Final Project - Breast

June 13, 2025

1 Breast Cancer Prediction

1.1 Binary Classification Prediction for type of Breast Cancer

[292]:
```
options(warn = -1)
```

Libraries

[ ]:
```
library(dplyr)
library(tidyr)
library(corrplot)
library(DataExplorer)
library(Amelia)
library(GGally)
library(caret)
# models
library(nnet)
library(kernlab)
library(klaR)
library(mda)
library(earth)
library(randomForest)
library(C50)
library(gbm)
library(pls)
library(glmnet)
library(pamr)
library(pROC)
```

1.2 Exploration Data Analysis

Importing the dataset

[294]:
```
breast_df <- read.csv('breast-cancer.csv')
```

Dropping the first column 'id'

[295]:
```
breast_df$id <- NULL
```

Checking dimensions

[296]:
```
dim <- dim(breast_df)
cat('Num Rows: ', dim[1], 'Num Col: ', dim[2])
```

```
Num Rows:  569 Num Col:  31
```

Showing first rows

[297]:
```
head(breast_df)
```

A data.frame: 6 × 31

	diagnosis <chr>	radius_mean <dbl>	texture_mean <dbl>	perimeter_mean <dbl>	area_mean <dbl>	smoothnes <dbl>
1	M	17.99	10.38	122.80	1001.0	0.11840
2	M	20.57	17.77	132.90	1326.0	0.08474
3	M	19.69	21.25	130.00	1203.0	0.10960
4	M	11.42	20.38	77.58	386.1	0.14250
5	M	20.29	14.34	135.10	1297.0	0.10030
6	M	12.45	15.70	82.57	477.1	0.12780

Showing Data types

[298]:
```
str(breast_df)
```

```
'data.frame':   569 obs. of  31 variables:
 $ diagnosis              : chr  "M" "M" "M" "M" …
 $ 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 …
```

Summary Statistics

[299]:
```
summary(breast_df)
```

```
  diagnosis           radius_mean      texture_mean   perimeter_mean  
 Length:569         Min.   : 6.981   Min.   : 9.71   Min.   : 43.79  
 Class :character   1st Qu.:11.700   1st Qu.:16.17   1st Qu.: 75.17  
 Mode  :character   Median :13.370   Median :18.84   Median : 86.24  
                    Mean   :14.127   Mean   :19.29   Mean   : 91.97  
                    3rd Qu.:15.780   3rd Qu.:21.80   3rd Qu.:104.10  
                    Max.   :28.110   Max.   :39.28   Max.   :188.50  
   area_mean      smoothness_mean   compactness_mean  concavity_mean   
 Min.   : 143.5   Min.   :0.05263   Min.   :0.01938   Min.   :0.00000  
 1st Qu.: 420.3   1st Qu.:0.08637   1st Qu.:0.06492   1st Qu.:0.02956  
 Median : 551.1   Median :0.09587   Median :0.09263   Median :0.06154  
 Mean   : 654.9   Mean   :0.09636   Mean   :0.10434   Mean   :0.08880  
 3rd Qu.: 782.7   3rd Qu.:0.10530   3rd Qu.:0.13040   3rd Qu.:0.13070  
 Max.   :2501.0   Max.   :0.16340   Max.   :0.34540   Max.   :0.42680  
 concave.points_mean symmetry_mean    fractal_dimension_mean   radius_se     
 Min.   :0.00000     Min.   :0.1060   Min.   :0.04996        Min.   :0.1115  
 1st Qu.:0.02031     1st Qu.:0.1619   1st Qu.:0.05770        1st Qu.:0.2324  
 Median :0.03350     Median :0.1792   Median :0.06154        Median :0.3242  
 Mean   :0.04892     Mean   :0.1812   Mean   :0.06280        Mean   :0.4052  
 3rd Qu.:0.07400     3rd Qu.:0.1957   3rd Qu.:0.06612        3rd Qu.:0.4789  
 Max.   :0.20120     Max.   :0.3040   Max.   :0.09744        Max.   :2.8730  
   texture_se      perimeter_se        area_se        smoothness_se     
 Min.   :0.3602   Min.   : 0.757   Min.   :  6.802   Min.   :0.001713  
 1st Qu.:0.8339   1st Qu.: 1.606   1st Qu.: 17.850   1st Qu.:0.005169  
 Median :1.1080   Median : 2.287   Median : 24.530   Median :0.006380  
 Mean   :1.2169   Mean   : 2.866   Mean   : 40.337   Mean   :0.007041  
 3rd Qu.:1.4740   3rd Qu.: 3.357   3rd Qu.: 45.190   3rd Qu.:0.008146  
 Max.   :4.8850   Max.   :21.980   Max.   :542.200   Max.   :0.031130  
 compactness_se      concavity_se     concave.points_se   symmetry_se      
 Min.   :0.002252   Min.   :0.00000   Min.   :0.000000   Min.   :0.007882  
 1st Qu.:0.013080   1st Qu.:0.01509   1st Qu.:0.007638   1st Qu.:0.015160  
 Median :0.020450   Median :0.02589   Median :0.010930   Median :0.018730  
 Mean   :0.025478   Mean   :0.03189   Mean   :0.011796   Mean   :0.020542  
 3rd Qu.:0.032450   3rd Qu.:0.04205   3rd Qu.:0.014710   3rd Qu.:0.023480  
 Max.   :0.135400   Max.   :0.39600   Max.   :0.052790   Max.   :0.078950  
 fractal_dimension_se  radius_worst    texture_worst   perimeter_worst 
 Min.   :0.0008948    Min.   : 7.93   Min.   :12.02   Min.   : 50.41  
 1st Qu.:0.0022480    1st Qu.:13.01   1st Qu.:21.08   1st Qu.: 84.11  
 Median :0.0031870    Median :14.97   Median :25.41   Median : 97.66  
 Mean   :0.0037949    Mean   :16.27   Mean   :25.68   Mean   :107.26  
```

```
3rd Qu.:0.0045580    3rd Qu.:18.79    3rd Qu.:29.72    3rd Qu.:125.40
Max.   :0.0298400    Max.   :36.04    Max.   :49.54    Max.   :251.20
  area_worst      smoothness_worst  compactness_worst concavity_worst
Min.   : 185.2   Min.   :0.07117   Min.   :0.02729   Min.   :0.0000
1st Qu.: 515.3   1st Qu.:0.11660   1st Qu.:0.14720   1st Qu.:0.1145
Median : 686.5   Median :0.13130   Median :0.21190   Median :0.2267
Mean   : 880.6   Mean   :0.13237   Mean   :0.25427   Mean   :0.2722
3rd Qu.:1084.0   3rd Qu.:0.14600   3rd Qu.:0.33910   3rd Qu.:0.3829
Max.   :4254.0   Max.   :0.22260   Max.   :1.05800   Max.   :1.2520
concave.points_worst symmetry_worst   fractal_dimension_worst
Min.   :0.00000      Min.   :0.1565   Min.   :0.05504
1st Qu.:0.06493      1st Qu.:0.2504   1st Qu.:0.07146
Median :0.09993      Median :0.2822   Median :0.08004
Mean   :0.11461      Mean   :0.2901   Mean   :0.08395
3rd Qu.:0.16140      3rd Qu.:0.3179   3rd Qu.:0.09208
Max.   :0.29100      Max.   :0.6638   Max.   :0.20750
```

Looking for Missing data

[300]:
```
colSums(is.na(breast_df))
```

diagnosis 0 **radius_mean** 0 **texture_mean** 0 **perimeter_mean** 0 **area_mean** 0 **smoothness_mean** 0 **compactness_mean** 0 **concavity_mean** 0 **concave.points_mean** 0 **symmetry_mean** 0 **fractal_dimension_mean** 0 **radius_se** 0 **texture_se** 0 **perimeter_se** 0 **area_se** 0 **smoothness_se** 0 **compactness_se** 0 **concavity_se** 0 **concave.points_se** 0 **symmetry_se** 0 **fractal_dimension_se** 0 **radius_worst** 0 **texture_worst** 0 **perimeter_worst** 0 **area_worst** 0 **smoothness_worst** 0 **compactness_worst** 0 **concavity_worst** 0 **concave.points_worst** 0 **symmetry_worst** 0 **fractal_dimension_worst** 0

This dataset doens't show any missing values in any column

Checking for Duplicates

[301]:
```
breast_df[duplicated(breast_df), ]
```

A data.frame: 0 × 31

diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_r
<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>

Changing 'diagnosis' column to category data type

[302]:
```
breast_df$diagnosis <- as.factor(breast_df$diagnosis)
```

Checking how many categories of each type exists in the dataset

[303]:
```
breast_table <- table(breast_df$diagnosis)
breast_table
```

```
  B   M
357 212
```

Calculating percentatge of class imbalance

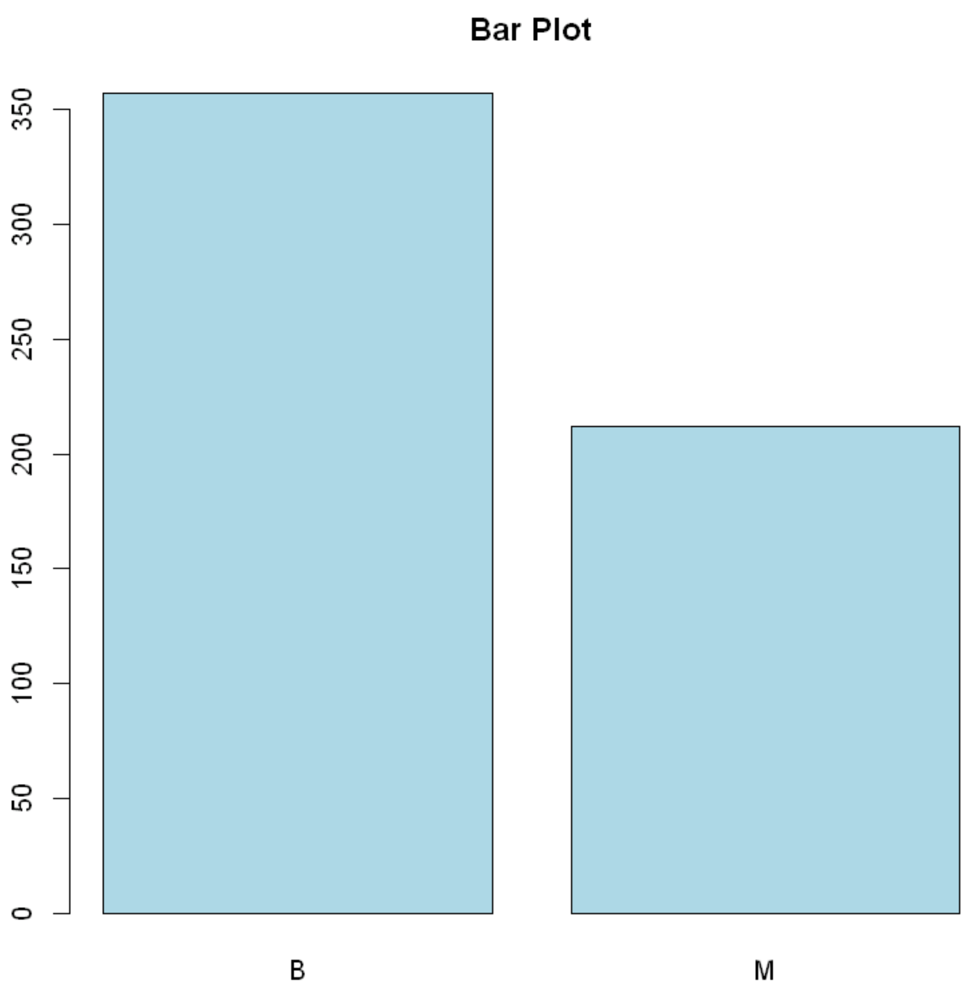
[304]:
```
total_class_imbalance <- breast_table[1] + breast_table[2]

breast_class_B <- breast_table[1] / total_class_imbalance
breast_class_M <- breast_table[2] / total_class_imbalance

cat("Quantity of Class B:", breast_class_B * 100, "%", "Quantity of Class M:",
 ↪breast_class_M * 100, "%")
```

```
Quantity of Class B: 62.74165 % Quantity of Class M: 37.25835 %
```

The calculations show a clear class imbalance between class B and class M

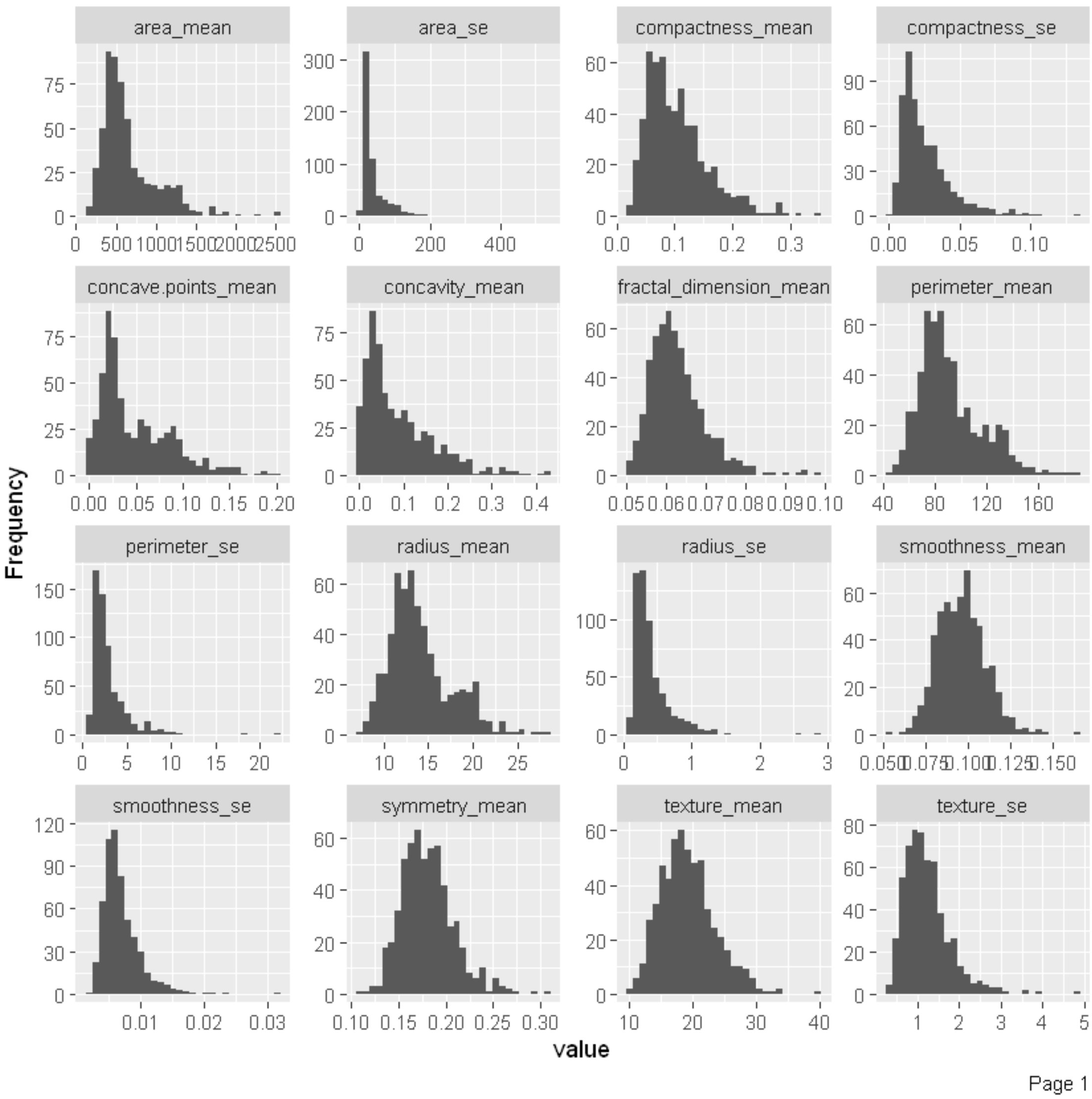
Visualization for Categorical Column

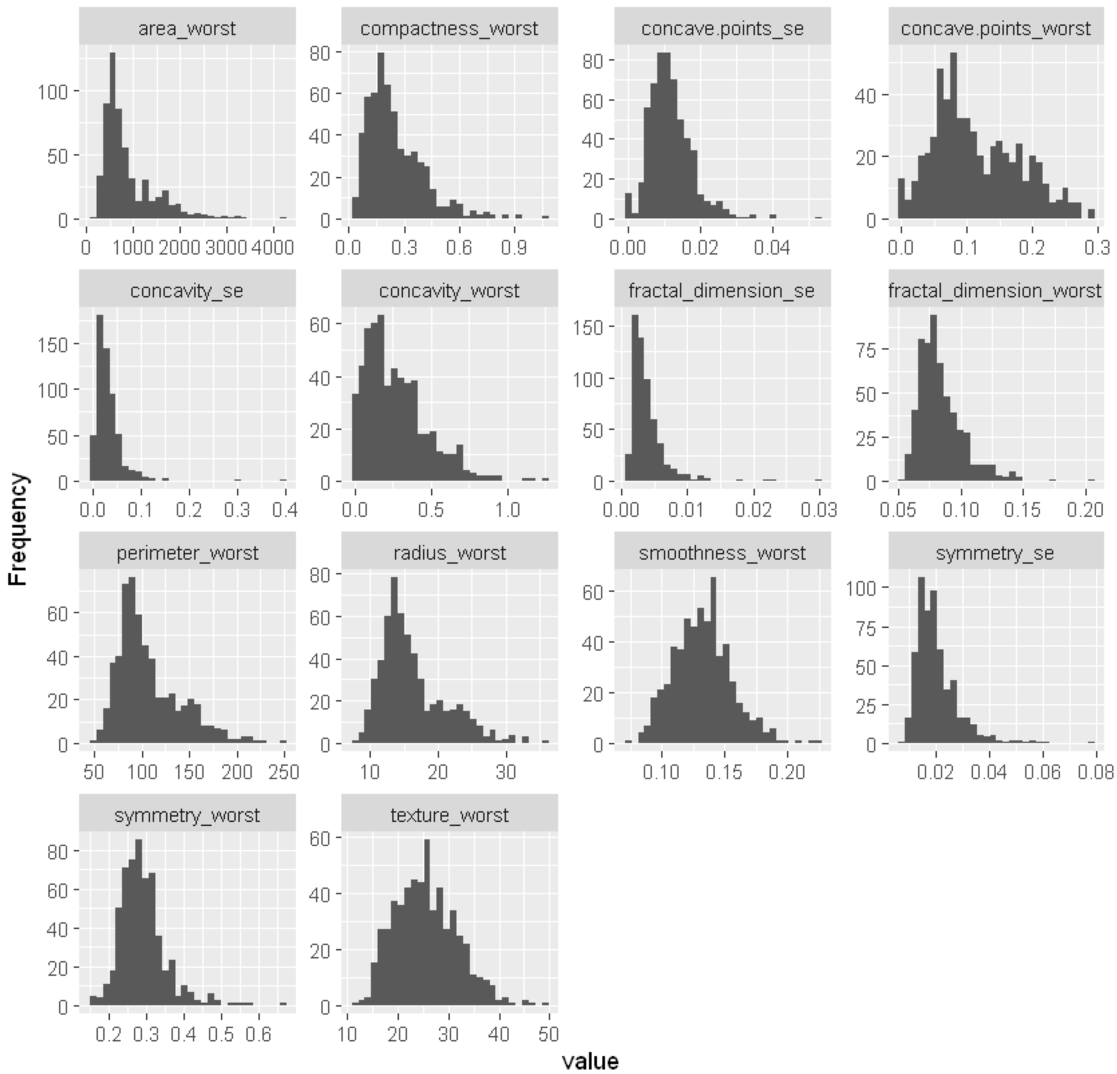
[305]:
```
barplot(table(breast_df$diagnosis), main = "Bar Plot", col = 'lightblue')
```



Visualizations for Numerical columns

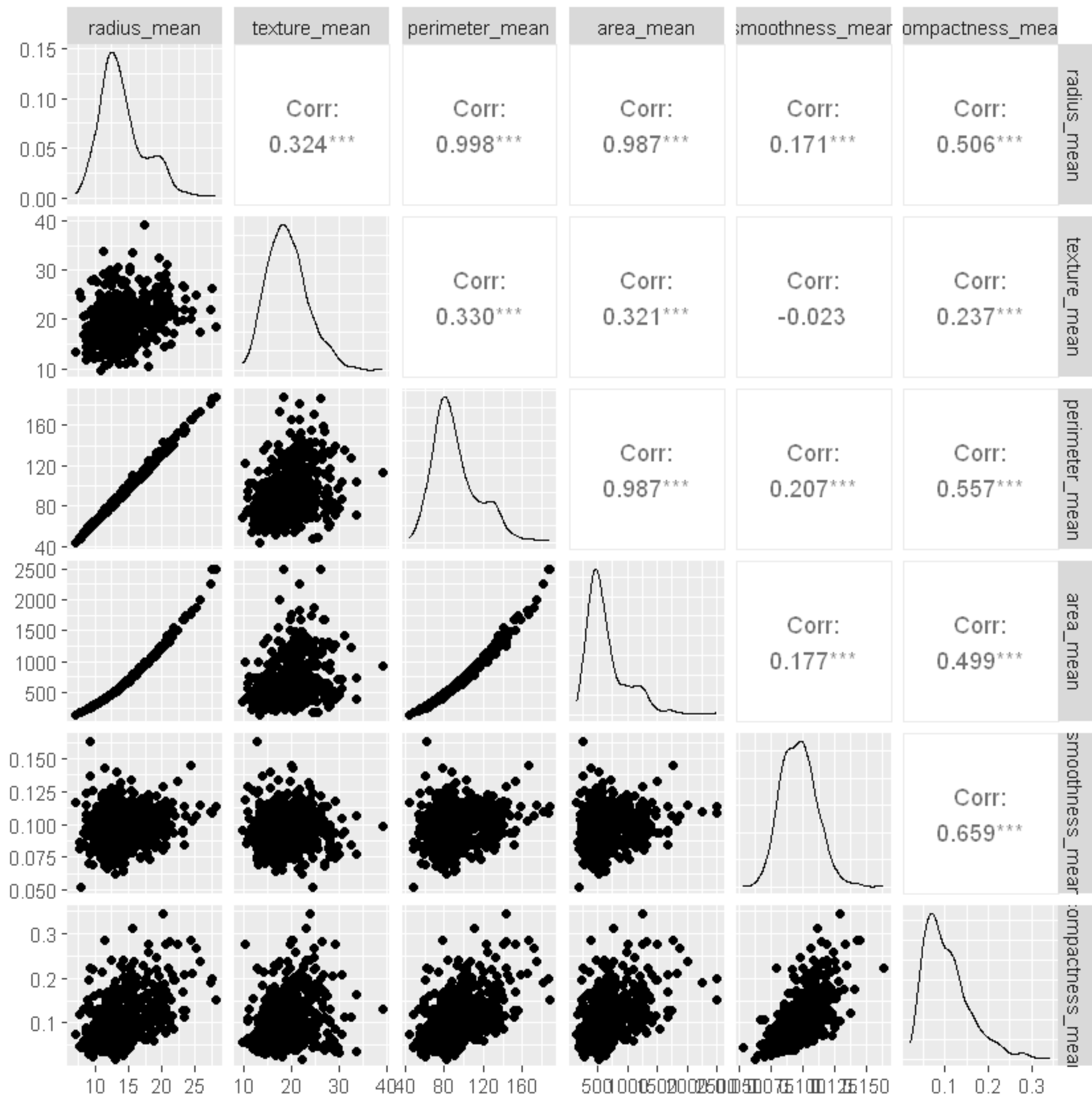
[306]:
```
plot_histogram(breast_df)
```





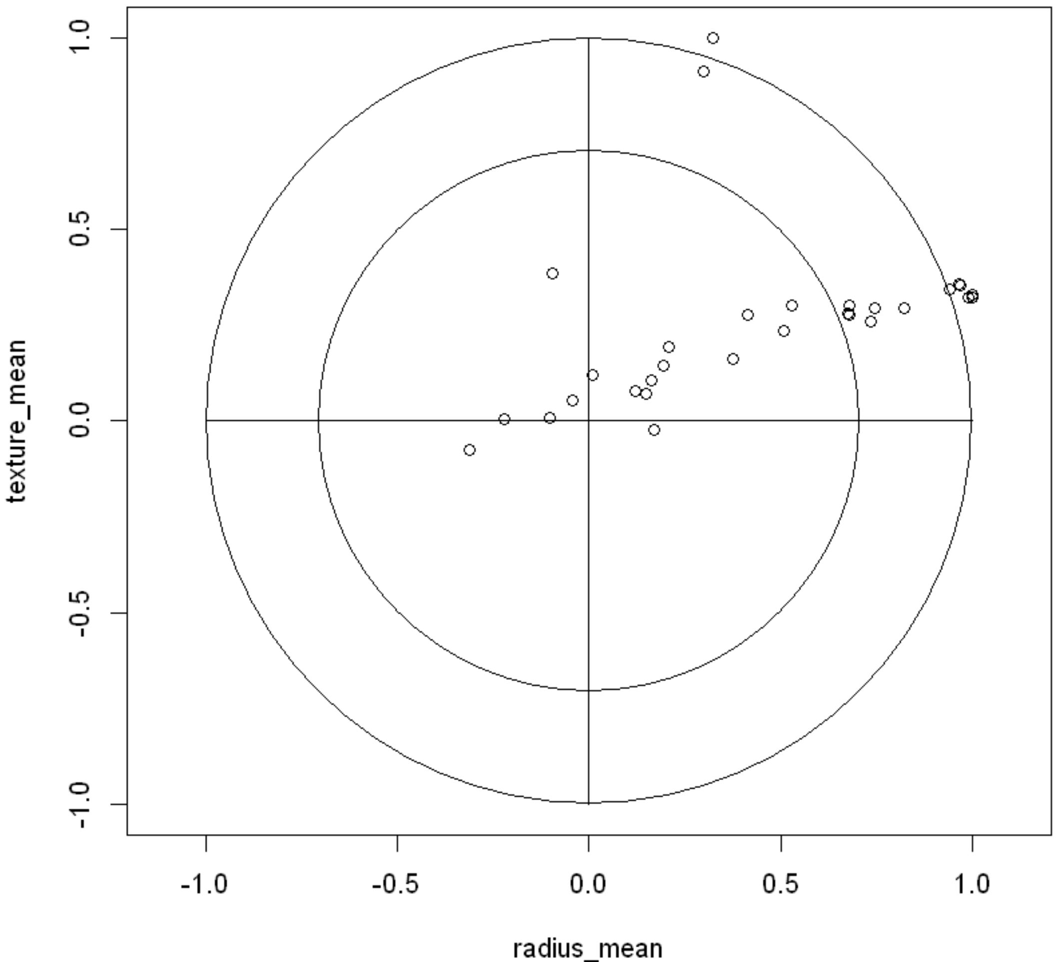
Page 2

[307]:
```
# Only select numeric columns
numeric_data <- breast_df[sapply(breast_df, is.numeric)]

# Pairwise scatterplots and correlations
ggpairs(numeric_data[ , 1:6])  # Try fewer columns if it's too dense
```



[308]:

```
# Correlation matrix
num_data <- select_if(breast_df, is.numeric)
cor_matrix <- cor(num_data, use = "complete.obs")

corrplot(cor_matrix, method = "color")
```



Data Splitting Using Stratified random sampling to maintain class proportions. Since this method works best for classification problems

[309]:
```r
# Setting up seed
set.seed(123)

# 60% into training
trainIndex <- createDataPartition(breast_df$diagnosis, p = 0.6, list = FALSE)

# Splitting the data
breast_train <- breast_df[trainIndex, ]
breast_test  <- breast_df[-trainIndex, ]
```

```
# Checking if the split is equally split
prop.table(table(breast_train$diagnosis))
prop.table(table(breast_test$diagnosis))
```

```
        B         M
0.6268222 0.3731778
```

```
        B         M
0.6283186 0.3716814
```

Yes, the split is even

Data Preprocessing (on training set) Since we have many skewed data points, we will use boxcox method

[310]:
```
# Fit preprocessing on training data (excluding the target variable "diagnosis")
preproc <- preProcess(breast_train[, -1], method = c("BoxCox","center",
  "scale"))
```

[311]:
```
# Apply preprocessing to both train and test
train_processed <- predict(preproc, breast_train[, -1])
test_processed  <- predict(preproc, breast_test[, -1])
```

[312]:
```
# Add back the target variable
train_processed$diagnosis <- breast_train$diagnosis
test_processed$diagnosis  <- breast_test$diagnosis
```

Computing correlation matrix before modeling

[313]:
```
cor_matrix <- cor(train_processed[, -which(names(train_processed) ==
  "diagnosis")]) # excluding the target variable and computes the correlation
  matrix for all predictor variables
```

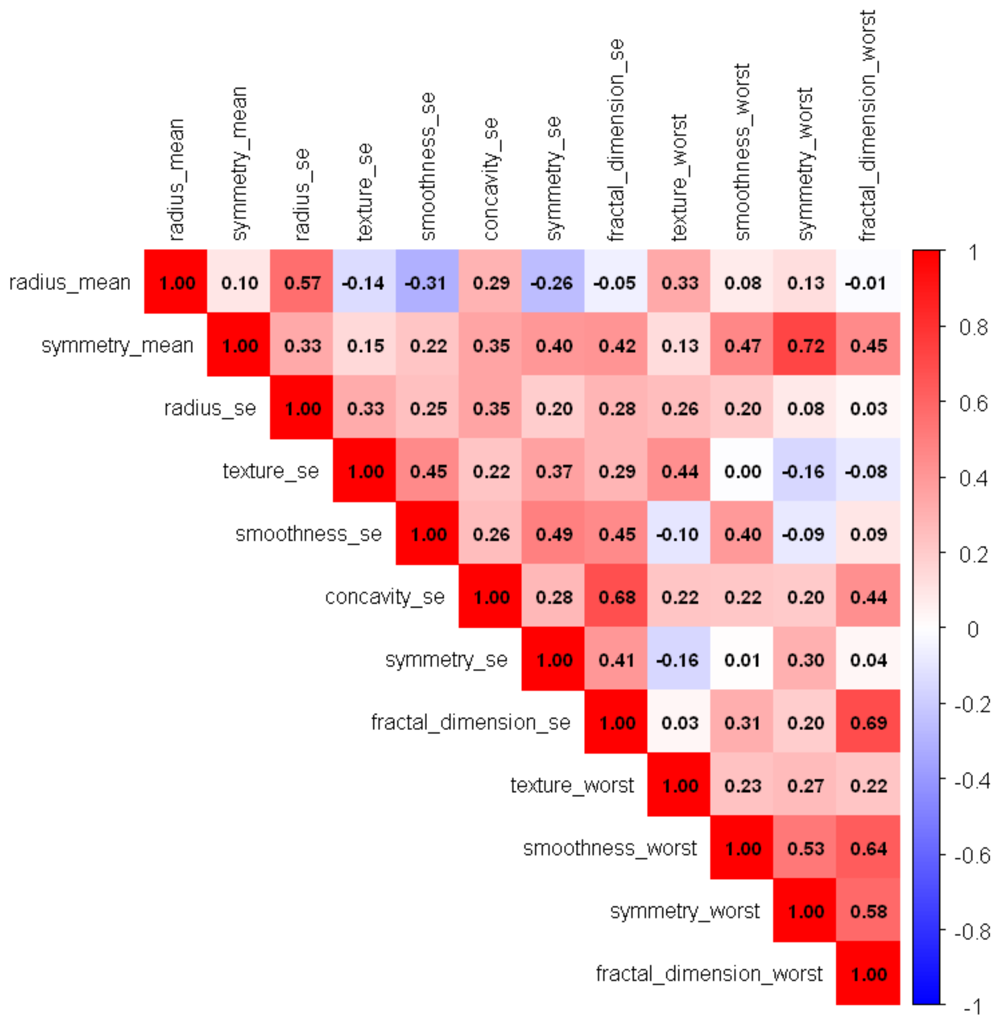
Finding predictors with correlations above 0.75

[314]:
```
highCorr <- findCorrelation(cor_matrix, cutoff = 0.75) # highCorr is a vector
  of column indices to remove.
```

[315]:
```
train_filtered <- train_processed[, -highCorr] # Removes the identified highly
  correlated columns
```

[316]:
```
filtered_predictors <- train_filtered[, !(names(train_filtered) %in%
  "diagnosis")]
cor_matrix_filtered <- cor(filtered_predictors)

# Plot the filtered correlation matrix
corrplot::corrplot(cor_matrix_filtered, method = "color", type = "upper",
         tl.cex = 0.8, tl.col = "black",
```

```
        col = colorRampPalette(c("blue", "white", "red"))(200),
        addCoef.col = "black", number.cex = 0.7)
```



We have reduced the number of predictors to 12 that are not highly correlated with one another

Checking the number of outliers

[317]:
```
# Remove target variable
predictors <- train_filtered[, !(names(train_filtered) %in% "diagnosis")]
```

[318]:
```
# Function to compute outlier counts
outlier_count <- function(x) {
  qnt <- quantile(x, probs=c(0.25, 0.75))
  iqr <- qnt[2] - qnt[1]
```

```
  lower <- qnt[1] - 1.5 * iqr
  upper <- qnt[2] + 1.5 * iqr
  sum(x < lower | x > upper)
}

# Apply to all predictors
sapply(predictors, outlier_count)
```

radius_mean 7 **symmetry_mean** 6 **radius_se** 2 **texture_se** 2 **smoothness_se** 3 **concavity_se** 17 **symmetry_se** 1 **fractal_dimension_se** 1 **texture_worst** 0 **smoothness_worst** 2 **symmetry_worst** 8 **fractal_dimension_worst** 1

1.3 Modelation

Defining Cross-validation

[319]:
```
ctrl <- trainControl(method = "cv", number = 10)
```

Neural Network

[320]:
```
nn_model <- train(diagnosis ~ ., data = train_filtered,
                  method = "nnet",
                  trControl = ctrl,
                  preProcess = NULL,
                  trace = FALSE,  # suppress training output
                  linout = FALSE)
```

Support Vector Machine (SVM)

[321]:
```
svm_model <- train(diagnosis ~ ., data = train_filtered,
                   method = "svmRadial",
                   trControl = ctrl,
                   preProcess = NULL)
```

k-Nearest Neighbors

[322]:
```
knn_model <- train(diagnosis ~ ., data = train_filtered,
                   method = "knn",
                   trControl = ctrl,
                   preProcess = NULL)
```

Naïve Bayes

[323]:
```
nb_model <- train(diagnosis ~ ., data = train_filtered,
                  method = "nb",
                  trControl = ctrl,
                  preProcess = NULL)
```

Flexible Discriminant Analysis (FDA)

[324]:
```
fda_model <- train(diagnosis ~ ., data = train_filtered,
                   method = "fda",
```

```
                   trControl = ctrl,
                   preProcess = NULL)
```

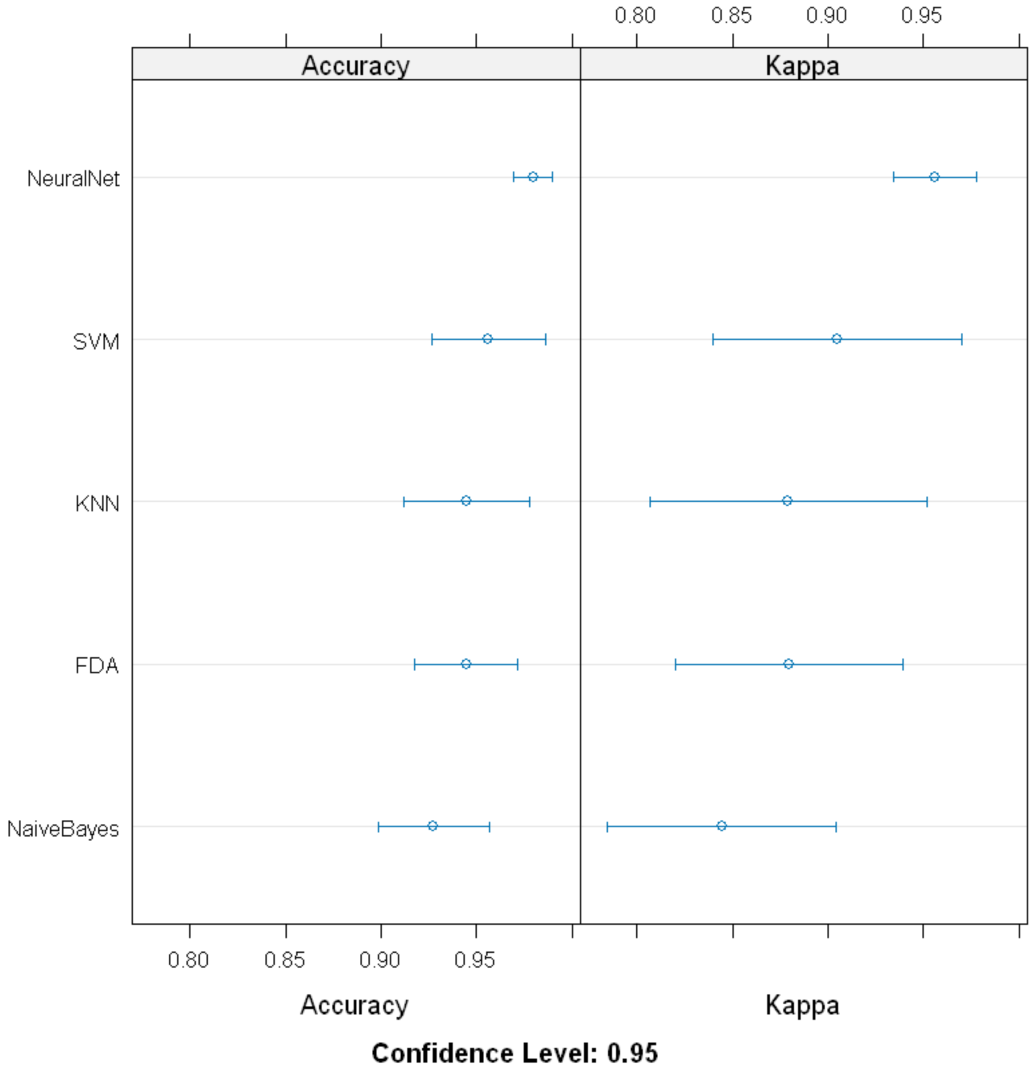
Putting all the models together

[325]:
```
models_list <- list(
  NeuralNet = nn_model,
  SVM = svm_model,
  KNN = knn_model,
  NaiveBayes = nb_model,
  FDA = fda_model
)
```

Compraing Results

[326]:
```
# Collect resampling results
results <- resamples(models_list)

# Summary table
summary(results)
dotplot(results)
```

```
Call:
summary.resamples(object = results)

Models: NeuralNet, SVM, KNN, NaiveBayes, FDA
Number of resamples: 10

Accuracy
                Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
NeuralNet  0.9705882 0.9705882 0.9710084 0.9795798 0.9928571 1.0000000    0
SVM        0.8823529 0.9210084 0.9705882 0.9563866 0.9926471 1.0000000    0
KNN        0.8823529 0.9142857 0.9420168 0.9450369 0.9924242 1.0000000    0
NaiveBayes 0.8285714 0.9142857 0.9411765 0.9275579 0.9424370 0.9705882    0
FDA        0.8823529 0.9123950 0.9567227 0.9446218 0.9705882 1.0000000    0

Kappa
                Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
NeuralNet  0.9343629 0.9370605 0.9382306 0.9560891 0.9846570 1.0000000    0
SVM        0.7433962 0.8266598 0.9368030 0.9046945 0.9842007 1.0000000    0
KNN        0.7354086 0.8088794 0.8726722 0.8790170 0.9833333 1.0000000    0
NaiveBayes 0.6440678 0.8111815 0.8735780 0.8443248 0.8770813 0.9343629    0
FDA        0.7354086 0.8139837 0.9052246 0.8795502 0.9368030 1.0000000    0
```



Among the models tested, the neural network achieved the highest cross-validated mean accuracy (97.96%) and Kappa (95.69%), followed closely by SVM (95.64% accuracy, 94.06% Kappa), while KNN, FDA, and Naive Bayes showed slightly lower performance with greater variability.

Classification tree (CART)

[327]:
```
cart_model <- train(diagnosis ~ ., data = train_filtered,
                    method = "rpart",
                    trControl = ctrl)
```

Bagged trees

[328]:
```
bagged_model <- train(diagnosis ~ ., data = train_filtered,
                      method = "treebag",
```

```
                        trControl = ctrl)
```

Random forest

[329]:
```r
rf_model <- train(diagnosis ~ ., data = train_filtered,
                  method = "rf",
                  trControl = ctrl)
```

Boosted trees (GBM)

[330]:
```r
boosted_model <- train(diagnosis ~ ., data = train_filtered,
                       method = "gbm",
                       trControl = ctrl,
                       verbose = FALSE)
```

C5.0

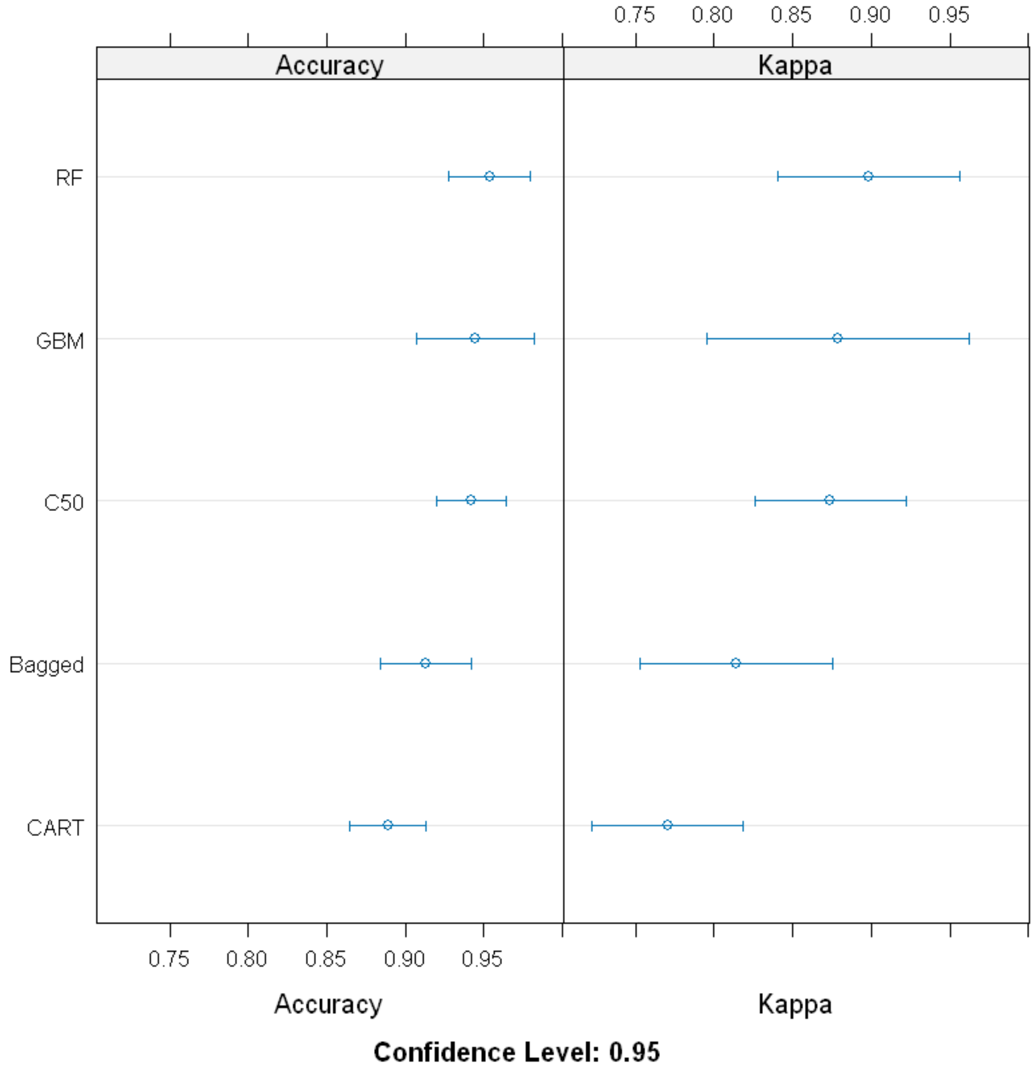
[331]:
```r
c50_model <- train(diagnosis ~ ., data = train_filtered,
                   method = "C5.0",
                   trControl = ctrl)
```

Comparing performance for Tree-based and Ensemble Models

[332]:
```r
models_list_tree <- list(CART = cart_model, Bagged = bagged_model, RF =␣
 ↪rf_model,
                         GBM = boosted_model, C50 = c50_model)

results_tree <- resamples(models_list_tree)
summary(results_tree)
dotplot(results_tree)
```

```
Call:
summary.resamples(object = results_tree)

Models: CART, Bagged, RF, GBM, C50
Number of resamples: 10

Accuracy
            Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
CART   0.8529412 0.8602941 0.8823529 0.8889076 0.9052521 0.9428571    0
Bagged 0.8285714 0.8922269 0.9130252 0.9129361 0.9411765 0.9696970    0
RF     0.8823529 0.9415966 0.9567227 0.9535294 0.9705882 1.0000000    0
GBM    0.8235294 0.9415966 0.9696970 0.9446957 0.9714286 1.0000000    0
C50    0.8823529 0.9205628 0.9420168 0.9415865 0.9705882 0.9714286    0

Kappa
            Min.   1st Qu.    Median      Mean   3rd Qu.      Max. NA's
CART   0.6931408 0.7171407 0.7613565 0.7703383 0.8002409 0.8776224    0
Bagged 0.6328671 0.7746361 0.8146918 0.8140209 0.8750050 0.9333333    0
RF     0.7424242 0.8721851 0.9052246 0.8987148 0.9381719 1.0000000    0
```

```
GBM    0.6031128 0.8731792 0.9333333 0.8791696 0.9392775 1.0000000    0
C50    0.7433962 0.8305072 0.8767674 0.8741912 0.9375755 0.9386282    0
```



Linear and Regularized Models

Logistic regression

```
[333]: log_model <- train(diagnosis ~ ., data = train_filtered,
                          method = "glm",
                          family = "binomial",
                          trControl = ctrl)
```

Linear Discriminant Analysis (LDA)

[334]:
```
lda_model <- train(diagnosis ~ ., data = train_filtered,
                   method = "lda",
                   trControl = ctrl)
```

Quadratic Discriminant Analysis (QDA)

[335]:
```
qda_model <- train(diagnosis ~ ., data = train_filtered,
                   method = "qda",
                   trControl = ctrl)
```

Partial Least Squares Discriminant Analysis (PLS-DA)

[336]:
```
plsda_model <- train(diagnosis ~ ., data = train_filtered,
                     method = "pls",
                     trControl = ctrl)
```

Penalized models

Ridge regression

[337]:
```
ridge_model <- train(diagnosis ~ ., data = train_filtered,
                     method = "glmnet",
                     trControl = ctrl,
                     tuneGrid = expand.grid(alpha = 0, lambda = seq(0.0001, 1,␣
 ↪length = 10)))
```

Lasso regression

[338]:
```
lasso_model <- train(diagnosis ~ ., data = train_filtered,
                     method = "glmnet",
                     trControl = ctrl,
                     tuneGrid = expand.grid(alpha = 1, lambda = seq(0.0001, 1,␣
 ↪length = 10)))
```

Elastic net

[339]:
```
elastic_model <- train(diagnosis ~ ., data = train_filtered,
                       method = "glmnet",
                       trControl = ctrl,
                       tuneLength = 10)  # automatically searches alpha & lambda
```

Nearest Shrunken Centroids

[340]:
```
nsc_model <- train(diagnosis ~ ., data = train_filtered,
                   method = "pam",
                   trControl = ctrl)
```

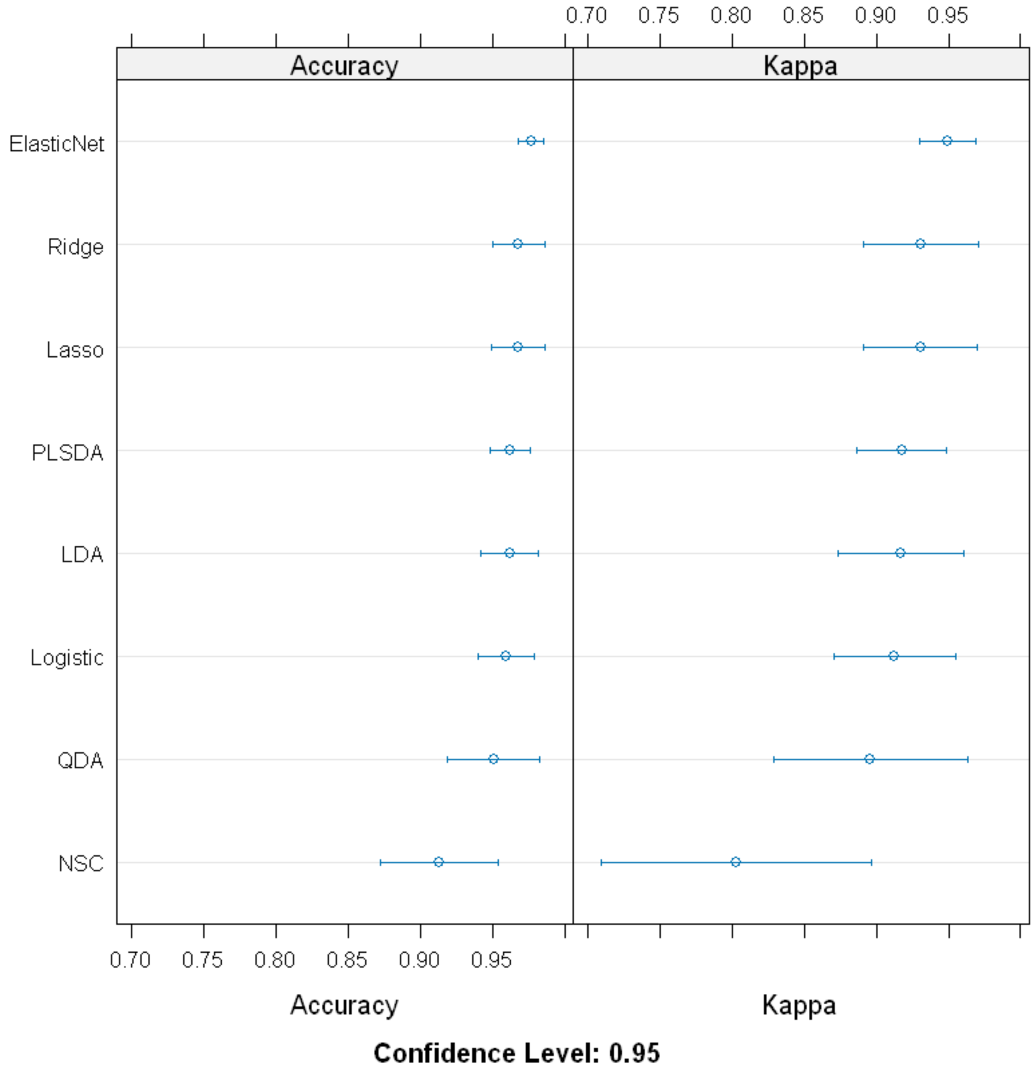
12345678910111213141516171819202122232425262728293011111111111

Comparing linear models

[341]:
```
models_list_linear <- list(Logistic = log_model, LDA = lda_model, QDA =␣
 ↪qda_model,
```

```r
                            PLSDA = plsda_model, Ridge = ridge_model, Lasso =
 ↪lasso_model,
                            ElasticNet = elastic_model, NSC = nsc_model)

results_linear <- resamples(models_list_linear)
summary(results_linear)
dotplot(results_linear)
```

```
Call:
summary.resamples(object = results_linear)

Models: Logistic, LDA, QDA, PLSDA, Ridge, Lasso, ElasticNet, NSC
Number of resamples: 10

Accuracy
                Min.   1st Qu.    Median      Mean   3rd Qu. Max. NA's
Logistic   0.9142857 0.9415966 0.9562771 0.9594067 0.9712185    1    0
LDA        0.9117647 0.9415966 0.9701426 0.9620117 0.9714286    1    0
QDA        0.8857143 0.9210084 0.9558824 0.9509244 0.9926471    1    0
PLSDA      0.9411765 0.9415966 0.9705882 0.9621008 0.9712185    1    0
Ridge      0.9411765 0.9415966 0.9710084 0.9679832 0.9928571    1    0
Lasso      0.9411765 0.9415966 0.9701426 0.9678100 0.9928571    1    0
ElasticNet 0.9696970 0.9705882 0.9710084 0.9765444 0.9714286    1    0
NSC        0.8235294 0.8922269 0.9142857 0.9127731 0.9424370    1    0

Kappa
                Min.   1st Qu.    Median      Mean   3rd Qu. Max. NA's
Logistic   0.8247078 0.8740991 0.9054779 0.9127371 0.9384294    1    0
LDA        0.8045977 0.8740991 0.9350177 0.9171101 0.9378330    1    0
QDA        0.7552448 0.8323824 0.9066832 0.8959101 0.9842007    1    0
PLSDA      0.8712121 0.8721851 0.9368030 0.9176256 0.9375755    1    0
Ridge      0.8716981 0.8740991 0.9373180 0.9306895 0.9849398    1    0
Lasso      0.8716981 0.8759990 0.9359807 0.9308197 0.9849398    1    0
ElasticNet 0.9333333 0.9368030 0.9373180 0.9494840 0.9392775    1    0
NSC        0.5903614 0.7552539 0.8073394 0.8031264 0.8731592    1    0
```



1.4 Summarizing all the models

[342]:

```
# Example data (replace with your actual numbers)
results_summary <- data.frame(
  Group = c("Linear & Regularized", "Tree & Ensemble", "Other classifiers"),
  Model = c("Elastic Net", "Random Forest", "Neural Net"),
  MeanAccuracy = c(0.9765, 0.9535, 0.9796),
  MeanKappa = c(0.9405, 0.8987, 0.9561)
)

print(results_summary)
```

```
                 Group         Model MeanAccuracy MeanKappa
```

```
1 Linear & Regularized   Elastic Net       0.9765    0.9405
2      Tree & Ensemble Random Forest       0.9535    0.8987
3    Other classifiers     Neural Net       0.9796    0.9561
```

Among all models, the neural network achieved the highest cross-validated mean accuracy (97.96%) and Kappa (95.61%), followed closely by elastic net (97.65% accuracy, 94.05% Kappa), while random forest led among tree-based models with 95.35% accuracy and 89.87% Kappa.

1.5 Preparing test dataset

Removing correlated columns

[343]:
```
test_filtered <- test_processed[, names(train_filtered)]
```

1.6 Making predictions with the best performance models

[344]:
```
# Neural network
pred_nn <- predict(nn_model, newdata = test_filtered)
cm_nn <- confusionMatrix(pred_nn, test_filtered$diagnosis)
```

[345]:
```
# Elastic net
pred_en <- predict(elastic_model, newdata = test_filtered)
cm_en <- confusionMatrix(pred_en, test_filtered$diagnosis)
```

[346]:
```
# Random forest
pred_rf <- predict(rf_model, newdata = test_filtered)
cm_rf <- confusionMatrix(pred_rf, test_filtered$diagnosis)
```

Comparison Table between models:

[347]:
```
# Create a data frame with selected metrics
results_table <- data.frame(
  Model = c("Neural Network", "Elastic Net", "Random Forest"),
  Accuracy = c(cm_nn$overall["Accuracy"],
               cm_en$overall["Accuracy"],
               cm_rf$overall["Accuracy"]),
  Kappa = c(cm_nn$overall["Kappa"],
            cm_en$overall["Kappa"],
            cm_rf$overall["Kappa"]),
  Sensitivity = c(cm_nn$byClass["Sensitivity"],
                  cm_en$byClass["Sensitivity"],
                  cm_rf$byClass["Sensitivity"]),
  Specificity = c(cm_nn$byClass["Specificity"],
                  cm_en$byClass["Specificity"],
                  cm_rf$byClass["Specificity"])
)

# Print the table
print(results_table)
```

```
           Model  Accuracy     Kappa Sensitivity Specificity
1 Neural Network 0.9690265 0.9341656   0.9647887   0.9761905
2    Elastic Net 0.9557522 0.9052649   0.9647887   0.9404762
3  Random Forest 0.9380531 0.8680127   0.9436620   0.9285714
```

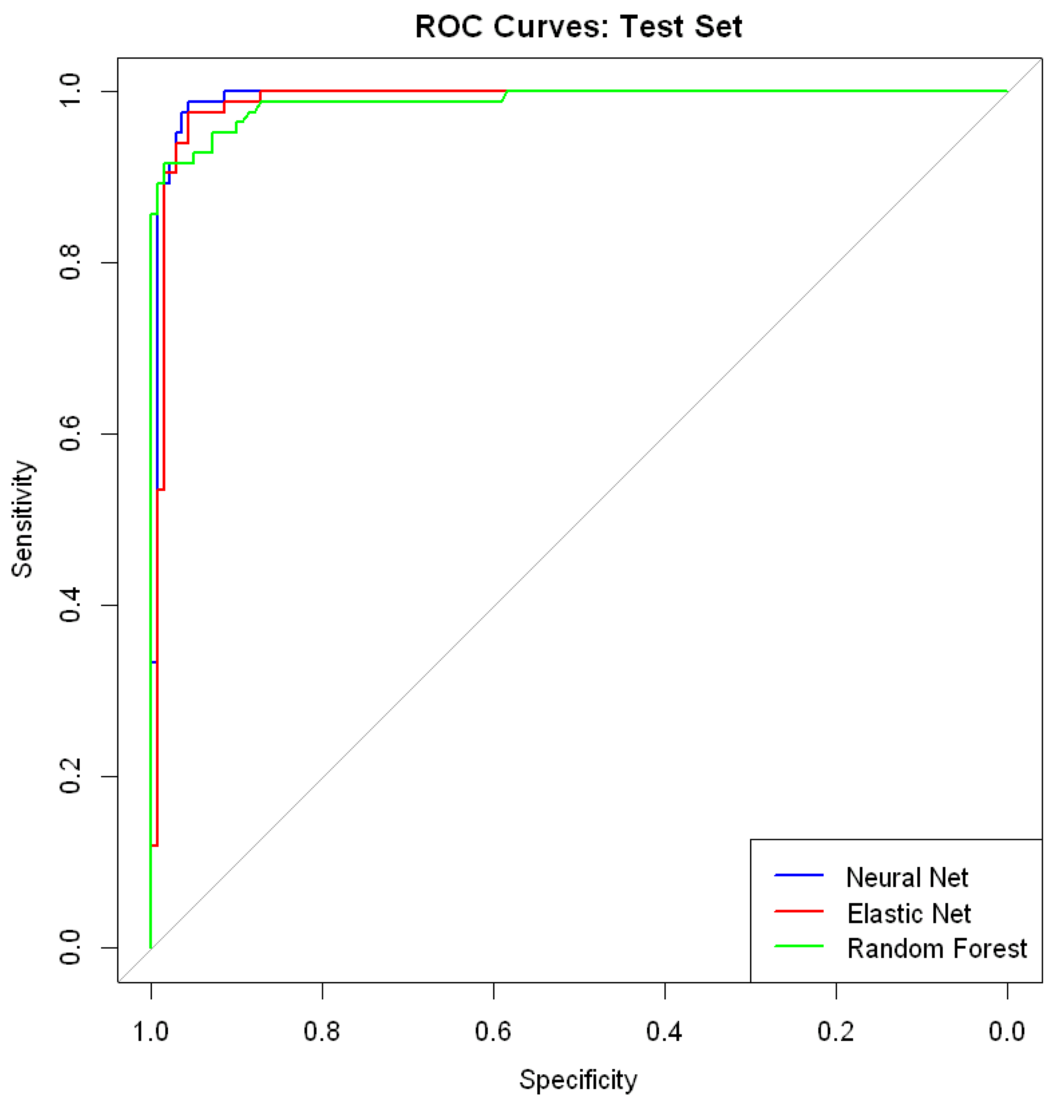
Generating ROC and AUC

[348]:
```
# Neural network
prob_nn <- predict(nn_model, newdata = test_filtered, type = "prob")
roc_nn <- roc(response = test_filtered$diagnosis, predictor = prob_nn[, "M"])

# Elastic Net
prob_en <- predict(elastic_model, newdata = test_filtered, type = "prob")
roc_en <- roc(response = test_filtered$diagnosis, predictor = prob_en[, "M"])

# Random Forest
prob_rf <- predict(rf_model, newdata = test_filtered, type = "prob")
roc_rf <- roc(response = test_filtered$diagnosis, predictor = prob_rf[, "M"])
```

```
Setting levels: control = B, case = M

Setting direction: controls < cases


Setting levels: control = B, case = M

Setting direction: controls < cases

Setting levels: control = B, case = M

Setting direction: controls < cases
```

1.7 ROC curves

[349]:
```
plot(roc_nn, col = "blue", main = "ROC Curves: Test Set")
plot(roc_en, col = "red", add = TRUE)
plot(roc_rf, col = "green", add = TRUE)
legend("bottomright", legend = c("Neural Net", "Elastic Net", "Random Forest"),
       col = c("blue", "red", "green"), lwd = 2)
```



AUC Values

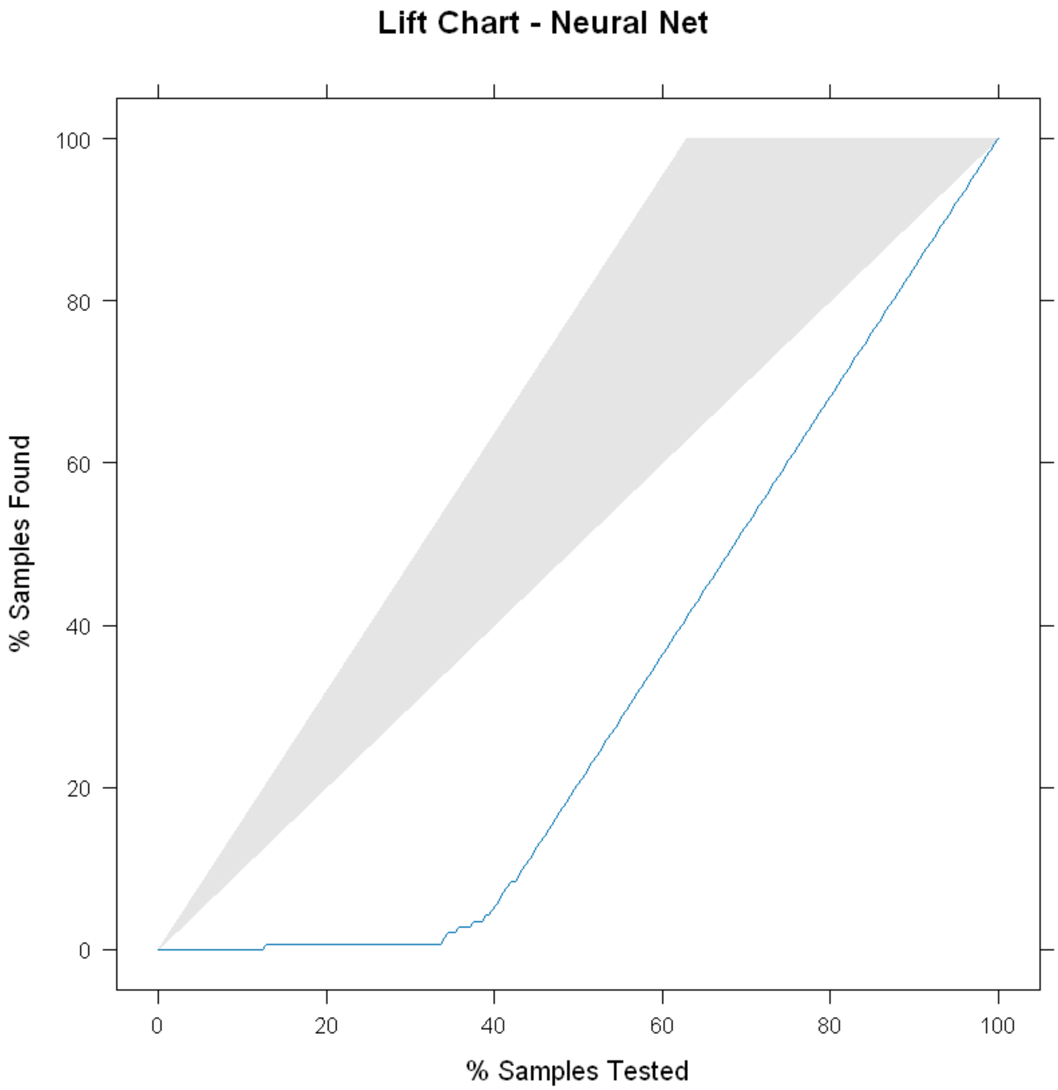
[350]:
```
cat("Neural Net AUC:", auc(roc_nn), "\n")
cat("Elastic Net AUC:", auc(roc_en), "\n")
cat("Random Forest AUC:", auc(roc_rf), "\n")
```

```
Neural Net AUC: 0.9922032
Elastic Net AUC: 0.9868377
Random Forest AUC: 0.9883048
```

On the test set, all models demonstrated excellent classification performance, with the neural network achieving the highest AUC (0.992), followed by random forest (0.988) and elastic net (0.987), indicating very high ability to distinguish malignant from benign cases.

Lift chart for best model: neural net

[351]:
```
# Predict probabilities
prob_nn <- predict(nn_model, newdata = test_filtered, type = "prob")

# Generate lift object
lift_nn <- lift(diagnosis ~ prob_nn[, "M"], data = test_filtered)

# Plot lift chart
plot(lift_nn, main = "Lift Chart - Neural Net")
```



This lift chart shows us how well the model ranks positive cases (M).

1.8 Conclusion

The classification models developed for breast cancer diagnosis showed excellent predictive performance on the test set. Among them, the neural network achieved the highest AUC (0.992) and strong accuracy, indicating superior ability to distinguish between malignant and benign cases. The elastic net (AUC 0.987) and random forest (AUC 0.988) models also performed exceptionally well, offering robust alternatives with comparable discrimination power. These results highlight that both linear regularized models and nonlinear ensemble methods can provide highly reliable predictions in this medical classification task. Future work could explore external validation on independent datasets and assess model interpretability for clinical use.