

Compulsory exercise 1: Group 12

Evgeni Vershinin, Kristina Ødegård

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Problem 1

a)

Quantative: Time, income earned, horsepower of a car. Qvalitative: Marital status, origin, Gender.

b) *KNN, LDA, QDA can be used for multi-class classifications.*

c)

*d) The nearest neighbour for $k=1$ is a blue dot, so our classification is blue. For $K=3$, two of the nearest neighbors are red and 1 blue. This gives $2/3$ red, so it is red. For $K=5$ we have $3/5$ red, so it is red.

```
data(Boston)
data = Boston

model = lm(medv ~ rm + age, data=data)
summary(model)

##
## Call:
## lm(formula = medv ~ rm + age, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.555  -2.882  -0.274   2.293  40.799
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -25.27740    2.85676  -8.848  < 2e-16 ***
## rm           8.40158    0.41208  20.388  < 2e-16 ***
## age        -0.07278    0.01029  -7.075 5.02e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.316 on 503 degrees of freedom
## Multiple R-squared:  0.5303, Adjusted R-squared:  0.5284
## F-statistic: 283.9 on 2 and 503 DF,  p-value: < 2.2e-16

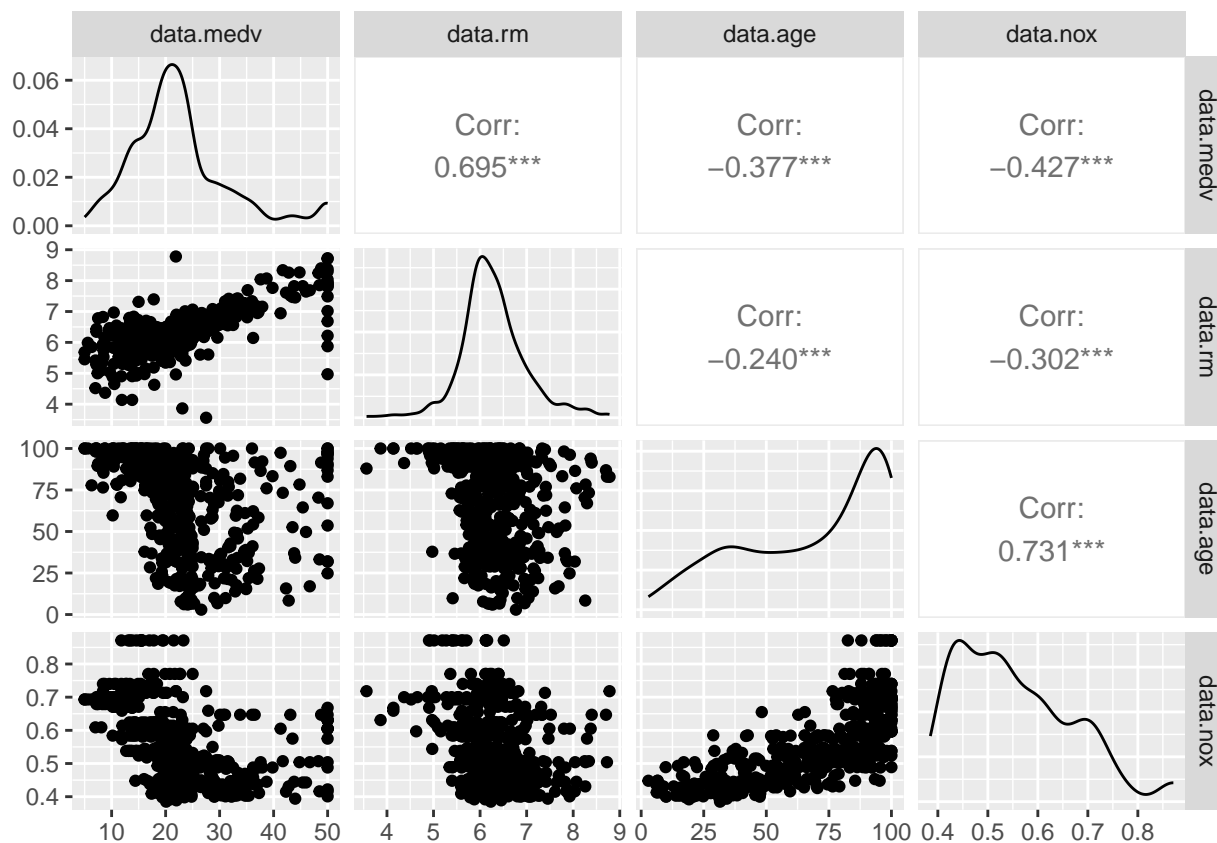
cor_matrix = cor(data.frame(data$medv, data$rm, data$age))
print(cor_matrix)
```

```
##          data.medv    data.rm    data.age
## data.medv 1.0000000 0.6953599 -0.3769546
## data.rm   0.6953599 1.0000000 -0.2402649
## data.age  -0.3769546 -0.2402649 1.0000000
```

```
model2 = lm(medv ~ rm + age + nox, data=data)
summary(model2)
```

```
##
## Call:
## lm(formula = medv ~ rm + age + nox, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.343  -3.168  -0.539   2.221  40.260
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -19.08308    3.33919  -5.715 1.88e-08 ***
## rm           8.12542    0.41525  19.568 < 2e-16 ***
## age        -0.03686    0.01449  -2.544 0.011269 *
## nox        -12.47877    3.58434  -3.481 0.000542 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.247 on 502 degrees of freedom
## Multiple R-squared:  0.5413, Adjusted R-squared:  0.5386
## F-statistic: 197.5 on 3 and 502 DF, p-value: < 2.2e-16
```

```
ggpairs(data.frame(data$medv, data$rm, data$age, data$nox))
```



e) IV Looking at the correlation between Age and NOX, it is 0.731, which is quite high which suggest it has multicollinearity, which means they give some of the same information for the model.

*Problem 2 a)

```
model3 = lm(medv ~ poly(rm, 2) + I(age*crim) + age + crim, data=data)
summary(model3)
```

```
##
## Call:
## lm(formula = medv ~ poly(rm, 2) + I(age * crim) + age + crim,
##     data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -34.314  -2.602   -0.369    2.136   35.081
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  28.096141   0.666283  42.169  < 2e-16 ***
## poly(rm, 2)1 123.366564   5.600727  22.027  < 2e-16 ***
## poly(rm, 2)2  64.836354   5.479728  11.832  < 2e-16 ***
## I(age * crim)  0.005792   0.003553   1.630   0.1037
## age         -0.067283   0.009342  -7.202 2.19e-12 ***
## crim        -0.796544   0.338946  -2.350   0.0192 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.369 on 500 degrees of freedom
## Multiple R-squared:  0.6626, Adjusted R-squared:  0.6592
## F-statistic: 196.3 on 5 and 500 DF,  p-value: < 2.2e-16

valuechanged = (-10*(-0.796544)+60*(-0.067283)+0.005792 * (-10 + 60))*1000
```

If the crime is reduced by 10 and age is 60, and then considering all other factor keeps equal our median value of the property is changed by 4218.06.'

**b) First thing we could do is to plot all our data with say ggpairs from GGally. We can then look how the data is spread and correlated. We want to carefully identify if we have any outliers. If most our points follow a specific pattern, but then one point stick out, we could carefully consider to remove it. One approach could be to look at the mean and std of a given data columns and if some point lie 2 standard deviations away from the mean we could remove them.

**c)

```
model4 <- lm(medv ~ crim + age + rm, data = Boston)
summary(model4)
```

```
##
## Call:
## lm(formula = medv ~ crim + age + rm, data = Boston)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.959  -3.143  -0.633   2.150  39.940
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -23.60556    2.76938  -8.524  < 2e-16 ***
## crim        -0.21102    0.03407  -6.195 1.22e-09 ***
## age         -0.05224    0.01046  -4.993 8.21e-07 ***
## rm           8.03284    0.40201  19.982 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.094 on 502 degrees of freedom
## Multiple R-squared:  0.5636, Adjusted R-squared:  0.561
## F-statistic: 216.1 on 3 and 502 DF,  p-value: < 2.2e-16
```

**i) A t-value is calculated with the follow formula: $t = \frac{\text{Coefficient Estimate}}{\text{Standard Error}} = \frac{10}{-0.052}$

The t-value for rm if the estimated coefficient was 10, but with the same standard error is 24.89.

The t-value is a measure of how many standard errors the estimated coefficient is from zero. This indicates how strong effect the variable has in the response variable. That is, how significant it is.

When the coefficient estimate is increased, taking it further away from zero, it increases the t-value, making it more statistically significant.

**ii)

```
f_test <- anova(model4)
print(f_test)
```

```
## Analysis of Variance Table
##
## Response: medv
##           Df Sum Sq Mean Sq F value    Pr(>F)
## crim       1  6440.8   6440.8 173.458 < 2.2e-16 ***
## age        1  2809.8   2809.8  75.671 < 2.2e-16 ***
## rm         1 14825.7 14825.7 399.275 < 2.2e-16 ***
## Residuals 502 18640.0     37.1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

An F-test was utilized to decide if at least one of the predictors is useful in predicting the response.

In this case, all three predictors has a p-value associated with the F-statistic that is $< 2.2^{-16}$. Since the p-value is essentially zero, we have strong evidence to reject the null hypothesis, which would be that none of the predictors were useful in predicting the response variable. Thus, at least one of the predictors is useful in predicting the response.

**iii)

```
model5 <- lm(medv ~ crim + age, data = Boston)
f_test_2 <- anova(model5)
print(f_test_2)
```

```
## Analysis of Variance Table
##
## Response: medv
##           Df Sum Sq Mean Sq F value    Pr(>F)
## crim       1   6441   6440.8  96.807 < 2.2e-16 ***
## age        1   2810   2809.8  42.232 1.954e-10 ***
## Residuals 503  33466     66.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value associated with F values, though increased for age in this model without the predictor rm, are still significantly lower than the typical significance level of 0.05. Thus the null hypothesis can be rejected for both predictors. We conclude that the model is still useful.

```
new_data <- data.frame(crim = 10, age = 90, rm = 5)
# Predict the response variable using the model for the confidence interval
prediction_c <- predict(model4, newdata = new_data, interval = "confidence", level = 0.99)

# Extract lower and upper bounds from the confidence interval prediction
lower_bound_c <- prediction_c[1]
upper_bound_c <- prediction_c[2]

# Print the results for the confidence interval
cat("Lower bound of 99% confidence interval:", lower_bound_c, "\n")
```

```
## Lower bound of 99% confidence interval: 9.746544
```

```
cat("Upper bound of 99% confidence interval:", upper_bound_c, "\n\n")
```

```
## Upper bound of 99% confidence interval: 8.25632
```

```
# Predict the response variable using the model for the prediction interval  
prediction_p <- predict(model4, newdata = new_data, interval = "prediction", level = 0.99)
```

```
# Extract lower and upper bounds from the prediction interval prediction  
lower_bound_p <- prediction_p[1]  
upper_bound_p <- prediction_p[2]
```

```
# Print the results for the prediction interval  
cat("Lower bound of 99% prediction interval:", lower_bound_p, "\n")
```

```
## Lower bound of 99% prediction interval: 9.746544
```

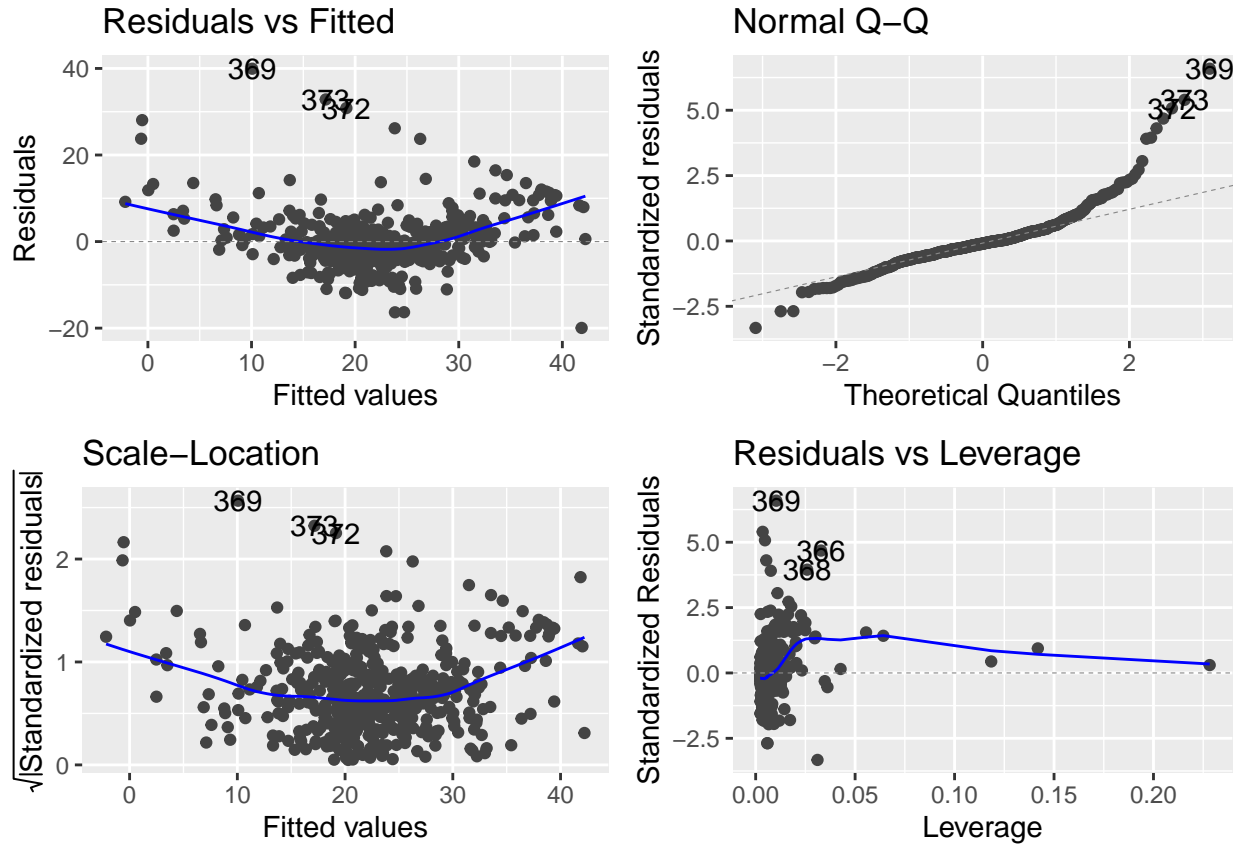
```
cat("Upper bound of 99% prediction interval:", upper_bound_p, "\n")
```

```
## Upper bound of 99% prediction interval: -6.079652
```

****iii)** The difference between confidence interval and prediction interval is that the confidence interval estimates the range in which the population mean response most likely will lie, and the prediction interval estimates the range in which a future individual observation most likely will fall within.

****iv)**

```
# Create diagnostic plots  
autoplot(model4, which = c(1, 2, 3, 5))
```



e) i) The gender is a binary qualitative variable. The student has used two binary variables to describe what only needs one. If two binary qualitative variables were used, it would in fact allow for four different cases:

Case 1: Male and Female
Case 2: Male and Not Female
Case 3: Not Male and Female
Case 4: Not Male and Not Female

$x_{male} = 1$ and $x_{female} = 1$
 $x_{male} = 1$ and $x_{female} = 0$
 $x_{male} = 0$ and $x_{female} = 1$
 $x_{male} = 0$ and $x_{female} = 0$

In reality, there are only two cases:

Case 1: Male (and Not Female) $x_{gender} = 1$
Case 2: Female (and Not Male) $x_{gender} = 0$

**ii) The formula should only have one binary quantitative variable to describe the gender.

$$y = \beta_0 + \beta_1 x_{gender} + \varepsilon$$

where

$$x_{gender} = \begin{cases} 1 & \text{if male} \\ 0 & \text{if female} \end{cases}$$

**iii) A formula for a linear model that predicts income based on the predictor education degree with three categories {Bachelor, Master, PhD} is:

$$y = \beta_0 + \beta_1 x_{education} + \varepsilon$$

where

$$x_{education} = \begin{cases} 2 & \text{if } PhD \\ 1 & \text{if } Master \\ 0 & \text{if } Bachelor \end{cases}$$

**f)

**i) True

**ii) False

**iii) True

**iv) False

***Problem 3 a)

```
data("titanic_train")
vars_to_be_removed <- c("PassengerId", "Name", "Ticket", "Cabin", "Embarked")
titanic_train <- titanic_train[, -which(names(titanic_train) %in% vars_to_be_removed)]
titanic_train$Pclass <- as.factor(titanic_train$Pclass)
train_idx <- sample(1:nrow(titanic_train), 0.8 * nrow(titanic_train))
titanic_test <- titanic_train[-train_idx, ]
titanic_train <- titanic_train[train_idx, ]
titanic_train <- na.omit(titanic_train)
titanic_test <- na.omit(titanic_test)
logReg = glm(Survived ~ Pclass + Sex + Age + SibSp + Parch + Fare, data = titanic_train, family = "binomial")
summary(logReg)
```

```
##
## Call:
## glm(formula = Survived ~ Pclass + Sex + Age + SibSp + Parch +
##      Fare, family = "binomial", data = titanic_train)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  4.048694   0.553988   7.308 2.71e-13 ***
## Pclass2      -1.230152   0.353680  -3.478 0.000505 ***
## Pclass3      -2.323032   0.368839  -6.298 3.01e-10 ***
## Sexmale      -2.675098   0.248332 -10.772 < 2e-16 ***
## Age          -0.042726   0.009268  -4.610 4.02e-06 ***
## SibSp        -0.420064   0.142759  -2.942 0.003256 **
## Parch        -0.099062   0.131840  -0.751 0.452422
## Fare          0.002732   0.002796   0.977 0.328516
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 763.63  on 564  degrees of freedom
## Residual deviance: 508.23  on 557  degrees of freedom
## AIC: 524.23
```



```
##
```

```
## Number of Fisher Scoring iterations: 5
```

```
predicted_probabilities <- predict(logReg, newdata = titanic_test, type = "response")
predicted_labels <- ifelse(predicted_probabilities > 0.5, 1, 0)
actual_labels <- titanic_test$Survived
misclassification_error <- mean(predicted_labels != actual_labels)
accuracy <- 1 - misclassification_error
print(accuracy)
```

```
## [1] 0.7919463
```

```
chitest = anova(logReg, test="Chisq")
chitest
```

```
## Analysis of Deviance Table
```

```
##
```

```
## Model: binomial, link: logit
```

```
##
```

```
## Response: Survived
```

```
##
```

```
## Terms added sequentially (first to last)
```

```
##
```

```
##
```

		Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
##	NULL			564	763.63	
##	Pclass	2	69.483	562	694.15	8.163e-16 ***
##	Sex	1	156.007	561	538.14	< 2.2e-16 ***
##	Age	1	17.682	560	520.46	2.611e-05 ***
##	SibSp	1	10.866	559	509.59	0.0009795 ***
##	Parch	1	0.289	558	509.30	0.5911460
##	Fare	1	1.074	557	508.23	0.3001461

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
newdata = data.frame(Pclass=as.factor(c(1,3)),Sex=c("female","female"),Age=c(40,40),SibSp=c(1,1),Parch=
newdata
```

	Pclass	Sex	Age	SibSp	Parch	Fare
## 1	1	female	40	1	0	200
## 2	3	female	40	1	0	20

```
casepredict = predict(logReg, newdata = newdata, type="response")
casepredict
```

```
##          1          2
## 0.9217204 0.4136693
```

Given a p value of less than 2.2×10^{-16} suggest it is really relevant predictor. Given that H_0 is predictor could just as well be 0, a low p value would break this hypothesis. Comparing the a woman with the all the same factors, except for class and fare price, the higher class woman has a 0.9217204 chance of survival, while the lower class woman has a 0.4136693 chance of survival.

```
ldamodel = lda(Survived ~ ., data = titanic_train)
print(ldamodel)
```

```
## Call:
## lda(Survived ~ ., data = titanic_train)
##
## Prior probabilities of groups:
##      0      1
## 0.5929204 0.4070796
##
## Group means:
##      Pclass2  Pclass3  Sexmale      Age      SibSp      Parch      Fare
## 0 0.2119403 0.6238806 0.8417910 30.74328 0.5432836 0.3820896 23.76219
## 1 0.2695652 0.2956522 0.3173913 28.71413 0.5000000 0.5217391 53.21353
##
## Coefficients of linear discriminants:
##              LD1
## Pclass2 -0.789073856
## Pclass3 -1.504574355
## Sexmale -2.068582677
## Age     -0.026553115
## SibSp   -0.251774569
## Parch   -0.086165420
## Fare    0.001778469
```

```
predicted <- predict(ldamodel, newdata = titanic_test)
predicted_labels <- predicted$class
actual_labels <- titanic_test$Survived
misclassification_error = mean(predicted_labels != actual_labels)
accuracy <- 1 - misclassification_error
print(accuracy)
```

```
## [1] 0.7919463
```

```
qdamodel = qda(Survived ~ ., data = titanic_train)
print(qdamodel)
```

```
## Call:
## qda(Survived ~ ., data = titanic_train)
##
## Prior probabilities of groups:
##      0      1
## 0.5929204 0.4070796
##
## Group means:
##      Pclass2  Pclass3  Sexmale      Age      SibSp      Parch      Fare
## 0 0.2119403 0.6238806 0.8417910 30.74328 0.5432836 0.3820896 23.76219
## 1 0.2695652 0.2956522 0.3173913 28.71413 0.5000000 0.5217391 53.21353
```

```
predicted <- predict(qdamodel, newdata = titanic_test)
predicted_labels <- predicted$class
```

```

actual_labels <- titanic_test$Survived
misclassification_error = mean(predicted_labels != actual_labels)
accuracy <- 1 - misclassification_error
print(accuracy)

```

```
## [1] 0.7986577
```

```

logreg_probs <- predict(logReg, newdata = titanic_test, type = "response")
lda_probs <- predict(ldamodel, newdata = titanic_test)$posterior[,2]
qda_probs <- predict(qdamodel, newdata = titanic_test)$posterior[,2]
actual_outcomes <- titanic_test$Survived

```

```

# ROC for Logistic Regression
roc_logreg <- roc(actual_outcomes, logreg_probs)

```

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

```
## Setting direction: controls < cases
```

```

# ROC for LDA
roc_lda <- roc(actual_outcomes, lda_probs)

```

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

```
## Setting direction: controls < cases
```

```

# ROC for QDA
roc_qda <- roc(actual_outcomes, qda_probs)

```

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

```
## Setting direction: controls < cases
```

```

# Plot ROC curve for Logistic Regression
plot(roc_logreg, main="ROC Curves Comparison", col="red")

```

```

# Add ROC curve for LDA
lines(roc_lda, col="blue")

```

```

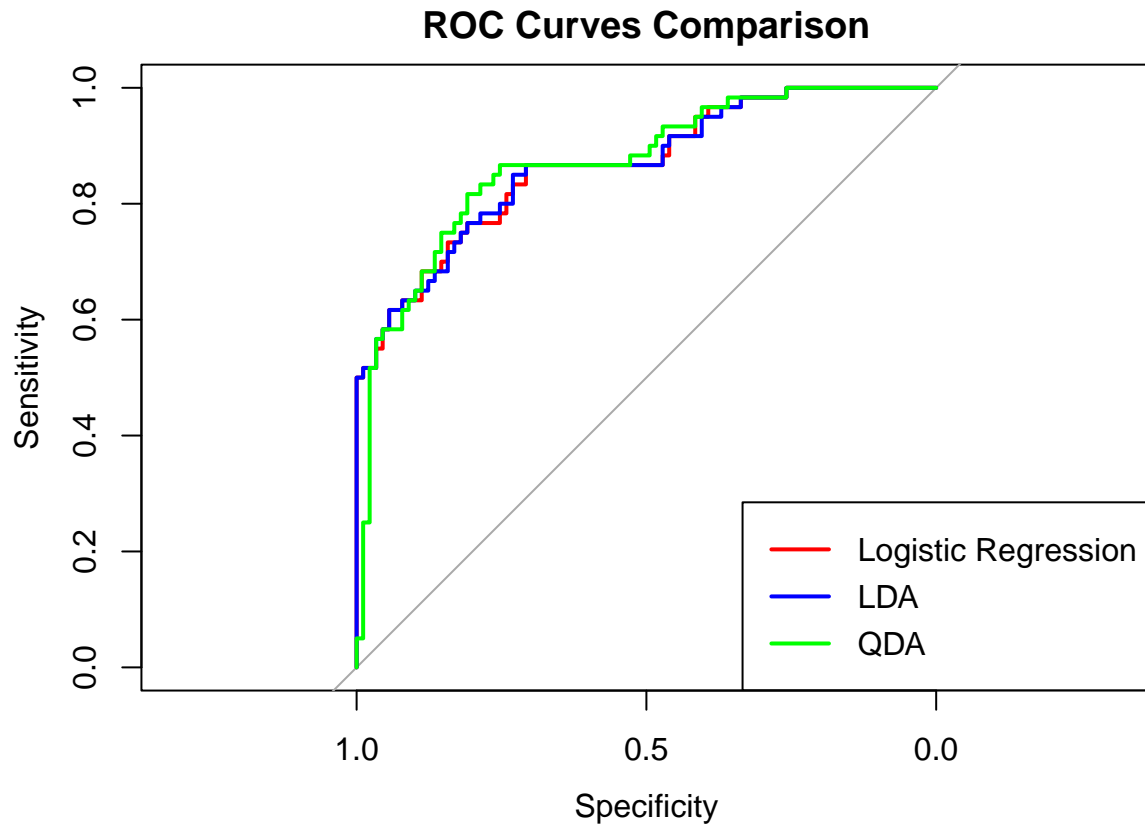
# Add ROC curve for QDA
lines(roc_qda, col="green")

```

```

# Add legend
legend("bottomright", legend=c("Logistic Regression", "LDA", "QDA"),
      col=c("red", "blue", "green"), lwd=2)

```



```
# AUC for Logistic Regression
auc_logreg <- roc_logreg$auc

# AUC for LDA
auc_lda <- roc_lda$auc

# AUC for QDA
auc_qda <- roc_qda$auc
# Print AUC values
cat("AUC for Logistic Regression:", auc_logreg, "\n")
```

```
## AUC for Logistic Regression: 0.8677903
```

```
cat("AUC for LDA:", auc_lda, "\n")
```

```
## AUC for LDA: 0.867603
```

```
cat("AUC for QDA:", auc_qda, "\n")
```

```
## AUC for QDA: 0.8702247
```

AUC over 0.8 is generally considered good. QDA performs slightly better than LDA and Logistic Regression. However Logistic regression is almost as accurate, but more interpretable, for one it gives clearer relationships between the predictors and they are linear.

****b)**

Diagnostic Paradigm:

The diagnostic paradigm in classification focuses on directly modeling the relationship between the predictors and the outcome (class labels). The primary goal is to diagnose the class of an observation based on its features. Models under this paradigm typically estimate the probability that an observation belongs to a certain class given its features. This approach is more deterministic, where the decision rule is often based on the estimated probabilities and predefined thresholds. **Sampling Paradigm:**

The sampling paradigm, on the other hand, is based on modeling the distribution of features for each class. It involves estimating how the data is generated or sampled for each class and then uses this information to classify new observations. This approach is more generative, as it tries to understand the underlying data generation process for each class and uses this generative model to make classification decisions.

Key Differences:

Modeling Focus: The diagnostic paradigm focuses on the direct relationship between features and classes, often modeling the conditional probability of a class given the features. The sampling paradigm focuses on modeling the distribution of features for each class, effectively capturing how data for each class is generated. **Approach:** Diagnostic models are more discriminative, directly seeking a decision boundary between classes. Sampling models are generative, aiming to understand the data generation process for each class. **Decision Rule:** In the diagnostic paradigm, classification decisions are often made based on estimated probabilities and thresholds. In the sampling paradigm, decisions are made based on likelihoods derived from the modeled distributions of features for each class.

ii) Classification Models and Their Paradigms

Logistic Regression: Belongs to the diagnostic paradigm. It models the probability of a class given the features directly using the logistic function.

KNN (K-Nearest Neighbors): Can be seen as part of the sampling paradigm. It classifies an observation based on the majority class among its K nearest neighbors, effectively using the local distribution of the data around an observation to make a classification decision.

Naive Bayes Classifier: Fits within the sampling paradigm. It is a generative model that assumes independence among features given the class and estimates the distribution of each feature within each class to compute the posterior probability of the class given an observation.

LDA (Linear Discriminant Analysis): Primarily fits within the sampling paradigm. LDA models the distribution of features in each class (assuming a Gaussian distribution with a common covariance matrix across classes) and uses this to classify new observations by finding the class that maximizes the posterior probability.

QDA (Quadratic Discriminant Analysis): Also belongs to the sampling paradigm. Similar to LDA, QDA models the distribution of features for each class, but it allows for class-specific covariance matrices, leading to quadratic decision boundaries. Like LDA, it uses the estimated distributions to compute class probabilities for classification.

*****Problem 4**

«««< HEAD a) iv) **True** ===== c)

- I) The decision boundary is given by setting by taking the log of each pdf and adding the log of the prior probability equal each other.

$$X|\{Y = 1\} \sim N(-2, 1.5^2)$$

$$X|\{Y = 2\} \sim N(2, 1.5^2)$$

$$\pi_1 = 0.3$$

$$\pi_2 = 0.7$$

$$g_1(x|\pi_1) = g_2(X|\pi_2)$$

$$\log\left(\frac{1}{\sqrt{2\pi}\sigma_1} + e^{-\frac{(x-\mu_1)^2}{2\sigma_1^2}}\right) + \log(\pi_1) = \log\left(\frac{1}{\sqrt{2\pi}\sigma_2} + e^{-\frac{(x-\mu_2)^2}{2\sigma_2^2}}\right) + \log(\pi_2)$$

$$\log\left(\frac{1}{\sqrt{2\pi}1.5} + e^{-\frac{(x+2)^2}{2 \cdot 1.5^2}}\right) + \log(0.3) = \log\left(\frac{1}{\sqrt{2\pi}1.5} + e^{-\frac{(x-2)^2}{2 \cdot 1.5^2}}\right) + \log(0.7)$$

$$\frac{(x-2)^2 - (x+2)^2}{4.5} + \log(0.3) - \log(0.7) = 0$$

$$\frac{x^2 - 4x + 4 - x^2 - 4x - 4}{4.5} + \log\left(\frac{0.3}{0.7}\right) = 0$$

$$\frac{-8x}{4.5} - 0.847 = 0$$

$$x = -0.477$$

For $x=-0.47$ is the point where the graphs cross, at this point a model would change its decision of which class our point belongs to.

```
# generate data for the two normal distributions
n_samples_class1 <- 3000
n_samples_class2 <- 7000
x1 <- rnorm(n_samples_class1, mean = -2, sd = 1.5)
x2 <- rnorm(n_samples_class2, mean = 2, sd = 1.5)
# create a data frame with the generated data
df <- data.frame(X1 = c(x1, x2), class = c(rep(1, n_samples_class1), rep(2, n_samples_class2)))
```

190c1bd (16.02)

b) i) Corrected three mistakes:

- Corrected the number of folds from 4 to 5.
-
- Corrected the RMSE formula.

```
# Import the Boston housing price dataset
data(Boston)
# select specific variables
selected_vars <- c("crim", "rm", "age", "medv")
boston_selected <- Boston[, selected_vars]

# manually perform the 5-fold cross-validation
folds <- createFolds(boston_selected$medv, k = 5) # CORRECTED to 5
rmse_list <- list()
for (i in 1:length(folds)) {
```

```

# get the training and validation sets
train <- boston_selected[-folds[[i]], ] # CORRECTED
val <- boston_selected[folds[[i]], ]
# fit a linear regression model
model <- lm(medv ~ ., data = train)
# compute RMSE on the validation set
pred <- predict(model, val)
rmse <- sqrt(mean((pred - val$medv)^2)) # CORRECTED squared error (RSME)
rmse <- rmse[1] # take out the value
# store rmse in rmse_list
rmse_list[[i]] <- rmse
}
# compute mean of rmse_list
rmse_mean <- mean(as.numeric(rmse_list))
cat("rmse_mean:", rmse_mean, "\n")

```

```
## rmse_mean: 6.058381
```

****ii)** Changed: `folds <- createFolds(boston_selected$medv, k = 5)` to : `folds <- createFolds(boston_selected$medv, k = nrow(boston_selected))`