

Salida R Parte 7

```
> conteos<-c(2114,246,626,293,2476,307,1326,512)
> Hospitalizado<-c("no","no","si","si","no","no","si","si")
> Sexo<-c("M","M","M","M","H","H","H","H")
> Diabetes<-c("no","si","no","si","no","si","no","si")
> datos2<-data.frame (conteos,Hospitalizado, Sexo, Diabetes)
> #Para elaborar mosaicplot con datos originales
> tabla<-xtabs(conteos~Hospitalizado+Sexo+Diabetes,datos2)
> tabla
, , Diabetes = no
      Sexo
Hospitalizado H    M
no          2476 2114
si          1326  626
, , Diabetes = si
      Sexo
Hospitalizado H    M
no           307  246
si           512  293

> modeloA<-glm(conteos~Hospitalizado+Sexo+Diabetes,family=poisson, data=datos2)
> summary(modeloA)

Call:
glm(formula = conteos ~ Hospitalizado + Sexo + Diabetes, family = poisson,
     data = datos2)

Deviance Residuals:
    1     2     3     4     5     6     7     8
 7.9869 -6.7194 -11.1426  6.3960 -0.3049 -10.0045 -0.2590 12.5970

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  7.82052    0.01762  443.79 <2e-16 ***
Hospitalizadosi -0.62349    0.02360  -26.41 <2e-16 ***
SexoM        -0.34307    0.02283  -15.03 <2e-16 ***
Diabetessi   -1.57223    0.02982  -52.72 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 5195.39  on 7  degrees of freedom
Residual deviance: 532.94  on 4  degrees of freedom
AIC: 607.9

Number of Fisher Scoring iterations: 4

> modeloB<-glm(conteos~Hospitalizado*Sexo*Diabetes,family=poisson, data=datos2)
> summary(modeloB)

Call:
glm(formula = conteos ~ Hospitalizado * Sexo * Diabetes, family = poisson,
     data = datos2)

Deviance Residuals:
[1] 0 0 0 0 0 0 0 0

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  7.81440    0.02010  388.840 < 2e-16 ***
Hospitalizadosi -0.62448    0.03403  -18.351 < 2e-16 ***
SexoM        -0.15806    0.02961   -5.338 9.42e-08 ***
Diabetessi   -2.08755    0.06051  -34.500 < 2e-16 ***
Hospitalizadosi:SexoM -0.59251    0.05682  -10.428 < 2e-16 ***
Hospitalizadosi:Diabetessi 1.13595    0.07980  14.235 < 2e-16 ***
SexoM:Diabetessi -0.06345    0.09055   -0.701  0.4835
Hospitalizadosi:SexoM:Diabetessi 0.25587    0.12616   2.028  0.0425 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 5.1954e+03  on 7  degrees of freedom
Residual deviance: 7.1987e-13  on 0  degrees of freedom
AIC: 82.956

Number of Fisher Scoring iterations: 2

> modeloC<-glm(conteos~Hospitalizado+Sexo*Diabetes,family=poisson, data=datos2)
> summary(modeloC)

Call:
```

```
glm(formula = conteos ~ Hospitalizado + Sexo * Diabetes, family = poisson,
     data = datos2)
```

```
Deviance Residuals:
    1      2      3      4      5      6      7      8
 7.5945 -5.9206 -11.4039  7.0647  0.0171 -10.6501 -0.0233 12.0247
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	7.81406	0.01819	429.580	<2e-16 ***
Hospitalizadosi	-0.62349	0.02360	-26.415	<2e-16 ***
SexoM	-0.32757	0.02506	-13.072	<2e-16 ***
Diabetessi	-1.53520	0.03852	-39.852	<2e-16 ***
SexoM:Diabetessi	-0.09080	0.06086	-1.492	0.136

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 5195.39 on 7 degrees of freedom
Residual deviance: 530.71 on 3 degrees of freedom
AIC: 607.66

Number of Fisher Scoring iterations: 4

```
> modeloD<-glm(conteos~Sexo+Hospitalizado*Diabetes,family=poisson, data=datos2)
> summary(modeloD)
```

```
Call:
glm(formula = conteos ~ Sexo + Hospitalizado * Diabetes, family = poisson,
     data = datos2)
```

```
Deviance Residuals:
    1      2      3      4      5      6      7      8
 4.7014  1.0745 -6.7433 -2.2986 -4.0849 -0.9237  5.3138  1.8686
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	7.89538	0.01754	450.11	<2e-16 ***
SexoM	-0.34307	0.02283	-15.03	<2e-16 ***
Hospitalizadosi	-0.85503	0.02702	-31.64	<2e-16 ***
Diabetessi	-2.11628	0.04501	-47.02	<2e-16 ***
Hospitalizadosi:Diabetessi	1.23051	0.06149	20.01	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 5195.39 on 7 degrees of freedom
Residual deviance: 123.28 on 3 degrees of freedom
AIC: 200.24

Number of Fisher Scoring iterations: 4

```
> modeloE<-glm(conteos~Diabetes+Hospitalizado*Sexo,family=poisson, data=datos2)
> summary(modeloE)
```

```
Call:
glm(formula = conteos ~ Diabetes + Hospitalizado * Sexo, family = poisson,
     data = datos2)
```

```
Deviance Residuals:
    1      2      3      4      5      6      7      8
 3.564 -8.558 -5.051  9.589  3.527 -8.392 -5.139 10.111
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	7.74266	0.01964	394.296	< 2e-16 ***
Diabetessi	-1.57223	0.02982	-52.724	< 2e-16 ***
Hospitalizadosi	-0.41485	0.03006	-13.802	< 2e-16 ***
SexoM	-0.16487	0.02798	-5.892	3.82e-09 ***
Hospitalizadosi:SexoM	-0.52828	0.04915	-10.749	< 2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 5195.39 on 7 degrees of freedom
Residual deviance: 414.92 on 3 degrees of freedom
AIC: 491.87

Number of Fisher Scoring iterations: 4

```
> modeloF<-glm(conteos~Hospitalizado+Sexo+Diabetes+Sexo*Diabetes+ Hospitalizado*Diabetes+Hospitalizado*Sexo, fami
ly=poisson, data=datos2)
> summary(modeloF)
```

```
Call:
glm(formula = conteos ~ Hospitalizado + Sexo + Diabetes + Sexo *
     Diabetes + Hospitalizado * Diabetes + Hospitalizado * Sexo,
```

```
family = poisson, data = datos2)
```

```
Deviance Residuals:
```

```
 1      2      3      4      5      6      7      8  
0.3502 -1.0026 -0.6366  0.9561 -0.3221  0.9332  0.4429 -0.7026
```

```
Coefficients:
```

```
                Estimate Std. Error z value Pr(>|z|)  
(Intercept)      7.82087    0.01978  395.426 < 2e-16 ***  
Hospitalizados  -0.64313    0.03286  -19.573 < 2e-16 ***  
SexoM            -0.17216    0.02880   -5.977 2.27e-09 ***  
Diabetessi      -2.14776    0.05399  -39.780 < 2e-16 ***  
SexoM:Diabetessi  0.06763    0.06315   1.071  0.284  
Hospitalizados:Diabetessi 1.23924    0.06206  19.969 < 2e-16 ***  
Hospitalizados:SexoM  -0.54089    0.05057  -10.695 < 2e-16 ***
```

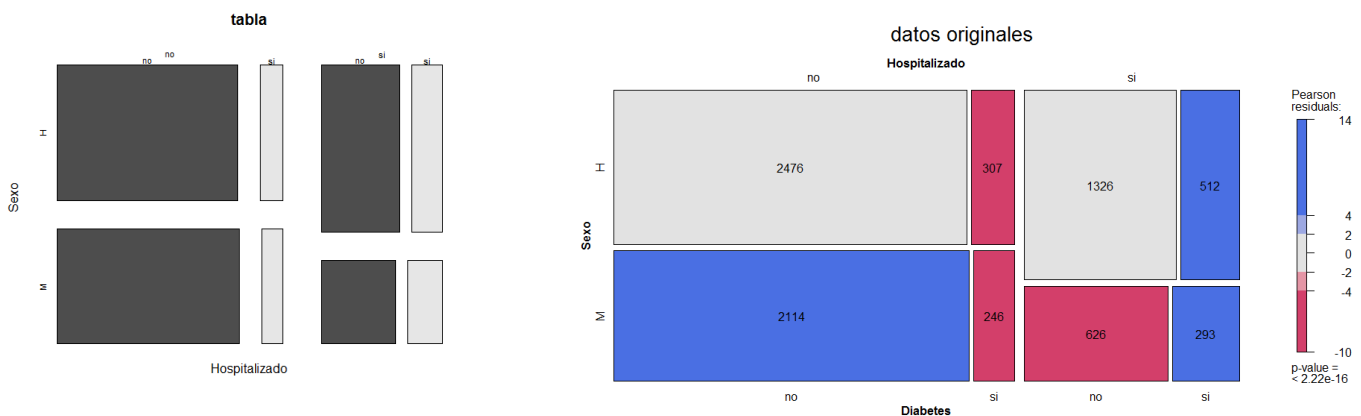
```
---  
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for poisson family taken to be 1)
```

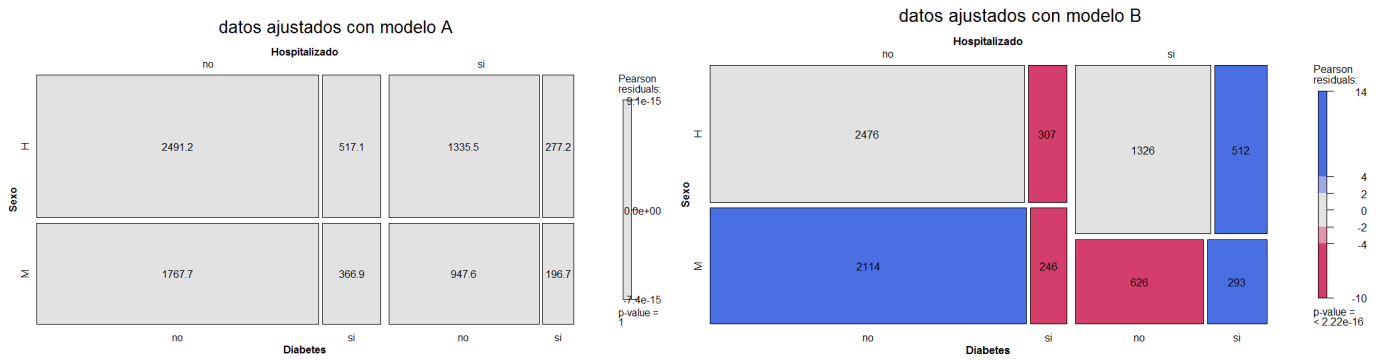
```
Null deviance: 5195.3853 on 7 degrees of freedom  
Residual deviance: 4.1116 on 1 degrees of freedom  
AIC: 85.068
```

```
Number of Fisher Scoring iterations: 3
```

```
> numero.ajustadosA <- fitted(modeloA)  
> datos2A <- data.frame(datos2, ajustadosA = numero.ajustadosA)  
> tabla.ajustadosA <- xtabs(ajustadosA ~ Hospitalizado+Sexo+Diabetes, datos2A )  
> numero.ajustadosB <- fitted(modeloB)  
> datos2B <- data.frame(datos2, ajustadosB = numero.ajustadosB)  
> tabla.ajustadosB <- xtabs(ajustadosB ~ Hospitalizado+Sexo+Diabetes, datos2B)  
> numero.ajustadosC <- fitted(modeloC)  
> datos2C <- data.frame(datos2, ajustadosC = numero.ajustadosC)  
> tabla.ajustadosC <- xtabs(ajustadosC ~ Hospitalizado+Sexo+Diabetes, datos2C)  
> numero.ajustadosD <- fitted(modeloD)  
> datos2D <- data.frame(datos2, ajustadosD = numero.ajustadosD)  
> tabla.ajustadosD <- xtabs(ajustadosD ~ Hospitalizado+Sexo+Diabetes, datos2D )  
> numero.ajustadosE <- fitted(modeloE)  
> datos2E <- data.frame(datos2, ajustadosE = numero.ajustadosE)  
> tabla.ajustadosE <- xtabs(ajustadosE ~ Hospitalizado+Sexo+Diabetes, datos2E )  
  
> numero.ajustadosF <- fitted(modeloF)  
> datos2F <- data.frame(datos2, ajustadosF = numero.ajustadosF)  
> tabla.ajustadosF <- xtabs(ajustadosF ~ Hospitalizado+Sexo+Diabetes, datos2F)  
  
> mosaicplot(~Hospitalizado+Sexo+Diabetes, data=tabla, color=T)  
> library("vcd")  
Loading required package: grid  
> mosaic(tabla, shade = TRUE, direction = "v", pop = FALSE, main="datos originales")  
> labeling_cells(text = as.table(tabla), margin = 0)(as.table(tabla))
```



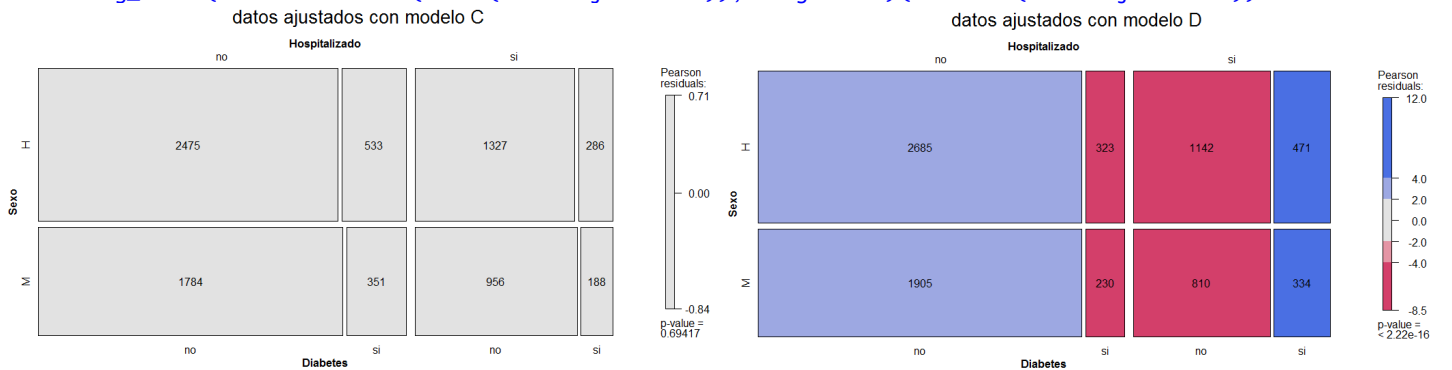
```
> mosaic(tabla.ajustadosA, shade = TRUE, direction = "v", pop = FALSE, main="datos ajustados con modelo A")  
> labeling_cells(text = as.table(round(tabla.ajustadosA,1)), margin = 0)(as.table(tabla.ajustadosA))  
> mosaic(tabla.ajustadosB, shade = TRUE, direction = "v", pop = FALSE, main="datos ajustados con modelo B")  
> labeling_cells(text = as.table(round(tabla.ajustadosB,1)), margin = 0)(as.table(tabla.ajustadosB))
```



```

> mosaic(tabla.ajustadosC, shade = TRUE, direction = "v", pop = FALSE, main="datos ajustados con modelo C"
)
> labeling_cells(text = as.table(round(tabla.ajustadosC)), margin = 0)(as.table(tabla.ajustadosC))
> mosaic(tabla.ajustadosD, shade = TRUE, direction = "v", pop = FALSE, main="datos ajustados con modelo D")
> labeling_cells(text = as.table(round(tabla.ajustadosD)), margin = 0)(as.table(tabla.ajustadosD))

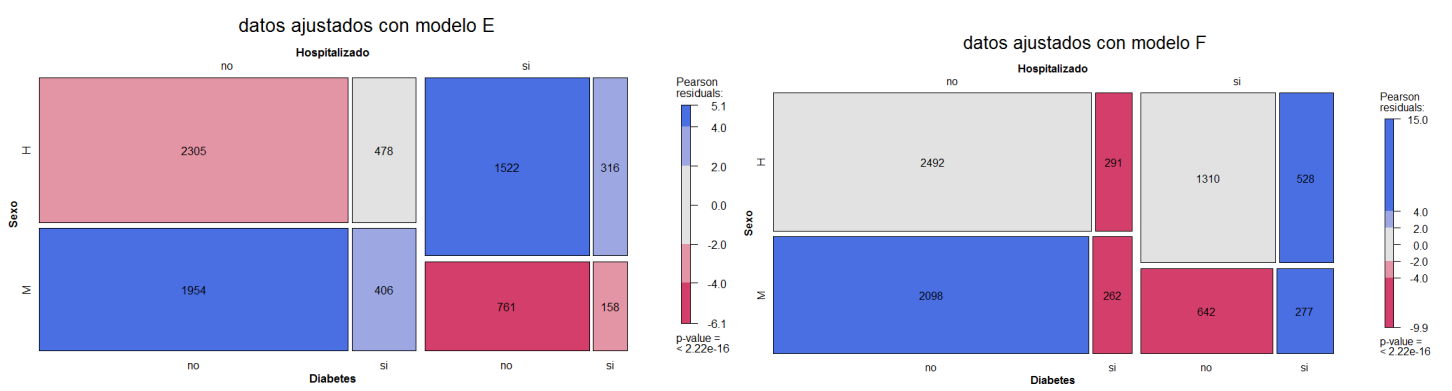
```



```

> mosaic(tabla.ajustadosE, shade = TRUE, direction = "v", pop = FALSE, main="datos ajustados con modelo E")
> labeling_cells(text = as.table(round(tabla.ajustadosE)), margin = 0)(as.table(tabla.ajustadosE))
> mosaic(tabla.ajustadosF, shade = TRUE, direction = "v", pop = FALSE, main="datos ajustados con modelo F")
> labeling_cells(text = as.table(round(tabla.ajustadosF)), margin = 0)(as.table(tabla.ajustadosF))

```



Salida R Parte 8

```

> Bacalao<-read.csv("C:/Users/Karla/Desktop/Cursos IIMAS/Categoricos/bacalao.csv")
> head(Bacalao)
  Station.ID Latitude Longitude Depth Temperature peces.capturados
1         356   71.10    22.43    349         3.95                44
2         357   71.32    23.68    382         3.75               138
3         358   71.60    24.90    294         3.45               675
4         359   71.27    25.88    304         3.65               357
5         363   71.52    28.12    384         3.35                76
6         364   71.48    29.10    344         3.65               368
> modelo2<-glm(peces.capturados~Latitude+Longitude+Temperature+Depth, family=poisson, data=Bacalao)
> modelo1<-glm(peces.capturados~Latitude+Longitude+Temperature, family=poisson, data=Bacalao)
> summary(modelo2)

```

call:

```
glm(formula = peces.capturados ~ Latitude + Longitude + Temperature + Depth, family = poisson, data = Bacalao)
```

```
Deviance Residuals:
```

Min	1Q	Median	3Q	Max
-24.280	-9.521	-3.173	2.118	49.442

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.6384251	0.6400393	-0.997	0.319
Latitude	0.0681683	0.0082264	8.286	<2e-16 ***
Longitude	0.0926485	0.0022925	40.414	<2e-16 ***
Temperature	0.1047362	0.0115462	9.071	<2e-16 ***
Depth	-0.0056388	0.0001372	-41.107	<2e-16 ***

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for poisson family taken to be 1)
```

```
Null deviance: 21533 on 88 degrees of freedom  
Residual deviance: 15468 on 84 degrees of freedom  
AIC: 16068
```

```
Number of Fisher Scoring iterations: 5
```

```
> summary(modelo1)
```

```
Call:
```

```
glm(formula = peces.capturados ~ Latitude + Longitude + Temperature, family = poisson, data = Bacalao)
```

```
Deviance Residuals:
```

Min	1Q	Median	3Q	Max
-24.691	-11.437	-4.987	3.259	50.310

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.765474	0.627919	4.404	1.06e-05 ***
Latitude	-0.013039	0.007901	-1.650	0.0989 .
Longitude	0.122820	0.002334	52.630	< 2e-16 ***
Temperature	0.047880	0.011449	4.182	2.89e-05 ***

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for poisson family taken to be 1)
```

```
Null deviance: 21533 on 88 degrees of freedom  
Residual deviance: 17095 on 85 degrees of freedom  
AIC: 17693
```

```
Number of Fisher Scoring iterations: 5
```

```
> anova(modelo1,modelo2, test="Chisq")
```

```
Analysis of Deviance Table
```

```
Model 1: peces.capturados ~ Latitude + Longitude + Temperature  
Model 2: peces.capturados ~ Latitude + Longitude + Temperature + Depth
```

	Resid. Df	Resid. Dev	Df	Deviance	Pr(>Chi)
1	85	17095			
2	84	15468	1	1627.2	< 2.2e-16 ***

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```