Chapter 530

Loglinear Models

Introduction

Loglinear models (LLM) studies the relationships among two or more discrete variables. Often referred to as multiway frequency analysis, it is an extension of the familiar chi-square test for independence in two-way contingency tables.

LLM may be used to analyze surveys and questionnaires which have complex interrelationships among the questions. Although questionnaires are often analyzed by considering only two questions at a time, this ignores important three-way (and multi-way) relationships among the questions. The use of LLM on this type of data is analogous to the use of multiple regression rather that simple correlations on continuous data.

There are several textbooks available that explain LLM in detail. We recommend the books by Tabachnick (1989) and Jobson (1992) which each have excellent chapters on LLM. Wickens (1989) is a book that is completely devoted to LLM.

Limitations and Assumptions

Since the use of LLM requires few assumptions about population distributions, it is remarkably free of limitations. It may be applied to almost any circumstance in which the variables are (or can be made) discrete. It can even be used to analyze continuous variables which fail to meet distributional assumptions (by collapsing the continuous variables into a few categories).

Three basic assumptions should be considered when using LLM.

1. *Observations are independent from each other*. In practice, this means that each observation comes from a different subject, that the subjects were randomly selected from the population of interest, and that no specific group of subjects is purposefully omitted.

2. *All observations are identically distributed*. This means that they are obtained in the same way. For example, you could not mix the results of a telephone survey with those of a door-to-door survey.

3. *The number of observations is large*. Since LLM makes use of large sample approximations, it requires large samples. The LLM algorithm begins by taking the natural logarithm of each of the cell frequencies, so empty cells (those with frequencies of zero) are not allowed. LLM appears to be less restrictive than traditional chi-square contingency tests, so rules that are used for those tests may be used for LLM analysis as well.

Fundamental Approach

LLM analysis requires two steps. It is easy to become lost in details of each of these steps, but it is important to keep in mind the overall purpose of each task.

1. *Selecting an appropriate model*. The first step is to find an appropriate model of the data. Several techniques may be used to find an appropriate LLM. One of the most popular is the step-down technique in which complex terms are removed until all terms remaining are significant.

This search for an appropriate model is restricted to those models which are *hierarchical*. Hierarchical models are those in which the inclusion of a term forces the inclusion of all components of that term. For example, the inclusion of the two-way interaction, AB, forces terms A and B to also be included.

Before the model is accepted, you should study the residuals to determine if the model fits the data reasonably well.

2. *Interpreting the selected model*. Once a model is selected, it must be interpreted. This is the step in which you determine what your data are telling you.

The Notation of Loglinear Models

Consider a two-way table in which the row-variable *A* has categories (levels) *i=1,...,I* and the column-variable *B* has categories *j=1,...,J*. A multiplicative model that reproduces the cell frequencies f_{ij} exactly is

$$m_{ij} = N\alpha_i\beta_j\gamma_{ij}$$

where $m_{ij} = E(f_{ij})$ is the expected frequency of the ith row and the jth column. When the m_{ij} are estimated using maximum likelihood, the results are denoted $\hat{m}_{ij}$. Also note that $N = \sum_{ij} f_{ij}$.

One aspect of the table that is of interest is whether *A* and *B* are independent. This is often tested using the familiar chi-square test. In the above formula, independence would be established if all γ_{ij} were equal to one.

Because of its multiplicative form, the above formula is difficult to work with. However, if we take the logarithm of both sides, we can rewrite it as

$$\ln(m_{ij}) = \theta + \lambda_i^A + \lambda_j^B + \lambda_{ij}^{AB}$$

The $\lambda's$ are called *effects*. The superscript indicates the variable(s) and the subscripts refer to the individual categories of those variables. The *order* of an effect is equal to the number of variables in the superscript.

Because this formulation is additive, it is called a *loglinear* model. Because of the logarithms, this model has the added constraint that none of the m_{ij} are zero.

Notice that the total number of $\lambda's$ in this model is *1+I+J+(IxJ)* which is greater than the number of cell frequencies (which is *IxJ*). When the number of parameters is greater than or equal to the number of cells, we say the model is *saturated*. A saturated model reproduces the observed frequencies exactly.

By testing whether certain of the $\lambda's$ are zero, you can test various interrelationships. For example, to test whether all of the frequencies are equal, you would test whether all first-order and second-order effects (the $\lambda^A{}'s$, $\lambda^B{}'s$, and $\lambda^{AB}{}'s$) are zero. Testing whether the $\lambda^{AB}{}'s$ are zero would test whether variables *A* and *B* are independent. Testing whether the $\lambda^A{}'s$ were zero would test whether the probabilities of the categories of *A* are equal. As you can see, this model will let you answer many interesting questions about factors *A* and *B*.

Hierarchical Models

The three-way LLM would be written as

$$\ln(m_{ijk}) = \theta + \lambda_i^A + \lambda_j^B + \lambda_{ij}^{AB} + \lambda_k^C + \lambda_{ik}^{AC} + \lambda_{jk}^{BC} + \lambda_{ijk}^{ABC}$$

or, using the familiar ANOVA syntax, it might be written as

$$y_{ijk} = mean + A_i + B_j + AB_{ij} + C_k + AC_{ik} + BC_{jk} + ABC_{ijk}$$

Various models that are subsets of this saturated model might be of interest. For example, the main-effects model, *A+B+C*, would be useful in testing whether the factors are independent.

Hierarchical models are a particular class of models in which no interaction term is specified unless all subset combinations of that term are also in the model.

Often, a shorthand notation is used to express these models in which only the largest terms are specified. The following examples, showing the hierarchical model on the left and the expanded model on the right, should give you the idea of how this notation works.

Hierarchical Notation	**Regular (Expanded) Notation**
ABC	A+B+AB+C+AC+BC+ABC
A,BC	A+B+C+BC
AB	A+B+AB
AB,BC	A+B+AB+C+BC
A,B	A+B
A,B,C	A+B+C
AB,AC,BC	A+B+AB+C+AC+BC

In the LLM analysis considered in this program, only hierarchical models are used. Hence, we adopt the shorthand model specification on the left, although we are actually fitting the expanded model on the right.

Goodness of Fit

When dealing with several competing models, the relative quality of each model must be considered. The quality of a model, as measured by its goodness of fit to the data, may be tested using either of two chi-square statistics:

The Pearson chi-square statistic

$$\chi^2 = 2\sum_{i,j,k} \frac{\left(f_{ijk} - \hat{m}_{ijk}\right)^2}{\hat{m}_{ijk}}$$

and the likelihood-ratio statistic

$$G^2 = 2\sum_{i,j,k} f_{ijk} \ln\left(\frac{f_{ijk}}{\hat{m}_{ijk}}\right)$$

Both of these statistics are distributed as a chi-square random variable when *N* is large and none of the $\hat{m}_{ijk}$ are small. If a few of the $\hat{m}_{ijk}$ are small, the chi-square approximation is still fairly close. Both of these statistics have *n-p* degrees of freedom where *n* is the number of cells in the table and *p* is the number of parameters in the model on which the $\hat{m}_{ijk}$ are based.

You should understand exactly what these two chi-square statistics are testing. They test whether the terms in the saturated model that are not included in the current model are significantly different from zero.

For example suppose the hierarchical model *AB, BC* is fit. The expanded version of this hierarchical model is *A+B+C+AB+BC*. Note that the terms *AC* and *ABC* are omitted. If the χ^2 and G^2 were computed using the $\hat{m}_{ijk}$ from this fit, they would test whether the *AC* and *ABC* effects are zero. That is, these chi-square statistics test whether any important effects have been left out of the model.

The likelihood-ratio statistic, G^2, enjoys a very useful property which the Pearson χ^2 does not have. It is additive under partitioning for nested models. To explain this, consider an example. Suppose the model *AB,AC,BC* is fit and the resulting value of G^2 is 17.8 with 8 degrees of freedom. A second model *A,B,C* is fit resulting in a G^2 value of 69.9 with 24 degrees of freedom. If you expand each of these models, you will find that the terms *AB*, *AC*, and *BC* are in the first model but not in the second. Also, note that the second model is nested (completely contained) in the first model. If you subtract the first G^2 from the second, you will get 52.1. This is also a valid chi-square statistic with degrees of freedom 24 - 8 = 16. It tests whether *AB, AC,* and *BC* are significant.

This additivity property is a very useful. It allows you to test the importance of various individual terms. For example, suppose the model *AB,AC,BC* is tested and the goodness-of-fit test is not significant. This means that this particular model, *A+B+C+AB+AC+BC*, fits the data adequately. The next question is whether all six of these terms are necessary. To test the significance of *BC* you would fit the model, *A+B+C+AB+AC,* and subtract the first G^2 value from the second. This would test the significance of *BC*.

A word of caution: the difference between the two G^2 is distributed as a chi-square only when the more complete model fits the data adequately. That means that the G^2 of the larger model should be nonsignificant. Because of the additivity property of G^2, it is very popular in LLM.

Again, this additivity property does not hold for the Pearson chi-square statistic. Why do we even compute this value? Why not just use the likelihood ratio statistic? For two reasons. First, some studies indicate that the Pearson goodness of fit test may be more accurate. Second, since both of these are asymptotic tests, you can be more comfortable with small sample results when both tests lead to the same conclusion.

Model Selection Techniques

One of the main tasks in working with LLM's is dealing with the large number of possible models that can be generated from a single data table. The number of terms in the saturated model doubles with each additional factor. For example, there are 16 effects in a four-factor study and 32 effects in a five-factor study. When you consider the number of possible models that can be created from the 16 effects in a four-factor study, you begin to see the magnitude of the task. Even limiting your search to just the hierarchical models still leaves you with a large number of models to consider. There are over 100 different hierarchical models in a four-factor study, and over a 1000 in a five-factor study.

Since your first task in the analysis is to find a well-fitting model with as few terms as possible, you must adopt some method to limit the number of models you consider. The program provides several possible model selection methods. The final model will result from applying several of these techniques to your data.

Standardized Parameter Estimates

This method screens models as follows. First, a standardized estimate of each λ in the saturated model is calculated. Next, a list is made of the largest effects (greater than some cutoff value like 2.0 or 3.0). Finally, a hierarchical model is selected which includes as few terms as possible while still including the list of significant effects. This model is tested for adequacy using the chi-square test. If the goodness-of-fit test is nonsignificant, the model is used. Otherwise, additional effects are added to the model (based on their standardized values) until an adequate model is found.

Tests of Marginal and Partial Association

This method computes two tests for each term (up to fourth order terms). These tests assume that terms of higher order are negligible. The two tests are for *partial* and *marginal* association. The partial association considers the

significance of a term after considering all other terms of the same order. The marginal association tests the significance of the term ignoring the influence of the other factors in the model.

The *partial association* test is constructed as follows. Fit a model containing all terms with the same order as the term being tested. Fit a second model identical with the first except with the term of interest. Subtract the first likelihood-ratio statistic from the second. The degrees of freedom are also determined by subtraction.

For example, to test that the partial association between *A* and *B* is zero in a four-way table, compute the values of G^2 for the models *AB,AC,AD,BC,BD,CD* and *AC,AD,BC,BD,CD*. The difference between these two values tests the partial association.

The *marginal association* test is constructed by collapsing the table until the term of interest is the highest-order interaction and there are no other terms of the same order. This term is then removed and the next lowest model is fit. The G^2 value tests the marginal association among the factors in the term.

For example, to test that the marginal association between *A* and *B* is zero in a four-way table, first collapse the table to the two-way table containing only *A* and *B*. Next fit the model *A,B* on the collapsed table and compute the value of G^2 . This G^2 value tests the marginal association between **A** and **B**.

By considering the results of these two tests for each term, you can gain a fairly good indication of which terms are significant and which are not. As before, to obtain the final model, make a list of all terms that are significant. Next, write down the minimal hierarchical model that includes these terms.

Simultaneous Order Tests

The program produces a report that simultaneously tests all terms of a given order and all terms of a given order and higher. These tests let you immediately reduce the number of models that must be considered. For example, if the test of second-order models and higher is significant while the test for third-order models and higher is not, you know that the maximum order that must be considered is two. This knowledge allows you to reduce your search to second-order models.

Step-Down Selection Procedure

This is probably the most popular model selection method. It is the method that is used by default in this program. This procedure begins with a specified model (often the saturated model is used since it fits the data well) and searches for a model with fewer terms that still fits well. The program uses a backward elimination selection technique, which works better than the forward selection technique.

This procedure works as follows. First, a significance level (alpha) is chosen for the goodness of fit test to signal a significant model (a model that does not fit the data). Next, each of the highest-order hierarchical terms is removed, being replaced with appropriate terms so that the resulting expanded model is only different by the term of interest. The G^2 values of the original model and the subset model are then differenced so that the term may be tested individually. The model picked is the sub-model having the largest significance probability. The procedure terminates when no sub-model can be found with a probability greater than alpha.

Analyzing the Residuals

Once a candidate model has been found, it must be further analyzed for adequacy. In addition to checking goodness of fit statistics, the residuals between the estimated and actual frequencies should be studied. If a particular cell seems to be causing distortion in the results, appropriate action must be taken (such as adding deleted terms back into the model).

Once the residuals appear to be okay, the various terms in the model must be interpreted. This is accomplished by considering the percentages in the corresponding collapsed tables.

Data Structure

The data may be entered in either raw or summarized form. In either case, each variable represents a factor and each row of data represents a cell. An optional variable may be used to give the frequency (count) of the number of individuals in that cell. When the frequency variable is left blank, each row receives a frequency of one.

The following data are a portion of the results of a study by Dyke and Patterson (1952) on the information sources people use to obtain their knowledge of cancer. The data are contained in the Loglin1 dataset.

Loglin1 dataset (subset)

Counts	Newspaper	Lecture	Radio	Reading	Knowledge
23	1	1	1	1	1
102	1	2	1	1	1
1	2	1	1	1	1
16	2	2	1	1	1
8	1	1	1	1	2
67	1	2	1	1	2
3	2	1	1	1	2
16	2	2	1	1	2
8	1	1	1	2	1
35	1	2	1	2	1

Procedure Options

This section describes the options available in this procedure.

Variables Tab

Specify the variables to be analyzed.

Factor Specification

Factor Variables (A-G)

At least two factor variables must be specified. Examples of factor variables are gender, age groups, "yes" or "no" responses, etc.

The factor categories need not be consecutive integers. You may use text or numeric identification codes. The treatment of text variables is specified for each variable by the Data Type option on the Variable Info sheet.

The first variable listed becomes factor A, the second becomes factor B, and so on. Up to seven factor variables may be designated.

Frequency Variable

Frequency Variable

This optional variable contains the count (frequency) of each cell in the table. If this variable is left blank, the frequency or each row in the dataset is assumed to be one.

Delta

Delta Value

This value is added to each cell count. It is used to add a small amount (between 0.1 and 0.9) to each cell count when zeros are present in the table. Remember that since the algorithm begins by taking the logarithm of each cell frequency and since the logarithm of zero is not defined, you cannot analyze a table with zero counts. This option lets you analyze data with zero frequencies.

When using this option, consider running your analysis over with two or three difference delta values to determine if the delta value is making a difference in the outcome (it should not).

Model Specification

Model

This option allows you to specify the hierarchical model to be fit. If a step-down selection is to be run, this model will serve as the starting point.

- **Full Model**

  This option causes the saturated model to be fit.

- **Up to (1,2,3,4)-Way**

  These options indicate that only terms up to and including that order are kept in the model.

  For example, if you are studying four factors and you specify "2Way," you would analyze the hierarchical model *AB,AC,AD,BC,BD,CD*.

- **Custom**

  Selecting this option causes the model specified in the Custom Model option (which is next) to be used.

Custom Model

This box specifies a hierarchical model of your choice. The syntax of hierarchical models is as follows:

Hierarchical terms refer to many actual terms. For example, suppose you have six factors (labeled A-F) and you specify the hierarchical model: *ABC,BCD,DE,F*. The expanded model would be:

Hierarchical Term	Expanded Terms
ABC	A,B,AB,C,AC,BC,ABC
BCD	B,C,BC,D,BD,CD,BCD
DE	D,E,DE
F	F

Notice that the simple terms B, C, and BC are contained in both the ABC list and the BCD list. Also, the term D is contained in both the BCD list and the DE list. The actual model fit would be the complete list, with each multiple-entry only listed once. Here, the expanded model would be:

A,B,AB,C,AC,BC,ABC,D,CD,BD,BCD,E,DE,F

If you want to specify a saturated model, you simply enter the highest order interaction. For example, the saturated four-factor model would be specified by entering "*ABCD*."

Step-Down Search Options

Perform Step-Down Search

Specifies whether the step-down model selection procedure is used. The procedure starts with the model specified in the Model option. The procedure is controlled by the Max Models and the Stopping Alpha options as explained below.

Note that the step-down search is a lengthy procedure and may require a few minutes to execute.

Max Models

This option specifies the maximum number of models that can be tried before the search is aborted. On slower computers, the search may go on for hours, so this option lets you abort the search after so many iterations. On Pentium class computers, the search will take only a few moments, so you can set this option very high.

Stopping Alpha

This option specifies the value of alpha which is the significance level for the goodness of fit tests. During the search, when no model is found whose probability level is greater than this amount, the search is ended. Remember that you are searching for a model the fits the data well and thus does not produce a significant goodness of fit test.

Although you might be in the habit of always selecting an alpha level of 0.05, you should consider using a larger value (say 0.15 or 0.25) because you want a model that fits the data well--that is not even close to significance. A model that is almost significant (has an alpha of 0.06 or 0.08) might be excluding important terms. When you use a value of 0.25, you can feel confident that your model really fits the data well.

Unfortunately, the appropriate value of alpha is also tied to the sample size. With small samples, a significance level of 0.25 might be due to a lack of the goodness of fit test's ability to reject any hypothesis and not a general agreement between the model and the data. Hence, with small sample sizes you can have a poor fit and a high alpha. On the other hand, large sample sizes may cause even slight deviations between model and fit to be significant at the 0.05 level. Hence, for large sample sizes, you would want the value of alpha to be closer to zero.

Maximum Likelihood Options

Max Iterations

This option specifies the maximum number of iterations. Usually, the algorithm will converge in less than five iterations, so the default value of twenty-five should be more than ample.

Max Difference

This option specifies the maximum difference between any of the actual frequencies and their corresponding predicted frequencies. Once the maximum is less than this amount, the maximum-likelihood procedure will terminate (has converged).

Reports Tab

The following options control which reports are displayed. Note that some reports are not produced in certain situations. If a report you want is not created, try rerunning the program with a specific model--with all Model Selection reports turned off.

Select Reports

Multi-Term Report - Table Report

Specifies whether the report is produced.

Report Options

Precision

Specify the precision of numbers in the report. Single precision will display seven-place accuracy, while double precision will display thirteen-place accuracy.

Variable Names

This option lets you select whether to display variable names, variable labels, or both.

Value Labels

Indicate whether to display the data values or their labels.

Example 1 – Loglinear Model Analysis

This section presents an example of how to run an analysis of the data contained in the Loglin1 dataset.

You may follow along here by making the appropriate entries or load the completed template **Example 1** by clicking on Open Example Template from the File menu of the Loglinear Models window.

1   Open the Loglin1 dataset.

- From the File menu of the NCSS Data window, select **Open Example Data**.
- Click on the file **Loglin1.NCSS**.
- Click **Open**.

2   Open the Loglinear Models window.

- Using the Analysis menu or the Procedure Navigator, find and select the **Loglinear Models** procedure.
- On the menus, select **File**, then **New Template**. This will fill the procedure with the default template.

3   Specify the variables.

- On the Loglinear Models window, select the **Variables tab**.
- Double-click in the **Factor A Variable** text box. This will bring up the variable selection window.
- Select **Newspaper** from the list of variables and then click **Ok**. "Newspaper" will appear in the Factor A Variables box.
- Double-click in the **Factor B Variable** text box. This will bring up the variable selection window.
- Select **Lecture** from the list of variables and then click **Ok**. "Lecture" will appear in the Factor B Variables box.
- Double-click in the **Factor C Variable** text box. This will bring up the variable selection window.
- Select **Radio** from the list of variables and then click **Ok**. "Radio" will appear in the Factor C Variables box.
- Double-click in the **Factor D Variable** text box. This will bring up the variable selection window.
- Select **Reading** from the list of variables and then click **Ok**. "Reading" will appear in the Factor D Variables box.
- Double-click in the **Factor E Variable** text box. This will bring up the variable selection window.
- Select **Knowledge** from the list of variables and then click **Ok**. "Knowledge" will appear in the Factor E Variables box.
- Double-click in the **Frequency Variable** text box. This will bring up the variable selection window.
- Select **Counts** from the list of variables and then click **Ok**. "Counts" will appear in the Frequency Variable box.

4   Run the procedure.

- From the Run menu, select **Run Procedure**. Alternatively, just click the green Run button.

Multiple-Term Test Section

Multiple-Term Test Section

K-Terms	DF	Like. Ratio Chi-Square	Prob Level	Pearson Chi-Square	Prob Level
1WAY & Higher	31	2666.19	0.0000	3811.81	0.0000
2WAY & Higher	26	596.84	0.0000	751.31	0.0000
3WAY & Higher	16	19.56	0.2406	21.21	0.1705
4WAY & Higher	6	3.23	0.7791	3.32	0.7680
5WAY & Higher	1	1.02	0.3116	1.01	0.3157

Note: Fit of all k-factor marginals. Simultaneous test that all interactions of order k and higher are zero.

K-Terms	DF	Like. Ratio Chi-Square	Prob Level
1WAY Only	5	2069.35	0.0000
2WAY Only	10	577.28	0.0000
3WAY Only	10	16.33	0.0906
4WAY Only	5	2.21	0.8196

Note: Simultaneous test that all interactions of order k are zero. These Chi-Squares are differences in the above table.

This report helps in the model selection process by isolating the highest order term(s) that need to be included in the final LLM.

The top table shows the significance of all terms of a given order and higher. For example, the 596.84 tests the significance of all terms of order two and above. The 3.23 tests the significance of all fourth- and fifth-order terms. Since there are only five factors in the table, the 1.02 tests the significance of the five-way interaction.

By glancing down the significance levels (Prob Level) of this table, you can quickly determine the maximum order that is significant. In the present example, note that the one-way and higher is significant, as is the two-way and higher. However, the three-way and higher is not significant, being only 0.2406 (we use a significance level of 0.20). Hence, all terms of order three or greater may be ignored.

The second table is formed by differencing the first. Since the Pearson chi-square cannot be differenced in this manner, only the likelihood-ratio chi-square tests are shown. These tests indicate the significance of all terms of a given order. They are used to substantiate the conclusions made from the first table.

In this example, you notice that the four-way and three-way terms are not significant, while the two-way and one-way terms are. Again, we are lead to the conclusion that second-order terms will be the highest that are needed in our final model.

Individual definitions of the columns of this report are as follows:

K-Terms

These are the terms that are being tested. In the first table they are the terms that are not in the model. Hence the goodness-of-fit chi-square test indicates whether these terms may be left out of the model. In the second table, these are the terms being tested.

DF

The degrees of freedom of the terms being tested. This is a parameter of the chi-square distribution. The degrees of freedom of the test are found by adding up the degrees of freedom of the individual terms left out of the model.

Like. Ratio Chi-Square

This is the value of the likelihood-ratio statistic calculated using the following formula:

$$G^2 = 2 \sum_{i,j,k} f_{ijk} \ln\left(\frac{f_{ijk}}{\hat{m}_{ijk}}\right)$$

This statistic follows the chi-square distribution in moderate to large samples. It is calculated using this formula in the top half of the report and by subtracting one row from the previous row in the bottom half of the report.

Note that strictly speaking, the likelihood-ratio statistics in the second table follow the central chi-square distribution only if the second chi-square (the one subtracted) is not significant.

Prob Level

This is the probability of obtaining the above chi-square value or larger by chance. When this value is less than some preset alpha level, say 0.15, the test statistic is said to be *significant*. Otherwise, the test statistic is *nonsignificant*. A nonsignificant model fits the data adequately. The choice of 0.15 is arbitrary, and you may use whatever value you feel comfortable with between 0.300 and 0.001.

Pearson Chi-Square

This is the value of the Pearson chi-square statistic calculated using the following formula,

$$\chi^2 = 2\sum_{i,j,k} \frac{\left(f_{ijk} - \hat{m}_{ijk}\right)^2}{\hat{m}_{ijk}}$$

Prob Level

This is the probability of obtaining the above chi-square value or larger by chance. When this value is less than some preset alpha level, say 0.15, the test statistic is said to be *significant*. Otherwise, the test statistic is *nonsignificant*. A nonsignificant model fits the data adequately. The choice of 0.15 is arbitrary, and you may use whatever value you feel comfortable with between 0.300 and 0.001.

Single-Term Test Section

Single-Term Test Section

Effect	DF	Partial Chi-Square	Prob Level	Marginal Chi-Square	Prob Level
A (Newspaper)	1	27.31	0.0000	27.31	0.0000
B (Lecture)	1	1449.22	0.0000	1449.22	0.0000
C (Radio)	1	498.12	0.0000	498.12	0.0000
D (Reading)	1	4.58	0.0323	4.58	0.0323
E (Knowledge)	1	90.11	0.0000	90.11	0.0000
AB	1	4.52	0.0335	21.60	0.0000
AC	1	46.15	0.0000	74.23	0.0000
AD	1	172.49	0.0000	253.71	0.0000
AE	1	31.75	0.0000	105.78	0.0000
BC	1	10.27	0.0014	18.95	0.0000
BD	1	7.33	0.0068	23.75	0.0000
BE	1	4.82	0.0282	17.16	0.0000
CD	1	0.42	0.5147	21.08	0.0000
CE	1	6.28	0.0122	24.25	0.0000
DE	1	79.58	0.0000	150.45	0.0000
ABC	1	1.48	0.2240	1.85	0.1733
ABD	1	0.01	0.9418	0.36	0.5470
ABE	1	3.16	0.0755	1.16	0.2820
ACD	1	1.25	0.2642	1.81	0.1790
ACE	1	0.00	0.9526	0.06	0.8089
ADE	1	2.75	0.0971	3.06	0.0800
BCD	1	1.50	0.2208	3.48	0.0621
BCE	1	1.39	0.2377	0.51	0.4740
BDE	1	3.86	0.0494	4.30	0.0381
CDE	1	0.01	0.9435	0.57	0.4486

This report presents partial and marginal association tests on terms of up to the third order. The actual computation was discussed earlier in the section of model selection, so we will not repeat it here except to note that the chi-squares are the difference between the likelihood-ratio statistics of two models. The validity of this procedure depends on the more complex model's likelihood ratio being nonsignificant.

You should remember that the partial chi-square statistic tests whether the term is significant after considering all other terms of the same order. The marginal-association chi-square tests whether the term is significant ignoring all other terms of the same order. Hence, when both tests are significant, you can be fairly certain that the term is

necessary. When neither test is significant, you can be fairly certain that the term is not necessary. And when one test is significant and the other is not, the term should be watched closely--it may or may not be important.

In this example, notice that only one three-way term, *BDE*, is significant. Almost all of the two-way terms are significant. Hence, our search for the best model might begin with the hierarchical model: *AB,AC,AD,AE,BC,BDE,CD,CE*. The *CD* term was not significant on the partial association test, so we might expect to see it omitted from the final model.

Notice that even though the simultaneous test of all third-order terms was not significant, this report indicated that *BDE* should be considered. There is always a possibility of this type of confusion among the various goodness of fit tests. This is why it is important to look at all of them. You can rationalize the difference in conclusions here by noting that the *BDE* is not highly significant, but only mildly significant.

Step-Down Model Search Section

Step-Down Model-Search Section

Step No	Best No	DF	Chi-Square	Prob Level	Term Deleted	DF	Chi-Square	Prob Level	Hierarchical Model
1	1	0	0.0	1.0000	None	0	0.0	0.0000	ABCDE
2	1	1	1.0	0.3116	ABCDE	1	1.0	0.3116	BCDE,ACDE,ABDE,ABCE,ABCD
3	2	2	1.3	0.5096	BCDE	1	0.3	0.5690	ACDE,ABDE,ABCE,ABCD
4	2	2	1.2	0.5463	ACDE	1	0.2	0.6670	BCDE,ABDE,ABCE,ABCD
5	2	2	1.8	0.4074	ABDE	1	0.8	0.3796	BCDE,ACDE,ABCE,ABCD
6	2	2	1.2	0.5598	ABCE	1	0.1	0.7117	BCDE,ACDE,ABDE,ABCD
7	2	2	1.4	0.4935	ABCD	1	0.4	0.5330	BCDE,ACDE,ABDE,ABCE
8	6	3	1.7	0.6464	BCDE	1	0.5	0.4808	ACDE,ABDE,ABCD,BCE
.	.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.	.
98	86	18	24.4	0.1420	AB	1	4.4	0.0354	CE,AC,BC,AD,AE,DE,BE,BD
99	86	18	100.7	0.0000	DE	1	80.7	0.0000	CE,AC,BC,AD,AE,AB,BE,BD
100	86	18	24.7	0.1324	BE	1	4.7	0.0293	CE,AC,BC,AD,AE,AB,DE,BD
101	86	18	27.7	0.0674	BD	1	7.7	0.0056	CE,AC,BC,AD,AE,AB,DE,BE
102	98	19	31.5	0.0360	CE	1	7.0	0.0079	AC,BC,AD,AE,DE,BE,BD
103	98	19	81.6	0.0000	AC	1	57.2	0.0000	CE,BC,AD,AE,DE,BE,BD
104	98	19	37.8	0.0064	BC	1	13.4	0.0003	CE,AC,AD,AE,DE,BE,BD
105	98	19	210.5	0.0000	AD	1	186.1	0.0000	CE,AC,BC,AE,DE,BE,BD
106	98	19	57.3	0.0000	AE	1	32.9	0.0000	CE,AC,BC,AD,DE,BE,BD
107	98	19	103.8	0.0000	DE	1	79.4	0.0000	CE,AC,BC,AD,AE,BE,BD
108	98	19	30.6	0.0449	BE	1	6.2	0.0130	CE,AC,BC,AD,AE,DE,BD
109	98	19	37.4	0.0070	BD	1	13.0	0.0003	CE,AC,BC,AD,AE,DE,BE
Best model found: CE,AC,BC,AD,AE,DE,BE,BD									
98	98	18	24.4	0.1420	AB	1	4.4	0.0354	CE,AC,BC,AD,AE,DE,BE,BD

This report documents the search algorithm's progress. It shows the results of each step. Remember that the algorithm uses a step down strategy. This means that it begins with the most complicated model possible (the saturated model) and proceeds by removing terms. Your main interest will be in the final model selected, but sometimes it is of interest to see how this model was arrived at.

Step No

This is the identification number of this model. This is the number referred to under Best.

Best No

The number of the model that is currently the designated as being the best.

DF

The degrees of freedom of the chi-square value. This is the degrees of freedom of the terms not in the model, since these are the terms being tested.

Chi-Square

The likelihood-ratio statistic, G^2, testing the goodness of fit of this model. This statistic tests the significance of the terms omitted from the model. Hence, when the G^2 is not significant, you can assume that all important terms are in the model. Of course, you might have included some negligible terms as well.

Prob Level

This is the probability value for the above chi-square statistic. If it is less than some small value, say 0.05, the chi-square is said to be significant and you assume that one of the terms left out of the model is important. If the probability is greater than the cutoff value, you assume that all significant terms are accounted for.

Term Deleted

This is the term that was removed from the current "best" model to obtain this model. Note that the model is reduced by that term only and not by all terms of lower order that were included because of it.

DF

The degrees of freedom of the term removed.

Chi Square

This value tests the significance of the removed term. It is calculated as the difference between the current chi-square statistic and the current best model's chi-square statistic. Since these are nested likelihood-ratio statistics, this difference is also a chi-square statistic.

Prob Level

The probability of rejecting the above chi-square value. If this value is greater than 0.05, you can assume that term is not necessary in the model.

Hierarchical Model

This is the hierarchical model that was fit.

Model Section

Model Section

Hierarchical Model: CE,AC,BC,AD,AE,DE,BE,BD

Model Term	Individual DF	Cumulative DF
Mean	1	1
A	1	2
B	1	3
C	1	4
AC	1	5
BC	1	6
D	1	7
AD	1	8
BD	1	9
E	1	10
AE	1	11
BE	1	12
CE	1	13
DE	1	14
Error	18	32

This report presents the expanded model (all terms are listed) as well as the associated degrees of freedom.

Chi-Square Test Section

Chi-Square Tests Section

DF	Like. Ratio Chi-Square	Prob Level	Pearson Chi-Square	Prob Level	Model
18	24.41	0.1420	24.49	0.1395	CE,AC,BC,AD,AE,DE,BE,BD

This report presents details of both the likelihood-ratio and the Pearson chi-square goodness of fit tests of the model selected. These terms are defined above.

Parameter Estimation Section

Parameter Estimation Section

Model Term	Number Cells	Count	Percent Count	Average Log(Count)	Effect (Lambda)	Effect Std. Error	Effect Z-Value
Mean	32	1729	100.00	3.0186	3.0186	0.0598	50.48
A: Newspaper							
1	16	973	56.28	3.3620	0.3434	0.0598	5.74
2	16	756	43.72	2.6752	-0.3434	0.0598	-5.74
B: Lecture							
1	16	135	7.81	1.8370	-1.1816	0.0598	-19.76
2	16	1594	92.19	4.2001	1.1816	0.0598	19.76
C: Radio							
1	16	412	23.83	2.5328	-0.4858	0.0598	-8.12
2	16	1317	76.17	3.5044	0.4858	0.0598	8.12
D: Reading							
1	16	820	47.43	3.1129	0.0944	0.0598	1.58
2	16	909	52.57	2.9242	-0.0944	0.0598	-1.58
E: Knowledge							
1	16	668	38.64	2.8902	-0.1283	0.0598	-2.15
2	16	1061	61.36	3.1469	0.1283	0.0598	2.15
AC: Newspaper,Radio							
1,1	8	306	17.70	3.1110	0.2349	0.0598	3.93
1,2	8	667	38.58	3.6129	-0.2349	0.0598	-3.93
2,1	8	106	6.13	1.9545	-0.2349	0.0598	-3.93
2,2	8	650	37.59	3.3959	0.2349	0.0598	3.93
BC: Lecture,Radio							
1,1	8	54	3.12	1.5274	0.1762	0.0598	2.95
1,2	8	81	4.68	2.1467	-0.1762	0.0598	-2.95
2,1	8	358	20.71	3.5381	-0.1762	0.0598	-2.95
2,2	8	1236	71.49	4.8622	0.1762	0.0598	2.95

(Report continues)

This report provides the details of the loglinear estimation of the specified model. This report was the goal of the LLM analysis. The definitions are as follows:

Model Term

The particular term in the model. Note that the levels of the term are also listed below the term. These levels would have printed out in words (like YES and NO) if Value Labels option had been set appropriately.

Number Cells

The number of cells involved in this term.

Count

The total of all cell counts at the indicated levels.

Percent Count

The percent the Count is of the table total. These percentages are used to understand why the term was significant.

Average Log(Count)

The average of LOG(count+delta) of all cells at the indicated levels.

Effect (Lambda)

The estimated value of λ for this term. These $\lambda's$ were identified in above and estimated using the routine of Haberman (1972).

Effect Std. Error

The asymptotic standard error of the above effect. When a saturated model is fit, the standard error is given by the square root of the variance of the effect. The variance is estimated using the formulas provided in Lee (1977). When an incomplete (less than saturated) model is estimated, the program uses the resulting estimated cell counts in the formulas appropriate for the saturated models. This is called the *approximate method* by Lee (1977). He states that these estimates may be a little large.

Effect Z-Value

This is the effect divided by the standard error. Since the number of cells included in a term differs from term to term, their estimation precision also differs. This z-value allows you to compare the relative magnitudes of the effects across all main-effects and interactions. These values represent the relative importance of that term in the loglinear model. The term *z-value* is used because these values are asymptotically normal. These were called the *standardized parameter estimates* in the Model Selection section of this chapter (presented earlier).

One model-selection rule of thumb is that you should keep all terms which have at least one z-value greater than some cutoff value (say 2.0 or 3.0) in absolute value.

Interpreting Significant Effects

The final task in loglinear analysis involves interpreting a significant term. This is usually accomplished by collapsing the table to the factors in the term of interest and then analyzing the percentages. For example, the term BC was significant. From above report, we can construct the following two-way table of percentages from the Percent Count column of the report. Note that we have arbitrarily decided to sum across the table. You could have summed down the table instead with no loss in analysis capability.

	Lectures		
<u>Radio</u>	**<u>Yes (B=1)</u>**	**<u>No (B=2)</u>**	**<u>Total</u>**
Yes (C=1)	**13%** = 100(3.12/23.83)	**87%** = 100(20.71/23.83)	**100%** = 100(23.83/23.83)
No (C=2)	**6%** = 100(4.68/76.17)	**94%** = 100(71.49/76.17)	**100%** = 100(76.17/76.17)

Looking at these percentages, we can now see why this term was significant. Notice that when factor C is 1, factor B changes from 13% to 87%. However, when factor C is 2, factor B changes from 6% to 94%. This difference in the amount of change is what causes BC to be significant. This type of table should be created for every significant term.

Data Table Section

Data Table Section

Reading	Radio	Lecture	Newspaper	Actual	Pred	Diff	Chi	FT-SR
Knowledge=1								
1	1	1	1	23.0	24.9	-1.9	-0.39	-0.34
1	1	1	2	1.0	2.7	-1.7	-1.05	-1.04
1	1	2	1	102.0	103.6	-1.6	-0.15	-0.13
1	1	2	2	16.0	11.4	4.6	1.38	1.31
1	2	1	1	27.0	24.7	2.3	0.47	0.50
1	2	1	2	3.0	6.9	-3.9	-1.49	-1.62
1	2	2	1	201.0	207.6	-6.6	-0.46	-0.44
1	2	2	2	67.0	58.2	8.8	1.15	1.14
2	1	1	1	8.0	4.3	3.7	1.77	1.55
2	1	1	2	4.0	2.0	2.0	1.39	1.22
2	1	2	1	35.0	36.2	-1.2	-0.19	-0.15
2	1	2	2	13.0	16.9	-3.9	-0.95	-0.94
2	2	1	1	7.0	4.3	2.7	1.32	1.22
2	2	1	2	2.0	5.1	-3.1	-1.38	-1.49
2	2	2	1	75.0	72.5	2.5	0.30	0.32
2	2	2	2	84.0	86.7	-2.7	-0.29	-0.27
Knowledge=2								
1	1	1	1	8.0	9.6	-1.6	-0.51	-0.44
1	1	1	2	3.0	2.0	1.0	0.68	0.71
1	1	2	1	67.0	63.8	3.2	0.40	0.42
1	1	2	2	16.0	13.5	2.5	0.68	0.71
1	2	1	1	18.0	13.0	5.0	1.37	1.31
1	2	1	2	8.0	7.1	0.9	0.35	0.42
1	2	2	1	177.0	175.8	1.2	0.09	0.11
1	2	2	2	83.0	95.2	-12.2	-1.25	-1.26
2	1	1	1	4.0	4.4	-0.4	-0.20	-0.08
2	1	1	2	3.0	4.0	-1.0	-0.49	-0.38
2	1	2	1	59.0	59.2	-0.2	-0.03	0.00
2	1	2	2	50.0	53.5	-3.5	-0.47	-0.45
2	2	1	1	6.0	6.0	0.0	0.00	0.09
2	2	1	2	10.0	13.9	-3.9	-1.04	-1.04
2	2	2	1	156.0	163.1	-7.1	-0.56	-0.55
2	2	2	2	393.0	376.9	16.1	0.83	0.83

This report presents the cell counts along with their predicted values and residuals. The main purpose of this report is to let you look for large residuals--cells that are predicted poorly by the LLM.

Actual

The cell count f_{ijk} which was read in or tabulated from the database.

Predicted

The predicted cell count m_{ijk} based on the current hierarchical model. The prediction equation is of the following form, with estimation by maximum likelihood.

$$\ln\left(m_{ijk}\right) = \theta + \lambda_i^A + \lambda_j^B + \lambda_{ij}^{AB} + \lambda_k^C + \lambda_{ik}^{AC} + \lambda_{jk}^{BC} + \lambda_{ijk}^{ABC}$$

The algorithm of Haberman (1972) is used to produce the maximum-likelihood estimates.

Difference

These residuals are Actual - Predicted. They are usually scanned to find cells that are not fit well by the model. Since the size of a residual must be judged in terms of the relative size of the cell count, you should avoid simply finding the largest residuals. Instead, you should look at a standardized residual, such as the Chi value in the last column.

Chi

This is a standardized residual. It is calculated using the formula

$$Chi = \frac{f_{ijk} - m_{ijk}}{\sqrt{m_{ijk}}}$$

It is the square root of the contribution of this cell to the overall Pearson chi-square goodness of fit statistic. This standardized residual lets you make direct comparisons among the fits of the various cells. Values of Chi larger than 1.96 in absolute value would be considered large.

FT-SR

This is the Freeman-Tukey standardized residual. Freeman and Tukey pointed out that for observations from a Poisson distribution, the quantity $\sqrt{x} + \sqrt{x+1}$ has a mean approximately equal to $\sqrt{4\mu+1}$ and a variance of one. Using this result, they formed this statistic which is written in our notation as

$$FTSR = \sqrt{f_{ijk}} + \sqrt{f_{ijk}+1} - \sqrt{4m_{ijk}+1}$$

Notice that this value does not suffer when the denominator is zero which is a real difficulty with the Chi statistic.

This value may also be considered as being from the unit normal distribution. Hence, like Chi, absolute values greater than 1.96 are considered larger.