

Arizona State University

From the Selected Works of Joseph M Hilbe

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Suppliment to Logistic Regression Models

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Available at: https://works.bepress.com/joseph_hilbe/26/

Supplement to *Logistic Regression Models*

Joseph M. Hilbe

Updated to 18 September, 2011

This document is intended to provide additional code, information, and updates to *Logistic Regression Models* (2009, Chapman & Hall/CRC). I will be adding to it on a periodical basis. Stata and R code may be copied and pasted into a text editor, and saved in ASCII or text format. Following the supplied code, which is displayed between double lines, I give sample output, which may come from the text.

A series of "0000000"s is given for half the page between sections. I have many more additions to make, which I intend to do by the end of November, 2011.

Converting Stata files to R data frames

TASK: Create an R data frame from a Stata *dta* file. The *Hmisc* package can convert Stata files versions 5-10 to R files. Use the command *saveold* to convert version 11 and 12 Stata files to version 10, which can be used by *Hmisc*.

```
. use heartlrm
. saveold heartlrm2
```

Below we assume that the Stata *heartlrm* file is stored in the `c://ado` directory. I save it to version 10 format, using a slightly different name. If I want to save this data as an R data frame in the `c://rfiles` directory, I can use the code below.

NOTE: *heartlrm2* is the same as *heart01*, but with no missing values and ordered in a meaningful way. *heart01* is used frequently in *Logistic Regression Models*.

```
library("Hmisc")
heart01 <- stata.get("c://ado/heartlrm2.dta")
save.image(file="c://rfiles/heart01.Rdata")
head(heart01)      # Check to make certain the data is correct
```

You may convert any Stata file to an R data frame in this manner.

CHAPTER 7

R code for Hosmer-Lemeshow test

Credit: Contributed by Robert A. LaBudde (c) 2007

```
=====
iQuantile <- function(x, breaks=15) {
  #indices in x[] of percentile steps by 1/breaks
  xo <- order(x) #sort indices
  n <- length(x)
  r <- rep(0, breaks+1)
  r[1]<- 1
  r[breaks+1]<- n
  r[2:breaks]<- round(1:(breaks-1)*n/breaks)
  return(list(index=r,cuts=x[xo[r]]))
}
hlGOF.test <- function(observed, predicted, breaks=15) {
  #H-L GOF test for logistic regression
  #observed and predicted should not have missing values and match by index
  cat("\n", 'Hosmer-Lemeshow GOF test', '\n')
  ndata <- length(predicted)
  cuts <- c(round(.75*breaks), breaks, round(1.25*breaks))
  pvals <- rep(1,cuts[3]) #p-values
  for (nCuts in cuts) {
    ip <- order(predicted)
    iq <- iQuantile(predicted, nCuts) #indices for cuts
    iqInd<- iq$index
    cat("\n", 'For # Cuts =', nCuts, ' # Data =', ndata, '\n')
    cat('Cut # Total #Patterns # Resp. # Pred. Mean Resp. Mean Pred.', '\n')

    x2 <- 0
    ntot <- 0
    for (i in 1:nCuts) {
      if (i==1) {
        isubs <- ip[1:iqInd[2]]
      } else {
        isubs <- ip[(iqInd[i]+1):iqInd[i+1]]
      }
      nsubs <- length(isubs)
      ntot <- ntot + nsubs
      aobs <- mean(observed[isubs])
      mobs <- sum(observed[isubs])
      ncvp <- length(unique(predicted[isubs]))
      apred <- mean(predicted[isubs])
      mpred <- apred*nsubs
      x2 <- x2 + (mobs-mpred)^2/mpred + ((nsubs-mobs) - (nsubs-mpred))^2/(nsubs-mpred)
      cat(sprintf('%3d', i), sprintf('%8d', nsubs), sprintf('%8d', ncvp), sprintf('%8d', mobs),
        sprintf('%10.2f', mpred), sprintf('%8.5f', aobs), sprintf('%8.5f', apred), '\n')
    }
    cat('Total # Data:', ndata, ' Total over cuts:', ntot, '\n')
    pvals[nCuts] <- pchisq(x2, nCuts-2, lower.tail=FALSE)
    cat('Chisq:', x2, ' d.f.:', sprintf('%d', nCuts-2), ' P-value:',
      sprintf('%8.5f', pvals[nCuts]), '\n')
  }
  cat("\n", 'Minimum P-value: ', sprintf('%8.5f', min(pvals)), '\n')
}
=====
```

OUTPUT: Chapter 7.2

```
> #SECTION 7.2: HOSMER-LEMESHOW GOF TEST

> fit7_2a<- glm(death ~ anterior + hcabg + kk2 + kk3 + kk4 +
+             age3 + age4, data=heart, family=binomial)

> summary(fit7_2a)
Call:
glm(formula = death ~ anterior + hcabg + kk2 + kk3 + kk4 + age3 +
age4, family = binomial, data = heart)

Deviance Residuals:
Min 1Q Median 3Q Max
-1.3724 -0.3257 -0.1745 -0.1270 3.1061

Coefficients:
              Estimate      Std. Error    z value    Pr(>|z|)
(Intercept)   -4.8159         0.1934    -24.896    < 2e-16 ***
anteriorAnterior 0.6387         0.1675     3.812    0.000138 ***
hcabg          0.7864         0.3527     2.229    0.025786 *
kk2            0.8249         0.1804     4.572    4.84e-06 ***
kk3            0.7967         0.2692     2.959    0.003083 **
kk4            2.6837         0.3565     7.529    5.11e-14 ***
age3           1.2668         0.2006     6.316    2.68e-10 ***
age4           1.9409         0.2080     9.329    < 2e-16 ***
---

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

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1486.2 on 4502 degrees of freedom
Residual deviance: 1276.3 on 4495 degrees of freedom
(885 observations deleted due to missingness)
AIC: 1292.3

Number of Fisher Scoring iterations: 7

> exp(coef(fit7_2a)) #ORs
      (Intercept) anteriorAnterior      hcabg      kk2
0.008099558      1.894095884 2.195519114 2.281692192
      kk3      kk4      age3      age4
2.218198595 14.639836908 3.549576517 6.964846706

> source('ralhlGOFtest.r') #macro for H-L GOF test
> heart2<- na.omit(heart) #drop rows with missing data

> hlGOF.test(heart2$death, predict(fit7_2a, heart2, type='response'), breaks=10)

Hosmer-Lemeshow GOF test
For # Cuts = 8 # Data = 4503
Cut # Total #Patterns # Resp. # Pred. Mean Resp. Mean Pred.
1 563 1 7 4.52 0.01243 0.00803
2 563 1 2 4.52 0.00355 0.00803
3 563 2 6 7.77 0.01066 0.01380
4 563 4 6 8.87 0.01066 0.01575
5 562 2 8 13.79 0.01423 0.02455
6 563 7 25 21.07 0.04440 0.03742
7 563 8 38 32.68 0.06750 0.05805
8 563 24 84 82.77 0.14920 0.14702
Total # Data: 4503 Total over cuts: 4503
Chisq: 8.334831 d.f.: 6 P-value: 0.21458
```

```
library(MASS)
library(nnet)
x1 <- rnorm(50000)
x2 <- rnorm(50000)
x3 <- rnorm(50000)
denom = 1+exp(.4*x1 -.5*x2 +1 ) + exp(-.3*x1+.25*x2 +2) + ///
        exp(-.25*x1 + .1*x2 +2.5)
p1 <- 1/denom
p2 <- exp( .4*x1 - .5*x2 + 1)/denom
p3 <- exp(-.3*x1 + .25*x2 + 2)/denom
p4 <- exp(-.25*x1 + .1*x2 + 2.5)/denom
u <- runif(50000)
y <- rep(1, length(u)) #start with all level 1 u<= p1)
p12 <- p1 + p2
y <- ifelse(u>p1 & u<= p12, 2, y)
p13 <- p1 + p2 +p3
y <- ifelse (u>p12 & u<= p13, 3, y)
y <- ifelse(u>p13, 4, y)
mlogit <- multinom( y ~ x1 + x2 )
summary(mlogit)
```

```

qui {
  clear
  set mem 50m
  set obs 50000
  gen x1 = invnorm(runiform())
  gen x2 = invnorm(runiform())
}

/* coefficients for y= 2 are .4, -.5 and 1
   coefficients for y= 3 are -.3, .25 and 2
   coefficients for y= 4 are -.25, .10 and 2.5 */
qui {
  gen denom = 1+exp(.4*x1 -.5*x2 +1 ) + exp(-.3*x1+.25*x2 +2) + ///
    exp(-.25*x1 + .1*x2 +2.5)
  gen p1 = 1/denom
  gen p2 = exp(.4*x1-.5*x2 + 1) / denom
  gen p3 = exp(-.3*x1+.25*x2 + 2) / denom
  gen p4 = exp(-.25*x1+.1*x2 + 2.5) / denom
  gen u = runiform()
  gen y = 1 if u <= p1
  gen p12 = p1 + p2
  replace y = 2 if y==. & u<=p12
  gen p13 = p1 +p2 + p3
  replace y = 3 if y==. & u<=p13
  replace y = 4 if y==.
}

```

| | | | |
|---------------------------------|---------------|---|---------|
| Multinomial logistic regression | Number of obs | = | 50000 |
| | LR chi2(6) | = | 4979.77 |
| | Prob > chi2 | = | 0.0000 |
| Log likelihood = -53562.977 | Pseudo R2 | = | 0.0444 |

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```
clear
use medpar
keep type died white hmo
mlogit type white died hmo, rrr
egen cp = group(died white hmo)
sort type cp
gen n = 1
by type cp: gen cnt = sum(n)
sort type cp
by type cp: keep if _n==_N
drop cp n
mlogit type died white hmo [fw=cnt], rrr
```

OBSERVATION-LEVEL DATA

```
. mlogit type white died hmo, rrr
```

| type | | RRR | Std. Err. | z | P> z | [95% Conf. Interval] | |
|-----------------|--|----------------|-----------|-------|-------|----------------------|----------|
| Elective_Admit | | (base outcome) | | | | | |
| Urgent_Admit | | | | | | | |
| white | | .4689032 | .1000123 | -3.55 | 0.000 | .3086957 | .7122555 |
| died | | 1.404759 | .1997158 | 2.39 | 0.017 | 1.063129 | 1.85617 |
| hmo | | .6174288 | .1279701 | -2.33 | 0.020 | .4113053 | .92685 |
| _cons | | .4388146 | .0898531 | -4.02 | 0.000 | .2937556 | .6555047 |
| Emergency_Admit | | | | | | | |
| white | | .6629189 | .2366041 | -1.15 | 0.249 | .3293487 | 1.334335 |
| died | | 1.905411 | .4113054 | 2.99 | 0.003 | 1.248093 | 2.908912 |
| hmo | | .1470197 | .0870809 | -3.24 | 0.001 | .0460471 | .4694064 |
| _cons | | .1130222 | .0392496 | -6.28 | 0.000 | .0572222 | .2232357 |

GROUPED FORMAT

```
. mlogit type white died hmo [fw=cnt], rrr
```

| | type | RRR | Std. Err. | z | P> z | [95% Conf. Interval] | |
|-----------------|----------------|----------|-----------|-------|-------|----------------------|----------|
| Elective_Admit | (base outcome) | | | | | | |
| Urgent_Admit | | | | | | | |
| | white | .4689032 | .1000123 | -3.55 | 0.000 | .3086957 | .7122555 |
| | died | 1.404759 | .1997158 | 2.39 | 0.017 | 1.063129 | 1.85617 |
| | hmo | .6174288 | .1279701 | -2.33 | 0.020 | .4113053 | .92685 |
| | _cons | .4388146 | .0898531 | -4.02 | 0.000 | .2937556 | .6555047 |
| Emergency_Admit | | | | | | | |
| | white | .6629189 | .2366041 | -1.15 | 0.249 | .3293487 | 1.334335 |
| | died | 1.905411 | .4113054 | 2.99 | 0.003 | 1.248093 | 2.908912 |
| | hmo | .1470197 | .0870809 | -3.24 | 0.001 | .0460471 | .4694064 |
| | _cons | .1130222 | .0392496 | -6.28 | 0.000 | .0572222 | .2232357 |

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SYNTHETIC LOGIT and PROBIT REGRESSION

R code

SYNTHETIC LOGISTIC REGRESSION

```
nobs <- 5000
x1  <- runif(nobs)
x2  <- runif(nobs)
xb  <- 2 + 0.75*x1 - 1.25*x2
exb <- 1/(1+exp(-xb))
by  <- rbinomial(nobs, size=1, p=exb)
lreg <- glm(by ~ x1 + x2, family=binomial(link="logit"))
summary(lreg)
```

SYNTHETIC PROBIT REGRESSION

```
nobs <- 5000
x1  <- runif(nobs)
x2  <- runif(nobs)
xb  <- 2 + 0.75*x1 - 1.25*x2
exb <- pnorm(xb)
py  <- rbinomial(nobs, size=1, p=exb)
preg <- glm(py ~ x1 + x2, family=binomial(link="probit"))
summary(preg)
```

SYNTHETIC BINOMIAL OR GROUPED LOGISTIC REGRESSION

```
nobs <- 5000
x1  <- runif(nobs)
x2  <- runif(nobs)
d   <- rep(1:5, each=10000, times=1) *100
xb  <- 2 + 0.75*x1 - 1.25*x2
exb <- 1/(1+exp(-xb))
by  <- rbinomial(nobs, size=d, p=exb)
dby <- d - by
mylogit <- data.frame(by, dby, x1, x2)
gby <- glm(cbind(by,dby) ~ x1 + x2, family=binomial(link="logit"), data=mylogit)
summary(gby)

or
library(msme) # forthcoming
mylogit <- data.frame(by, d, x1, x2)
lreg <- irls(by ~ x1 + x2, family=binomial, m=d, data=mylogit)
summary(lreg)
```

MONTE CARLO LOGISTIC REGRESSION

```
# mc.logit.r // Joseph Hilbe 31Jul 2011 100 replications
# Displays vectors of coefficients and of standard errors
logitmc <- function()
{
  nobs <- 50000
  x1 <- runif(nobs)
  x2 <- runif(nobs)
  xb <- 2 + .75*x1 - 1.25*x2
  exb <- 1/(1+exp(-xb))
  by <- rbinom(nobs, size = 1, prob = exb)
  lry <- glm(by ~ x1 + x2, family=binomial(link="logit"))
  beta <- lry$coef
  pr <- sum(residuals(lry, type="pearson")^2)
  prdisp <- pr/lry$df.residual
  return(list(coef = coef(lry),
             se = sqrt(diag(vcov(lry)))/sqrt(prdisp)))
}
B <- replicate(100, logitmc())
apply(matrix(unlist(B[1,]), 3, 100), 1, mean)
apply(matrix(unlist(B[2,]), 3, 100), 1, mean)
```

MONTE CARLO GROUPED LOGISTIC REGRESSION

```
# mc.glogit.r // Joseph Hilbe 31Jul 2011
glogitmc <- function()
{
  nobs <- 50000
  x1 <- runif(nobs)
  x2 <- runif(nobs)
  d <- rep(1:5, each=10000, times=1)*100 # denominator
  xb <- 2 + .75*x1 - 1.25*x2
  exb <- 1/(1+exp(-xb))
  by <- rbinom(nobs, size = d, p = exb)
  dby = d - by
  gby <- glm(cbind(by,dby) ~ x1 + x2, family=binomial(link="logit"))
  beta <- gby$coef
  pr <- sum(residuals(gby, type="pearson")^2)
  prdisp <- pr/gby$df.residual
  se <- sqrt(diag(vcov(gby)))/prdisp
  list(beta, se)
}
B <- replicate(100, glogitmc())
apply(matrix(unlist(B[1,]), 3, 100), 1, mean)
mean(unlist(B[2,]))
```

SYNTHETIC LOGIT and PROBIT REGRESSION

Stata code

SYNTHETIC BERNOULLI-LOGIT DATA

```
* x1=.75, x2=-1.25, _cons=2
clear
set obs 50000
set seed 13579
gen x1 = invnorm(runiform())
gen x2 = invnorm(runiform())
gen xb = 2 + 0.75*x1 - 1.25*x2
gen exb = 1/(1+exp(-xb))
gen by = rbinomial(1, exb)
glm by x1 x2, nolog fam(bin 1)
```

SYNTHETIC BERNOULLI-PROBIT DATA

```
* x1=.75, x2=-1.25, _cons=2
clear
set obs 50000
set seed 19375
gen x1 = invnorm(runiform())
gen x2 = invnorm(runiform())
gen xb = 2 + 0.75*x1 - 1.25*x2
gen double exb = normprob(xb)
* replace exb=.99999999 if exb>.99999999 // add if need 50000 obs
gen double py = rbinomial(1, exb)
glm py x1 x2, nolog fam(bin 1) link(probit)
```

SYNTHETIC BINOMIAL-LOGIT DATA

```
* x1=.75, x2=-1.25, _cons=2
clear
set obs 50000
set seed 13579
gen x1 = invnorm(runiform())
gen x2 = invnorm(runiform())
* =====
* Select one: user specified or random denominator
* gen d = 100+100*int((_n-1)/10000)
gen d = ceil(10*runiform())
* =====
gen xb = 2 + 0.75*x1 - 1.25*x2
gen exb = 1/(1+exp(-xb))
gen by = rbinomial(d, exb)
glm by x1 x2, nolog fam(bin d)
```

*** SYNTHETIC ORDERED LOGIT WITH 3 LEVELS**

```
di in ye "Defined Coefficients/cuts:"
di in ye "b1 = .75; b2 = 1.25"
di in ye "Cut1=2; Cut2=3; Cut3=4"
qui {
drop _all
set obs 50000
set seed 13444
gen double x1 = 3*uniform()+1
gen double x2 = 2*uniform()-1
gen err = uniform()
gen y = .75*x1 + 1.25*x2 + log(err/(1-err))
gen int ys = 1 if y<=2
replace ys=2 if y<=3 & y>2
replace ys=3 if y<=4 & y>3
replace ys=4 if y>4
* save syn_logit
}
ologit ys x1 x2, nolog
* predict double (olpr1 olpr2 olpr3 olpr4), pr
```

*** SYNTHETIC ORDERED LOGIT MODEL WITH 4 LEVELS**

```
qui {
drop _all
set obs 50000
set seed 13444
gen double x1 = 3*runiform()+1
gen double x2 = 2*runiform()-1
gen double x3 = runiform()
gen err = runiform()
gen y = .5*x1 + 1.75*x2 - 1.25*x3 + log(err/(1-err))
gen int ys = 1 if y<=.8
replace ys=2 if y<=1.6 & y>.8
replace ys=3 if y<=2.4 & y>1.6
replace ys=4 if y<=3.2 & y>2.4
replace ys=5 if y>3.2
* save syn_logit
}
ologit ys x1 x2 x3, nolog
predict double (olpr1 olpr2 olpr3 olpr4 olpr5), pr
noi di in ye "Defined Coefficients/cuts:"
noi di in ye "b1 = .5; b2 = 1.75; b3 = -1.25"
noi di in ye "Cut1=.8; Cut2=1.6; Cut3=2.4; Cut4=3.2"
```

*** SYNTHETIC BINOMIAL-PROBIT DATA AND MODEL**

```
* x1=.75, x2=-1.25, _cons=2
clear
set obs 50000
set seed 070785
gen x1 = invnorm(runiform())
gen x2 = invnorm(runiform())
* =====
* Select one: user specified or random denominator
* gen d = 100+100*int((_n-1)/10000)
gen d = ceil(10*runiform())
* =====
gen xb = 2 + 0.75*x1 - 1.25*x2
gen double exb = normprob(xb)
* replace exb=.99999999 if exb>.99999999 and want exactly 50000
gen double by = rbinomial(d, exb)
glm by x1 x2, nolog fam(bin d) link(probit)
```

*** SYNTHETIC ORDERED PROBIT DATA AND MODEL**

```
di in ye "b1 = .75; b2 = 1.25"
di in ye "Cut1=2; Cut2=3,; Cut3=4"
qui {
drop _all
set obs 50000
set seed 12345
gen double x1 = 3*uniform()+1
gen double x2 = 2*uniform()-1
gen double y = .75*x1 + 1.25*x2 + invnorm(uniform())
gen int ys = 1 if y<=2
replace ys=2 if y<=3 & y>2
replace ys=3 if y<=4 & y>3
replace ys=4 if y>4
* save syn_probit
}
oprobit ys x1 x2, nolog
* predict double (olpr1 olpr2 olpr3 olpr4), pr
```

*** SYNTHETIC MULTINOMIAL LOGIT MODEL**

```
* y=2: x1= 0.4, x2=-0.5, _cons=1.0
* y=3: x1=-3.0, x2=0.25, _cons=2.0
qui {
clear
set mem 50m
* set seed 111322
set obs 100000
gen x1 = runiform()
gen x2 = runiform()
gen denom = 1+exp(.4*x1 - .5*x2 + 1) + exp(-.3*x1+.25*x2 + 2)
gen p1 = 1/denom
gen p2 = exp(.4*x1-.5*x2 + 1) / denom
gen p3 = exp(-.3*x1+.25*x2 + 2) / denom
gen u = runiform()
gen y = 1 if u <= p1
gen p12 = p1 + p2
replace y = 2 if y==. & u<=p12
replace y = 3 if y==.
}
mlogit y x1 x2, baseoutcome(1) nolog
```