Compulsory exercise 1: Group 37

TMA4268 Statistical Learning V2022

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17 February, 2022

Problem 1

a)

$E[(y_0 - \hat{f}(x_0))^2]$
$= E[y_0^2 - 2y_0\hat{f}(x_0) + \hat{f}(x_0)^2]$
$= E[y_0^2] - 2E[y_0\hat{f}(x_0)] + E[\hat{f}(x_0)^2]$
$= E[y_0]^2 + Var[y_0] - 2E[y_0\hat{f}(x_0)] + E[\hat{f}(x_0)]^2 + Var[\hat{f}(x_0)]$
$= E[f(x_0) + \epsilon]^2 + Var[f(x_0) + \epsilon] - 2E[(f(x_0) + \epsilon)\hat{f}(x_0)] + E[\hat{f}(x_0)]^2 + Var[\hat{f}(x_0)]$
It is assumed that ϵ is independent of x, and that $E[\epsilon] = 0$.
$= E[f(x_0) + \epsilon]^2 + Var[f(x_0) + \epsilon] - 2E[\epsilon\hat{f}(x_0)] - 2E[f(x_0)\hat{f}(x_0)] + E[\hat{f}(x_0)]^2 + Var[\hat{f}(x_0)]$
$= E[f(x_0)]^2 + Var[f(x_0)] + Var[\epsilon] - 2E[\epsilon\hat{f}(x_0)] - 2E[f(x_0)\hat{f}(x_0)] + E[\hat{f}(x_0)]^2 + Var[\hat{f}(x_0)]$
$= E[f(x_0)]^2 - 2E[f(x_0)\hat{f}(x_0)] + E[\hat{f}(x_0)]^2 + Var[\hat{f}(x_0)] + Var[\epsilon]$
$= f(x_0)^2 - 2f(x_0)E[\hat{f}(x_0)] + E[\hat{f}(x_0)]^2 + Var[\hat{f}(x_0)] + Var[\epsilon]$
$= (f(x_0) - E[\hat{f}(x_0)])^2 + Var[\hat{f}(x_0)] + Var[\epsilon]$
Where
$Var[\epsilon]$ is the irreducible error,
$Var[\hat{f}(x_0)]$ is the variance of the prediction, and
$(f(x_0) - E[\hat{f}(x_0)])^2$

b)

Irreducible error: - The irreducible error is the error made by the true function f, implying that the irreducible error will always exist no matter how well the model is fit. It may stem from factors that are not captured by the covariates or an inherent stochastisity in the response variable. Reducible error: - The reducible error is caused by the discrepency between the fitted model and the true relationship, and it is the sum of the square of the bias, and the variance Variance: - The variance is typically caused by overfitting the model to the training data. This implies that a new set of training could result in a vastly different model. Bias: - The bias is typically caused by underfitting the model. A high bias is usually found in an inflexible model that fails to capture nuances in the relationship.

c)

1. True
2. False
3. True
4. False

d)

1. True
2. False
3. False
4. False

e)

(iii) 0.76

Problem 2

Here is a code chunk:

```r
library(palmerpenguins) # Contains the data set "penguins".
data(penguins)
head(penguins)
```

```
## # A tibble: 6 x 8
##   species island bill_length_mm bill_depth_mm flipper_length_~ body_mass_g sex
##   <fct>   <fct>           <dbl>         <dbl>            <int>       <int> <fct>
## 1 Adelie  Torge~           39.1          18.7              181        3750 male
## 2 Adelie  Torge~           39.5          17.4              186        3800 fema~
## 3 Adelie  Torge~           40.3          18                195        3250 fema~
## 4 Adelie  Torge~           NA            NA                 NA          NA <NA>
## 5 Adelie  Torge~           36.7          19.3              193        3450 fema~
## 6 Adelie  Torge~           39.3          20.6              190        3650 male
## # ... with 1 more variable: year <int>
```

a)

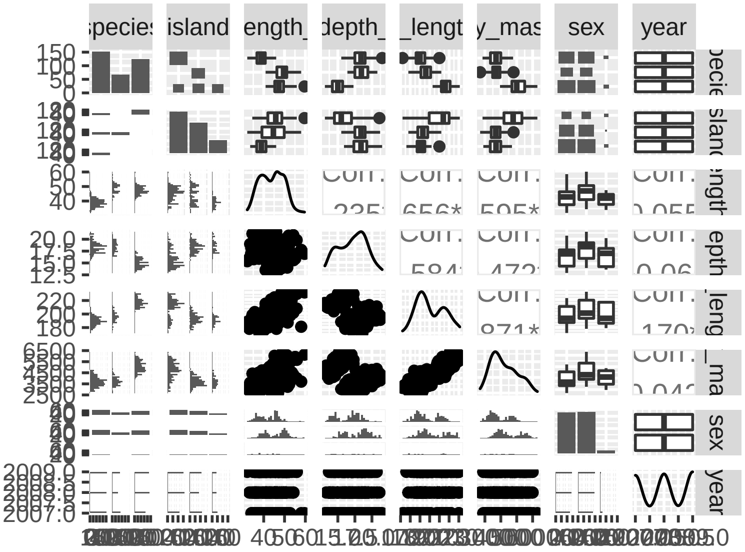
Error 1: - The sex covariate is rejected on the basis of a low p-value. This is wrong because a low p-value indicates that the probability of observing a more extreme value given the null hypothesis is low. In this case, the p-value is way too low to be ignored.

Error 2: - The null hypothesis is tested separately for the categorical covariate. This is incorrect when the covariate has more than two categories, because the dummy variables truly represent the same covariate. Hence, the F-test must be applied in order to evaluate the significance of the categorical covariate, as it can test multiple variables at the same time. The basis on which he kept the species covariate is therefore invalid.

Error 3: - The assumption that the Chinstrap penguins are the largest is possibly wrong, as the interaction term between bill depth and species must also be taken into account.

b)

```r
library(GGally)
ggpairs(penguins)
```



The pairs functions helps with identifying correlations in the data. In this case, the boxplot between sex and body weight indicates a relationship.

c)

```
############## =^._.^= ~~~Oskar and Halvor'S CODE~~~ =^._.^= ##############
############## install.packages('palmerpenguins') # Run if you haven't installed this before.
library(ggfortify)
library(palmerpenguins) # Contains the data set 'penguins'.
data(penguins)
# We do not discard island, as the pairs plot suggests a correlation with body mass.
Penguins <- subset(penguins, select = -c(year))

# Fit the model as specified in advance based on expert knowledge with the inclusion of island:
penguin.model <- lm(body_mass_g ~ flipper_length_mm + sex + bill_depth_mm * species + island,
data = Penguins)

# Look at the model coefficients
summary(penguin.model)$coefficients
```

```
##                                  Estimate Std. Error  t value     Pr(>|t|)
## (Intercept)                   -1385.27845 652.738847 -2.1222552 3.457699e-02
## flipper_length_mm                17.71249   2.941999  6.0205607 4.721257e-09
## sexmale                         430.56261  44.848586  9.6003609 2.304069e-19
## bill_depth_mm                    83.59180  22.449873  3.7234864 2.317818e-04
## speciesChinstrap               1474.29960 681.997594  2.1617372 3.137259e-02
## speciesGentoo                   632.57985 545.520709  1.1595891 2.470726e-01
## islandDream                     -21.35204  58.304464 -0.3662163 7.144434e-01
## islandTorgersen                 -51.77579  60.839901 -0.8510170 3.953904e-01
## bill_depth_mm:speciesChinstrap  -84.58980  37.117784 -2.2789561 2.332189e-02
## bill_depth_mm:speciesGentoo      34.87807  34.595615  1.0081645 3.141301e-01
```

```
anova(penguin.model)
```

```
## Analysis of Variance Table
##
## Response: body_mass_g
##                      Df    Sum Sq   Mean Sq   F value    Pr(>F)
## flipper_length_mm     1 164047703 164047703 1986.9804 < 2.2e-16 ***
## sex                   1   9416589   9416589  114.0557 < 2.2e-16 ***
## bill_depth_mm         1   3667377   3667377   44.4200 1.145e-10 ***
## species               2  10670525   5335262   64.6218 < 2.2e-16 ***
## island                2     59488     29744    0.3603   0.69777
## bill_depth_mm:species   2    730681    365341    4.4251   0.01271 *
## Residuals           323  26667303     82561
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

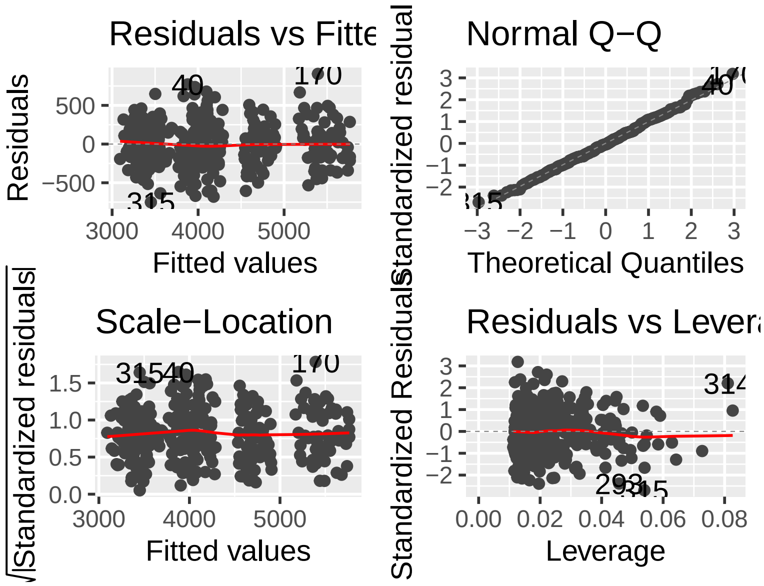
```
# We see from the f test that island is likely not important after all. We do, however, see that the in

# Fit final model with sex
final.model <- lm(body_mass_g ~ flipper_length_mm + bill_depth_mm * species + sex, data = Penguins)

summary(final.model)
```

```
##
## Call:
## lm(formula = body_mass_g ~ flipper_length_mm + bill_depth_mm *
##     species + sex, data = Penguins)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -751.2 -183.8   -9.8  191.1  906.9
##
## Coefficients:
##                                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)                     -1336.58     646.92  -2.066 0.039615 *
## flipper_length_mm                  17.38       2.91   5.971 6.17e-09 ***
## bill_depth_mm                      82.98      22.32   3.717 0.000237 ***
## speciesChinstrap                 1460.15     680.39   2.146 0.032610 *
## speciesGentoo                     644.88     542.57   1.189 0.235481
## sexmale                           432.90      44.63   9.699  < 2e-16 ***
## bill_depth_mm:speciesChinstrap   -83.53      37.01  -2.257 0.024666 *
## bill_depth_mm:speciesGentoo       36.17      34.48   1.049 0.294955
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 286.8 on 325 degrees of freedom
##   (11 observations deleted due to missingness)
## Multiple R-squared:  0.8758, Adjusted R-squared:  0.8732
## F-statistic: 327.5 on 7 and 325 DF,  p-value: < 2.2e-16
```

```
anova(final.model)
```

```
## Analysis of Variance Table
##
## Response: body_mass_g
##                       Df    Sum Sq   Mean Sq   F value  Pr(>F)
## flipper_length_mm       1 164047703 164047703 1994.7424 < 2e-16 ***
## bill_depth_mm           1    338887    338887    4.1207 0.04318 *
## species                 2  15483131   7741565   94.1338 < 2e-16 ***
## sex                     1   7932472   7932472   96.4551 < 2e-16 ***
## bill_depth_mm:species   2    729458    364729    4.4349 0.01258 *
## Residuals             325  26728014     82240
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
autoplot(final.model,smooth.colour="red")
```



REPORT: PREDICTION OF PENGUIN BODY MASS, by Oskar and Halvor :3 We begin with a linear regression model with body mass as the response, and flipper length, bill depth, species, island and sex as covariates, as well as an interaction effect between bill depth and species. We see that the island term has a large p-value and it is therefore discarded, as it does not seem to be correlated with body mass. From the f-test we see that both the categorical variables are probably significant. The final model can be described depending on the species of the penguin:

$$\hat{y}_{adelie} = \hat{\beta}_0 + \hat{\beta}_{flipper\_length}x_{flipper\_length} + \hat{\beta}_{sex\_male}x_{sex\_male} + \hat{\beta}_{bill\_depth}x_{bill\_depth}$$

$$\hat{y}_{chinstrap} = \hat{\beta}_0 + \hat{\beta}_{flipper\_length}x_{flipper\_length} + \hat{\beta}_{sex\_male}x_{sex\_male} + (\hat{\beta}_{bill\_depth} + \hat{\beta}_{bill\_depth:chinstrap})x_{bill\_depth} + \hat{\beta}_{chinstra}$$

$$\hat{y}_{gentoo} = \hat{\beta}_0 + \hat{\beta}_{flipper\_length}x_{flipper\_length} + \hat{\beta}_{sex\_male}x_{sex\_male} + (\hat{\beta}_{bill\_depth} + \hat{\beta}_{bill\_depth:gentoo})x_{bill\_depth} + \hat{\beta}_{gentoo}$$

(where $\hat{y}_{adelie}$ is the predicted body mass for Adelie penguins, $\hat{\beta}_0$ is the estimated intercept, $x_{flipper\_length}$ is the flipper length covariate, $\hat{\beta}_{flipper\_length}$ is the estimated flipper length coefficient, etc.) Note that x_{sex_male} is 1 if the penguin is male and 0 if female. In the final model, all terms have small (<0.05) f-values, signaling a strong correlation with the response. The assumptions of a linear model can be checked with the four plot supplied by the autoplot() function. From the qq-plot we see strong evidence that the residuals are normally distributed. From the Tukey-Anscombe diagram we see evidence of the residuals having expectation 0 and equal σ^2. This is also backed up by the scale location plot. There is also no apparent pattern in the T-A diagram, suggesting that the residuals are independent. The leverage plot is useful for determining outliers with high leverage. There is one data point in particular that warrants further inspection, as it has quite high leverage and might be an outlier.

Problem 3

a)

```
library(tidyverse)
library(GGally)
# Create a new boolean variable indicating whether or not the penguin is an
# Adelie penguin
Penguins$adelie <- ifelse(Penguins$species == "Adelie", 1, 0)
# Select only relevant variables and remove all rows with missing values in body
# mass, flipper length, sex or species.
Penguins_reduced <- Penguins %>% dplyr::select(body_mass_g, flipper_length_mm, adelie) %>%
mutate(body_mass_g = as.numeric(body_mass_g), flipper_length_mm = as.numeric(flipper_length_mm)) %>%drop
set.seed(4268)
# 70% of the sample size for training set
training_set_size <- floor(0.7 * nrow(Penguins_reduced))
train_ind <- sample(seq_len(nrow(Penguins_reduced)), size = training_set_size)
train <- Penguins_reduced[train_ind, ]
test <- Penguins_reduced[-train_ind, ]
```

(i)

```
penguin.glm = glm(adelie ~ ., data=train, family="binomial")
penguin.glm.probs = predict(penguin.glm, type="response", newdata=test)
penguin.glm.preds = ifelse(penguin.glm.probs > 0.5, 1, 0)
conf.glm = table(penguin.glm.preds, test$adelie)
```

(ii)

```
library(MASS)
penguin.qda = qda(adelie ~ ., data=train)
penguin.qda.probs = predict(penguin.qda, newdata=test)$posterior
penguin.qda.preds = predict(penguin.qda, newdata=test)$class
conf.qda = table(penguin.qda.preds, test$adelie)
```

(iii)

```
library(class)
penguin.knn = knn(train = train, test = test, cl = train$adelie, k=25, prob=T)
penguin.knn.probs = attributes(penguin.knn)$prob
not.adelie = which(penguin.knn == 0)
```

```
penguin.knn.probs[not.adelie] = 1-penguin.knn.probs[not.adelie]
conf.knn = table(penguin.knn, test$adelie)
```

(iv)

```
#True positive rate
sensitivity = function(table){
  return (table[2,2]/(table[2,2]+table[1,2]))
}
#True negative rate
specificity = function(table){
  return (table[1,1]/(table[1,1]+table[2,1]))
}

cat("Sensitivity for logistic regression:", sensitivity(conf.glm), "\n")
```

```
## Sensitivity for logistic regression: 0.9767442
```

```
cat("Specificity for logistic regression:", specificity(conf.glm), "\n")
```

```
## Specificity for logistic regression: 0.8666667
```

```
cat("Sensitivity for QDA:", sensitivity(conf.qda), "\n")
```

```
## Sensitivity for QDA: 0.9767442
```

```
cat("Specificity for QDA:", specificity(conf.qda), "\n")
```

```
## Specificity for QDA: 0.7666667
```

```
cat("Sensitivity for KNN:", sensitivity(conf.knn), "\n")
```

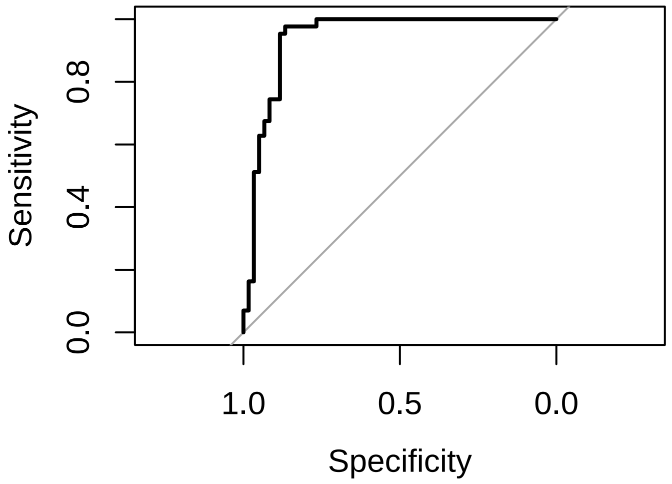
```
## Sensitivity for KNN: 0.9534884
```

```
cat("Specificity for KNN:", specificity(conf.knn), "\n")
```

```
## Specificity for KNN: 0.5833333
```

b)

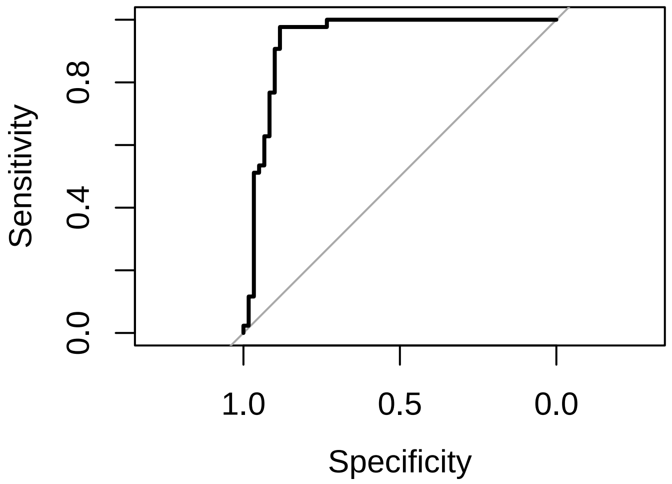
```
library(pROC)
library(plotROC)
roc.glm = roc(response = test$adelie, predictor = penguin.glm.probs, direction = "<")
plot(roc.glm)
```



```
auc(roc.glm)
```

```
## Area under the curve: 0.9391
```

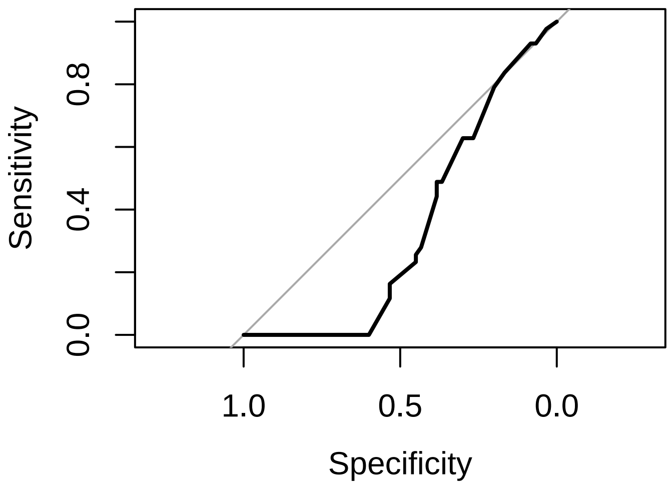
```
roc.qda = roc(response = test$adelie, predictor = penguin.qda.probs[,2], direction = "<")
plot(roc.qda)
```



```
auc(roc.qda)
```

```
## Area under the curve: 0.938
```

```
roc.knn = roc(response = test$adelie, predictor = penguin.knn.probs, direction = "<")
plot(roc.knn)
```



```
auc(roc.knn)
```

```
## Area under the curve: 0.3374
```

Problem 4