Detecting Small Taxa Using Simulated Comparison Data: A Reanalysis of Beach, Amir, and Bau's (2005) Data

John Ruscio
The College of New Jersey

David K. Marcus
University of Southern Mississippi

On the basis of taxometric analyses of data sets that they created to pose interpretive challenges, S. R. H. Beach, N. Amir, and J. J. Bau (2005) cautioned that using comparison data simulated by J. Ruscio's programs can lead to inaccurate conclusions. Careful examination of S. R. H. Beach et al.'s methods and results plus reanalysis of their data fails to substantiate this concern: Using comparison data identified the taxonic structure of S. R. H. Beach et al.'s data sets, even when the taxon base rate was very low. The authors show that J. Ruscio's simulation programs generate comparison data appropriately and that analyzing these data provides a useful interpretive aid. Additionally, the authors discuss and illustrate the effective use of the inchworm consistency test to disambiguate taxometric results for small taxa and dimensional constructs with positively skewed indicators.

Keywords: taxometrics, latent structure, data simulation, comparison data, inchworm consistency test

The taxometric method pioneered by Meehl (1995) is an increasingly popular method for distinguishing categorical (taxonic) and continuous (dimensional) latent constructs. Not only has the method been applied in psychopathology research (for a review, see J. Ruscio, Haslam, & Ruscio, 2006) but it also has been used to examine the structure of constructs underlying assessment instruments, such as the Beck Depression Inventory (A. M. Ruscio & Ruscio, 2002) and the Infrequency scales of the Minnesota Multiphasic Personality Inventory—2 (Strong, Greene, & Schinka, 2000). The target construct under investigation typically involves a rare phenomenon within the population studied, so the base rate of a putative taxon is low, and the variables used in taxometric research usually are positively skewed. This skew can result from the mixture of two groups of unequal size (e.g., a small taxon and its larger complement), respondents' decreasing likelihood of endorsing items or selecting response options indicative of more severe disturbance, or both. Small putative taxa and skewed indicators can make it difficult to differentiate taxonic and dimensional data (J. Ruscio, Ruscio, & Keane, 2004).

Beach, Amir, and Bau (2005) used the maximum eigenvalue (MAXEIG; Waller & Meehl, 1998) taxometric procedure to examine these challenges. A MAXEIG analysis requires three or more valid indicators of the construct under study. Cases are sorted using one variable, referred to as the input indicator, which forms the x axis of a MAXEIG graph. The sample is then divided into a series of ordered subsamples, or windows. Within each window, one calculates the largest eigenvalue of the covariance matrix constructed from the two

or more remaining indicators. The covariance matrix is the usual variance–covariance matrix with the diagonal of variances replaced by zeros to leave only off-diagonal covariances. The largest eigenvalue of such a matrix is used to index the extent to which the indicators covary, and the series of conditional eigenvalues is plotted as the y values of a MAXEIG graph. For taxonic data, the window with the most even mix of taxon and complement members often yields the largest eigenvalue, resulting in a peaked curve. A low frequency taxon can yield a MAXEIG graph that cusps at the right side of the graph—but so can a dimensional construct with positively skewed indicators.

J. Ruscio et al. (2004) suggested two techniques for dealing with this interpretational ambiguity: (a) analyzing taxonic and dimensional comparison data to provide an interpretive aid and (b) performing the inchworm consistency test (ICT; Waller & Meehl, 1998) to see whether results change in a manner more consistent with taxonic or dimensional structure. With the former technique, one generates both taxonic and dimensional comparison data sets that reproduce key properties of the research data. If the graphical results for analyses of the research data are more similar to those for the taxonic than the dimensional comparison data, this pattern supports an inference of taxonic latent structure, with the opposite true as well. To conduct the ICT, one should perform MAXEIG analyses with an increasing number of windows. The graphs for a small taxon can change from cusped to peaked at the right side of the curve as the number of windows increases, provided that eventually there are windows containing more taxon members than complement members. In contrast, the graphs for a dimensional construct measured with skewed indicators ordinarily continue to be cusped at the right side of the curve.

Beach et al. (2005) raised concerns about both of these strategies. To test the ability to detect small taxa using simulated comparison data (SCD) and the ICT, they generated a series of taxonic data sets, most of which had low taxon base rates, as well as SCD to accompany each target data set. To implement the ICT, the number of windows in the MAXEIG analyses varied from 10

---

to 100. Beach et al. reported that for many of their data sets, curves for taxonic and dimensional comparison data were similar despite the fact that the target data were taxonic. In addition, estimates of latent parameters (e.g., separation between groups) calculated from the results of MAXEIG analyses of the taxonic comparison data differed from the parameters used to generate the target data sets. Because Beach et al. believed that cusped curves for their target data correctly identified taxonic structure, they concluded that (a) the use of SCD would have failed to detect many of these small taxa, (b) the use of SCD would have led to the rejection of many of these data sets as unsuitable for taxometric analysis, (c) requiring that the ICT yields a peaked—rather than cusped—curve to infer taxonic structure is too stringent a standard, and (d) the programs to simulate comparison data are biased in their reproduction of important characteristics of target data sets. We address each of these concerns in light of Beach et al.'s findings as well as our reanalyses of their data.

Does the Analysis of SCD Help to Detect Small Taxa?

We agree with Beach et al. (2005) that the question of whether SCD can be used to help detect small taxa is crucial. They presented MAXEIG curves for a few data sets with small taxa ($p = .09, .10$, and $.11$; see their Figures 1, 2, and 3, respectively). The target data and comparison data yielded cusped curves, even with 100 windows; any taxonic peaks were ambiguous, at best. However, until the scaling of the y axis was held constant across analyses in their Figure 6, the similarities between curves for target and taxonic comparison data were obscured, as were the differences between curves for target and dimensional comparison data. When graphed as in their Figure 6, Beach et al.'s findings show that the use of SCD identified taxonic structure in each analysis.

Because few of Beach et al.'s (2005) taxometric curves were presented and both their and our interpretations are subjective, we obtained and reanalyzed their data sets using SCD and an objective index. We analyzed the 50 data sets in which 10 taxon base rates ($p = .05, .06, .07, .08, .09, .10, .15, .20, .25$, and $.30$) were crossed with five levels of within-group correlation ($r_{wg} = .00, .05, .10, .15$, and $.20$), and the 18 additional data sets in which three taxon base rates ($p = .09, .10$, and $.11$) were crossed with six levels of within-group correlation ($r_{wg} = .03, .04, .05, .06, .07$, and $.08$); all data sets contained $N = 4,000$ cases and six indicators. Generating taxonic comparison data necessitates assigning cases to groups so that indicator distributions and correlations can be reproduced within groups (and therefore between them as well). For each of the 68 data sets, we classified cases in three ways. First, actual group membership was used to classify cases infallibly. Second, Bayes' Theorem was used to classify cases using the results of an initial taxometric analysis (Waller & Meehl, 1998); this is what Beach et al. had done. Third, a base-rate classification technique was used by cutting along the distribution of indicator total scores at a point determined by the base rate estimated through an initial taxometric analysis (J. Ruscio et al., 2006).

For each data set, MAXEIG was performed using 50 windows that overlapped 90% with one another, and each variable served as the input indicator once with the remaining five indicators serving as output indicators. Using only 50 windows provides a very conservative test for the detection of taxa because this leaves $n = 678$ cases within each window (formula in Waller & Meehl, 1998,

p. 42), and many of the taxa were considerably smaller than this. To interpret results objectively, we calculated the comparison curve fit index (CCFI) to quantify the extent to which results for the target data are more similar to those for the taxonic or dimensional comparison data (J. Ruscio et al., 2006; J. Ruscio, Ruscio, & Meron, in press). CCFI values can range from 0 to 1, with higher values suggesting better fit for taxonic structure. The index is symmetric about .50, in that this middle value represents equivalent fit for both structures.

The panels on the left side of Figure 1 show the MAXEIG curves for Beach et al.'s (2005) data sets with $p = .09, .10$, and $.11$, with $r_{wg} = .08$ in each case. The dark lines connecting data points are the averaged curves for the target data; in each two-graph panel, the left graph superimposes the results for the target data on the results for 10 samples of taxonic comparison data, with the upper and lower bounds representing ± 1 SE within that sampling distribution of results; the right graph superimposes the results for the target data on the results for 10 samples of dimensional comparison data. CCFI values above .50 correctly identify taxonic structure. For these three data sets, CCFI $= .884, .879$, and $.834$, respectively.

The CCFI values for all 68 of Beach et al.'s (2005) data sets, using all three criteria for generating taxonic comparison data, are shown in Tables 1 and 2. Every CCFI exceeded .50, usually by a substantial margin. CCFI values in the .80s, akin to results as clear as those in Figure 1, were the norm; nearly 80% of all CCFI values exceeded .80 (including 35% that exceeded .90), and 99% of all CCFI values exceeded .70. These results indicate that the use of SCD can reliably detect the taxa in Beach et al.'s data sets. Both their analysis (with results graphed as in their Figure 6) and our reanalysis provide considerable support for the utility of SCD in detecting the small taxa in these data. Whereas Beach et al. did not evaluate how well their proposed decision rules perform with dimensional data, J. Ruscio et al. (in press) demonstrated that the accuracy with which the use of SCD—quantified using the CCFI—identifies small taxa does not result from mistaking dimensional for taxonic data.

The ICT

Beach et al. (2005) performed MAXEIG using 10, 20, 40, and 100 windows. The formula provided by Waller and Meehl (1998, p. 42) shows that for Beach et al.'s total sample size of $N = 4,000$ and the conventional 90% overlap between adjacent windows, even using 100 windows still leaves too many cases in each ($n = 367$) to detect small taxa by means of a peaked curve. For example, with a base rate of .05 in a sample of $N = 4,000$, there are only 200 taxon members. Because taxon members would not appreciably outnumber complement members even in the uppermost windows, a MAXEIG analysis with such large windows would not be expected to yield a peaked curve (barring sampling error).

Nonetheless, analyses of Beach et al.'s (2005) low-base-rate data sets can yield peaked curves when a sufficiently large number of windows is used. Panels on the right side of Figure 1 contain the MAXEIG curves for analyses using 500 windows (which yield $n = 79$ within each). The distinction between the peaked curves for taxonic data and the cusped curves for dimensional data is clear and mitigates the risk of falsely concluding that the target data sets are unsuitable for taxometric analysis. Table 2 includes CCFI values for
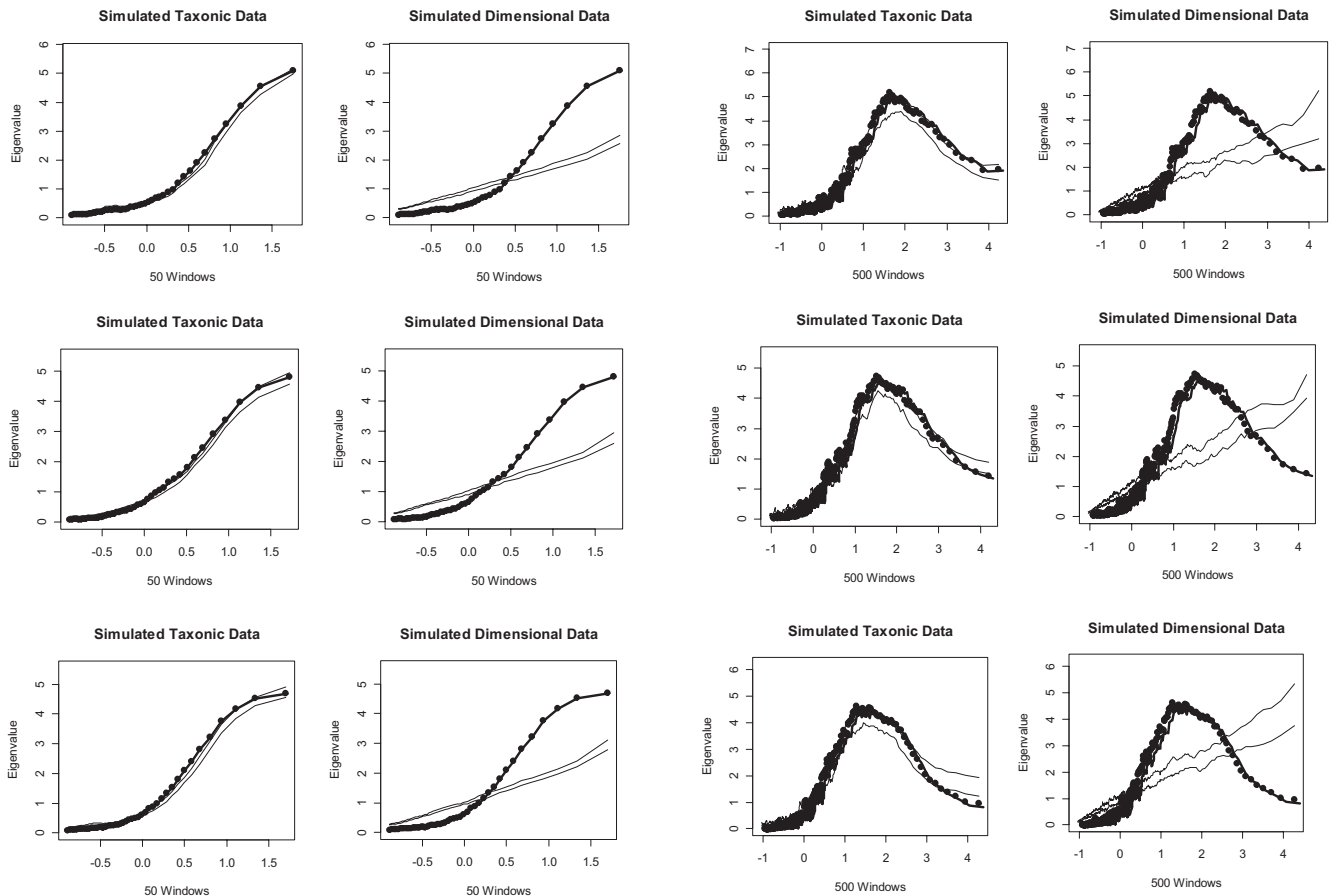
Figure 1. MAXEIG analysis, using 50 windows (left panels) and 500 windows (right panels) that overlapped 90% with one another, of Beach et al.'s (2005) data: $N = 4,000$; six indicators; $r_{wg} = .08$; and $p = .09$ (top row), .10 (middle row), and .11 (bottom row). Dark lines connecting data points depict the averaged curve for the target data. In the left (right) graph of each panel, the curve for the target data is superimposed on the results for 10 taxonic (dimensional) comparison data sets; the upper and lower bounds depict ± 1 *SE* within this sampling distribution of results. Taxonic comparison data were generated using a fallible assignment of cases to groups (Bayes' Theorem).

analyses of the 18 low-base-rate data sets that Beach et al. analyzed to suggest that the use of SCD would lead to the rejection of taxonic data as inadequate for taxometrics. Regardless of the technique used to classify cases to generate taxonic comparison data (actual group membership, Bayes' Theorem, or base-rate classification) or the number of windows used in the analysis (50 or 500), all CCFI values correctly identified taxonic structure. A necessary condition for obtaining a CCFI value that diverges from .50 is that curve shapes for taxonic and dimensional comparison data differ. Thus, the taxonic CCFI values—99% of which exceeded .70—show that the use of SCD supports the adequacy of every data set for analysis and correctly identifies its taxonic structure.

Although interpretational guidelines for the ICT warrant further study, Beach et al.'s (2005) conclusion that requiring a peaked curve is too stringent and would fail to detect many small taxa appears premature. With a large sample and a sufficiently large number of windows, peaks can emerge even for taxa with very low base rates. In the absence of a peak, or when a peak is ambiguous in that it may be due to sampling error within the uppermost window(s), two types of

inferential errors are possible: one might fail to identify a small taxon if a peak is required but does not emerge for taxonic data, or one might falsely identify a small taxon if a peak is not required and dimensional data yield a cusped curve. Beach et al.'s proposed guideline—that cusped curves constitute evidence of taxonic structure—reduces the chance of missing genuine taxa but increases the chance of identifying pseudo-taxa. Without dimensional target data sets, it was not possible for Beach et al. to determine the risk of identifying pseudo-taxa from a decision rule that recommends taxonic conclusions based on cusped curves. When the ICT yields cusped curves even with many windows, we advise researchers to withhold judgment of latent structure.

Alternatively, investigators may be able to disambiguate a stubbornly cusped curve by using SCD (not mutually exclusive with using the ICT). When doing so, we agree with Beach et al. (2005) that a peak should not be required to reach an inference of taxonic structure and that one should examine the entire curve, not simply its upper end. Our CCFI results for just 50 windows demonstrate that one need not observe a peak to identify a taxon. If the CCFI is nontrivially

Table 1

Comparison Curve Fit Index (CCFI) values for MAXEIG Analyses of Beach et al.'s (2005) 50 Data Sets

p	r_{wg}	Classification of cases			p	r_{wg}	Classification of cases		
		Infallible	Bayesian	Base-rate			Infallible	Bayesian	Base-rate
.05	.00	.985	.850	.719	.10	.00	.936	.810	.839
.05	.05	.988	.872	.724	.10	.05	.939	.800	.859
.05	.10	.984	.870	.746	.10	.10	.914	.795	.916
.05	.15	.984	.872	.706	.10	.15	.931	.818	.890
.05	.20	.983	.875	.714	.10	.20	.911	.863	.846
.06	.00	.968	.865	.784	.15	.00	.943	.776	.808
.06	.05	.966	.887	.768	.15	.05	.947	.794	.890
.06	.10	.984	.903	.807	.15	.10	.927	.744	.918
.06	.15	.958	.895	.842	.15	.15	.894	.791	.807
.06	.20	.978	.942	.850	.15	.20	.808	.805	.625
.07	.00	.973	.881	.859	.20	.00	.945	.822	.850
.07	.05	.972	.916	.875	.20	.05	.969	.815	.871
.07	.10	.976	.883	.885	.20	.10	.902	.741	.867
.07	.15	.972	.915	.877	.20	.15	.856	.743	.769
.07	.20	.967	.935	.924	.20	.20	.749	.684	.554
.08	.00	.977	.891	.862	.25	.00	.931	.845	.905
.08	.05	.976	.888	.887	.25	.05	.944	.763	.906
.08	.10	.981	.904	.905	.25	.10	.939	.820	.881
.08	.15	.966	.928	.916	.25	.15	.936	.823	.829
.08	.20	.974	.916	.939	.25	.20	.856	.807	.869
.09	.00	.963	.881	.896	.30	.00	.943	.850	.934
.09	.05	.974	.911	.926	.30	.05	.907	.831	.895
.09	.10	.967	.896	.946	.30	.10	.919	.782	.886
.09	.15	.970	.886	.969	.30	.15	.911	.766	.847
.09	.20	.956	.918	.929	.30	.20	.865	.803	.802

Note.   We performed all analyses using 50 windows that overlapped 90% with one another, and each variable served once as the input indicator with the remaining five variables serving as output indicators. MAXEIG = maximum eigenvalue; p = taxon base rate; r_{wg} = within-group correlation.

above .50, this supports an inference of taxonic structure, and no peak is required. It must be remembered, however, that it is possible to obtain cusped curves that are more consistent with dimensional structure (a CCFI well below .50 would indicate this), or cusped curves that remain ambiguous (a CCFI near .50 would indicate this). Even when SCD are used and the full shapes of the curves are compared, cusped curves may remain uninterpretable.

Do the Programs to Generate Comparison Data Yield Biased Results?

Unfortunately, when describing how comparison data are generated, Beach et al. (2005) conflated two different approaches. Throughout their article, Beach et al. cite both A. M. Ruscio and Ruscio (2002) and J. Ruscio et al. (2004). The later study used programs that did not exist at the time of the earlier study, which used an ad hoc technique. Not distinguishing between these two studies' simulation methods can be misleading because they differ in several important ways. Other aspects of Beach et al.'s description of the simulation programs were inaccurate. For example, they state that to generate dimensional comparison data, "pairings among the indicators are shuffled with an iterative procedure until the pairings of indicator values attain a *preset criterion* that matches, as closely as possible, the *mean intercorrelation* of the indicators in the parent distribution" (p. 448) and later note that "the algorithm is focused on maintaining *average indicator skew*"

(p. 459). In addition, Beach et al. state that "to simulate a taxon, *a constant is added to a proportion of cases* equal to the estimated base rate of the putative taxon. This *simulates the average validity* of the indicators" (p. 449). The italicized phrases (our emphasis in each case) are incorrect; for details on how each program works, see J. Ruscio et al. (2006, in press).

Beach et al. (2005) observed discrepancies between the parameters used to generate their target data sets and the parameter estimates provided by taxometric analysis of the taxonic comparison data. They suggested that other algorithms may be required to simulate comparison data, which implies that the program they used was responsible for the discrepancies they observed. However, Beach et al.'s test confounded the performance of the program with three factors: (1) parameter estimation error in the initial taxometric analysis, (2) classification error when assigning cases to putative groups, and (3) parameter estimation error in the subsequent taxometric analysis. J. Ruscio et al. (in press) performed tests free of these confounds and found that the simulation programs reproduce data with good precision and negligible, if any, bias. The biases observed by Beach et al. are not attributable to the simulation programs but to confounding factors. Distinguishing and understanding all of the factors that influence the utility of SCD is essential to implementing this approach most effectively. We briefly explain the confounds in Beach et al.'s test and show that no bias is observed when they are removed.

Table 2

Comparison Curve Fit Index (CCFI) values for MAXEIG Analyses of Beach et al.'s (2005) 18 Data Sets

		Classification of Cases		
p	r_{wg}	Infallible	Bayesian	Base-rate
.09	.03	.944	.829 (.783)	.741 (.843)
.09	.04	.950	.789 (.761)	.737 (.860)
.09	.05	.963	.846 (.779)	.765 (.838)
.09	.06	.949	.813 (.814)	.758 (.839)
.09	.07	.965	.833 (.750)	.778 (.868)
.09	.08	.930	.884 (.812)	.751 (.865)
.10	.03	.969	.822 (.783)	.731 (.862)
.10	.04	.967	.838 (.752)	.761 (.848)
.10	.05	.963	.858 (.809)	.735 (.871)
.10	.06	.972	.848 (.829)	.714 (.853)
.10	.07	.940	.871 (.770)	.743 (.859)
.10	.08	.962	.879 (.825)	.745 (.860)
.11	.03	.969	.847 (.815)	.708 (.895)
.11	.04	.965	.825 (.791)	.752 (.877)
.11	.05	.957	.855 (.792)	.743 (.873)
.11	.06	.944	.843 (.808)	.761 (.861)
.11	.07	.954	.849 (.801)	.749 (.863)
.11	.08	.947	.834 (.805)	.733 (.858)

Note. We performed all analyses using windows that overlapped 90% with one another, and each variable served once as the input indicator with the remaining five variables serving as output indicators. We obtained values in parentheses using 500 windows; we obtained all other values using 50 windows. MAXEIG = maximum eigenvalue; p = taxon base rate; r_{wg} = within-group correlation.

Beach et al. (2005) performed taxometric analyses to estimate latent parameters of the taxonic structural model, including the taxon base rate and each indicator's valid and false positive rates. Using these estimates, Bayes' Theorem was applied to classify cases. At both stages, error is introduced such that the resulting fallible classification of cases (C_F) will not correspond to true group membership (C). Beach et al. provided the simulation program with the criterion variable C_F and then evaluated its performance using criterion variable C as the standard; this introduces Factors (1) and (2) as confounds. Moreover, their test was confounded by Factor (3) because they estimated latent parameters of the simulated data indirectly, through taxometric analyses, rather than via direct calculation.

To demonstrate that apparent biases disappear when these confounds are removed, we generated 10 samples of SCD for each of Beach et al.'s (2005) 68 taxonic data sets, used actual group membership to generate taxonic comparison data, and calculated within-group correlations directly from the SCD. These precautions allowed us to evaluate the performance of the simulation program itself, free of the confounds described above. This test yielded 20,400 residual correlations (r in the target data minus r in the taxonic comparison data): 68 samples $\times$ 2 groups (taxon, complement) $\times$ 15 correlations within each group (six indicators yield 15 intercorrelations) $\times$ 10 replications per sample. Results reveal no detectable bias ($M = .000$) and good precision ($SD = .027$). This does not reflect offsetting biases across samples: Averaging the 300 residuals for each sample yielded 68 means that ranged from a low of $-.003$ to a high of .002.

We are not asserting that John Ruscio's programs are an optimal solution to the problem of generating SCD, and we recognize that future programs may function even better. Our demonstration is consistent with extensive research showing that J. Ruscio's programs reproduce characteristics of the data provided to them with good precision and negligible, if any, bias and that using these SCD is very helpful in distinguishing taxonic and dimensional data (J. Ruscio, in press; J. Ruscio et al., in press).

Conclusions

The results of any data-analytic technique should be interpreted using a standard that can be applied reliably by other researchers and that has been validated by prior research. Both Beach et al.'s (2005) analyses and our reanalyses support the use of SCD, and we propose that this meets both of the requirements set forth above. An objective index, such as the CCFI, should improve reliability of interpretation. Mounting evidence (e.g., J. Ruscio, in press; J. Ruscio et al., in press) suggests that the CCFI differentiates taxonic and dimensional data more effectively than many conventional tests in the taxometric literature (e.g., examining the consistency of multiple estimates of the taxon base rate).

Trends evident in published taxometric investigations suggest that researchers, reviewers, and editors have become acutely aware of the need for a reliable and valid interpretive standard for taxometric results and that SCD are being used to help meet this need. Since the development of programs to generate comparison data and the validation of their use as an interpretive aid, it has become unorthodox for a taxometric study not to include SCD. We believe it would be unwise to return to the interpretation of taxometric results using only the illustrative graphs obtained under highly idealized data conditions and procedural implementations that can differ substantially from the data and analytic approach used in a particular investigation. Whereas this traditional approach has not been subjected to a challenging test, SCD can be used to provide a custom-tailored panel of comparison curves and to interpret taxometric results in an objective—but not infallible—manner, and there is considerable empirical support from rigorous testing to support this approach (J. Ruscio, in press; J. Ruscio et al., in press).

We would like to draw attention to one critical step to using SCD: assigning cases to groups to generate taxonic comparison data. The program to simulate taxonic data requires this, and the utility of the results depends on how this is done. In our reanalysis, we used three techniques for assigning cases to groups: actual group membership, Bayes' Theorem, and base-rate classification. The first technique is not an option for investigators; we included it only for comparative purposes and to underscore the importance of judging the output of a simulation program against its input. Along with other methods (e.g., the application of thresholds to scores on assessment instruments or the use of formal diagnostic algorithms), researchers can use Bayes' Theorem or base-rate classification to assign cases to groups.

Our reanalysis provides no grounds for preferring one of these methods to the other. Moreover, we hesitate to draw conclusions on the basis of the limited range of data conditions generated by Beach et al. (2005), especially because no dimensional data sets were included. The results of J. Ruscio et al.'s (in press) more extensive analyses suggest that CCFI values better discriminate taxonic and dimensional data when cases are assigned to groups using the base-rate method than Bayes' Theorem. Further research is needed, and researchers should bear in mind that the use of SCD

requires thoughtful application to obtain informative results. This is neither a blindly mechanical nor an infallible technique.

J. Ruscio et al. (2004) recommended the use of SCD and the ICT as tools for disambiguating cusped taxometric curves. Both Beach et al.'s (2005) analysis and our reanalysis shed light on important issues. We agree that research is needed to determine how best to assign cases to groups to generate taxonic comparison data, that data simulation has not been optimized and may be improved, that one should interpret an entire taxometric curve in an objective manner, and that careless use of SCD can yield misleading results. Most fundamentally, we agree with Beach et al. that researchers must adopt a rigorous, empirically grounded approach to implementing the taxometric method and interpreting results.

References

Beach, S. R. H., Amir, N., & Bau, J. J. (2005). Can sample-specific simulations help detect low base-rate taxonicity? *Psychological Assessment, 17,* 446–461.

Meehl, P. E. (1995). Bootstraps taxometrics: Solving the classification problem in psychopathology. *American Psychologist, 50,* 266–274.

Ruscio, A. M., & Ruscio, J. (2002). The latent structure of analogue depression: Should the BDI be used to classify groups? *Psychological Assessment, 14,* 135–145.

Ruscio, J. (in press). Taxometric analysis: An empirically-grounded approach to implementing the method. *Criminal Justice and Behavior.*

Ruscio, J., Haslam, N., & Ruscio, A. M. (2006). *Introduction to the taxometric method: A practical guide.* Mahwah, NJ: Erlbaum.

Ruscio, J., Ruscio, A. M., & Keane, T. M. (2004). Using taxometric analysis to distinguish a small latent taxon from a latent dimension with positively skewed indicators: The case of involuntary defeat syndrome. *Journal of Abnormal Psychology, 113,* 145–154.

Ruscio, J., Ruscio, A. M., & Meron, M. (in press). Applying the bootstrap to taxometric analysis: Generating empirical sampling distributions to help interpret results. *Multivariate Behavioral Research.*

Strong, D. R., Greene, R. L., & Schinka, J. A. (2000). Taxometric analysis of MMPI–2 infrequency scales [F and $F(p)$] in clinical settings. *Psychological Assessment, 12,* 166–173.

Waller, N. G., & Meehl, P. E. (1998). *Multivariate taxometric procedures: Distinguishing types from continua.* Thousand Oaks, CA: Sage.

AMERICAN PSYCHOLOGICAL ASSOCIATION
SUBSCRIPTION CLAIMS INFORMATION

Today's Date:_____

We provide this form to assist members, institutions, and nonmember individuals with any subscription problems. With the appropriate information we can begin a resolution. If you use the services of an agent, please do **NOT** duplicate claims through them and directly to us. **PLEASE PRINT CLEARLY AND IN INK IF POSSIBLE.**

PRINT FULL NAME OR KEY NAME OF INSTITUTION

ADDRESS

CITY   STATE/COUNTRY   ZIP

YOUR NAME AND PHONE NUMBER

MEMBER OR CUSTOMER NUMBER (MAY BE FOUND ON ANY PAST ISSUE LABEL)

DATE YOUR ORDER WAS MAILED (OR PHONED)

____PREPAID ____CHECK ____CHARGE
                    CHECK/CARD CLEARED DATE:_____

(If possible, send a copy, front and back, of your cancelled check to help us in our research of your claim.)

ISSUES: ____ MISSING ____ DAMAGED

TITLE   **VOLUME OR YEAR**   **NUMBER OR MONTH**

Thank you. Once a claim is received and resolved, delivery of replacement issues routinely takes 4–6 weeks.

——————— **(TO BE FILLED OUT BY APA STAFF)** ———————

DATE RECEIVED: _____   DATE OF ACTION: _____
ACTION TAKEN: _____   INV. NO. & DATE: _____
STAFF NAME: _____   LABEL NO. & DATE:_____

Send this form to APA Subscription Claims, 750 First Street, NE, Washington, DC 20002-4242

PLEASE DO NOT REMOVE. A PHOTOCOPY MAY BE USED.