Project

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```
library(leaps)
## Warning: package 'leaps' was built under R version 4.3.3
library(tidyverse)
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr
             1.1.2 v readr
                                    2.1.4
## v forcats 1.0.0
                                    1.5.0
                        v stringr
## v ggplot2 3.4.2
                        v tibble
                                    3.2.1
## v lubridate 1.9.2
                        v tidyr
                                    1.3.0
## v purrr
              1.0.1
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                    masks stats::lag()
## i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become error
library(caret)
## Warning: package 'caret' was built under R version 4.3.3
## Loading required package: lattice
## Attaching package: 'caret'
## The following object is masked from 'package:purrr':
##
##
       lift
library(pROC)
## Warning: package 'pROC' was built under R version 4.3.3
## Type 'citation("pROC")' for a citation.
## Attaching package: 'pROC'
## The following objects are masked from 'package:stats':
##
      cov, smooth, var
##
```

```
library(glmnet)
## Loading required package: Matrix
##
## Attaching package: 'Matrix'
## The following objects are masked from 'package:tidyr':
##
##
       expand, pack, unpack
##
## Loaded glmnet 4.1-7
library(r02pro)
## Warning: package 'r02pro' was built under R version 4.3.3
library(MASS)
##
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##
       select
library(ISLR)
heart <- read.csv("heart.csv")</pre>
```

Feature Selection

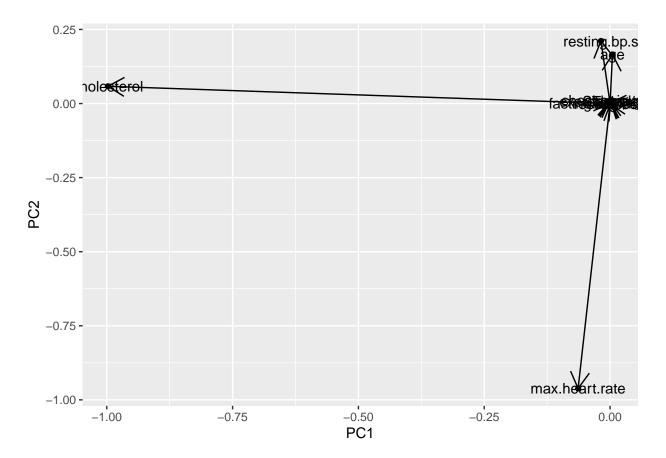
0.1842095787

##

```
# Forward Stepwise Selection with adjusted R~2
forward_fit <- regsubsets(target ~., data = heart, method = "forward", nvmax = 8)</pre>
forward_sum <- summary(forward_fit)</pre>
best_ind_for <- which.max(forward_sum$adjr2)</pre>
best_model_forward <- coef(forward_fit, best_ind_for)</pre>
best_model_forward
##
           (Intercept)
                                                  chest.pain.type
                                                                           cholesterol
                                         sex
         -0.0745320857
                                                                         -0.0003344296
##
                               0.1868783023
                                                     0.1191827974
## fasting.blood.sugar
                             max.heart.rate
                                                 exercise.angina
                                                                               oldpeak
                                                     0.1776171859
                                                                          0.0600706989
##
          0.1295000003
                              -0.0021876808
##
              ST.slope
```

```
# Backward Stepwise Selection with Cp
backward_fit <- regsubsets(target ~ ., data = heart, method = "backward", nvmax = 8)
backward_sum <- summary(backward_fit)
best_ind_back <- which.min(backward_sum$cp)
best_model_backward <- coef(backward_fit, best_ind_back)
best_model_backward</pre>
```

```
##
           (Intercept)
                                        sex
                                                chest.pain.type
                                                                         cholesterol
##
         -0.0745320857
                               0.1868783023
                                                   0.1191827974
                                                                       -0.0003344296
## fasting.blood.sugar
                            max.heart.rate
                                                exercise.angina
                                                                             oldpeak
          0.1295000003
                             -0.0021876808
                                                   0.1776171859
                                                                        0.0600706989
##
##
              ST.slope
          0.1842095787
##
```

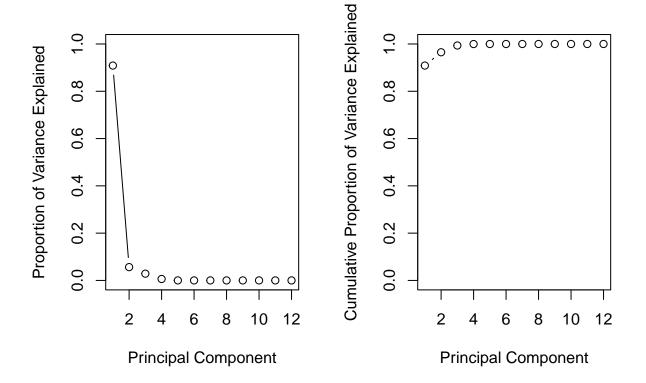


```
pr.var <- pr.out$sdev^2
pve <- pr.var / sum(pr.var)

cum_var <- cumsum(pve)
n_components <- which(cum_var >= 0.8)[1]

par(mfrow = c(1, 2))
```

```
par(mfrow = c(1, 2))
plot(pve, xlab = "Principal Component", ylab = "Proportion of Variance Explained", ylim = c(0, 1), type
plot(cumsum(pve), xlab = "Principal Component", ylab = "Cumulative Proportion of Variance Explained", y
```



Split to train and test data

```
library(dplyr)
set.seed(1)
```

```
heart <- dplyr::select(heart,
    `chest.pain.type`, `cholesterol`, `fasting.blood.sugar`,
    `max.heart.rate`, `exercise.angina`, `oldpeak`, `ST.slope`, `target`
)
tr_ind <- sample(1:nrow(heart), 0.8 * nrow(heart))
heart_train <- heart[tr_ind, ]
heart_test <- heart[-tr_ind, ]</pre>
```

Logistic Regression

```
logistic_model <- glm(target ~., data = heart_train, family = "binomial")</pre>
summary(logistic_model)
##
## Call:
## glm(formula = target ~ ., family = "binomial", data = heart_train)
## Coefficients:
                       Estimate Std. Error z value Pr(>|z|)
## (Intercept)
                     -2.2204080 0.7864720 -2.823 0.004754 **
## chest.pain.type
                      0.7356541 0.1022968 7.191 6.41e-13 ***
                      ## cholesterol
## fasting.blood.sugar 0.8008350 0.2264151 3.537 0.000405 ***
                    -0.0150355 0.0039974 -3.761 0.000169 ***
## max.heart.rate
## exercise.angina
                      1.0956566 0.2047066 5.352 8.68e-08 ***
                       0.4709970 0.1042426 4.518 6.23e-06 ***
## oldpeak
## ST.slope
                       1.1197392  0.1764426  6.346  2.21e-10 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
##
      Null deviance: 1318.24 on 951 degrees of freedom
## Residual deviance: 791.39 on 944 degrees of freedom
## AIC: 807.39
##
## Number of Fisher Scoring iterations: 5
predict_train_prob <- predict(logistic_model, type = "response")</pre>
predict_train_label <- ifelse(predict_train_prob > 0.5, "1", "0")
train_error <- mean(predict_train_label != heart_train$target)</pre>
print(train_error)
## [1] 0.1764706
predict_test_prob <- predict(logistic_model, newdata = heart_test, type = "response")</pre>
predict_test_label <- ifelse(predict_test_prob > 0.5, "1", "0")
test_error <- mean(predict_test_label != heart_test$target)</pre>
print(test_error)
```

[1] 0.1722689

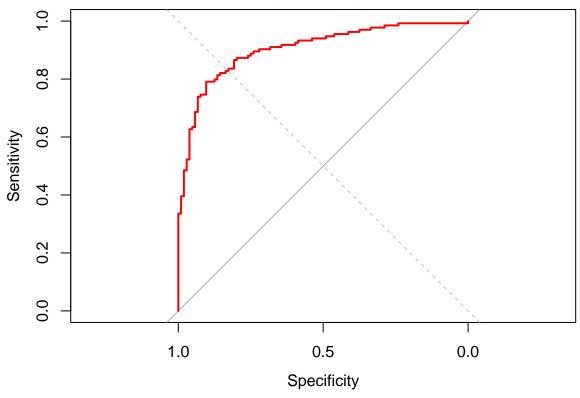
```
# aucroc
roc_logistic <- roc(heart_test$target, predict_test_prob)

## Setting levels: control = 0, case = 1

## Setting direction: controls < cases

auc_logistic <- auc(roc_logistic)
plot(roc_logistic, col = "red", lwd = 2, main = "ROC Curve - Logistic Regression (Test Set)")
abline(a = 0, b = 1, lty = 2, col = "gray")</pre>
```

ROC Curve – Logistic Regression (Test Set)



```
mean(heart$target[fold_ind == j] != pred_label)
  }))
error_lr
## [1] 0.1786873
set.seed(1)
X train <- heart train[, -which(names(heart train) == "target")]</pre>
Y_train <- heart_train$target</pre>
X_test <- heart_test[, -which(names(heart_test) == "target")]</pre>
Y_test <- heart_test$target</pre>
Y_test <- as.factor(Y_test)</pre>
# Set up the trainControl for 5-fold cross-validation
ctrl <- trainControl(method = "cv", number = 5)</pre>
# Define the tuning grid for alpha and lambda
grid \leftarrow expand.grid(alpha = seq(0, 1, by = 0.1), lambda = seq(0.05, 0.1, by = 0.002))
#Perform 5-fold cross-validation to tune hyperparameters
logi_reg_model <- train(x = X_test,y = Y_test,method = "glmnet",trControl = ctrl,</pre>
                        tuneGrid = grid,metric = "Accuracy")
print(logi_reg_model)
## glmnet
##
## 238 samples
##
    7 predictor
##
     2 classes: '0', '1'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 190, 191, 191, 190, 190
## Resampling results across tuning parameters:
##
##
     alpha lambda Accuracy
                               Kappa
##
     0.0
           0.050
                    0.8277482 0.6494130
##
     0.0
           0.052
                    0.8277482 0.6494130
                   0.8277482 0.6494130
##
     0.0
           0.054
##
     0.0
           0.056
                   0.8277482 0.6494130
##
     0.0
           0.058
                  0.8277482 0.6494130
##
     0.0
           0.060
                  0.8277482 0.6494130
##
           0.062
                   0.8277482 0.6494130
     0.0
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     0.0
                    0.8277482 0.6494130
##
           0.066
                   0.8277482 0.6494130
     0.0
           0.068 0.8277482 0.6494130
##
     0.0
##
           0.070 0.8234929 0.6411552
     0.0
##
     0.0
           0.072 0.8234929 0.6411552
##
           0.074 0.8193262 0.6331673
     0.0
##
     0.0
           0.076 0.8193262 0.6331673
           ##
     0.0
```

```
##
     0.0
             0.080
                     0.8193262
                                 0.6331673
##
             0.082
     0.0
                     0.8193262
                                 0.6331673
##
     0.0
             0.084
                     0.8193262
                                 0.6331673
##
     0.0
             0.086
                     0.8193262
                                 0.6331673
##
     0.0
             0.088
                     0.8193262
                                 0.6331673
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     0.0
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     0.1
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             0.058
                     0.8362589
                                  0.6671656
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                                 0.6578168
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```

```
##
     0.2
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             0.056
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             0.060
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     0.3
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##
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                                 0.6053661
```

```
1.0 0.100 0.8070035 0.6053661
##
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were alpha = 0.1 and lambda = 0.058.
logi_reg_model$bestTune
##
      alpha lambda
## 31 0.1 0.058
# training error
train_predict_logiregu <- predict(logi_reg_model, X_train)</pre>
train_error_logiregu <- mean(train_predict_logiregu != Y_train)</pre>
train_error_logiregu
## [1] 0.1838235
# test error
test_predict_logiregu <- predict(logi_reg_model, X_test)</pre>
test_error_logiregu <- mean(test_predict_logiregu != Y_test)</pre>
test_error_logiregu
## [1] 0.1554622
# rocauc
roc_logiregu <- roc(Y_test, as.numeric(test_predict_logiregu), levels = rev(levels(Y_test)))</pre>
## Setting direction: controls > cases
auc_logiregu <- auc(roc_logiregu)</pre>
auc_logiregu
## Area under the curve: 0.8415
```

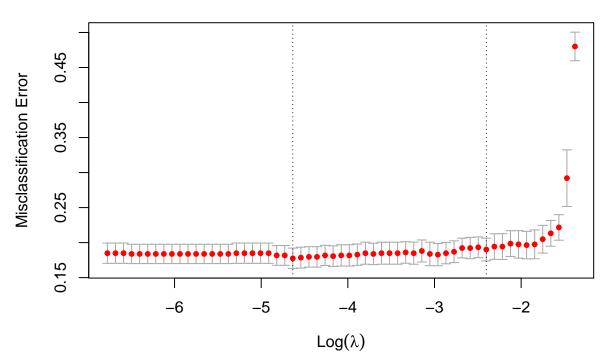
Lasso Regression

```
set.seed(1)

x_train <- model.matrix(target ~ ., data = heart_train)[, -1]
y_train <- heart_train$target
x_test <- model.matrix(target ~ ., data = heart_test)[, -1]
y_test <- heart_test$target

cv_fit <- cv.glmnet(x_train, y_train, alpha = 1, family = "binomial", type.measure = "class", nfolds = plot(cv_fit)</pre>
```

7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 5 5 4 3 1



```
best_lambda <- cv_fit$lambda.min
cat("Best lambda:", best_lambda, "\n")</pre>
```

Best lambda: 0.009707011

```
lasso_model <- glmnet(x_train, y_train, family="binomial", alpha=1, lambda=best_lambda)</pre>
```

```
pred_prob_train <- predict(lasso_model, newx = x_train, type = "response")
pred_prob_test <- predict(lasso_model, newx = x_test, type = "response")

pred_class_train <- ifelse(pred_prob_train > 0.5, "1", "0")
pred_class_test <- ifelse(pred_prob_test > 0.5, "1", "0")

train_error_lasso <- mean((pred_class_train != y_train)^2)
test_error_lasso <- mean((pred_class_test != y_test)^2)

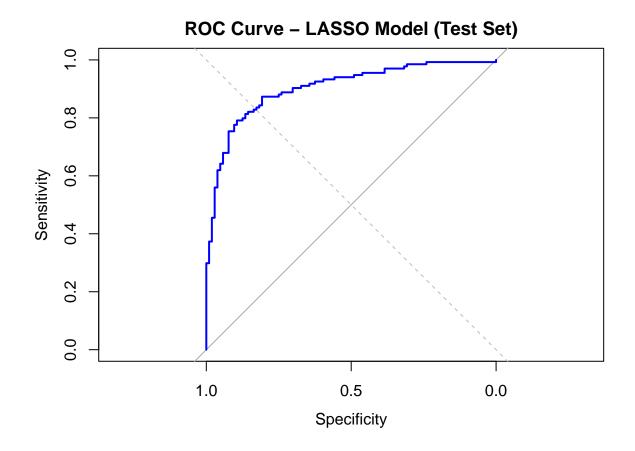
print(train_error_lasso)</pre>
```

[1] 0.1722689

```
print(test_error_lasso)
```

[1] 0.1722689

```
# cross-validation
set.seed(1)
K <- 5
n_all <- nrow(heart)</pre>
fold_ind <- sample(1:K, n_all, replace = TRUE)</pre>
x <- model.matrix(target ~ ., data = heart)[, -1]</pre>
y <- heart$target
error_lasso <- mean(sapply(1:K, function(j) {</pre>
  # Training and validation split
  x_train <- x[fold_ind != j, ]</pre>
  y_train <- y[fold_ind != j]</pre>
  x_valid <- x[fold_ind == j, ]</pre>
  y_valid <- y[fold_ind == j]</pre>
  # Fit LASSO model with CV on training set to get best lambda
  cv_fit <- cv.glmnet(x_train, y_train, family = "binomial", alpha = 1, type.measure = "class")
  best_lambda <- cv_fit$lambda.min</pre>
  # Predict on validation fold
  pred_prob <- predict(cv_fit, newx = x_valid, s = best_lambda, type = "response")</pre>
  pred_label <- ifelse(pred_prob > 0.5, 1, 0)
  # Misclassification error
  mean(y_valid != pred_label)
}))
error lasso
## [1] 0.1745477
library(pROC)
# Ensure both are numeric vectors of the same length
roc_lasso <- roc(as.numeric(y_test), as.numeric(pred_prob_test[, 1]))</pre>
## Setting levels: control = 0, case = 1
## Setting direction: controls < cases
# AUC value
auc_lasso <- auc(roc_lasso)</pre>
cat("LASSO Test AUC:", round(auc_lasso, 4), "\n")
## LASSO Test AUC: 0.9032
# Plot ROC
plot(roc_lasso, col = "blue", lwd = 2, main = "ROC Curve - LASSO Model (Test Set)")
abline(a = 0, b = 1, lty = 2, col = "gray")
```



Compare AIC

```
set.seed(1)
aic_lr <- AIC(logistic_model)
deviance_lasso <- deviance(lasso_model)
df_lasso <- lasso_model$df
aic_lasso <- deviance_lasso + 2 * df_lasso
cat("AIC - Logistic Regression (glm):", round(aic_lr, 2), "\n")

## AIC - Logistic Regression (glm): 807.39

cat("AIC - LASSO (glmnet):", round(aic_lasso, 2), "\n")

## AIC - LASSO (glmnet): 809.04

library(MASS)
library(tree)

## Warning: package 'tree' was built under R version 4.3.3</pre>
```

```
library(readr)
library(caret)
library(randomForest)
## Warning: package 'randomForest' was built under R version 4.3.3
## randomForest 4.7-1.2
## Type rfNews() to see new features/changes/bug fixes.
##
## Attaching package: 'randomForest'
## The following object is masked from 'package:dplyr':
##
       combine
## The following object is masked from 'package:ggplot2':
##
##
       margin
library(forcats)
set.seed(1)
#Load data
heart_data <- read_csv("heart.csv")</pre>
## Rows: 1190 Columns: 12
## -- Column specification -----
## Delimiter: ","
## dbl (12): age, sex, chest pain type, resting bp s, cholesterol, fasting bloo...
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
#Recode sex
heart_data$sex <- as.factor(heart_data$sex)</pre>
heart_data$sex <- fct_recode(heart_data$sex, "male" = "1", "female" = "0")
#Recode target to valid R variable names
heart_data$target <- as.factor(heart_data$target)</pre>
heart_data$target <- fct_recode(heart_data$target, "No" = "0", "Yes" = "1")
#Creation of train/test data
h_ind <- createDataPartition(heart_data$target, p = 0.8, list = FALSE)
heart_train <- heart_data[h_ind, ]</pre>
heart_test <- heart_data[-h_ind, ]</pre>
#PCA for variable selection (exclude target and separate numeric/categorical)
```

```
numeric_cols <- sapply(heart_train, is.numeric) & colnames(heart_train) != "target"</pre>
heart_train_numeric <- heart_train[, numeric_cols]</pre>
categorical_cols <- !numeric_cols & colnames(heart_train) != "target"</pre>
heart_train_categorical <- heart_train[, categorical_cols, drop = FALSE]
# Scale numeric predictors
heart_scale <- scale(heart_train_numeric)</pre>
#Perform PCA on numeric predictors
pca_result <- prcomp(heart_scale, center = TRUE, scale. = TRUE)</pre>
loadings <- pca_result$rotation</pre>
important_vars <- names(sort(abs(loadings[, 1]), decreasing = TRUE))[1:5] # Top 5 from PC1</pre>
important_vars <- unique(c(important_vars, names(sort(abs(loadings[, 2]), decreasing = TRUE))[1:4])) #</pre>
important_vars2 <- important_vars[!important_vars %in% c("target", "resting ecg")] # Exclude target and
#Combine selected numeric variables with all categorical variables
selected_cols <- c(important_vars2, colnames(heart_train_categorical))</pre>
train_selected <- heart_train[, selected_cols]</pre>
test_selected <- heart_test[, selected_cols]</pre>
#Prepare training data for Random Forest
rf_train_data <- data.frame(train_selected, target = as.factor(heart_train$target))
#Convert categorical predictors to factors
if ("st slope" %in% colnames(rf_train_data)) rf_train_data$`st slope` <- as.factor(rf_train_data$`st sl
if ("resting ecg" %in% colnames(rf_train_data)) rf_train_data$`resting ecg` <- as.factor(rf_train_data$
if ("exercise angina" %in% colnames(rf_train_data)) rf_train_data$`exercise angina` <- as.factor(rf_tra
if ("sex" %in% colnames(rf_train_data)) rf_train_data$sex <- as.factor(rf_train_data$sex)
if ("chest pain type" %in% colnames(rf_train_data)) rf_train_data$`chest pain type` <- as.factor(rf_tra
#Define custom summary function to include Accuracy, Kappa, ROC, Sens, Spec
customSummary <- function(data, lev = NULL, model = NULL) {</pre>
  out <- c(defaultSummary(data, lev, model), twoClassSummary(data, lev, model))</pre>
}
#Define 5-fold cross-validation
train_control <- trainControl(</pre>
  method = "cv",
  number = 5,
  savePredictions = "final",
  classProbs = TRUE,
  summaryFunction = customSummary, # Includes Accuracy, Kappa, ROC, Sens, Spec
  returnResamp = "all"
#Train Random Forest with 5-fold CV
rf_cv_model <- train(</pre>
  target ~ .,
  data = rf_train_data,
  method = "rf",
  trControl = train_control,
  ntree = 500,
  tuneGrid = data.frame(mtry = sqrt(ncol(rf_train_data) - 1)),
```

```
metric = "Accuracy"
)
#Cross-validation training error
cv_accuracy <- mean(rf_cv_model$results$Accuracy)</pre>
cv_error <- 1 - cv_accuracy</pre>
cat("5-Fold CV Training Error:", cv_error, "\n")
## 5-Fold CV Training Error: 0.09024073
#Explicit training error (predict on full training data)
train_predictions <- predict(rf_cv_model, newdata = rf_train_data, type = "raw")</pre>
train_confusion <- table(rf_train_data$target, train_predictions)</pre>
train_accuracy <- sum(diag(train_confusion)) / sum(train_confusion)</pre>
train_error <- 1 - train_accuracy</pre>
cat("Training Error (Explicit):", train_error, "\n")
## Training Error (Explicit): 0
#Print CV results
print(rf_cv_model)
## Random Forest
##
## 953 samples
##
    9 predictor
    2 classes: 'No', 'Yes'
##
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 762, 762, 764, 762, 762
## Resampling results:
##
##
    Accuracy
                           ROC
                Kappa
                                       Sens
                                                  Spec
     0.9097593 0.8184171 0.9542393 0.8797753 0.9364752
##
##
## Tuning parameter 'mtry' was held constant at a value of 3
#Prepare test data for prediction
rf_test_data <- data.frame(test_selected, target = as.factor(heart_test$target))
#Convert categorical predictors to factors in test data
if ("st slope" %in% colnames(rf_test_data)) rf_test_data$`st slope` <- as.factor(rf_test_data$`st slope
if ("resting ecg" %in% colnames(rf_test_data)) rf_test_data$`resting ecg` <- as.factor(rf_test_data$`re
if ("exercise angina" %in% colnames(rf_test_data)) rf_test_data$`exercise angina` <- as.factor(rf_test_
if ("sex" %in% colnames(rf_test_data)) rf_test_data$sex <- as.factor(rf_test_data$sex)
if ("chest pain type" %in% colnames(rf_test_data)) rf_test_data$`chest pain type` <- as.factor(rf_test_
#Predict on test data
test_predictions <- predict(rf_cv_model, newdata = rf_test_data, type = "raw")</pre>
```

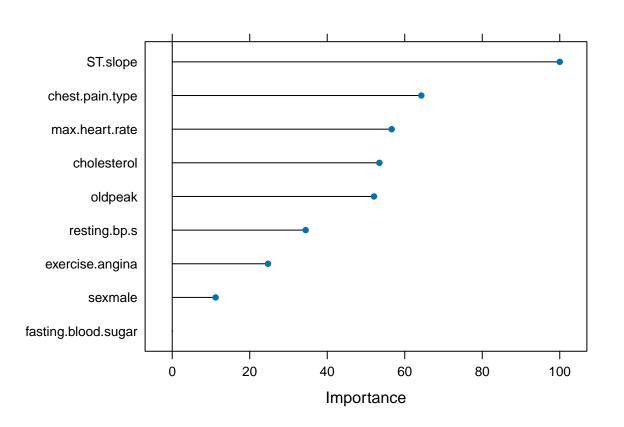
```
#Test error
test_confusion <- table(rf_test_data$target, test_predictions)
test_accuracy <- sum(diag(test_confusion)) / sum(test_confusion)
test_error <- 1 - test_accuracy
cat("Test Error:", test_error, "\n")</pre>
```

Test Error: 0.05485232

```
#Variable importance
varImp(rf_cv_model)
```

```
## rf variable importance
##
                       Overall
##
## ST.slope
                        100.00
## chest.pain.type
                         64.29
## max.heart.rate
                         56.62
## cholesterol
                         53.46
                         52.07
## oldpeak
## resting.bp.s
                         34.44
## exercise.angina
                         24.70
## sexmale
                         11.21
## fasting.blood.sugar
                          0.00
```

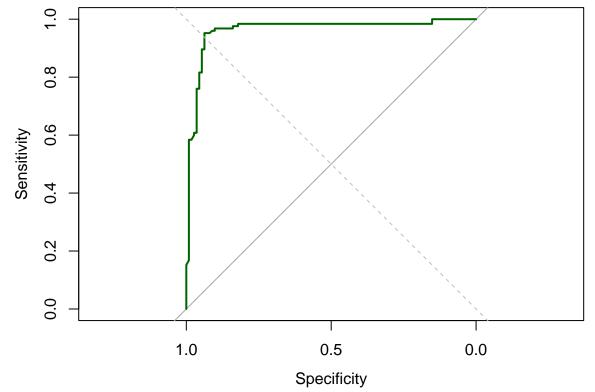
plot(varImp(rf_cv_model))



Random Forest Test AUC: 0.9622

```
# Plot ROC curve
plot(roc_rf, col = "darkgreen", lwd = 2, main = "ROC Curve - Random Forest (Test Set)")
abline(a = 0, b = 1, lty = 2, col = "gray")
```





Comparison of ROC Curves

