Multiple Logistic Example

To illustrate multiple logistic regression, I again used data from the Late Life Study of Social Exchanges (LLSSE; Sorkin & Rook, 2004) to predict self-reported heart disease. Predictors included sex (w1sex; men=0, women=1), vigorous physical activity (w1activ), depression symptomatology from the brief 9-item version (Santor & Coyne, 1997) of the Center for Epidemiologic Studies-Depression scale (Radloff, 1977), and a measure of negative social exchanges (w1neg; Newsom, Rook, Nishishiba, Sorkin, & Mahan, 2005), which assesses the frequency of interpersonal conflicts.

SPSS¹

logistic regression vars=wlhheart with wlsex wlactiv wlcesd9 wlneg
/print=summary ci(95) iter(1).

Exerpts from output:

Block 0: Beginning Block

Iteration	History	a,b,c
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Iteration		-2 Log likelihood	Coefficients Constant
Step 0	1	633.358	-1.329
	2	625.763	-1.581
	3	625.718	-1.602
	4	625.718	-1.603

a. Constant is included in the model.

b. Initial -2 Log Likelihood: 625.718

c. Estimation terminated at iteration number 4 because parameter estimates changed by less than .001.

Omnibus Tests of Model Coefficients

		Chi-square	df	Sig.
Step 1	Step	23.238	4	<.001
	Block	23.238	4	<.001
	Model	23.238	4	<.001

Model Summary

Stop	-2 Log	Cox & Snell R	Nagelkerke R
Step	likelihood	Square	Square
1	602.480 ^a	.033	.055

a. Estimation terminated at iteration number 5 because parameter estimates changed by less than .001.

Variables in the Equation

								95% C.I.for EXP(B)	
		В	S.E.	Wald	df	Sig.	Exp(B)	Lower	Upper
Step 1 ^a	A1-sex of R	978	.214	20.824	1	<.001	.376	.247	.572
	N11-how often vigerous phy activities (Health)	041	.048	.721	1	.396	.960	.874	1.055
	9-item CES-D	.035	.022	2.550	1	.110	1.036	.992	1.082
	negative exchanges-total (mean)	.068	.186	.132	1	.716	1.070	.743	1.542
	Constant	-1.199	.206	33.922	1	<.001	.301		

a. Variable(s) entered on step 1: A1-sex of R, N11-how often vigerous phy activities (Health), 9-item CES-D, negative exchanges-total (mean).

¹ Note that the ci(95) keyword uses whole numbers to refer to percents not decimals. Also, adding the word goodfit to the /print subcommand will produce the Hosmer-Lemeshow test if desired (not recommended unless N > 400).

R

The glm procedure in R does not provide the likelihood ratio ("chi-square" test), so I used the lmtest package to compute that. The chi-square is the difference between the Block 0 (or null) model and the full model, so each has to be tested separately and then the lrtest function computes the difference between the -2 log likelihoods. To test the null model, the glm function is used but with a 1 instead of the predictors. Note that the N must be the same, so I use a listwise deletion routine for the variables in the full model before testing either model (always be sure to check descriptives to make sure it was done correctly before proceeding). The modEvA package is used to obtain pseudo- R^2 values.

```
> #listwise deletion so Ns the same for nested test
> d = d[complete.cases(d[,c("w1hheart","w1sex","w1activ","w1cesd9","w1neg")]),]
> #test null/block 0 model--a 1 is used in place of variables--for chi-square
> rm(logmodn)
  logmodn <- glm(w1hheart ~ 1, data = d, family = "binomial")</pre>
> summary(logmodn)
Call
qlm(formula = w1hheart ~ 1, family = "binomial", data = d)
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
                             0.1018 -15.75 <2e-16 ***
(Intercept) -1.6025
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
     Null deviance: 625.72 on 691 degrees of freedom
Residual deviance: 625.72 on 691 degrees of freedom
AIC: 627.72
Number of Fisher Scoring iterations: 3
> rm(logmod2)
> logmod2 <- glm(w1hheart ~ w1sex + w1activ + w1cesd9 + w1neg, data = d, family = "binomial")
> summary(logmod2)
Call:
glm(formula = w1hheart ~ w1sex + w1activ + w1cesd9 + w1neg, family = "binomial",
     data = d
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
                                      -5.824 5.74e-09 ***
                            0.20588
(Intercept) -1.19911
w1sex
              -0.97841
                            0.21440
                                      -4.563 5.03e-06 ***
w1activ
              -0.04065
                            0.04788
                                      -0.849
                                                  0.396
               0.03539
                            0.02216
                                       1.597
                                                  0.110
w1cesd9
w1neg
               0.06780
                            0.18643
                                       0.364
                                                  0.716
signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 625.72
                               on 691
                                        degrees of freedom
Residual deviance: 602.48
                               on 687
                                        degrees of freedom
AIC: 612.48
Number of Fisher Scoring iterations: 4
> #easy way to get odds ratios
> measy way to get odds ratios
> exp(cbind(OR=coef(logmod2), confint(logmod2)))
Waiting for profiling to be done...
OR 2.5 % 97.5 %
(Intercept) 0.3014610 0.1998632 0.4485558
wlsex
             0.3759076 0.2458771 0.5707173
0.9601616 0.8724972 1.0530681
w1sex
w1activ
w1cesd9
              1.0360220 0.9909311 1.0812665
w1nea
              1.0701472 0.7324376 1.5282734
  #get chi-square (LR) test comparing logmodn and logmod2
> library(lmtest)
> lrtest(logmodn,logmod2)
Likelihood ratio test
Model 1: w1hheart ~ 1
Model 2: w1hheart ~ w1sex + w1activ + w1cesd9 + w1neg
 #Df LogLik Df Chisq Pr(>Chisq)
L 1 -312.86
1
2 5 -301.24 4 23.238 0.0001135 ***
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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```
> #obtain psuedo-R-sq values with modEvA package
> library(modEvA)
> RsqGLM(model=logmod2) #model on right of equal sign is name I gave my model above
$coxsnell
[1] 0.03302352
$Nagelkerke
[1] 0.05548855
$McFadden
[1] 0.03713834
$Tjur
[1] 0.03423869
$sqPearson
[1] 0.03373417
```

Sample Write-Up

To identify factors that predict self-reported heart disease in a sample of older adults, a multiple logistic regression analysis was conducted, simultaneously entering gender, self-reported physical activity, depression scores, and negative social exchanges into the model. The results indicated that, together, the predictors accounted for a significant amount of variance in success, likelihood ratio $\chi^2(4) = 23.238$, p < .001. The Nagelkerke pseudo- R^2 indicated approximately 6% of the variance in heart disease was accounted for by the predictors overall. Out of all of the predictors in the model, only gender was a significant independent predictor of heart disease, B = .978, SE = .214, p <.001, with women more than two and a half times less likely to report heart disease, OR = .376, 95% CI[.247,.572] (where the odds for men vs. women = 1/.376 = 2.660) after controlling for activity level, B = .041, SE = .048, p = .396, OR = .960, 95% CI[.847,1.1055], depression, B = .035, SE = .022, p = .110, OR = 1.036, 95% CI[.992,1.082], and negative social exchanges, B = .068, SE = .186, p = .716, OR = 1.070, 95% CI[.743,.1.542].²

Nested Test Example

Any two nested models in which the same *N* is used and one model has a subset of predictors can be compared with a likelihood ratio test. This is akin to the *F*-test for the change in *R*-square, although we are only getting significance test, not the increment in *R*-square (I see no reason you could not also report the difference in pseudo *R*-square as long as you refer to it as an "approximate" increment). I'll illustrate a comparison of the model with just wlcesd9 and the full model. In SPSS (omitted here), you can add /method=enter subcommands to the logistic regression command as in OLS regression, and, in R (below), you can conduct the significance test with lrtest function in the same manner we used above for comparing to the null model. This analysis answers the question as to whether adding the three additional variables (wlsex, wlactiv, and wlneg) accounted for a significant amount of additional variance in the outcome. I omitted some of the output.

```
> #listwise deletion so Ns the same for nested test
> d = d[complete.cases(d[,c("w1hheart","w1sex","w1activ","w1cesd9","w1neg")]),]
> rm(logmod1)
> #simple logistic with continuous predictor
> logmod1 <- glm(w1hheart ~ w1cesd9, data = d, family = "binomial")
> summary(logmod1)
Null deviance: 625.72 on 691 degrees of freedom
Residual deviance: 623.72 on 690 degrees of freedom
> rm(logmod2)
> logmod2 <- glm(w1hheart ~ w1sex + w1activ + w1cesd9 + w1neg, data = d, family = "binomial")
> summary(logmod2)
Null deviance: 625.72 on 691 degrees of freedom
Residual deviance: 625.72 on 691 degrees of freedom
AL: 612.48
> #get LR chi-square nested test
> library(Imtest)
> lrtest(logmod2, logmod1)
Likelihood ratio test
Model 1: w1hheart ~ w1sex + w1activ + w1cesd9 + w1neg
Model 2: w1hheart ~ w1sex + w1activ + w1cesd9 + w1neg
Model 2: w1hheart ~ w1cesd9
```

² Had negative social exchanges been significant, we might say that the odds of heart disease increased by about 7% for each unit increase on the scale, OR = 1.070. Depending on the number of predictors and whether there is a table used to present results, non-significant coefficients might or might not be reported in practice. (Please present nonsignificant results for the HW, however).

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```
#Df LogLik Df Chisq Pr(>Chisq)
1 5 -301.24
2 2 -311.86 -3 21.239 9.391e-05 ***
---
signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The likelihood ratio test is simply the difference between the two -2 log likelihood values (R calls them "residual deviance"): $\chi^2 = 623.72 - 602.48 = 21.239$. The result is a chi-square value tested with df = 690 - 687 = 3. Note that the Imtest package takes the difference in loglikelihoods (rather than -2 × the likelihood), which is half the -2 log likelihood (residual deviance) values, and then it multiplies the difference by 2 at the end to arrive at the same result.

References

Newsom, J. T., Rook, K. S., Nishishiba, M., Sorkin, D. H., & Mahan, T. L. (2005). Understanding the relative importance of positive and negative social exchanges: Examining specific domains and appraisals. *The Journals of Gerontology Series B: Psychological Sciences and Social Sciences*, 60(6), P304-P312.

Radloff, L. S. (1977). The CES-D scale: A self-report depression scale for research in the general population. Applied psychological measurement, 1(3), 385-401.

Santor, D. A., & Coyne, J. C. (1997). Shortening the CES–D to improve its ability to detect cases of depression. *Psychological assessment*, 9(3), 233-243.

Sorkin, D. H., & Rook, K. S. (2004). Interpersonal control strivings and vulnerability to negative social exchanges in later life. *Psychology and Aging*, 19(4), 555-564.