Logistic Regression

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For this model the first step is preparing the split to create two sets from the original dataset: training and testing sets, in this case we are going to use 80 percent of the sample for training the model and the other 20 percent will be used to validate de model's quality. The distribution of the observation in the two set is made over a random simple sampling applied over the index.

```
# Random sample indexes
train_index <- sample(1:nrow(cangrejos), 0.8 * nrow(cangrejos))
test_index <- setdiff(1:nrow(cangrejos), train_index)

# Build X_train
X_train <- cangrejos[train_index,]
X_test <- cangrejos[test_index,]</pre>
```

For the model selection we are going to use the Step aic and the R function glm will be used to compute de logistic regression, specifying the option family = binomial, that means the response variable is binary. AIC penalizes increasing the number of parameters into de model, and the best option will be the model with the smallest.

```
fit <- glm(y ~ 1 + w + c + s + c*s + c*w + s*w, family=binomial, data=X_train)
stepAIC(fit)</pre>
```

```
## Start: AIC=159.97
## y ~ 1 + w + c + s + c * s + c * w + s * w
##
##
          Df Deviance
                          AIC
## - c:s
           1
               146.48 158.48
##
  - w:s
           1
               146.84 158.84
## - w:c
           1
               147.95 159.95
               145.97 159.97
## <none>
##
## Step: AIC=158.48
  y ~ w + c + s + w:c + w:s
##
##
          Df Deviance
## - w:s
               147.25 157.25
               148.40 158.40
## - w:c
           1
               146.48 158.48
## <none>
##
## Step: AIC=157.25
  y ~ w + c + s + w:c
##
##
          Df Deviance
                          AIC
## - w:c
           1
               148.43 156.43
## - s
           1
               148.52 156.52
## <none>
               147.25 157.25
##
## Step: AIC=156.43
## y ~ w + c + s
```

```
##
##
         Df Deviance
                         ATC
## - s
               149.48 155.48
               148.43 156.43
## <none>
## - c
           1
               152.35 158.35
               169.16 175.16
## - w
           1
## Step: AIC=155.48
## y ~ w + c
##
          Df Deviance
## <none>
               149.48 155.48
## - c
          1
               152.45 156.45
## - w
              170.94 174.94
          1
## Call: glm(formula = y ~ w + c, family = binomial, data = X_train)
##
## Coefficients:
## (Intercept)
                                      с1
##
      -11.9728
                     0.4675
                                  0.6923
##
## Degrees of Freedom: 137 Total (i.e. Null); 135 Residual
## Null Deviance:
                        179.5
## Residual Deviance: 149.5
                                AIC: 155.5
After running the aic step the best model is described below
######## Estimación del modelo #######
fit2 <- glm(y ~ 1 + w, family=binomial, data=cangrejos)</pre>
summary(fit2)
##
## Call:
## glm(formula = y ~ 1 + w, family = binomial, data = cangrejos)
## Deviance Residuals:
       Min
                 1Q
                     Median
                                   30
                                           Max
## -2.0281 -1.0458 0.5480
                                        1.6942
                               0.9066
##
## Coefficients:
               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -12.3508
                            2.6287 -4.698 2.62e-06 ***
## w
                            0.1017
                                    4.887 1.02e-06 ***
                 0.4972
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
##
       Null deviance: 225.76 on 172 degrees of freedom
## Residual deviance: 194.45 on 171 degrees of freedom
## AIC: 198.45
##
## Number of Fisher Scoring iterations: 4
```

The second one model has small AIC however not all the coefficient are significat at 5% level

```
fit3 <- glm(y ~ 1 + w + c, family=binomial, data=cangrejos)</pre>
summary(fit3)
##
## Call:
## glm(formula = y ~ 1 + w + c, family = binomial, data = cangrejos)
## Deviance Residuals:
##
               1Q
                    Median
                                3Q
      Min
                                       Max
## -2.1080 -0.9708
                    0.5346
                            0.8958
                                     1.8188
##
## Coefficients:
             Estimate Std. Error z value Pr(>|z|)
##
## (Intercept) -11.9501
                          2.6643 -4.485 7.28e-06 ***
               0.4670
                                  4.506 6.61e-06 ***
                          0.1037
## c1
               0.6531
                          0.3571
                                 1.829
                                        0.0675 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## (Dispersion parameter for binomial family taken to be 1)
##
##
      Null deviance: 225.76 on 172 degrees of freedom
## Residual deviance: 191.12 on 170 degrees of freedom
## AIC: 197.12
## Number of Fisher Scoring iterations: 4
anova(fit2, fit3 , test="Chisq")
## Analysis of Deviance Table
## Model 1: y ~ 1 + w
## Model 2: y \sim 1 + w + c
    Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1
          171
                 194.45
## 2
          170
                 191.12 1
                            3.3344 0.06785 .
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
When x=26, we would like to know the probability that the event occurs.
x < -c(1,26)
eta <- sum(x*coef(fit2))</pre>
prob <- exp(eta)/(1+exp(eta))</pre>
prob
## [1] 0.6404177
Now, using the function predict
newdata \leftarrow data.frame(w = c(20, 26))
probabilities <- fit2 %>% predict(newdata, type = "response")
probabilities
```

##

1

0.08270068 0.64041770

Conidence interval for the coeficent

```
alpha <- 0.05
li <- coef(fit2)[-1] - qnorm(1-alpha/2)*diag(vcov(fit2))[-1]
ls <- coef(fit2)[-1] + qnorm(1-alpha/2)*diag(vcov(fit2))[-1]
li <- exp(li)
ls <- exp(ls)
c(li,ls)</pre>
```

```
## w w
## 1.611144 1.677855
```

Predicting the value for in the testing set, for this case the threshold is 0.7, that means that if the probability is greater than 0.7 the observation will be associated with 1 and in another case will be mark with 0.

```
rev<-predict(fit2,X_test,type = "response")
X_test$predicted.classes<- ifelse(rev > 0.7, "1", "0")
X_test
```

```
##
              w y predicted.classes
       c s
       0 0 26.0 1
## 2
## 3
       0 0 25.6 0
                                  0
                                  0
## 11
      1 1 26.1 1
## 16
      0 0 24.5 1
                                  0
                                  0
## 18
      1 0 26.2 1
## 20
      1 0 25.4 1
                                  0
## 33 1 1 24.9 1
                                  0
## 38 1 0 30.0 1
                                  1
## 40 1 0 23.9 1
                                  0
## 41 1 0 26.0 1
                                  0
## 46 1 0 23.8 0
                                  0
## 56 1 0 28.2 1
                                  1
## 69 0 0 24.5 1
                                  0
## 77
      1 1 24.5 1
                                  0
## 79
      1 1 25.0 1
                                  0
## 86 0 0 24.1 0
                                  0
## 89
       0 1 24.7 0
                                  0
## 90 1 0 25.8 0
                                  0
## 97 1 0 27.9 1
                                  1
## 104 1 0 26.2 0
                                  0
## 107 1 0 25.1 1
                                  0
## 110 1 1 26.8 0
                                  1
## 114 1 0 29.0 1
                                  1
## 121 1 0 24.9 0
                                  0
## 123 1 1 24.3 0
                                   0
## 127 0 1 29.8 1
                                   1
## 142 1 0 28.5 1
                                  1
## 145 0 0 27.1 0
                                   1
## 147 1 1 26.5 0
                                  0
## 148 0 0 23.0 0
                                  0
## 149 0 1 26.0 1
                                  0
## 155 1 0 28.2 1
                                  1
## 156 1 1 25.2 1
                                  0
## 166 1 0 25.8 0
                                  0
## 171 1 0 26.5 1
                                  0
```

To check the model accuracy we are going to see the percent associated with values that were classified right.

```
# Model accuracy
mean(X_test$predicted.classes == X_test$y)
```

[1] 0.5142857

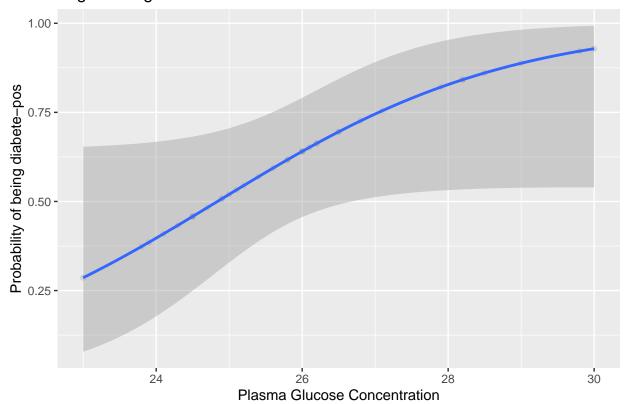
Finally to check the well know s-shape for the logistic regreesion we are going to use the ggplot library

```
library(ggplot2)
X_test$rev<-predict(fit2,X_test,type = "response")

X_test %>%
    ggplot(aes(w, rev)) +
    geom_point(alpha = 0.1) +
    geom_smooth(method = "glm", method.args = list(family = "binomial")) +
    labs(
        title = "Logistic Regression Model",
        x = "Plasma Glucose Concentration",
        y = "Probability of being diabete-pos"
    )
```

Warning in eval(family\$initialize): non-integer #successes in a binomial
glm!

Logistic Regression Model



```
table(X_test$y,X_test$predicted.classes)
```

##

```
## 0 1
## 0 11 2
## 1 15 7
```

References

- R Core Team (2018). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/.
- H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York, 2016.
- Hadley Wickham, Romain François, Lionel Henry and Kirill Müller (2019). dplyr: A Grammar of Data Manipulation. R package version 0.8.3. https://CRAN.R-project.org/package=dplyr

http://www.sthda.com/english/articles/36-classification-methods-essentials/151-logistic-regression-essentials-in-r/logistic-regression-e