

Categorical Data Analysis

Lab material #5-2

```

data wash;
input treatmnt $ washblty $ count @@;
cards;
water low 27 water medium 14 water high 5
standard low 10 standard medium 17 standard high 26
super low 5 super medium 12 super high 50
;
run;

proc freq order=data;
weight count;
tables treatmnt*washblty / chisq cmh;
run;

data wash2;
set wash;
select (treatmnt);
when('water') u=0;
when('standard') u=1;
when('super') u=2;
end;
select (washblty);
when('low') v=1;
when('medium') v=2;
when('high') v=3;
end;
run;

proc genmod data=wash2 data=order;
class treatmnt washblty;
model count = treatmnt washblty treatmnt*washblty / dist=poisson link=log; /* saturated model */
run;
proc genmod data=wash2 data=order;
class treatmnt washblty;
model count = treatmnt washblty u*v / dist=poisson link=log; /* reduced model : linear-by-linear model or Uniform Association Model */
run;

```

Output 1 Results

The FREQ Procedure

Table of treatmnt by washblty

treatmnt		washblty			
		Frequency			
		Percent			
		Row Pct			
Col Pct		low	medium	high	Total
-----+-----+-----+-----+					
water		27	14	5	46
		16.27	8.43	3.01	27.71
		58.70	30.43	10.87	
		64.29	32.56	6.17	
-----+-----+-----+-----+					
standard		10	17	26	53

		6.02		10.24		15.66		31.93	
		18.87		32.08		49.06			
		23.81		39.53		32.10			
-----+-----+-----+-----+									
super		5		12		50		67	
		3.01		7.23		30.12		40.36	
		7.46		17.91		74.63			
		11.90		27.91		61.73			
-----+-----+-----+-----+									
Total		42		43		81		166	
		25.30		25.90		48.80		100.00	

Statistics for Table of treatmnt by washblty

Statistic	DF	Value	Prob

Chi-Square	4	55.0879	<.0001
Likelihood Ratio Chi-Square	4	58.0366	<.0001
Mantel-Haenszel Chi-Square	1	50.6016	<.0001
Phi Coefficient		0.5761	
Contingency Coefficient		0.4992	
Cramer's V		0.4073	

Sample Size = 166

Summary Statistics for treatmnt by washblty

Cochran-Mantel-Haenszel Statistics (Based on Table Scores)

Statistic	Alternative Hypothesis	DF	Value	Prob

1	Nonzero Correlation	1	50.6016	<.0001
2	Row Mean Scores Differ	2	52.7786	<.0001
3	General Association	4	54.7560	<.0001

Total Sample Size = 166

The GENMOD Procedure

Model Information

Data Set	WORK.WASH2
Distribution	Poisson
Link Function	Log
Dependent Variable	count

Number of Observations Read	9
Number of Observations Used	9

Class Level Information

Class	Levels	Values
treatmnt	3	standard super water
washblty	3	high low medium

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	0	0.0000	.
Scaled Deviance	0	0.0000	.
Pearson Chi-Square	.	0.0000	.
Scaled Pearson X2	.	0.0000	.
Log Likelihood		357.3498	
Full Log Likelihood		-20.3101	
AIC (smaller is better)		58.6202	
AICC (smaller is better)		.	
BIC (smaller is better)		60.3953	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square
Intercept		1	2.6391	0.2673	2.1152	3.1629	97.50
treatmnt	standard	1	0.1942	0.3609	-0.5132	0.9015	0.29
treatmnt	super	1	-0.1542	0.3934	-0.9252	0.6169	0.15
treatmnt	water	0	0.0000	0.0000	0.0000	0.0000	.
washblty	high	1	-1.0296	0.5210	-2.0507	-0.0085	3.91
washblty	low	1	0.6568	0.3293	0.0113	1.3023	3.98
washblty	medium	0	0.0000	0.0000	0.0000	0.0000	.
treatmnt*washblty	standard high	1	1.4545	0.6072	0.2644	2.6446	5.74
treatmnt*washblty	standard low	1	-1.1874	0.5170	-2.2007	-0.1741	5.27
treatmnt*washblty	standard medium	0	0.0000	0.0000	0.0000	0.0000	.
treatmnt*washblty	super high	1	2.4567	0.6122	1.2569	3.6566	16.11
treatmnt*washblty	super low	1	-1.5322	0.6259	-2.7591	-0.3054	5.99
treatmnt*washblty	super medium	0	0.0000	0.0000	0.0000	0.0000	.
treatmnt*washblty	water high	0	0.0000	0.0000	0.0000	0.0000	.
treatmnt*washblty	water low	0	0.0000	0.0000	0.0000	0.0000	.
treatmnt*washblty	water medium	0	0.0000	0.0000	0.0000	0.0000	.
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates

Parameter		Pr > ChiSq
Intercept		<.0001
treatmnt	standard	0.5906
treatmnt	super	0.6952
treatmnt	water	.
washblty	high	0.0481
washblty	low	0.0461
washblty	medium	.
treatmnt*washblty	standard high	0.0166
treatmnt*washblty	standard low	0.0216
treatmnt*washblty	standard medium	.
treatmnt*washblty	super high	<.0001
treatmnt*washblty	super low	0.0144
treatmnt*washblty	super medium	.
treatmnt*washblty	water high	.
treatmnt*washblty	water low	.

```
treatmnt*washblty  water      medium      .
Scale
```

NOTE: The scale parameter was held fixed.

The GENMOD Procedure

Model Information

```
Data Set          WORK.WASH2
Distribution       Poisson
Link Function      Log
Dependent Variable count
```

```
Number of Observations Read      9
Number of Observations Used      9
```

Class Level Information

```
Class      Levels  Values
treatmnt      3  standard super water
washblty      3  high low medium
```

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	3	1.9138	0.6379
Scaled Deviance	3	1.9138	0.6379
Pearson Chi-Square	3	1.9558	0.6519
Scaled Pearson X2	3	1.9558	0.6519
Log Likelihood		356.3929	
Full Log Likelihood		-21.2670	
AIC (smaller is better)		54.5340	
AICC (smaller is better)		96.5340	
BIC (smaller is better)		55.7174	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Wald Chi-Square	Pr > ChiSq
Intercept	1	2.5703	0.2066	2.1653	2.9754	154.71	<.0001
treatmnt standard	1	-1.7858	0.3444	-2.4609	-1.1108	26.89	<.0001
treatmnt super	1	-4.0981	0.7445	-5.5574	-2.6389	30.30	<.0001
treatmnt water	0	0.0000	0.0000	0.0000	0.0000	.	.
washblty high	1	-0.6845	0.3029	-1.2783	-0.0907	5.11	0.0239
washblty low	1	0.7007	0.2369	0.2363	1.1650	8.75	0.0031
washblty medium	0	0.0000	0.0000	0.0000	0.0000	.	.
u*v	1	1.0228	0.1632	0.7029	1.3428	39.26	<.0001
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.