```
> fibrinogeno<-c(2.52,2.56,2.19,2.18,3.41,2.46,3.22,2.21,3.15,2.60,2.29,2.35,5.06,3.34,2.38,3.15,3.53,2.68,2.
6,2.23,2.88,
+                 2.65,2.09,2.28,2.67,2.29,2.15,2.54,3.93,3.34,2.99,3.32)
> gammaglobulin<-c(38,31,33,31,37,36,38,37,39,41,36,29,37,32,37,36,46,34,38,37,30,46,44,36,39,31,31,28,32,30,
36,35)
> response<-c(rep(0,12),rep(1,3),0,1,rep(0,5),1,rep(0,5),1,0,0,0)
> eritrocitos.data<-data.frame(fibrinogeno,gammaglobulin,response)
> modelo1<-glm(response~fibrinogeno ,family=binomial,eritrocitos.data)
> summary(modelo1)
Call:
glm(formula = response ~ fibrinogeno, family = binomial, data = eritrocitos.data)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9298  -0.5399  -0.4382  -0.3356   2.4794
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -6.8451     2.7703  -2.471   0.0135 *
fibrinogeno   1.8271     0.9009   2.028   0.0425 *
 (Dispersion parameter for binomial family taken to be 1)
    Null deviance: 30.885  on 31  degrees of freedom
Residual deviance: 24.840  on 30  degrees of freedom
AIC: 28.84
> modelo2<-glm(response~gammaglobulin ,family=binomial,eritrocitos.data)
> summary(modelo2)
Call:
glm(formula = response ~ gammaglobulin, family = binomial, data = eritrocitos.data)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.1150  -0.6649  -0.5680  -0.4164   2.1009
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    -6.5289     3.8344  -1.703   0.0886 .
gammaglobulin   0.1387     0.1022   1.358   0.1745
    Null deviance: 30.885  on 31  degrees of freedom
Residual deviance: 28.945  on 30  degrees of freedom
AIC: 32.945
> modelo3<-glm(response~fibrinogeno+ gammaglobulin,family=binomial,eritrocitos.data)
> summary(modelo3)
Call:
glm(formula = response ~ fibrinogeno + gammaglobulin, family = binomial,
    data = eritrocitos.data)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9683  -0.6122  -0.3458  -0.2116   2.2636
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -12.7921     5.7963  -2.207   0.0273 *
fibrinogeno     1.9104     0.9710   1.967   0.0491 *
gammaglobulin   0.1558     0.1195   1.303   0.1925
    Null deviance: 30.885  on 31  degrees of freedom
Residual deviance: 22.971  on 29  degrees of freedom
AIC: 28.971
> anova(modelo0,modelo1,modelo3)
Analysis of Deviance Table

Model 1: response ~ 1
Model 2: response ~ fibrinogeno
Model 3: response ~ fibrinogeno + gammaglobulin
  Resid. Df Resid. Dev Df Deviance
1        31     30.885
2        30     24.840  1   6.0446
3        29     22.971  1   1.8692
>
```

Los datos están desagrupados, i.e son binarios

modelo 1 y modelo 2 SI son significativamente diferentes.

modelo 2 y modelo 3   NO son significativamente diferentes

```
> 1-pchisq(1.8692,1)
[1] 0.1715667
> 1-pchisq(6.0446,1)
[1] 0.01394889
```

Ahora veamos que tal ajusta

```
> logitgof(response, fitted(modelo51),g=8)

         Hosmer and Lemeshow test (binary model)

data:  response, fitted(modelo51)
X-squared = 8.9824, df = 6, p-value = 0.1746

Warning message:
In logitgof(response, fitted(modelo51), g = 8) :
  At least one cell in the expected frequencies table is < 1. Chi-square approximation may be incorrect.

> hosmerlem(response, fitted(modelo51),g=8)
$chisq
[1] 8.982414
$p.value
[1] 0.1745695

> hosmerlem(response, fitted(modelo51),g=10)
$chisq
[1] 8.900193
$p.value
[1] 0.3507854

> logitgof(response, fitted(modelo51),g=10)

         Hosmer and Lemeshow test (binary model)
data:  response, fitted(modelo51)
X-squared = 8.9002, df = 8, p-value = 0.3508
Warning message:
In logitgof(response, fitted(modelo51), g = 10) :
  At least one cell in the expected frequencies table is < 1. Chi-square approximation may be incorrect.
```