Term Project - Predictive Modeling

Loding important packages

```
library(readr,  warn.conflicts=F)
library(RColorBrewer,  warn.conflicts=F) #Rcolorbrewer palette
library(corrplot,  warn.conflicts=F)
```

```
## corrplot 0.84 loaded
```

```
library(ggcorrplot,  warn.conflicts=F)
```

```
## Loading required package: ggplot2
```

```
library(plotly,  warn.conflicts=F)
library(ggplot2, warn.conflicts=F)
library(reshape, warn.conflicts=F)
library(viridis, warn.conflicts=F)
```

```
## Loading required package: viridisLite
```

```
library(tidyverse, warn.conflicts=F)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --

## v tibble  3.1.0     v dplyr   1.0.5
## v tidyr   1.1.2     v stringr 1.4.0
## v purrr   0.3.4     v forcats 0.5.0

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x tidyr::expand() masks reshape::expand()
## x dplyr::filter() masks plotly::filter(), stats::filter()
## x dplyr::lag()    masks stats::lag()
## x dplyr::rename() masks reshape::rename(), plotly::rename()
```

```
library(hrbrthemes, warn.conflicts=F)
```

```
## NOTE: Either Arial Narrow or Roboto Condensed fonts are required to use these themes.

##       Please use hrbrthemes::import_roboto_condensed() to install Roboto Condensed and

##       if Arial Narrow is not on your system, please see https://bit.ly/arialnarrow
```

```
library(psych, warn.conflicts=F)
library(class, warn.conflicts=F)
library(caret, warn.conflicts = F)
```

```
## Loading required package: lattice
```

```
library(DescTools)
```

```
##
## Attaching package: 'DescTools'

## The following objects are masked from 'package:caret':
##
##     MAE, RMSE

## The following objects are masked from 'package:psych':
##
##     AUC, ICC, SD
```

```
library(sjPlot)
```

```
## #refugeeswelcome
```

```
set.seed(123456789)
```

Importing Dataset

```
data <- read.csv("~/Breast-Cancer-Prediction/data/data.csv",  header=T)
cancerData <- read.csv("~/Breast-Cancer-Prediction/data/data.csv",  header=T)
```

Looking at dataset

```
head(data)
```

```
##         id diagnosis radius_mean texture_mean perimeter_mean area_mean
## 1   842302         M       17.99        10.38         122.80    1001.0
## 2   842517         M       20.57        17.77         132.90    1326.0
## 3 84300903         M       19.69        21.25         130.00    1203.0
## 4 84348301         M       11.42        20.38          77.58     386.1
## 5 84358402         M       20.29        14.34         135.10    1297.0
## 6   843786         M       12.45        15.70          82.57     477.1
##   smoothness_mean compactness_mean concavity_mean concave.points_mean
## 1         0.11840          0.27760         0.3001             0.14710
## 2         0.08474          0.07864         0.0869             0.07017
## 3         0.10960          0.15990         0.1974             0.12790
## 4         0.14250          0.28390         0.2414             0.10520
## 5         0.10030          0.13280         0.1980             0.10430
## 6         0.12780          0.17000         0.1578             0.08089
##   symmetry_mean fractal_dimension_mean radius_se texture_se perimeter_se
```

```
## 1        0.2419                0.07871    1.0950     0.9053        8.589
## 2        0.1812                0.05667    0.5435     0.7339        3.398
## 3        0.2069                0.05999    0.7456     0.7869        4.585
## 4        0.2597                0.09744    0.4956     1.1560        3.445
## 5        0.1809                0.05883    0.7572     0.7813        5.438
## 6        0.2087                0.07613    0.3345     0.8902        2.217
##   area_se smoothness_se compactness_se concavity_se concave.points_se
## 1  153.40      0.006399        0.04904      0.05373           0.01587
## 2   74.08      0.005225        0.01308      0.01860           0.01340
## 3   94.03      0.006150        0.04006      0.03832           0.02058
## 4   27.23      0.009110        0.07458      0.05661           0.01867
## 5   94.44      0.011490        0.02461      0.05688           0.01885
## 6   27.19      0.007510        0.03345      0.03672           0.01137
##   symmetry_se fractal_dimension_se radius_worst texture_worst perimeter_worst
## 1     0.03003             0.006193        25.38         17.33          184.60
## 2     0.01389             0.003532        24.99         23.41          158.80
## 3     0.02250             0.004571        23.57         25.53          152.50
## 4     0.05963             0.009208        14.91         26.50           98.87
## 5     0.01756             0.005115        22.54         16.67          152.20
## 6     0.02165             0.005082        15.47         23.75          103.40
##   area_worst smoothness_worst compactness_worst concavity_worst
## 1     2019.0           0.1622            0.6656          0.7119
## 2     1956.0           0.1238            0.1866          0.2416
## 3     1709.0           0.1444            0.4245          0.4504
## 4      567.7           0.2098            0.8663          0.6869
## 5     1575.0           0.1374            0.2050          0.4000
## 6      741.6           0.1791            0.5249          0.5355
##   concave.points_worst symmetry_worst fractal_dimension_worst  X
## 1               0.2654         0.4601                0.11890 NA
## 2               0.1860         0.2750                0.08902 NA
## 3               0.2430         0.3613                0.08758 NA
## 4               0.2575         0.6638                0.17300 NA
## 5               0.1625         0.2364                0.07678 NA
## 6               0.1741         0.3985                0.12440 NA
```

Columns in dataset

```
colnames(data)
```

```
##  [1] "id"                     "diagnosis"
##  [3] "radius_mean"            "texture_mean"
##  [5] "perimeter_mean"         "area_mean"
##  [7] "smoothness_mean"        "compactness_mean"
##  [9] "concavity_mean"         "concave.points_mean"
## [11] "symmetry_mean"          "fractal_dimension_mean"
## [13] "radius_se"              "texture_se"
## [15] "perimeter_se"           "area_se"
## [17] "smoothness_se"          "compactness_se"
## [19] "concavity_se"           "concave.points_se"
## [21] "symmetry_se"            "fractal_dimension_se"
## [23] "radius_worst"           "texture_worst"
## [25] "perimeter_worst"        "area_worst"
## [27] "smoothness_worst"       "compactness_worst"
```

```
## [29] "concavity_worst"          "concave.points_worst"
## [31] "symmetry_worst"           "fractal_dimension_worst"
## [33] "X"
```

Checking for null values

```
lapply(data,function(x) { length(which(is.na(x)))})
```

```
## $id
## [1] 0
##
## $diagnosis
## [1] 0
##
## $radius_mean
## [1] 0
##
## $texture_mean
## [1] 0
##
## $perimeter_mean
## [1] 0
##
## $area_mean
## [1] 0
##
## $smoothness_mean
## [1] 0
##
## $compactness_mean
## [1] 0
##
## $concavity_mean
## [1] 0
##
## $concave.points_mean
## [1] 0
##
## $symmetry_mean
## [1] 0
##
## $fractal_dimension_mean
## [1] 0
##
## $radius_se
## [1] 0
##
## $texture_se
## [1] 0
##
## $perimeter_se
## [1] 0
##
```

```
## $area_se
## [1] 0
##
## $smoothness_se
## [1] 0
##
## $compactness_se
## [1] 0
##
## $concavity_se
## [1] 0
##
## $concave.points_se
## [1] 0
##
## $symmetry_se
## [1] 0
##
## $fractal_dimension_se
## [1] 0
##
## $radius_worst
## [1] 0
##
## $texture_worst
## [1] 0
##
## $perimeter_worst
## [1] 0
##
## $area_worst
## [1] 0
##
## $smoothness_worst
## [1] 0
##
## $compactness_worst
## [1] 0
##
## $concavity_worst
## [1] 0
##
## $concave.points_worst
## [1] 0
##
## $symmetry_worst
## [1] 0
##
## $fractal_dimension_worst
## [1] 0
##
## $X
## [1] 569
```

We can notice, that there seems to be three category in dataset. They're: mean, se and worst

DATA WRANGLING Deleting X column as it seems to be a mistake while importing the dataset

```
drops <- c("X")
data <- data[ , !(names(data) %in% drops)]
```

```
lapply(data,function(x) { length(which(is.na(x)))})
```

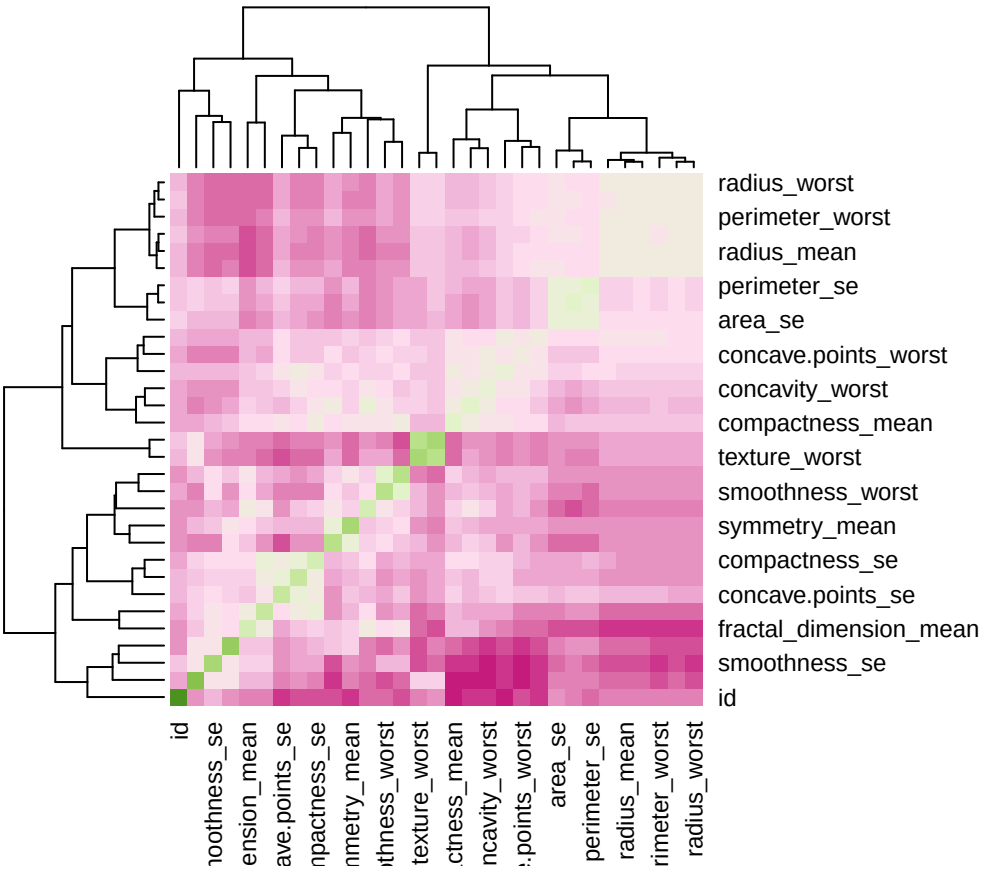
```
## $id
## [1] 0
##
## $diagnosis
## [1] 0
##
## $radius_mean
## [1] 0
##
## $texture_mean
## [1] 0
##
## $perimeter_mean
## [1] 0
##
## $area_mean
## [1] 0
##
## $smoothness_mean
## [1] 0
##
## $compactness_mean
## [1] 0
##
## $concavity_mean
## [1] 0
##
## $concave.points_mean
## [1] 0
##
## $symmetry_mean
## [1] 0
##
## $fractal_dimension_mean
## [1] 0
##
## $radius_se
## [1] 0
##
## $texture_se
## [1] 0
##
## $perimeter_se
## [1] 0
##
```

```
## $area_se
## [1] 0
##
## $smoothness_se
## [1] 0
##
## $compactness_se
## [1] 0
##
## $concavity_se
## [1] 0
##
## $concave.points_se
## [1] 0
##
## $symmetry_se
## [1] 0
##
## $fractal_dimension_se
## [1] 0
##
## $radius_worst
## [1] 0
##
## $texture_worst
## [1] 0
##
## $perimeter_worst
## [1] 0
##
## $area_worst
## [1] 0
##
## $smoothness_worst
## [1] 0
##
## $compactness_worst
## [1] 0
##
## $concavity_worst
## [1] 0
##
## $concave.points_worst
## [1] 0
##
## $symmetry_worst
## [1] 0
##
## $fractal_dimension_worst
## [1] 0
```

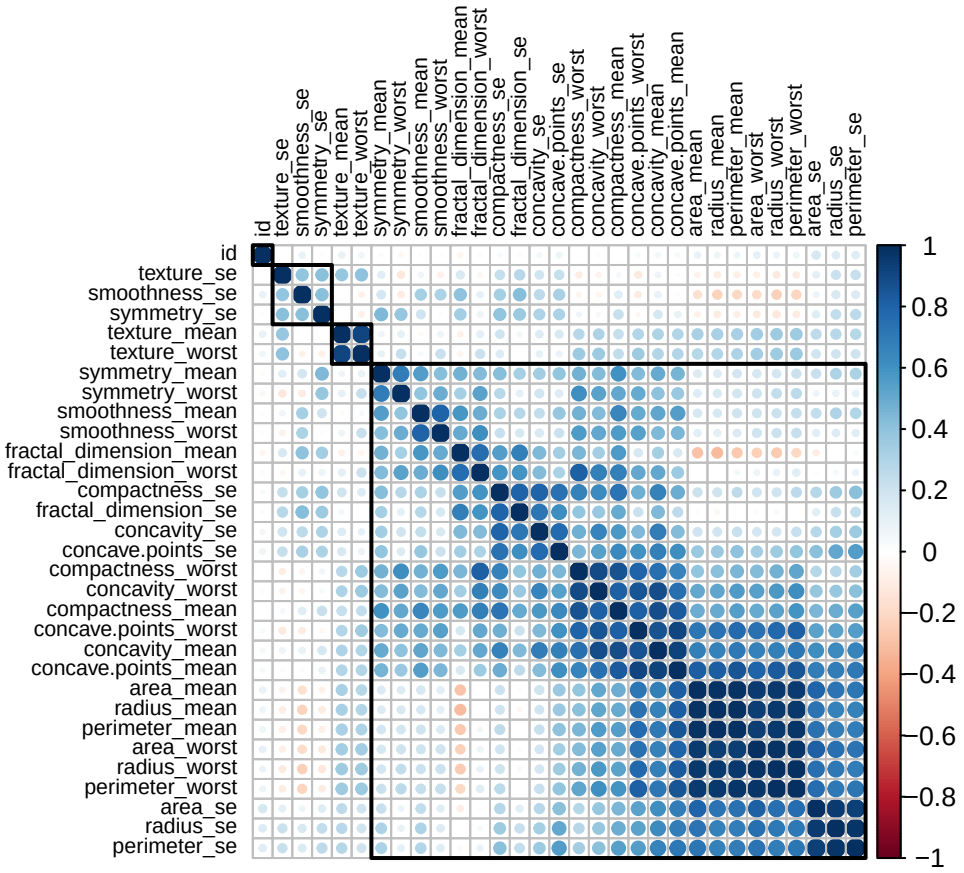
As we can notice now we do not have any missing data

Let's looking into correlation matrix to see correlation between all the variables

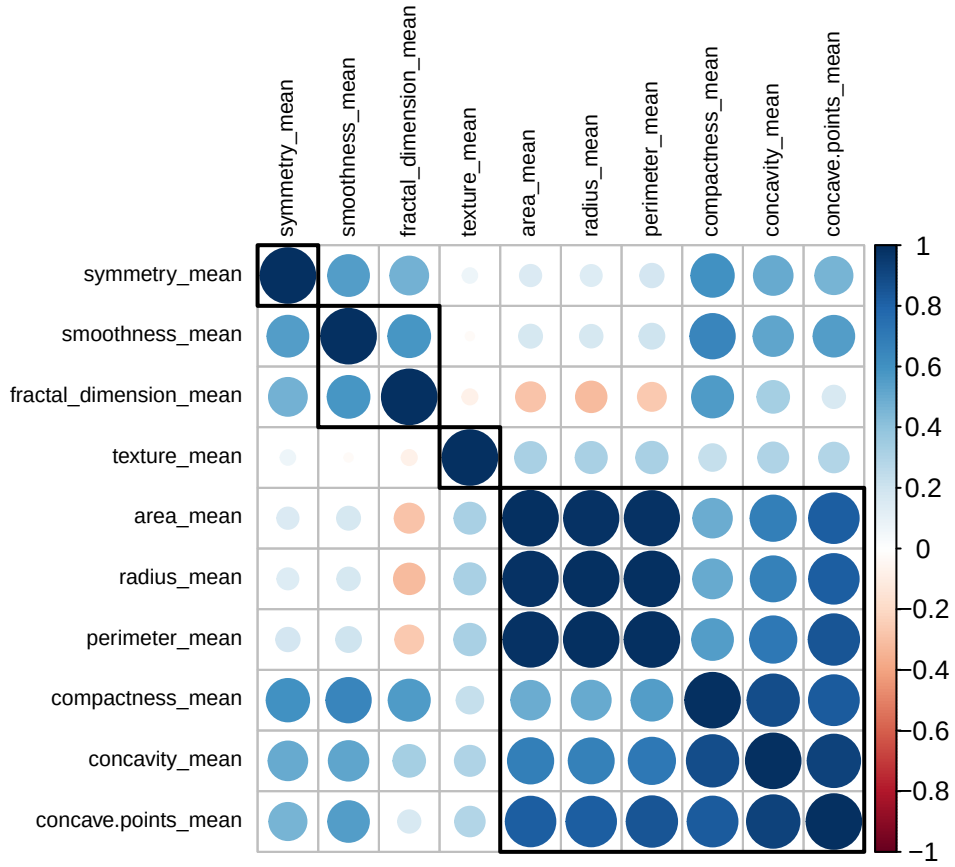
```
matrixData <- cor(data[sapply(data,is.numeric)], method="pearson")
# Rcolorbrewer palette
coul <- colorRampPalette(brewer.pal(8, "PiYG"))(25)
heatmap(matrixData, scale="column", col = coul)
```



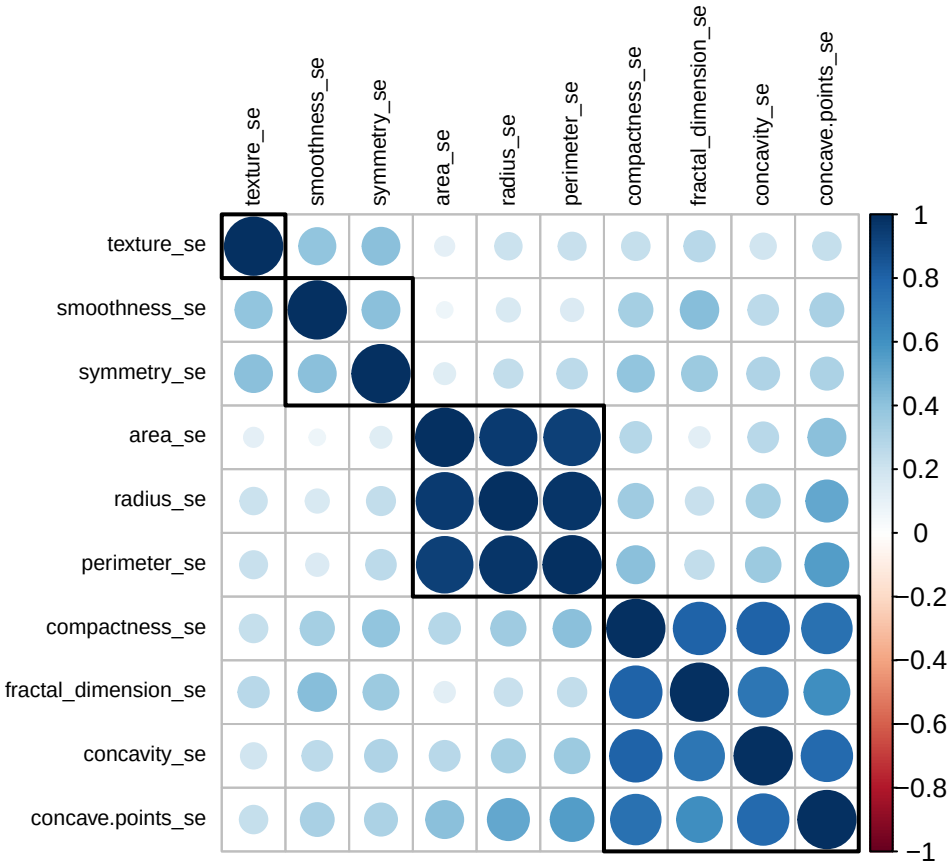

```
corrplot(matrixData, tl.col = "black", order = "hclust", hclust.method = "average", addrect = 4, tl.cex
```



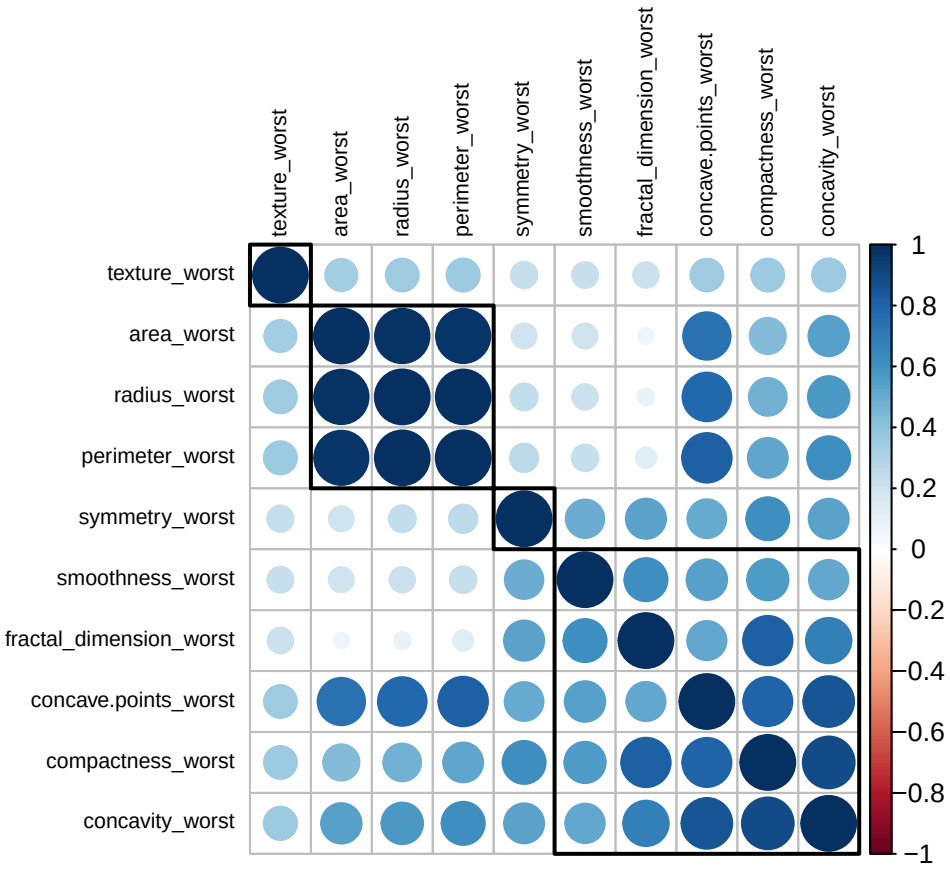

```
#data <- sapply(data,is.numeric)
data.mean <- cor(data[,c(3:12)],method="pearson")
data.se <- cor(data[,c(13:22)],method="pearson")
data.worst <- cor(data[,c(23:32)],method="pearson")


corrplot(data.mean, tl.col = "black", order = "hclust", hclust.method = "average", addrect = 4, tl.cex =
```




```
corrplot(data.se, tl.col = "black", order = "hclust", hclust.method = "average", addrect = 4, tl.cex = 0
```




```
corrplot(data.worst, tl.col = "black", order = "hclust", hclust.method = "average", addrect = 4, tl.cex
```



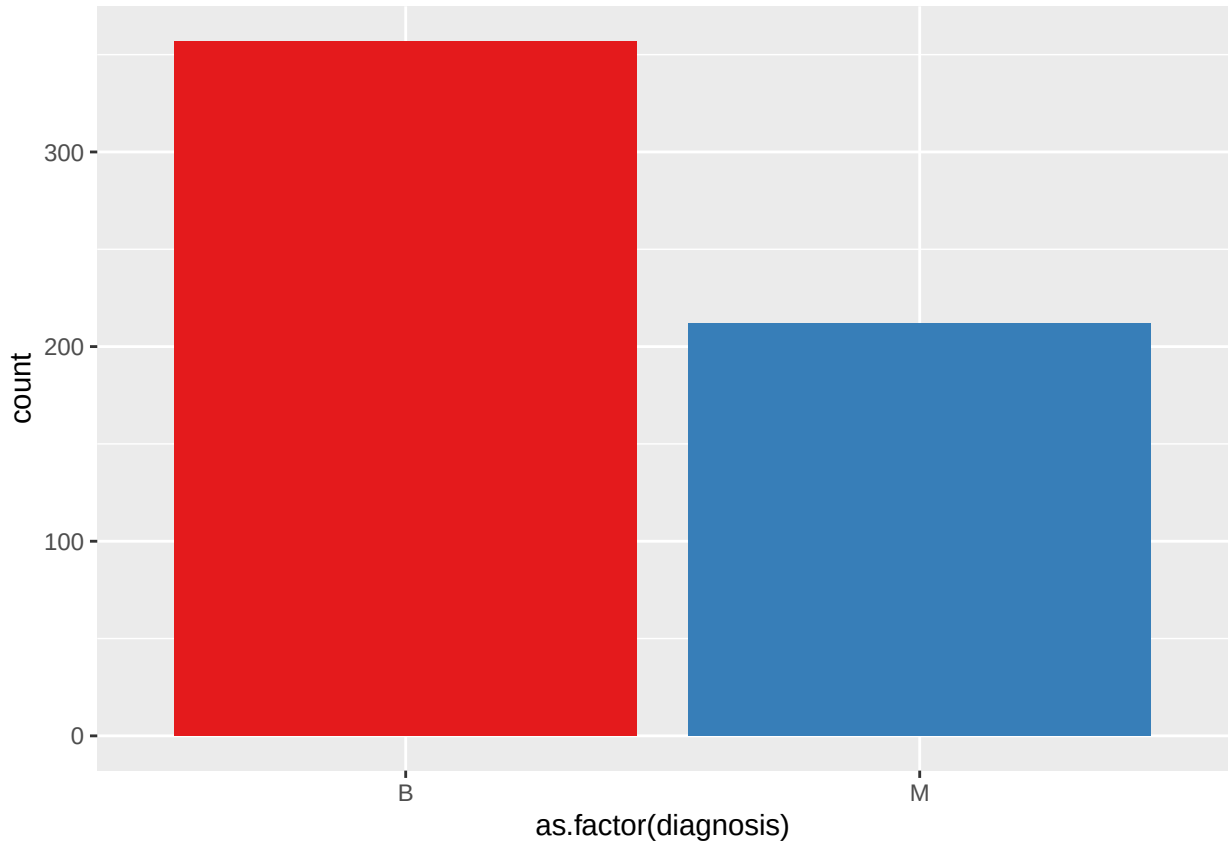

```
table(data$diagnosis)
```

```
##
##   B   M
## 357 212
```

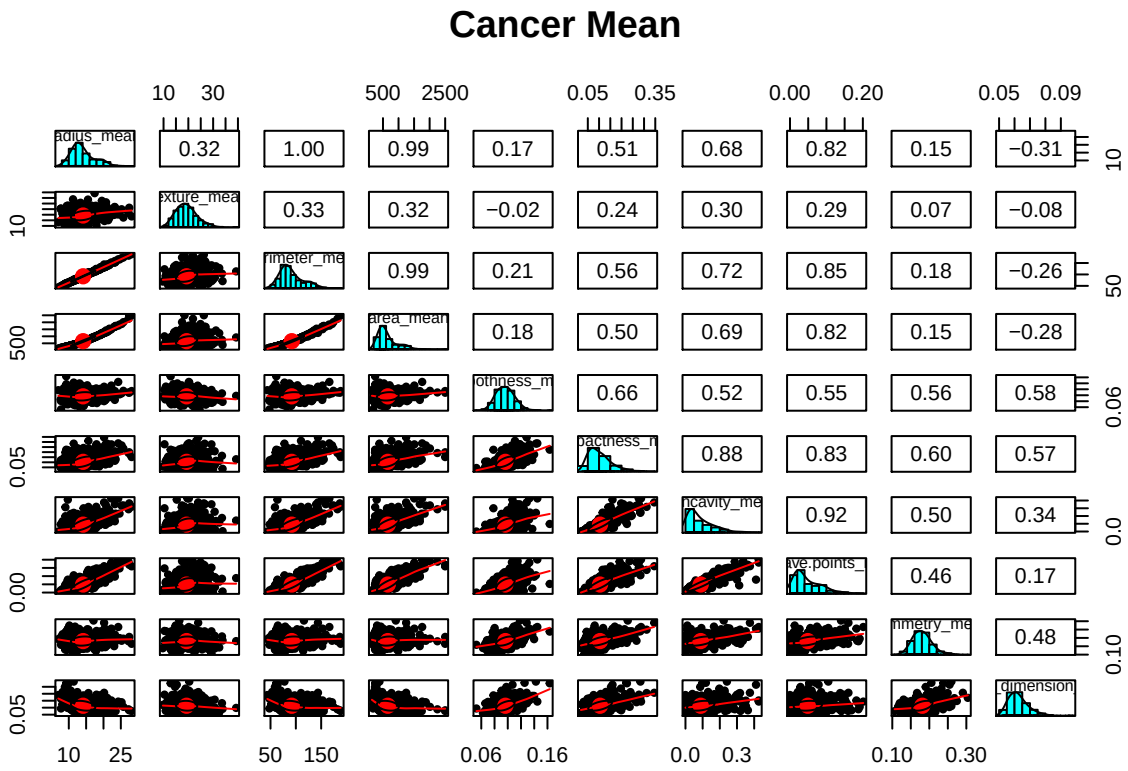
```
prop.table(table(data$diagnosis))*100
```

```
##
##        B        M
## 62.74165 37.25835
```

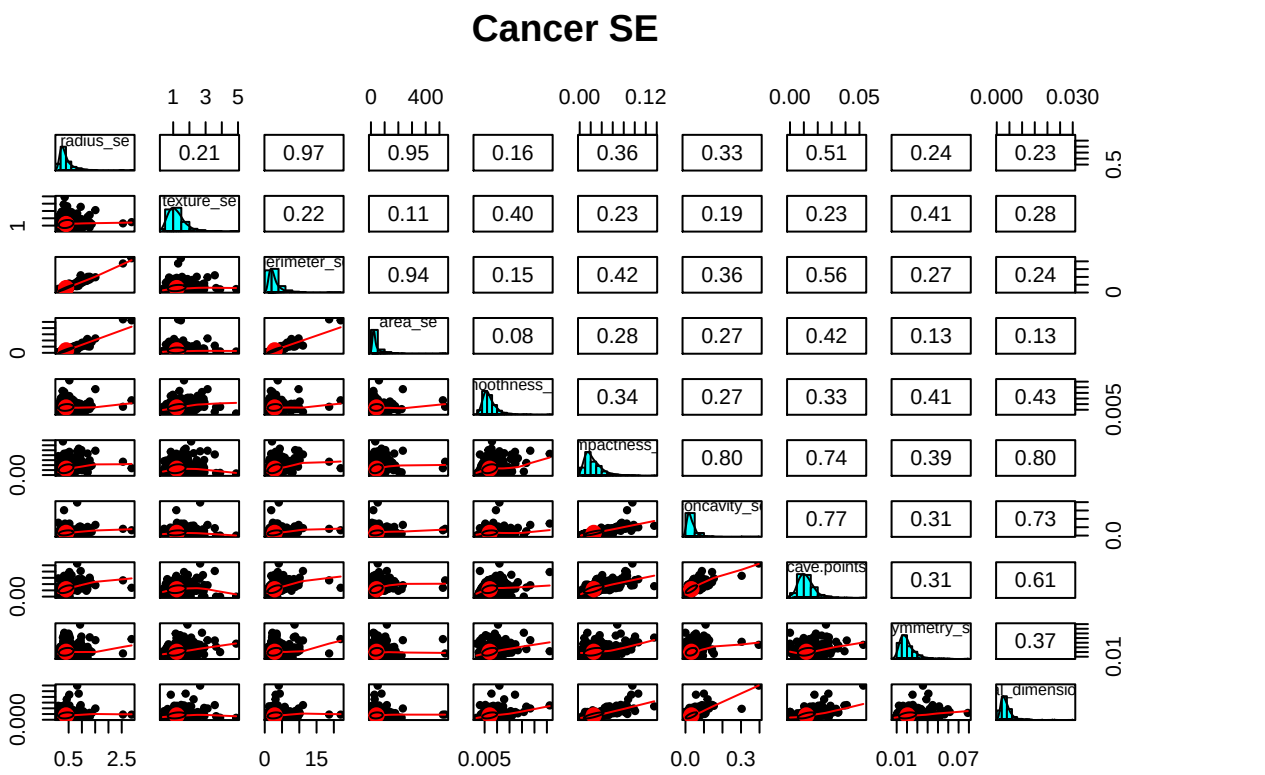
```
ggplot(data, aes(x=as.factor(diagnosis), fill=as.factor(diagnosis) )) +
  geom_bar( ) +
  scale_fill_brewer(palette = "Set1") +
  theme(legend.position="none")
```



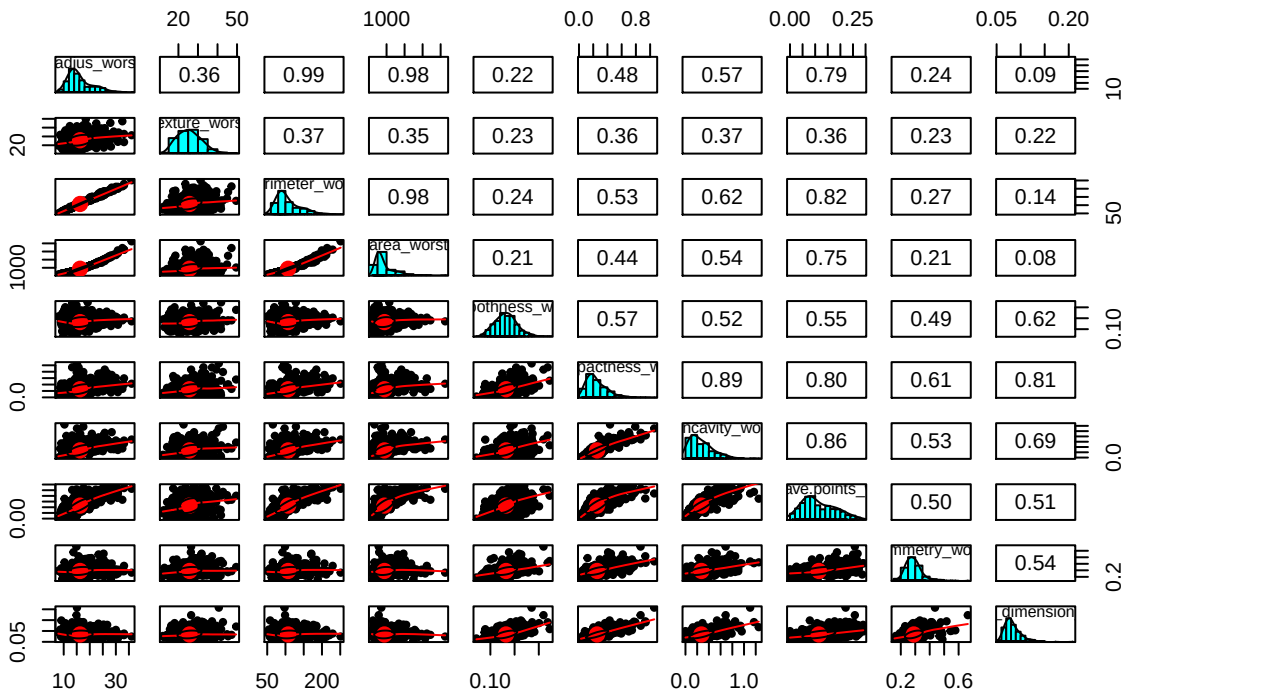

```
pairs.panels(data[,c(3:12)], main="Cancer Mean")
```



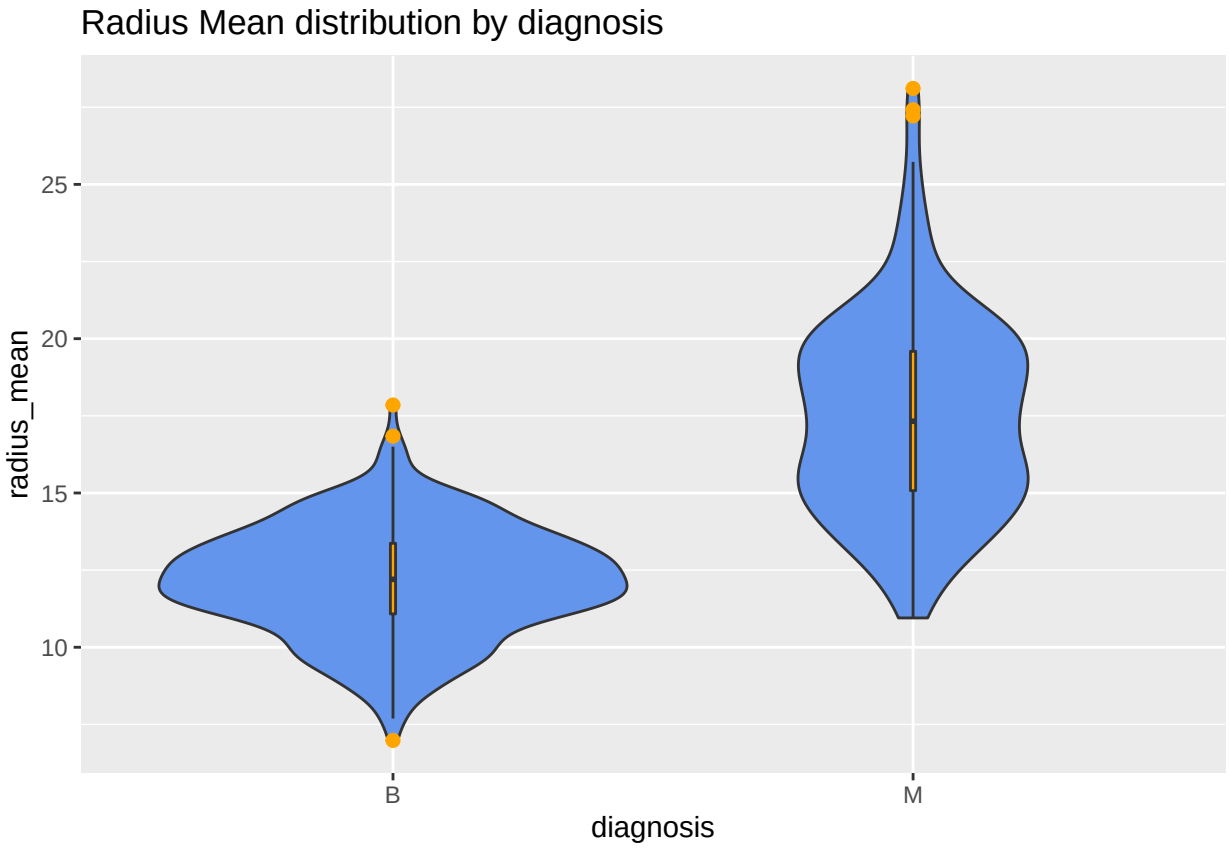
```
pairs.panels(data[,c(13:22)], main="Cancer SE")
```



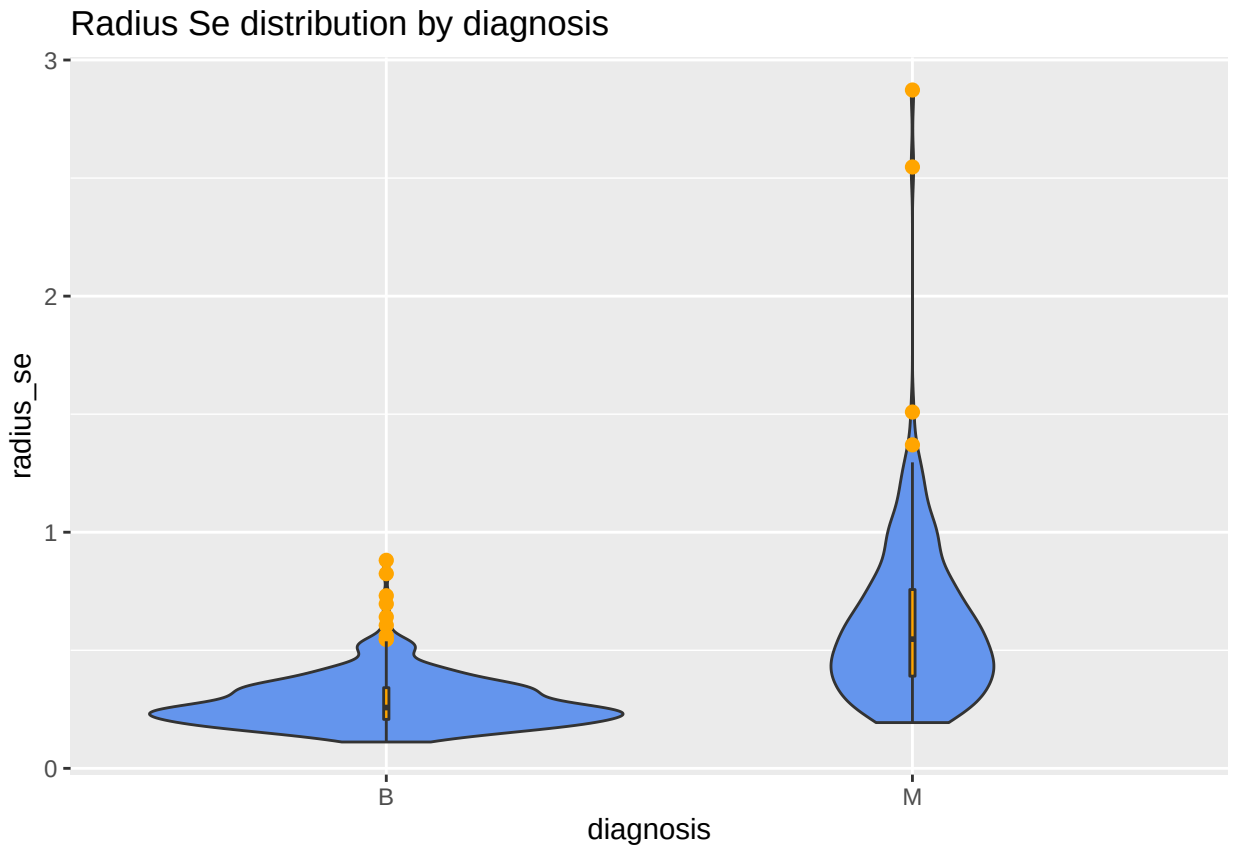

```
pairs.panels(data[,c(23:32)], main="Cancer Worst")
```



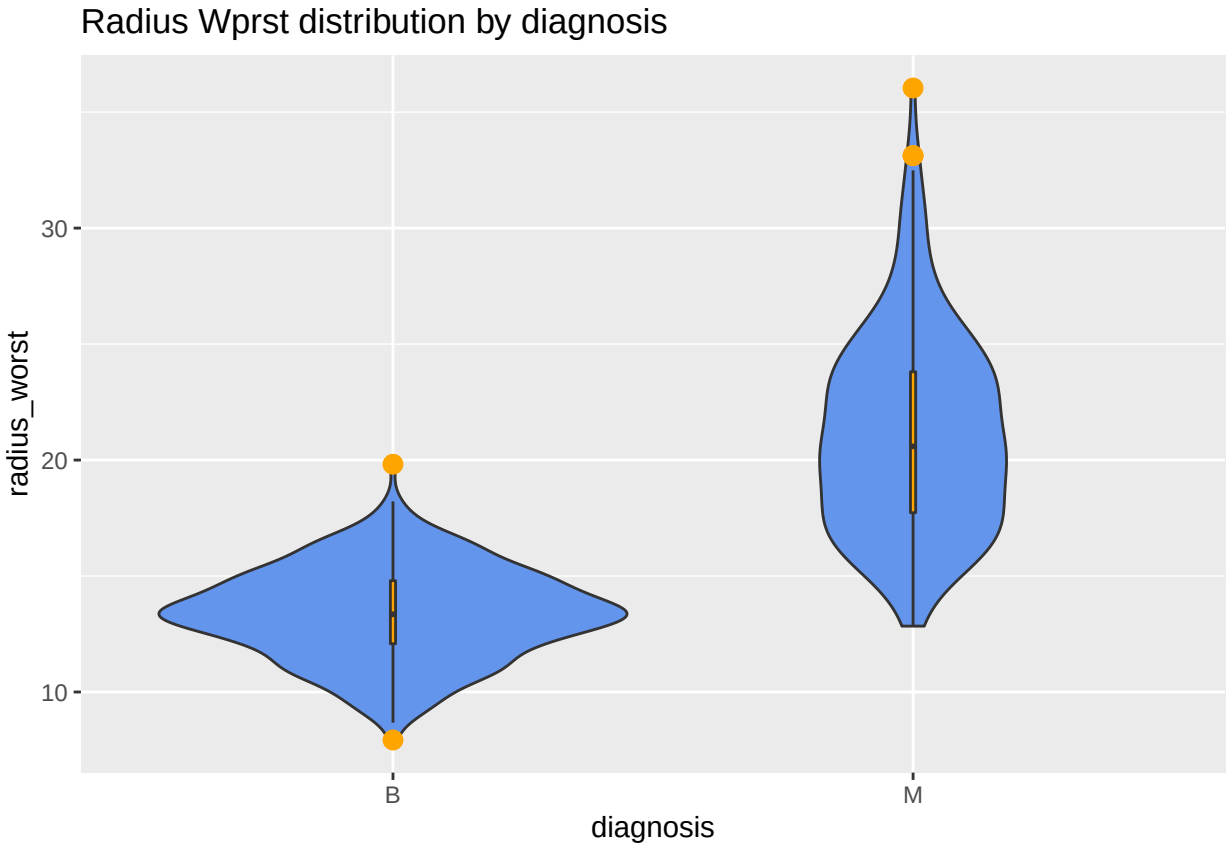
```
ggplot(data, aes(x = diagnosis,
y = radius_mean)) + geom_violin(fill = "cornflowerblue") + geom_boxplot(width = .01,
fill = "orange", outlier.color = "orange", outlier.size = 2) +
labs(title = "Radius Mean distribution by diagnosis")
```




```
ggplot(data, aes(x = diagnosis,
y = radius_se)) + geom_violin(fill = "cornflowerblue") + geom_boxplot(width = .01,
fill = "orange", outlier.color = "orange", outlier.size = 2) +
labs(title = "Radius Se distribution by diagnosis")
```




```
ggplot(data, aes(x = diagnosis,
y = radius_worst)) + geom_violin(fill = "cornflowerblue") + geom_boxplot(width = .01,
fill = "orange", outlier.color = "orange", outlier.size = 3) +
labs(title = "Radius Wprst distribution by diagnosis")
```



Let's split the data now to see how tumors differ for M and B

```
dataNew <- split(data, data$diagnosis)
dataB <- dataNew$B
dataM <- dataNew$M
```

Now we have two different datasets for B and M
####(I will do this work later, I can't find perfect visualization technique for this)

Model Building

```
str(cancerData)
```

```
## 'data.frame':    569 obs. of  33 variables:
##  $ id                     : int  842302 842517 84300903 84348301 84358402 843786 844359 84458202 844
##  $ diagnosis              : Factor w/ 2 levels "B","M": 2 2 2 2 2 2 2 2 2 2 ...
##  $ radius_mean            : num  18 20.6 19.7 11.4 20.3 ...
##  $ texture_mean           : num  10.4 17.8 21.2 20.4 14.3 ...
##  $ perimeter_mean         : num  122.8 132.9 130 77.6 135.1 ...
##  $ area_mean              : num  1001 1326 1203 386 1297 ...
##  $ smoothness_mean        : num  0.1184 0.0847 0.1096 0.1425 0.1003 ...
##  $ compactness_mean       : num  0.2776 0.0786 0.1599 0.2839 0.1328 ...
##  $ concavity_mean         : num  0.3001 0.0869 0.1974 0.2414 0.198 ...
##  $ concave.points_mean    : num  0.1471 0.0702 0.1279 0.1052 0.1043 ...
##  $ symmetry_mean          : num  0.242 0.181 0.207 0.26 0.181 ...
```

```
##  $ fractal_dimension_mean : num  0.0787 0.0567 0.06 0.0974 0.0588 ...
##  $ radius_se              : num  1.095 0.543 0.746 0.496 0.757 ...
##  $ texture_se             : num  0.905 0.734 0.787 1.156 0.781 ...
##  $ perimeter_se           : num  8.59 3.4 4.58 3.44 5.44 ...
##  $ area_se                : num  153.4 74.1 94 27.2 94.4 ...
##  $ smoothness_se          : num  0.0064 0.00522 0.00615 0.00911 0.01149 ...
##  $ compactness_se         : num  0.049 0.0131 0.0401 0.0746 0.0246 ...
##  $ concavity_se           : num  0.0537 0.0186 0.0383 0.0566 0.0569 ...
##  $ concave.points_se      : num  0.0159 0.0134 0.0206 0.0187 0.0188 ...
##  $ symmetry_se            : num  0.03 0.0139 0.0225 0.0596 0.0176 ...
##  $ fractal_dimension_se   : num  0.00619 0.00353 0.00457 0.00921 0.00511 ...
##  $ radius_worst           : num  25.4 25 23.6 14.9 22.5 ...
##  $ texture_worst          : num  17.3 23.4 25.5 26.5 16.7 ...
##  $ perimeter_worst        : num  184.6 158.8 152.5 98.9 152.2 ...
##  $ area_worst             : num  2019 1956 1709 568 1575 ...
##  $ smoothness_worst       : num  0.162 0.124 0.144 0.21 0.137 ...
##  $ compactness_worst      : num  0.666 0.187 0.424 0.866 0.205 ...
##  $ concavity_worst        : num  0.712 0.242 0.45 0.687 0.4 ...
##  $ concave.points_worst   : num  0.265 0.186 0.243 0.258 0.163 ...
##  $ symmetry_worst         : num  0.46 0.275 0.361 0.664 0.236 ...
##  $ fractal_dimension_worst: num  0.1189 0.089 0.0876 0.173 0.0768 ...
##  $ X                      : logi  NA NA NA NA NA NA ...
```

```
cancerData <- select(cancerData, -id, -X)
cancerData$diagnosis<- as.numeric(as.factor(cancerData$diagnosis))

library(kernlab)
```

```
##
## Attaching package: 'kernlab'

## The following object is masked from 'package:psych':
##
##     alpha

## The following object is masked from 'package:purrr':
##
##     cross

## The following object is masked from 'package:ggplot2':
##
##     alpha
```

```
ind <- sample(1:dim(cancerData)[1],170)
train <- cancerData[-ind, ]
test <- cancerData[ind, ]
```

```
library(e1071)

svmfit = svm(diagnosis~ ., data = train, kernel = "linear", cost = 5, scale = FALSE)
tune.out <- tune(svm, diagnosis~., data = train, kernel = "linear",
                 ranges = list(cost = c(0.001, 0.01, 0.1, 1, 5, 10, 100)))
# extract the best model
(bestmod <- tune.out$best.model)
```

```
##
## Call:
## best.tune(method = svm, train.x = diagnosis ~ ., data = train, ranges = list(cost = c(0.001,
##     0.01, 0.1, 1, 5, 10, 100)), kernel = "linear")
##
##
## Parameters:
##    SVM-Type:  eps-regression
##  SVM-Kernel:  linear
##        cost:  0.1
##       gamma:  0.03333333
##     epsilon:  0.1
##
##
## Number of Support Vectors:  321
```

```
prediction <- predict(bestmod,test)
prediction_train <- predict(bestmod,train)
```

```
library(Metrics)
```

```
##
## Attaching package: 'Metrics'

## The following objects are masked from 'package:caret':
##
##     precision, recall
```

```
cor(test$diagnosis,prediction)*100
```

```
## [1] 85.40166
```

```
cmBest = table(test[,1], prediction)
#cm
cm2Best = table(train[,1], prediction_train )
#cm2
```

```
classifier = svm(formula = diagnosis ~ .,
                 data = train,
                 type = 'C-classification',
                 kernel = 'linear')

y_pred = predict(classifier, test)
y_train_pred = predict(classifier, train)
```

```
cmBEST = table(test[,1], y_pred)
cmBEST
```

```
##    y_pred
##      1  2
##   1 99  2
##   2  1 68
```

```
cm2BEST = table(train[,1], y_train_pred )
cm2BEST
```

```
##    y_train_pred
##       1   2
##   1 255   1
##   2   3 140
```

```
#cor(test$diagnosis,y_pred)*100
```

#7 inccorect in train and 2 incorrect in test

```
library(caret)
confusionMatrix(cmBEST)
```

```
## Confusion Matrix and Statistics
##
##    y_pred
##      1  2
##   1 99  2
##   2  1 68
##
##                Accuracy : 0.9824
##                  95% CI : (0.9493, 0.9963)
##     No Information Rate : 0.5882
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9635
##
##  Mcnemar's Test P-Value : 1
##
##             Sensitivity : 0.9900
##             Specificity : 0.9714
##          Pos Pred Value : 0.9802
##          Neg Pred Value : 0.9855
##              Prevalence : 0.5882
##          Detection Rate : 0.5824
##    Detection Prevalence : 0.5941
##       Balanced Accuracy : 0.9807
##
##        'Positive' Class : 1
##
```

```
confusionMatrix(cm2BEST)
```

```
## Confusion Matrix and Statistics
##
##    y_train_pred
##       1   2
##   1 255   1
##   2   3 140
```

```
##
##                Accuracy : 0.99
##                  95% CI : (0.9745, 0.9973)
##     No Information Rate : 0.6466
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.9781
##
##  Mcnemar's Test P-Value : 0.6171
##
##             Sensitivity : 0.9884
##             Specificity : 0.9929
##          Pos Pred Value : 0.9961
##          Neg Pred Value : 0.9790
##              Prevalence : 0.6466
##          Detection Rate : 0.6391
##    Detection Prevalence : 0.6416
##       Balanced Accuracy : 0.9906
##
##        'Positive' Class : 1
##
```

Model accuracy of 98% obtained on test set and also 98% on train set.