

# Taxometrics, Polytomous Constructs, and the Comparison Curve Fit Index: A Monte Carlo Analysis

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The taxometric method effectively distinguishes between dimensional (1-class) and taxonic (2-class) latent structure, but there is virtually no information on how it responds to polytomous (3-class) latent structure. A Monte Carlo analysis showed that the mean comparison curve fit index (CCFI; Ruscio, Haslam, & Ruscio, 2006) obtained with 3 taxometric procedures—mean above minus below a cut (MAMBAC), maximum covariance (MAXCOV), and latent mode factor analysis (L-Mode)—accurately identified 1-class (dimensional) and 2-class (taxonic) samples and produced taxonic results when applied to 3-class (polytomous) samples. From these results it is concluded that using the simulated data curve approach and averaging across procedures is an effective way of distinguishing between dimensional (1-class) and categorical (2 or more classes) latent structure.

*Keywords:* taxometric, polytomous data, comparison curve fit index

Interest in taxometrics has grown exponentially in recent years. In just the last decade, there has been a 514% increase in the number of peer-reviewed journal articles published on Meehl's taxometric method (Meehl & Golden, 1982).<sup>1</sup> Moreover, taxometric procedures are no longer—if, in fact, they ever were—the exclusive province of abnormal psychology. There is nothing in Meehl's (1992, 1995, 2004) writings or procedures to suggest that his approach can be applied only to the psychopathological conditions that inspired him to experiment with coherent cut kinetics and develop the taxometric method. Researchers have accordingly responded by expanding the scope of taxometric research and applying taxometric procedures to a variety of nonpathological conditions and assessment constructs. In fact, a quarter of the peer-reviewed journal articles on taxometrics in the last 2 years were published in three assessment journals: *Psychological Assessment*, *Assessment*, and *Journal of Personality Assessment*. Taxometrics have been used to assess the latent structure of perfectionism (Broman-Fulks, Hill, & Green, 2008), marital discord (Whisman, Beach, & Snyder, 2008), disgust sensitivity (Olatunji & Broman-Fulks, 2007), and exaggerated health complaints (Walters, Berry, Lanyon, & Murphy, 2009). It is all the more

important, then, that we understand the strengths and weaknesses of this relatively new and increasingly popular approach for assessing the latent structure of psychological constructs.

The taxometric method is designed to distinguish between continuous and discontinuous structure but can assess only one taxonic boundary at a time. Accordingly, problems may arise when polytomous (three or more ordered classes) constructs are evaluated with the taxometric method. In the assessment field there are several plausible polytomous constructs that could potentially work their way into a taxometric analysis and give false or misleading results. Consider, for example, Moffitt's (1993) life-course-persistent/adolescence-limited/nondelinquent taxonomy. Assuming that this putative three-class typology exists, it could have a profound effect on taxometric research conducted on criminal justice or developmental psychopathology topics. Depending on whether polytomous constructs yield taxonic, dimensional, or ambiguous results they could produce pseudodimensional, pseudotaxonic, or indeterminate findings in a study on delinquency. This is a situation that could be made even more complicated by nonlinear and interactive forces that alter the latent structure patterns of polytomous constructs on the basis various sample or indicator characteristics. Major depression has generated inconsistent results in several taxometric studies based, in part, on sample (clinical vs. analogue) and indicator (self-report vs. rating scale) variations (Beach & Amir, 2003; Ruscio, Ruscio, & Kean, 2004; Solomon, Ruscio, Seeley, & Lewinsohn, 2006). Perhaps

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The assertions and opinions contained herein are the private views of the authors and should not be construed as official or as reflecting the views of the Federal Bureau of Prisons or the United States Department of Justice. Taxometric graphs not included in this article are available upon request.

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<sup>1</sup> A search of the PsycINFO database on April 4, 2009 uncovered 36 peer-reviewed journal articles published between 2006 and 2008 in which the terms *taxometric* or *taxometrics* were included in the title, abstract, or keyword section, compared to seven peer-reviewed journal articles published between 1996 and 1998.

these inconsistent findings are the result of an underlying three-class structure involving bipolar disorder, unipolar endogenous/melancholic depression, and unipolar exogenous depressive disorders.

McGrath (2008) recently subjected an ordered three-class construct to taxometric analysis using a Monte Carlo design and determined that in many cases false inferences of either dimensional or taxonic latent structure were obtained. Across the 40 Monte Carlo scenarios included in the McGrath study, inconsistency was the rule. Whereas the majority of mean above minus below a cut (MAMBAC) curves suggested dimensional latent structure, the majority of maximum covariance (MAXCOV) and maximum eigenvalue (MAXEIG) curves showed signs of a taxonic peak. The latent mode factor analysis (L-Mode) curves, on the other hand, were fairly evenly split between dimensional and taxonic latent structure. The McGrath study was limited, however, by a relatively restricted set of sample parameters and reliance on procedures (i.e., visual inspection of curve shape, base rate consistency, Bayesian probabilities, congruence between the observed variance–covariance matrix and the anticipated taxonic variance–covariance matrix as measured by the goodness-of-fit index) that have performed poorly in Monte Carlo research (Haslam & Cleland, 2002; Ruscio, 2007).

Two inferential frameworks guide taxometric research. First, there is the traditional method (Meehl, 1995, 2004; Meehl & Yonce, 1994, 1996; Waller & Meehl, 1998) in which the primary goal is the detection of taxonic structure. This approach treats dimensional structure essentially as the null hypothesis, taxonic structure as the alternative hypothesis, and failure to reject the null hypothesis as evidence of nontaxonic structure. Then, there is the competing hypotheses approach, which treats taxonic and dimensional latent structure as equally viable possibilities and bases its conclusions on the relative fit of the research data to the two models (Ruscio & Kaczetow, 2009; Ruscio, Ruscio, & Meron, 2007). The former approach would tend to treat indeterminate results as evidence of dimensional structure, so that polytomous data should tend to support the null hypothesis. Any one of three possibilities, however, might be consistent with the views of someone affiliated with the competing hypotheses approach. First, polytomous constructs could be interpreted as evidence of dimensional structure (De Boeck, Wilson, & Acton, 2005), perhaps because multiple categories are interpreted as points along a dimension. Second, polytomous constructs could produce category-like taxometric results (De Boeck et al., 2005) given the taxometric procedure's sensitivity to taxonic boundaries, even when there is more than one. Finally, polytomous constructs could produce ambiguous taxometric results to the extent that they fit neither the taxonic nor dimensional models.

The comparison curve approach has recently emerged as an important tool for decision-making from the competing hypotheses perspective on taxometric analysis. The relative fit between an observed data curve and simulated data curves derived using taxonic and dimensional structure is quantified in the comparison curve fit index (CCFI; Ruscio, Haslam, & Ruscio, 2006). CCFI scores range from 0 to 1, with scores above .50 indicating better fit between the data curve and simulated taxonic curve and scores below .50 indicating better fit between the data curve and simulated dimensional curve. The CCFI can be calculated for all three primary taxometric procedures (MAMBAC, MAXCOV/MAXEIG,

and L-Mode) and the results averaged (Ruscio & Kaczetow, 2009; Ruscio et al., 2007). Ruscio, Walters, Marcus, and Kaczetow (2010) recommended that taxometric researchers use an indeterminate category, either .45 to .55 or .40 to .60, to avoid interpreting ambiguous results as evidence of a taxon or dimension. Use of an indeterminate category improved the accuracy of the mean CCFI from 98.0% to 99.4% (.45 to .55 indeterminate) and 99.9% (.40 to .60 indeterminate) but at the cost of 5% (.45 to .55 indeterminate) to 14% (.40 to .60 indeterminate) unclassified cases (Ruscio et al., 2010). The CCFI is the most empirically supported objective measure of latent structure currently available for use with the taxometric method. As such, its use should make it possible to determine whether polytomous constructs generate taxonic, dimensional, or indeterminate results.

The principal goal of this study was to examine the effect of a three-class ordered polytomous construct on an objective estimate of latent structure (CCFI) measured using three different taxometric procedures (MAMBAC, MAXCOV, and L-Mode) for the purpose of determining what to expect if polytomous (three or more classes) data are unintentionally entered into a taxometric analysis. To do this, a large Monte Carlo analysis was performed using three latent structures: a one-class (dimensional) condition, a two-class (taxonic) condition, and a three-class (polytomous) condition. From this point forward, dimensional, taxonic, and polytomous structure are referred to as one-class, two-class, and three-class, respectively. It was hypothesized that the CCFI would consistently fall below .50 (single threshold), .45 (narrow dual thresholds), and .40 (broad dual thresholds) in the one-class samples and consistently rise above .50 (single threshold), .55 (narrow dual thresholds), and .60 (broad dual thresholds) in the two-class samples. From the mixed and inconsistent results obtained by McGrath (2008) it was possible that three-class samples would produce ambiguous CCFI results (.45 to .55 or .40 to .60), although values consistent with one-class or two-class structure could also arise depending on certain characteristics of the local maxima that sometimes emerge in the distributions generated by taxometric procedures. Assuming that the polytomous samples produce consistent CCFI findings, a secondary objective of this study was to determine whether it is possible to distinguish between three-class samples and samples with genuine two-class (in the event three-class data yield taxonic outcomes), genuine one-class (in the event three-class data yield dimensional outcomes), or genuine indeterminate (in the event three-class data yield indeterminate outcomes) structure.

## Method

### Dataset Generation

All datasets were created using the iterative algorithm described by Ruscio and Kaczetow (2008), which can be used to produce datasets that vary in their sample size, the number of indicators, the target correlation between the indicators, the asymmetry in the indicator distributions, and the relative weighting of the tails of the distributions. This algorithm was used to form one-class (dimensional), two-class (taxonic), and three-class (polytomous) datasets for this study. Parameters for the datasets were randomly sampled from uniform distributions for sample size ( $N = 300$ – $1,000$ ), asymmetry ( $g = .00$ – $.30$ ), and tail weight ( $h = .00$ – $.15$ ).

Discontinuous datasets were generated by creating two (for two-class) or three (for three-class) subsamples such that the total  $N$  across subsamples matched the randomly selected value for the dataset. Additional parameters were based on uniform random distributions for the base rate used for the two- and three-class groups (two-class:  $p = .10-.50$ ; three-class:  $P1 = P2 = .10-.33$ ), mean separation between adjoining classes ( $d = 1.25-2.00$ ), level of within-subsample correlation ( $r_{wg} = .00-.30$ ), and the taxon: complement variance ratio ( $VR = 1-4$ , integers only). Two-class datasets were generated by combining the two subsamples after setting the mean for the taxon subsample to achieve the desired  $d$  value when compared with the complement subsample and increasing the variance of the taxon group to match  $VR$ . Three-class datasets were generated by increasing the mean for the first taxon subsample to achieve the desired  $d$  value when compared with the complement subsample, setting the mean of the second taxon subsample to achieve twice the desired  $d$  value, and setting the variance of both taxon groups to equal  $VR$ .

The one-class dataset was created using some of the same parameters as the two- and three-class datasets with the exceptions being those that are irrelevant to the construction of one-class samples (i.e.,  $P$ ,  $d$ ,  $r$ , and  $VR$ ). In their place correlations between indicators were randomly sampled from a range of values ( $r_{xy} = .10-.65$ ). Crossing the three structural conditions (one-class, two-class, three-class) with three different numbers of indicators (four, five, six) yielded nine different structure-indicator combinations. Five hundred datasets were generated for each of the nine combinations to produce 4,500 samples: 1,500 dimensional samples, 1,500 taxonic samples, and 1,500 polytomous samples.

A subgroup of samples was identified for follow-up analysis to address the possibility that CCFI scores for the three-class dataset might yield consistent dimensional or taxonic results. Every 20th one-class (dimensional) sample, every 20th two-class (taxonic) sample, and every 20th three-class (polytomous) sample was selected for possible inclusion in the follow-up analyses. Hence, if the three-class dataset produced consistent dimensional results, the 75 preselected one-class samples and the 75 preselected three-class samples would be compared. Likewise, if the three-class dataset produced consistent taxonic results, the 75 preselected two-class samples and the 75 preselected three-class samples would be compared.

## Taxometric Analyses

Three taxometric procedures were included in the current investigation: mean above minus below a cut (MAMBAC; Meehl & Yonce, 1994), maximum covariance (MAXCOV; Meehl & Yonce, 1996), and latent mode factor analysis (L-Mode; Waller & Meehl, 1998). Each procedure was calculated using Ruscio's (2009b) taxometric program for R language. MAMBAC arranges the input indicator along the  $x$ -axis and then plots mean differences on the output indicator for scores falling above and below a series of evenly spaced cuts (50 in the present study). A peak or bump on the MAMBAC curve suggests the presence of a taxon, whereas a concave or dish-shaped curve is more consistent with dimensional latent structure (Meehl & Yonce, 1994). Indicators were arranged in all possible two-variable combinations to create 12 to 30 individual curves, depending on the number of indicators, which were then averaged and compared to simulated taxonic and dimensional

datasets. Cases were assigned to the taxon and complement groups for the purpose of generating simulated data using the base rate classification procedure built into the MAMBAC program.

After arranging the input indicator along the  $x$ -axis, MAXCOV computes the covariance between two output indicators in equally sized subgroups of the input indicator. Subgroups for this study were formed using 50 sliding windows with 90% overlap. A peak on the MAXCOV curve is normally indicative of a taxon, whereas a relatively flat or nonpeaked curve suggests the presence of a dimension (Meehl & Yonce, 1996). MAXCOV was implemented using all possible indicator triplets (one indicator serving as the input and two indicators serving as the output). With four to six indicators, traditional MAXCOV will produce 12 to 60 individual curves, although the mean curve was the principal focus of the current investigation. Cases were assigned to the taxon and complement groups using the base rate classification procedure.

L-Mode calculates scores on the first (and largest) principal factor of the indicators and then plots the distribution of scores on this single latent factor using Bartlett's (1937) weighted least squares method. A bimodal or double-humped L-Mode curve generally suggests the presence of a taxon or discontinuity in the distribution, whereas a unimodal or single-humped L-Mode curve suggests a dimension or continuity in the distribution. That said, taxa have been known to generate unimodal patterns, and bimodal configurations have sometimes been observed in dimensional data (Waller & Meehl, 1998). McGrath (2008) observed trimodal L-Mode curves in several three-class samples in his small-scale Monte Carlo analysis. The L-Mode procedure generates a taxon base rate by averaging base rate estimates calculated from the locations of the latent modes.

Simulated taxonic and dimensional datasets were created for MAMBAC, MAXCOV, and L-Mode using a bootstrapping technique (10 simulated datasets for taxonic structure and 10 simulated datasets for dimensional structure) that samples with replacement and reproduces the unique distributional and correlational characteristics of the data (Ruscio & Kaczetow, 2009; Ruscio et al., 2007). The CCFI is the ratio of the root-mean-square residual (RMSR) of fit between the data graph and simulated dimensional graph to the sum of the RMSR of fit between the data graph and simulated dimensional graph and the RMSR of fit between the data graph and simulated taxonic graph:  $RMSR_{Dim}/(RMSR_{Dim} + RMSR_{Tax})$ . Whereas CCFI values above .5 (to a maximum of 1) are consistent with taxonic latent structure, values below .5 (to a minimum of 0) are consistent with dimensional latent structure, and values around .5 are ambiguous. The accuracy of the CCFI has been established through Monte Carlo research (Ruscio, 2007; Ruscio & Marcus, 2007; Ruscio et al., 2007, 2010; Walters & Ruscio, 2009).

## Results

Table 1 lists the percentages of one-class, two-class, and three-class samples achieving CCFIs above and below .500 (first column), above .549 and below .450 (second column), and above .599 and below .400 (third column). Consistent with prior research (Ruscio, 2007; Ruscio et al., 2007, 2010), the CCFIs of the individual procedures achieved at least 85% accuracy without an indeterminate category and at least 95% accuracy with an indeterminate category. The mean CCFI for the three procedures, as in

Table 1  
Proportion of CCFI Values in the Single and Dual Threshold Categories

Dataset	Single threshold		Narrow dual threshold			Broad dual threshold		
	<.500	>.500	<.450	.450-.549	>.550	<.400	.400-.599	>.600
MAMBAC								
One-class	92.6	7.4	86.4	9.3	4.3	75.9	21.9	2.1
Two-class	0.3	99.7	0.1	0.1	99.7	0.1	0.5	99.5
Three-class	0.0	100.0	0.0	0.0	100.0	0.0	0.0	100.0
MAXCOV								
One-class	96.4	3.6	91.3	7.2	1.5	81.9	17.7	0.3
Two-class	7.4	92.6	4.2	8.4	87.4	1.6	16.7	81.7
Three-class	9.5	90.5	2.3	19.6	78.1	0.3	39.9	59.8
L-Mode								
One-class	99.0	1.0	97.5	2.1	0.5	95.2	4.7	0.1
Two-class	13.7	86.3	7.1	18.1	74.7	3.3	40.7	56.0
Three-class	0.9	99.1	0.1	6.5	93.4	0.0	21.1	78.9
Mean								
One-class	99.9	0.1	98.3	1.7	0.0	93.7	6.3	0.0
Two-class	1.0	99.0	0.5	3.2	96.3	0.1	8.9	90.9
Three-class	0.0	100.0	0.0	0.0	100.0	0.0	1.1	98.9

Note. Numbers directly under each heading are comparison curve fit index (CCFI) values. Numbers in the columns of the table are percentages; each percentage is based on 1,500 samples. MAMBAC = mean above minus below a cut; MAXCOV = maximum covariance; L-Mode = latent mode factor analysis; mean = average of the three procedures; one-class = dimensional; two-class = taxonic; three-class = polytomous.

past studies, attained an accuracy level in excess of 99%. Whereas the one-class samples consistently achieved markedly lower CCFI scores than samples with two- and three-class structure, the two-class samples produced CCFI results that were largely indistinguishable from the CCFI results obtained with the three-class samples.

Of the 75 three-class and 75 two-class samples preselected for follow-up analysis, the 40 taxon-leaning (CCFI  $\geq .500$ ) three-class and 40 taxon-learning two-class samples with the largest  $N$ s were subjected to Ruscio and Ruscio's (2004b) two-step procedure. Using the base rate classification technique, each sample was divided into a taxon and complement according to the mean taxon base rate for MAMBAC, MAXCOV, and L-Mode.<sup>2</sup> A follow-up (Step 2) taxometric analysis was then performed on the taxonic group from the original (Step 1) analysis, defined by ranking individuals according to the size of their summed score across indicators and assigning them to the taxon group until the proportion of cases matched the mean base rate estimate. This summative procedure has been found to be superior to other methods involving Bayesian classification of cases (Ruscio, 2009a). The results, as outlined in Table 2, indicate good sensitivity (i.e., identifying subtaxa in the three-class samples) but weak specificity (i.e., identifying subtaxa in the two-class samples as well).

Further analysis of the 80 two- and three-class samples revealed a significant positive correlation between the true size of the first step taxon ( $n_t$ ) and the accuracy of the mean CCFI ( $r = .29, p < .01$ ) and a significant negative correlation between the true-estimated taxon base rate discrepancy ( $P - P_{est}$ ) and the accuracy of the mean CCFI ( $r = -.42, p < .001$ ). There was also evidence that inaccurate three-class second step results occurred more often when the first step taxon base rate was underestimated (thus creating a pseudodimension by excluding some of the lower scoring taxon members from the Step 2 analysis), whereas inaccurate two-class second step results occurred more often when the first

step taxon base rate was overestimated (thus creating a pseudotaxon by including some of the higher scoring complement members in the Step 2 analysis).

Three different base rate estimates were used to approximate the Step 1 taxon base rate: a conservative estimate (MAXCOV), a liberal estimate (L-Mode), and an intermediate estimate (average of MAMBAC, MAXCOV, and L-Mode). Because the L-Mode base rates were twice as high as the MAXCOV base rates, with the averaged base rates falling in between, the estimated first step  $n_t$  (taxon sample size) was set at 250 or more for the MAXCOV base rates, 500 or more for the L-Mode base rates, and 375 for the average base rates. Analyses revealed that the CCFI was most effective in identifying Step 2 taxa in three-class structures when samples were selected using L-Mode base rates, that the CCFI was most effective in identifying Step 2 dimensions in two-class structures when samples were selected using MAXCOV base rates, and that the best overall results were achieved with the MAXCOV base rates (see Table 3).

Qualitative analysis of taxometric results is ordinarily discouraged because it can be unreliable and overly subjective. An interesting qualitative effect did surface, nonetheless, when the L-Mode curves were visually inspected. A pattern of three convex curves with deflection downward on either side separated by two concave curves with deflection upward on either side was observed in several curves. This trimodal pattern, referred to as the "Halloween ghost," was considered a marker of three-class structure by McGrath (2008). Whereas 10 out of 40 (25%) three-class L-Mode curves displayed this pattern, none of the 40 two-class L-Mode

<sup>2</sup> In the full complement of 80 two- and three-class samples the mean taxon base rate calculated across the three procedures ( $P_{est}$ ) was more similar, on average, to the actual taxon base rate than the base rate for any single procedure or combination of two procedures.

Table 2  
Results of a Step 2 Analysis of the Step 1 Taxonic Group in Three- and Two-Class Samples

Procedure	Three-class sample					Two-class sample					$\eta^2$
	<i>M</i>	<i>SD</i>	>.500	>.550	>.600	<i>M</i>	<i>SD</i>	>.500	>.550	>.600	
MAMBAC	.703	.180	82.5	86.1 (10.0)	94.4 (10.0)	.494	.202	57.5	52.9 (15.0)	50.0 (25.0)	.237
MAXCOV	.652	.106	92.5	94.8 (12.5)	96.7 (25.0)	.549	.169	72.5	73.5 (15.0)	70.0 (25.0)	.120
L-Mode	.634	.134	77.5	90.0 (25.0)	100.0 (42.5)	.459	.119	30.0	42.8 (22.5)	30.8 (67.5)	.331
Mean CCFI	.663	.114	87.5	94.3 (12.5)	96.8 (22.5)	.501	.137	60.0	52.0 (37.5)	55.0 (50.0)	.302

Note. MAMBAC = mean above minus below a cut; MAXCOV = maximum covariance; L-Mode = latent mode factor analysis; Mean CCFI = average of three procedures for the comparison curve fit index; >.500 = proportion of samples with CCFI scores equal to or greater than .500 (single threshold criterion); >.550 = proportion of samples out of all nonambiguous samples with CCFI scores equal to or greater than .550 (narrow dual threshold criterion; with number in parentheses representing the proportion of cases where the CCFI fell between .450 and .549); >.600 = proportion of three-class samples out of all nonambiguous samples with CCFI scores equal to or greater than .600 (broad dual threshold criterion; with number in parentheses representing the proportion of cases where the CCFI fell between .400 and .599);  $\eta^2$  = eta-squared for structure (two-class vs. three-class) in a two-way analysis of variance with indicators as the other variable (eta-squared values for indicator and for the Indicator  $\times$  Structure interaction were all <.03); each structure is represented by the 40 two-class and 40 three-class taxon-leaning (mean CCFI > .500) samples with the largest sample sizes in a group of 75 randomly selected datasets representing each structure.

curves showed evidence of trimodality. A logistic regression analysis of the 40 three-class datasets revealed that the trimodal pattern was most likely to occur when *k*, *VR*, *d*, and *h* were high and *r<sub>wg</sub>* and *g* were low. One of the trimodal patterns obtained in the current Monte Carlo study is reproduced in Figure 1.

### Discussion

As the taxometric method becomes a fixture in psychological assessment research it is imperative that we consider its strengths and weaknesses and understand the boundaries of its overall utility. A potential weakness of the taxometric method is that because it was designed to differentiate between one-class continuous (dimensional) distributions and two-class discontinuous (taxonic) distributions it may be incapable of distinguishing between one- and two-class distributions and constructs with multiple taxonic boundaries. The approach taken by the taxometric method contrasts sharply with procedures like cluster analysis and finite mixture modeling which detect latent structure in ways that allow for more than two options. On the one hand, the taxometric method's ability to identify discontinuity in a distribution accurately is one of its principal strengths. On the other hand, the

method's inability to differentiate between two- and three-class samples may be one of its principal weaknesses. This conclusion may be premature, however, in that higher order analysis using procedures like the two-step method introduced by Ruscio and Ruscio (2004b) may have value in taxometrically distinguishing between two- and three-class constructs, although the practical utility of the procedure still needs to be determined.

The results of the two-step analyses revealed that whereas a significant portion of taxa in the three-class samples partitioned into subtaxa during the second step, so did a sizeable portion of the two-class samples. When a conservative MAXCOV-generated estimate of the first step taxon base rate (*n<sub>t</sub>*) was employed, the CCFI's ability to identify two-class structure improved significantly. Of the three taxometric procedures examined in this study, L-Mode appeared to generate the strongest Step 2 effect, both qualitatively (one-quarter trimodal curves for three-class samples vs. no trimodal curves for two-class samples) and quantitatively (CCFI using the broad dual threshold criterion achieved 85% accuracy in the 80-database sample). Datasets were dichotomized according to the presence or absence of the Halloween ghost pattern in the L-Mode curve, and a logistic regression was per-

Table 3  
Results of Step 2 Analyses on the Mean CCFI Using MAXCOV, L-Mode, and Averaged Base Rate-Defined Samples

Procedure	Three-class sample						Two-class sample					
	<i>N</i>	<i>M</i>	<i>SD</i>	>.500	>.550	>.600	<i>N</i>	<i>M</i>	<i>SD</i>	>.500	>.550	>.600
MAXCOV BR > 250	22	.638	.134	77.3	88.8 (18.2)	92.8 (36.4)	12	.374	.140	25.0	20.0 (16.7)	11.1 (25.0)
L-Mode BR > 500	19	.711	.096	94.7	100.0 (5.3)	100.0 (10.5)	14	.503	.127	57.1	44.4 (35.7)	50.0 (57.1)
Average BR > 375	15	.681	.125	86.7	100.0 (20.0)	100.0 (26.7)	3	.496	.133	66.7	50.0 (33.3)	50.0 (33.3)

Note. MAXCOV BR > 250 = estimated taxon base rate for maximum covariance indicates a taxon sample size (*n<sub>t</sub>*) of 250 cases or more; L-Mode BR > 500 = estimated taxon base rate for latent mode factor analysis indicates an *n<sub>t</sub>* of 500 cases or more; average BR > 350 = the averaged estimated taxon base rate across the three procedures (mean above minus below a cut [MAMBAC], MAXCOV, and L-Mode) indicates an *n<sub>t</sub>* of 350 cases or more; >.500 = proportion of samples with comparison curve fit index (CCFI) scores equal to or greater than .500 (single threshold criterion); >.550 = proportion of samples out of all nonambiguous samples with CCFI scores equal to or greater than .550 (narrow dual threshold criterion; with number in parentheses representing the proportion of cases where the CCFI fell between .450 and .549); >.600 = proportion of three-class samples out of all nonambiguous samples with CCFI scores equal to or greater than .600 (broad dual threshold criterion; with number in parentheses representing the proportion of cases where the CCFI fell between .400 and .599); all CCFIs are averaged across the three procedures (MAMBAC, MAXCOV, L-Mode).

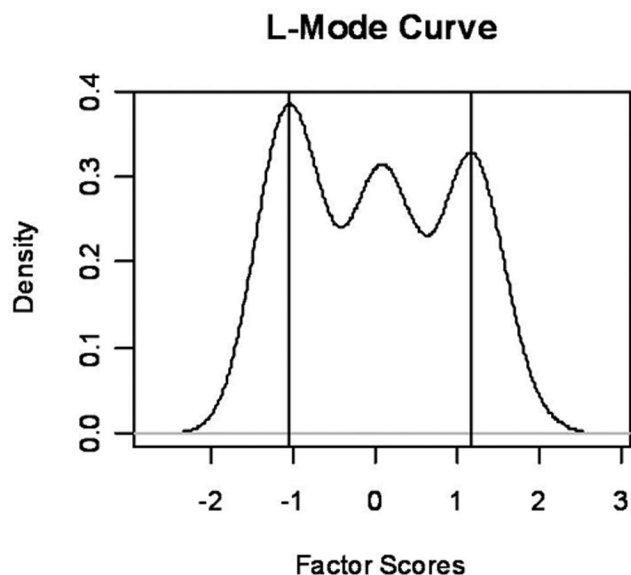


Figure 1. An L-Mode graph of a three-class sample with six indicators.

formed using the parameters for the datasets as predictors. The results indicated that the trimodal pattern was more likely to emerge with more indicators, a higher ratio of the base rate for the taxa versus complement classes, good between-group separation, greater tail weight, a manageable level of within-group (nuisance) covariance, and low indicator skew.

The question the current study sought to answer was whether the taxometric method responds in a predictable fashion to constructs with polytomous (three or more classes) latent structure. Previously, McGrath (2008) observed pseudotaxonic, pseudodimensional, and indeterminate results in a Monte Carlo analysis of three-class samples subjected to taxometric analysis, but the statistics used to evaluate the findings were problematic (see Haslam & Cleland, 2002; Ruscio, 2007; Ruscio et al., 2006). In the current Monte Carlo study, one-class, two-class, and three-class datasets were analyzed with Ruscio's (2007) comparison curve approach and CCFI. The results revealed that the CCFI accurately identified dimensional structure in the one-class datasets, accurately identified taxonic structure in the two-class datasets, and supported a taxonic (two-class) conclusion in the three-class datasets. These findings indicate that three-class polytomous constructs give rise to taxonic CCFI results using Ruscio's comparison curve approach. Hence, use of the CCFI in conjunction with an indeterminate category can help researchers avoid mistaking three-class polytomous constructs for one-class dimensional constructs, although it may be less helpful in differentiating between two-class taxonic and three-class polytomous constructs.

The current investigation illustrates the value of generating simulated taxonic and dimensional data curves that reflect the unique statistical characteristics of the indicators for use in assessing the relative fit of the actual data curve, the results of which are quantified in the CCFI. There are several advantages to the CCFI, a number of which are highlighted in the current investigation. First, the CCFI is an objective and highly accurate procedure (Ruscio, 2007; Ruscio et al., 2010), in direct contrast to the more subjective and less reliable approaches traditionally used to assess

taxometric data (i.e., base rate consistency, Bayesian probabilities, curve shape). Second, because the CCFI is based on the simulated curve approach, it is better able to handle nonnormal data than traditional approaches to taxometric analysis. Third, the CCFI is compatible with Meehl's notion of consistency testing. Meehl (1995, 2004) recommended that taxometrics be performed using multiple nonredundant and quasi-independent procedures such as MAMBAC, MAXCOV, and L-Mode. Consistency across different taxometric procedures is consequently a precondition for concluding that a construct is dimensional or taxonic. The CCFI provides an objective procedure for determining the consistency of results using either a single threshold ( $<.500$ ,  $\geq.500$ ), narrow dual threshold ( $<.450$ ,  $>.550$ ), or broad dual threshold ( $<.400$ ,  $>.600$ ) criterion and has the added advantage of being amenable to averaging. Results from the current study indicate that the narrow and broad dual threshold models were equally effective in identifying dimensional structure in the one-class dataset, taxonic structure in the two-class dataset, and taxonic structure in the three-class dataset.

As was previously mentioned, at least two different inferential frameworks have been suggested for the taxometric method: the traditional taxon-detection approach (Meehl, 1995, 2004; Meehl & Yonce, 1994, 1996; Waller & Meehl, 1998) and the competing hypotheses approach (Ruscio & Kaczetow, 2009; Ruscio et al., 2007). In the taxon-detection approach dimensional results are treated as error, noise, or the null hypothesis, whereas in the competing hypotheses approach taxonic and dimensional latent structure are construed as alternative hypotheses of equal weight and importance. Even though the current study did not directly compare these two inferential frameworks, the results seem to provide greater support for the competing hypotheses approach than for the taxon-detection approach (as does the possibility of polytomous structure in general). The three-class polytomous samples fit the simulated taxonic model as well as the two-class taxonic samples, and neither fit the dimensional model particularly well. This is inconsistent with the taxon-detection approach because instead of being identified as nontaxonic (dimensional or ambiguous), the three-class samples were "misidentified" (from the standpoint of the taxon-detection model) as taxonic. The current results appear to be more consistent with the view that dimensional and categorical results reflect alternative structures and that polytomous constructs, at least three-class ones, can be classified as categorical. Because the CCFI with a dual threshold criterion identifies polytomous constructs as taxonic, taxometric researchers using the comparison curve approach can rest assured that they are probably not working with a polytomous construct when they get consistent dimensional results.

Taxometric research has important implications for research and practice in psychological assessment, which is probably why the procedure is so popular with researchers in the psychological assessment field. Ruscio et al. (2006) emphasized that taxometric findings can be helpful in selecting and constructing items for various and sundry assessment procedures. A construct with a taxonic or categorical latent structure is most efficiently assessed with a relatively small number of highly focused items capable of sorting cases into a few discrete categories. A dimensional construct, by contrast, is best measured with a relatively large number of diverse items that cover the entire range of the dimension rather than dividing the distribution into mutually exclusive categories.

An equally important implication of taxometric research for the field of psychological assessment is its use in determining the construct validity of psychological test scores. The taxometric method is designed to assess the latent structure of the construct that underpins the psychological procedure rather than the latent structure of the procedure itself. If a test designed to measure a construct generally believed to be dimensional, such as intelligence, produces ambiguous or taxonic results or a construct generally believed to be taxonic, such as gender, produces ambiguous or dimensional results, this automatically brings the construct integrity of this assessment procedure into question.

The principal limitation of the research described in this article is the uncertain generalizability of the results to other contexts. The Monte Carlo analyses were based on an algorithm created by Ruscio and Kaczetow (2008) and the number of indicators, which was the only parameter other than structure that was systemically varied, comprised only three levels (four, five, and six). The latter parameter restriction was introduced because a review of the literature on taxometric analysis revealed that few studies used more than four to six indicators. In addition, polytomous structure was confined to a three-class typology and so it is uncertain whether the taxonic CCFI results obtained with the three-class samples in this study would generalize to polytomous constructs composed of four or more categories. One possibility is that as the number of categories increases the CCFI becomes less aligned with the taxonic model and more aligned with the dimensional model. In fact, it could even be argued that once we reach a certain number of categories (e.g., eight to 10) there is little practical value to be found in differentiating between dimensional and categorical latent structure. Using taxometric results to guide development of an assessment procedure for an eight-class categorical construct may not differ that much from the taxometric guidelines used to create an assessment procedure for a dimensional construct. For practical reasons the eight categories would need to be ordered quantitatively (otherwise, we would probably need to create eight separate measures). This is similar to how a dimensional construct is assessed at different points along its continuum.

Ruscio and Ruscio (2004a) have discussed the role of taxometrics in a comprehensive program of structural research. They recommended that for constructs with multiple taxonic boundaries the taxometric method can be used to search for taxonic boundaries in a construct iteratively, with the process being repeated within each class defined in the previous step. Given the tendency of hierarchical cluster analysis and latent class/profile analysis to overidentify the number of boundaries in a construct (McLachlan & Peel, 2001), there is a need for a procedure that can identify multiple taxonic boundaries and estimate the maximum number of such boundaries. A two-step procedure, which can be extended to a multistep procedure, has been advocated by Ruscio and Ruscio (2004a, 2004b) for this very purpose. The two-step procedure involves subjecting a taxon identified in a previous taxometric analysis to further taxometric analysis to determine whether it forms a dimension (two-class structure) or taxon (three-class structure). If a taxon is identified then a third taxometric analysis can be performed to see whether it forms a dimension (three-class structure) or taxon (four-class structure). The results of the current study indicate that the multistep procedure does a good job of identifying taxonic structure but is much less effective in identifying dimensional structure at the second step of the process.

Further analysis revealed the importance of an accurate base rate estimate when using the two-step procedure, something that is not under the researcher's control. What is under the researcher's control is selection of the base rate estimate. To the extent that overestimating the first step taxon base rate appears to have a more deleterious effect on the CCFI's ability to identify second step dimensionality in two-class samples than underestimating the first step taxon base rate has on the CCFI's ability to identify second step taxonicity in three-class samples, investigators may want to use a conservative procedure like MAXCOV to estimate the taxon base rate.

As the results of this and previous studies indicate, the CCFI is effective in differentiating between dimensional (continuous) and taxonic (discontinuous) latent structure. Results indicative of discontinuous structure, however, should not be taken as prima facie evidence of two-class structure because the three-class samples in the current study also achieved elevated CCFI scores. Hence, the current results do not provide a definitive answer to the question of whether taxometric analysis can be used to differentiate between divergent categorical structures. Categorical results can be explored further with cluster analysis or latent class/profile analysis, although as Ruscio et al. (2006) pointed out, each of these procedures tends to overestimate the number of clusters or distinct categories in a distribution and are not particularly adept at identifying taxonic boundaries. The two-step sequential process introduced by Ruscio and Ruscio (2004b) has potential but requires a relatively large taxonic subsample ( $n_t$ ) and an accurate or at least a more conservative estimate of the first step taxon base rate to operate efficiently for the purpose of distinguishing between different categorical structures. Trimodality in the L-Mode curve may be exclusive to three-class constructs, but it occurred in only 25% of the 40 three-class samples included in the two-step analyses and in about 25% of the three-class samples included in the McGrath (2008) study. Similar problems may arise when attempting to identify the number of dimensions in a continuous construct. The taxometric method and CCFI do a good job of answering Stage 1 questions (i.e., is the construct dimensional or categorical?). Now we need a procedure or set of procedures that can answer Stage 2 questions (i.e., how many dimensions or categories are there?). The future of research using latent structure procedures requires that we identify and validate procedures for answering these important Stage 2 questions.

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