

Illustration of the Equivalence of Loglinear and Chi-Square Models for Two Binary Variables

Below I use SPSS to illustrate the equivalence of chi square and loglinear analyses. The first model is a test of the saturated model with the association term. Test of the association term is a test of the same hypothesis but will only be asymptotically equivalent to the nested test (which follows).

```
output close *.
```

```
*show equivalence to the chi-square handout.
```

```
* Two-way analysis with chi-square.
crosstabs /tables=agegrp by voted
          /cells=count row column
          /statistics=chisq phi.
```

agegrp * voted voted in 2020 general election Crosstabulation

		voted voted in 2020 general election			
		0 no	1 yes	Total	
agegrp	.00 youngest age group	Count	35	50	85
		% within agegrp	41.2%	58.8%	100.0%
		% within voted voted in 2020 general election	16.1%	5.7%	7.8%
	1.00 older ages	Count	183	824	1007
		% within agegrp	18.2%	81.8%	100.0%
		% within voted voted in 2020 general election	83.9%	94.3%	92.2%
Total		Count	218	874	1092
		% within agegrp	20.0%	80.0%	100.0%
		% within voted voted in 2020 general election	100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymptotic Significance (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	25.960 ^a	1	<.001		
Continuity Correction ^b	24.540	1	<.001		
Likelihood Ratio	21.952	1	<.001		
Fisher's Exact Test				<.001	<.001
Linear-by-Linear Association	25.936	1	<.001		
N of Valid Cases	1092				

a. 0 cells (0.0%) have expected count less than 5. The minimum expected count is 16.97.

b. Computed only for a 2x2 table

Saturated model, used for comparison, but overall tests are not meaningful. Association tests for the 2 × 2 independence hypothesis that is the same as the chi-square test.

*square of z-value for association variable or nested likelihood test is approx equal to Pearson chi-square or is equal to likelihood ratio test from crosstab.

```
compute assoc = agegrp*voted.
genlog agegrp voted with assoc
/print=est/plot=none
/design = agegrp voted assoc.
```

Goodness-of-Fit Tests ^{a,b}

	Value	df	Sig.
Likelihood Ratio	.000	0	.
Pearson Chi-Square	.000	0	.

- a. Model: Poisson
- b. Design: Constant + agegrp + voted + assoc

Parameter Estimates ^{b,c}

Parameter	Estimate	Std. Error	Z	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant	5.565	.231	24.076	<.001	5.112	6.018
[agegrp = .00]	-1.643	.183	-8.959	<.001	-2.002	-1.283
[agegrp = 1.00]	0 ^a
[voted = 0]	-.352	.219	-1.609	.108	-.782	.077
[voted = 1]	0 ^a
assoc	1.150	.234	4.921	<.001	.692	1.608

- a. This parameter is set to zero because it is redundant.
- b. Model: Poisson
- c. Design: Constant + agegrp + voted + assoc

The “Z” value for the `assoc` variable is a test of the independence of the two variables, and is very close to the likelihood ratio from the chi-square test, $z^2 = (-4.921)^2 \approx 21.952$.

This second model tests lack of fit without the association term (i.e., **nonsaturated model**). The discrepancy in fit is due to whatever dependence there is between the two variables. So, the chi-squares match those in the crosstab analysis.

*the goodness of fit test from this model matches the linear-by-linear output from the chi-genlog agegrp voted

```

/print=est
/plot=none
/design = agegrp voted.
```

Goodness-of-Fit Tests ^{a,b}

	Value	df	Sig.
Likelihood Ratio	21.952	1	<.001
Pearson Chi-Square	25.960	1	<.001

- a. Model: Poisson
- b. Design: Constant + agegrp + voted

Parameter Estimates ^{b,c}

Parameter	Estimate	Std. Error	Z	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
Constant	6.692	.035	191.478	<.001	6.624	6.761
[agegrp = .00]	-2.472	.113	-21.887	<.001	-2.693	-2.251
[agegrp = 1.00]	0 ^a
[voted = 0]	-1.389	.076	-18.342	<.001	-1.537	-1.240
[voted = 1]	0 ^a

- a. This parameter is set to zero because it is redundant.
- b. Model: Poisson
- c. Design: Constant + agegrp + voted