Logistic Regression

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September 4, 2019

Dataset

For this statistical method, we are going to use the data set crabs avaible in R through the library MASS, its variables are:

- *sp:* species - "B" or "O" for blue or orange.
- *sex:* M for male and F for female
- *index:* 1:50 within each of the four groups.
- *FL:* frontal lobe size (mm).
- *RW:* rear width (mm).
- *CL:* carapace length (mm).
- *CW:* carapace width (mm).
- *BD:* body depth (mm).

The function summary will be used to have a first idea of the data structure.Notice that the variable indice is deleted because we will supose that all of the crabs belogns to the same group.

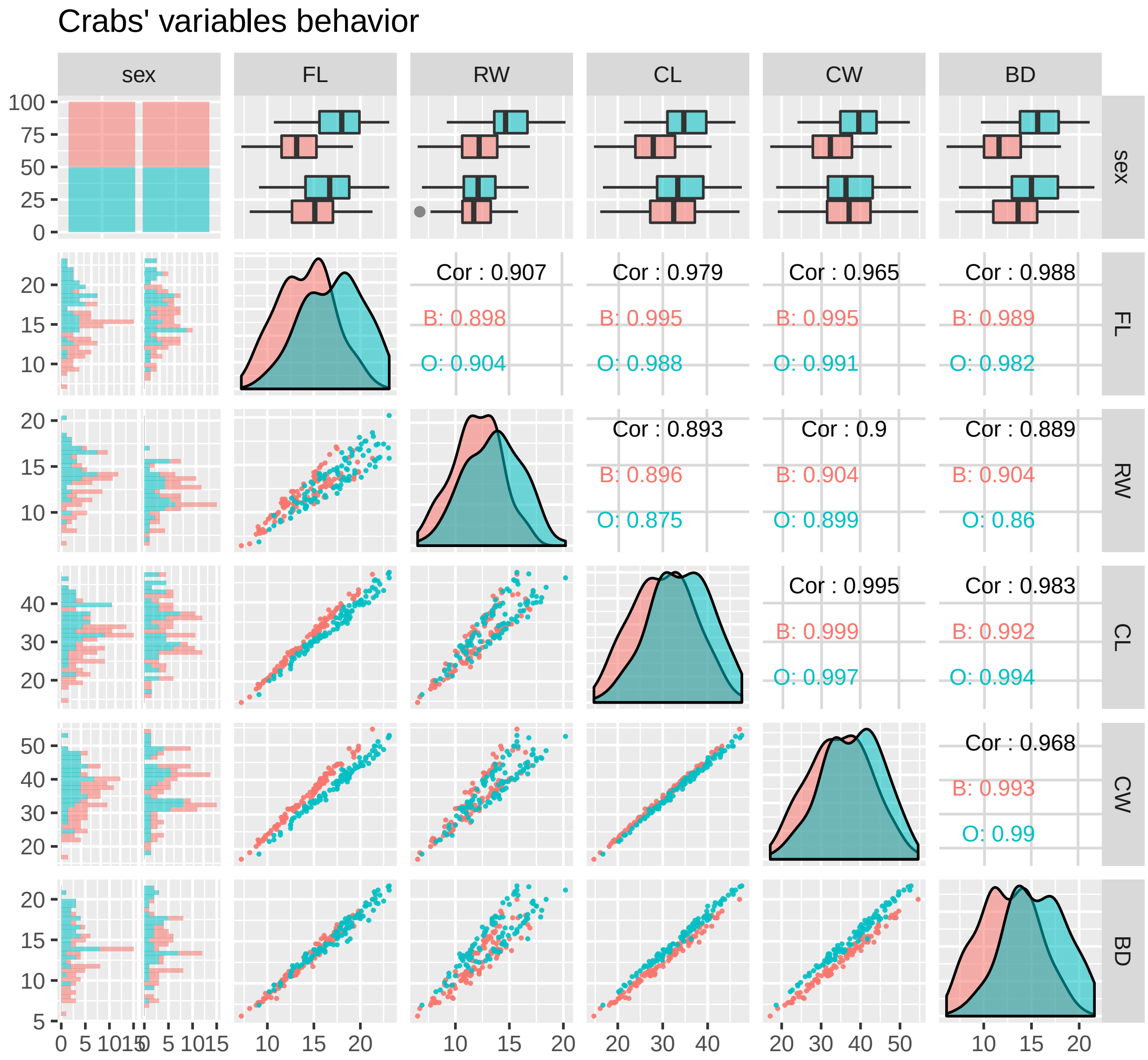
```
Packages <- c("MASS","dplyr","ggplot2","readr", "pscl","ROCR", "GGally")
lapply(Packages, library, character.only = TRUE)
set.seed(3)
```

```
data(crabs)
crabs<-crabs[,-3]
summary(crabs)
```

```
##  sp      sex           FL              RW              CL       
##  B:100   F:100   Min.   : 7.20   Min.   : 6.50   Min.   :14.70  
##  O:100   M:100   1st Qu.:12.90   1st Qu.:11.00   1st Qu.:27.27  
##                  Median :15.55   Median :12.80   Median :32.10  
##                  Mean   :15.58   Mean   :12.74   Mean   :32.11  
##                  3rd Qu.:18.05   3rd Qu.:14.30   3rd Qu.:37.23  
##                  Max.   :23.10   Max.   :20.20   Max.   :47.60  
##        CW              BD       
##  Min.   :17.10   Min.   : 6.10  
##  1st Qu.:31.50   1st Qu.:11.40  
##  Median :36.80   Median :13.90  
##  Mean   :36.41   Mean   :14.03  
##  3rd Qu.:42.00   3rd Qu.:16.60  
##  Max.   :54.60   Max.   :21.60  
```

In the data set we have two category variables: sp that is our target and sex,the others are quantitatives, that is the reason why in sex appears barplots and the other variables have density distribution plots and scatter plots. The two colors are associeted with the break up of sp wich has two levels, pink is associated with level B and blue with the second level (B). Notice that the sex distribution is the same for both of the levels because the two barplots have the same structure, with the box plots we can see that the behaviour of the other variables is different in the levels for sex and sp. Even when we havenÂ´t examine the correlation is easy to see that there is a strong linear relation between the varaibles and in some cases like CL vs. RW the dispersion increase when the variables take high values.

```
ggpairs(crabs, columns = 2:ncol(crabs), title = "Crabs' variables behavior",
  axisLabels = "show", mapping = aes(colour=sp,alpha = 5),
  upper = list(continuous = wrap("cor", size =3)),
  lower = list(continuous = wrap("points", alpha = 0.9,    size=0.3)))
```



To create the model, the first step is preparing the split over the database to create two sets: training and testing datasets, 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.

```
train_index <- sample(1:nrow(crabs), 0.8 * nrow(crabs))
test_index <- setdiff(1:nrow(crabs), train_index)
# Build X_train and X_test
X_train <- crabs[train_index,]
X_test <- crabs[test_index,]
```

Correlation

We can see that the variables have a strong correlation almost all of them, that is a problem if we would try to put in the model all of these variables. The just the varaibles sex,FL,RW and CL will keep to start the model.

```
cor(X_train[,3:ncol(crabs)])
```

```
##           FL        RW        CL        CW        BD
## FL 1.0000000 0.9027495 0.9800157 0.9661302 0.9897178
## RW 0.9027495 1.0000000 0.8918536 0.9007618 0.8879675
## CL 0.9800157 0.8918536 1.0000000 0.9951218 0.9830334
## CW 0.9661302 0.9007618 0.9951218 1.0000000 0.9681736
## BD 0.9897178 0.8879675 0.9830334 0.9681736 1.0000000
```

Model identification

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. Not all the variables are in the inicial model because of the high correlation between them as I said before.

```
fit <- glm(sp ~ 1 + sex+FL+RW+CL+sex*FL+sex*RW, family=binomial, data=X_train)
stepAIC(fit)
```

```
## Start:  AIC=27.11
## sp ~ 1 + sex + FL + RW + CL + sex * FL + sex * RW
##
##          Df Deviance     AIC
## - sex:RW  1   13.224  25.224
## - sex:FL  1   13.467  25.467
## <none>        13.106  27.106
## - CL      1  130.058 142.058
##
## Step:  AIC=25.22
## sp ~ sex + FL + RW + CL + sex:FL
##
##          Df Deviance     AIC
## - sex:FL  1   13.945  23.945
## <none>        13.224  25.224
## - RW      1   20.569  30.569
## - CL      1  130.706 140.706
##
## Step:  AIC=23.95
## sp ~ sex + FL + RW + CL
##
##        Df Deviance     AIC
## <none>      13.945  23.945
## - RW    1   21.049  29.049
## - sex   1   24.175  32.175
## - CL    1  166.631 174.631
## - FL    1  200.546 208.546
```

```
##
## Call:  glm(formula = sp ~ sex + FL + RW + CL, family = binomial, data = X_train)
```

```
##
## Coefficients:
## (Intercept)         sexM           FL           RW           CL
##     -58.985       11.901       29.294        4.451      -14.158
##
## Degrees of Freedom: 159 Total (i.e. Null);  155 Residual
## Null Deviance:       221.6
## Residual Deviance: 13.95     AIC: 23.95
```

Well, let see the best model in detail:

```
fit<-glm(formula = sp ~ sex + FL + CL, family = binomial, data = X_train)
summary(fit)
```

```
##
## Call:
## glm(formula = sp ~ sex + FL + CL, family = binomial, data = X_train)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.66885  -0.02286   0.00000   0.00221   2.13687
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -23.412      7.579  -3.089  0.00201 **
## sexM           2.101      1.229   1.710  0.08732 .
## FL            19.546      6.150   3.178  0.00148 **
## CL            -8.675      2.742  -3.163  0.00156 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 221.582  on 159  degrees of freedom
## Residual deviance:  21.049  on 156  degrees of freedom
## AIC: 29.049
##
## Number of Fisher Scoring iterations: 10
```

There is enough statistical evindence that there is no overdispersion (null hipotesis)

```
deviance(fit) ##Compare N-p
```

```
## [1] 21.0486
```

```
nrow(X_train)-4
```

```
## [1] 156
```

```
pchisq(fit$deviance, df=fit$df.residual, lower.tail=FALSE)
```

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

We would like to know the probability that the event occurs when we have a male, with FL=11.1 and CL=23.8.

```
x <- c(1,1,11.1,23.8)
eta <- sum(x*coef(fit))
prob <- exp(eta)/(1+exp(eta)) ;prob
```

```
## [1] 1.993698e-05
```

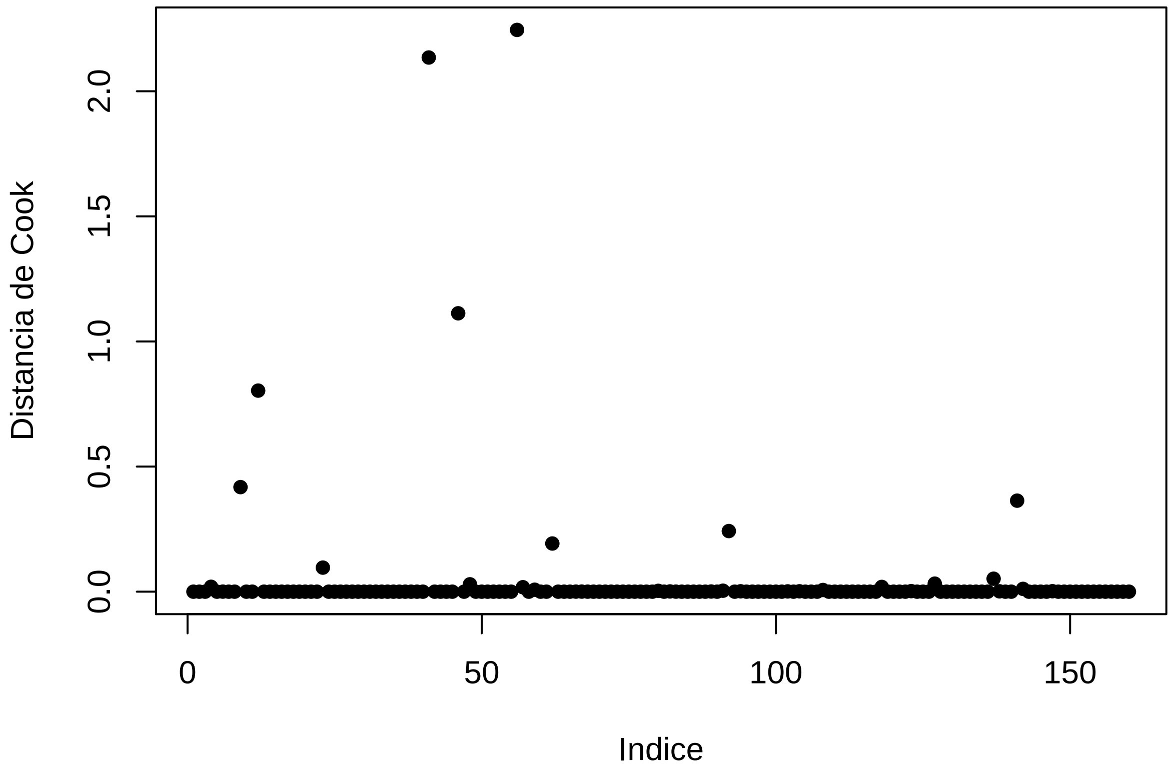
R has a function predict which enables us to calculate quickly probabilities just entry the values of each variable.

```
newdata <- data.frame( sex='M',FL=11.1,RW=9.9,CL=23.8,CW=27.1,BD=9.8)
probabilities <- fit %>% predict(newdata, type = "response")
probabilities
```

```
##            1
## 1.993698e-05
```

The cook distance to identify leverage points.

```
source("macros.txt") ##professor Vanegas
dC(fit, identify=4)
```



```
## integer(0)
```

Residuals behavior

```
bc(fit, rep=100, alpha=0.9)
```

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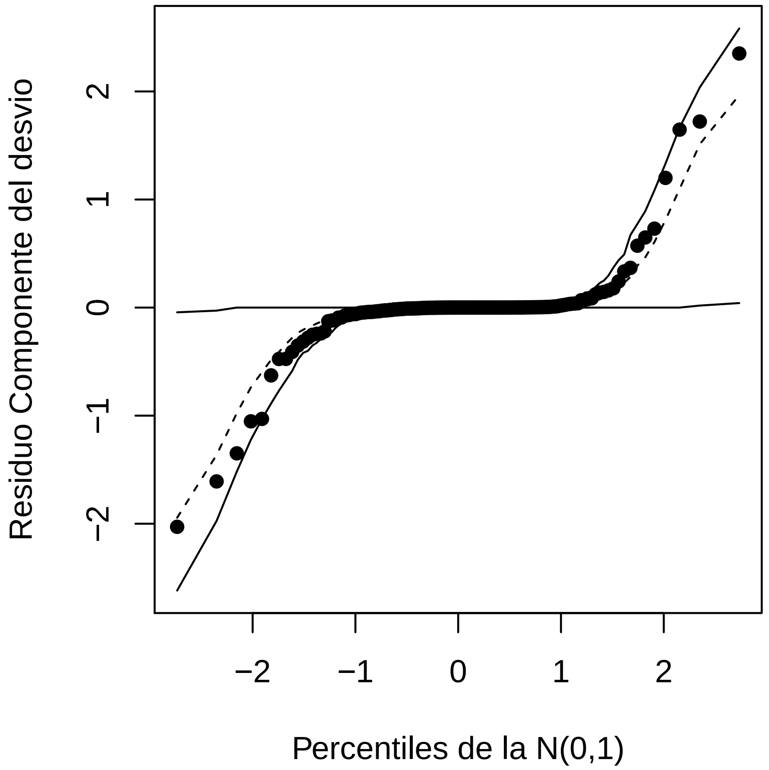


Testing the model

It is using the probability that we are going to validade our model, predicting the value in the testing set for this is necessary define a threshold, in this case will be 0.4, that means that if the probability is greater than 0.4 the observation will be associated with the level *O* and in another case will be mark with *B*.

```
rev<-predict(fit,X_test,type = "response")
 X_test$predicted.classes<- ifelse(rev > 0.4, "O", "B")
 head(X_test,3)
```

```
##    sp sex   FL   RW   CL   CW   BD predicted.classes
## 1   B   M  8.1  6.7 16.1 19.0  7.0                 B
## 6   B   M 10.8  9.0 23.0 26.5  9.8                 B
## 10  B   M 11.8 10.5 25.2 29.3 10.3                 B
```

```
 tail(X_test,3)
```

```
##     sp sex   FL   RW   CL   CW   BD predicted.classes
## 186  O   F 19.7 16.7 39.9 43.6 18.2                 O
## 190  O   F 20.1 17.2 39.8 44.1 18.6                 O
## 193  O   F 20.6 17.5 41.5 46.2 19.2                 O
```

To check the model accuracy we are going to see the percent associated with values that were classified right.The 92.5% of the observations were right classified.

```
mean(X_test$predicted.classes == X_test$sp)
```

```
## [1] 0.925
```

Pseudo R2

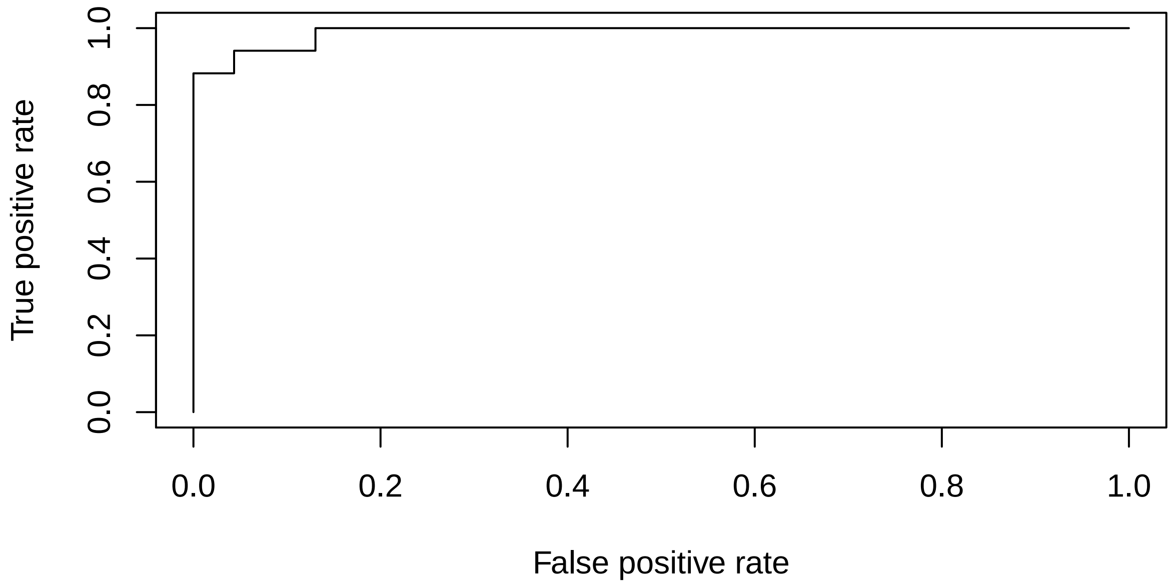
McFadden measure is 0.88 that is a really good value because this metric ranges from 0 to just under 1, with values closer to zero indicating that the model has no predictive power.

```
pR2(fit)
```

```
##          llh      llhNull           G2     McFadden         r2ML 
##  -10.5242979 -110.7910225  200.5334492    0.9050077    0.7144488 
##         r2CU 
##    0.9530456
```

Roc curve.

```
prob <- predict(fit, newdata=X_test, type="response")
pred <- prediction(prob, X_test$sp)
perf <- performance(pred, measure = "tpr", x.measure = "fpr")
plot(perf)
```



We exmaine the ROC curve which shows the trade off between the rate at which you can correctly predict something with the rate of incorrectly predicting something.

Parameters interpretation

```
fit$coefficients
```

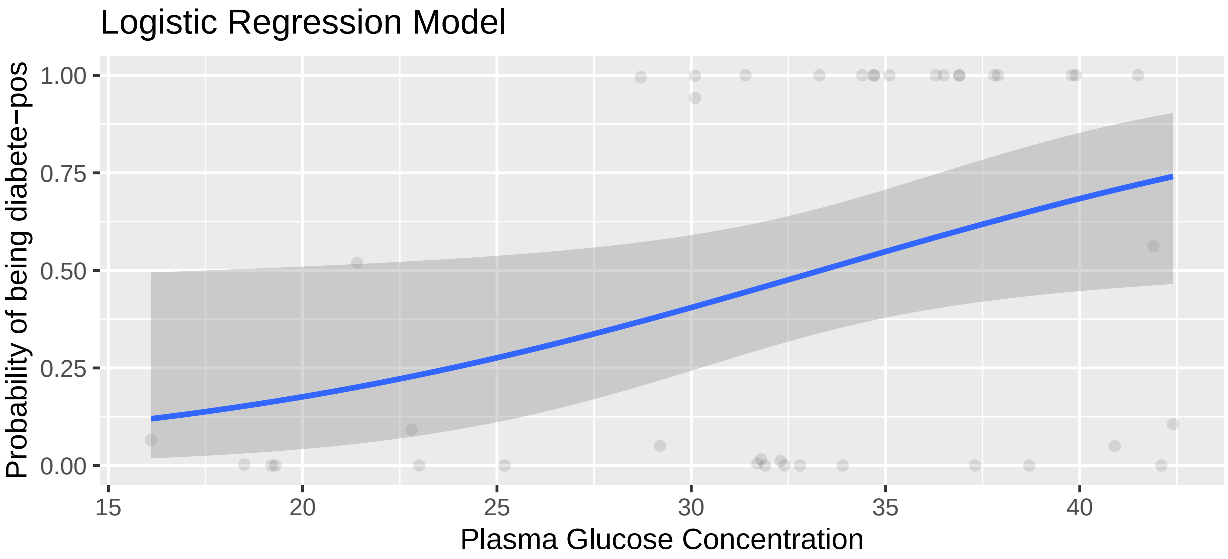
```
## (Intercept)        sexM          FL          CL
##  -23.412346    2.100512   19.545675   -8.675129
```

Our final model is $y = B_0 + B_1 Sex_{male} + B_2 Fl + B_3 Cl$

- e^{B_1} when the crab is male the odds of sucess increase in $e^{2.100512}$ 8.166 times, that mean that males have 8.16 times of being O than females
- e^{B_2} for each adittional unit in FL the odss of sucess (being O) increase in $e^{19.55}$
- e^{B_3} for each adittional unit in CL the odds of being O decrease in $e^{-8.87}$
- e^{B_0} when the crab is female and have 0 value in FL and CL the odds of being O is $e^{-23.41}$

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

```
X_test$rev<-predict(fit,X_test,type = "response")
X_test %>%
  ggplot(aes(CL, 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"
    )
```



References

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Barret Schloerke, Jason Crowley, Di Cook, Francois Briatte, Moritz Marbach, Edwin Thoen, Amos Elberg and Joseph Larmarange (2018). GGally: Extension to 'ggplot2'. R package version 1.4.0. https://CRAN.R-project.org/package=GGally

Vanegas Luis Hernando who share the macro.txt to examine the residuals.