

Partial output based on R codes and Packages

Basic output

```
model= glm( y ~ x2 + x3 + x4 + x5, binomial, data = logitreg)

summary(model)
```

```
Call:
glm(formula = y ~ x2 + x3 + x4 + x5, family = binomial, data = logitreg)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.7943 -0.2618 -0.0092  0.0002  4.6541

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
x2          8.727e-04  4.056e-01   0.002  0.99828
x3          1.553e+00  3.398e-01   4.572 4.83e-06 ***
x4          8.922e+00  1.922e+00   4.642 3.45e-06 ***
x5          1.960e+00  7.448e-01   2.631 0.00851 **
(Intercept) -1.600e+01  3.347e+00  -4.779 1.76e-06 ***

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

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 554.518  on 399  degrees of freedom
Residual deviance:  57.759  on 395  degrees of freedom
AIC: 67.759

Number of Fisher Scoring iterations: 10
```

Other simple functions such as `exp(coef(model))` and `confint(model)` are also available.

The main packages used are **LOGIT** and **pscl**.

Examples:

```
Library(LOGIT)
toOR(model)

            or      delta  zscore pvalue exp.loci.  exp.upci.
x2          1.0009    0.4060  0.0022 0.9983    0.4520    2.2164
x3          4.7274    1.6061  4.5721 0.0000    2.4290    9.2006
x4       7494.4430 14403.4858  4.6423 0.0000   173.3104 324081.3469
x5          7.0972    5.2859  2.6312 0.0085    1.6486   30.5527
(Intercept)  0.0000    0.0000 -4.7795 0.0000    0.0000    0.0001
```

```

library(psc1)
pr2(model)
      llh      llhNull      G2      McFadden      r2ML      r2CU
-28.8795704 -277.2588722  496.7586037   0.8958390   0.7111641   0.9482188

```

llh The log-likelihood from the fitted model

llhNull The log-likelihood from the intercept-only restricted model

G2 Minus two times the difference in the log-likelihoods

McFadden McFadden's pseudo r-squared

r2ML Maximum likelihood pseudo r-squared (Cox & Snell)

r2CU Cragg and Uhler's pseudo r-squared (Nagelkerke)

```

library(LOGIT)
library(MASS)
model= glm(y ~ x2 + x3 + x4 + x5, binomial, data = logitreg)
grp10<-HLTest(obj=model, g=10)
cbind(grp10$observed, round(grp10$expect, digits = 1))
grp10

```

```

In HLTest(obj = model, g = 10) :
  Some expected counts are less than 5. Use smaller number of groups
> cbind(grp10$observed, round(grp10$expect, digits = 1))
      Y0 Y1 Y0hat Y1hat
[1.97895757072e-05,0.00440654403756] 39  1  39.9   0.1
(0.00440654403756,0.0247458953312] 39  1  39.6   0.4
(0.0247458953312,0.0337175161903] 40  0  38.7   1.3
(0.0337175161903,0.0337514797517] 40  0  38.7   1.3
(0.0337514797517,0.194655431685] 38  2  37.7   2.3
(0.194655431685,0.999970128639]  4 36  5.4  34.6
(0.999970128639,0.9999981883]  0 40  0.0  40.0
(0.9999981883,0.99999999083]  0 40  0.0  40.0
(0.99999999083,0.9999999997]  0 40  0.0  40.0
(0.9999999997,1]  0 40  0.0  40.0
> grp10

      Hosmer and Lemeshow goodness-of-fit test with 10 bins

data:  model
x2 = 14.559, df = 8, p-value = 0.06832

```