

ADS 503 Final Project

April Chia

2025-06-05

Packages used

```
library(caret)
library(tidyverse)
library(ggplot2)
library(reshape2)
library(corrplot)
library(Hmisc)
library(mlbench)
library(e1071)
library(randomForest)
library(gt)
library(pls)
library(elasticnet)
library(pROC)
```

Import dataset

```
cancer_data <- read.csv("breast-cancer.csv")
head(cancer_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
## 1           0.2654      0.4601      0.11890
## 2           0.1860      0.2750      0.08902
## 3           0.2430      0.3613      0.08758
## 4           0.2575      0.6638      0.17300
## 5           0.1625      0.2364      0.07678
## 6           0.1741      0.3985      0.12440
```

EDA

```
summary(cancer_data)
```

```
##      id      diagnosis      radius_mean      texture_mean
## Min.   :    8670 Length:569 Min.    : 6.981 Min.    : 9.71
## 1st Qu.:  869218 Class :character 1st Qu.:11.700 1st Qu.:16.17
## Median :  906024 Mode  :character Median :13.370 Median :18.84
## Mean   : 30371831 Mean   :14.127 Mean   :19.29
## 3rd Qu.:  8813129 3rd Qu.:15.780 3rd Qu.:21.80
## Max.   :911320502 Max.   :28.110 Max.   :39.28
## perimeter_mean      area_mean      smoothness_mean      compactness_mean
## Min.    : 43.79 Min.    : 143.5 Min.    :0.05263 Min.    :0.01938
## 1st Qu.: 75.17 1st Qu.: 420.3 1st Qu.:0.08637 1st Qu.:0.06492
## Median : 86.24 Median : 551.1 Median :0.09587 Median :0.09263
## Mean    : 91.97 Mean    : 654.9 Mean    :0.09636 Mean    :0.10434
## 3rd Qu.:104.10 3rd Qu.: 782.7 3rd Qu.:0.10530 3rd Qu.:0.13040
## Max.    :188.50 Max.    :2501.0 Max.    :0.16340 Max.    :0.34540
## concavity_mean      concave.points_mean symmetry_mean      fractal_dimension_mean
## Min.    :0.00000 Min.    :0.00000 Min.    :0.1060 Min.    :0.04996
## 1st Qu.:0.02956 1st Qu.:0.02031 1st Qu.:0.1619 1st Qu.:0.05770
## Median :0.06154 Median :0.03350 Median :0.1792 Median :0.06154
## Mean    :0.08880 Mean    :0.04892 Mean    :0.1812 Mean    :0.06280
## 3rd Qu.:0.13070 3rd Qu.:0.07400 3rd Qu.:0.1957 3rd Qu.:0.06612
## Max.    :0.42680 Max.    :0.20120 Max.    :0.3040 Max.    :0.09744
```

```
##      radius_se      texture_se      perimeter_se      area_se
## Min.   :0.1115   Min.   :0.3602   Min.   : 0.757   Min.   : 6.802
## 1st Qu.:0.2324   1st Qu.:0.8339   1st Qu.: 1.606   1st Qu.: 17.850
## Median :0.3242   Median :1.1080   Median : 2.287   Median : 24.530
## Mean   :0.4052   Mean   :1.2169   Mean   : 2.866   Mean   : 40.337
## 3rd Qu.:0.4789   3rd Qu.:1.4740   3rd Qu.: 3.357   3rd Qu.: 45.190
## Max.   :2.8730   Max.   :4.8850   Max.   :21.980   Max.   :542.200
## smoothness_se      compactness_se      concavity_se      concave.points_se
## Min.   :0.001713   Min.   :0.002252   Min.   :0.00000   Min.   :0.000000
## 1st Qu.:0.005169   1st Qu.:0.013080   1st Qu.:0.01509   1st Qu.:0.007638
## Median :0.006380   Median :0.020450   Median :0.02589   Median :0.010930
## Mean   :0.007041   Mean   :0.025478   Mean   :0.03189   Mean   :0.011796
## 3rd Qu.:0.008146   3rd Qu.:0.032450   3rd Qu.:0.04205   3rd Qu.:0.014710
## Max.   :0.031130   Max.   :0.135400   Max.   :0.39600   Max.   :0.052790
## symmetry_se      fractal_dimension_se      radius_worst      texture_worst
## Min.   :0.007882   Min.   :0.0008948   Min.   : 7.93   Min.   :12.02
## 1st Qu.:0.015160   1st Qu.:0.0022480   1st Qu.:13.01   1st Qu.:21.08
## Median :0.018730   Median :0.0031870   Median :14.97   Median :25.41
## Mean   :0.020542   Mean   :0.0037949   Mean   :16.27   Mean   :25.68
## 3rd Qu.:0.023480   3rd Qu.:0.0045580   3rd Qu.:18.79   3rd Qu.:29.72
## Max.   :0.078950   Max.   :0.0298400   Max.   :36.04   Max.   :49.54
## perimeter_worst      area_worst      smoothness_worst      compactness_worst
## Min.   : 50.41   Min.   : 185.2   Min.   :0.07117   Min.   :0.02729
## 1st Qu.: 84.11   1st Qu.: 515.3   1st Qu.:0.11660   1st Qu.:0.14720
## Median : 97.66   Median : 686.5   Median :0.13130   Median :0.21190
## Mean   :107.26   Mean   : 880.6   Mean   :0.13237   Mean   :0.25427
## 3rd Qu.:125.40   3rd Qu.:1084.0   3rd Qu.:0.14600   3rd Qu.:0.33910
## Max.   :251.20   Max.   :4254.0   Max.   :0.22260   Max.   :1.05800
## concavity_worst      concave.points_worst      symmetry_worst      fractal_dimension_worst
## Min.   :0.0000   Min.   :0.00000   Min.   :0.1565   Min.   :0.05504
## 1st Qu.:0.1145   1st Qu.:0.06493   1st Qu.:0.2504   1st Qu.:0.07146
## Median :0.2267   Median :0.09993   Median :0.2822   Median :0.08004
## Mean   :0.2722   Mean   :0.11461   Mean   :0.2901   Mean   :0.08395
## 3rd Qu.:0.3829   3rd Qu.:0.16140   3rd Qu.:0.3179   3rd Qu.:0.09208
## Max.   :1.2520   Max.   :0.29100   Max.   :0.6638   Max.   :0.20750
```

```
# Data types
str(cancer_data)
```

```
## 'data.frame':   569 obs. of  32 variables:
## $ id              : int  842302 842517 84300903 84348301 84358402 843786 844359 84458202 844...
## $ 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 ...
```

```
# Missing values
```

```
sum(is.na(cancer_data))
```

```
## [1] 0
```

```
# Duplicates
```

```
sum(duplicated(cancer_data))
```

```
## [1] 0
```

```
# Distribution of predictors
```

```
cancer_data |>
```

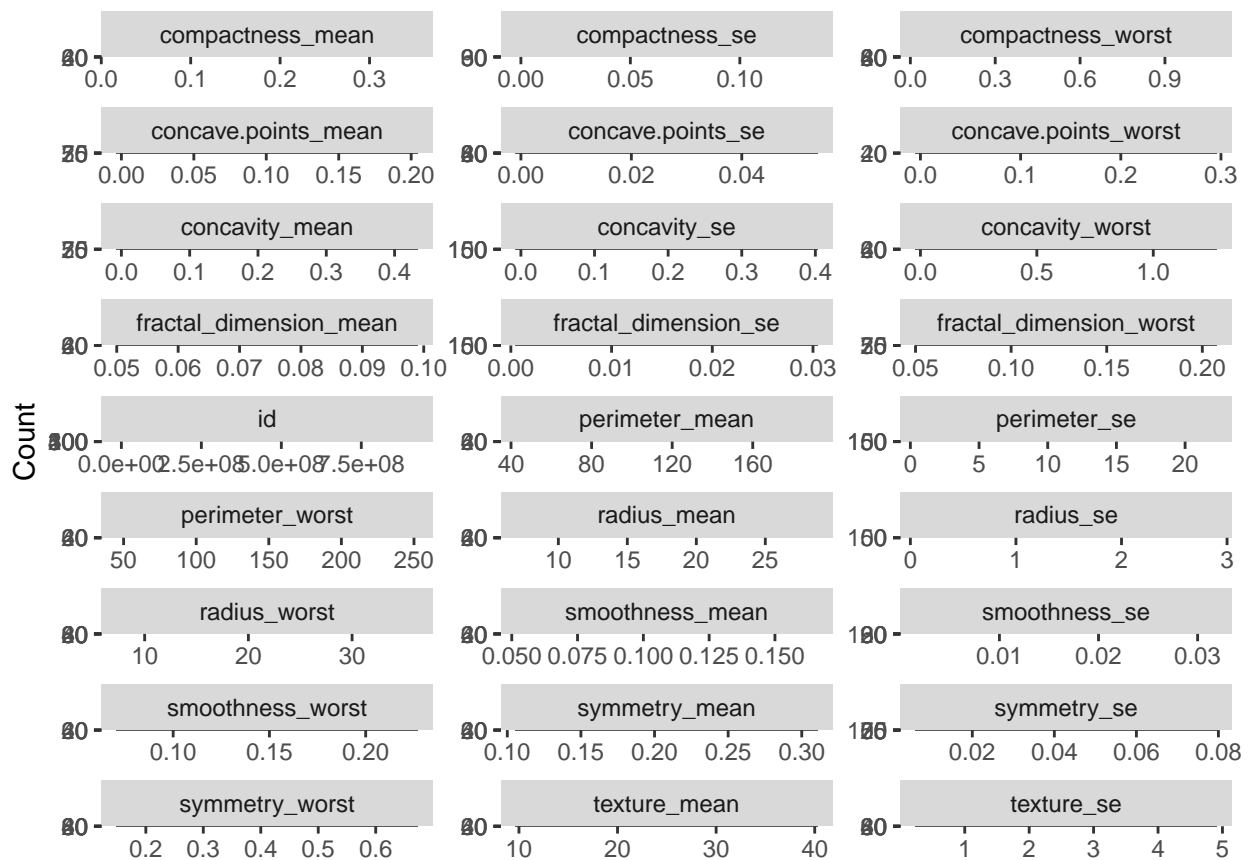
```
  pivot_longer(-diagnosis, names_to = 'feature', values_to = 'value') |>
```

```
  ggplot(aes(x = value)) +
```

```
  geom_histogram(bins = 30) +
```

```
  facet_wrap(~ feature, scales = "free", ncol = 3) +
```

```
  labs(title = 'Glass Data Features', x = "values", y = "Count")
```



Distribution of diagnosis classes

```
table(cancer_data$diagnosis)
```

```
##
```

```
##      B      M
```

```
## 357 212
```

```
prop.table(table(cancer_data$diagnosis))
```

```
##
```

```
##           B           M
```

```
## 0.6274165 0.3725835
```

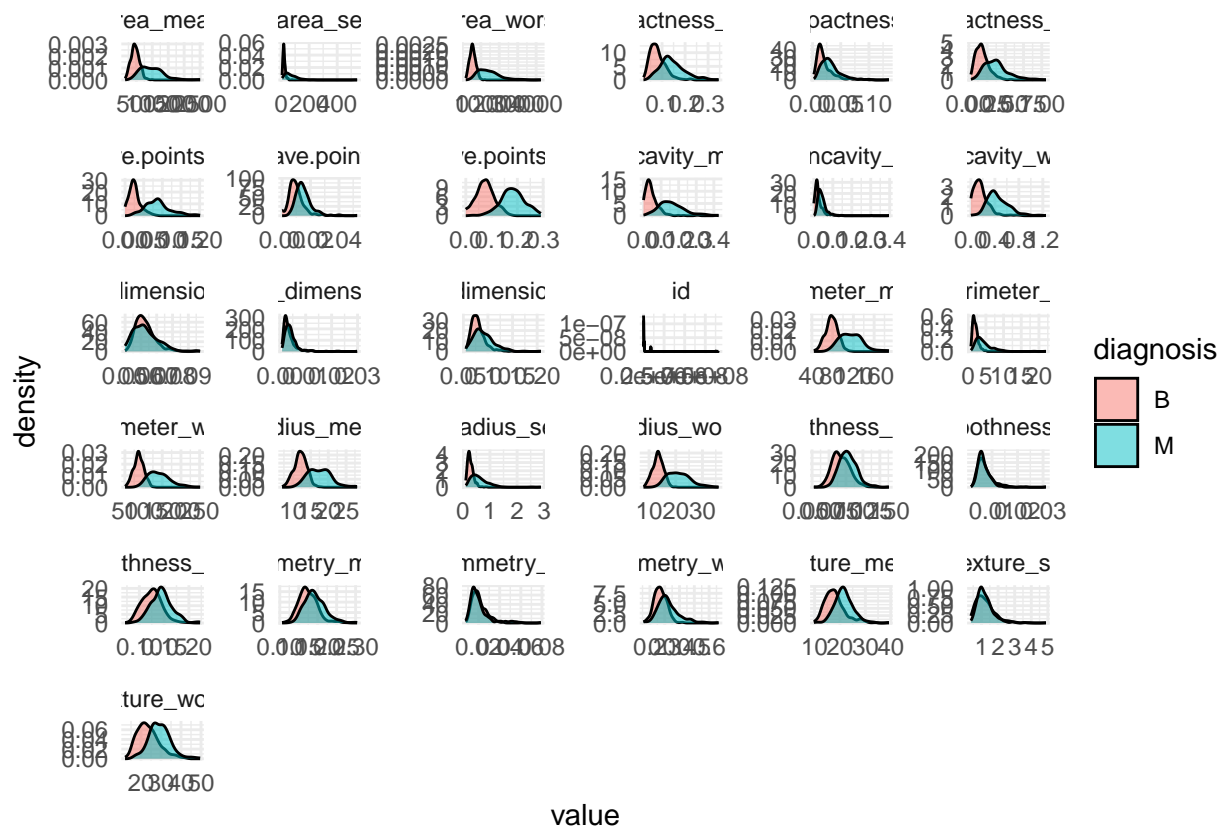
Relationship between predictors and response

```
predictor_data <- cancer_data[, names(cancer_data) != "diagnosis"]
```

Convert to long format

```
df_long <- data.frame(
  diagnosis = rep(cancer_data$diagnosis, times = ncol(predictor_data)),
  feature = rep(names(predictor_data), each = nrow(cancer_data)),
  value = as.vector(as.matrix(predictor_data))
)
```

```
ggplot(df_long, aes(x = value, fill = diagnosis)) +
  geom_density(alpha = 0.5) +
  facet_wrap(~ feature, scales = "free") +
  theme_minimal()
```



```
# Predictors w/ near zero variance
degenerate <- nearZeroVar(predictor_data)
print(degenerate)
```

```
## integer(0)
```

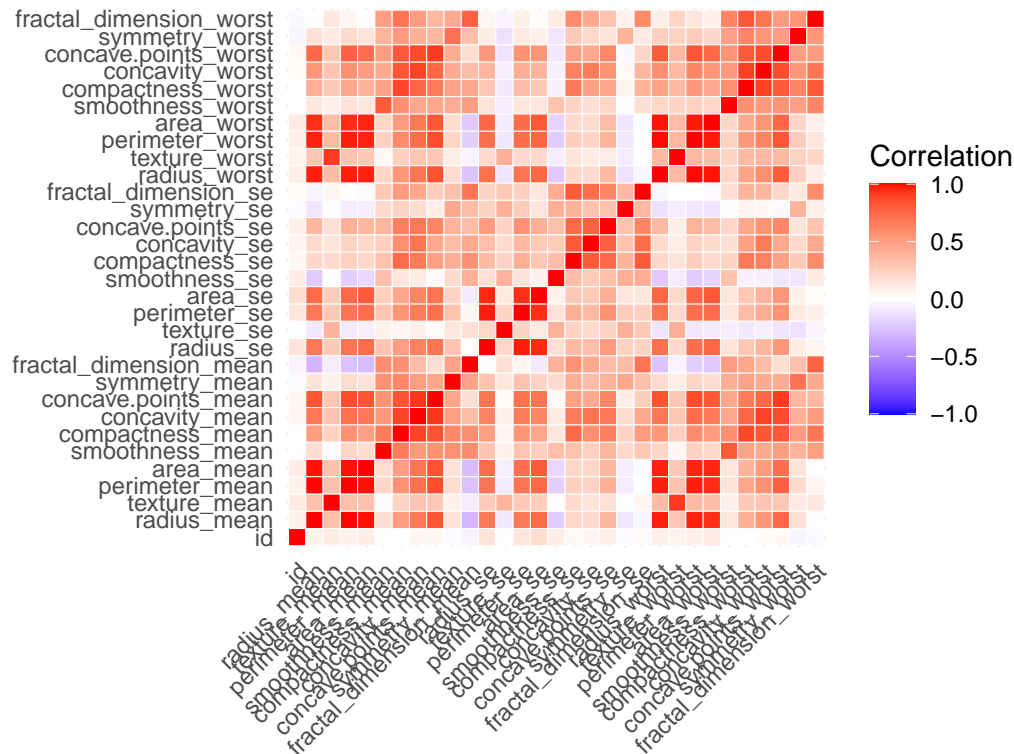
```
# Correlation between predictors
```

```
cor_matrix <- cor(predictor_data)
```

```
cor_long <- melt(cor_matrix)
```

```
ggplot(cor_long, aes(Var1, Var2, fill = value)) +
  geom_tile(color = "white") +
  scale_fill_gradient2(low = "blue", high = "red", mid = "white",
    midpoint = 0, limit = c(-1, 1), space = "Lab",
    name = "Correlation") +
  theme_minimal() +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1)) +
  coord_fixed() +
  labs(title = "Predictor Correlation Heatmap", x = "", y = "")
```

Predictor Correlation Heatmap



Skewness

```
apply(cancer_data[, -2], 2, skewness)
```

```
##          id          radius_mean          texture_mean
##      6.4396595          0.9374168          0.6470241
##      perimeter_mean          area_mean          smoothness_mean
##      0.9854334          1.6370654          0.4539207
##      compactness_mean          concavity_mean          concave.points_mean
##      1.1838556          1.3938008          1.1650124
##      symmetry_mean          fractal_dimension_mean          radius_se
##      0.7217877          1.2976191          3.0723468
##      texture_se          perimeter_se          area_se
##      1.6377733          3.4254803          5.4185001
##      smoothness_se          compactness_se          concavity_se
##      2.3022616          1.8922032          5.0835502
##      concave.points_se          symmetry_se          fractal_dimension_se
##      1.4370701          2.1835728          3.9033041
##      radius_worst          texture_worst          perimeter_worst
##      1.0973059          0.4956970          1.1222227
##      area_worst          smoothness_worst          compactness_worst
##      1.8495814          0.4132383          1.4657948
##      concavity_worst          concave.points_worst          symmetry_worst
##      1.1441794          0.4900213          1.4263764
## fractal_dimension_worst
##      1.6538237
```

Pre-processing

```
# Remove unnecessary columns
df <- cancer_data[, -which(names(cancer_data) == "id")]
head(df)
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean
## 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

	compactness_mean	concavity_mean	concave.points_mean	symmetry_mean
## 1	0.27760	0.3001	0.14710	0.2419
## 2	0.07864	0.0869	0.07017	0.1812
## 3	0.15990	0.1974	0.12790	0.2069
## 4	0.28390	0.2414	0.10520	0.2597
## 5	0.13280	0.1980	0.10430	0.1809
## 6	0.17000	0.1578	0.08089	0.2087

	fractal_dimension_mean	radius_se	texture_se	perimeter_se	area_se
## 1	0.07871	1.0950	0.9053	8.589	153.40
## 2	0.05667	0.5435	0.7339	3.398	74.08
## 3	0.05999	0.7456	0.7869	4.585	94.03
## 4	0.09744	0.4956	1.1560	3.445	27.23
## 5	0.05883	0.7572	0.7813	5.438	94.44
## 6	0.07613	0.3345	0.8902	2.217	27.19

	smoothness_se	compactness_se	concavity_se	concave.points_se	symmetry_se
## 1	0.006399	0.04904	0.05373	0.01587	0.03003
## 2	0.005225	0.01308	0.01860	0.01340	0.01389
## 3	0.006150	0.04006	0.03832	0.02058	0.02250
## 4	0.009110	0.07458	0.05661	0.01867	0.05963
## 5	0.011490	0.02461	0.05688	0.01885	0.01756
## 6	0.007510	0.03345	0.03672	0.01137	0.02165

	fractal_dimension_se	radius_worst	texture_worst	perimeter_worst	area_worst
## 1	0.006193	25.38	17.33	184.60	2019.0
## 2	0.003532	24.99	23.41	158.80	1956.0
## 3	0.004571	23.57	25.53	152.50	1709.0
## 4	0.009208	14.91	26.50	98.87	567.7
## 5	0.005115	22.54	16.67	152.20	1575.0
## 6	0.005082	15.47	23.75	103.40	741.6

	smoothness_worst	compactness_worst	concavity_worst	concave.points_worst
## 1	0.1622	0.6656	0.7119	0.2654
## 2	0.1238	0.1866	0.2416	0.1860
## 3	0.1444	0.4245	0.4504	0.2430
## 4	0.2098	0.8663	0.6869	0.2575
## 5	0.1374	0.2050	0.4000	0.1625
## 6	0.1791	0.5249	0.5355	0.1741

	symmetry_worst	fractal_dimension_worst
## 1	0.4601	0.11890
## 2	0.2750	0.08902
## 3	0.3613	0.08758
## 4	0.6638	0.17300
## 5	0.2364	0.07678


```
## 6          0.3985          0.12440

# Convert diagnosis to factor
df$diagnosis <- factor(df$diagnosis, levels = c("B", "M"))

# BoxCox Transformation
non_bct_cols <- c("smoothness_mean", "texture_worst", "smoothness_worst", "concave.points_worst")
bct_cols <- setdiff(names(df), non_bct_cols)

params <- preProcess(df[, bct_cols], method = "BoxCox")
df_transformed <- predict(params, df[, bct_cols])
df[, bct_cols] <- df_transformed

# Confirm transformation
apply(df_transformed[, -1], 2, skewness)
```

##	radius_mean	texture_mean	perimeter_mean
##	-0.018084005	-0.013801528	-0.018259725
##	area_mean	compactness_mean	concavity_mean
##	0.283456808	-0.033906489	1.393800804
##	concave.points_mean	symmetry_mean	fractal_dimension_mean
##	1.165012377	0.001737667	0.150646585
##	radius_se	texture_se	perimeter_se
##	0.027176088	0.029036809	0.069227942
##	area_se	smoothness_se	compactness_se
##	0.115303422	-0.024011982	-0.004019758
##	concavity_se	concave.points_se	symmetry_se
##	5.083550174	1.437070137	0.054910585
##	fractal_dimension_se	radius_worst	perimeter_worst
##	0.012191507	0.026399596	0.061225231
##	area_worst	compactness_worst	concavity_worst
##	0.067682043	-0.220675829	1.144179410
##	symmetry_worst	fractal_dimension_worst	
##	-0.056548989	0.047053460	

Data splitting

```
set.seed(123)
trainIndex <- createDataPartition(df_transformed$diagnosis, p = 0.8, list = FALSE)

train <- df_transformed[trainIndex, ]
test <- df_transformed[-trainIndex, ]
```

Models

```
ctrl <- trainControl(method = "cv",
                     number = 10,
                     summaryFunction = twoClassSummary,
                     classProbs = TRUE,
                     savePredictions = TRUE)

set.seed(123)
# Logistic Regression
lr_model <- train(x = train[, -1],
```

```

y = train$diagnosis,
method = "glm",
preProcess = c("center", "scale"),
metric = "ROC",
trControl = ctrl)

```

```

## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: algorithm did not converge
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred

```

```
lr_model
```

```

## Generalized Linear Model
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results:
##
## ROC      Sens      Spec
## 0.9667959 0.9506158 0.9352941

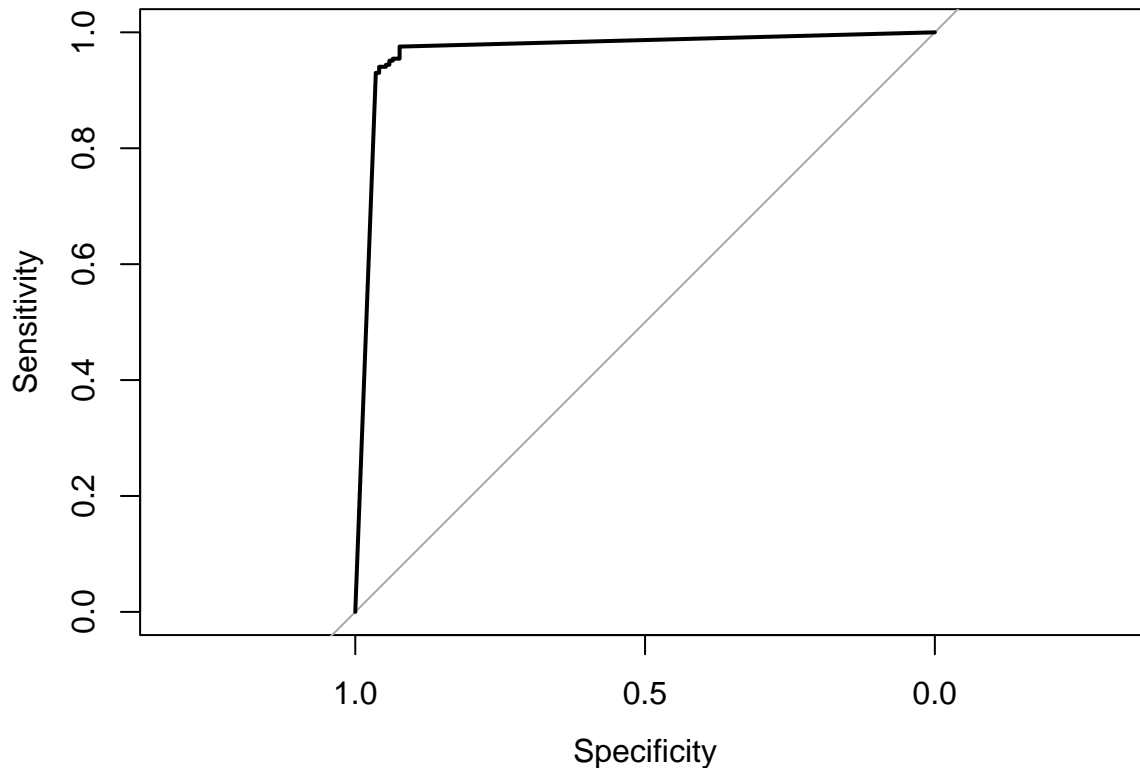
```

```
testResults <- data.frame(obs = test$diagnosis, LogReg = predict(lr_model, test[, -1]))
```

```
# ROC curve for log reg
lr_roc <- roc(response = lr_model$pred$obs,
              predictor = lr_model$pred$M,
              levels = rev(levels(lr_model$pred$obs)))
```

```
## Setting direction: controls > cases
```

```
plot(lr_roc, legaces.axes = TRUE)
```



```
# Confusion Matrix
confusionMatrix(testResults$LogReg, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction  B  M
```

```
##           B 68  1
```

```
##           M  3 41
```

```
##
```

```
##           Accuracy : 0.9646
```

```
##           95% CI : (0.9118, 0.9903)
```

```
##           No Information Rate : 0.6283
```

```
##           P-Value [Acc > NIR] : <2e-16
```

```
##
```

```
##           Kappa : 0.9249
```

```
##
```

```
##           McNemar's Test P-Value : 0.6171
```

```
##
```

```
##          Sensitivity : 0.9762
##          Specificity : 0.9577
##          Pos Pred Value : 0.9318
##          Neg Pred Value : 0.9855
##          Prevalence : 0.3717
##          Detection Rate : 0.3628
##          Detection Prevalence : 0.3894
##          Balanced Accuracy : 0.9670
##
##          'Positive' Class : M
##
```

```
# Penalized Logistic Regression
plrGrid <- expand.grid(alpha = c(0, .1, .2, .4, .6, .8, 1),
                      lambda = seq(.01, .2, length = 10))

set.seed(123)
plr_model <- train(x = train[, -1],
                  y = train$diagnosis,
                  method = "glmnet",
                  tuneGrid = plrGrid,
                  preProcess = c("center", "scale"),
                  metric = "ROC",
                  trControl = ctrl)

plr_model
```

```
## glmnet
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results across tuning parameters:
##
##   alpha  lambda      ROC      Sens      Spec
##   0.0    0.01000000  0.9947117  0.9791872  0.9294118
##   0.0    0.03111111  0.9947117  0.9791872  0.9294118
##   0.0    0.05222222  0.9936902  0.9791872  0.9235294
##   0.0    0.07333333  0.9926615  0.9756158  0.9117647
##   0.0    0.09444444  0.9918357  0.9756158  0.9058824
##   0.0    0.11555556  0.9910099  0.9756158  0.9058824
##   0.0    0.13666667  0.9901985  0.9720443  0.8882353
##   0.0    0.15777778  0.9889670  0.9720443  0.8823529
##   0.0    0.17888889  0.9885540  0.9720443  0.8823529
##   0.0    0.20000000  0.9883512  0.9720443  0.8823529
##   0.1    0.01000000  0.9949218  0.9896552  0.9411765
##   0.1    0.03111111  0.9938931  0.9860837  0.9235294
##   0.1    0.05222222  0.9918502  0.9791872  0.9176471
##   0.1    0.07333333  0.9910316  0.9757389  0.9117647
##   0.1    0.09444444  0.9895972  0.9757389  0.9058824
##   0.1    0.11555556  0.9891843  0.9756158  0.8941176
##   0.1    0.13666667  0.9885613  0.9756158  0.8823529
```

##	0.1	0.15777778	0.9885613	0.9756158	0.8764706
##	0.1	0.17888889	0.9885613	0.9756158	0.8764706
##	0.1	0.20000000	0.9885613	0.9756158	0.8705882
##	0.2	0.01000000	0.9951246	0.9860837	0.9411765
##	0.2	0.03111111	0.9924660	0.9826355	0.9235294
##	0.2	0.05222222	0.9912417	0.9791872	0.9176471
##	0.2	0.07333333	0.9896045	0.9791872	0.9117647
##	0.2	0.09444444	0.9894016	0.9791872	0.8941176
##	0.2	0.11555556	0.9891843	0.9756158	0.8882353
##	0.2	0.13666667	0.9887786	0.9756158	0.8882353
##	0.2	0.15777778	0.9889815	0.9756158	0.8823529
##	0.2	0.17888889	0.9889815	0.9791872	0.8764706
##	0.2	0.20000000	0.9887641	0.9791872	0.8647059
##	0.4	0.01000000	0.9941032	0.9789409	0.9411765
##	0.4	0.03111111	0.9912489	0.9860837	0.9235294
##	0.4	0.05222222	0.9900174	0.9826355	0.9117647
##	0.4	0.07333333	0.9896045	0.9791872	0.8882353
##	0.4	0.09444444	0.9898073	0.9826355	0.8882353
##	0.4	0.11555556	0.9891843	0.9826355	0.8823529
##	0.4	0.13666667	0.9889670	0.9896552	0.8764706
##	0.4	0.15777778	0.9889597	0.9896552	0.8411765
##	0.4	0.17888889	0.9885468	0.9931034	0.8352941
##	0.4	0.20000000	0.9875254	0.9931034	0.8294118
##	0.6	0.01000000	0.9932918	0.9825123	0.9411765
##	0.6	0.03111111	0.9910461	0.9860837	0.9117647
##	0.6	0.05222222	0.9904231	0.9895320	0.9117647
##	0.6	0.07333333	0.9904086	0.9895320	0.8941176
##	0.6	0.09444444	0.9895900	0.9895320	0.8764706
##	0.6	0.11555556	0.9887496	0.9965517	0.8588235
##	0.6	0.13666667	0.9889525	0.9965517	0.8352941
##	0.6	0.15777778	0.9885323	0.9965517	0.8117647
##	0.6	0.17888889	0.9881266	0.9965517	0.8000000
##	0.6	0.20000000	0.9875109	0.9965517	0.7941176
##	0.8	0.01000000	0.9926760	0.9825123	0.9411765
##	0.8	0.03111111	0.9904303	0.9860837	0.9117647
##	0.8	0.05222222	0.9908287	0.9895320	0.9058824
##	0.8	0.07333333	0.9895755	0.9895320	0.8705882
##	0.8	0.09444444	0.9889380	0.9929803	0.8588235
##	0.8	0.11555556	0.9885323	0.9894089	0.8235294
##	0.8	0.13666667	0.9875036	0.9965517	0.8117647
##	0.8	0.15777778	0.9873008	0.9965517	0.8000000
##	0.8	0.17888889	0.9873080	0.9965517	0.7823529
##	0.8	0.20000000	0.9871124	1.0000000	0.7705882
##	1.0	0.01000000	0.9924804	0.9825123	0.9352941
##	1.0	0.03111111	0.9906259	0.9895320	0.9235294
##	1.0	0.05222222	0.9902057	0.9895320	0.8941176
##	1.0	0.07333333	0.9889525	0.9894089	0.8588235
##	1.0	0.09444444	0.9862793	0.9858374	0.8352941
##	1.0	0.11555556	0.9856781	0.9929803	0.8235294
##	1.0	0.13666667	0.9836352	0.9929803	0.8000000
##	1.0	0.15777778	0.9830194	0.9929803	0.7705882
##	1.0	0.17888889	0.9830194	0.9964286	0.7235294
##	1.0	0.20000000	0.9830194	1.0000000	0.6823529
##					

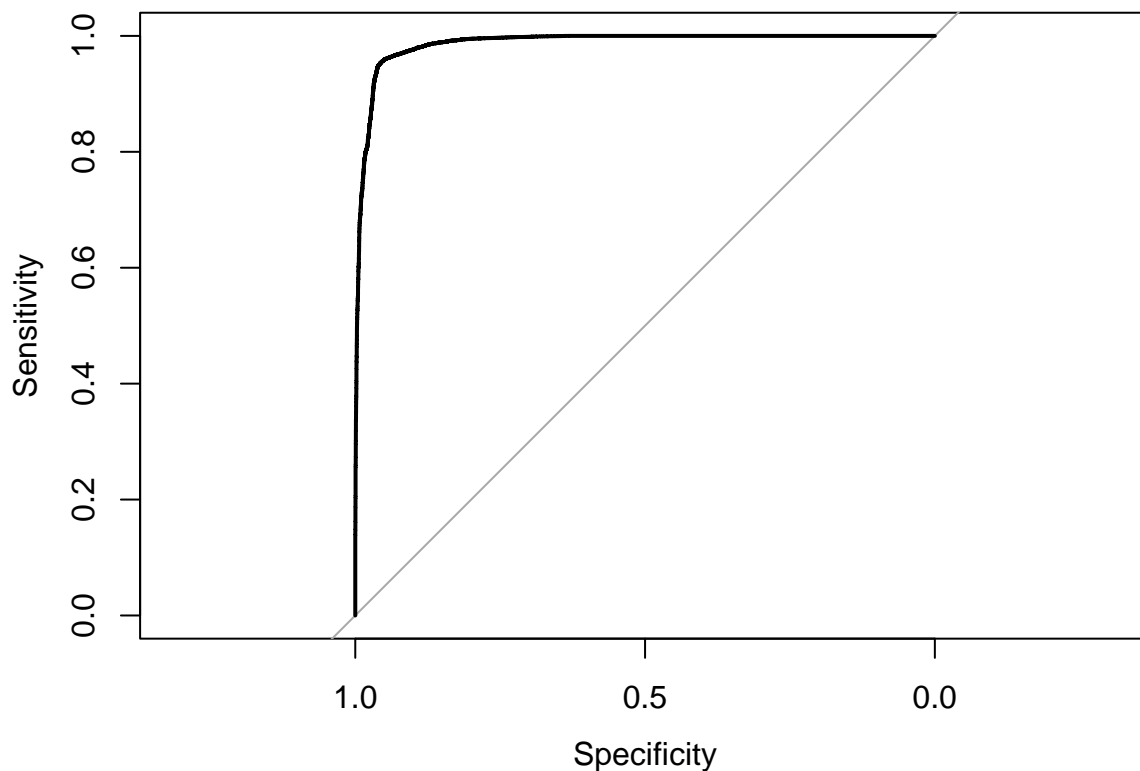
```
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were alpha = 0.2 and lambda = 0.01.
```

```
testResults$PLR <- predict(plr_model, test[, -1])
```

```
# ROC curve for penalized log reg
plr_roc <- roc(response = plr_model$pred$obs,
               predictor = plr_model$pred$M,
               levels = rev(levels(plr_model$pred$obs)))
```

```
## Setting direction: controls > cases
```

```
plot(plr_roc, legaces.axes = TRUE)
```



```
# Confusion Matrix
confusionMatrix(testResults$PLR, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction B  M
```

```
##           B 70  1
```

```
##           M  1 41
```

```
##
```

```
##           Accuracy : 0.9823
```

```
##           95% CI : (0.9375, 0.9978)
```

```
##           No Information Rate : 0.6283
```

```
##           P-Value [Acc > NIR] : <2e-16
```

```
##
```

```
##           Kappa : 0.9621
```

```
##
```

```

## McNemar's Test P-Value : 1
##
##      Sensitivity : 0.9762
##      Specificity : 0.9859
##      Pos Pred Value : 0.9762
##      Neg Pred Value : 0.9859
##      Prevalence : 0.3717
##      Detection Rate : 0.3628
##      Detection Prevalence : 0.3717
##      Balanced Accuracy : 0.9811
##
##      'Positive' Class : M
##

# LDA
set.seed(123)
lda_model <- train(x = train[, -1],
                  y = train$diagnosis,
                  method = "lda",
                  preProcess = c("center", "scale"),
                  metric = "ROC",
                  trControl = ctrl)
lda_model

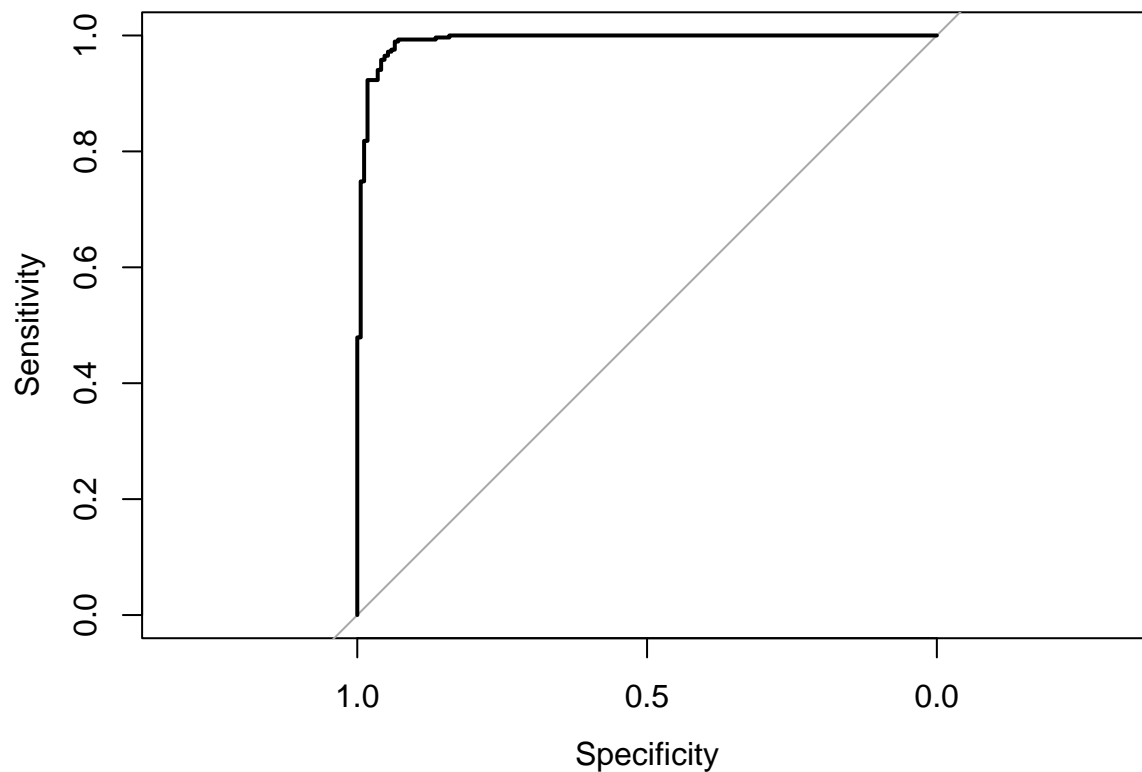
## Linear Discriminant Analysis
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results:
##
##      ROC      Sens      Spec
## 0.9930745 0.9929803 0.8941176

testResults$LDA <- predict(lda_model, test[, -1])

# ROC curve for LDA
lda_roc <- roc(response = lda_model$pred$obs,
              predictor = lda_model$pred$M,
              levels = rev(levels(lda_model$pred$obs)))

## Setting direction: controls > cases
plot(lda_roc, legaces.axes = TRUE)

```



```
# Confusion Matrix
confusionMatrix(testResults$LDA, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##           B 71  3
##           M  0 39
##
##           Accuracy : 0.9735
##           95% CI : (0.9244, 0.9945)
##           No Information Rate : 0.6283
##           P-Value [Acc > NIR] : <2e-16
##
##           Kappa : 0.9423
##
##           McNemar's Test P-Value : 0.2482
##
##           Sensitivity : 0.9286
##           Specificity : 1.0000
##           Pos Pred Value : 1.0000
##           Neg Pred Value : 0.9595
##           Prevalence : 0.3717
##           Detection Rate : 0.3451
##           Detection Prevalence : 0.3451
##           Balanced Accuracy : 0.9643
##
##           'Positive' Class : M
```



```
##
# PLSDA
plsGrid <- expand.grid(ncomp = 1:20)

set.seed(123)
pls_model <- train(x = train[, -1],
  y = train$diagnosis,
  method = "pls",
  tuneGrid = plsGrid,
  preProcess = c("center", "scale"),
  metric = "ROC",
  trControl = ctrl)

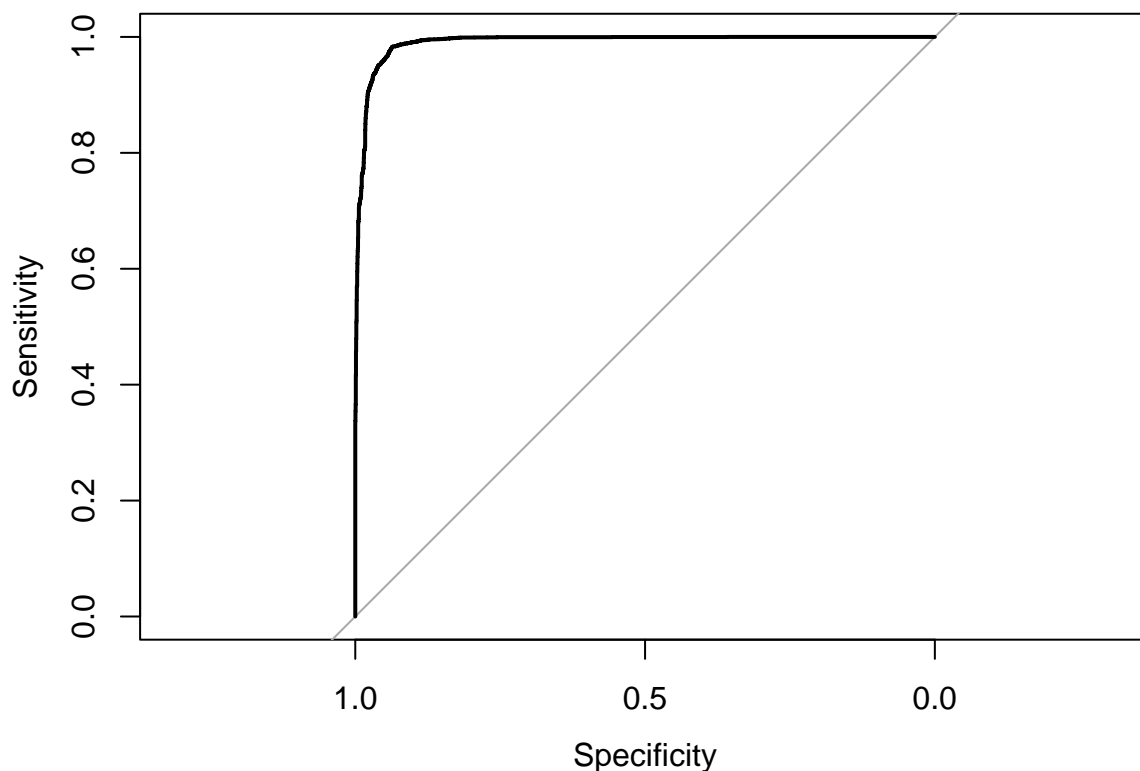
pls_model

## Partial Least Squares
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results across tuning parameters:
##
##  ncomp  ROC      Sens      Spec
##  1      0.9797015 0.9685961 0.8588235
##  2      0.9887569 0.9757389 0.9000000
##  3      0.9880107 0.9929803 0.9176471
##  4      0.9939076 0.9965517 0.8941176
##  5      0.9939003 0.9929803 0.9058824
##  6      0.9918574 0.9965517 0.9058824
##  7      0.9922704 0.9894089 0.9058824
##  8      0.9932701 0.9929803 0.8941176
##  9      0.9928644 1.0000000 0.8941176
## 10      0.9930817 1.0000000 0.9000000
## 11      0.9916618 0.9964286 0.8882353
## 12      0.9924732 0.9928571 0.8941176
## 13      0.9904158 0.9894089 0.8941176
## 14      0.9922704 0.9928571 0.9058824
## 15      0.9916691 0.9894089 0.9000000
## 16      0.9924804 0.9929803 0.9058824
## 17      0.9941104 0.9929803 0.8941176
## 18      0.9943060 0.9929803 0.8941176
## 19      0.9945161 0.9929803 0.8941176
## 20      0.9932918 0.9929803 0.8882353
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was ncomp = 19.
testResults$PLS <- predict(pls_model, test[, -1])
```

```
# ROC curve for PLS
pls_roc <- roc(response = pls_model$pred$obs,
               predictor = pls_model$pred$M,
               levels = rev(levels(pls_model$pred$obs)))
```

```
## Setting direction: controls > cases
```

```
plot(pls_roc, legaces.axes = TRUE)
```



```
# Confusion Matrix
confusionMatrix(testResults$PLS, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction  B  M
```

```
##           B 71  3
```

```
##           M  0 39
```

```
##
```

```
##           Accuracy : 0.9735
```

```
##           95% CI : (0.9244, 0.9945)
```

```
##           No Information Rate : 0.6283
```

```
##           P-Value [Acc > NIR] : <2e-16
```

```
##
```

```
##           Kappa : 0.9423
```

```
##
```

```
##           McNemar's Test P-Value : 0.2482
```

```
##
```

```
##           Sensitivity : 0.9286
```

```
##           Specificity : 1.0000
```

```

##          Pos Pred Value : 1.0000
##          Neg Pred Value : 0.9595
##          Prevalence : 0.3717
##          Detection Rate : 0.3451
##          Detection Prevalence : 0.3451
##          Balanced Accuracy : 0.9643
##
##          'Positive' Class : M
##

# MDA
mdaGrid <- expand.grid(subclasses = 1:3)

set.seed(123)
mda_model <- train(x = train[, -1],
                  y = train$diagnosis,
                  method = "mda",
                  tuneGrid = mdaGrid,
                  preProcess = c("center", "scale"),
                  metric = "ROC",
                  trControl = ctrl)
mda_model

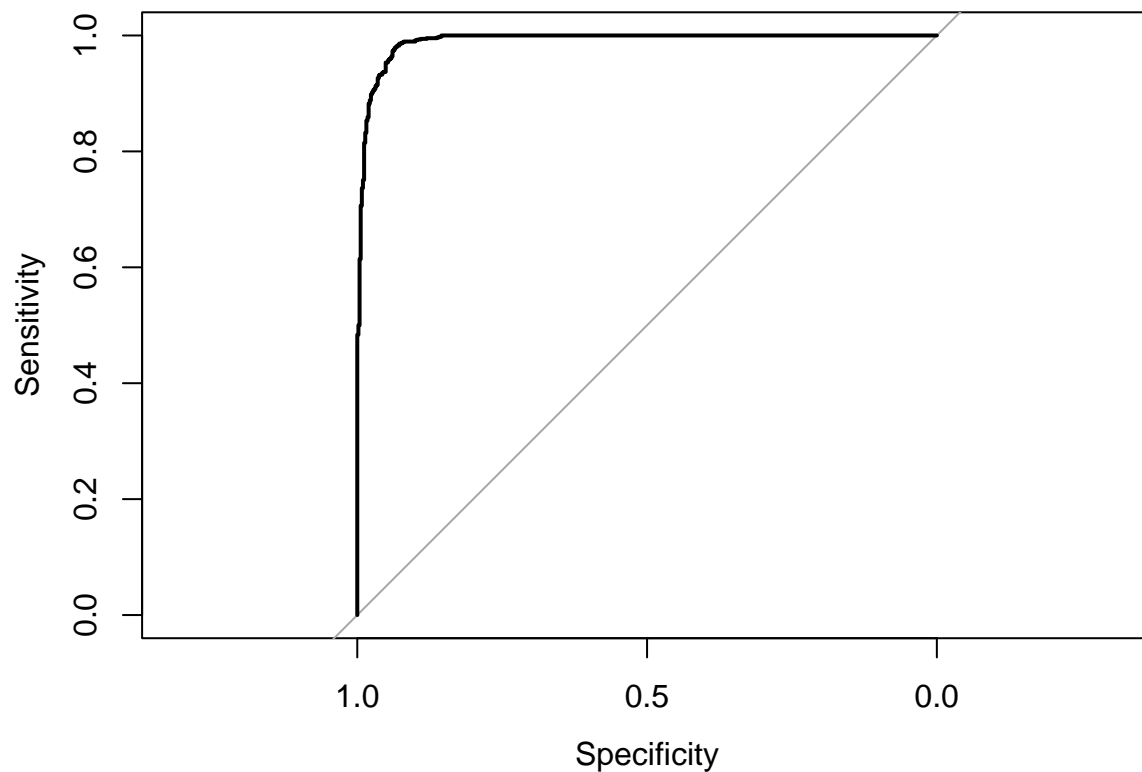
## Mixture Discriminant Analysis
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results across tuning parameters:
##
## subclasses ROC Sens Spec
## 1 0.9930745 0.9929803 0.8941176
## 2 0.9895972 0.9929803 0.9000000
## 3 0.9949073 0.9894089 0.9058824
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was subclasses = 3.

testResults$MDA <- predict(mda_model, test[, -1])

# ROC curve for MDA
mda_roc <- roc(response = mda_model$pred$obs,
              predictor = mda_model$pred$M,
              levels = rev(levels(mda_model$pred$obs)))

## Setting direction: controls > cases
plot(mda_roc, legaces.axes = TRUE)

```



```
# Confusion Matrix
confusionMatrix(testResults$MDA, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##      B 70  1
##      M  1 41
##
##           Accuracy : 0.9823
##           95% CI : (0.9375, 0.9978)
##      No Information Rate : 0.6283
##      P-Value [Acc > NIR] : <2e-16
##
##           Kappa : 0.9621
##
##  McNemar's Test P-Value : 1
##
##           Sensitivity : 0.9762
##           Specificity : 0.9859
##      Pos Pred Value : 0.9762
##      Neg Pred Value : 0.9859
##           Prevalence : 0.3717
##      Detection Rate : 0.3628
##      Detection Prevalence : 0.3717
##      Balanced Accuracy : 0.9811
##
##           'Positive' Class : M
```

```
##
# Decision Trees
set.seed(123)
rpart_model <- train(x = train[, -1],
                     y = train$diagnosis,
                     method = "rpart",
                     tuneLength = 30,
                     preProcess = c("center", "scale"),
                     metric = "ROC",
                     trControl = ctrl)
rpart_model

## CART
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results across tuning parameters:
##
##   cp          ROC      Sens      Spec
## 0.00000000 0.9395791 0.9301724 0.8882353
## 0.02778905 0.9162743 0.9334975 0.8764706
## 0.05557809 0.9166872 0.9369458 0.8941176
## 0.08336714 0.9143763 0.9405172 0.8882353
## 0.11115619 0.9143763 0.9405172 0.8882353
## 0.13894523 0.9143763 0.9405172 0.8882353
## 0.16673428 0.9143763 0.9405172 0.8882353
## 0.19452333 0.9143763 0.9405172 0.8882353
## 0.22231237 0.9143763 0.9405172 0.8882353
## 0.25010142 0.9143763 0.9405172 0.8882353
## 0.27789047 0.9143763 0.9405172 0.8882353
## 0.30567951 0.9143763 0.9405172 0.8882353
## 0.33346856 0.9143763 0.9405172 0.8882353
## 0.36125761 0.9143763 0.9405172 0.8882353
## 0.38904665 0.9143763 0.9405172 0.8882353
## 0.41683570 0.9143763 0.9405172 0.8882353
## 0.44462475 0.9143763 0.9405172 0.8882353
## 0.47241379 0.9143763 0.9405172 0.8882353
## 0.50020284 0.9143763 0.9405172 0.8882353
## 0.52799189 0.9143763 0.9405172 0.8882353
## 0.55578093 0.9143763 0.9405172 0.8882353
## 0.58356998 0.9143763 0.9405172 0.8882353
## 0.61135903 0.9143763 0.9405172 0.8882353
## 0.63914807 0.9143763 0.9405172 0.8882353
## 0.66693712 0.9143763 0.9405172 0.8882353
## 0.69472617 0.9143763 0.9405172 0.8882353
## 0.72251521 0.9143763 0.9405172 0.8882353
## 0.75030426 0.9143763 0.9405172 0.8882353
## 0.77809331 0.9143763 0.9405172 0.8882353
## 0.80588235 0.6529774 0.9647783 0.3411765
```

```
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was cp = 0.
```

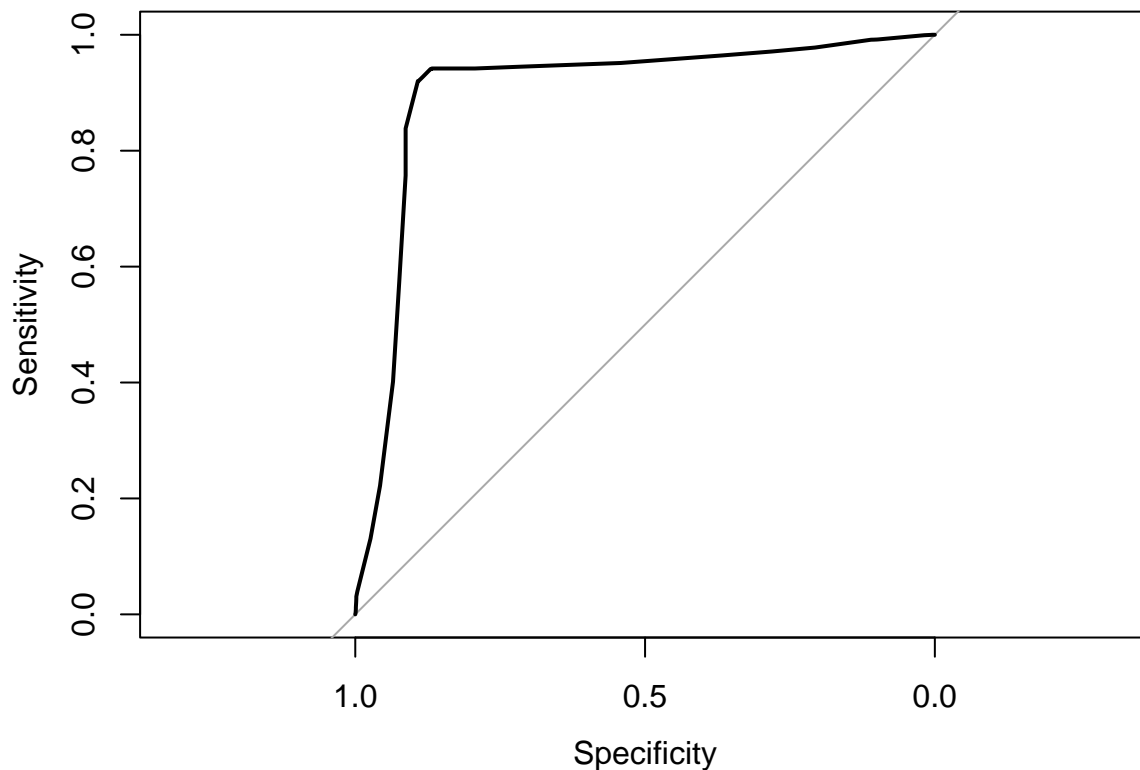
```
testResults$DecisionTree <- predict(rpart_model, test[, -1])
```

```
# ROC curve for decision trees
```

```
rpart_roc <- roc(response = rpart_model$pred$obs,
  predictor = rpart_model$pred$M,
  levels = rev(levels(rpart_model$pred$obs)))
```

```
## Setting direction: controls > cases
```

```
plot(rpart_roc, legaces.axes = TRUE)
```



```
# Confusion Matrix
```

```
confusionMatrix(testResults$DecisionTree, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction  B  M
```

```
##           B 64  5
```

```
##           M  7 37
```

```
##
```

```
##           Accuracy : 0.8938
```

```
##           95% CI : (0.8218, 0.9439)
```

```
##           No Information Rate : 0.6283
```

```
##           P-Value [Acc > NIR] : 1.762e-10
```

```
##
```

```
##           Kappa : 0.7748
```

```
##
## McNemar's Test P-Value : 0.7728
##
##      Sensitivity : 0.8810
##      Specificity : 0.9014
##      Pos Pred Value : 0.8409
##      Neg Pred Value : 0.9275
##      Prevalence : 0.3717
##      Detection Rate : 0.3274
##      Detection Prevalence : 0.3894
##      Balanced Accuracy : 0.8912
##
```

```
##      'Positive' Class : M
##
```

```
# Random Forest
```

```
mtryValues <- seq(1, 10, 1)
rfGrid <- data.frame(mtry = mtryValues)

set.seed(123)
rf_model <- train(x = train[, -1],
                  y = train$diagnosis,
                  method = "rf",
                  ntree = 1000,
                  preProcess = c("center", "scale"),
                  tuneGrid = rfGrid,
                  metric = "ROC",
                  trControl = ctrl)

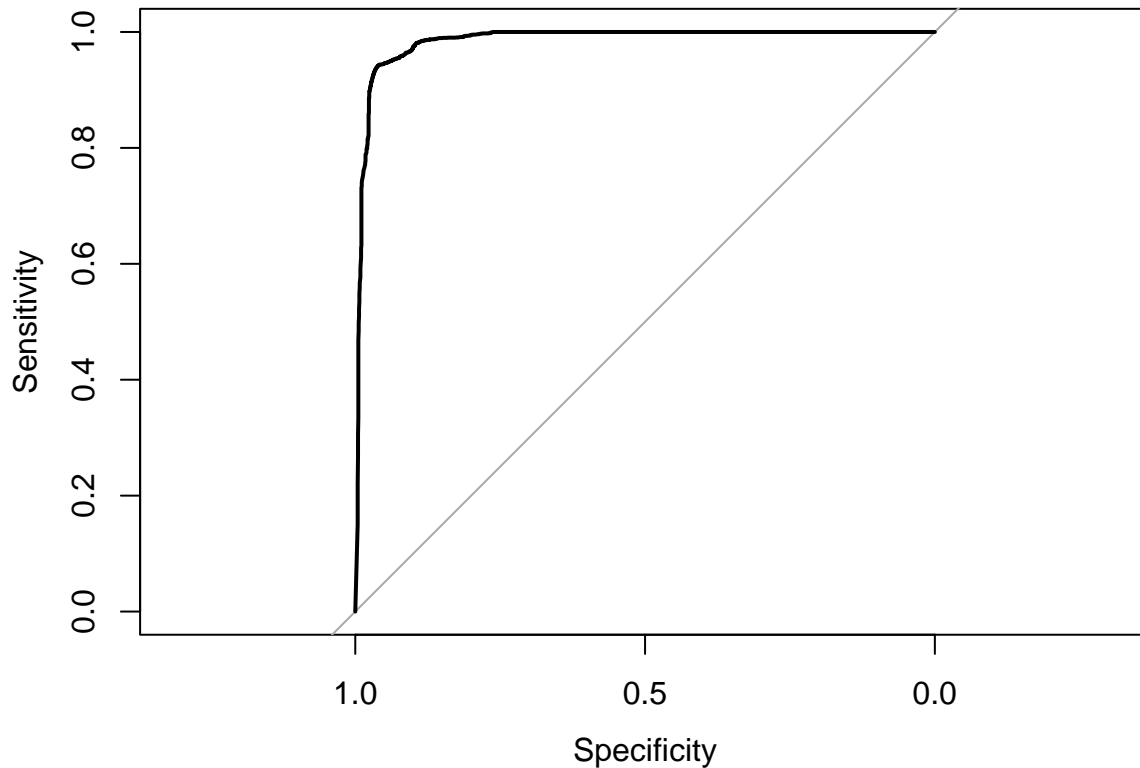
rf_model
```

```
## Random Forest
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results across tuning parameters:
##
##  mtry  ROC      Sens      Spec
##  1     0.9881339 0.9580049 0.9235294
##  2     0.9869168 0.9545567 0.9235294
##  3     0.9886410 0.9580049 0.9235294
##  4     0.9867068 0.9509852 0.9294118
##  5     0.9872139 0.9545567 0.9176471
##  6     0.9872102 0.9545567 0.9294118
##  7     0.9869168 0.9545567 0.9294118
##  8     0.9873153 0.9580049 0.9235294
##  9     0.9874167 0.9545567 0.9235294
## 10     0.9872139 0.9511084 0.9176471
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 3.
```

```
testResults$RF <- predict(rf_model, test[, -1])

# ROC curve for random forest
rf_roc <- roc(response = rf_model$pred$obs,
              predictor = rf_model$pred$M,
              levels = rev(levels(rf_model$pred$obs)))

## Setting direction: controls > cases
plot(rf_roc, legaces.axes = TRUE)
```



```
# Confusion Matrix
confusionMatrix(testResults$RF, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##           B 68  3
##           M  3 39
##
##               Accuracy : 0.9469
##               95% CI : (0.888, 0.9803)
##       No Information Rate : 0.6283
##       P-Value [Acc > NIR] : 1.866e-15
##
##               Kappa : 0.8863
##
##       McNemar's Test P-Value : 1
##
```



```
##          Sensitivity : 0.9286
##          Specificity : 0.9577
##          Pos Pred Value : 0.9286
##          Neg Pred Value : 0.9577
##          Prevalence : 0.3717
##          Detection Rate : 0.3451
##          Detection Prevalence : 0.3717
##          Balanced Accuracy : 0.9432
##
##          'Positive' Class : M
##
```

```
# Boosted Trees
gbmGrid <- expand.grid(interaction.depth = c(1, 3, 5, 7, 9),
                      n.trees = (1:20)*100,
                      shrinkage = c(.01, .1),
                      n.minobsinnode = 5)

set.seed(123)
gbm_model <- train(x = train[, -1],
                  y = train$diagnosis,
                  method = "gbm",
                  preProcess = c("center", "scale"),
                  tuneGrid = gbmGrid,
                  verbose = FALSE,
                  metric = "ROC",
                  trControl = ctrl)

gbm_model
```

```
## Stochastic Gradient Boosting
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results across tuning parameters:
##
## shrinkage interaction.depth n.trees ROC Sens Spec
## 0.01 1 100 0.9782599 0.9545567 0.8529412
## 0.01 1 200 0.9838670 0.9509852 0.8705882
## 0.01 1 300 0.9859461 0.9509852 0.8823529
## 0.01 1 400 0.9873660 0.9651478 0.9000000
## 0.01 1 500 0.9877644 0.9651478 0.9176471
## 0.01 1 600 0.9889815 0.9615764 0.9176471
## 0.01 1 700 0.9891915 0.9651478 0.9176471
## 0.01 1 800 0.9898073 0.9615764 0.9176471
## 0.01 1 900 0.9904158 0.9615764 0.9176471
## 0.01 1 1000 0.9906114 0.9615764 0.9235294
## 0.01 1 1100 0.9904086 0.9615764 0.9294118
## 0.01 1 1200 0.9908143 0.9650246 0.9235294
## 0.01 1 1300 0.9906042 0.9650246 0.9294118
## 0.01 1 1400 0.9906042 0.9650246 0.9352941
```

##	0.01	1	1500	0.9901912	0.9650246	0.9352941
##	0.01	1	1600	0.9901912	0.9650246	0.9352941
##	0.01	1	1700	0.9908070	0.9684729	0.9352941
##	0.01	1	1800	0.9906042	0.9684729	0.9352941
##	0.01	1	1900	0.9910171	0.9684729	0.9352941
##	0.01	1	2000	0.9914155	0.9684729	0.9352941
##	0.01	3	100	0.9869023	0.9650246	0.8882353
##	0.01	3	200	0.9889597	0.9615764	0.9117647
##	0.01	3	300	0.9899957	0.9650246	0.9235294
##	0.01	3	400	0.9910171	0.9614532	0.9294118
##	0.01	3	500	0.9907998	0.9578818	0.9294118
##	0.01	3	600	0.9910026	0.9578818	0.9352941
##	0.01	3	700	0.9914155	0.9578818	0.9411765
##	0.01	3	800	0.9916256	0.9614532	0.9411765
##	0.01	3	900	0.9920313	0.9650246	0.9411765
##	0.01	3	1000	0.9922414	0.9650246	0.9411765
##	0.01	3	1100	0.9926543	0.9650246	0.9411765
##	0.01	3	1200	0.9928499	0.9650246	0.9411765
##	0.01	3	1300	0.9932556	0.9650246	0.9411765
##	0.01	3	1400	0.9932483	0.9684729	0.9411765
##	0.01	3	1500	0.9930382	0.9684729	0.9411765
##	0.01	3	1600	0.9928354	0.9684729	0.9411765
##	0.01	3	1700	0.9930455	0.9684729	0.9411765
##	0.01	3	1800	0.9932483	0.9684729	0.9352941
##	0.01	3	1900	0.9932483	0.9684729	0.9352941
##	0.01	3	2000	0.9932483	0.9684729	0.9352941
##	0.01	5	100	0.9840771	0.9721675	0.9058824
##	0.01	5	200	0.9883512	0.9650246	0.9235294
##	0.01	5	300	0.9895827	0.9614532	0.9294118
##	0.01	5	400	0.9908070	0.9650246	0.9294118
##	0.01	5	500	0.9912127	0.9684729	0.9411765
##	0.01	5	600	0.9922414	0.9614532	0.9352941
##	0.01	5	700	0.9922414	0.9650246	0.9352941
##	0.01	5	800	0.9926471	0.9650246	0.9411765
##	0.01	5	900	0.9928499	0.9650246	0.9411765
##	0.01	5	1000	0.9926471	0.9650246	0.9411765
##	0.01	5	1100	0.9926471	0.9650246	0.9411765
##	0.01	5	1200	0.9928499	0.9615764	0.9352941
##	0.01	5	1300	0.9928499	0.9615764	0.9352941
##	0.01	5	1400	0.9930455	0.9615764	0.9352941
##	0.01	5	1500	0.9932483	0.9615764	0.9352941
##	0.01	5	1600	0.9932483	0.9684729	0.9352941
##	0.01	5	1700	0.9934512	0.9684729	0.9352941
##	0.01	5	1800	0.9930455	0.9684729	0.9352941
##	0.01	5	1900	0.9932483	0.9684729	0.9352941
##	0.01	5	2000	0.9934512	0.9684729	0.9352941
##	0.01	7	100	0.9859751	0.9685961	0.9058824
##	0.01	7	200	0.9895465	0.9685961	0.9235294
##	0.01	7	300	0.9915966	0.9685961	0.9352941
##	0.01	7	400	0.9915966	0.9614532	0.9294118
##	0.01	7	500	0.9922124	0.9614532	0.9294118
##	0.01	7	600	0.9920023	0.9614532	0.9352941
##	0.01	7	700	0.9926253	0.9614532	0.9411765
##	0.01	7	800	0.9924225	0.9650246	0.9235294

##	0.01	7	900	0.9926326	0.9615764	0.9294118
##	0.01	7	1000	0.9926326	0.9615764	0.9294118
##	0.01	7	1100	0.9926326	0.9615764	0.9294118
##	0.01	7	1200	0.9930382	0.9615764	0.9352941
##	0.01	7	1300	0.9930382	0.9615764	0.9411765
##	0.01	7	1400	0.9934512	0.9615764	0.9411765
##	0.01	7	1500	0.9936540	0.9615764	0.9411765
##	0.01	7	1600	0.9936540	0.9650246	0.9411765
##	0.01	7	1700	0.9934512	0.9650246	0.9411765
##	0.01	7	1800	0.9934512	0.9650246	0.9411765
##	0.01	7	1900	0.9934512	0.9684729	0.9411765
##	0.01	7	2000	0.9932483	0.9684729	0.9411765
##	0.01	9	100	0.9881121	0.9685961	0.9000000
##	0.01	9	200	0.9889597	0.9651478	0.9235294
##	0.01	9	300	0.9916111	0.9650246	0.9294118
##	0.01	9	400	0.9916039	0.9650246	0.9294118
##	0.01	9	500	0.9913938	0.9650246	0.9294118
##	0.01	9	600	0.9915966	0.9614532	0.9294118
##	0.01	9	700	0.9922124	0.9580049	0.9294118
##	0.01	9	800	0.9917995	0.9580049	0.9294118
##	0.01	9	900	0.9922052	0.9580049	0.9294118
##	0.01	9	1000	0.9921979	0.9615764	0.9352941
##	0.01	9	1100	0.9921979	0.9615764	0.9352941
##	0.01	9	1200	0.9930310	0.9615764	0.9352941
##	0.01	9	1300	0.9928209	0.9615764	0.9294118
##	0.01	9	1400	0.9926181	0.9615764	0.9352941
##	0.01	9	1500	0.9928209	0.9615764	0.9352941
##	0.01	9	1600	0.9930238	0.9615764	0.9352941
##	0.01	9	1700	0.9928209	0.9650246	0.9352941
##	0.01	9	1800	0.9928209	0.9650246	0.9294118
##	0.01	9	1900	0.9930310	0.9650246	0.9352941
##	0.01	9	2000	0.9924152	0.9684729	0.9352941
##	0.10	1	100	0.9895827	0.9615764	0.9352941
##	0.10	1	200	0.9895755	0.9615764	0.9411765
##	0.10	1	300	0.9920385	0.9719212	0.9411765
##	0.10	1	400	0.9930527	0.9719212	0.9411765
##	0.10	1	500	0.9932628	0.9719212	0.9352941
##	0.10	1	600	0.9924442	0.9753695	0.9294118
##	0.10	1	700	0.9926543	0.9753695	0.9294118
##	0.10	1	800	0.9922341	0.9753695	0.9294118
##	0.10	1	900	0.9918285	0.9753695	0.9294118
##	0.10	1	1000	0.9922341	0.9753695	0.9294118
##	0.10	1	1100	0.9924370	0.9753695	0.9294118
##	0.10	1	1200	0.9922414	0.9753695	0.9294118
##	0.10	1	1300	0.9924442	0.9753695	0.9294118
##	0.10	1	1400	0.9920241	0.9753695	0.9294118
##	0.10	1	1500	0.9924442	0.9753695	0.9352941
##	0.10	1	1600	0.9920313	0.9753695	0.9411765
##	0.10	1	1700	0.9916329	0.9753695	0.9352941
##	0.10	1	1800	0.9918357	0.9753695	0.9352941
##	0.10	1	1900	0.9922414	0.9753695	0.9352941
##	0.10	1	2000	0.9920313	0.9753695	0.9352941
##	0.10	3	100	0.9924152	0.9719212	0.9352941
##	0.10	3	200	0.9924225	0.9720443	0.9352941

##	0.10	3	300	0.9930382	0.9754926	0.9294118
##	0.10	3	400	0.9934512	0.9754926	0.9352941
##	0.10	3	500	0.9932338	0.9719212	0.9294118
##	0.10	3	600	0.9930310	0.9754926	0.9352941
##	0.10	3	700	0.9928282	0.9719212	0.9352941
##	0.10	3	800	0.9926326	0.9754926	0.9411765
##	0.10	3	900	0.9936540	0.9719212	0.9411765
##	0.10	3	1000	0.9936540	0.9719212	0.9411765
##	0.10	3	1100	0.9932411	0.9684729	0.9352941
##	0.10	3	1200	0.9930382	0.9684729	0.9352941
##	0.10	3	1300	0.9926326	0.9684729	0.9352941
##	0.10	3	1400	0.9926326	0.9684729	0.9352941
##	0.10	3	1500	0.9926326	0.9684729	0.9352941
##	0.10	3	1600	0.9926326	0.9684729	0.9352941
##	0.10	3	1700	0.9924225	0.9684729	0.9352941
##	0.10	3	1800	0.9922124	0.9684729	0.9352941
##	0.10	3	1900	0.9903868	0.9684729	0.9411765
##	0.10	3	2000	0.9908070	0.9684729	0.9352941
##	0.10	5	100	0.9901478	0.9614532	0.9411765
##	0.10	5	200	0.9916039	0.9719212	0.9235294
##	0.10	5	300	0.9914010	0.9684729	0.9235294
##	0.10	5	400	0.9924152	0.9684729	0.9294118
##	0.10	5	500	0.9926108	0.9684729	0.9294118
##	0.10	5	600	0.9924080	0.9684729	0.9294118
##	0.10	5	700	0.9928209	0.9684729	0.9294118
##	0.10	5	800	0.9928137	0.9684729	0.9294118
##	0.10	5	900	0.9928137	0.9684729	0.9352941
##	0.10	5	1000	0.9928137	0.9684729	0.9411765
##	0.10	5	1100	0.9928137	0.9719212	0.9352941
##	0.10	5	1200	0.9929151	0.9719212	0.9294118
##	0.10	5	1300	0.9908867	0.9719212	0.9352941
##	0.10	5	1400	0.9908867	0.9719212	0.9352941
##	0.10	5	1500	0.9912924	0.9719212	0.9411765
##	0.10	5	1600	0.9889597	0.9719212	0.9411765
##	0.10	5	1700	0.9915966	0.9684729	0.9411765
##	0.10	5	1800	0.9915025	0.9684729	0.9470588
##	0.10	5	1900	0.9915025	0.9684729	0.9411765
##	0.10	5	2000	0.9917270	0.9684729	0.9411765
##	0.10	7	100	0.9909591	0.9580049	0.9235294
##	0.10	7	200	0.9917488	0.9615764	0.9235294
##	0.10	7	300	0.9921689	0.9719212	0.9235294
##	0.10	7	400	0.9923790	0.9719212	0.9235294
##	0.10	7	500	0.9926036	0.9719212	0.9176471
##	0.10	7	600	0.9928137	0.9719212	0.9176471
##	0.10	7	700	0.9922052	0.9719212	0.9176471
##	0.10	7	800	0.9930310	0.9719212	0.9176471
##	0.10	7	900	0.9931324	0.9719212	0.9235294
##	0.10	7	1000	0.9909954	0.9719212	0.9235294
##	0.10	7	1100	0.9889742	0.9719212	0.9235294
##	0.10	7	1200	0.9889815	0.9719212	0.9235294
##	0.10	7	1300	0.9893871	0.9719212	0.9235294
##	0.10	7	1400	0.9916256	0.9719212	0.9235294
##	0.10	7	1500	0.9915314	0.9754926	0.9235294
##	0.10	7	1600	0.9917415	0.9720443	0.9294118

```

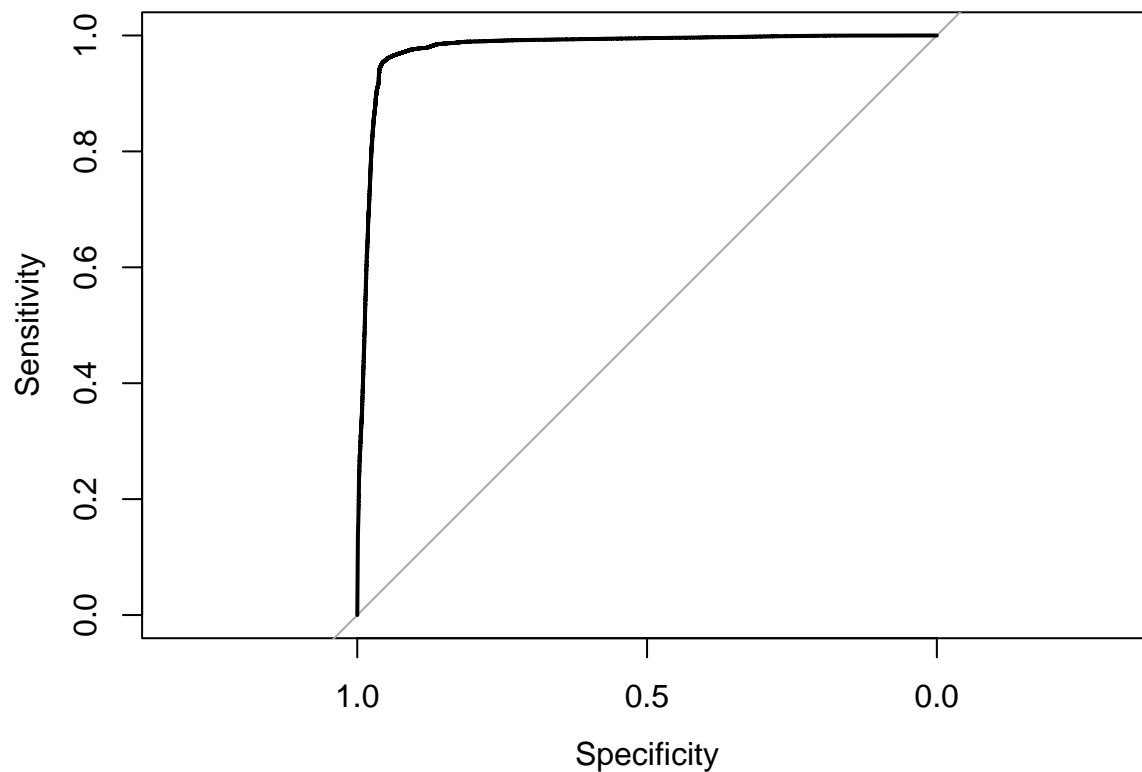
## 0.10      7      1700    0.9907346 0.9685961 0.9352941
## 0.10      7      1800    0.9930672 0.9651478 0.9470588
## 0.10      7      1900    0.9926615 0.9651478 0.9470588
## 0.10      7      2000    0.9924587 0.9616995 0.9470588
## 0.10      9       100    0.9901550 0.9650246 0.9235294
## 0.10      9       200    0.9920023 0.9650246 0.9411765
## 0.10      9       300    0.9928282 0.9650246 0.9411765
## 0.10      9       400    0.9932411 0.9685961 0.9470588
## 0.10      9       500    0.9930455 0.9720443 0.9411765
## 0.10      9       600    0.9930600 0.9720443 0.9529412
## 0.10      9       700    0.9930672 0.9720443 0.9411765
## 0.10      9       800    0.9923573 0.9720443 0.9352941
## 0.10      9       900    0.9909374 0.9720443 0.9352941
## 0.10      9      1000    0.9892133 0.9720443 0.9352941
## 0.10      9      1100    0.9890032 0.9720443 0.9411765
## 0.10      9      1200    0.9894089 0.9685961 0.9411765
## 0.10      9      1300    0.9890104 0.9687192 0.9411765
## 0.10      9      1400    0.9885975 0.9651478 0.9470588
## 0.10      9      1500    0.9906259 0.9651478 0.9529412
## 0.10      9      1600    0.9911475 0.9651478 0.9588235
## 0.10      9      1700    0.9904303 0.9651478 0.9588235
## 0.10      9      1800    0.9908432 0.9616995 0.9647059
## 0.10      9      1900    0.9910533 0.9616995 0.9647059
## 0.10      9      2000    0.9906476 0.9581281 0.9647059
##
## Tuning parameter 'n.minobsinnode' was held constant at a value of 5
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were n.trees = 900, interaction.depth =
## 3, shrinkage = 0.1 and n.minobsinnode = 5.

testResults$BoostedTree <- predict(gbm_model, test[, -1])

# ROC curve for boosted trees
gbm_roc <- roc(response = gbm_model$pred$obs,
               predictor = gbm_model$pred$M,
               levels = rev(levels(gbm_model$pred$obs)))

## Setting direction: controls > cases
plot(gbm_roc, legaxes.axes = TRUE)

```



```
# Confusion Matrix
confusionMatrix(testResults$BoostedTree, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction  B  M
##           B 71  1
##           M  0 41
##
##           Accuracy : 0.9912
##           95% CI : (0.9517, 0.9998)
##           No Information Rate : 0.6283
##           P-Value [Acc > NIR] : <2e-16
##
##           Kappa : 0.981
##
## Mcnemar's Test P-Value : 1
##
##           Sensitivity : 0.9762
##           Specificity : 1.0000
##           Pos Pred Value : 1.0000
##           Neg Pred Value : 0.9861
##           Prevalence : 0.3717
##           Detection Rate : 0.3628
##           Detection Prevalence : 0.3628
##           Balanced Accuracy : 0.9881
##
##           'Positive' Class : M
```

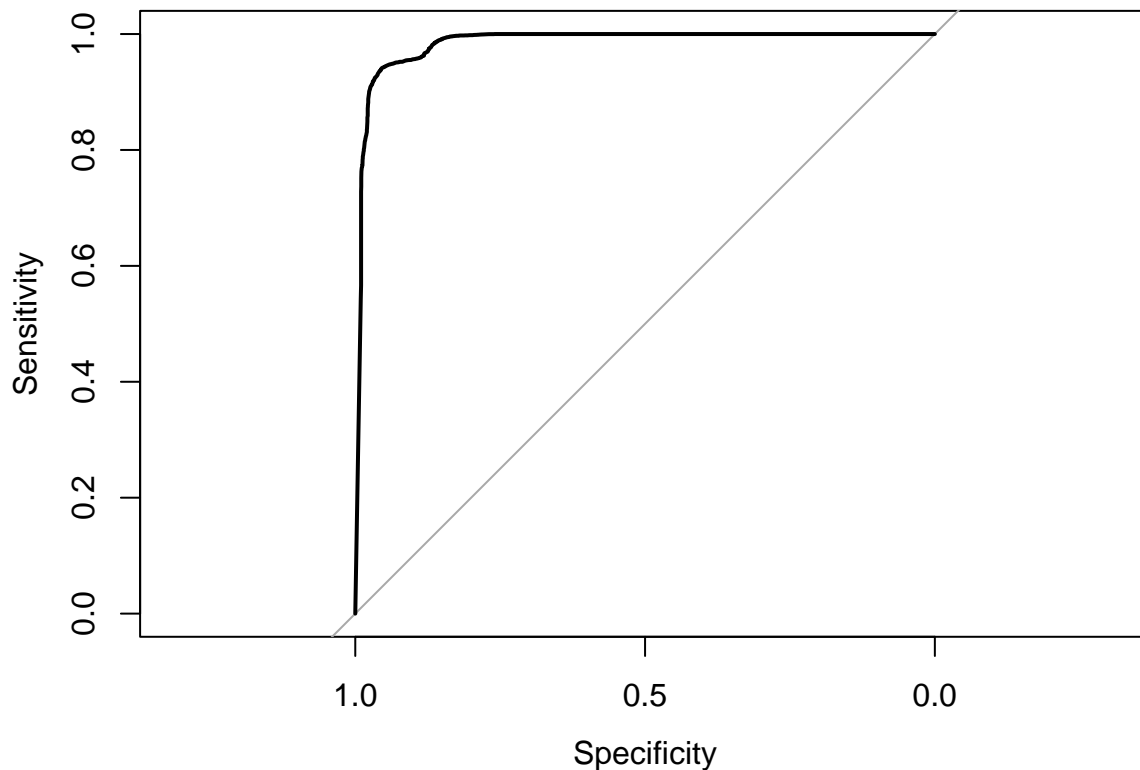
```
##
# KNN
set.seed(123)
knn_model <- train(x = train[, -1],
                   y = train$diagnosis,
                   method = "knn",
                   preProcess = c("center", "scale"),
                   tuneLength = 20,
                   metric = "ROC",
                   trControl = ctrl)
knn_model

## k-Nearest Neighbors
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results across tuning parameters:
##
##  k   ROC      Sens      Spec
##  5  0.9867611  0.9791872  0.9058824
##  7  0.9863590  0.9720443  0.9235294
##  9  0.9854390  0.9651478  0.9058824
## 11  0.9847146  0.9687192  0.8941176
## 13  0.9840988  0.9651478  0.8882353
## 15  0.9858881  0.9685961  0.8941176
## 17  0.9854970  0.9582512  0.8941176
## 19  0.9850949  0.9616995  0.8941176
## 21  0.9852941  0.9651478  0.8882353
## 23  0.9882353  0.9650246  0.8764706
## 25  0.9872139  0.9650246  0.8705882
## 27  0.9868045  0.9546798  0.8705882
## 29  0.9872102  0.9546798  0.8647059
## 31  0.9871124  0.9581281  0.8647059
## 33  0.9868118  0.9616995  0.8647059
## 35  0.9865003  0.9616995  0.8647059
## 37  0.9857759  0.9616995  0.8647059
## 39  0.9853702  0.9651478  0.8647059
## 41  0.9875072  0.9685961  0.8647059
## 43  0.9876159  0.9685961  0.8647059
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was k = 23.
testResults$KNN <- predict(knn_model, test[, -1])

# ROC curve for KNN
knn_roc <- roc(response = knn_model$pred$obs,
               predictor = knn_model$pred$M,
               levels = rev(levels(knn_model$pred$obs)))
```

```
## Setting direction: controls > cases
```

```
plot(knn_roc, legaces.axes = TRUE)
```



```
# Confusion Matrix
```

```
confusionMatrix(testResults$KNN, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction  B  M
```

```
##           B 69  2
```

```
##           M  2 40
```

```
##
```

```
##           Accuracy : 0.9646
```

```
##           95% CI : (0.9118, 0.9903)
```

```
##           No Information Rate : 0.6283
```

```
##           P-Value [Acc > NIR] : <2e-16
```

```
##
```

```
##           Kappa : 0.9242
```

```
##
```

```
##           McNemar's Test P-Value : 1
```

```
##
```

```
##           Sensitivity : 0.9524
```

```
##           Specificity : 0.9718
```

```
##           Pos Pred Value : 0.9524
```

```
##           Neg Pred Value : 0.9718
```

```
##           Prevalence : 0.3717
```

```
##           Detection Rate : 0.3540
```

```
##           Detection Prevalence : 0.3717
```



```

##          Balanced Accuracy : 0.9621
##
##          'Positive' Class : M
##

# Neural Network Model
nnetGrid <- expand.grid(size = 1:2, decay = c(0, .1, .2, .3, .4, .5, 1))

set.seed(123)
nnet_model <- train(x = train[, -1],
                    y = train$diagnosis,
                    method = "nnet",
                    preProcess = c("center", "scale"),
                    tuneGrid = nnetGrid,
                    metric = "ROC",
                    linout = FALSE,
                    trace = FALSE,
                    maxit = 1000,
                    trControl = ctrl)

nnet_model

## Neural Network
##
## 456 samples
## 26 predictor
## 2 classes: 'B', 'M'
##
## Pre-processing: centered (26), scaled (26)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 410, 410, 411, 411, 410, 411, ...
## Resampling results across tuning parameters:
##
##  size  decay  ROC          Sens          Spec
##  1      0.0   0.9691937  0.9757389  0.9470588
##  1      0.1   0.9930310  0.9753695  0.9588235
##  1      0.2   0.9944726  0.9823892  0.9529412
##  1      0.3   0.9948855  0.9823892  0.9470588
##  1      0.4   0.9953057  0.9858374  0.9470588
##  1      0.5   0.9953057  0.9858374  0.9470588
##  1      1.0   0.9951101  0.9894089  0.9470588
##  2      0.0   0.9636048  0.9578818  0.9529412
##  2      0.1   0.9938569  0.9754926  0.9529412
##  2      0.2   0.9936468  0.9753695  0.9470588
##  2      0.3   0.9951029  0.9788177  0.9529412
##  2      0.4   0.9947044  0.9823892  0.9470588
##  2      0.5   0.9942915  0.9823892  0.9470588
##  2      1.0   0.9951101  0.9859606  0.9470588
##
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were size = 1 and decay = 0.5.

testResults$NNet <- predict(nnet_model, test[, -1])

# ROC curve for neural network
nnet_roc <- roc(response = nnet_model$pred$obs,

```

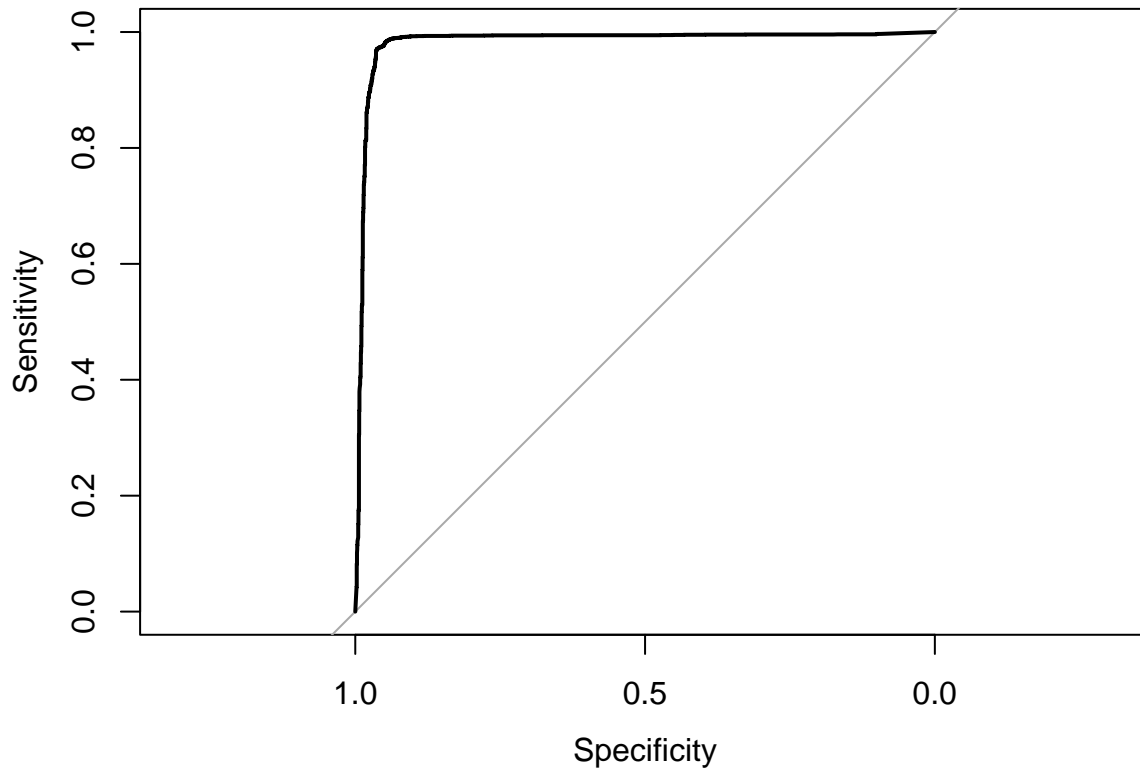
```

predictor = nnet_model$pred$M,
levels = rev(levels(nnet_model$pred$obs)))

```

```
## Setting direction: controls > cases
```

```
plot(nnet_roc, legaces.axes = TRUE)
```



```
# Confusion Matrix
```

```
confusionMatrix(testResults$NNet, testResults$obs, positive = "M")
```

```
## Confusion Matrix and Statistics
```

```
##
```

```
##           Reference
```

```
## Prediction  B  M
```

```
##           B 69  0
```

```
##           M  2 42
```

```
##
```

```
##           Accuracy : 0.9823
```

```
##           95% CI : (0.9375, 0.9978)
```

```
## No Information Rate : 0.6283
```

```
## P-Value [Acc > NIR] : <2e-16
```

```
##
```

```
##           Kappa : 0.9625
```

```
##
```

```
## McNemar's Test P-Value : 0.4795
```

```
##
```

```
##           Sensitivity : 1.0000
```

```
##           Specificity : 0.9718
```

```
## Pos Pred Value : 0.9545
```

```
## Neg Pred Value : 1.0000
```

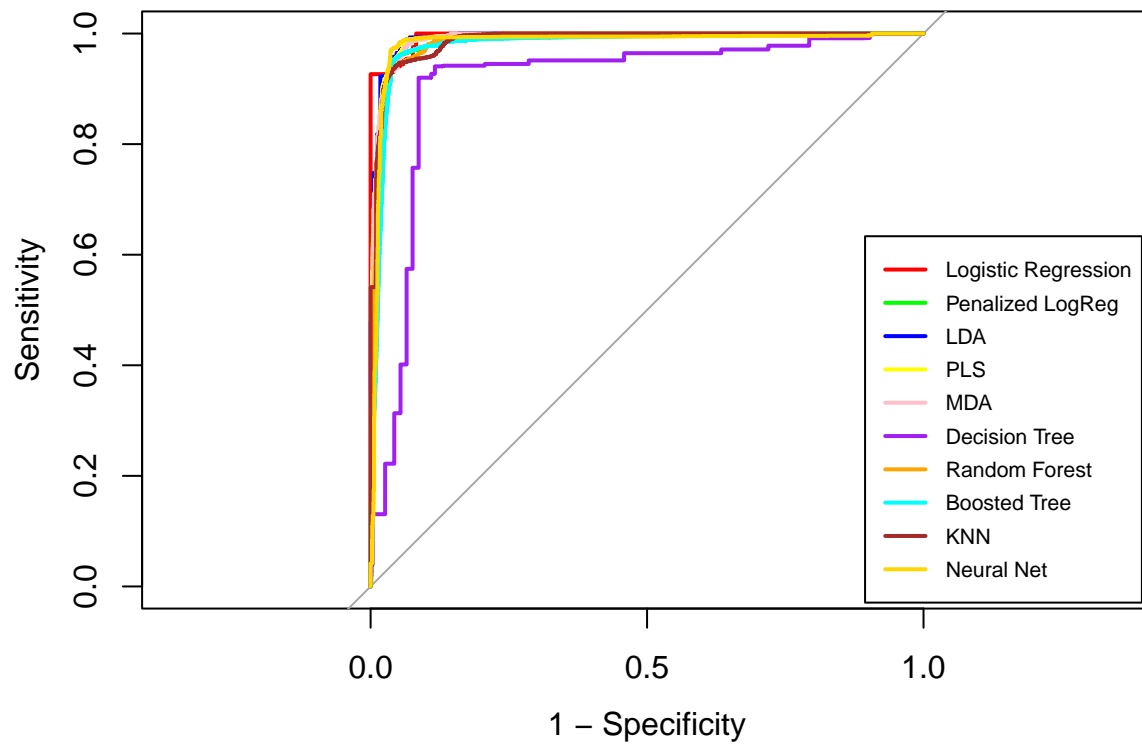
```
##           Prevalence : 0.3717
##       Detection Rate : 0.3717
## Detection Prevalence : 0.3894
##       Balanced Accuracy : 0.9859
##
##       'Positive' Class : M
##
```

Compare Models

```
par(oma = c(0, 0, .75, 0))

plot(lr_roc, type = "s", col = 'red', legacy.axes = TRUE, lwd = 2)
plot(plr_roc, type = "s", add = TRUE, col = 'green', legacy.axes = TRUE, lwd = 2)
plot(lda_roc, type = "s", add = TRUE, col = 'blue', legacy.axes = TRUE, lwd = 2)
plot(pls_roc, type = "s", add = TRUE, col = 'yellow', legacy.axes = TRUE, lwd = 2)
plot(mda_roc, type = "s", add = TRUE, col = 'pink', legacy.axes = TRUE, lwd = 2)
plot(rpart_roc, type = "s", add = TRUE, col = 'purple', legacy.axes = TRUE, lwd = 2)
plot(rf_roc, type = "s", add = TRUE, col = 'orange', legacy.axes = TRUE, lwd = 2)
plot(gbm_roc, type = "s", add = TRUE, col = 'cyan', legacy.axes = TRUE, lwd = 2)
plot(knn_roc, type = "s", add = TRUE, col = 'brown', legacy.axes = TRUE, lwd = 2)
plot(nnet_roc, type = "s", add = TRUE, col = 'gold', legacy.axes = TRUE, lwd = 2)
legend("bottomright",
      legend = c("Logistic Regression", "Penalized LogReg", "LDA", "PLS",
                  "MDA", "Decision Tree", "Random Forest", "Boosted Tree",
                  "KNN", "Neural Net"),
      col = c("red", "green", "blue", "yellow", "pink",
              "purple", "orange", "cyan", "brown", "gold"),
      lwd = 2,
      cex = 0.7,
      inset = 0.01)
title(main = "Comparison of ROC Curves by Model", outer = TRUE)
```

Comparison of ROC Curves by Model



```
# Dot plot comparing models
```

```
models <- list(LogisticRegression = lr_model, PLR = plr_model, LDA = lda_model, PLS = pls_model, MDA = mda_model)
```

```
results_models <- resamples(models)
```

```
dotplot(results_models)
```

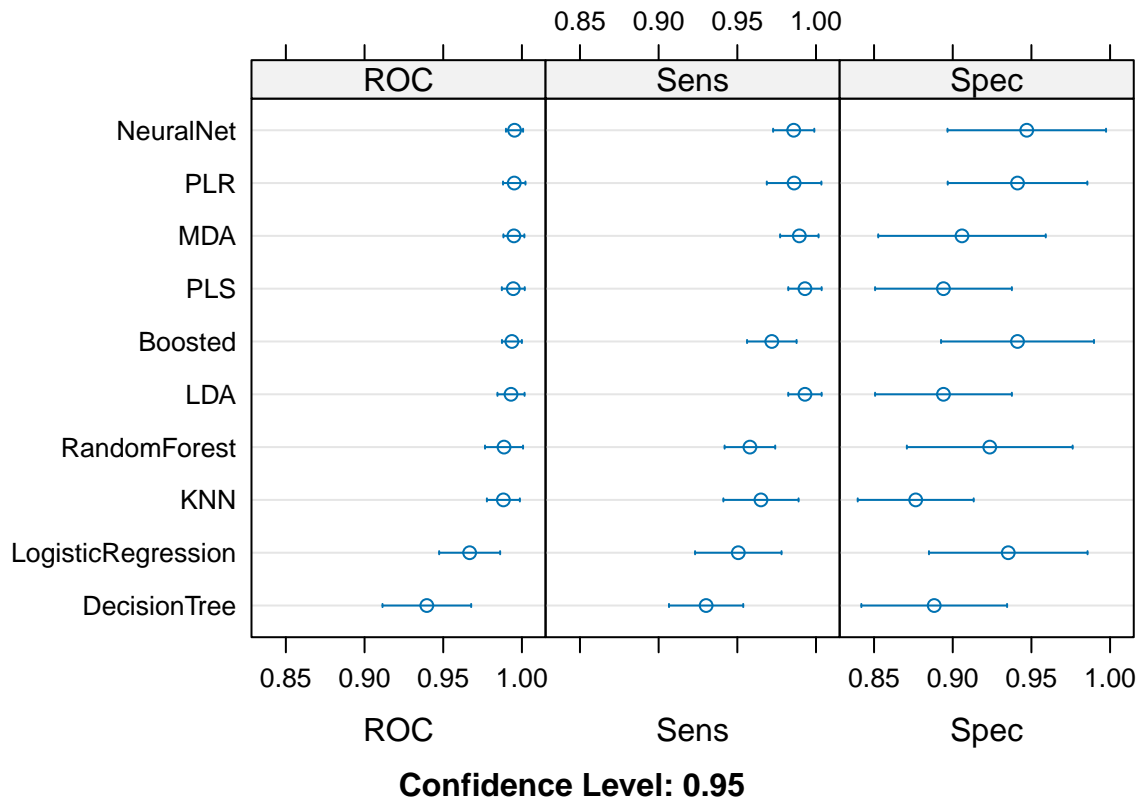


Table comparing performance metrics

```
results_table <- data.frame(
  Models = c("Logistic Regression", "Penalized LogReg", "LDA", "PLS", "MDA",
    "Decision Tree", "Random Forest", "Boosted Tree", "KNN", "Neural Net"),
  ROC_Train = c(0.9667959, 0.9951246, 0.9930745, 0.9945161, 0.9949073, 0.9395791, 0.9886410, 0.9936540,
    Sensitivity_Train = c(0.9506158, 0.9860837, 0.9929803, 0.9929803, 0.9894089, 0.9301724, 0.9580049, 0.
    Sensitivity_Test = c(0.9762, 0.9762, 0.9286, 0.9286, 0.9762, 0.8810, 0.9286, 0.9762, 0.9524, 1.0000),
    Specificity_Train = c(0.9352941, 0.9411765, 0.8941176, 0.8941176, 0.9058824, 0.8882353, 0.9235294, 0.
    Specificity_Test = c(0.9577, 0.9859, 1.0000, 1.0000, 0.9859, 0.9014, 0.9577, 1.0000, 0.9718, 0.9718)
)

print(results_table)
```

##	Models	ROC_Train	Sensitivity_Train	Sensitivity_Test
## 1	Logistic Regression	0.9667959	0.9506158	0.9762
## 2	Penalized LogReg	0.9951246	0.9860837	0.9762
## 3	LDA	0.9930745	0.9929803	0.9286
## 4	PLS	0.9945161	0.9929803	0.9286
## 5	MDA	0.9949073	0.9894089	0.9762
## 6	Decision Tree	0.9395791	0.9301724	0.8810
## 7	Random Forest	0.9886410	0.9580049	0.9286
## 8	Boosted Tree	0.9936540	0.9719212	0.9762
## 9	KNN	0.9882353	0.9650246	0.9524
## 10	Neural Net	0.9953057	0.9858374	1.0000
##	Specificity_Train	Specificity_Test		
## 1	0.9352941	0.9577		
## 2	0.9411765	0.9859		
## 3	0.8941176	1.0000		
## 4	0.8941176	1.0000		

## 5	0.9058824	0.9859
## 6	0.8882353	0.9014
## 7	0.9235294	0.9577
## 8	0.9411765	1.0000
## 9	0.8764706	0.9718
## 10	0.9470588	0.9718