DATA 622 Assignment 1

CUNY: Spring 2021

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```r
library(palmerpenguins)
library(dplyr)
library(ggplot2)
library(tidyr)
library(caret)
library(MASS)
library(pROC)
library(nnet) # Used for multinomial logistic regression
library(mlogit)
library(stargazer)
library(popbio)
theme_set(theme_minimal())
```

The palmer penguins dataset consists of 8 variables, 7 independent variables and 1 dependent variable (species).

Variables

species: species of the penguin observed island: consider it (No NA) bill_length_mm: penguin bill length in millimeters bill_depth_mm: penguin bill depth in millimeters flipper_length_mm: penguin flipper length in millimeters body_mass_g: penguin body mass in grams sex: penguin sex year: year of observation

```r
ds <- penguins

head(ds)
```

```
## # 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>
```

```r
summary(ds)
```

```
##       species          island    bill_length_mm  bill_depth_mm  
##  Adelie   :152   Biscoe   :168   Min.   :32.10   Min.   :13.10  
##  Chinstrap: 68   Dream    :124   1st Qu.:39.23   1st Qu.:15.60  
##  Gentoo   :124   Torgersen: 52   Median :44.45   Median :17.30  
##                                  Mean   :43.92   Mean   :17.15  
##                                  3rd Qu.:48.50   3rd Qu.:18.70  
##                                  Max.   :59.60   Max.   :21.50  
##                                  NA's   :2       NA's   :2      
##  flipper_length_mm  body_mass_g       sex           year     
##  Min.   :172.0     Min.   :2700   female:165   Min.   :2007  
##  1st Qu.:190.0     1st Qu.:3550   male  :168   1st Qu.:2007  
##  Median :197.0     Median :4050   NA's  : 11   Median :2008  
##  Mean   :200.9     Mean   :4202                Mean   :2008  
##  3rd Qu.:213.0     3rd Qu.:4750                3rd Qu.:2009  
##  Max.   :231.0     Max.   :6300                Max.   :2009  
##  NA's   :2         NA's   :2
```

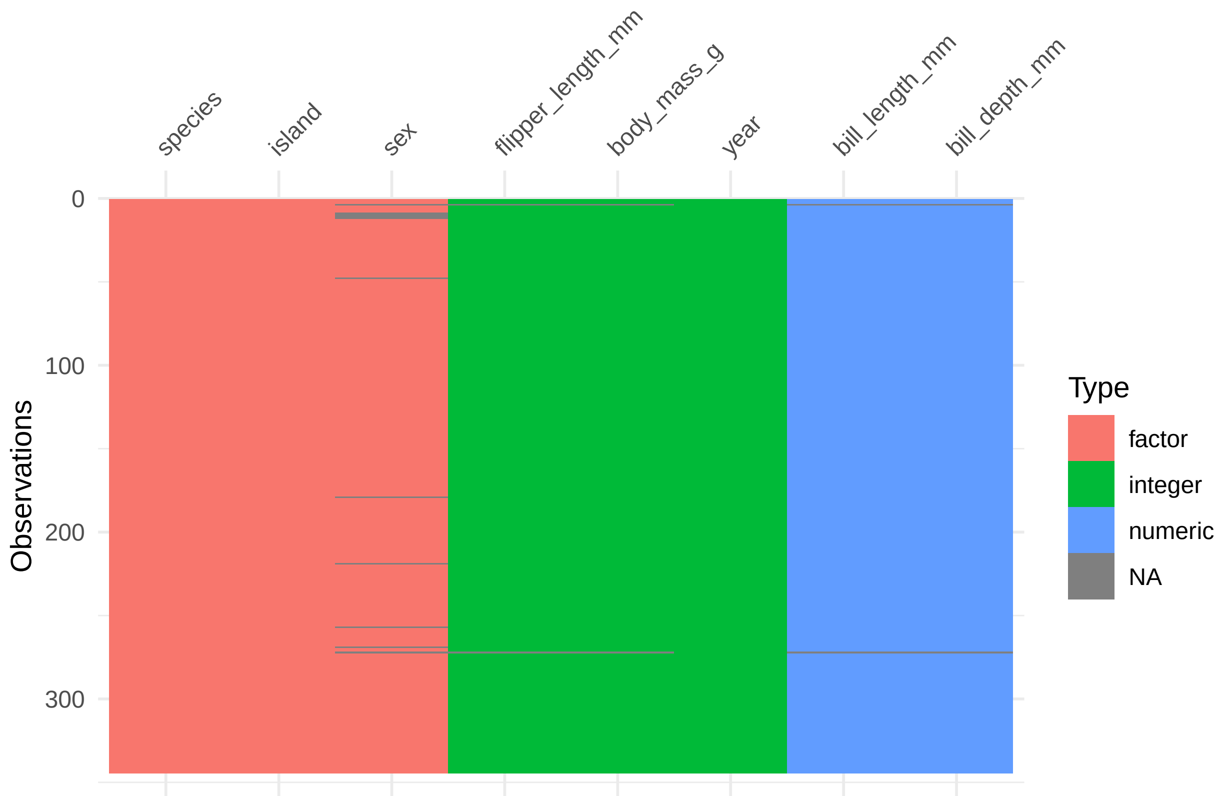
```r
dim(ds)
```

```
## [1] 344   8
```

```r
glimpse(ds)
```

```
## Rows: 344
## Columns: 8
## $ species           <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, A...
## $ island            <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torge...
## $ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34....
## $ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18....
## $ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, ...
## $ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 347...
## $ sex               <fct> male, female, female, NA, female, male, female, m...
## $ year              <int> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2...
```

```r
visdat::vis_dat(ds)
```




```
# Penguins data has three factor variables
ds %>%
  dplyr::select(where(is.factor)) %>%
  glimpse()
```

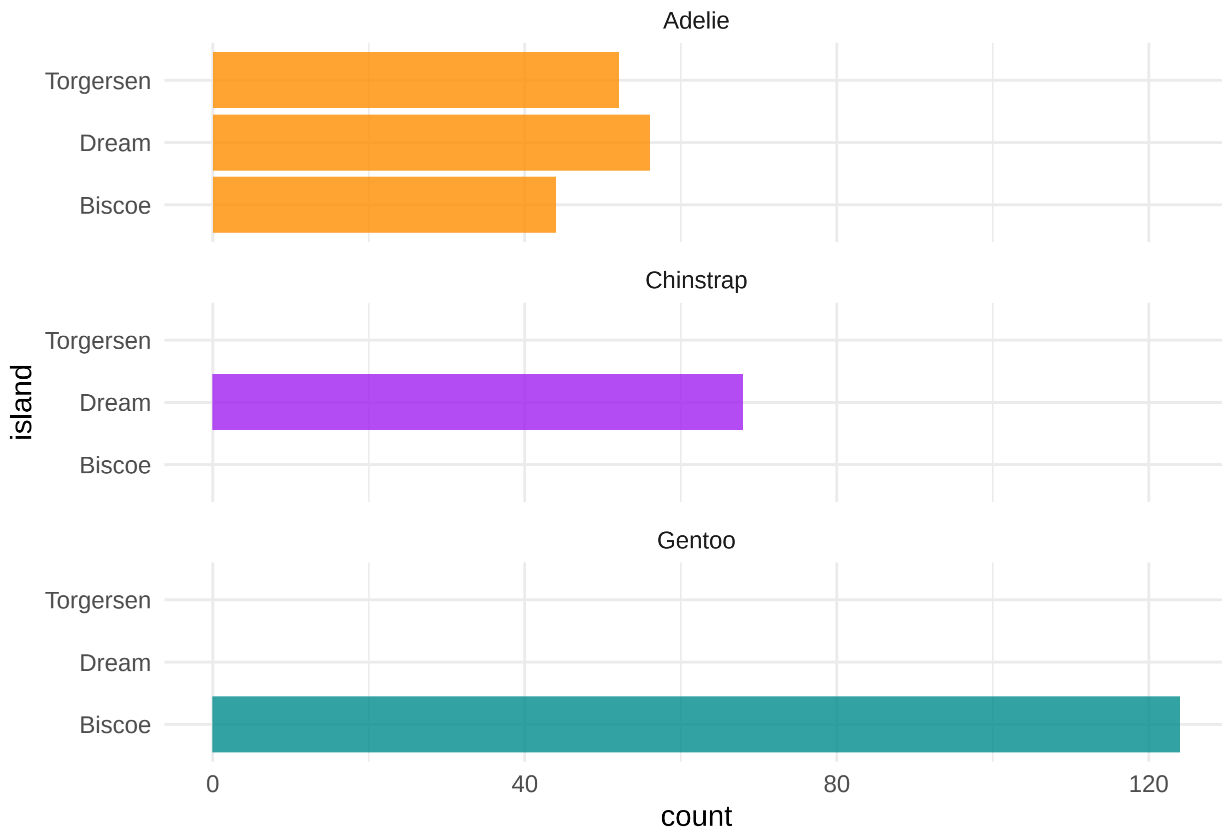
```
## Rows: 344
## Columns: 3
## $ species <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Ade...
## $ island  <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torgersen, Torg...
## $ sex     <fct> male, female, female, NA, female, male, female, male, NA, N...
```

```
# Count penguins for each species / island
ds %>%
  count(species, island, .drop=F)
```

```
## # A tibble: 9 x 3
##   species   island        n
##   <fct>     <fct>     <int>
## 1 Adelie    Biscoe       44
## 2 Adelie    Dream        56
## 3 Adelie    Torgersen    52
## 4 Chinstrap Biscoe        0
## 5 Chinstrap Dream        68
## 6 Chinstrap Torgersen     0
## 7 Gentoo    Biscoe      124
```

```
## 8 Gentoo    Dream         0
## 9 Gentoo    Torgersen     0
```

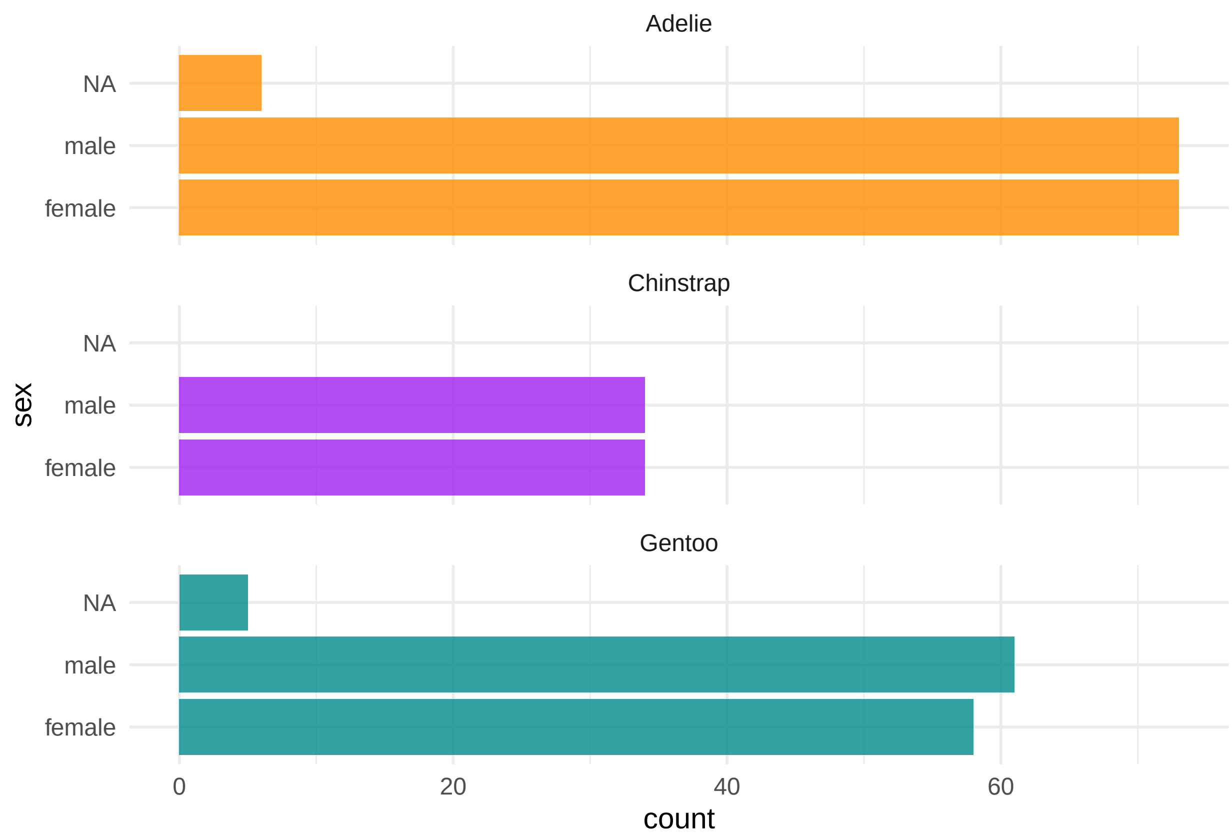
```r
ggplot(ds, aes(x = island, fill = species)) +
  geom_bar(alpha = 0.8) +
  scale_fill_manual(values = c("darkorange", "purple", "cyan4"),
                    guide = F) +
  theme_minimal() +
  facet_wrap(~species, ncol = 1) +
  coord_flip()
```




```r
# Count penguins for each species / sex
ds %>%
  count(species, sex, .drop = F)
```

```
## # A tibble: 8 x 3
##   species   sex        n
##   <fct>     <fct>  <int>
## 1 Adelie    female    73
## 2 Adelie    male      73
## 3 Adelie    <NA>       6
## 4 Chinstrap female    34
## 5 Chinstrap male      34
## 6 Gentoo    female    58
## 7 Gentoo    male      61
## 8 Gentoo    <NA>       5
```

```r
ggplot(ds, aes(x = sex, fill = species)) +
  geom_bar(alpha = 0.8) +
  scale_fill_manual(values = c("darkorange", "purple", "cyan4"),
                    guide = F) +
  theme_minimal() +
  facet_wrap(~species, ncol = 1) +
  coord_flip()
```



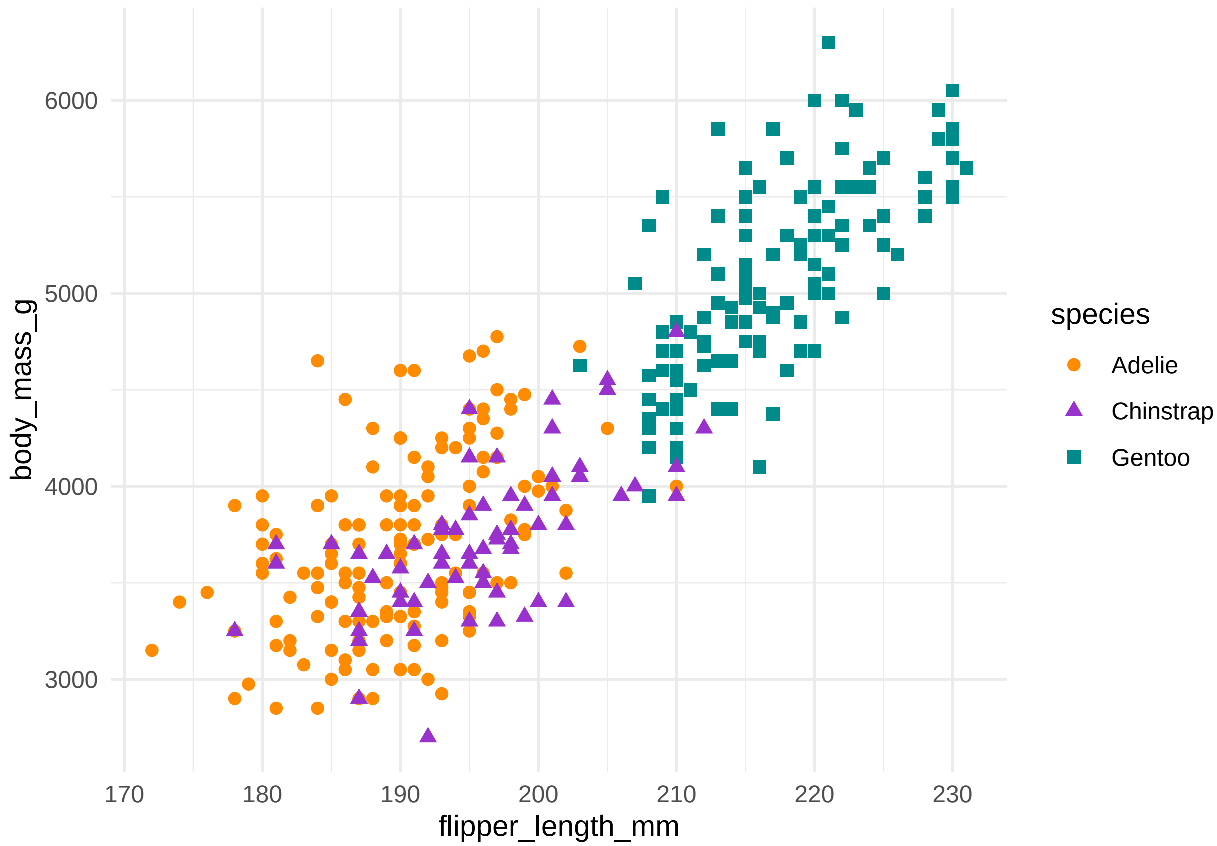

```r
# Penguins data also has four continuous variables, making six unique scatterplots
ds %>%
  dplyr::select(body_mass_g, ends_with("_mm")) %>%
  glimpse()
```

```
## Rows: 344
## Columns: 4
## $ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 347...
## $ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34....
## $ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18....
## $ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, ...
```

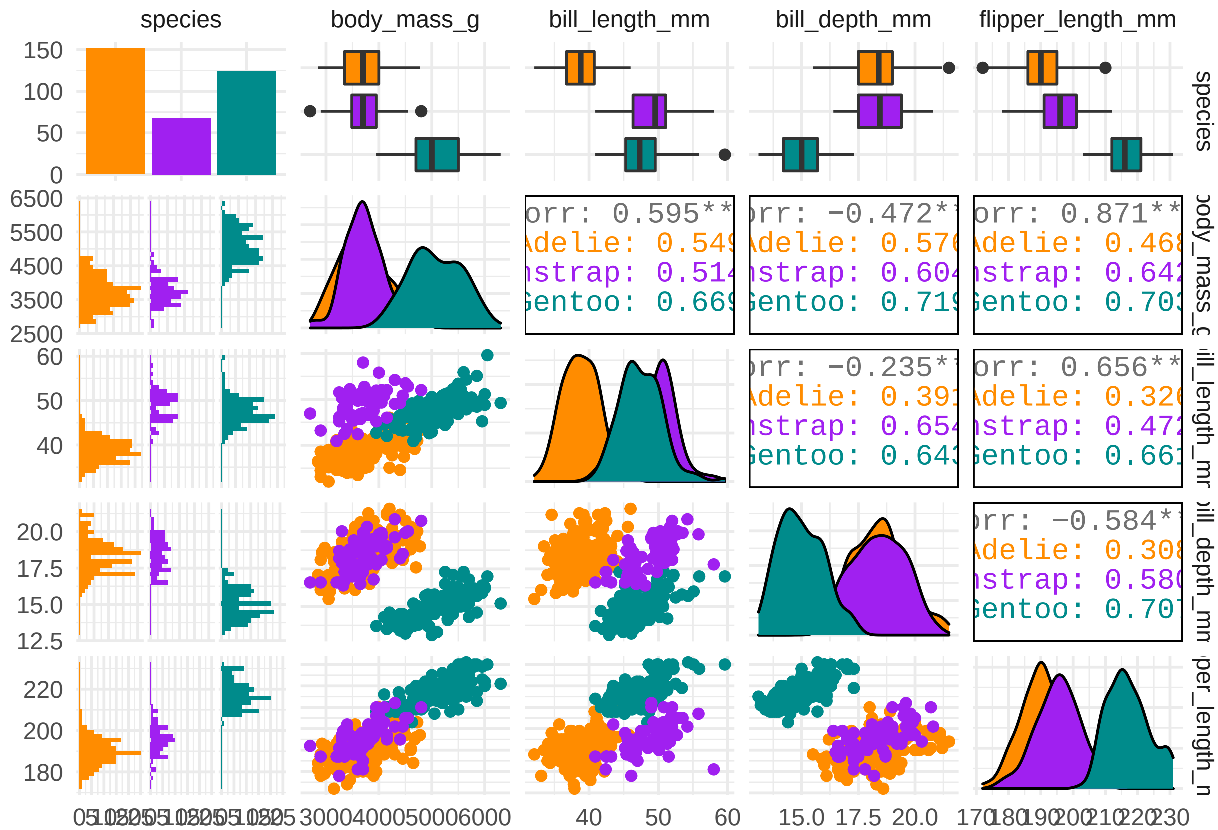
```r
# Scatterplot example 1: penguin flipper length versus body mass
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species,
                 shape = species),
```

```
            size = 2) +
  scale_color_manual(values = c("darkorange", "darkorchid", "cyan4"))
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```




```
ds %>%
  dplyr::select(species, body_mass_g, ends_with("_mm")) %>%
  GGally::ggpairs(aes(color = species)) +
  scale_color_manual(values = c("darkorange","purple","cyan4")) +
  scale_fill_manual(values = c("darkorange","purple","cyan4"))
```




```r
# Create dataset for binary logistic regression: species Gentoo or Not
data_binary <- penguins

# Only use complete instances ... actually come back to this as I don't want to exclude because of sex
train_data_binary <- na.omit(data_binary)

dim(train_data_binary)
```

```
## [1] 333   8
```

Based on the result, 11 rows are removed, which would equal the number of NAs in variable *sex*.

Binary Logistic Regression

The following approach attempts to construct a logistic regression model based on a binary outcome. As the penguins dataset is based on a dependent variable (species) containing three values, a dummy variable *Gentoo* is defined to identify penguins of the species Gentoo or of the other two values (Adelie and Chinstrap). Based on the exploratory data analysis indicating independent variable overlap for body mass, bill depth, and flipper length between the Adelie and Chinstrap species, the decision was made to group these two species based on the similarities.

```r
# Create new column
train_data_binary$gentoo <- ifelse(train_data_binary$species=="Gentoo", 1, 0)
```

```r
summary(train_data_binary)
```

```
##       species          island    bill_length_mm  bill_depth_mm
##  Adelie   :146   Biscoe   :163   Min.   :32.10   Min.   :13.10
##  Chinstrap: 68   Dream    :123   1st Qu.:39.50   1st Qu.:15.60
##  Gentoo   :119   Torgersen: 47   Median :44.50   Median :17.30
##                                  Mean   :43.99   Mean   :17.16
##                                  3rd Qu.:48.60   3rd Qu.:18.70
##                                  Max.   :59.60   Max.   :21.50
##  flipper_length_mm  body_mass_g       sex           year          gentoo
##  Min.   :172       Min.   :2700   female:165   Min.   :2007   Min.   :0.0000
##  1st Qu.:190       1st Qu.:3550   male  :168   1st Qu.:2007   1st Qu.:0.0000
##  Median :197       Median :4050                Median :2008   Median :0.0000
##  Mean   :201       Mean   :4207                Mean   :2008   Mean   :0.3574
##  3rd Qu.:213       3rd Qu.:4775                3rd Qu.:2009   3rd Qu.:1.0000
##  Max.   :231       Max.   :6300                Max.   :2009   Max.   :1.0000
```

With the derived dummy variable *Gentoo*, the variable *species* is removed from the initial dataset, so as not to impact the logistic regression models.

```r
# Drop species column, as now just using gentoo column as Y variable

drops <- c("species")
train_data_binary <- train_data_binary[ , !(names(train_data_binary) %in% drops)]

summary(train_data_binary)
```

```
##        island    bill_length_mm  bill_depth_mm   flipper_length_mm
##  Biscoe   :163   Min.   :32.10   Min.   :13.10   Min.   :172
##  Dream    :123   1st Qu.:39.50   1st Qu.:15.60   1st Qu.:190
##  Torgersen: 47   Median :44.50   Median :17.30   Median :197
##                  Mean   :43.99   Mean   :17.16   Mean   :201
##                  3rd Qu.:48.60   3rd Qu.:18.70   3rd Qu.:213
##                  Max.   :59.60   Max.   :21.50   Max.   :231
##   body_mass_g       sex           year          gentoo
##  Min.   :2700   female:165   Min.   :2007   Min.   :0.0000
##  1st Qu.:3550   male  :168   1st Qu.:2007   1st Qu.:0.0000
##  Median :4050                Median :2008   Median :0.0000
##  Mean   :4207                Mean   :2008   Mean   :0.3574
##  3rd Qu.:4775                3rd Qu.:2009   3rd Qu.:1.0000
##  Max.   :6300                Max.   :2009   Max.   :1.0000
```

In order to validate the models property, the initial penguins dataset is partitioned into training data at 70% of the given dataset with the remaining 30% used as test data completely unseen by the model.

```r
set.seed(123)
trainIndex <-createDataPartition(train_data_binary$gentoo, p = 0.7, list = FALSE, times = 1)
train <- train_data_binary[trainIndex,]
test <- train_data_binary[-trainIndex,]
```

Three versions of a binary logistic regression model are constructed in order to evaluate the accuracy of each and also provide to narrow the model to the least number of variables to identify the most parsimomious model.

Baseline Model

The first model uses all the available independent variables in order to define a baseline evaluation of the model.

```
# All variables
model1 <- glm(gentoo ~ ., data = train, family = "binomial"(link="logit"))
#Accuracy 100%, AIC is 18
summary(model1)
```

```
##
## Call:
## glm(formula = gentoo ~ ., family = binomial(link = "logit"),
##     data = train)
##
## Deviance Residuals:
##        Min          1Q      Median          3Q         Max
## -3.722e-05  -2.100e-08  -2.100e-08   2.100e-08   2.985e-05
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)        7.439e+03  1.581e+08       0        1
## islandDream       -1.043e+01  1.197e+05       0        1
## islandTorgersen   -1.180e+01  1.124e+05       0        1
## bill_length_mm     7.064e-01  1.136e+04       0        1
## bill_depth_mm     -9.278e+00  3.578e+04       0        1
## flipper_length_mm  9.491e-01  6.324e+03       0        1
## body_mass_g        1.516e-02  1.527e+02       0        1
## sexmale            1.990e+00  1.590e+05       0        1
## year              -3.773e+00  7.865e+04       0        1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3.0884e+02  on 233  degrees of freedom
## Residual deviance: 4.3248e-09  on 225  degrees of freedom
## AIC: 18
##
## Number of Fisher Scoring iterations: 25
```

Resulting AIC: 18.

Stepwise Model

Next, the *stepAIC* function is applied to the full model to determine the most ??meaningful?? variables for the model.

```
# All variables then applied with stepAIC
model2 <- glm(gentoo ~ ., data = train, family = "binomial"(link="logit")) %>% stepAIC(trace=F, directi
# Accuracy 100% an AIC is 6
summary(model2)
```

```
##
```

```
## Call:
## glm(formula = gentoo ~ bill_depth_mm + flipper_length_mm, family = binomial(link = "logit"),
##     data = train)
##
## Deviance Residuals:
##        Min          1Q      Median          3Q         Max
## -6.826e-05  -2.100e-08  -2.100e-08   2.100e-08   6.510e-05
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)         -428.130 474946.766  -0.001    0.999
## bill_depth_mm        -14.834  12021.243  -0.001    0.999
## flipper_length_mm      3.274   1957.819   0.002    0.999
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 3.0884e+02  on 233  degrees of freedom
## Residual deviance: 9.5967e-09  on 231  degrees of freedom
## AIC: 6
##
## Number of Fisher Scoring iterations: 25
```

Resulting AIC: 6.

Hand Selected Model

Finally, a hand-selected list of independent variables are selected based on the evaluation of the exploratory data analysis.

```
# Hand selected variables
model3 <- glm(gentoo ~ island + bill_depth_mm + flipper_length_mm + body_mass_g, data = train, family =
# Accuracy 100%, AIC is 12
summary(model3)
```

```
##
## Call:
## glm(formula = gentoo ~ island + bill_depth_mm + flipper_length_mm +
##     body_mass_g, family = binomial(link = "logit"), data = train)
##
## Deviance Residuals:
##        Min          1Q      Median          3Q         Max
## -4.069e-05  -2.100e-08  -2.100e-08   2.100e-08   2.804e-05
##
## Coefficients:
##                     Estimate Std. Error z value Pr(>|z|)
## (Intercept)       -1.402e+02  6.440e+05   0.000    1.000
## islandDream       -1.390e+00  4.055e+04   0.000    1.000
## islandTorgersen   -5.044e+00  7.407e+04   0.000    1.000
## bill_depth_mm     -1.049e+01  1.142e+04  -0.001    0.999
## flipper_length_mm  1.098e+00  3.818e+03   0.000    1.000
## body_mass_g        1.958e-02  5.657e+01   0.000    1.000
##
## (Dispersion parameter for binomial family taken to be 1)
```

```
##
##     Null deviance: 3.0884e+02  on 233  degrees of freedom
## Residual deviance: 4.7527e-09  on 228  degrees of freedom
## AIC: 12
##
## Number of Fisher Scoring iterations: 25
```

Resulting AIC: 12.

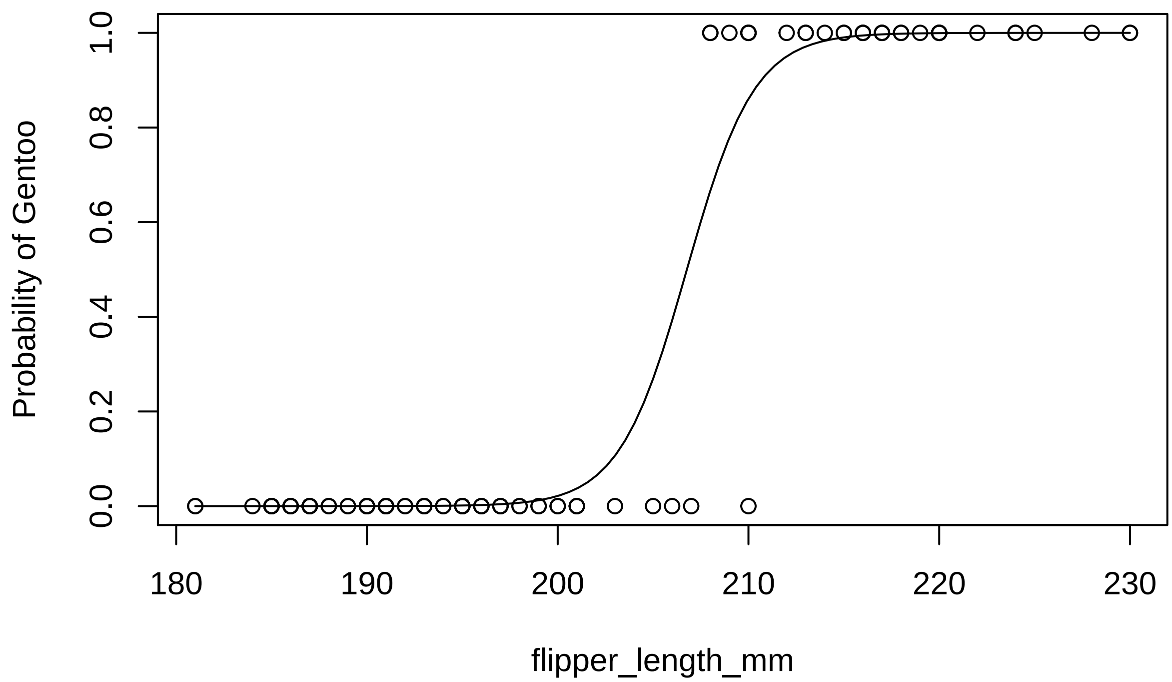
```r
## use the test data set to make predictions for the 3 models
mod1.predict.probs <- predict.glm(model1, type="response", newdata=test)
mod1.predict.manual <- ifelse(mod1.predict.probs > 0.5, '1','0')
attach(test)

mod2.predict.probs <- predict.glm(model2, type="response", newdata=test)
mod2.predict.manual <- ifelse(mod2.predict.probs > 0.5, '1','0')
attach(test)
```

```
## The following objects are masked from test (pos = 3):
##
##     bill_depth_mm, bill_length_mm, body_mass_g, flipper_length_mm,
##     gentoo, island, sex, year
```

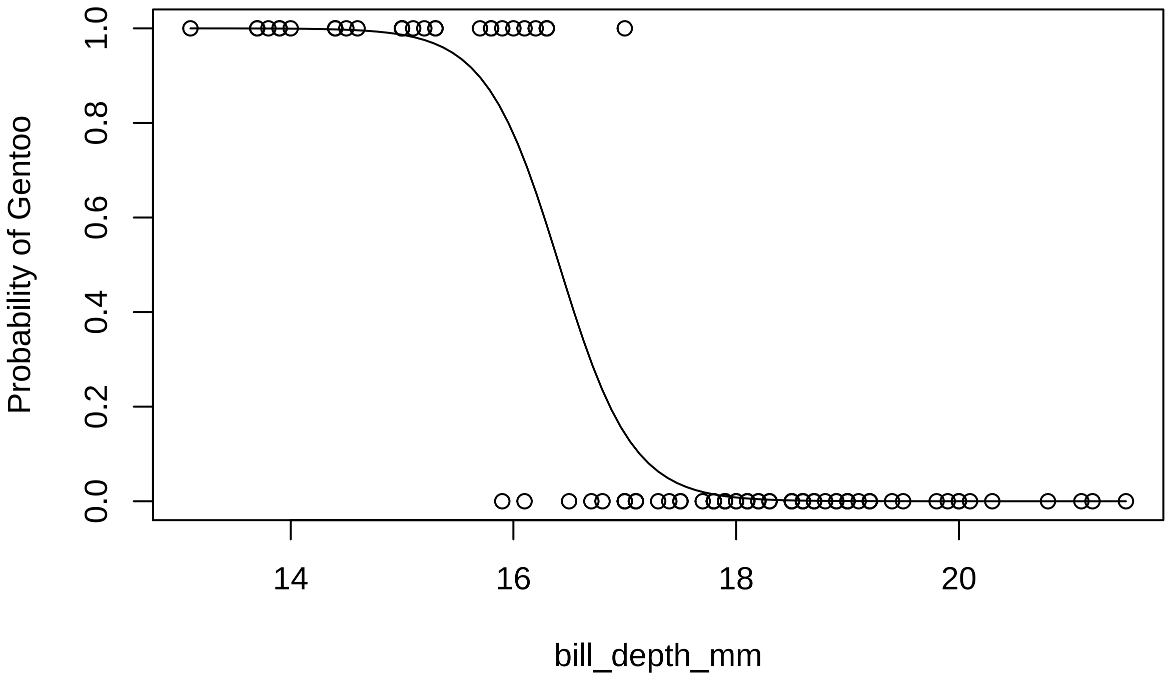
```r
mod3.predict.probs <- predict.glm(model3, type="response", newdata=test)
mod3.predict.manual <- ifelse(mod3.predict.probs > 0.5, '1','0')
attach(test)
```

```
## The following objects are masked from test (pos = 3):
##
##     bill_depth_mm, bill_length_mm, body_mass_g, flipper_length_mm,
##     gentoo, island, sex, year

## The following objects are masked from test (pos = 4):
##
##     bill_depth_mm, bill_length_mm, body_mass_g, flipper_length_mm,
##     gentoo, island, sex, year
```

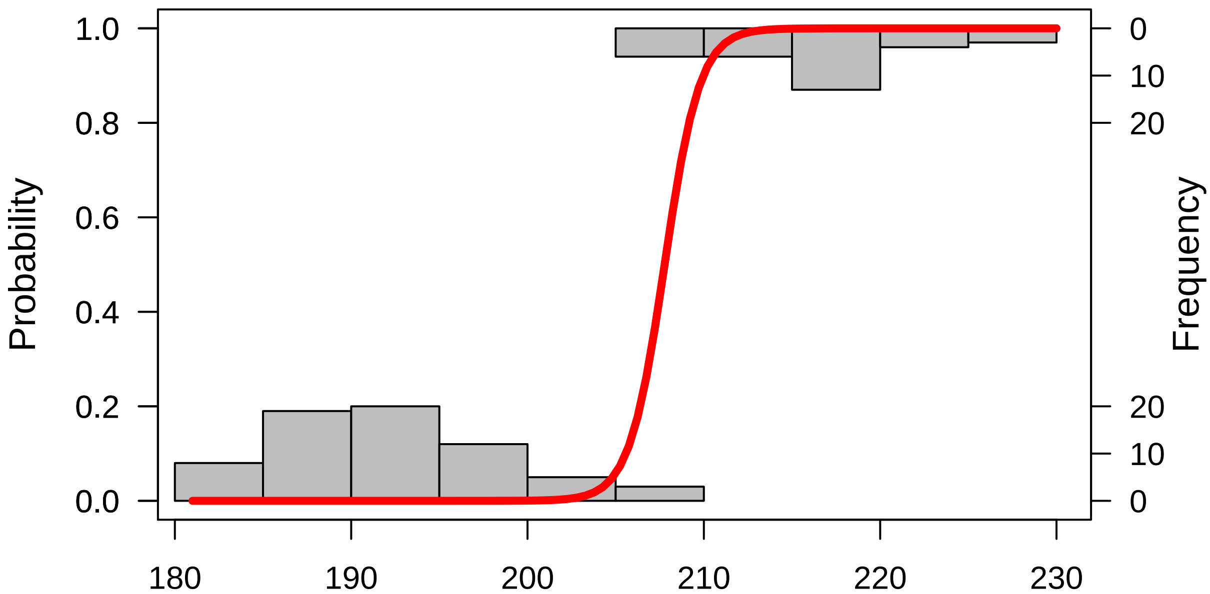
```r
# Plot the dependent variable interpretation
# https://sites.google.com/site/daishizuka/toolkits/plotting-logistic-regression-in-r

# plot with flipper_length_mm on x-axis and Gentoo species (0 or 1) on y-axis
plot(flipper_length_mm,gentoo,xlab="flipper_length_mm",ylab="Probability of Gentoo")
g=glm(gentoo ~ flipper_length_mm, data = train, family = "binomial"(link="logit"))
curve(predict(g,data.frame(flipper_length_mm=x),type="resp"),add=TRUE)
```




```r
# plot with bill_depth_mm on x-axis and Gentoo species (0 or 1) on y-axis
plot(bill_depth_mm,gentoo,xlab="bill_depth_mm",ylab="Probability of Gentoo")
g=glm(gentoo ~ bill_depth_mm, data = train, family = "binomial"(link="logit"))
curve(predict(g,data.frame(bill_depth_mm=x),type="resp"),add=TRUE)
```




```r
# plot using another function
logi.hist.plot(flipper_length_mm,gentoo,boxp=FALSE,type="hist",col="gray")
```



Model 1 Results

```
# Model1
# now can use the caret function
cm.var <- caret::confusionMatrix(factor(mod1.predict.manual), factor(test$gentoo), positive='1')
cm.var$table
```

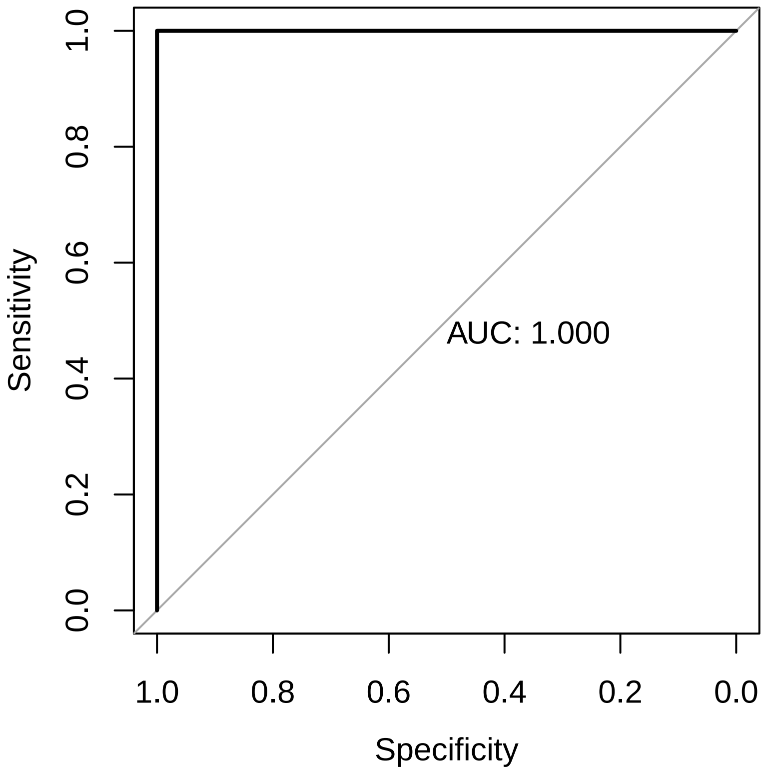
```
##           Reference
## Prediction  0  1
##          0 67  0
##          1  0 32
```

```
# print metrics
mod1.CMmetrics <- c(cm.var$overall[c(1)], cm.var$byClass[c(1,2,5,6,7)])
mod1.CMmetrics
```

```
##    Accuracy Sensitivity Specificity   Precision      Recall          F1
##           1           1           1           1           1           1
```

```
# ROC and AUC
par(pty="s")
roc.stepwise <- roc(train$gentoo, model1$fitted.values, plot=TRUE, print.auc=TRUE)
```

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

## Setting direction: controls < cases
```




```r
# Dispersion Statistic
E2 <- resid(model1, type = "pearson")
N  <- nrow(train)
p  <- length(coef(model1)) + 1 # '+1' is due to theta
mod1.dispersion <- dispesion <-sum(E2^2) / (N - p)
```

Model 2 Results

```r
# Model2
# now can use the caret function
cm.var <- caret::confusionMatrix(factor(mod2.predict.manual), factor(test$gentoo), positive='1')
cm.var$table
```

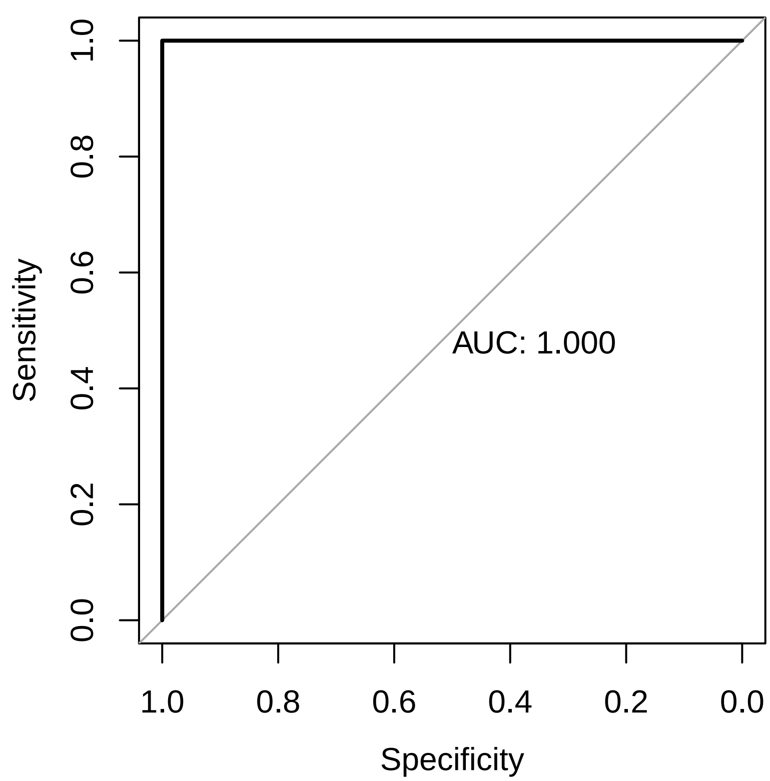
```
##           Reference
## Prediction  0  1
##          0 67  0
##          1  0 32
```

```r
# print metrics
mod2.CMmetrics <- c(cm.var$overall[c(1)], cm.var$byClass[c(1,2,5,6,7)])
mod2.CMmetrics
```

```
##    Accuracy Sensitivity Specificity   Precision      Recall          F1
##           1           1           1           1           1           1
```

```r
# ROC and AUC
par(pty="s")
roc.stepwise <- roc(train$gentoo, model2$fitted.values, plot=TRUE, print.auc=TRUE)
```

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

## Setting direction: controls < cases
```




```r
# Dispersion Statistic
E2 <- resid(model2, type = "pearson")
N  <- nrow(train)
p  <- length(coef(model2)) + 1 # '+1' is due to theta
mod2.dispersion <- dispesion <-sum(E2^2) / (N - p)
```

Model 3 Results

```r
# Model3
# now can use the caret function
cm.var <- caret::confusionMatrix(factor(mod3.predict.manual), factor(test$gentoo), positive='1')
cm.var$table
```

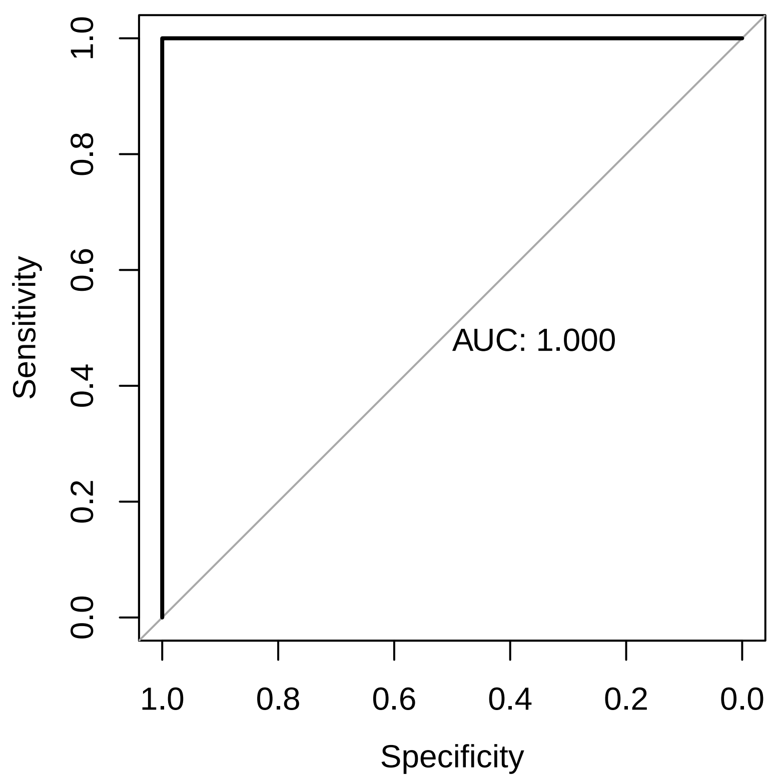
```
##           Reference
## Prediction  0  1
##          0 67  0
##          1  0 32
```

```r
# print metrics
mod3.CMmetrics <- c(cm.var$overall[c(1)], cm.var$byClass[c(1,2,5,6,7)])
mod3.CMmetrics
```

```
##    Accuracy Sensitivity Specificity   Precision      Recall          F1
##           1           1           1           1           1           1
```

```r
# ROC and AUC
par(pty="s")
roc.stepwise <- roc(train$gentoo, model3$fitted.values, plot=TRUE, print.auc=TRUE)
```

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

## Setting direction: controls < cases
```



```r
# Dispersion Statistic
E2 <- resid(model3, type = "pearson")
N  <- nrow(train)
p  <- length(coef(model3)) + 1 # '+1' is due to theta
mod3.dispersion <- dispesion <-sum(E2^2) / (N - p)
```

Multinomial Logistic Regression

```r
# Initial walk-through: https://stats.idre.ucla.edu/r/dae/multinomial-logistic-regression/

# Start with initial dateset
mlr_data <- penguins

summary(mlr_data)
```

```
##       species          island    bill_length_mm  bill_depth_mm
##  Adelie   :152   Biscoe   :168   Min.   :32.10   Min.   :13.10
##  Chinstrap: 68   Dream    :124   1st Qu.:39.23   1st Qu.:15.60
##  Gentoo   :124   Torgersen: 52   Median :44.45   Median :17.30
##                                  Mean   :43.92   Mean   :17.15
##                                  3rd Qu.:48.50   3rd Qu.:18.70
##                                  Max.   :59.60   Max.   :21.50
##                                  NA's   :2       NA's   :2
##  flipper_length_mm  body_mass_g       sex           year
##  Min.   :172.0     Min.   :2700   female:165   Min.   :2007
##  1st Qu.:190.0     1st Qu.:3550   male  :168   1st Qu.:2007
##  Median :197.0     Median :4050   NA's  : 11   Median :2008
##  Mean   :200.9     Mean   :4202                Mean   :2008
##  3rd Qu.:213.0     3rd Qu.:4750                3rd Qu.:2009
##  Max.   :231.0     Max.   :6300                Max.   :2009
##  NA's   :2         NA's   :2
```

```r
mlr_data$species2 <- relevel(mlr_data$species, ref = "Gentoo")
test <- multinom(species2 ~ body_mass_g + bill_length_mm + bill_depth_mm + flipper_length_mm + island,
```

```
## # weights:  24 (14 variable)
## initial  value 375.725403
## iter  10 value 20.138634
## iter  20 value 1.481353
## iter  30 value 0.035234
## iter  40 value 0.000933
## iter  50 value 0.000233
## final  value 0.000089
## converged
```

```r
summary(test)
```

```
## Call:
## multinom(formula = species2 ~ body_mass_g + bill_length_mm +
```

```
##     bill_depth_mm + flipper_length_mm + island, data = mlr_data)
##
## Coefficients:
##           (Intercept) body_mass_g bill_length_mm bill_depth_mm
## Adelie       179.0566 -0.01156190     -11.117549     15.793011
## Chinstrap   -151.2783 -0.04191271       4.802821     -5.639087
##           flipper_length_mm islandDream islandTorgersen
## Adelie            0.4109570    22.48619        69.34019
## Chinstrap         0.6913637   117.34484        16.71717
##
## Std. Errors:
##           (Intercept) body_mass_g bill_length_mm bill_depth_mm
## Adelie       0.736784   0.4581624       49.98112      14.88575
## Chinstrap    0.732472   0.7914301       49.74986      14.71006
##           flipper_length_mm islandDream islandTorgersen
## Adelie             6.554627    0.732472    1.236702e-24
## Chinstrap          6.545027    0.732472    1.876044e-50
##
## Residual Deviance: 0.0001778793
## AIC: 28.00018
```

```
stargazer(test, type="text", out="test.htm")
```

```
##
## ==============================================
##                       Dependent variable:
##                   ----------------------------
##                       Adelie       Chinstrap
##                        (1)            (2)
## ----------------------------------------------
## body_mass_g           -0.012         -0.042
##                      (0.458)        (0.791)
##
## bill_length_mm       -11.118          4.803
##                      (49.981)      (49.750)
##
## bill_depth_mm         15.793         -5.639
##                      (14.886)      (14.710)
##
## flipper_length_mm     0.411          0.691
##                      (6.555)        (6.545)
##
## islandDream          22.486***     117.345***
##                      (0.732)        (0.732)
##
## islandTorgersen      69.340***      16.717***
##                      (0.000)        (0.000)
##
## Constant             179.057***    -151.278***
##                      (0.737)        (0.732)
##
## ----------------------------------------------
## Akaike Inf. Crit.     28.000         28.000
## ==============================================
```

```
## Note:              *p<0.1; **p<0.05; ***p<0.01
```

```
test.rrr = exp(coef(test))
test.rrr
```

```
##            (Intercept) body_mass_g bill_length_mm bill_depth_mm
## Adelie    5.798378e+77   0.9885047   1.484942e-05  7.224660e+06
## Chinstrap 1.998367e-66   0.9589535   1.218537e+02  3.556113e-03
##           flipper_length_mm  islandDream islandTorgersen
## Adelie             1.508260 5.829443e+09    1.300353e+30
## Chinstrap          1.996436 9.166779e+50    1.820439e+07
```

```
stargazer(test, type="text", coef=list(test.rrr), p.auto=FALSE, out="testrrr.htm")
```

```
##
## ==========================================================================================================
##
##                    -------------------------------------------------------------------------------------------
##                                                                    Adelie
##                                                                     (1)
## ----------------------------------------------------------------------------------------------------------
## body_mass_g                                                         0.989
##                                                                    (0.458)
##
## bill_length_mm                                                     0.00001
##                                                                   (49.981)
##
## bill_depth_mm                                                   7,224,660.000
##                                                                   (14.886)
##
## flipper_length_mm                                                   1.508
##                                                                    (6.555)
##
## islandDream                                                  5,829,443,146.000***
##                                                                    (0.732)
##
## islandTorgersen                                 1,300,352,545,036,810,191,042,951,249,920.000***
##                                                                    (0.000)
##
## Constant           579,837,803,916,479,821,887,587,742,166,729,353,269,199,669,971,417,058,436,431,37
##                                                                    (0.737)
##
## ----------------------------------------------------------------------------------------------------------
## Akaike Inf. Crit.                                                  28.000
## ==========================================================================================================
## Note:
```

```
# Again with https://www.r-bloggers.com/2020/05/multinomial-logistic-regression-with-r/

index <- createDataPartition(mlr_data$species, p = .70, list = FALSE)
train <- mlr_data[index,]
test <- mlr_data[-index,]
```

```r
# Set the reference
train$species <- relevel(train$species, ref = "Adelie")

# Training the multinomial model
#multinom_model <- multinom(species ~ ., data = mlr_data)

multinom_model <- multinom(species ~ island + bill_depth_mm + bill_length_mm, data = mlr_data)
```

```
## # weights:  18 (10 variable)
## initial  value 375.725403
## iter  10 value 7.109357
## iter  20 value 3.080002
## iter  30 value 1.165609
## iter  40 value 0.972679
## iter  50 value 0.791804
## iter  60 value 0.629141
## iter  70 value 0.239584
## iter  80 value 0.210170
## iter  90 value 0.197773
## iter 100 value 0.180365
## final  value 0.180365
## stopped after 100 iterations
```

```r
#multinom_model <- multinom(species ~ flipper_length_mm + body_mass_g, data = mlr_data)


#with flipper length, and with body mass, will also get to one hundred accuracy
# but these 3 are required for 100: island + bill_depth_mm + bill_length_mm

# Checking the model
summary(multinom_model)
```

```
## Call:
## multinom(formula = species ~ island + bill_depth_mm + bill_length_mm,
##     data = mlr_data)
##
## Coefficients:
##           (Intercept) islandDream islandTorgersen bill_depth_mm bill_length_mm
## Chinstrap -94.4661532     4.04063       -16.83291     -14.19469       8.083423
## Gentoo     -0.9047992   -18.48151       -14.78798     -21.82820       9.070280
##
## Std. Errors:
##           (Intercept) islandDream islandTorgersen bill_depth_mm bill_length_mm
## Chinstrap    82.71917    55.74159       107.82684      13.12430       6.673409
## Gentoo       10.28023    86.00558        87.37543      23.86346       9.995773
##
## Residual Deviance: 0.3607304
## AIC: 20.36073
```

```r
# Convert the coefficients to odds by taking the exponential of the coefficients.
exp(coef(multinom_model))
```

```
##            (Intercept)  islandDream islandTorgersen bill_depth_mm
## Chinstrap 9.416097e-42 5.686217e+01    4.892843e-08  6.844208e-07
## Gentoo    4.046231e-01 9.409816e-09    3.781492e-07  3.312341e-10
##           bill_length_mm
## Chinstrap       3240.307
## Gentoo          8693.059
```

```r
head(round(fitted(multinom_model), 2))
```

```
##   Adelie Chinstrap Gentoo
## 1      1         0      0
## 2      1         0      0
## 3      1         0      0
## 5      1         0      0
## 6      1         0      0
## 7      1         0      0
```

```r
# Predicting and validating the model

# Predicting the values for train dataset
train$speciesPredicted <- predict(multinom_model, newdata = train, "class")

# Building classification table
tab <- table(train$species, train$speciesPredicted)

# Calculating accuracy - sum of diagonal elements divided by total obs
round((sum(diag(tab))/sum(tab))*100,2)
```

```
## [1] 100
```

```r
# Predicting the class for test dataset
test$speciesPredicted <- predict(multinom_model, newdata = test, "class")

# Building classification table
tab <- table(test$species, test$speciesPredicted)
tab
```

```
##
##             Adelie Chinstrap Gentoo
##   Adelie        44         0      0
##   Chinstrap      0        20      0
##   Gentoo         0         0     37
```

Sex doesn't matter, Considering that I'm grouping Orange and Purple, probably don't use bill_length_mm, as that one shows purple and green have similar distribution

Prompt

Data – 622 Homework # 1 Due date Feb 19, 2021- 11:59 EST Let's use the Penguin dataset for our assignment. To learn more about the dataset, please visit: https://allisonhorst.github.io/palmerpenguins/

articles/intro.html For this assignment, let us use 'species' as our outcome or the dependent variable. 1. Logistic Regression with a binary outcome. (40) a. The penguin dataset has 'species' column. Please check how many categories you have in the species column. Conduct whatever data manipulation you need to do to be able to build a logistic regression with binary outcome. Please explain your reasoning behind your decision as you manipulate the outcome/dependent variable (species). b. Please make sure you are evaluating the independent variables appropriately in deciding which ones should be in the model. c. Provide variable interpretations in your model. 2. For your model from #1, please provide: AUC, Accuracy, TPR, FPR, TNR, FNR (20) 3. Multinomial Logistic Regression. (40) a. Please fit it a multinomial logistic regression where your outcome variable is 'species'. b. Please be sure to evaluate the independent variables appropriately to fit your best parsimonious model. c. Please be sure to interpret your variables in the model. 4. Extra credit: what would be some of the fit statistics you would want to evaluate for your model in question #3? Feel free to share whatever you can provide. (10)

Considers for multinomial wald test LR test: likelihood ratio Cross validation parallel lines assumption

Ideas here: https://stats.stackexchange.com/questions/145203/how-to-assess-if-a-model-is-good-in-multinomial-logistic-regression