lattice
Loading required package: ggplot2
```

```
In [35]: intrain <- createDataPartition(y = df$type, p= 0.8, list = FALSE)
         train <- df[intrain,]
         test <- df[-intrain,]
```

```
In [36]: dim(train)
```

1. 158 2. 8

```
In [37]: dim(test)
```

1. 37 2. 8

E. Use the support vector machine (SVM) method with a linear basis function kernel from R's caret library to generate a machine learning model for the 7 types of wheat seeds based on some or all features provided in the data set. Using the caret library's trainControl() function, check your model parameter and feature selection by performing repeated cross-validation (with 5-folds) on the training data for your model. Consult the caret library documentation as needed.

```
In [33]: train[["type"]] = factor(train[["type"]])
```

```
In [43]: unique(train['type'])
```

A data.frame: 3 Œ 1

	type <fct>
2	A
69	B
138	C

```
In [44]: # using repeated CV with 5 folds

         trctrl <- trainControl(method = "repeatedcv", number = 5)
```

```
In [47]: # Using SVM with linear basis function

         svm_linear <- train(type ~., data = train, method = "svmLinear",trControl=trctrl, tune
```

```
In [48]: svm_linear
```

```
Support Vector Machines with Linear Kernel

158 samples
  7 predictor
  3 classes: 'A', 'B', 'C'

No pre-processing
Resampling: Cross-Validated (5 fold, repeated 1 times)
Summary of sample sizes: 127, 126, 126, 127, 126
Resampling results:

  Accuracy   Kappa
  0.9243952  0.8865593

Tuning parameter 'C' was held constant at a value of 1
```

F. Use the test data set (i.e. the 20% of the data that was kept aside earlier) to generate a final validation for your model with the predict() function in the caret library. Comment on the accuracy of the model.

In [49]:
```
# let's apply our model to the test set

test_pred <- predict(svm_linear, newdata = test)
test_pred
```

1. A 2. A 3. A 4. A 5. A 6. A 7. A 8. A 9. A 10. A 11. A 12. A 13. A 14. B 15. B 16. B 17. B 18. B 19. B 20. B 21. B 22. B 23. B 24. B 25. B 26. B 27. C 28. C 29. C 30. A 31. C 32. C 33. C 34. C 35. A 36. A 37. A

Levels: 1. 'A' 2. 'B' 3. 'C'

In [ ]:
```
# Compute model prediction accuracy rate

mean(test_pred == test$type)
```

In [52]:
```
confusionMatrix(table(test_pred, test$type))
```

```
Confusion Matrix and Statistics


test_pred  A  B  C
        A 13  0  4
        B  0 13  0
        C  0  0  7

Overall Statistics

               Accuracy : 0.8919
                 95% CI : (0.7458, 0.9697)
    No Information Rate : 0.3514
    P-Value [Acc > NIR] : 1.275e-11

                  Kappa : 0.8359

 Mcnemar's Test P-Value : NA

Statistics by Class:

                     Class: A Class: B Class: C
Sensitivity            1.0000   1.0000   0.6364
Specificity            0.8333   1.0000   1.0000
Pos Pred Value         0.7647   1.0000   1.0000
Neg Pred Value         1.0000   1.0000   0.8667
Prevalence             0.3514   0.3514   0.2973
Detection Rate         0.3514   0.3514   0.1892
Detection Prevalence   0.4595   0.3514   0.1892
Balanced Accuracy      0.9167   1.0000   0.8182
```

0.3.1 The accuracy of the model is 89.19%

G. Based on your model, classify the beans provided in the unlabeled /public/bmort/R/wheat-unknown.csv data set. Indicate which classification of the 7 available types has been assigned to each of the unlabeled seeds

```
In [60]: unknown = read.csv('/public/bmort/R/wheat-unknown.csv')
         dim(unknown)
```

1. 10 2. 7

```
In [61]: test_pred <- predict(svm_linear, newdata = unknown)
         test_pred
```

1. B 2. B 3. B 4. B 5. B 6. B 7. B 8. B 9. B 10. B
Levels: 1. 'A' 2. 'B' 3. 'C'

```
In [62]: unknown$type = test_pred
```

```
In [63]: unknown
```

A data.frame: 10 Œ 8

area	perimeter	compactness	length	width	asymmetry	groove	type
<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<fct>
11.56	13.31	0.8198	5.363	2.683	4.062	5.182	B
14.79	14.52	0.8819	5.545	3.291	2.704	5.111	B
10.82	12.83	0.8256	5.180	2.630	4.853	5.089	B
13.32	13.94	0.8613	5.541	3.073	7.035	5.440	B
11.49	13.22	0.8263	5.304	2.695	5.388	5.310	B
10.83	12.96	0.8099	5.278	2.641	5.182	5.185	B
15.11	14.54	0.8986	5.579	3.462	3.128	5.180	B
11.19	13.05	0.8253	5.250	2.675	5.813	5.219	B
12.02	13.33	0.8503	5.350	2.810	4.271	5.308	B
17.99	15.86	0.8992	5.890	3.694	2.068	5.837	B

0.4 Approach - 2 Without normalizing and not removing the outliers as outliers have some significant information

```
In [1]: df = read.csv("/public/bmort/R/wheat.csv")
```

```
In [2]: # finding mode value

        find_mode <- function(x) {
          u <- unique(x)
          tab <- tabulate(match(x, u))
          u[tab == max(tab)]
        }

        mode_val = find_mode(df$width)
```

In [3]:
```
# replacing null value with mode value

# which(is.na(df$width))
df$width[8] = mode_val
```

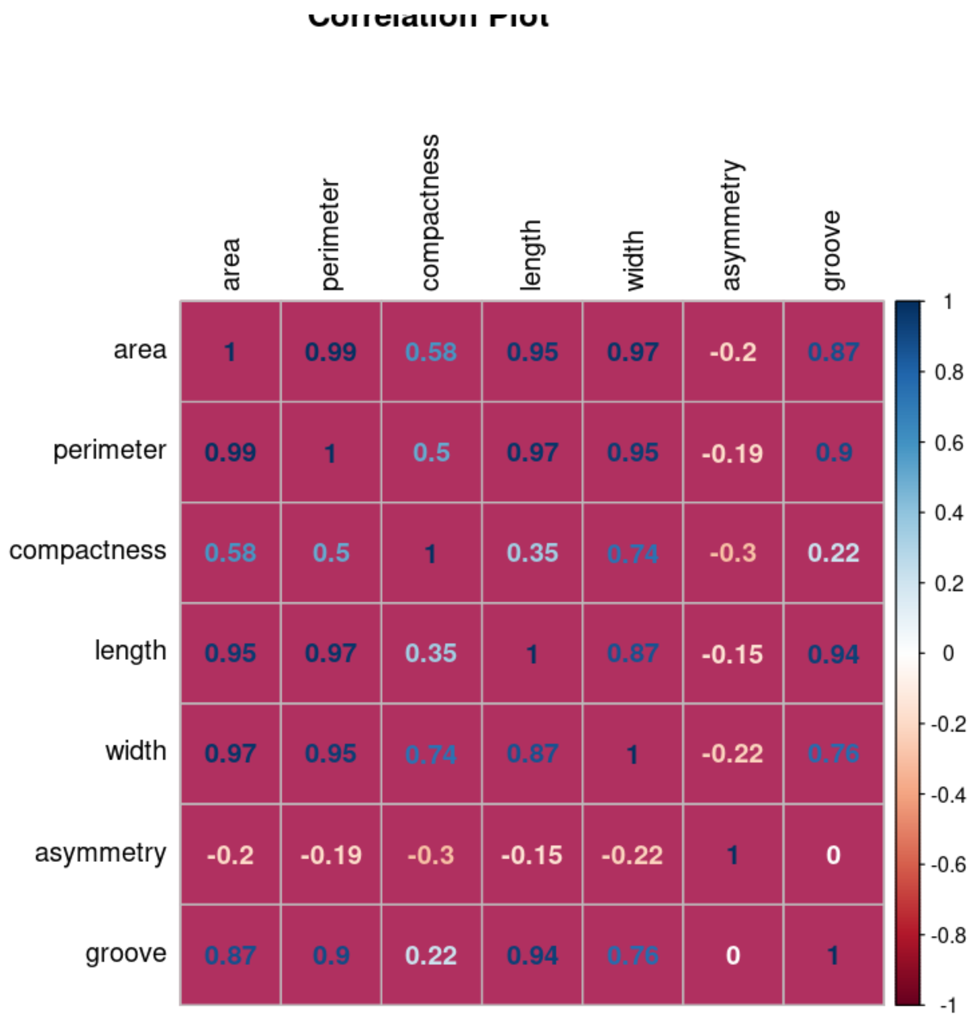
In [4]:
```
sapply(df, function(x) sum(is.na(x)))
```

area 0 **perimeter** 0 **compactness** 0 **length** 0 **width** 0 **asymmetry** 0 **groove** 0 **type** 0

In [5]:
```
summary(df)
```

```
      area          perimeter      compactness         length     
 Min.   :10.59   Min.   :12.41   Min.   :0.8081   Min.   :4.899  
 1st Qu.:12.38   1st Qu.:13.47   1st Qu.:0.8583   1st Qu.:5.257  
 Median :14.40   Median :14.38   Median :0.8745   Median :5.534  
 Mean   :14.94   Mean   :14.60   Mean   :0.8721   Mean   :5.639  
 3rd Qu.:17.41   3rd Qu.:15.78   3rd Qu.:0.8879   3rd Qu.:6.009  
 Max.   :21.18   Max.   :17.25   Max.   :0.9183   Max.   :6.675  
     width         asymmetry          groove      type  
 Min.   :2.642   Min.   :0.7651   Min.   :4.519   A:68  
 1st Qu.:2.965   1st Qu.:2.4935   1st Qu.:5.043   B:69  
 Median :3.244   Median :3.5915   Median :5.226   C:63  
 Mean   :3.272   Mean   :3.6627   Mean   :5.414         
 3rd Qu.:3.564   3rd Qu.:4.7043   3rd Qu.:5.879         
 Max.   :4.033   Max.   :8.4560   Max.   :6.550         
```

In [7]:
```
library(corrplot)
out = df[1:7]
relation = cor(out)
corrplot(relation, title='Correlation Plot', bg='maroon', method='number', tl.col='bla
```




```
In [9]: intrain <- createDataPartition(y = df$type, p= 0.8, list = FALSE)
        train <- df[intrain,]
        test <- df[-intrain,]

In [10]: train[["type"]] = factor(train[["type"]])

In [11]: # using repeated CV with 5 folds

         trctrl <- trainControl(method = "repeatedcv", number = 5)

In [12]: # Using SVM with linear basis function

         svm_linear <- train(type ~., data = train, method = "svmLinear",trControl=trctrl, tune
```

In [13]: svm_linear

```
Support Vector Machines with Linear Kernel

162 samples
  7 predictor
  3 classes: 'A', 'B', 'C'

No pre-processing
Resampling: Cross-Validated (5 fold, repeated 1 times)
Summary of sample sizes: 130, 130, 128, 130, 130
Resampling results:

  Accuracy   Kappa
  0.9378676  0.9067272

Tuning parameter 'C' was held constant at a value of 1
```

In [14]:
```
# let's apply our model to the test set

test_pred <- predict(svm_linear, newdata = test)
test_pred
```

1. A 2. A 3. A 4. C 5. A 6. A 7. A 8. A 9. A 10. A 11. A 12. C 13. A 14. B 15. B 16. B 17. B 18. B 19. B 20. B 21. B 22. B 23. B 24. B 25. B 26. B 27. C 28. C 29. C 30. C 31. C 32. C 33. C 34. C 35. C 36. C 37. A 38. A

Levels: 1. 'A' 2. 'B' 3. 'C'

In [15]:
```
# Compute model prediction accuracy rate

mean(test_pred == test$type)
```

0.894736842105263

In [16]: confusionMatrix(table(test_pred, test$type))

```
Confusion Matrix and Statistics


test_pred  A  B  C
        A 11  0  2
        B  0 13  0
        C  2  0 10

Overall Statistics

               Accuracy : 0.8947
                 95% CI : (0.752, 0.9706)
```

```
    No Information Rate : 0.3421
    P-Value [Acc > NIR] : 2.13e-12

                  Kappa : 0.842

 Mcnemar's Test P-Value : NA

Statistics by Class:

                     Class: A Class: B Class: C
Sensitivity            0.8462   1.0000   0.8333
Specificity            0.9200   1.0000   0.9231
Pos Pred Value         0.8462   1.0000   0.8333
Neg Pred Value         0.9200   1.0000   0.9231
Prevalence             0.3421   0.3421   0.3158
Detection Rate         0.2895   0.3421   0.2632
Detection Prevalence   0.3421   0.3421   0.3158
Balanced Accuracy      0.8831   1.0000   0.8782
```

```
In [17]: unknown = read.csv('/public/bmort/R/wheat-unknown.csv')
         dim(unknown)
```

1. 10 2. 7

```
In [18]: test_pred <- predict(svm_linear, newdata = unknown)
         test_pred
```

1. C 2. A 3. C 4. C 5. C 6. C 7. A 8. C 9. C 10. B
Levels: 1. 'A' 2. 'B' 3. 'C'

```
In [19]: unknown$type = test_pred
```

```
In [20]: unknown
```

A data.frame: 10 Œ 8

area <dbl>	perimeter <dbl>	compactness <dbl>	length <dbl>	width <dbl>	asymmetry <dbl>	groove <dbl>	type <fct>
11.56	13.31	0.8198	5.363	2.683	4.062	5.182	C
14.79	14.52	0.8819	5.545	3.291	2.704	5.111	A
10.82	12.83	0.8256	5.180	2.630	4.853	5.089	C
13.32	13.94	0.8613	5.541	3.073	7.035	5.440	C
11.49	13.22	0.8263	5.304	2.695	5.388	5.310	C
10.83	12.96	0.8099	5.278	2.641	5.182	5.185	C
15.11	14.54	0.8986	5.579	3.462	3.128	5.180	A
11.19	13.05	0.8253	5.250	2.675	5.813	5.219	C
12.02	13.33	0.8503	5.350	2.810	4.271	5.308	C
17.99	15.86	0.8992	5.890	3.694	2.068	5.837	B

0.4.1 The accuracy of the model is 89.47%

0.5 Even though Approach - 2 has slightly higher accuracy, I would say Approach - 1 is better as we removed outliers and scaled the data values in each column