CME Article

Biostatistics 306. Log-linear models: poisson regression

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Log-linear models are used to determine whether there are any significant relationships in multiway contingency tables that have three or more categorical variables and/or to determine if the distribution of the counts among the cells of a table can be explained by a simpler, underlying structure ***(restricted model)***. The ***saturated model*** contains all the variables being analysed and all possible interactions between the variables.

Let us use a simple 2X2 cross-tabulation (over-eating versus over-weight, Table Ia) to illustrate the log-linear model analysis. Table Ib shows the SPSS data structure and their association could easily be assessed using the chi-square test[1] (test of independence). Table Ic shows that there is no association (phew!), p=0.065 and Table Id shows the corresponding risk estimates.

Table Ia. Over-eating x over-weight.

Over-eating * over-weight cross-tabulation

			Over-weight		
			Yes	No	Total
Over-eating	Yes	Count	58	41	99
		% within over-weight	55.8%	42.7%	49.5%
	No	Count	46	55	101
		% within over-weight	44.2%	57.3%	50.5%
Total		Count	104	96	200
		% within over-weight	100.0%	100.0%	100.0%

Table Ib. SPSS data structure for over-eating x over-weight.

Over-eating	Over-weight	Count
Yes	Yes	58
Yes	No	41
No	Yes	46
No	No	55

Coding Yes = 1 & No = 2.

Table Ic. Chi-square test.

Chi-square tests

	Value	df	Asymp sig. (2-sided)	Exact sig. (2-sided)	Exact sig. (1-sided)
Pearson chi-square	3.407[b]	1	.065		
Continuity correction[a]	2.904	1	.088		
Likelihood ratio	3.417	1	.065		
Fisher's exact test				.068	.044
Linear-by-linear association	3.390	1	.066		
No. of valid cases	200				

a. Computed only for a 2x2 table.

b. 0 cells (.0%) have expected count less than 5. The minimum expected count is 47.52.

Table Id. Risk estimate table.

Risk estimate

		95% confidence interval	
	Value	Lower	Upper
Odds ratio for over-eating (yes/no)	1.691	.966	2.960
For cohort over-weight = yes	1.286	.982	1.685
For cohort over-weight = no	.761	.567	1.021
No. of valid cases	200		

We shall use the log-linear model analysis for the above 2X2 table.

Before running the analysis for the log-linear model, we have to "weight cases" using the variable Count first. Go to ***Data, Weight Cases*** to get Template I. Check on the "Weight cases by" and input "Count" to the Frequency Variable option.

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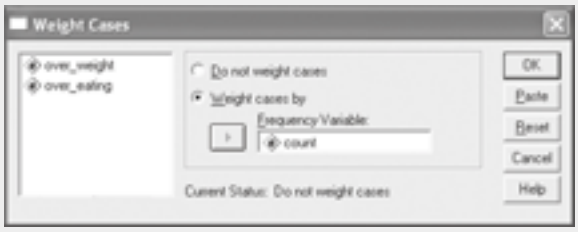
Template I. Declaring "count" as the "Weight cases by".

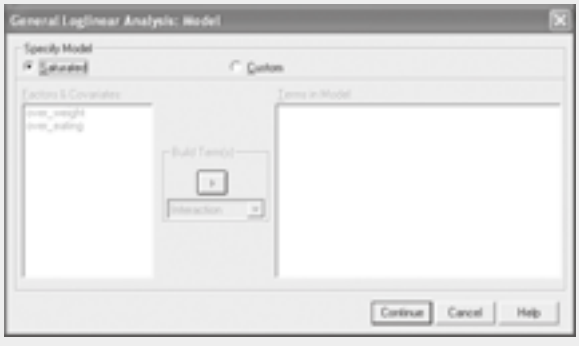


Go to ***Analyze, Loglinear, General*** to get Template II. Put Over-weight and Over-eating into the Factors option (a maximum of 10 categorical variables could be included).

Template II. Declaring only categorical variables.

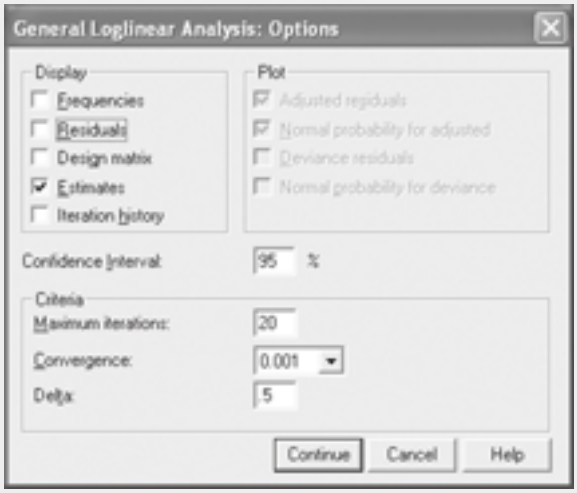
Leave the "Distribution of Cell Counts" as Poisson, then click on the Model folder, and see Template III. The Saturated model gives all possible interactions between the categorical variables. In this case, the model will be Over-weight + Over-eating + Over-eating X Over-weight.

Template III. Defining the saturated model.



Click on the Options folder in Template II to get Template IV.

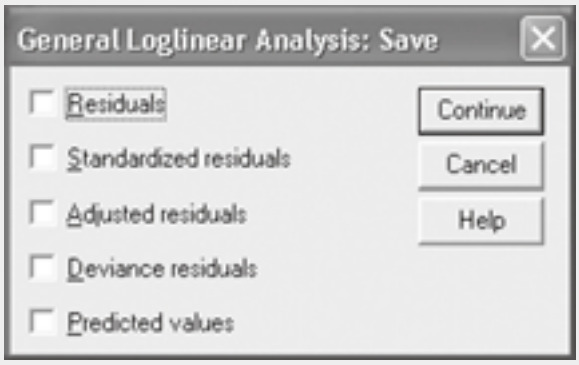
Template IV. Display options.



Check the Estimates box.

The following options are available in the Saved folder (Template V). Leave them unchecked.

Template V. Save options.



The model information and goodness-of-fit statistics will be automatically displayed.

SPSS output – Saturated Model (only relevant tables shown)

Table II shows the goodness-of-fit test, which will always result in a chi-square value of 0 because the saturated model will fully explain all the relationships among the variables.

Table II. Goodness-of-fit test.

Goodness-of-fit tests[a,b]			
	Value	df	Sig.
Likelihood ratio	.000	0	.
Pearson chi-square	.000	0	.

[a] Model: Poisson.

[b] Design: Constant + over_weight + over_eating + over_weight* over_eating.

Table III. Saturated model – parameter estimates.

Parameter estimates[b,c]						
					95% confidence interval	
Parameter	Estimate	Std. error	Z	Sig.	Lower bound	Upper bound
Constant	4.016	.134	29.922	.000	3.753	4.279
[over_weight = 1.00]	-.177	.199	-.890	.373	-.567	.213
[over_weight = 2.00]	0[a]	.	.	.	.	.
[over_eating = 1.00]	-.291	.205	-1.417	.157	-.693	.112
[over_eating = 2.00]	0[a]	.	.	.	.	.
[over_weight = 1.00]* [over_eating = 1.00]	.525	.284	1.831	.067	-.037	1.077
[over_weight = 1.00]* [over_eating = 2.00]	0[a]	.	.	.	.	.
[over_weight = 2.00]* [over_eating = 1.00]	0[a]	.	.	.	.	.
[over_weight = 2.00]* [over_eating = 2.00]	0[a]	.	.	.	.	.

a. This parameter is set to zero because it is redundant.

b. Model: Poisson

c. Design: Constant + over_weight + over_eating + over_weight * over_eating

Table III shows the parameter estimates of the saturated model. Taking the exponential (exp) of the estimate gives the odds ratio. We are particularly interested in the interaction term [over_weight = 1.00] * [over_eating = 1.00] which assesses the association between the 2 variables. This interaction's estimate is 0.525 and exp (0.525) = 1.691 with a p-value of 0.067 – which is exactly the same results obtained using Chi-square test (Tables Ic & Id).

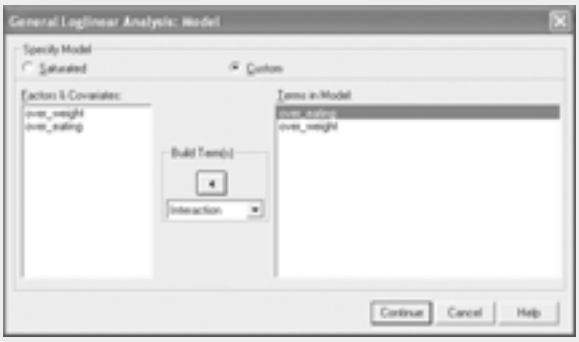
The main effect ([over_weight = 1.00] and [over_eating = 1.00]) tests on the null hypothesis that the subjects are distributed evenly over the levels of each variable. Here we have both variables quite evenly distributed (over-weight: 52% vs 48% and over-eating: 49.5% vs 50.5%, Table Ib), thus p>0.05 for both main effects.

The standardised form (Z) can be used to assess which variables/interactions in the model are the most or least important to explain the data. The higher the absolute of Z, the more "important".

If our interest is to determine relationships, we can stop here. But if we want to develop a simpler model, then the next simpler (restricted) model will be Over-weight + Over-eating (ignoring their interaction, since the 2 variables are independent).

To define this Over-weight + Over-eating restricted model, click on the custom button in Template III. Put Over-weight and Over-eating to the Terms in Model option (Template VI).

Template VI. Defining the restricted over-weight + over-eating model.



In Template IV, check on the Residuals and Frequencies options, and clear all the plot options.

SPSS outputs – Restricted model: Over-weight + Over-eating.

Table IVa. Goodness-of-fit test: Over-weight + Over-eating.

Goodness-of-fit tests[a,b]			
	Value	df	Sig.
Likelihood ratio	3.417	1	.065
Pearson chi-square	3.407	1	.065

a. Model: Poisson.

b. Design: Constant + over_eating + over_weight.

Table IVb. Residual analysis for Over-weight + Over-eating.

Cell counts and residuals[a,b]									
		Observed		Expected					
Over-weight	Over-eating	Count	%	Count	%	Residual	Standardised residual	Adjusted residual	Deviance
Yes	Yes	58	29.0%	51.480	25.7%	6.520	.909	1.843	.890
	No	46	23.0%	52.520	26.3%	-6.520	-.900	-1.843	-.919
No	Yes	41	20.5%	47.520	23.8%	-6.520	-.946	-1.843	-.969
	No	55	27.5%	48.480	24.2%	6.520	.936	1.843	.917

a. Model: Poisson.

b. Design: Constant + over_eating + over_weight.

The goodness-of-fit test (Table IVa) compares whether this restricted model (Over-weight + Over-eating) is an adequate fit to the data. We want the p-value (sig) to be >0.05. In this case, we have p=0.065 which means that this restricted model is adequate to fit the data.

Residual analysis helps us to spot outlier cells, where the restricted model is not fitting well. The *Residual* is the difference of the expected frequencies and the observed cell frequencies. The smaller the residual, the better the model is working for that cell. The *Standardized residuals* (normalised against the mean and standard deviation) should have values <1.96 for a good fit. The *Adjusted (Studentized) residuals* penalise for the fact that large expected values tend to have larger residuals. Cells with the largest adjusted residuals show where the model is working least well. The *Studentized deviance residuals* (Deviance) are a more accurate version of adjusted residuals.

If we decide that over-weight is a response variable and over-eating is the independent, a logistic regression (taking into account of other covariates) could be performed[2].

But if both are dependent variables (I over-eat thus I am over-weight or I am over-weight thus I over-eat), then a logistic model will not be appropriate. Let us extend the above over-weight, over-eating analysis by taking into consideration their gender (Table Va).

Table Va. Cross-tabulation of Over-weight, Over-eating and Gender.

Over-eating	Over-weight	Count	Male	Female
Yes	Yes	58	44	14
Yes	No	41	23	18
No	Yes	46	26	20
No	No	55	23	32

Table Vb shows the SPSS structure.

Table Vb. SPSS data structure for Over-weight, Over-eating and Gender.

Over-eating	Over-weight	Gender	Count
Yes	Yes	Male	44
Yes	No	Male	23
No	Yes	Male	26
No	No	Male	23
Yes	Yes	Female	14
Yes	No	Female	18
No	Yes	Female	20
No	No	Female	32

Coding: Yes = 1 & No = 2. Male = 1 & Female = 2.

We can start by constructing the saturated model and then remove the non-significant terms, or start from the basic main effects model (without interaction terms) and then build up. Let us use the latter.

Table Vc shows the goodness-of-fit for the restricted model of Over-weight + Over-eating + Gender (main effects only). The p-value is <0.05, which shows that this model is not adequate to explain the data

Table Vc. Goodness-of-fit test for Over-weight + Over-eating + Gender.

Goodness-of-fit tests[a,b]			
	Value	df	Sig.
Likelihood ratio	17.446	4	.002
Pearson chi-square	18.761	4	.001

a. Model: Poisson.

b. Design: Constant + gender + over_eating + over_weight.

Let us use all two-way interactions: Over-weight + Over-eating + Gender + Over-weight X Over-eating + Over-weight X Gender + Over-eating X Gender. To get this model, in Template III, custom with the

main effects and all two-way interactions (Template VII). Table Vd shows that this model does fit the data adequately (p=0.606).

Template VII. Restricted model with main effects and all two-way interactions.

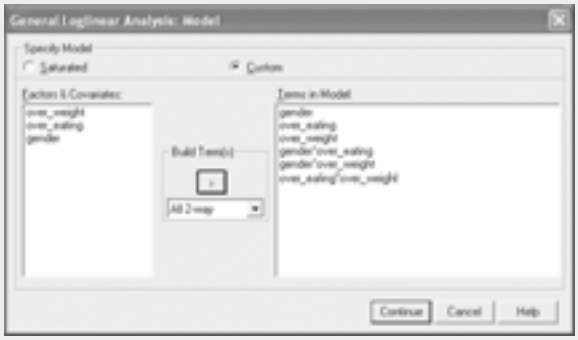


Table Vd. Goodness-of-fit test for main effects and all two-way interactions.

Goodness-of-fit tests[a,b]			
	Value	df	Sig.
Likelihood ratio	.265	1	.606
Pearson chi-square	.265	1	.606

a. Model: Poisson.

b. Design: Constant + gender + over_eating + over_weight + over_eating * gender + over_weight * gender + over_eating * over_weight.

Two significant relationships were found (Table Ve). Over-eating X Gender (p=0.015) and Over-weight X Gender (p=0.014) interactions. This means that males compared to females are both more likely to

Table Ve. Parameter estimates for main effects and all two-way interactions.

Parameter estimates[b,c]						
					95% confidence interval	
Parameter	Estimate	Std. error	Z	Sig.	Lower bound	Upper bound
Constant	3.492	.167	20.936	.000	3.165	3.819
[gender = 1.00]	-.395	.244	-1.619	.105	-.873	.083
[gender = 2.00]	0[a]	.	.	.	.	.
[over-eating = 1.00]	-.651	.258	-2.523	.012	-1.157	-.145
[over-eating = 2.00]	0[a]	.	.	.	.	.
[over_weight = 1.00]	-.541	.252	-2.146	.032	-1.035	-.047
[over_weight = 2.00]	0[a]	.	.	.	.	.
[over_eating = 1.00]* [gender = 1.00]	.726	.298	2.435	.015	.142	1.311
[over_eating = 1.00]* [gender = 2.00]	0[a]	.	.	.	.	.
[over_eating = 2.00]* [gender = 1.00]	0[a]	.	.	.	.	.
[over_eating = 2.00]* [gender = 2.00]	0[a]	.	.	.	.	.
[over_weight = 1.00]* [gender = 1.00]	.734	.297	2.469	.014	.151	1.317
[over_weight = 1.00]* [gender = 2.00]	0[a]	.	.	.	.	.
[over_weight = 2.00]* [gender = 1.00]	0[a]	.	.	.	.	.
[over_weight = 2.00]* [gender = 2.00]	0[a]	.	.	.	.	.
[over_eating = 1.00]* [over_weight = 1.00]	.398	.294	1.356	.175	-.177	.974
[over_eating = 1.00]* [over_weight = 2.00]	0[a]	.	.	.	.	.
[over_eating = 2.00]* [over_weight = 1.00]	0[a]	.	.	.	.	.
[over_eating = 2.00]* [over_weight = 2.00]	0[a]	.	.	.	.	.

a. This parameter is set to zero because it is redundant.

b. Model: Poisson.

c. Design: Constant + gender + over-eating + over_weight + over_eating * gender + over-weight * gender + over_eating * over_weight.

over-eat (OR = exp (0.726) = 2.07, 95% CI exp (0.142) = 1.15 to exp (1.311) = 3.71) and be over-weight (OR = exp (0.734) = 2.08, 95% CI exp (0.151) = 1.16 to exp (1.317) = 3.73). The standardised form (Z) for both interactions are of similar sizes (2.435 & 2.469) which implies that both relationships are equally important to explain this set of data. We can stop here if our interest is to determine what relationships are available in the data. We can proceed to "reduce" the model by removing the interaction terms that are not significant if one wants the most **Parsimonious** model.

You are absolutely right! We can arrive at the same results by performing 3 pair-wise chi-square tests for the 3 variables – i.e. do chi-square tests for Over-weight with Gender, Over-weight with Over-eating, and Over-eating with Gender, separately.

The interpretation of the results gets more complicated with more categorical variables and these variables can have more than 2 levels (for example, Race). The discussion of log-linear analysis here is far from comprehensive – the aim here is to introduce to you what log-linear models can do. Do seek help from a standard statistical text or biostatistician in the event that you have more "challenging" data, say 5 categorical variables and some of them may have more than 3 levels of responses.

One last caution: cells with zero frequencies may cause non-convergence of the estimates. It is recommended that the sample size should be 5 times the number of cells in the table. For example, for a 2X2X2, we should have n = 5X8 = 40 (at least). There are 2 types of zeros - Structural and Random (sampling). Structural zeros are those where a situation can never happen (e.g. a man getting pregnant!). Before analysis, such cells need to be deleted from the table. Random (sampling) zeros arise from sampling error, small sample size or too many variables. Before analysis, set these cells with zeros to have a very small number like 1E-12.

Poisson Regression is used to model the number of occurrences of an event of interest (Example 1) or the rate of occurrence of an event (Example 2) as a function of some independent variables, and the assumption of a normally distributed dependent does not apply.

Example 1. Modeling the number of occurrences of an event – the length of stay (LOS).

Table VIa shows the data for 10 subjects.

Table VIa. Data for the modeling of occurrences.

Gender	Race	Age	LOS
male	chinese	11	3
male	malay	15	4
male	malay	24	7
male	indian	14	4
female	chinese	13	4
female	chinese	16	5
female	malay	19	6
female	malay	13	3
female	indian	15	4
female	malay	20	7

Coding: Male = 1 & Female = 2. Chinese = 1, Malay = 2 & Indian = 3.

We can perform a linear regression analysis[3] on LOS if we have a larger dataset. The issue is that we may have grouped data in which linear regression would be impossible. Using linear regression would quantify the LOS difference between Gender, while poisson regression would provide the Relative Risk (RR) on having a longer LOS between Gender.

Before performing a poisson regression, we have to first "weight cases" using the variable LOS. Then go to Analyze, Loglinear, General. Let us use Gender + Race first (Template II). Custom the Main effects model Gender + Race (Template III). Click on Estimates option (Template IV).

Table VIb shows that the main effects model (Gender + Race) is a good fit (p>0.05). Thus, we do not require the interaction term.

Table VIb. Goodness-of-fit for Gender + Race model.

Goodness-of-fit tests[a,b]			
	Value	df	Sig.
Likelihood ratio	1.472	2	.479
Pearson chi-square	1.430	2	.489

[a] Model: Poisson.

[b] Design: Constant + gender + race.

Table VIc shows that [race = 2] compares with [race = 3], i.e. Malays compared to Indians, were at a higher risk (RR = exp (1.216) = 3.37, 95% CI exp (0.428) = 1.5 to exp (2.0) = 7.39) of having a longer LOS.

In order to include a quantitative variable, Age, in the poisson model (Gender + Race + Age), a unique ID has to be created for each subject. If "Id" variable is not present, go to ***Transform, Compute*** (Template VIII). Type ID in Target Variable option and $casenum in the Numeric Expression option. This will create a new variable ID with numbers 1 to 10.

Table VIc. Parameter estimates for Gender + Race model.

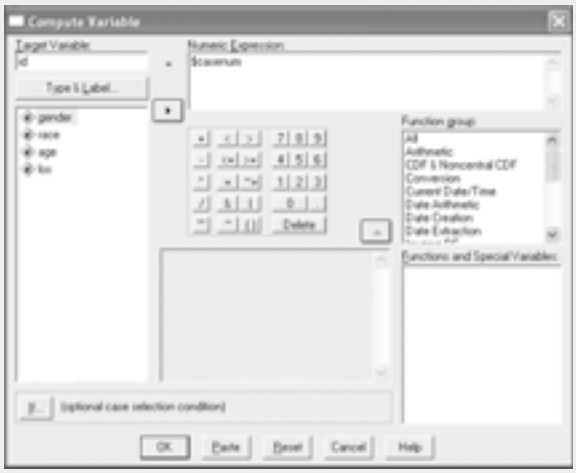
Parameter estimates[b,c]						
					95% confidence interval	
Parameter	Estimate	Std. error	Z	Sig.	Lower bound	Upper bound
Constant	1.597	.372	4.295	.000	.868	2.325
[gender = 1]	-.477	.300	-1.590	.112	-1.065	.111
[gender = 2]	0[a]	.	.	.	.	.
[race = 1]	.405	.456	.888	.374	-.489	1.300
[race = 2]	1.216	.402	3.022	.003	.428	2.005
[race = 3]	0[a]	.	.	.	.	.

[a] This parameter is set to zero because it is redundant.

[b] Model: Poisson.

[c] Design: Constant + gender + race.

Template VIII. Computing ID = $casenum.



Go to Template II, put Gender, Race and ID to the Factors option and Age to the Cell Covariates option (Template IX). Then custom (Template III) the model Gender + Race + Age (leave ID alone).

Template IX. General log-linear analysis.

The following message will appear:

Click ok.

Table VIIa shows that no interaction terms are required for this Gender + Race + Age model. With Age included in the model, Race became not significant. A one-year increase in age results in an increased of exp (0.248) = 1.28 or 28% in risk of having a longer LOS (Table VIIb).

Table VIIa. Goodness-of-fit for Gender + Race + Age model.

Goodness-of-fit tests[a,b]			
	Value	df	Sig.
Likelihood ratio	19.391	55	1.000
Pearson chi-square	19.488	55	1.000

[a] Model: Poisson.

[b] Design: Constant + age + gender + race.

Example 2. Modeling the incidence rate of an infection.

The number of infections reported in three high-risk wards of four hospitals were collected (Table VIIIa). "Infected" refers to the number of cases of the infections reported and "Total" is the total number of subjects at risk.

Table VIIb. Parameter estimates for Gender + Race + Age model.

Parameter estimates[b,c]						
					95% confidence interval	
Parameter	Estimate	Std. error	Z	Sig.	Lower bound	Upper bound
Constant	-2.267	.505	-4.489	.000	-3.257	-1.277
age	.248	.030	8.180	.000	.189	.308
[gender = 1]	-.436	.318	-1.372	.170	-1.058	.187
[gender = 2]	0[a]	.	.	.	.	.
[race = 1]	.126	.462	.272	.786	-.779	1.030
[race = 2]	-.783	.481	-1.630	.103	-1.725	.159
[race = 3]	0[a]	.	.	.	.	.

a. This parameter is set to zero because it is redundant.

b. Model: Poisson.

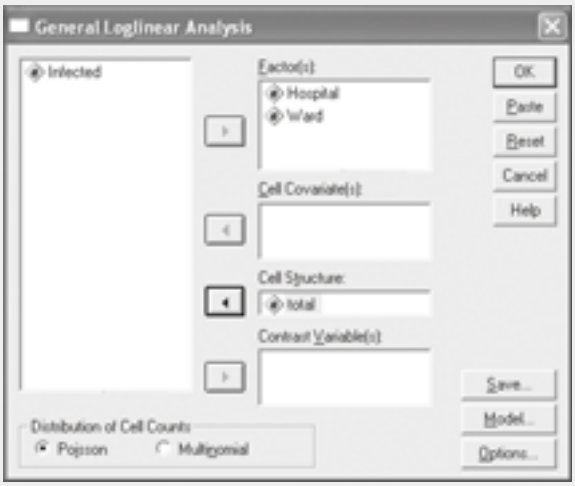
c. Design: Constant + age + gender + race.

Table VIIIa. Number of infections by hospital by ward.

Hospital	Ward	Infected	Total
1	1	10	51125
1	2	14	44660
1	3	31	76345
2	1	76	513578
2	2	62	335943
2	3	20	99884
3	1	45	263862
3	2	18	135490
3	3	10	39106
4	1	15	61728
4	2	12	56329
4	3	13	54459

Weight cases by Infected, then use the log-linear model. Put Hospital and Ward in the Factors option and Total in the Cell Structure option (Template X). Custom the Hospital + Ward model.

Template X. General log-linear analysis.



The goodness-of-fit (Table VIIIb) for the Hospital + Ward model shows that no interaction terms are required. The results (Table VIIIc) show that the risk of infections is independent of hospitals but patients in Ward type 3 compared to Ward type 1 are more prone to have infections (RR=exp (0.343) = 1.41, p=0.025).

Table VIIIb. Goodness-of-fit for Hospital + Ward model.

Goodness-of-fit tests[a,b]			
	Value	df	Sig.
Likelihood ratio	4.778	6	.573
Pearson chi-square	4.640	6	.591

a. Model: Poisson.

b. Design: Constant + Hospital + Ward.

Table VIIIc. Parameter estimates.

Parameter estimates[b,c]						
					95% confidence interval	
Parameter	Estimate	Std. error	Z	Sig.	Lower bound	Upper bound
Constant	-8.178	.181	-45.201	.000	-8.532	-7.823
[Hospital = 1]	.283	.209	1.354	.176	-.126	.692
[Hospital = 2]	-.257	.181	-1.425	.154	-.611	.097
[Hospital = 3]	-.246	.201	-1.227	.220	-.640	.147
[Hospital = 4]	0[a]	.	.	.	.	.
[Ward = 1]	-.343	.153	-2.240	.025	-.644	-.043
[Ward = 2]	-.243	.159	-1.528	.126	-.554	.069
[Ward = 3]	0[a]	.	.	.	.	.

a. This parameter is set to zero because it is redundant.

b. Model: Poisson.

c. Design: Constant + Hospital + Ward.

We can use Table VIIIc to predict the incidence for Hospital A Ward 1 = exp (-8.178 + 0.283 – 0.343) = exp (-8.238) = 0.000264 which is about 3 in 10,000.

We have carried out a very simplistic overview of poison regression using SPSS. One note of caution is that the present SPSS version is not the suitable software to perform a proper poisson regression analysis. SAS and STATA would be preferred. The reason is that SPSS does not allow us to check for the assumptions of **Over/ Under Dispersion** of the model, which is a crucial assumption for a poisson regression model and does not have the capability to rectify when the assumptions are not satisfied.

A poisson distribution has this special property that mean is equal to the variance. Thus an over dispersion means that the variance is much greater than the mean (the reverse for under dispersion) and this will produce severe underestimates of the standard errors and thus overestimates the p-values (more likely to be <0.05). This potential problem is easily rectified by using a Negative Binomial Regression that is available in SAS/STATA.

Our next article will be Biostatistics 307. Conjoint analysis and canonical correlation.

REFERENCES

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Multiple Choice Questions (Code SMJ 200508A)

	True	False
Question 1. Which model in the log-linear analysis has a non-zero chi-square for its goodness-of-fit test?		
(a) The parsimonious model.	❑	❑
(b) The saturated model.	❑	❑
(c) The restricted model.	❑	❑
(d) All of the above.	❑	❑
Question 2. In the log-linear model parameter estimates table, which column gives an indication on the "importance" of the main effect/interaction term contributing to the data?		
(a) The p-value.	❑	❑
(b) The estimates.	❑	❑
(c) The standardised form (Z).	❑	❑
(d) All of the above.	❑	❑
Question 3. The exponential of the parameter estimates in log-linear model gives:		
(a) The odds ratios.	❑	❑
(b) The hazard ratios.	❑	❑
(c) The relative risks.	❑	❑
(d) None of the above.	❑	❑
Question 4. The exponential of the parameter estimates in poisson regression gives:		
(a) The odds ratios.	❑	❑
(b) The hazard ratios.	❑	❑
(c) The relative risks.	❑	❑
(d) None of the above.	❑	❑
Question 5. Under dispersion in poisson regression means:		
(a) The mean is greater than the variance.	❑	❑
(b) The mean is smaller than the variance.	❑	❑
(c) The mean is equal to the variance.	❑	❑
(d) None of the above.	❑	❑

Doctor's particulars:

Name in full: _____

MCR number: _____ Specialty: _____

Email address: _____

Submission instructions:

A. Using this answer form

1. Photocopy this answer form.
2. Indicate your responses by marking the "True" or "False" box ☑
3. Fill in your professional particulars.
4. Post the answer form to the SMJ at 2 College Road, Singapore 169850.

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1. Log on at the SMJ website: URL <http://www.sma.org.sg/cme/smj> and select the appropriate set of questions.
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