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ABSTRACT
        This LISREL study examines the robustness of the
maximum likelihood estimates under varying degrees of measurement
model misspecification. A true model containing five latent variables
(two endogenous and three exogenous) and two indicator variables per
latent variable was used. Measurement model misspecification
considered included errors of omission, errors of inclusion, and
simultaneous errors of omission and inclusion. A sample size of 200
was used for all replications. LISREL programs were written for each
of six models to be tested. The PC version of LISREL VII was used to
estimate the models. Assessments of results were based on average
parameter estimates for each model across replications, average
chi-square value across replications, modification indices for errors
of omission, and t-values for errors of inclusion. Results indicate
that minor misspecifications in LISREL measurement models in the LY
matrix are the most problematic, particularly for compound errors. In
general, the ability of the LISREL program to detect measurement
model misspecification is quite good. One figure illustrating the
true population model and six data tables are included. (TJH)

MEASUREMENT MODEL SPECIFICATION ERROR IN LISREL STRUCTURAL EQUATION MODELS

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Researchers using LISREL or similar programs for the purpose of estimating the parameters of structural equation models must make important assumptions. Statistically, the researcher must assume large sample sizes (asymptotic theory) and a multivariate normal distribution of indicator variables in the measurement model. In addition, theoretical assumptions as to the appropriateness of model specification are necessary. Unfortunately, usually one or more of these assumptions are violated. Much Monte Carlo research that has been done has been primarily concerned with non-normality and sample size (such as Boomsma, 1983; Gerbing & Anderson, 1985). Other studies have been concerned with the use of categorical or dichotomous data (Ethington, 1985), model misspecification (such as Gallini & Mandeville, 1983; MacCallum, 1986; Silvia & MacCallum, 1988; Baldwin, 1987) and the test statistics used for model fitting (such as Kaplan, 1988). This study examines the robustness of ML estimates under varying degrees of measurement model misspecification.

Techniques

A true model containing five latent variables (two endogenous and three exogenous) and two indicator variables per latent variable was used (from MacCallum, 1986). Figure 1 illustrates the true model. Three types of measurement model misspecification were considered: (1) errors of omission, i.e., where a true fac-

tor loading is omitted; (2) errors of inclusion, i.e., where an
extra factor loading is added to the model; and (3) simultaneous
errors of omission and inclusion. A sample size of N=200 was used
for all replications.

Using the assigned true parameter values, the model was spe-
cified, and the population covariance matrix genera' using the
PROC IML program (SAS Institute, 1988). The population covariance
matrix Σ was used as input to the GENRAW and PRELIS programs
{Joreskog & Sorbom, 1988) to generate 20 sample covariance mat-
rices S for each model to be tested. Each variable was specified
to be continuous with a mean of zero. LISREL programs were writ-
ten for each of the six models to be tested. The PC version of
LISREL VII (Joreskog & Sorbom, 1989) was used to estimate the
models.

The relevant output from the program runs consisted of the
maximum likelihood parameter estimates, the standard errors of
the estimates, t-values for all parameters being esti-
mated, modification indices for all parameters that were not
being estimated, and the chi-square goodness-of-fit value with
the associated degrees of freedom.

Assessment of the results was based on the following crite-
ria:

(1) Average parameter estimates for each model across repli-
cations (bias of sample estimates): Does the average sample
parameter estimate differ from the actual parameter value?

This relative difference was judged by computing a statistic which was the difference between the average parameter estimate and the parameter value divided by the parameter value and multiplied by 100. The relative difference represents the percentage increase or decrease in the value of the estimate as compared to the true parameter value.

(2) Average chi-square value across replications: Would a misspecified model still be considered a good fit? What is the rate of rejection for misspecified models?

(3) Modification indices for errors of omission

    A. Average modification index for a particular error.

    B. Percentage of cases in which the index is highest for the particular misspecification made: Does the modification index correctly indicate the adjustment to be made to yield a properly specified model?

(4) T-values for errors of inclusion

    A. Average t-value for error: Is the t-value significant?

    B. Percentage of cases in which the t-value is insignificant: Does the t-value correctly

indicate that the misspecified parameter should be set equal to zero and thus yield a properly specified model?

In addition to analyzing information about model misspecification, parameter bias, and resultant goodness-of-fit, it is also of interest to consider the occurrences of improper solutions and nonconvergence in a Monte Carlo study. Improper solutions result when maximum likelihood estimates of variances are negative. These negative variances indicate that the solution is unstable. Nonconvergence was defined as the inability of the program to find a unique solution which meets the convergence criteria within 250 iterations.

At the onset of this study, it was decided that improper solutions were to be included in the analysis. It was also decided that a minimum of 20 converged solutions was necessary for model analysis.

Results

Model 1A. Model 1A includes LX(6,2) as a factor loading. This error of inclusion means that the true model is contained within the misspecified model. The average parameter estimate for the misspecification was -.03 (t_{25} = -.16, p>.05). All other estimated parameters were significant. The only estimate that

substantially differed from the parameter value was PS(1,1). The average chi-square value indicates that the model would be considered plausible. The maximum modification indices were small and randomly scattered; thus, recovery from the misspecification would be expected.

Model 1B. Model 1B omits LX(6,3). All estimated parameters were significant. GA(1,3) was underestimated due to the influence that the omission had on the latent variable. PH(3,3) indicates an increase in error variance. The maximum modification indices correctly indicated that LX(6,3) should be added to the model in every replication. The average chi-square value indicates that the model should not be considered plausible. Overall, deletion of a parameter as in this model appears to be more serious than inclusion as in Model 1A.

Model 1C. Model 1C includes LX(6,2) and omits LX(6,3). The t-value for the included estimate did not indicate that the parameter should be set to zero ($t_{27} = 3.47$, $p<.05$). However, the modification indices would alert the researcher to the omitted element, yielding Model 1A. Thus, using a two-step process, recovery from the misspecifications would be likely. The misspecification was correctly identified in every replication. As in Model 1B, GA(1,3) was underestimated, and PH(3,3) was overestimated. The chi-square values were large for every replication, thus indicating that the model is not plausible.

Model 2A. Model 2A added LY(4,1) to the population model. As

for Model 1A, all parameter loadings were significant except for the misspecification (t_{25} = .26, p>.05). The chi-square goodness-of-fit index indicates an acceptable model. PS(1,1) was under-estimated.

Model 2B. LY(4,2) was omitted from the population model. Parameter estimates for elements of GA, PS, TE, and TD were affected by the misspecification. PS(2,2) was overestimated by 112%, and TE(4,4) was overestimated by 212%. The chi-square values indicate that the model is unacceptable, and the maximum modification indices correctly flag the LY(4,2) factor loading in 19 of the 20 replications.

Model 2C. Model 2C simultaneously contains an error of inclusion (LY(4,1)) and an error of omission (LY(4,2)). Such errors on the "endogenous side" of the model presented many more estimation problems than for Model 1C. Values for BE(2,1), GA(1,1), and PS(2,2) were overestimated, while values for GA(2,1), GA(2,2), and PS(1,1) were underestimated. T-values indicated that GA(2,2) should be deleted from the model, while LY(4,1) should be retained. In 16 of 20 replications, LY(4,2) had the highest modification index. The average chi-square value is significant. Overall, this model shows that measurement misspecification can seriously distort the estimated values of structural coefficients and fail to give the information necessary to correct the model.

Importance of the Study

Questions as to the appropriateness of parameters derived from structural equation modeling under specific violations of assumptions have only been partially answered. Past research has concentrated on aspects of non-normality and sample size with fewer studies investigating issues such as model misspecification, level of measurement, and goodness-of-fit. Researchers must be aware of the effects of violating assumptions when using sophisticated statistical programs such as LiSREL. This knowledge is essential to statisticians concerned with the development of covariance structure analysis as well as applied researchers in the field using structural equation modeling for theory development.

This paper provides specific information as to the problems of measurement model misspecification for a model typical of those most often used in applied research. Overall, minor mis-specifications in LISREL measurement models in the LY matrix are the most problematic, particularly for compound errors, **even when the structural model is properly specified and the sample size is adequate.** In general, the ability of the LISREL program to detect measurement model misspecification is quite good. Thus, users can be relatively assured that program output (when combined with strong substantive theory supporting an adjustment) will aid them

in correcting a misspecification.

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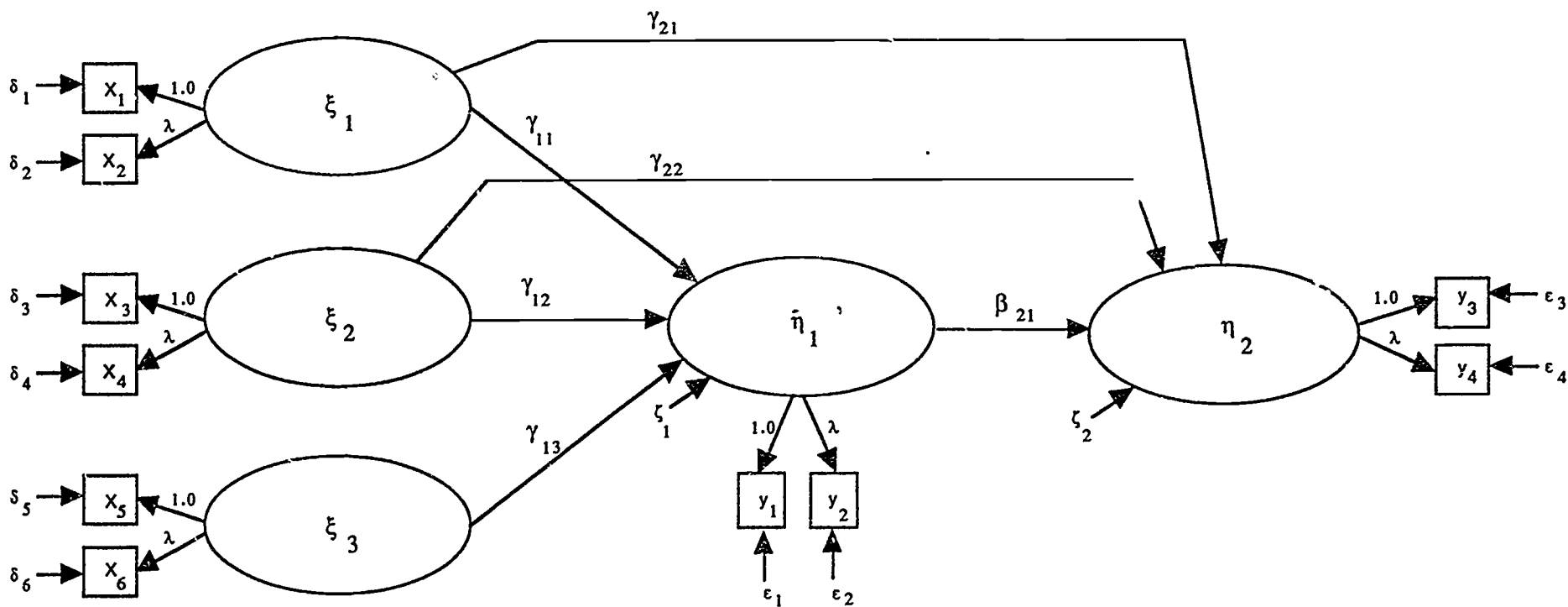
Figure 1. True population model.

NOTE: ϕ_{21} ϕ_{31} ϕ_{32} are estimated as well.

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PARAMETER	PARAMETER VALUE	MEAN ESTIMATE	RELATIVE DIFF.	t
LY 1,1	1.0*			
LY 2,1	.8	.81	-**	11.55
LY 3,2	1.0			
LY 4,2	.8	.75	-	13.69
LX 1,1	1.0			
LX 2,1	.8	.79	-	7.86
LX 3,2	1.0			
LX 4,2	.8	.83	-	7.95
LX 6,2	-	-.03	-	-.16
LX 5,3	1.0			
LX 6,3	.8	.81	-	4.43
BE 2,1	.4	.41	-	2.82
GA 1,1	.4	.40	-	3.79
GA 2,1	.6	.63	-	4.32
GA 1,2	.6	.58	-	5.17
GA 2,2	.4	.44	-	2.81
GA 1,3	.4	.40	-	3.52
PH 1,1	1.0	1.01	-	5.47
PH 2,1	.3	.32	-	3.09
PH 3,1	.3	.31	-	3.26
PH 2,2	1.0	1.01	-	5.51
PH 3,2	.3	.30	-	2.78
PH 3,3	1.0	1.06	-	4.16
PS 1,1	.5	.43	-14	3.63
PS 2,2	.5	.48	-	3.65
TE 1,1	.6	.63	-	5.64
TE 2,2	.6	.58	-	6.91
TE 3,3	.6	.60	-	4.93
TE 4,4	.6	.59	-	6.66
TD 1,1	.6	.61	-	4.82
TD 2,2	.6	.60	-	6.70
TD 3,3	.6	.58	-	4.84
TD 4,4	.6	.60	-	6.46
TD 5,5	.6	.54	-	3.03
TD 6,6	.6	.60	-	4.58

AVG MAX MI = 3.8 FOR LY 4,1 IN 3 OF 20 REPLICATIONS
     All others were smaller and randomly scattered.

CHI-SQUARE = 23.51 with 25 df (p>.05)

Number of converged replications = 20
Number of nonconvergent solutions = 0
Number of improper solutions   = 0

* factor loadings of 1.0 are fixed for manifest variables
** indicates a relative difference of 10% or less

TABLE 1. RESULTS FOR MODEL 1A

PARAMETER	PARAMETER VALUE	MEAN ESTIMATE	RELATIVE DIFF.	t
LY 1,1	1.0*			
LY 2,1	.8	.81	-**	11.33
LY 3,2	1.0			
LY 4,2	.8	.81	-	13.02
LX 1,1	1.0			
LX 2,1	.8	.81	-	7.48
LX 3,2	1.0			
LX 4,2	.8	.81	-	7.59
LX 5,3	1.0			
BE 2,1	.4	.43	-	3.26
GA 1,1	.4	.42	-	3.88
GA 2,1	.6	.63	-	4.37
GA 1,2	.6	.67	12	5.67
GA 2,2	.4	.39	-	2.32
GA 1,3	.4	.22	-45	3.39
PH 1,1	1.0	.97	-	5.24
PH 2,1	.3	.27	-	2.64
PH 3,1	.3	.30	-	2.86
PH 2,2	1.0	1.02	-	5.35
PH 3,2	.3	.29	-	2.73
PH 3,3	1.0	1.55	55	9.98
PS 1,1	.5	.57	14	4.16
PS 2,2	.5	.48	-	3.69
TE 1,1	.6	.57	-	5.02
TE 2,2	.6	.62	-	5.92
TE 3,3	.6	.61	-	4.97
TE 4,4	.6	.62	-	6.60
TD 1,1	.6	.61	-	4.88
TD 2,2	.6	.56	-	6.07
TD 3,3	.6	.60	-	4.76
TD 4,4	.6	.60	-	6.35
TD 6,6	.6	1.23	-	9.98

AVG MAX MI = 64.2 FOR LX 6,3 IN 20 OF 20 REPLICATIONS

CHI-SQUARE = 114.29 with 28 df (p<.05)

Number of converged replications = 20
Number of nonconvergent solutions = 0
Number of improper solutions   = 0

* factor loadings of 1.0 are fixed for manifest variables
** indicates a relative difference of 10% or less

TABLE 2. RESULTS FOR MODEL 1B

PARAMETER	PARAMETER VALUE	MEAN ESTIMATE	RELATIVE DIFF.	t
LY 1,1	1.0*			
LY 2,1	.8	.78	-**	11.34
LY 3,2	1.0			
LY 4,2	.8	.80	-	13.45
LX 1,1	1.0			
LX 2,1	.8	.79	-	7.87
LX 3,2	1.0			
LX 4,2	.8	.84	-	7.93
LX 6,2	-	.33	-	3.47
LX 5,3	1.0			
BE 2,1	.4	.37	-	2.69
GA 1,1	.4	.44	-	4.17
GA 2,1	.6	.63	-	4.63
GA 1,2	.6	.70	17	5.64
GA 2,2	.4	.44	-	2.55
GA 1,3	.4	.20	-50	3.02
PH 1,1	1.0	1.07	-	5.50
PH 2,1	.3	.29	-	2.91
PH 3,1	.3	.27	-	2.52
PH 2,2	1.0	.96	-	5.32
PH 3,2	.3	.36	20	3.33
PH 3,3	1.0	1.60	60	9.98
PS 1,1	.5	.57	14	4.09
PS 2,2	.5	.47	-	3.68
TE 1,1	.6	.58	-	4.98
TE 2,2	.6	.60	-	6.95
TE 3,3	.6	.60	-	5.04
TE 4,4	.6	.57	-	6.49
TD 1,1	.6	.92	53	4.75
TD 2,2	.6	.59	-	6.46
TD 3,3	.6	.66	-	5.55
TD 4,4	.6	.58	-	9.73
TD 5,5	.6	.54	-	3.03
TD 6,6	.6	.60	-	4.58

AVG MAX MI = 57.7 FOR LX 6,3 IN 20 OF 20 REPLICATIONS

CHI-SQUARE = 94.26 with 27 df (p<.05)

Number of converged replications = 20
Number of nonconvergent solutions = 0
Number of improper solutions   = 0

* factor loadings of 1.0 are fixed for manifest variables
** indicates a relative difference of 10% or less

TABLE 3. RESULTS FOR MODEL 1C

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PARAMETER	PARAMETER VALUE	MEAN ESTIMATE	RELATIVE DIFF.	t
LY 1,1	1.0*			
LY 2,1	.8	.81	-**	11.17
LY 4,1	-	.01	-	.26
LY 3,2	1.0			
LY 4,2	.8	.79	-	4.42
LX 1.1	1.0			
LX 2,1	.8	.80	-	8.02
LX 3,2	1.0			
LX 4,2	.8	.82	-	7.90
LX 6,3	.8	.81	-	5.55
BE 2,1	.4	.45	-	2.95
GA 1,1	.4	.39	-	3.96
GA 2,1	.6	.60	-	4.30
GA 1,2	.6	.60	-	5.41
GA 2,2	.4	.37	-	2.39
GA 1,3	.4	.40	-	3.53
PH 1,1	1.0	1.06	-	5.60
PH 2,1	.3	.31	-	3.03
PH 3,1	.3	.26	-	2.59
PH 2,2	1.0	1.00	-	5.51
PH 3,2	.3	.28	-	2.79
PH 3,3	1.0	.99	-	4.47
PS 1,1	.5	.44	-12	3.53
PS 2,2	.5	.52	-	2.80
TE 1,1	.6	.64	-	5.70
TE 2,2	.6	.57	-	7.09
TE 3,3	.6	.57	-	3.40
TE 4,4	.6	.58	-	5.13
TD 1,1	.6	.56	-	4.62
TD 2,2	.6	.57	-	6.36
TD 3,3	.6	.57	-	4.79
TD 4,4	.6	.55	-	6.21
TD 5,5	.6	.54	-	3.36
TD 6,6	.6	.59	-	4.98

AVG M\X MI = 4.0 FOR LX 1,3 IN 3 OF 20 REPLICATIONS
          All others were smaller and randomly scattered.

CHI-SQUARE = 27.01 with 25 df (p>.05)

Number of converged replications = 20
Number of nonconvergent solutions = 0
Number of improper solutions   = 0

* factor loadings of 1.0 are fixed for manifest variables
** indicates a relative difference of 10% or less

TABLE 4. RESULTS FOR MODEL 2A

PARAMETER	PARAMETER VALUE	MEAN ESTIMATE	RELATIVE DIFF.	t
LY 1,1	1.0*			
LY 2,1	.8	.80	-**	11.80
LY 3,2	1.0			
LX 1,1	1.0			
LX 2,1	.8	.82	-	7.15
LX 3,2	1.0			
LX 4,2	.8	.80	-	7.95
LX 6,3	.8	.86	-	6.14
BE 2,1	.4	.41	-	2.72
GA 1,1	.4	.37	-	3.59
GA 2,1	.6	.58	-	4.05
GA 1,2	.6	.64	-	5.68
GA 2,2	.4	.41	-	2.49
GA 1,3	.4	.45	12.5	3.85
PH 1,1	1.0	1.01	-	5.17
PH 2,1	.3	.27	-	2.57
PH 3,1	.3	.29	-	2.84
PH 2,2	1.0	1.04	-	5.51
PH 3,2	.3	.31	-	3.00
PH 3,3	1.0	.93	-	4.63
PS 1,1	.5	.49	-	3.77
PS 2,2	.5	1.06	112	7.99
TE 1,1	.6	.57	-	5.02
TE 2,2	.6	.60	-	6.83
TE 4,4	.6	1.87	212	9.98
TD 1,1	.6	.61	-	4.51
TD 2,2	.6	.60	-	6.00
TD 3,3	.6	.60	-	4.86
TD 4,4	.6	.58	-	6.42
TD 5,5	.6	.92	53	4.33
TD 6,6	.6	.54	-	4.79

AVG MAX MI = 105.2 FOR LY 4,2
        LY 4,2 had the MMI in 19 of 20 replications.

CHI-SQUARE = 196.87 with 28 df (p<.05)

Number of converged replications = 20
Number of nonconvergent solutions = 0
Number of improper solutions   = 0

* factor loadings of 1.0 are fixed for manifest variables
** indicates a relative difference of 10% or less

TABLE 5. RESULTS FOR MODEL 2B

PARAMETER	PARAMETER VALUE	MEAN ESTIMATE	RELATIVE DIFF.	t
LY 1,1	1.0*			
LY 2,1	.8	.84	-**	10.94
LY 4,1	-	.91	-	11.13
LY 3,2	1.0			
LX 1,1	1.0			
LX 2,1	.8	.84	-	7.73
LX 3,2	1.0			
LX 4,2	.8	.78	-	7.50
LX 6,3	.8	.77	-	5.98
BE 2,1	.4	.84	110	3.98
GA 1,1	.4	.54	35	5.21
GA 2,1	.6	.29	-52	1.76
GA 1,2	.6	.59	-	5.54
GA 2,2	.4	.14	-65	.71
GA 1,3	.4	.30	-25	3.41
PH 1,1	1.0	.96	-	5.31
PH 2,1	.3	.27	-	2.75
PH 3,1	.3	.30	-	2.81
PH 2,2	1.0	.97	-	5.33
PH 3,2	.3	.31	-	2.85
PH 3,3	1.0	1.15	15	4.78
PS 1,1	.5	.25	-50	2.68
PS 2,2	.5	.86	72	7.39
TE 1,1	.6	.81	35	7.70
TE 2,2	.6	.73	22	8.24
TE 4,4	.6	.77	28	8.06
TD 1,1	.6	.63	-	5.21
TD 2,2	.6	.59	-	6.27
TD 3,3	.6	.59	-	4.79
TD 4,4	.6	.60	-	6.70
TD 5,5	.6	.56	-	3.16
TD 6,6	.6	.64	-	5.33

AVG MAX MI = 35.8 FOR LY 4,2
        LY 4,2 had the MMI in 16 of 20 replications.

CHI-SQUARE = 71.62 with 27 df (p<.05)

Number of converged replications   = 20
Number of nonconvergent solutions = 0
Number of improper solutions   = 0

* factor loadings of 1.0 are fixed for manifest variables
** indicates a relative difference of 10% or less

TABLE 6. RESULTS FOR MODEL 2C