

R Analysis Example Replication C8

```
# Set up data sets for C8
ncsr <- read.table(file = "P://ASDA 2/Data sets/ncsr/ncsr_sub_5apr2017.csv", sep = ",", header = T, as.is=T)

#create factor versions with labels
ncsr$racec <- factor(ncsr$racecat, levels = 1: 4, labels =c("Other", "Hispanic", "Black", "White"))
ncsr$mar3catc <- factor(ncsr$MAR3CAT, levels = 1: 3, labels =c("Married", "Previously Married", "Never
Married"))
ncsr$ed4catc <- factor(ncsr$ED4CAT, levels = 1: 4, labels =c("0-11", "12", "13-15", "16+"))
ncsr$sexc <- factor(ncsr$SEX, levels = 1:2, labels=c("Male", "Female"))
ncsr$ag4catc <- factor(ncsr$ag4cat, levels = 1:4, labels=c("18-29", "30-44", "45-59", "60+"))
ncsr$mdec <- factor(ncsr$mde, level = 1:2, labels=c("No", "Yes"))

ncsrsvyp1 <- svydesign(strata=~SESTRAT, id=~SECLUSTR, weights=~NCSRWTSH, data=ncsr, nest=T)
names (ncsrsvyp1)
ncsrp2 <- subset(ncsr, !is.na(NCSRWTLG))

ncsrsvyp2 <- svydesign(strata=~SESTRAT, id=~SECLUSTR, weights=~NCSRWTLG, data=ncsrp2, nest=T)
names (ncsrsvyp2)

# Bivariate chisq tests for Example 8.1
# MDE by Sex, Age, ALD, Education, and Marital Status
ex8_1sex <- svyby(~factor(mde), ~sexc, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
ex8_1sex

ex8_1age <- svyby(~factor(mde), ~ag4catc, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
ex8_1age

ex8_1ald <- svyby(~factor(mde), ~ald, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
ex8_1ald

ex8_1ed <- svyby(~factor(mde), ~ed4catc, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
ex8_1ed

ex8_1mar <- svyby(~factor(mde), ~mar3catc, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
ex8_1mar

# ChiSq Tests
svychisq(~mde + ag4cat, ncsrsvyp2)
svychisq(~mde + sexc, ncsrsvyp2)
svychisq(~mde + ald, ncsrsvyp2)
svychisq(~mde + ED4CAT, ncsrsvyp2)
svychisq(~mde + MAR3CAT, ncsrsvyp2)

# Model 8.1
mod81 <- svyglm(mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) + factor(mar3catc), family=quasibinomial,
design=ncsrsvyp2)
summary(mod81)
#exp of coefficients
exp(mod81$coef)

# Lumley AIC (design-adjusted) test for first model
AIC(mod81)
```

```

# tests of parameters
regTermTest(mod81, ~factor(ag4catc))
regTermTest(mod81, ~factor(ed4catc))
regTermTest(mod81, ~factor(mar3catc))

# Currently checking on ability to do average marginal effects of ALD on MDE by Age Groups
# Similar to margins, dydx(ald) by (ag4cat) in Stata

#add interactions to model
mod81_int <- svyglm(mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) + factor(mar3catc) +
sexm*factor(ag4catc) + sexm*ald + sexm*factor(ed4catc) + sexm*factor(mar3catc), family=quasibinomial,
design=ncsrsvyp2)
summary(mod81_int)
# AIC for 2nd model
AIC(mod81_int)

# Test interactions of sex by all other predictors
regTermTest(mod81_int, ~sexm:factor(ag4catc))
regTermTest(mod81_int, ~sexm:ald)
regTermTest(mod81_int, ~sexm:factor(ed4catc))
regTermTest(mod81_int, ~sexm:factor(mar3catc))

# Design-Adjusted LRT test in R, tests model 1 v. model 2 with interactions
anova(mod81, mod81_int, test="Chisq", method="LRT")

# Model 8.2 with logit, probit, and cloglog comparison
summary(ex82_logit <- svyglm(ald ~ factor(ag4catc) + sexm + factor(ed4catc) + factor(mar3catc),
family=quasibinomial, design=ncsrsvyp2))
regTermTest(ex82_logit, ~factor(ag4catc))
regTermTest(ex82_logit, ~factor(ed4catc))
regTermTest(ex82_logit, ~factor(mar3catc))

summary(ex82_probit <- svyglm(ald ~ factor(ag4catc) + sexm + factor(ed4catc) + factor(mar3catc),
family=quasibinomial(link=probit), design=ncsrsvyp2))
regTermTest(ex82_probit, ~factor(ag4catc))
regTermTest(ex82_probit, ~factor(ed4catc))
regTermTest(ex82_probit, ~factor(mar3catc))

summary(ex82_cloglog <- svyglm(ald ~ factor(ag4catc) + sexm + factor(ed4catc) + factor(mar3catc),
family=quasibinomial(link=cloglog), design=ncsrsvyp2))
regTermTest(ex82_cloglog, ~factor(ag4catc))
regTermTest(ex82_cloglog, ~factor(ed4catc))
regTermTest(ex82_cloglog, ~factor(mar3catc))

```

Output R Analysis Example Replication C8

```
> # MDE by Sex, Age, ALD, Education, and Marital Status
> ex8_1sex <- svyby(~factor(mde), ~sexc, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
> ex8_1sex
      sexc factor(mde)0 factor(mde)1 se.factor(mde)0 se.factor(mde)1
Male   Male   0.8471074   0.1528926   0.009137590   0.009137590
Female Female  0.7738295   0.2261705   0.006727609   0.006727609

> ex8_1age <- svyby(~factor(mde), ~ag4catc, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
> ex8_1age
      ag4catc factor(mde)0 factor(mde)1 se.factor(mde)0 se.factor(mde)1
18-29  18-29   0.8160119   0.1839881   0.008853615   0.008853615
30-44  30-44   0.7712342   0.2287658   0.011044532   0.011044532
45-59  45-59   0.7766733   0.2233267   0.012606600   0.012606600
60+    60+    0.8893912   0.1106088   0.009562657   0.009562657

> ex8_1ald <- svyby(~factor(mde), ~ald, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
> ex8_1ald
      ald factor(mde)0 factor(mde)1 se.factor(mde)0 se.factor(mde)1
0  0   0.8230860   0.1769140   0.006506907   0.006506907
1  1   0.5484091   0.4515909   0.029025055   0.029025055

> ex8_1ed <- svyby(~factor(mde), ~ed4catc, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
> ex8_1ed
      ed4catc factor(mde)0 factor(mde)1 se.factor(mde)0 se.factor(mde)1
0-11   0-11   0.8369163   0.1630837   0.01212127   0.01212127
12     12     0.8145033   0.1854967   0.00827191   0.00827191
13-15  13-15  0.7875147   0.2124853   0.01043948   0.01043948
16+    16+    0.8033254   0.1966746   0.01087591   0.01087591

> ex8_1mar <- svyby(~factor(mde), ~mar3catc, svymean, design=ncsrsvyp2, se=T, na.rm=T, ci=T)
> ex8_1mar
      mar3catc factor(mde)0 factor(mde)1 se.factor(mde)0
Married      Married      0.8267385   0.1732615   0.007419619
Previously Married Previously Married  0.7609794   0.2390206   0.014493869
Never Married      Never Married  0.8060058   0.1939942   0.011549336
      se.factor(mde)1
Married      0.007419619
Previously Married  0.014493869
Never Married  0.011549336
```

```
> # ChiSq Tests
> svychisq(~mde + ag4cat, ncsrsvyp2)

Pearson's X^2: Rao & Scott adjustment

data: svychisq(~mde + ag4cat, ncsrsvyp2)
F = 26.39, ndf = 2.7612, ddf = 115.9700, p-value = 1.965e-12

> svychisq(~mde + sexc, ncsrsvyp2)

Pearson's X^2: Rao & Scott adjustment

data: svychisq(~mde + sexc, ncsrsvyp2)
F = 44.834, ndf = 1, ddf = 42, p-value = 3.965e-08

> svychisq(~mde + ald, ncsrsvyp2)

Pearson's X^2: Rao & Scott adjustment

data: svychisq(~mde + ald, ncsrsvyp2)
F = 120.03, ndf = 1, ddf = 42, p-value = 6.86e-14

> svychisq(~mde + ED4CAT, ncsrsvyp2)

Pearson's X^2: Rao & Scott adjustment

data: svychisq(~mde + ED4CAT, ncsrsvyp2)
F = 4.3043, ndf = 2.903, ddf = 121.930, p-value = 0.006916

> svychisq(~mde + MAR3CAT, ncsrsvyp2)

Pearson's X^2: Rao & Scott adjustment

data: svychisq(~mde + MAR3CAT, ncsrsvyp2)
F = 11.085, ndf = 1.8987, ddf = 79.7450, p-value = 7.616e-05
```

```
> # Model 8.1
> mod81 <- svyglm(mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) + factor(mar3catc), family=quasibinomial,
design=ncsrsvyp2)
> summary(mod81)
```

Call:

```
svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
factor(mar3catc), family = quasibinomial, design = ncsrsvyp2)
```

Survey design:

```
svydesign(strata = ~SESTRAT, id = ~SECLUSTER, weights = ~NCSRWTLG,
data = ncsrp2, nest = T)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-1.58308	0.12066	-13.120	2.01e-14	***
factor(ag4catc)30-44	0.25562	0.09438	2.708	0.0108	*
factor(ag4catc)45-59	0.20645	0.09153	2.256	0.0311	*
factor(ag4catc)60+	-0.67579	0.14130	-4.783	3.74e-05	***
sexm	-0.57735	0.07722	-7.477	1.64e-08	***
ald	1.42368	0.15416	9.235	1.53e-10	***
factor(ed4catc)12	0.07925	0.09690	0.818	0.4194	
factor(ed4catc)13-15	0.23051	0.09307	2.477	0.0187	*
factor(ed4catc)16+	0.16293	0.11061	1.473	0.1505	
factor(mar3catc)Previously Married	0.48642	0.08542	5.694	2.63e-06	***
factor(mar3catc)Never Married	0.11558	0.10787	1.071	0.2920	

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

(Dispersion parameter for quasibinomial family taken to be 1.001564)

Number of Fisher Scoring iterations: 4

```
> #exp of coefficients
```

```
> exp(mod81$coef)
```

(Intercept)	0.2053424	factor(ag4catc)30-44	1.2912600
factor(ag4catc)45-59	1.2293019	factor(ag4catc)60+	0.5087563
sexm	0.5613867	ald	4.1523575
factor(ed4catc)12	1.0824803	factor(ed4catc)13-15	1.2592434
factor(ed4catc)16+	1.1769489	factor(mar3catc)Previously Married	1.6264870
factor(mar3catc)Never Married	1.1225236		

```
> # Lumley AIC (design-adjusted) test for first model
```

```
> AIC(mod81)
```

eff.p	AIC	deltabar
9.7757533	5288.0774889	0.9775753

```
> # tests of parameters
> regTermTest(mod81, ~factor(ag4catc))
Wald test for factor(ag4catc)
  in svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
    factor(mar3catc), family = quasibinomial, design = ncsrsvyp2)
F = 19.98292 on 3 and 32 df: p= 1.7536e-07
> regTermTest(mod81, ~factor(ed4catc))
Wald test for factor(ed4catc)
  in svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
    factor(mar3catc), family = quasibinomial, design = ncsrsvyp2)
F = 2.236337 on 3 and 32 df: p= 0.10303
> regTermTest(mod81, ~factor(mar3catc))
Wald test for factor(mar3catc)
  in svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
    factor(mar3catc), family = quasibinomial, design = ncsrsvyp2)
F = 17.00766 on 2 and 32 df: p= 9.2915e-06
```

```

> #add interactions to model 8.1
> mod81_int <- svyglm(mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) + factor(mar3catc) +
sexm*factor(ag4catc) + sexm*ald + sexm*factor(ed4catc) + sexm*factor(mar3catc), family=quasibinomial,
design=ncsrsvyp2)
> summary(mod81_int)

```

```

Call:
svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
factor(mar3catc) + sexm * factor(ag4catc) + sexm * ald +
sexm * factor(ed4catc) + sexm * factor(mar3catc), family = quasibinomial,
design = ncsrsvyp2)

```

```

Survey design:
svydesign(strata = ~SESTRAT, id = ~SECLUSTR, weights = ~NCSRWTLG,
data = ncsrp2, nest = T)

```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-1.599889	0.134010	-11.939	2.45e-11	***
factor(ag4catc)30-44	0.220404	0.113761	1.937	0.06507	.
factor(ag4catc)45-59	0.214641	0.102494	2.094	0.04746	*
factor(ag4catc)60+	-0.645556	0.175192	-3.685	0.00123	**
sexm	-0.546442	0.357168	-1.530	0.13967	
ald	1.553140	0.211023	7.360	1.74e-07	***
factor(ed4catc)12	0.130518	0.083710	1.559	0.13261	
factor(ed4catc)13-15	0.297324	0.117042	2.540	0.01829	*
factor(ed4catc)16+	0.242218	0.151870	1.595	0.12438	
factor(mar3catc)Previously Married	0.417786	0.110525	3.780	0.00097	***
factor(mar3catc)Never Married	0.017337	0.129782	0.134	0.89489	
factor(ag4catc)30-44:sexm	0.096743	0.200840	0.482	0.63458	
factor(ag4catc)45-59:sexm	0.002637	0.212817	0.012	0.99022	
factor(ag4catc)60+:sexm	-0.037809	0.302028	-0.125	0.90146	
sexm:ald	-0.200417	0.242241	-0.827	0.41654	
sexm:factor(ed4catc)12	-0.137780	0.271016	-0.508	0.61603	
sexm:factor(ed4catc)13-15	-0.168790	0.269350	-0.627	0.53705	
sexm:factor(ed4catc)16+	-0.194018	0.344159	-0.564	0.57838	
sexm:factor(mar3catc)Previously Married	0.182504	0.207867	0.878	0.38903	
sexm:factor(mar3catc)Never Married	0.231898	0.211963	1.094	0.28526	

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

(Dispersion parameter for quasibinomial family taken to be 1.001859)

Number of Fisher Scoring iterations: 4

```

> # AIC for 2nd model
> AIC(mod81_int)
      eff.p      AIC  deltabar
19.51813 5303.89335   1.02727

> # Test interactions of sex by all other predictors
> regTermTest(mod81_int, ~sexm:factor(ag4catc))
Wald test for sexm:factor(ag4catc)
  in svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
    factor(mar3catc) + sexm * factor(ag4catc) + sexm * ald +
    sexm * factor(ed4catc) + sexm * factor(mar3catc), family = quasibinomial,
    design = ncsrsvyp2)
F = 0.259966 on 3 and 23 df: p= 0.85346
> regTermTest(mod81_int, ~sexm:ald)
Wald test for sexm:ald
  in svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
    factor(mar3catc) + sexm * factor(ag4catc) + sexm * ald +
    sexm * factor(ed4catc) + sexm * factor(mar3catc), family = quasibinomial,
    design = ncsrsvyp2)
F = 0.6845 on 1 and 23 df: p= 0.41654
> regTermTest(mod81_int, ~sexm:factor(ed4catc))
Wald test for sexm:factor(ed4catc)
  in svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
    factor(mar3catc) + sexm * factor(ag4catc) + sexm * ald +
    sexm * factor(ed4catc) + sexm * factor(mar3catc), family = quasibinomial,
    design = ncsrsvyp2)
F = 0.1318233 on 3 and 23 df: p= 0.94015
> regTermTest(mod81_int, ~sexm:factor(mar3catc))
Wald test for sexm:factor(mar3catc)
  in svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
    factor(mar3catc) + sexm * factor(ag4catc) + sexm * ald +
    sexm * factor(ed4catc) + sexm * factor(mar3catc), family = quasibinomial,
    design = ncsrsvyp2)
F = 0.783767 on 2 and 23 df: p= 0.4685

```



```
> # Design-Adjusted LRT test in R, tests model 1 v. model 2 with interactions
> anova(mod81, mod81_int, test="Chisq", method="LRT")
Working (Rao-Scott) LRT for factor(ag4catc):sexm sexm:ald sexm:factor(ed4catc) sexm:factor(mar3catc)
in svyglm(formula = mde ~ factor(ag4catc) + sexm + ald + factor(ed4catc) +
  factor(mar3catc) + sexm * factor(ag4catc) + sexm * ald +
  sexm * factor(ed4catc) + sexm * factor(mar3catc), family = quasibinomial,
  design = ncsrsvyp2)
Working 2logLR = 3.412191 p= 0.90812
(scale factors: 3 1.5 1.1 0.84 0.78 0.65 0.57 0.34 0.23 )
```

```
> # Model 8.2 with logit, probit, and cloglog comparison
> summary(ex82_logit <- svyglm(ald ~ factor(ag4catc) + sexm + factor(ed4catc) + factor(mar3catc),
family=quasibinomial, design=ncsrsvyp2))
```

Call:

```
svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
factor(mar3catc), family = quasibinomial, design = ncsrsvyp2)
```

Survey design:

```
svydesign(strata = ~SESTRAT, id = ~SECLUSTER, weights = ~NCSRWTLG,
data = ncsrp2, nest = T)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-3.12432	0.22527	-13.869	2.54e-15	***
factor(ag4catc)30-44	0.14628	0.17813	0.821	0.417443	
factor(ag4catc)45-59	-0.05071	0.14392	-0.352	0.726833	
factor(ag4catc)60+	-1.12034	0.21248	-5.273	8.25e-06	***
sexm	0.99799	0.11910	8.379	1.11e-09	***
factor(ed4catc)12	-0.26844	0.19373	-1.386	0.175150	
factor(ed4catc)13-15	-0.26448	0.17614	-1.502	0.142716	
factor(ed4catc)16+	-0.73623	0.19719	-3.734	0.000712	***
factor(mar3catc)Previously Married	0.51783	0.14206	3.645	0.000910	***
factor(mar3catc)Never Married	0.06532	0.16871	0.387	0.701130	

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

(Dispersion parameter for quasibinomial family taken to be 0.9751118)

Number of Fisher Scoring iterations: 6

```
> regTermTest(ex82_logit, ~factor(ag4catc))
Wald test for factor(ag4catc)
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
factor(mar3catc), family = quasibinomial, design = ncsrsvyp2)
F = 12.66092 on 3 and 33 df: p= 1.1402e-05
> regTermTest(ex82_logit, ~factor(ed4catc))
Wald test for factor(ed4catc)
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
factor(mar3catc), family = quasibinomial, design = ncsrsvyp2)
F = 5.037044 on 3 and 33 df: p= 0.005531
> regTermTest(ex82_logit, ~factor(mar3catc))
Wald test for factor(mar3catc)
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
factor(mar3catc), family = quasibinomial, design = ncsrsvyp2)
F = 6.696711 on 2 and 33 df: p= 0.003622
```

```
> summary(ex82_probit <- svyglm(ald ~ factor(ag4catc) + sexm + factor(ed4catc) + factor(mar3catc),
family=quasibinomial(link=probit), design=ncsrsvyp2))
```

Call:

```
svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
  factor(mar3catc), family = quasibinomial(link = probit),
  design = ncsrsvyp2)
```

Survey design:

```
svydesign(strata = ~SESTRAT, id = ~SECLUSTER, weights = ~NCSRWTLG,
  data = ncsrp2, nest = T)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.71944	0.10648	-16.149	< 2e-16 ***
factor(ag4catc)30-44	0.06532	0.08541	0.765	0.449852
factor(ag4catc)45-59	-0.03447	0.06734	-0.512	0.612141
factor(ag4catc)60+	-0.53128	0.09372	-5.669	2.56e-06 ***
sexm	0.47084	0.05695	8.268	1.51e-09 ***
factor(ed4catc)12	-0.12378	0.09497	-1.303	0.201457
factor(ed4catc)13-15	-0.12438	0.08504	-1.463	0.153028
factor(ed4catc)16+	-0.33956	0.09237	-3.676	0.000836 ***
factor(mar3catc)Previously Married	0.25478	0.07014	3.633	0.000942 ***
factor(mar3catc)Never Married	0.03895	0.07795	0.500	0.620593

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

(Dispersion parameter for quasibinomial family taken to be 0.9825414)

Number of Fisher Scoring iterations: 6

```
> regTermTest(ex82_probit, ~factor(ag4catc))
```

Wald test for factor(ag4catc)

```
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
  factor(mar3catc), family = quasibinomial(link = probit),
  design = ncsrsvyp2)
```

F = 16.00526 on 3 and 33 df: p= 1.3479e-06

```
> regTermTest(ex82_probit, ~factor(ed4catc))
```

Wald test for factor(ed4catc)

```
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
  factor(mar3catc), family = quasibinomial(link = probit),
  design = ncsrsvyp2)
```

F = 5.005033 on 3 and 33 df: p= 0.0057059

```
> regTermTest(ex82_probit, ~factor(mar3catc))
```

Wald test for factor(mar3catc)

```
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
  factor(mar3catc), family = quasibinomial(link = probit),
  design = ncsrsvyp2)
```

F = 6.701662 on 2 and 33 df: p= 0.0036093

```
> summary(ex82_cloglog <- svyglm(ald ~ factor(ag4catc) + sexm + factor(ed4catc) + factor(mar3catc),
family=quasibinomial(link=cloglog), design=ncsrsvyp2))
```

Call:

```
svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
  factor(mar3catc), family = quasibinomial(link = cloglog),
  design = ncsrsvyp2)
```

Survey design:

```
svydesign(strata = ~SESTRAT, id = ~SECLUSTER, weights = ~NCSRWTLG,
  data = ncsrp2, nest = T)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-3.14840	0.21716	-14.498	7.19e-16	***
factor(ag4catc)30-44	0.14304	0.17125	0.835	0.409556	
factor(ag4catc)45-59	-0.04524	0.13967	-0.324	0.748043	
factor(ag4catc)60+	-1.08287	0.20816	-5.202	1.02e-05	***
sexm	0.96522	0.11494	8.398	1.06e-09	***
factor(ed4catc)12	-0.26010	0.18467	-1.408	0.168358	
factor(ed4catc)13-15	-0.25556	0.16843	-1.517	0.138700	
factor(ed4catc)16+	-0.71265	0.19042	-3.743	0.000694	***
factor(mar3catc)Previously Married	0.49354	0.13522	3.650	0.000898	***
factor(mar3catc)Never Married	0.06049	0.16369	0.370	0.714073	

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

(Dispersion parameter for quasibinomial family taken to be 0.9745877)

Number of Fisher Scoring iterations: 6

```
> regTermTest(ex82_cloglog, ~factor(ag4catc))
```

Wald test for factor(ag4catc)

```
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
  factor(mar3catc), family = quasibinomial(link = cloglog),
  design = ncsrsvyp2)
```

F = 12.18828 on 3 and 33 df: p= 1.5779e-05

```
> regTermTest(ex82_cloglog, ~factor(ed4catc))
```

Wald test for factor(ed4catc)

```
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
  factor(mar3catc), family = quasibinomial(link = cloglog),
  design = ncsrsvyp2)
```

F = 5.0184 on 3 and 33 df: p= 0.0056322

```
> regTermTest(ex82_cloglog, ~factor(mar3catc))
```

Wald test for factor(mar3catc)

```
in svyglm(formula = ald ~ factor(ag4catc) + sexm + factor(ed4catc) +
  factor(mar3catc), family = quasibinomial(link = cloglog),
  design = ncsrsvyp2)
```

F = 6.710508 on 2 and 33 df: p= 0.0035866