

TAXOMETRIC ANALYSIS WITH DICHOTOMOUS  
INDICATORS: THE MODIFIED MAXCOV PROCEDURE  
AND A CASE-REMOVAL CONSISTENCY TEST<sup>1,2</sup>

JOHN RUSCIO

*Elizabethtown College*

*Summary.*—Previous Monte Carlo simulations and empirical trials have demonstrated the power with which taxometric procedures distinguish between taxonic (categorical) and dimensional (continuous) latent structures. However, questions have been raised about results obtained using procedures modified to accommodate dichotomous indicators. The present investigation shows that the most widely used taxometric procedure (MAXCOV) can distinguish between latent structures when adapted for use with dichotomous indicators, although particularly large samples and substantially valid indicators are required. This study also illustrates the value of including a case removal consistency test as one component of a taxometric investigation.

Taxometric procedures are designed to help assess whether the latent structure of a given psychological construct is taxonic (categorical) or dimensional (continuous). This analytic approach was developed by Meehl and colleagues (e.g., Meehl, 1973, 1995, 1999; Meehl & Golden, 1982; Meehl & Yonce, 1994, 1996; Waller & Meehl, 1998) to test a conjectured two-group latent class model. Meehl (1995) reviewed a considerable body of research using empirical data as well as Monte Carlo simulations that demonstrates the efficacy of the taxometric method. Although most of the available procedures were designed for use with continuous indicators, a number of taxometric investigations have been conducted with indicators that are either inherently dichotomous or formed from items that have been dichotomized. In the absence of a study of the robustness of taxometric procedures with dichotomous indicators, questions have been raised about the interpretability of these results (Meehl, 1995; Meehl & Yonce, 1996; Miller, 1996). This paper presents the results of a Monte Carlo investigation which addresses these questions and evaluates a consistency test.

LOGIC OF THE MAXCOV PROCEDURE

The most widely used procedure within Meehl's coherent cut kinetics approach to taxometrics is MAXCOV, short for "MAXimum COVariance"

<sup>1</sup>Address correspondence to John Ruscio, Department of Psychology, Elizabethtown College, Elizabethtown, PA 17022 or e-mail (rusciojp@etown.edu).

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(Meehl, 1973; Meehl & Yonce, 1996). MAXCOV utilizes three indicators, each of which is hypothesized to differentiate between (or "separate") two conjectured latent classes (the "taxon" and "complement"). One of the indicators (the "input") is divided into a series of distinct intervals. The covariance of the remaining two indicators is then computed within each successive interval. The shape of the curve formed by plotting each covariance above its corresponding input interval on the abscissa indicates the latent structure. Taxonic data yield curves that are markedly peaked whereas dimensional data yield curves that are relatively flat.

Using dichotomous—rather than continuous—indicators requires modifying the MAXCOV procedure (Gangestad & Snyder, 1985). Two indicators are set aside for the calculation of covariances, and those that remain are summed to form an input variable. A series of MAXCOV curves is generated by graphing the covariance plot for each possible pair of indicators. Previous research has often used eight dichotomous indicators to strike a balance between the number of input intervals and the stability of the covariance values within these intervals. With too few intervals, it would be difficult to discern the shape of the MAXCOV curve, whereas with too many intervals, the stability of within-interval covariances would be compromised. The resultant curves have not been presented in a panel but averaged to stabilize further the covariance estimates and thereby aid interpretation.<sup>3</sup>

To date, researchers have drawn dichotomous indicators primarily from items on self-report questionnaires, on the assumption that total scores on a valid scale should distinguish between a conjectured taxon and complement. An initial pool of potential indicators is formed by selecting items with the highest corrected item-total correlations. Item content is then examined to retain qualitatively distinct indicators from the initial pool, thereby minimizing nuisance covariation within the conjectured groups.

#### MONTE CARLO TESTS OF THE MODIFIED MAXCOV PROCEDURE

Three critical questions can be raised regarding the use of dichotomous indicators in the MAXCOV procedure. First, can the obtained curves be interpreted in the same manner as curves derived from continuous indicators? In a Monte Carlo demonstration, Miller (1996) showed that dichotomous indicator MAXCOV curves calculated from dimensional data are not flat. The

<sup>3</sup>The present study diverges from the tradition of smoothing MAXCOV curves. Whereas continuous indicator curves may contain many covariance points, dichotomous indicator curves contain few. With few points, any smoothing procedure begins to flatten severely—rather than simply smooth—a curve, weighting endpoints too heavily into more central covariance values and potentially masking a taxonic peak. This is particularly problematic with iterative smoothing procedures, such as Tukey's "3RH, twice" method, which has been used extensively in previous taxometric research. Especially when curves are averaged, there remains little need for smoothing. Therefore, only "raw" curves are used in this study.

troubling implication is that these curves could be misinterpreted as evidence of taxonic structure. However, Miller did not provide a corresponding set of curves for taxonic data, making it difficult to judge whether a reliable difference in curve shape exists across latent structures. Compounding this problem, Miller—like researchers who have conducted taxometric investigations—did not provide a rationale for his scaling of the ordinate axis. The rounded hump that Miller obtained would be stretched into a tall, peaked curve if an inappropriately small ordinate scale was chosen. Whereas Miller's note raises the possibility of pseudotaxonic results, there is one series of studies in which a taxonic solution uncovered in MAXCOV analyses using dichotomous indicators (Lenzenweger & Korfine, 1992; Korfine & Lenzenweger, 1995) was corroborated using continuous indicators (Lenzenweger, 1999). Although this provides no general assurance of the trustworthiness of the modified MAXCOV procedure, that modification may be useful when the procedure is carried out—and the results are interpreted—by an informed taxometrician exercising due caution.

Second, how does the modified MAXCOV procedure perform under a variety of conditions? Given the loss of information inherent in dichotomization and the instability of covariance estimates based on dichotomous variables, it is imperative that we understand the effects of factors such as sample size, base rate, and indicator separation on dichotomous indicator MAXCOV curves.

Third, what additional tests may be used to evaluate conjectures of taxonicity with dichotomous indicators? Taxometric investigations depend heavily on the convergence of results, and consistency tests provide essential tools for the corroboration or refutation of latent structures.

#### *The Monte Carlo Procedure*

The guiding questions outlined above were addressed via a Monte Carlo investigation by matching the variance-covariance matrices of taxonic and dimensional samples that each contained eight continuously distributed variables, following the procedure described by Meehl and Yonce (1994, 1996), dichotomizing these variables,<sup>4</sup> and performing the modified MAXCOV procedure on the manifestly dichotomous indicators.

<sup>4</sup>To dichotomize the indicators, cases were sorted and cut according to an average endorsement rate which, to simulate research data, was pulled from .50 toward the base rate. For all analyses presented here, the average endorsement rate was set at .80 times the size of the taxon plus .20 times the size of the complement, e.g., for a base rate of .10, average endorsement rate =  $.80 \times .10 + .20 \times .90$ , or .26. For dimensional samples, the base-rate equivalent of the latent interitem correlation was used for this calculation. (In previous analyses, different methods of dichotomizing the indicators yielded qualitatively similar results.) To avoid the possibility of detecting pseudotaxa based on a "bunching" of endorsement rates (Grayson, 1987), they were spread using increments of  $-.10, -.07, -.04, -.01, +.01, +.04, +.07$ , and  $+.10$ , e.g., for a base rate of .10, the eight indicators were dichotomized such that endorsement rates equaled .16, .19, .22, .25, .27, .30, .33, and .36.

To generate MAXCOV curves, each possible pair of indicators was removed, in turn, and the remaining six indicators were summed to create a 7-point input scale ranging in value from 0 to 6. The covariance of the two output indicators was calculated at each value of the input but set to zero when too few cases (<12) were present to permit reliable estimation.<sup>5</sup> This procedure was repeated for each pair of output indicators. The results were combined to produce one MAXCOV curve by plotting the median covariance value at each point, thereby minimizing the influence of outliers. This MAXCOV curve was used to compute an estimate of the base rate of taxon members in the sample (see formulae in Meehl & Yonce, 1996).

The final step was to carry out a case removal consistency test, the logic of which is simply that, if an estimate of the base rate of taxon membership denotes a latent parameter, it should be altered in a predictable manner by the systematic removal of cases. To maximize the expected change in base-rate estimates between the full and the reduced sample, cases were removed (on the basis of their total scores on all indicators) from that end of the distribution containing the smaller putative latent class (taxon or complement). Removing cases from the larger latent class would effect less change in the expected base rates of the reduced sample. Trial and error indicated that the removal of one quartile of cases balanced two competing demands reasonably well. It removed a sufficient proportion of cases such that a significant change in base rate was expected but did not remove so many cases that the remaining sample size prohibited subsequent taxometric analysis.

A reasonable expected value for a reduced-sample base-rate estimate can readily be calculated. Suppose that the full-sample base-rate estimate was .40 (40 taxon members out of every 100 cases). Removal of the upper quartile (mostly taxon members) would result in a new sample containing about 15 (40 - 25) taxon members out of every 75 (100 - 25) cases, yielding a new base rate of .20.<sup>6</sup> In the event that the removal of a full quartile of

<sup>5</sup>Setting covariances to zero—rather than omitting them—when too few cases were available for reliable estimation prevented severe errors when later estimating the taxon base rate from the MAXCOV curve. By simply omitting covariances within small-*n* intervals, the median covariance would have been based on a handful of estimates whose sample sizes barely exceeded the allowed minimum. In early testing, this frequently caused spurious spikes to emerge at the ends of the MAXCOV curves. Particularly in the case of positive spikes, this dramatically affected the estimate of the taxon base rate, which is a crucial parameter for drawing inferences of latent structure. In contrast, setting the unstable covariances to zero removed these spikes without otherwise compromising the interpretability of the MAXCOV curves. A low covariance value in one interval cannot create a spurious peak in another interval. Moreover, when there are so few cases in an interval, its covariance will have a negligible effect on the estimation of the taxon base rate.

<sup>6</sup>To the extent that the latent classes are poorly separated, this expected base rate will be too extreme because some of the 25 cases in the upper quartile would be complement members. Unfortunately, in the context of a taxometric investigation one does not know for certain that there are in fact latent classes, much less the precise extent of their separation. Thus, one should bear in mind the potential for bias in this estimate even if its magnitude cannot be determined.

cases would have pushed the expected base rate of the reduced sample below .10 or above .90, a smaller number of cases was removed such that the expected base rate would equal .10 or .90.

The design of this Monte Carlo study was factorial, systematically varying three parameters: sample size, base rate, and the separation between latent classes. The levels of each factor were chosen to afford comparisons with the Monte Carlo work of Meehl and Yonce (1994, 1996) and to explore the boundary conditions under which dichotomous indicator MAXCOV analyses are effective. The simulations therefore included sample sizes of 200, 300, 600, 1,000, and 1,500 cases; taxon base rates of .50, .25, and .10; and separations of 2.00, 1.75, 1.50, 1.25, and 1.00 within-group standard deviations. Within each factorial combination, 100 taxonic and 100 dimensional samples were generated and analyzed.

#### *Monte Carlo Results*

With regard to the first of the three critical questions raised above, it appears that MAXCOV results *can* help to differentiate taxonic and dimensional latent structures when dichotomous indicators are used. Fig. 1 displays the MAXCOV curves and base-rate estimates for the first three taxonic samples of  $N=1,500$ , base rate = .50, and  $2.00\sigma$  separation and the first three corresponding dimensional samples ( $N=1,500$ ,  $r_{xy} = .50$ ). Even at a glance, one can readily see the striking difference between the MAXCOV curves for taxonic and dimensional samples. Consistent with continuous indicator analyses, taxonic samples yielded centrally located peaks that tapered toward zero at the endpoints. Consistent with Miller's (1996) findings, dimensional data tended to yield low, smooth, humped curves whose endpoints did not reach zero.

Two quantitative indices of taxonicity were further evaluated, (a) covariance peaks and (b) discrepancies between expected and observed reduced-sample base-rate estimates. The average covariance peak of all 100 taxonic samples with the parameters of those shown in Fig. 1 was quite high ( $M = .11$ ,  $SD = .01$ ), and reduced-sample base-rate estimates were in good accord with expectations, as all 100 reduced-sample base-rate estimates fell within .01 of the expected value. The average covariance peak of all 100 dimensional comparison samples was fairly low ( $M = .03$ ,  $SD = .01$ ), and there was not a single case of impressive agreement between expected and observed reduced-sample base-rate estimates; discrepancies ranged from .06 to .44 ( $M = .23$ ).

These analyses suggest that the MAXCOV procedure can be effectively adapted for use with dichotomous indicators. Because the number of samples generated across all cells in the factorial design prohibits a comprehensive display of MAXCOV curves, results are presented solely in terms of the

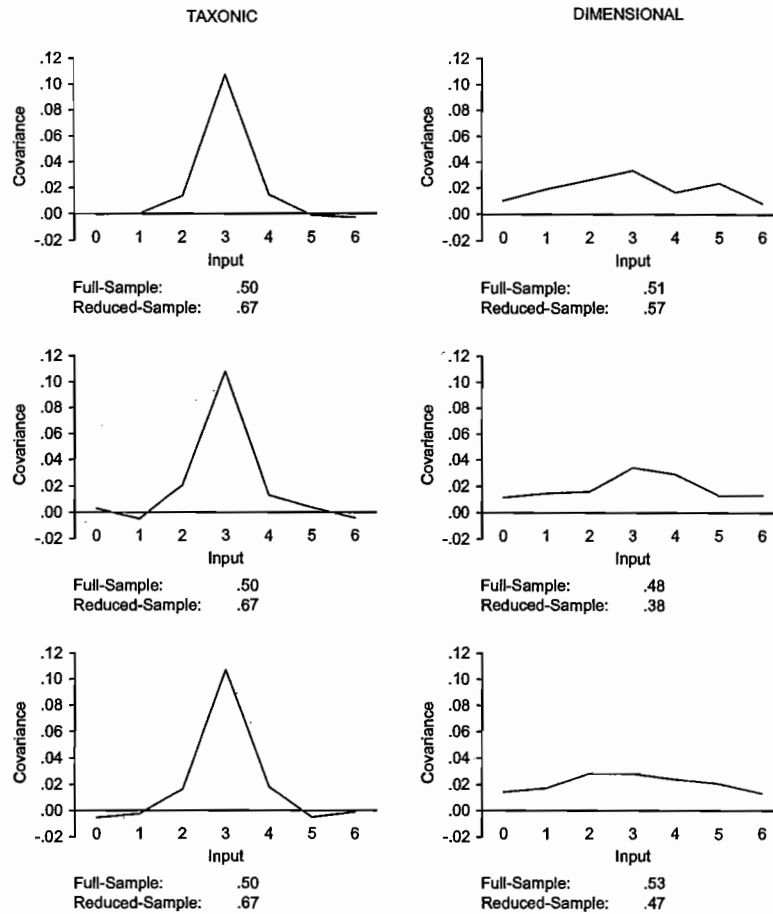


FIG. 1. MAXCOV curves for the first three taxonic samples (left;  $N=1,500$ , base rate = .50,  $2.00\sigma$  separation) and the first three corresponding dimensional samples (right;  $N=1,500$ ,  $\bar{r}_{xy} = .50$ ). Below each graph, the full-sample and reduced-sample base-rate estimates are listed.

quantitative indices of covariance peak and reduced-sample base-rate estimate consistency. Covariance peaks in excess of .05 were scored as consistent with taxonicity, as were agreements within .05 between expected and observed base-rate estimates. These cutoff values—identical sheerly by coincidence—were determined through an iterative process combining analytical considerations and a prudent eyeballing of results. Although strict cutoffs were implemented here to afford quantitative comparisons across study conditions, researchers are encouraged to use these as guidelines flexibly to assist their evaluation of results. In applied taxometric work, a principled argu-

ment based on the consistency with which all evidence supports one latent structure over another is far preferable to the reification of arbitrary cutoff values that mechanize interpretations.

TABLE 1  
PROPORTION OF TAXONIC (DIMENSIONAL) SAMPLES WITH COVARIANCE PEAK  $> .50$  AND  
REDUCED-SAMPLE BASE-RATE ESTIMATE WITHIN  $.05$  OF EXPECTED VALUE

Base Rate Separation		$N=200$	$N=300$	$N=600$	$N=1,000$	$N=1,500$
.50	$2.00\sigma$	.17 (.33)	.83 (.27)	.98 (.14)	.99 (.04)	1.00 (.00)
.50	$1.75\sigma$	.82 (.25)	.97 (.12)	.98 (.05)	.98 (.02)	1.00 (.01)
.50	$1.50\sigma$	.89 (.21)	.87 (.07)	.88 (.01)	.90 (.01)	.90 (.00)
.50	$1.25\sigma$	.57 (.05)	.51 (.03)	.60 (.03)	.60 (.01)	.57 (.00)
.50	$1.00\sigma$	.30 (.07)	.20 (.07)	.13 (.03)	.09 (.00)	.04 (.00)
.25	$2.00\sigma$	.15 (.14)	.61 (.16)	1.00 (.06)	1.00 (.03)	1.00 (.00)
.25	$1.75\sigma$	.46 (.13)	.86 (.13)	.99 (.06)	.98 (.00)	.99 (.02)
.25	$1.50\sigma$	.50 (.19)	.69 (.15)	.78 (.10)	.81 (.04)	.80 (.03)
.25	$1.25\sigma$	.31 (.14)	.42 (.13)	.33 (.06)	.19 (.04)	.22 (.03)
.25	$1.00\sigma$	.23 (.13)	.22 (.14)	.17 (.14)	.08 (.10)	.05 (.07)
.10	$2.00\sigma$	.03 (.15)	.11 (.19)	.95 (.31)	1.00 (.21)	1.00 (.05)
.10	$1.75\sigma$	.24 (.10)	.38 (.21)	.98 (.18)	.96 (.21)	.99 (.14)
.10	$1.50\sigma$	.35 (.08)	.67 (.24)	.91 (.10)	.81 (.22)	.83 (.16)
.10	$1.25\sigma$	.19 (.01)	.51 (.11)	.71 (.06)	.51 (.07)	.47 (.03)
.10	$1.00\sigma$	.19 (.07)	.31 (.18)	.27 (.04)	.25 (.04)	.13 (.01)

Table 1 shows the proportions of taxonic and dimensional samples passing both covariance peak and case removal consistency test thresholds. These results suggest two boundary conditions for acceptable MAXCOV performance. First, regardless of other parameters, MAXCOV performed poorly with indicator separations of  $1.25\sigma$  or less. Second, sample size set a limit on the extremity of the base rates detected. With samples as small as 300 cases, results with base rates of .50 were arguably quite satisfactory: false positive and false negative error rates were nearly all below 20%, and most were below 10%. To achieve comparable results for base rates as extreme as .10, however, the requisite sample size appeared to be closer to 600 cases. To provide a sense for what results may look like under suboptimal—but satisfactory—conditions, Fig. 2 displays the MAXCOV curves and base-rate estimates for the first three taxonic samples of  $N=600$ , base rate = .25, and  $1.50\sigma$  separation and the first three corresponding dimensional samples ( $N=600$ ,  $\bar{r}_{xy} = .30$ ). The contrast between taxonic and dimensional latent structures is still apparent, although less stark than in Fig. 1. Moreover, by the quantitative tests of taxonicity used in this study, only two samples of the three for each latent structure are correctly classified. The middle taxonic curve fails a test (its reduced-sample base rate fails to drop sufficiently) and the middle dimensional curve passes both tests (it exceeds a height of

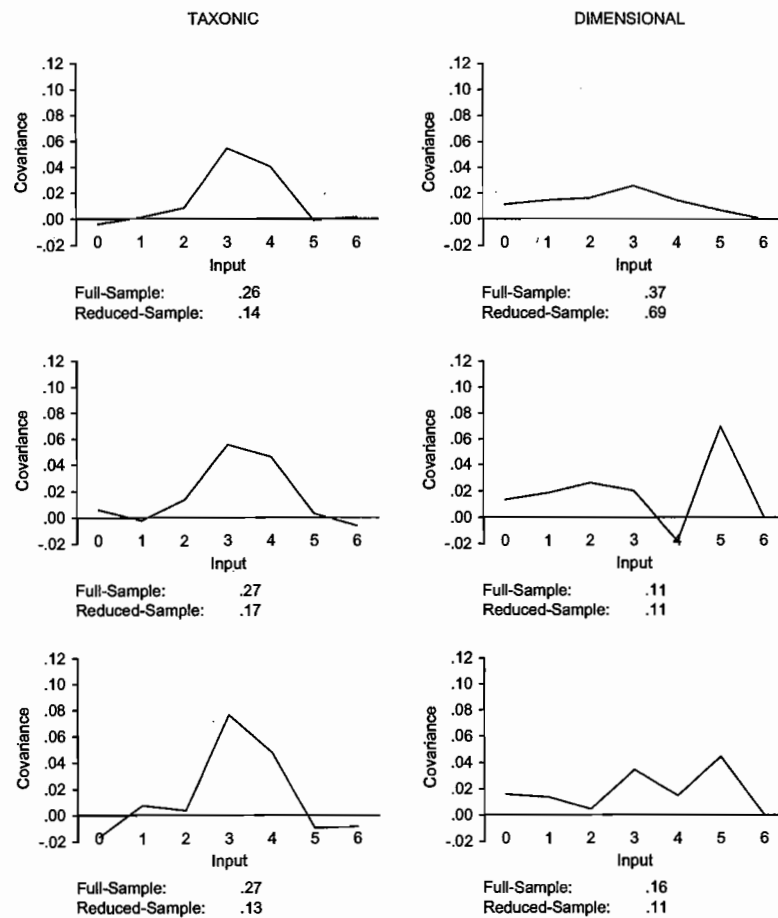


FIG. 2. MAXCOV curves for the first three taxonic samples (left;  $N=600$ , base rate = .25,  $1.50\sigma$  separation) and the first three corresponding dimensional samples (right;  $N=600$ ,  $\bar{r}_{xy} = .30$ ). Below each graph, the full-sample and reduced-sample base-rate estimates are listed.

.05 and, because its base rate was so low to begin with, its reduced sample base rate is consistent with expectations). This underscores the need for more flexible interpretation and, especially, for the evaluation of consistency across multiple tests.

#### DISCUSSION

The Monte Carlo investigation presented above, based on a wide array of parameters encountered in research, showed that the modified MAXCOV procedure—accompanied by a case-removal consistency test—can be used to



uncover latent structure. Thus, despite skepticism regarding its utility, the present investigation supports the use of MAXCOV even when only dichotomous indicators are available.

The finding that the modified MAXCOV procedure can be used to distinguish between taxonic and dimensional latent structures does not, however, represent an unconditional green light to researchers planning to dichotomize items before submitting them to taxometric analyses. Whenever data *need not* be dichotomized, they *should not* be. If a potential indicator contains sufficient variation such that it can be divided into intervals and used as an input indicator, there is no reason to dichotomize it. In cases where individual items cannot be used continuously, there are many alternatives to dichotomization. For example, items on the Beck Depression Inventory, which range in value from 0 to 3, can be summed in pairs to create 7-point indicators, merged into larger composites, or removed in pairs as output indicators with all remaining items summed to form input indicators (see Ruscio & Ruscio, in press). The modified MAXCOV procedure outlined here is perhaps best viewed as a last-resort approach, useful when only inherently dichotomous indicators are available for analysis and there are too few such indicators available to create composites.

There are notable similarities and differences between the present results, the results of Monte Carlo trials with continuous indicators (Meehl & Yonce, 1996), and the advice that Meehl (1995) has offered based on decades of work on the taxometric method. The degradation in clarity of results uncovered in the present study under unfavorable parameter conditions, e.g., smaller sample sizes, more extreme base rates, lower separations, is predictable from sampling theory and parallels the findings obtained by Meehl and Yonce (1996). However, whereas Meehl (1995) advocated samples of no less than 300 cases and at least  $1.25\sigma$  separation, more stringent requirements seem warranted if dichotomous indicators are employed. A safer rule of thumb for the modified MAXCOV procedure might be a sample containing no less than 600 cases and indicators that achieve at least  $1.50\sigma$  of separation (at the latent level).

The case-removal consistency test presented and evaluated here is similar to what Meehl and Yonce (1994) proposed and relies on the same logic. If latent taxa exist, reanalysis following the targeted removal of cases should yield predictable results. The present consistency test involved removing cases from the *smaller* of the putative latent classes to effect the most sizable change in expected base rates for a given reduction in sample size. Although this works well when the initial taxon base-rate estimate is moderate, e.g., within the .25 to .75 range, it is not feasible when that estimate is more extreme, e.g., closer to 0 or to 1, because one simply cannot remove many cases from the smaller latent class. Thus, in the event of an extreme base-

rate estimate it seems wise to follow Meehl and Yonce's advice by removing a random subset of cases from the *larger* latent class to construct a sample whose new base rates are expected to be equal. This approach will require a particularly large sample.

In light of the results of the present findings, prior taxometric investigations that have included dichotomous indicator MAXCOV analyses warrant a careful reconsideration. Given that dimensional data *do not* yield the flat curve expected by researchers using the modified MAXCOV procedure and that scaling of the ordinate axis (as well as the aspect ratio) has been somewhat haphazard,<sup>7</sup> reevaluations of past results should consider both qualitative criteria (curve shape) and the quantitative indices (covariance peak and case removal) refined here. Although case removal would require a reanalysis, the graphs reported in the literature can easily be inspected. Doing so suggests many curves have been interpreted as evidence for taxonicity that actually appear more consistent with the low peaks (covariance < .05) of dimensional data [e.g., Gangestad & Snyder, 1985, p. 327; Strube, 1989, p. 982; Haslam & Beck, 1994, p. 689 (top left); Tyrka, Cannon, Haslam, Mednick, Schulsinger, Schulsinger, & Parnas, 1995, p. 178; Oakman & Woody, 1996, p. 982 (Fig. 1)], as well as others that are consistent with the tall peaks (covariance > .05) of taxonic data [e.g., Lenzenweger & Korfine, 1992, p. 570; Harris, Rice, & Quinsey, 1994, p. 393 (panel a); Haslam, 1994, p. 71; Korfine & Lenzenweger, 1995, p. 29; Oakman & Woody, 1996, p. 982 (Fig. 2)]. Interestingly, one study contained a MAXCOV curve with a dramatic, right-end covariance peak of about .20 (Trull, Widiger, & Guthrie, 1990, p. 45)—highly consistent with a low base-rate taxon—that was interpreted as evidence of dimensionality. The reinterpretations offered here do not necessarily challenge the conclusions of studies whose MAXCOV curves might have been misjudged, as these curves were only part of the evidence on which conclusions were based in each case. Nonetheless, it should be clear that dichotomous indicator MAXCOV curves need to be interpreted with great care and accompanied by additional tests of the latent class model.

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<sup>7</sup>Computer-generated graphs typically default to a scaling that encompasses the range of observed values and little more. This (or other arbitrary scaling practices) can produce highly misleading results. For example, each of the curves for dimensional samples presented in Fig. 1 would appear peaked with an ordinate that runs only up to .04. As is discussed below, it is possible that some researchers have misinterpreted dichotomous indicator MAXCOV curves.

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