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## On the Use of Path Analysis and Related Procedures for the Investigation of Ecological Problems

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Smith et al. (1997) recently drew attention to some pitfalls that can arise when trying to predict the responses of experimental manipulations from nonexperimental data using path analysis. Based on their analyses of experimental and nonexperimental data on rodent community interactions, they drew several conclusions: correlation coefficients and standardized path coefficients varied depending on the data set used, results based on nonexperimental data did not predict the effects of experimental treatments, results obtained from the long-term manipulation did not reveal certain known processes for one of the affected species, the pocket mouse, and they were unable to assess the overall fit of the path model to their data because the model was “just-identified” (i.e., they had an equal number of known and estimated parameters, which leaves no degrees of freedom for testing model fit). Based on these findings, the authors have pointed out potential limitations in the use of nonexperimental data as a means to analyze underlying mechanisms. In this note, we attempt to provide some additional insights into the issues raised by Smith et al. (1997). First, we discuss some difficulties with the interpretation of traditional path analysis results. Second, we reconstruct their covariance matrices and then use structural equation modeling (SEM) to perform a multigroup analysis and to make comparisons between predicted and observed mice densities. Third, we discuss the question of what we can reasonably expect from path modeling methods.

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### Historical Perspective

Path analysis was originally developed by Sewall Wright (1918, 1921, 1934, 1960) for the purpose of partitioning direct and indirect relationships among variables. From its initial conception, path analysis dealt with dependency relationships in the sense that the investigator specified the order of dependence among variables (e.g.,  $A \rightarrow B \rightarrow C$ ) and, based on that assumption, partitioned relationships among different pathways. In this original form, path analysis was not a simultaneous method (in the sense that all parameters were estimated simultaneously) nor did it include overall tests of model fit to data. In the early 1970s, more general procedures were developed for analyzing covariance relationships (Keesling 1972; Jöreskog 1973), and path analysis has since come to be superseded by the more general approach of structural equation modeling (SEM). At present, SEM is used by thousands of researchers in fields ranging from the social sciences to chemistry and biology, and there are a large number of modern presentations of SEM and associated procedures (e.g., Hayduk 1987, 1996; Loehlin 1987; Bollen 1989; Lohmöller 1989; Spirtes et al. 1993; Hair et al. 1995; Hoyle 1995; Marcoulides and Schumacker 1996; Schumacker and Lomax 1996). Ecologists have been slow to adopt path analysis, though in recent years the number of applications has increased substantially (e.g., Schemske and Horvitz 1988; Farris and Lechowicz 1990; Kingsolver and Schemske 1991; Wesser and Armbruster 1991; Mitchell 1993, 1994; Wootton 1994a, 1994b; Walker et al. 1994; Smith 1995; Shipley 1997). Even less common in ecology has been the use of SEM (Johnson et al. 1991; Mitchell 1992; Pugesek and Tomer 1995, 1996; Grace and Pugesek 1997; Shipley, in press).

### Smith et al.'s Criticisms

The main criticism made by Smith et al. (1997, p. 29) was that, “Path analysis gave varying . . . results when applied to data from unmanipulated and manipulated systems.” In this case, the data being compared were from unmanipulated control plots, short-term species removal plots, and long-term species removal plots. The model

being considered was one where kangaroo rats may influence mice populations either directly or indirectly through effects on grass cover. To consider their argument, there are two problems to address here: the changes in correlations among data sets and the question of extrapolation from unmanipulated to manipulated plots.

With regard to the first problem, the following quote from Smith et al. (1997, p. 35) illustrates the problem: "When applied to data on harvest mice, path analysis yielded results that differed substantially across the three applications. Analysis of the unmanipulated system revealed a modest overall negative effect of kangaroo rats on harvest mice ( $r_{y1} = -0.303$ ). . . . The short-term removal experiment yielded a substantially larger overall correlation ( $r_{y1} = -0.710$ ). . . . The long-term experiment also revealed a large overall negative effect of kangaroo rats on harvest mice ( $r_{y1} = -0.760$ )." In this case,  $r_{y1}$  is the correlation coefficient between rats and mice. We argue that this change in correlation coefficients is expected and does not have a bearing on whether or not the data sets are consistent or inconsistent in their predictions. Figure 1 illustrates the matter. Imagine a hypothetical case where some set of unmanipulated plots is represented by 10 replicates containing some degree of variation in the actual values of the  $x$  variable. The relationship between the  $x$  and  $y$  variables can be summarized by the correlation coefficient ( $r$ ), the regression coefficient ( $b_1$ ), and the intercept ( $b_0$ ). In the case of a simple path model

$$X \rightarrow Y,$$

the standardized path coefficient would be the same as the correlation coefficient ( $r$ ) and the unstandardized path coefficient would be the regression coefficient ( $b_1$ ). If a number of replicates are added which have  $x$  values of zero, they can be expected to act as "influential points" (Hair et al. 1995) and cause a substantial increase in the correlation coefficient even though they fall along the same regression line. Thus, in this example, changes in correlation structure in a data set do not provide insight into the question of whether the added points can be predicted from the original ones. Only analysis of the unstandardized coefficients can provide an assessment of whether the added points fall along the same line.

With regard to extrapolation from unmanipulated to manipulated systems, procedures such as path analysis (or SEM) are only able to analyze the relationships in the input data set. They are subject to the same cautions about extrapolation beyond the data as any other statistical procedure. If a process has a fairly constant effect for that data set, such as might be the case for the control plots for an experiment, then there will be no systematic

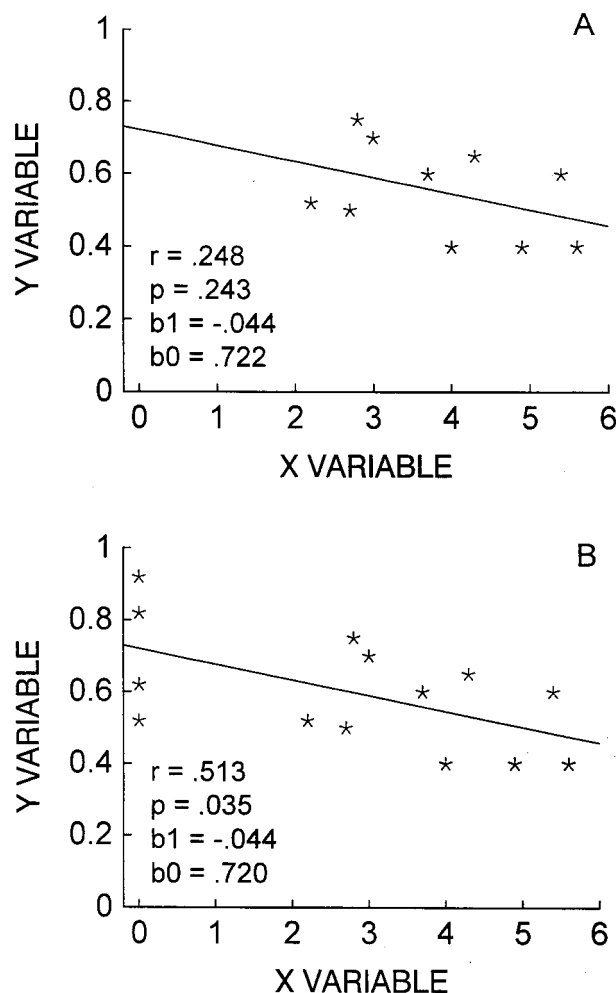


Figure 1: Hypothetical example of data showing the impact of adding four data points with zero values of the  $x$  variable (as might result from an exclusion treatment) to 10 data points with a narrower range of values.  $r$  = correlation coefficient,  $p$  =  $p$ -value for  $r$ ,  $b_1$  = slope of relationship, and  $b_0$  = the intercept. A, Ten data points with a nonsignificant relationship between  $x$  and  $y$ . B, With four additional data points added to the original 10, correlation coefficient increases while slope of the line is unchanged.

covariance between variables to reflect the presence of that underlying process. In this case, in order to predict the results of manipulations from unmanipulated plots, either the unmanipulated plots must span a wide range of natural variation in rat densities, including plots with no rats, or they must accurately estimate the slope of a linear relationship that applies to the new condition examined. Whether either assumption has been met in their example is questionable. Typically, the control plots for an experiment are selected so as to minimize variance among plots, whereas data sets collected for the purpose of prediction (cf. Grace and Pugsek 1997; L. Gough and

**Table 1:** Reconstructed covariance matrices from Smith et al. (1997) for the three data sets for each of the two target species, harvest mice and pocket mice

	<i>Harvest mice</i>			<i>Pocket mice</i>		
	<i>Mice</i>	<i>Rats</i>	<i>Grass</i>	<i>Mice</i>	<i>Rats</i>	<i>Grass</i>
Data set A ( $n = 10$ ):						
Mice	.0729			.0144		
Rats	-.1014	1.5376		-.0315	1.5376	
Grass	.0062	-.0103	.0024	.0023	-.0103	.0024
Data set B ( $n = 14$ ):						
Mice	.0702			.0471		
Rats	-.2023	1.1556		-.1292	1.1556	
Grass	.0022	.0026	.0018	.0008	.0026	.0018
Data set C ( $n = 14$ ):						
Mice	.0870			.1568		
Rats	-.2412	1.1578		-.1542	1.1578	
Grass	.0231	-.0560	.0092	.0276	-.0560	.0092

J. B. Grace, unpublished manuscript), seek to maximize the variance among plots.

Structural equation modeling methods can be used, in fact, to determine whether data sets possess commonality with regard to a set of structural (dependence) relationships and whether the results of manipulations can be predicted from unmanipulated data. The problem can be approached by either using a multigroup analysis (Jöreskog and Sörbom 1996) to compare the structure of two or more data sets, or by using unstandardized path coefficients from the unmanipulated plots to predict values for the manipulated plots (i.e., prediction from regression). Here we present a reanalysis of the data from Smith et al. (1997) using these two approaches.

#### Reanalysis Using LISREL

Given that standardized coefficients are not the best method for assessing the commonality of results among data sets, the question remains, do their data support the contention that the manipulated plots are inconsistent with the unmanipulated ones? In order to address this question, we first reconstructed the covariance (unstandardized) matrices using their correlations in combination with estimated standard deviations for data sets A, B, and C. Recall that data set A contains 10 unmanipulated plots, B contains those 10 plots plus the four plots subjected to short-term manipulation, and C contains the 10 unmanipulated plots plus the four plots subjected to long-term manipulation. The reconstructed covariance matrices are presented in table 1.

#### Multigroup Test of Commonality among Data Sets

The first analysis of the commonality of the data sets is a multigroup analysis in LISREL (Jöreskog and Sörbom 1996). In a multigroup test, a hypothesized model is simultaneously fit to the data of each group being considered while path coefficients, variances, and error terms are constrained to be equal between groups. This test determines if the data from the different groups fit exactly the same model. If a significant difference is found between models for a parameter (path coefficient, variance, or error term), this indicates that this constraint (equality of a parameter) is false and a less constrained model is indicated. We should point out that for the data of Smith et al. (1997) two assumptions normally required for multigroup analyses are violated, data set independence and adequate sample size (the same criticisms can be made of the comparisons made by Smith et al. 1997). The purpose of our application here is to demonstrate how SEM can be employed to test hypotheses about commonality of groups. Interpretations of these results must consider the assumptions that are violated.

LISREL (Jöreskog and Sörbom 1996) was used to conduct a comparison of data sets A, B, and C using the reconstructed covariance matrices (apps. A and B). In multigroup analyses, equality constraints across groups produce degrees of freedom even when individual models are "just-identified" (i.e., saturated), thus allowing for a test of significance. As summarized in table 2, for both harvest mice and pocket mice, a common model fit all three data sets quite well for both mice species ( $\chi^2 = 7.8400$ ,  $df = 9$ ,  $P = .5503$  for harvest mice and  $\chi^2 = 9.6308$ ,  $df = 7$ ,  $P = .2919$  for pocket mice). Note that a

**Table 2:** LISREL results for analysis of covariance matrices using multigroup analysis (see app. B)

<i>Harvest mice</i>		<i>Pocket mice</i>	
<i>A. Multigroup goodness-of-fit statistic</i>			
<i>N</i> for multigroup analysis = 38		<i>N</i> for multigroup analysis = 38	
$\chi^2$ with 9 df = 7.8400 ( <i>P</i> = .5503)		$\chi^2$ with 8 df = 9.6308 ( <i>P</i> = .2919)	
Group A $\chi^2$ = 3.2771		Group A $\chi^2$ = 4.6998	
Group B $\chi^2$ = 1.7419		Group B $\chi^2$ = 2.2934	
Group C $\chi^2$ = 2.8210		Group C $\chi^2$ = 2.6376	
<i>B. R<sup>2</sup> values for fit to general model</i>			
<i>Mice</i>	<i>Grass</i>	<i>Mice</i>	<i>Grass</i>
Group A = .4522	. . .	Group A = .2782	. . .
Group B = .3977	. . .	Group B = .2483	. . .
Group C = .6640	.2938	Group C = .2880	.2938
<i>C. Unstandardized estimates for general model</i>			
<i>Groups 1, 2, and 3</i>		<i>Groups 1, 2, and 3</i>	
mice = 1.7526 × grass − .1207 × rats (.4836) (.0297) [3.6242] [−4.0659]		mice = 1.5051 × grass − .0643 × rats (.5998) (.0299) [2.5094] [−2.1503]	
<i>Group 3</i>		<i>Group 3</i>	
grass = −.0484 × rats (.0211) [−2.2919]		grass = −.0484 × rats (.0211) [−2.2919]	

Note: A.  $\chi^2$  values for the group model as well as the contribution from each individual group to the total  $\chi^2$ .  $P$  values (in parentheses) indicate no significant difference in parameters between groups when they exceed  $P$  = .05. B.  $R^2$  values for each group based on the general model. C. Numbers in parentheses are standard errors; numbers in brackets are  $t$ -values. All  $t$ -values shown are significant at  $P$  = .05.

nonsignificant  $\chi^2$  test indicates a good fit between the model and the data. We, therefore, have no basis to reject the hypothesis that the same path model applies to both manipulated and unmanipulated data sets. Based on this analysis and using single degree of freedom  $\chi^2$  tests, some individual differences were found between groups for some parameters. The variances in some measured variables differed in a couple of cases. The variance of grass cover (a parameter in both the models for harvest and pocket mice) was higher in group C than in the other groups ( $\Delta\chi^2$  = 5.59 and 6.07 for harvest and pocket mice data sets respectively,  $P$  < .05). For pocket mice, the variance in mice density was also higher in group C ( $\Delta\chi^2$  = 5.14,  $P$  < .05). This disproportion is to be ex-

pected since group C contains the long-term manipulations that tended to produce conditions not observed in unmanipulated plots. These are incidental differences that do not affect the main interpretation of the data (the basis of which can be seen in Smith et al. 1997, table 1). The main difference of importance was that the model for data set C (including the long-term manipulations) showed a significant negative effect of rats on grass cover, which was not observed in data sets A and B ( $t$ -values for this path in data sets A and B were both  $t$  = -0.903,  $P$  = .27). This effect represents the long-term impact of kangaroo rats on grass reported by Smith et al. (1997). However, the slopes of the relationships for the other two major paths, from rats to mice and from grass to mice,

were not different between data sets, contradicting the conclusions of Smith et al. (1997) that coefficients were generally inconsistent.

Table 2 also presents the  $R^2$  values and the unstandardized estimates for the general models. Mice densities were found to be significantly related to both rats and grass. The  $R^2$  values for the fit of the data sets to the general model were fairly good for harvest mice (mean = 0.5053) but not as good for pocket mice (mean = 0.2715). These values were comparable to those in Smith et al. (1997, calculated from  $e_y$  in their table 3) except that the multigroup analysis produced more consistent values across groups.

#### *Prediction Based on the Unmanipulated Plots*

Another application of SEM that can be made is to make predictions from the unmanipulated plots and to test those predictions against the values obtained from short- and long-term manipulations. In essence, this tests the extrapolative ability of a data set. We should emphasize that extrapolative ability is not a necessary criterion for the validity of a model based on a set of data. Whether a model can be used for prediction of new situations is separate from the question of validity for that data set. Very few ecological studies have a demonstrated ability to extrapolate to new situations (for an exception, see Shipley et al. 1991; Wootton 1994b). Nonetheless, this is an issue of considerable interest, and here we provide such a test using the data from Smith et al. (1997).

Using means and covariances, we generated LISREL estimates for both harvest and pocket mice models based solely on the unmanipulated plots (table 3). Using the values for rats and grass from Smith et al. (1997, table 1), we calculated predicted values for mice for both the short-term and long-term experiments. While it is possible to calculate variance measures for these estimates, testing the predicted versus observed values with error associated with the predictions would constitute a very conservative test given the small sample size, and for this reason we treat the predicted values as deterministic. The bias created by this approach favors the interpretation of Smith et al. (1997; that manipulated plots are not consistent with nonmanipulated plots) and disfavors our interpretation. As shown in table 3, observed values for the manipulated plots were higher than predicted. The results for harvest mice in the short-term experiment showed the greatest discrepancy while the pocket mice densities in the long-term experiment showed the least. However, only the case for harvest mice in the short-term experiment showed differences that were statistically significant. All other differences were nonsignificant.

Thus, based on the available data, we are not able to show that the mice densities found in the long-term experiment differ significantly from those predicted from the unmanipulated plots using linear extrapolation. Yet, even if there were significant differences, this would only indicate that the relationship between rats and mice is not linear, not that the statistical method was unfit.

#### **Interpretation of the Analyses**

Overall, these analyses show some of the capabilities of path modeling methods for the investigation of ecological systems. Given the extremely small sample sizes and the fact that this was a post facto use of the method instead of a planned evaluation, we feel that the path modeling results presented in this note provide a reasonable summarization of the data (with the reservations stated above). In addition to estimating path coefficients and the commonality among data sets, these analyses also allow for a comparison between expectations and data. As an example, one feature of the data that Smith et al. (1997) found to be inconsistent with their biological understanding of the system was a strong positive relationship between grass cover and pocket mice density (we found the same result, table 2). Based on their previous studies, they do not believe that grass cover positively affects pocket mice. However, the discrepancy here is between their data and their expectations, not a flaw in the statistical methods. This kind of discrepancy is exactly the kind of result that endorses SEM as a way of contributing to scientific progress by pointing out differences between expectations and observations.

Another important point to make is that path modeling methods can only extract the information available in the data being analyzed. One question that these methods can address is, How much of the observed variation in mice densities can be attributed to observed variation in rats and grass? The value of the results of that analysis will depend on how well the investigators understand the relationships among variables and how good a data set is for analyzing the relationships. If one wishes to explore the utility of path modeling methods for extracting information from a data set, it will usually be most effective to use simulations that can generate data from a number of assumptions (e.g., Pugsek and Tomer 1995).

#### **What Can We Gain from Path Modeling Methods?**

The question of fundamental importance that we would like to consider in this section is, What can we expect to learn from the analysis of path models? Here we provide a quote from the classic work by Bollen (1989): "The



**Table 3:** Mice densities predicted by the unmanipulated plots using LISREL model results for group A alone (not including any manipulated plots)

<i>Predicted vs. observed responses</i>	<i>Harvest mice</i>	<i>Pocket mice</i>
Predicted mice with rats excluded:		
Short-term experiment	.573	.218
Long-term experiment	.974	.370
Observed (mean $\pm$ SD):		
Short-term experiment	1.01 $\pm$ .25	.530 $\pm$ .38
Long-term experiment	1.26 $\pm$ .36	.500 $\pm$ .66
<i>t</i> -values:		
Short-term experiment	3.496*	1.642 <sup>a</sup>
Long-term experiment	1.589 <sup>a</sup>	.394 <sup>a</sup>

Note: The equation for harvest mice was as follows:  $MICE = .374 - .0501 \times RATS + 2.358 \times GRASS$ . The equation for pocket mice was as follows:  $MICE = .1422 - .01452 \times RATS + .08926 \times GRASS$ . Values for RATS and GRASS were taken from Smith et al. (1997, table 1). Predictions are presented without error (see discussion in text). Observed values represent the means and standard deviations of four replicates.

<sup>a</sup>Not significant.

\* $P < .05$ .

purpose of [SEM] is to determine if the *causal inferences* of a researcher are *consistent* with the data. If the path model does not fit the data, then revisions are needed, since one or more of the model assumptions are in error. If the path model is consistent with the data, this does not prove causation. Rather, it shows that our assumptions are not contradicted and may be valid. We only can say 'may be valid' because other models and assumptions also may fit the data."

It should be clear from this statement that experienced practitioners of SEM realize that this methodology is no "magic wand," and, in fact, it has significant limitations. First, it cannot yield results that necessarily extend beyond the data used in the analysis (unlike analytical or simulation models). Second, it cannot prove causation (though it can lead to the falsification of causal hypotheses). Third, there are significant data requirements, both in terms of the number of measured variables (allowing for overidentification and model testing) and in terms of replication. Fourth, one must consider the nature of the data and the ability of the analysis to conform to the assumptions of the test. Fortunately, much progress has been made in this area, and there are now strategies for dealing with most limitations (e.g., nonnormality, nonlinearity, collinearity, nonindependent samples, nonadditivity, categorical variables, small sample size, etc.). Despite these limitations, SEM represents a powerful methodology for addressing multivariate problems.

One important point about what can be accomplished by confirmatory methods such as SEM has to do with the

relationship between a causal hypothesis and a confirmatory test of a path model. The specified path model represents, in essence, a set of expectations resulting from an underlying mechanistic hypothesis about how system components influence one another. The path model itself represents the expected covariance structure for a set of data intended to evaluate that hypothesis, and the structure of that path model implies certain constraints on the expected patterns of covariances among variables. The number of these constraints determines the degrees of freedom available for testing between expected and observed covariances. If the model places no constraints on the data, there can be no test. When a test for goodness of fit (using a chi-square or other criterion test) shows a significant deviation between expected and observed, it means that the data are not consistent with the mechanisms underlying the specified model, and our causal hypothesis about the system is rejected. It is in this fashion that confirmatory statistical methods are used to evaluate underlying mechanistic hypotheses. Of course, when our test criterion is nonsignificant we do not prove our hypothesis to be true since either limitations on statistical power or unconsidered, equivalent models might be involved. Ultimately, it is the continued evaluation with additional data that leads to greater confidence in the acceptance of a model.

In conclusion, path modeling methods such as SEM, while far from perfect, represent one of the most powerful approaches available for analyzing complex multivariate relationships. These tools have been shown to have

utility in many other disciplines, where they are now used extensively. Only through continued attempts to use such methods can we discover the degree of their utility for ecological problems.

### Acknowledgments

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## APPENDIX A

Table A1: Data sets used in the analyses

	<i>Correlations</i>		
	<i>Rats</i>	<i>Grass</i>	<i>Mice</i>
Harvest mice:			
Group A (file = ah.dat):			
Rats	1.0		
Grass	-.170	1.0	
Mice	-.303	.467	1.0
SE	1.24	.049	.27
Group B (file = bh.dat):			
Rats	1.0		
Grass	.057	1.0	
Mice	-.710	.195	1.0
SE	1.075	.043	.265
Group C (file = ch.dat):			
Rats	1.0		
Grass	-.542	1.0	
Mice	-.760	.816	1.0
SE	1.076	.096	.295
Pocket mice:			
Group A (file = ap.dat):			
Rats	1.0		
Grass	-.170	1.0	
Mice	-.212	.390	1.0
SE	1.24	.049	.12
Group B (file = bp.dat):			
Rats	1.0		
Grass	.057	1.0	
Mice	-.554	.081	1.0
SE	1.075	.043	.217
Group C (file = cp.dat):			
Rats	1.0		
Grass	-.542	1.0	
Mice	-.362	.727	1.0
SE	1.076	.096	.396

Note: SE refers to standard errors of the mean.

## APPENDIX B

### SIMPLIS Command Statements Used to Analyze the Data under LISREL

Group 1. Analysis of Data Set A—Harvest Mice  
 observed variables: rats grass hmice  
 correlations from file = ah.dat  
 standard deviations from file = ah.dat  
 sample size: 10  
 relationships:  
 hmice = rats grass

Group 2. Analysis of Data Set A + B—Harvest Mice  
 correlations from file = bh.dat  
 standard deviations from file = bh.dat  
 sample size: 14

Group 3. Analysis of Data Set A + C—Harvest Mice  
 correlations from file = ch.dat  
 standard deviations from file = ch.dat  
 sample size: 14  
 set the path from rats to grass free  
 set the variance of grass free  
 options: ss, sc, nd = 4  
 end of problem

Group 1. Analysis of Data Set A—Pocket Mice  
 observed variables: rats grass pmice  
 correlations from file = ap.dat  
 standard deviations from file = ap.dat  
 sample size: 10  
 relationships: pmice = rats grass

Group 2. Analysis of Data Set A + B—Pocket Mice  
 correlations from file = bp.dat  
 standard deviations from file = bp.dat  
 sample size: 14

Group 3. Analysis of Data Set A + C—Pocket Mice  
 correlations from file = cp.dat  
 standard deviations from file = cp.dat  
 sample size: 14  
 set the variance of pmice free  
 set the variance of grass free  
 set the path from rats to grass free  
 options: ss, sc, nd = 4  
 end of problem



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