```
> #Multiple Logistic Regression in R
> if (FALSE)
+ {"
+ The data, taken from Lee (1974), consist of patient characteristics and
+ whether or not cancer remission occurred, and are saved in the data set
+ Remission. The variable remiss is the cancer remission indicator variable
+ with a value of 1 for remission and a value of 0 for nonremission.  The other
+ six variables are the risk factors thought to be related to cancer remission.
+ "}
>
> library(faraway)
>
> #read in the data which is in a csv file
> remission <- read.csv("C:/Users/jmard/OneDrive/Desktop/RegressionMethodsSpring2020/
                        Lecture 12 14APR2020/remission.csv",header = TRUE)
> head(remission,3L)
  remiss cell smear infil  li blast  temp
1      1  0.8  0.83  0.66 1.9 1.100 0.996
2      1  0.9  0.36  0.32 1.4 0.740 0.992
3      0  0.8  0.88  0.70 0.8 0.176 0.982
>
> logistic <- glm(remiss ~ cell + smear + infil + li + blast + temp,family=binomial(logit),data=remission)
> summary(logistic)

Call:
glm(formula = remiss ~ cell + smear + infil + li + blast + temp,
    family = binomial(logit), data = remission)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.95165  -0.66491  -0.04372   0.74304   1.67069

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  58.0385    71.2364   0.815   0.4152
cell         24.6615    47.8377   0.516   0.6062
smear        19.2936    57.9500   0.333   0.7392
infil       -19.6013    61.6815  -0.318   0.7507
li            3.8960     2.3371   1.667   0.0955 .
```

```
blast         0.1511     2.2786   0.066   0.9471
temp        -87.4339    67.5735  -1.294   0.1957
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 34.372  on 26  degrees of freedom
Residual deviance: 21.751  on 20  degrees of freedom
AIC: 35.751

Number of Fisher Scoring iterations: 8

> anova(logistic, test="Chisq")
Analysis of Deviance Table

Model: binomial, link: logit

Response: remiss

Terms added sequentially (first to last)


      Df Deviance Resid. Df Resid. Dev Pr(>Chi)
NULL                     26     34.372
cell   1   2.5800        25     31.792 0.108223
smear  1   0.5188        24     31.273 0.471347
infil  1   0.2927        23     30.980 0.588500
li     1   6.7818        22     24.199 0.009209 **
blast  1   0.3215        21     23.877 0.570724
temp   1   2.1264        20     21.751 0.144782
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
>
> library(DescTools) #install package if needed
> PseudoR2(logistic,which="all")

McFadden     McFaddenAdj        CoxSnell      Nagelkerke   AldrichNelson
0.36719420   -0.04011686      0.37340108      0.51859997      0.31854514
```

```
VeallZimmermann    Efron         McKelveyZavoina
0.56877141       0.38771143        0.83061406

   AIC             BIC            logLik         logLik0             G2
35.75065229    44.82151035    -10.87532614    -17.18588254    12.62111280
```

Null deviance: 34.372
Residual deviance: 21.751

34.372 - 21.751 = 12.621

```
>
> if (FALSE)
+ {"
+ McFadden pseudo-R2
+ McFadden adjusted pseudo-R2
+ Cox and Snell pseudo-R2 (also known as ML pseudo-R2)
+ Nagelkerke pseudoR2 (also known as CraggUhler R2)
+ AldrichNelson AldrichNelson pseudo-R2
+ VeallZimmermann pseudo-R2
+ McKelvey and Zavoina pseudo-R2
+ Efron pseudo-R2
+ Tjur’s pseudo-R2
+ Akaike’s information criterion
+ log-Likelihood for the fitted model (by maximum likelihood)
+ log-Likelihood for the null model. The null model will include the offset,
  and an intercept if there is one in the model.
+ G2 - difference of the null deviance - model deviance
+ "}
>
> remission2_7 <-cbind(remission$cell,remission$smear,remission$infil,remission$li,
          remission$blast,remission$temp)
> HosmerLemeshowTest(fit = fitted(logistic), obs = remission[,1], X = remission2_7)
$C

        Hosmer-Lemeshow C statistic

data:  fitted(logistic) and remission[, 1]
X-squared = 10.69, df = 8, p-value = 0.2199


$H
```

```
        Hosmer-Lemeshow H statistic

data:  fitted(logistic) and remission[, 1]
X-squared = 12.839, df = 8, p-value = 0.1175


$gof

        le Cessie-van Houwelingen-Copas-Hosmer global goodness of fit test

data:  fitted(logistic) and remission[, 1]
z = 0.13535, p-value = 0.8923


>
```