Testing the Construct Validity of Meehl's Taxonic Model of Schizotypy:

Taxometric Search Techniques Applied to Self-Report Measures of Schizotypic Signs

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Running Head: IDENTIFYING A SCHIZOTYPAL TAXONOMY

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Abstract

Two taxometric search procedures developed by Meehl and associates (MAXCOV and MAMBAC) were applied to data from three self-report measures of schizotypic signs (Perceptual Aberration, Magical Ideation, and Cognitive Slippage) in a sample of 5255 college students. The MAMBAC procedure, which is sensitive to the existence of an underlying taxonomy, suggested that Meehl's model of a schizotypal taxonomy is viable. The MAXCOV procedure suggested cutoff scores on each measure for classifying subjects as schizotypal and also estimated the base rate for schizotypy in this sample (averaging 9%). These findings provide additional construct validation for Meehl's model of schizotypy and for the Chapman scales of psychosis proneness. Additional work is underway to refine the scales and to rule out potential psychometric artifacts.

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Since there is substantial evidence for genetic influences in schizophrenia [See Gottesman (1991) for a review], attention has turned to issues such as the mode of inheritance, where there is a lively debate. Gottesman (19xx) argues for a polygenic mode of inheritance, while Meehl (1962, 1989, 1990) argues for a single gene model with the added influence of polygenic potentiators. Meehl's model acknowledges that other genetic influences can increase or decrease the impact of the hypothesized schizogene on behavior. A single gene model has the advantage of being more parsimonious than a polygenic model, and it makes several precise predictions.

Meehl's (1962, 1990) diathesis/stress model of schizophrenia proposed that a genetic diathesis (schizotaxia) was a necessary but not sufficient condition for the development of schizophrenia. Meehl used the term schizotypy to refer to the typical pattern of behavior that develops in someone who inherits this schizotaxia. He suggested that schizotypes could be identified by these behavior patterns, which he called schizotypic signs (Meehl 1964). The Chapmans and their students have developed reliable self-report measures for many of these schizotypic signs (e.g., Chapman, Chapman, & Raulin, 1976, 1978; Eckblad & Chapman, 1983; Miers & Raulin, 1985).

Meehl's proposed model is taxonic—that is, he argues that the schizotype is different in kind, and not just degree, from the non-schizotype. By contrast, a polygenic model of risk for schizophrenia would predict a dimension of risk, with some individuals low on that dimension and others high. There is no clear taxonomy in a polygenic model, although polygenic models with a sharp threshold may appear to be taxonic. Biological sex is an example of a genetically-determined taxonomy with essentially two taxonomic categories—females and males (ignoring for the moment rare categories such as XYY individuals).

The key to Meehl's model of schizophrenia is the accurate identification of schizotypes, the majority of whom will never develop schizophrenia. Meehl (1964) proposed a checklist approach to identify schizotypes, while the Chapmans and their colleagues (Chapman, Chapman, Raulin, & Edell, 1978) proposed the use of self-report psychometric instruments to measure schizotypic signs. Extensive research [see Edell (in press) for a review] shows that the Chapman scales identify subjects who show characteristics suggestive of risk for schizophrenia. Furthermore, a follow-up study (Chapman, Chapman, Kwapil, Eckblad, and Zinser, 1994) suggests that at least some of these scales do indeed identify individuals with an increased risk for psychosis. These data support the validity of these psychometric measures of schizotypy, but do not address the construct validity of Meehl's hypothesis of a schizotypal taxonomy.

Meehl addressed the construct validation of schizotypy by developing a series of mathematically-based taxometric search techniques. The term "coherent cut kinetics" refers to the general strategy used in all of these techniques (Meehl & Yonce, 1994). We illustrate in Figure 1 the problem and the coherent cut kinetics strategy. Assume for the moment the existence of an underlying taxonomy, and also assume that we have developed measures that are moderately valid indicators of that taxonomy. A moderately valid indicator will show a mean difference between the two taxonomic classes (or taxa), but the distributions for the two classes will overlap. Several of the Chapman Scales may be promising measures for this task. Figure 1(a) illustrates the underlying assumption of this model for a single moderately valid indicator. We have drawn these curves assuming a base rate for schizotypy of 10%—about what one would expect based on genetic data (Meehl, 1990). Because we currently have no perfect criterion for schizotypy, we are unable to construct directly the underlying distributions on our indicator shown by dotted lines in Figure 1(a). In fact, we do not even know if the hypothesized underlying taxonomy exists. Our task is to (1) demonstrate that our hypothesis of an underlying taxonomy is likely to be true, (2) identify the cutoff score (termed HITMAX) on the indicator measures that correctly classifies the largest number of subjects, and (3) estimate taxon parameters. HITMAX is the point at which the two distributions cross as shown in Figure 1(b). It is the

point on our indicator variable that maximizes the total number of correct classifications of subjects. Meehl's general strategy for finding HITMAX and validating the underlying assumption of a taxonomy is to use a sliding interval (a sliding cut with some procedures) as shown in Figure 1(c). For each possible interval, the subjects that score within that interval are included in mathematical computations, which are derived from the assumption of a taxonomy. For example, the Maximum Covariance Procedure (MAXCOV) uses three moderately valid indicators of the presumed underlying taxa. One of the three variables is designated as the input variable, and sliding intervals are determined for that variable. The other two variables are called output variables. If we assume that these three indicators are pairwise uncorrelated within each taxon, then any interval on the input variable that contains only schizotypes or only non-schizotypes will show zero covariance between the two output variables. Furthermore, the maximum covariance between the output variables will occur when the interval contains a 50/50 mixture of schizotypes and non-schizotypes (Meehl, 1965, 1973), which conveniently enough occurs only at the HITMAX location [see Figure 1(c)]. Figure 1(d) illustrates the expected covariance curve for the MAXCOV procedure. Fortunately, Monte Carlo studies (Golden & Meehl, 1973b; Golden, Tyan, & Meehl, 1974c) suggest that the MAXCOV procedure is robust to the assumption of a zero correlation between variables within each taxonomy, since this assumption is unlikely to be literally true.

Insert Figure 1 about here

This study used three self-report measures of schizotypic signs (Perceptual Aberration, Magical Ideation, and Cognitive Slippage) with a sample of over 5000 college students to address the construct validity of Meehl's taxonic model of schizotypy. Two of the most extensively studied of Meehl's taxometric techniques were used—the Maximum Covariance (MAXCOV) procedure described above and MAMBAC (Mean above minus below a cut; Meehl & Yonce, 1994). The purpose of the present study was to (1) evaluate the likelihood of an underlying taxonomy, and if a taxonomy seems likely, (2) locate scale

cutoff scores that maximize the number of correct classifications, (3) estimate of the base rate of schizotypy; and (4) identify the latent parameters for the indicator variables for both the schizotypal and non-schizotypal taxa.

Method

Subjects

The subjects included 6291 college students who completed a research form containing three scales of schizotypic signs and an Infrequency Scale as part of a requirement of the undergraduate introductory psychology course. Subjects were dropped if they skipped more than 4 items from any of the three schizotypic signs scales or if they endorsed more than one item on the 5-item Infrequency Scale (Raulin, 1984). The Infrequency Scale, designed to detect random responding, contains items that are endorsed in the keyed direction by fewer than one percent of respondents (e.g., "I find that I often walk with a limp which is the result of a skydiving accident."). These strict criteria for inclusion reduced the sample to 5255 subjects (2752 males and 2503 females). Although gender differences were statistically significant because of the large sample sizes, they were not large enough to be clinically significant (average effect size < .10). Therefore, males and females were combined for the analyses.

Measures (Indicator Set)

Three measures of schizotypic signs were used: Perceptual Aberration (Chapman, Chapman, & Raulin, 1978), Magical Ideation (Eckblad & Chapman, 1983), and Cognitive Slippage (Miers & Raulin, 1985). All of these scales use a true/false format, and all have been developed using procedures to maximize internal consistency and minimize the effects of method variance such as social desirability and acquiescence response set biases. Longitudinal data suggest that these measures have high test-retest reliability (Mahler, Raulin, O'Gorman, & Furash, 1987). The Perceptual Aberration Scale measures deviant or distorted perceptions, feelings, and beliefs primarily in relation to one's body (e.g., "I have felt that something outside of my body was part of my body."). The Magical Ideation Scale measures a belief in causal connections between behavior and events that are not, in reality, related (e.g., "If reincarnation were true, it would explain a number of

unusual experiences that I have had."). The Cognitive Slippage Scale measures a mild form of thought disorder (e.g., "Often when I am talking I feel that I am not making sense."). Previous research (Propper et al., 1987) suggested that these three scales were measuring the same construct. Meehl (1964) suggested that anhedonia would also be a suitable candidate as an indicator measure, but factor-analytic research (Propper et al., 1987) suggests that anhedonia is sensitive to a different underlying construct than the measures used in this study.

Using several indicators, as we are doing, provides several estimates of latent parameters such as base rates, thus giving us increased confidence in the results. In addition, having more than one indicator measure permits the computation of the Bayesian probability of taxon membership for each subject using the individual scores for the subjects—a procedure more powerful for classification than relying on the cutoff from a single indicator.

Taxon Search Procedures

We will be using two taxometric search procedures—the MAMBAC and MAXCOV procedures. These are described briefly below, but the interested reader is referred to Meehl and Yonce (1994, in press) for more details.

MAMBAC. MAMBAC stands for Mean Above Minus Below a Cut. The procedure requires two measures—each a moderately valid indicator of the underlying taxon. One measure is designated as the input variable, and a sliding cut is used with this variable. For each cut, the mean on the second indicator variable is computed for the subjects who score above and below this cut, and a difference score (absolute value) is computed. This mean difference should theoretically reach a peak at the point where the cut is closest to defining pure groups of schizotypes and non-schizotypes (i.e., the HITMAX location). Meehl and Yonce (1994) have found in Monte Carlo studies that the shape of the MAMBAC curve is strongly affected by whether the data are taxonomic as shown in Figure 2(a). If there is no underlying taxonomy, MAMBAC produces a dish-shaped curve. In a taxonic situation, the MAMBAC curve shows a peak that varies in location depending on the base rate of the taxa. We used the MAMBAC procedure to test for taxonicity and to

get rough estimates of the HITMAX location and base rates. We used the MAXCOV procedure to identify the HITMAX cut and underlying taxon parameters.

Insert Figure 2 about here

MAXCOV. The Maximum Covariance procedure (MAXCOV) requires three moderately valid indicators of a single hypothesized taxonomy. These indicators are assumed to be uncorrelated with one another within each taxon. However, in a mixture of the two taxa, a correlation would be observed because both are sensitive to the underlying taxonomy represented in the mixture. The logic of this phenomenon is as follows: Assume that schizotypes on average have a higher mean than non-schizotypes on each indicator variable. In this situation, the XY pairs of scores for schizotypes would be shifted up and to the right in a scatterplot relative to the non-schizotypes, thus creating a correlation in a mixed group. In fact, we can predict the covariance in a mixture of two groups from the base rates (p and q) and the covariance in each group using Equation 1 (these equations taken from Meehl, 1973). The subscripts $_s$ and $_n$ are used to designate the hypothesized schizotypal and non-schizotypal taxa.

$$\mathrm{cov}(xy) = p\big[\mathrm{cov}_s(xy)\big] + q\big[\mathrm{cov}_n(xy)\big] + pq\big[(\overline{X}_s - \overline{X}_n)(\overline{Y}_s - \overline{Y}_n)\big] \tag{1}$$

The only other assumption behind the MAXCOV procedure is that the distribution of each indicator variable is unimodal within each taxon. One variable is arbitrarily designated as the input variable, and a sliding interval on this variable is used. For each interval on the input variable, the covariance of the other two variables is computed for the subjects who score within the sliding interval. That covariance should rise to a peak as the sliding interval approaches HITMAX and then fall beyond the HITMAX interval. Furthermore, since we know that the base rates of the two taxa are equal in the interval that contains HITMAX, it is possible to derive an equation that will give the relative base rates of the taxa within each interval. Under the assumption of zero correlation within each taxon, the first two terms of Equation 1 drop out, leaving us with Equation 2 (covariance is the

product of three terms: the base rates (p and q) and a constant, which is itself the product

of the mean differences between the taxa for each variable).

$$\text{cov}(xy) = pq\left[(\overline{X}_s - \overline{X}_n)(\overline{Y}_s - \overline{Y}_n)\right] = pq\left[K\right] \tag{2}$$

In the HITMAX interval, the base rates are equal (p = q = .5), so Equation 2 simplifies to

Equation 3, which allows us to estimate the constant K.

$$\text{cov}(xy) = (.5)(.5)\left[K\right] = .25\left[K\right] \tag{3}$$

Once K is estimated, we can use the observed covariance in each interval and our

estimate of K to estimate the proportion of schizotypes in each interval using Equation 4,

which can be written in the form of a quadratic equation.

$$\text{cov}(xy) = pq\left[K\right] = p(1-p)\left[K\right] \quad \Rightarrow \quad Kp^2 - Kp + \text{cov}(xy) = 0 \tag{4}$$

With the relative base rate of schizotypes and non-schizotypes in each interval and the

actual frequency of subjects in each interval, one can literally trace the shapes of the

underlying distributions for each taxon.

Extensive validation work has been completed on the MAXCOV procedure (Meehl &

Yonce, in press). In Monte Carlo trials, the Maximum Covariance method produced

accurate estimates of the proportion of cases in each taxon (Golden & Meehl, 1973b;

Golden, Tyan, & Meehl, 1974b) and was robust to violations of the assumption of zero

intra-taxon correlation between the indicator variables provided that the correlations of

each indicator pair within each taxon are approximately equal and less than .4 (Meehl,

1965). Furthermore, the MAXCOV procedure correctly estimated appropriate HITMAX

cuts and base rates for detecting gender (male and female taxonomies) using MMPI

scales drawn from the items of Scale 5 (Golden & Meehl, 1973a; Meehl, Lykken, Burdick,

& Schoener, 1969).

Results

MAMBAC. Results of the MAMBAC analyses are displayed in the bottom three panels

of Figure 2. With three indicator variables, there are six MAMBAC curves—two for each

possible input variable. Meehl and Yonce (1994) showed in Monte Carlo work that in the situation where there is an underlying taxonomy, some but not necessarily all of these MAMBAC curves will show the characteristic shape suggesting a taxonic situation and none of the curves will show the shape suggesting a non-taxonomic situation. In this case, all of the curves show a characteristic rise on the right, suggesting the presence of a low base rate taxon. None of the curves show the U-shaped function typically found in non-taxonic situations. Taken together, these data suggest the presence of an underlying schizotypal taxon with a relatively low base rate. The procedure recommended by Meehl and Yonce (1994) for estimating base rates with MAMBAC yielded estimates for the schizotypal taxon ranging from 16% to 37%, with a mean base rate estimate of 25%. These estimates seem high in comparison with other research findings (e.g., Korfine & Lenzenweger, 1995; Lenzenweger & Korfine, 1992). They also seem high given the shape of the MAMBAC curves, which suggest a smaller base rate for the schizotypal taxon. This issue will be addressed in the discussion section.

MAXCOV. The MAXCOV curves for the Perceptual Aberration, Magical Ideation, and Cognitive Slippage Scales are presented in Figure 3. For the curves shown in these figures, we used an interval width of three scores and slid the interval up one score to create the next interval. In addition, we smoothed the resulting covariance curve. Covariances between output indicators were plotted only for intervals that contain 20 or more cases.

Insert Figure 3 about here

Under the assumptions of the MAXCOV procedure, as the interval on the input variable moves from left to right there should be a gradual increase in covariance to a maximum (HITMAX) and then a gradual decrease. Given that the base rate of schizotypy is presumed to be around 10% (Meehl, 1990) and schizotypes are indicated by elevated scale scores, HITMAX should be located in the upper range of scores for each variable. Thus, the covariance curves should be unimodal and negatively skewed. This prediction was generally confirmed, although curiously, there was a drop in covariance just before

the curve rose again to its peak for each indicator variable, a drop that was most dramatic in the Perceptual Aberration covariance curve.

Estimating Base Rates, Taxon Parameters, and the Shape of the Latent Distributions. We constructed the latent distributions shown in Figure 4 using Equations (3) and (4) and estimated the base rates of the two hypothesized taxonomic categories. If these base rate estimates agree with one another and with external estimates from other data sources (e.g., genetic studies), then one can be more confident of the results. The base rate estimates were 7%, 10%, and 8% from the Perceptual Aberration, Magical Ideation, and Cognitive Slippage Scales, respectively. These estimates of the base rate of schizotypy are not only consistent with one another, but also consistent with other data sources (Meehl, 1990). These figures are also close to the base rate estimates for schizotypy reported by Lenzenweger and Korfine (1992) and Korfine and Lenzenweger (1995), although they disagree with the estimates from the MAMBAC procedure. By summing the latent distributions one can estimate the parameters of these distributions. Table 1(a) gives these estimates.

Insert Table 1 about here

Insert Figure 4 about here

Nuisance Covariance. Since it is unlikely that the assumption behind the MAXCOV procedure (zero within-taxa correlations between each pair of variables) is literally true, one might question the effects of violations of this assumption. As mentioned previously, Monte Carlo studies suggested that the MAXCOV procedure is generally robust to this assumption. If we assume for the moment that nuisance correlations exist but are approximately equal in each taxonomy, Equation 2 simplifies to Equation 5, where $cov_n(xy)$ is the nuisance (i.e., within taxa) covariance. At HITMAX, Equation 5 becomes Equation 6, suggesting that the constant K is overestimated by an amount equal to 25%

of the nuisance covariance. Furthermore, the observed covariance in each interval should be corrected by an amount equal to the nuisance covariance when computing the relative base rates in each interval (derived from Equation 5).

$$\text{cov}(xy) = [p+q]\text{cov}_n(xy) + pq[K] = \text{cov}_n(xy) + pq[K] \tag{5}$$

$$\text{cov}(xy) = \text{cov}(xy)_n + .25[K] \quad \Rightarrow \quad \text{cov}(xy) - \text{cov}(xy)_n = .25[K] \tag{6}$$

These observations give us a method to try to reduce the effects of nuisance covariance on the generation of the latent distributions by factoring in estimates of the nuisance covariance into both the computation of the constant K and the later computations of p and q in each interval. We can estimate the size of the nuisance covariance for the non-schizotypic taxonomy by averaging the covariance estimates in the first few intervals on each scale based on the assumption that these intervals are likely to be close to 100% non-schizotypes. Unfortunately, we cannot use the same procedure to estimate the size of the nuisance covariance in the schizotypal taxonomy because the presumed low base rate of this taxonomy makes it unlikely that even the top of the scale contains mostly schizotypes. Therefore, we have assumed in the following analyses that the nuisance covariance is equal in the two taxonomies.

Table 1(b) shows revised estimates of the latent parameters compensating for the nuisance covariance. We used as the estimate of nuisance covariance the observed covariance in the first four intervals on each input variable (scores of 0 to 3). With the exception of the Perceptual Aberration Scale, these revised parameter estimates are quite reasonable. It appears that the strategy that we used for estimating the degree of nuisance covariance for the Perceptual Aberration Scale overestimates the nuisance covariance because the covariance for the first four intervals was high—higher in fact than some other points in the covariance curve. This suggests that these first few intervals are probably not homogeneous. We conducted a second analysis for the Perceptual Aberration Scale using as our estimate of nuisance covariance the lowest point on the covariance curve. This analysis produced much more reasonable results—a base rate

estimate for schizotypy of 8% and estimates of 7.54 and 6.50 for the mean and standard deviation in the schizotypal taxon, respectively. Figure 5 shows the latent distributions of Figure 4 recomputed using these estimates of nuisance covariance in the computation of K and in the later computation of the relative base rates within each interval.

Insert Figure 5 about here

Discussion

The results presented here generally support Meehl's hypothesis of a schizotypal taxon and the validity of the Perceptual Aberration, Magical Ideation, and Cognitive Slippage Scales as indicators of this taxon. A conservative interpretation of the results of the current study is that there appears to be an underlying taxon that is tapped by the three scales of schizotypic signs used, but there is no direct evidence that the taxon being tapped is schizotypy (i.e., the hypothesized genetic risk factor for schizophrenia). Caution is warranted given that the longitudinal data of Chapman et al. (1994) suggest that the Perceptual Aberration and Magical Ideation scales identify people with elevated risk for psychosis, but not necessarily schizophrenia.

Shape of the Covariance Curves. The shape of the covariance curves presents an interesting puzzle. Given the large sample used in this study (5000+ subjects), it is not likely that the minor peak consistently observed to the left of the major peak is a chance finding, especially since it was observed for all three of our measures. Lenzenweger, Korfine, and Loranger (1993) found a similar pattern in a MAXCOV study of several personality disorders, but this pattern was not observed in an earlier empirical study of detecting gender (Golden & Meehl, 1973a). One speculative possibility is that the measures used in this study are sensitive to more than one taxonomy, although perhaps not equally sensitive. Looking at the content of the items from these three measures, it certainly seems plausible that each scale may, for example, tap risk for both schizophrenia and bipolar disorder. As noted earlier, Chapman et al. (1994) reported that the combined Perceptual Aberration/Magical Ideation Scale identified subjects at risk for

psychosis, but elevated rates of both schizophrenia and bipolar disorder were represented in their ten-year follow-up. Although Meehl and his associates have done extensive study of the MAXCOV procedure in both taxonic and non-taxonic situations, little is known about the behavior of these techniques in situations of multiple taxa. Additional Monte Carlo studies might help to clarify this situation and give us guidance on (1) how to proceed and (2) what the limitations of this taxometric methodology might be. Carving nature at its joints is always a challenge; but nature has a lot of joints, and carving just one at a time takes exquisite care.

However, the answer to the puzzling shape of the covariance curves (Figure 3) may actually be quite simple. Each shows a dip before a rise to the eventual peak. This certainly does not fit the model for the MAXCOV procedure that was illustrated in Figure 1, but the clue to what might be going on lies in the graph of the latent distributions (Figure 4). These distributions suggest a mean difference between the two suspected taxa, but with considerable overlap. The overlap is an even greater problem given the low expected base rate for schizotypy. We illustrate in Figure 6, what we think is responsible for the puzzling dip in the covariance curves. We created two frequency distributions using a standard normal table. The distributions were created with a total frequency of 90,000 and 10,000 cases, respectively. We set up the standard deviation of the smaller distribution at half the standard deviation of the larger distribution and shifted the mean of the smaller distribution 1.6 standard deviation units above the mean of the larger distribution. The critical portion of the two resulting curves is shown in Figure 6(a). Notice that unlike Figure 1(a), the curves cross at two points rather than one. Either increasing the base rate of the smaller distribution or separating the curves more would be sufficient to recreate the situation shown in Figure 1(a). Figure 6(c) graphs the proportion of schizotypes in each interval shown for the curves in Figure 6(a). Notice that the curve crosses the .50 value (HITMAX) twice. In Figure 6(b), we modified the larger distribution to give it a strong positive skew. The distribution of scores on the Perceptual Aberration Scale in an unselected sample shows a similar strong positive skew. In this situation the curves also cross twice, but there is a more dramatic swing in the proportion of schizotypes between

the two points where the curves cross as shown in Figure 6(d). If we were conducting a

MAXCOV analysis on the situation on Figure 6(a), we would expect two peaks with a

slight valley between the peaks. The same analysis on the situation in Figure 6(b) would

also produce two peaks, but with a much deeper valley. This is almost exactly what we

found. In the scale that was highly skewed (Perceptual Aberration), we got a deep valley

between two peaks and in the other scales a smaller, but still distinct, valley. Of course,

this post hoc explanation does not prove that our data came from the situation we just

described. It only shows that such an explanation (a combination of too small a mean

difference between schizotypes and non-schizotypes on our indicator variables coupled

with the large base rate differences) is feasible. The latent parameter estimates suggest a

mean separation in the approximate range needed to achieve these results, although the

variance estimates for the schizotypal taxon are a bit larger than those in our scenario.

However, this interpretation of the data has the advantage of parsimony.

Insert Figure 6 about here

Another issue in the current data is the discrepancy between the base rate estimates

produced by MAMBAC and MAXCOV. We believe that the problem lies with the MAMBAC

base rate estimates. The MAMBAC base rate estimation procedure relies on comparing

data from the extreme ends of the distribution under the assumption that the individuals at

one end will be exclusively schizotypes and the individuals at the other end will be

exclusively non-schizotypes. But the latent distributions produced by the MAXCOV

procedure suggest that this assumption of pure groups at the extremes may be

unwarranted for these scales.

Taxometric search techniques are dramatically different from the traditional null

hypothesis testing paradigms that dominate most of psychology (Cohen, 1994; Lykken,

1968; Meehl, 1967). With sample sizes in excess of 5000, any group difference that we

might have evaluated would be virtually guaranteed to be statistically significant

regardless of whether it had any scientific or clinical significance. In the paradigms

popularized by R. A. Fisher, larger sample sizes provide a weaker test of a hypothesis because it is easier to reject the null hypothesis due to the increased power. But the taxometric procedures used in this study make specific point predictions about the shapes of curves, the locations of their peaks, and the estimates of bases rates for the suspected taxa. Larger sample sizes provide a tougher test of the hypothesis because deviations from the expected results are easier to detect. It was the consistent deviation from the expected shape of the covariance curves, coupled with the fact that similar deviations had shown up in other research, that forced the analysis of the effects of mean separation and shapes of the latent distributions just described. We would argue that, even with this bit of post hoc reasoning, the consistency with which we matched multiple point predictions—predictions that were all based on a single assumption of an underlying taxonomy—is a strikingly powerful finding. It certainly strengthens Meehl's argument for the existence of a schizotypal taxon.

Potential Psychometric Artifacts. Now that we have argued that the data support Meehl's concept of a schizotypal taxonomy, we would like to add a cautionary note. During some of our follow-up work (described below), we became concerned about the possibility of psychometric artifacts masquerading as taxa. One has to be careful when working with psychometric measures. We illustrate the problem that can develop with a simple example. Assume that you have a distribution of a variable like height. To avoid the possibility of an underlying taxa, we will assume that the distribution is for females only. Suppose we develop a psychometric instrument with a series of Likert Scale items of the form "I am taller than X inches." If we create a scale with 80 items by varying X from 1 to 80 in units of one, our scale would produce a distribution very similar in shape to the latent distribution of height. We often assume that psychometric instruments give us this approximate correspondence to nature, but that assumption is rarely true. For example, if our scale included 80 items, most of them clustered near a single value (e.g., 68), we will get a bimodal distribution. The extreme situation is where our scale has 80 items, each asking if the person is taller than 68 inches. Only two scores are possible here: 0 for those shorter than or equal to 68 and 80 for those taller than 68. The distribution of item

difficulties in a psychometric measure clearly affects what one observes irrespective of the true state of nature, as Chapman and Chapman (1973) demonstrated in another context more than two decades ago.

This concern for the possibility of a psychometric artifact is not just academic. The possibility exists that the scale development procedures for each of the measures of schizotypal signs used in the current study may have inadvertently created just such an artifact. Because the scales were each developed to measure characteristics of a low base rate phenomenon (schizotypy), a deliberate strategy of selecting items with low endorsement frequencies was used, essentially clustering the items in a narrow range of item difficulty. Although a reasonable psychometric decision because it maximized discrimination of the scale where it would do the most good, it is possible that this procedure may have created a subtle psychometric artifact that was undetectable until Meehl's powerful taxometric search procedures were applied. We have begun to evaluate the feasibility of this scenario with Monte Carlo studies, but until those data are in it would be wise to interpret the data from this study cautiously.

Directions for Future Research. Assuming for the moment that we can rule out the possibility of psychometric artifacts, then the most reasonable interpretation of the current data is that there appears to be an underlying schizotypal taxon with a base rate close to what one would expect for schizotypy. The schizotypy measures used in this study appear to be moderately valid indicators of this taxonomy, but their sensitivity needs to be improved if we want to really nail down the construct of schizotypy.

One advantage of this taxometric search approach is that it offers a method to bootstrap our way to more refined measures of schizotypy. By using the information from initial taxometric search analyses with promising measures, we can perform item analyses designed to create revised measures that are more sensitive or more specific to the underlying taxa. It is theoretically possible to use population parameter estimates based on moderately valid measures to guide the construction of refined measures that would give better prediction. This process could then be repeated, bootstrapping our way to refined measures (Dawes & Meehl, 1966).

We have been experimenting with such item analysis techniques in our laboratory using both the sample from this study and Monte Carlo generated samples. Refinement of promising measures could substantially enhance the performance of Meehl's taxometric search techniques. It was this work, however, that sensitized us to the possibility of a psychometric artifact. We noticed that several of our selection criteria led to the selection of items in a narrow range of item difficulty. It would be very foolish to do this scale-refinement work using a blind empirical approach. Our intention is to use Monte Carlo techniques extensively throughout this process to get a feel for the subtleties of these scale refinement procedures.

Although we believe that the unusual shape of the covariance curve is probably the result of less than optimal discrimination for our indicator measures as described above, we cannot yet rule out alternative explanations such as the presence of more than two taxa. This area deserves more study—primarily Monte Carlo studies of the behavior of these taxometric techniques when multiple taxa are present.

Summary. The goals in this construct validation research are (1) to identify the likely state of nature regarding risk for schizophrenia and (2) measure the relevant variables with the greatest precision possible. Of course, these points are interrelated. Cleaner measures give us a better look at the state of nature, and the right model of nature guides the production of better measures. Although issues still need to be resolved about the current data (e.g., the possibility of a psychometric artifact or more than two taxa), we believe that the current study gives us insight into point #1 and the data necessary to make advances on point #2.

The results of this study are a testament to the power of the taxometric techniques developed by Meehl and his colleagues. Even with the correction for nuisance covariance, the latent distributions for our three variables are well short of optimal. Even still, the techniques provide converging evidence for the existence of a pair of taxa—perhaps one of which is the schizotypal taxon hypothesized by Meehl. Theoretical and empirically-guided refinement of these measures could provide us with the precision needed to truly test the construct validity of the concept of schizotypy.

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Author Notes

Table 1

Parameter Estimates of the Three Indicator Variables for Each Taxon
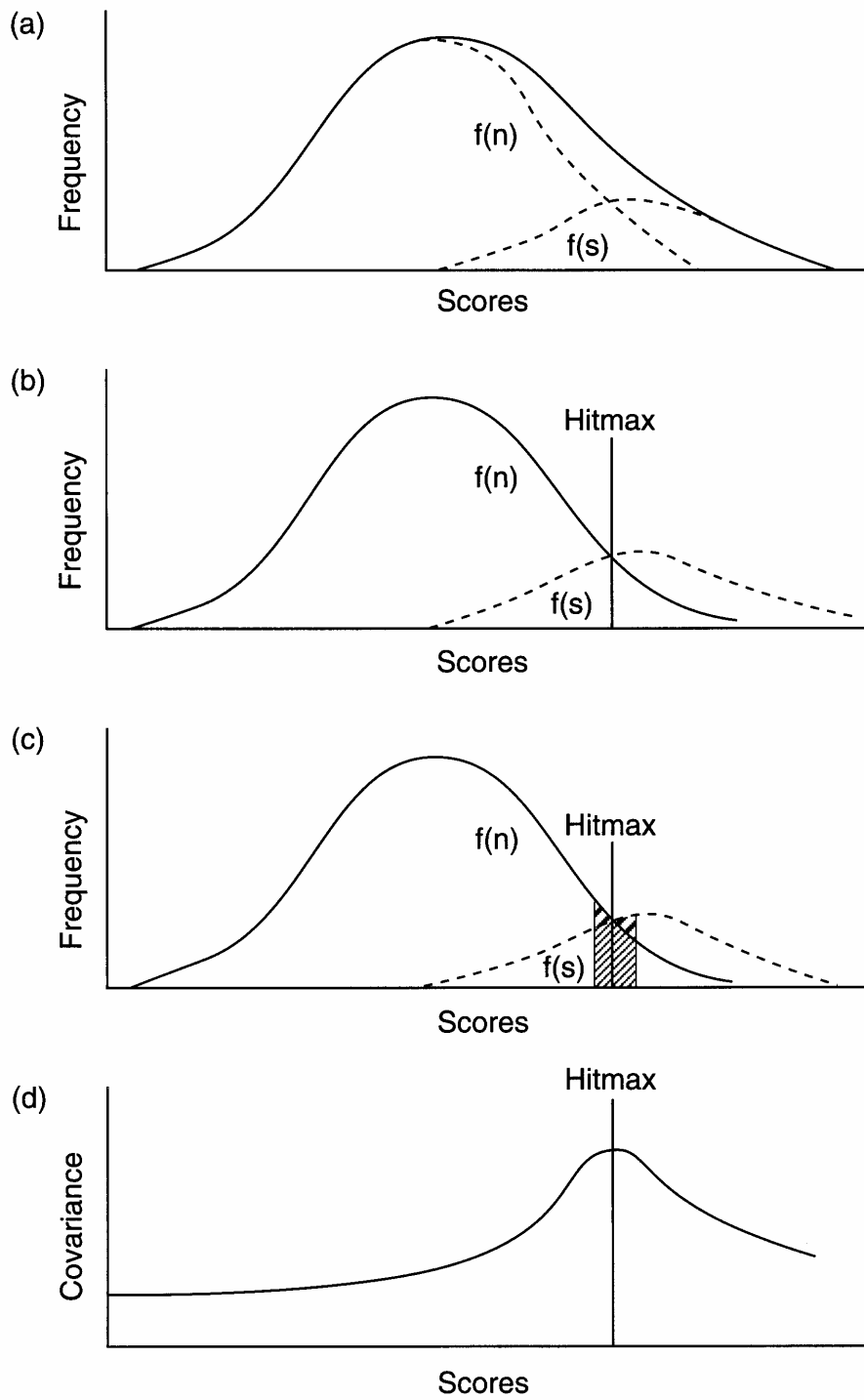
(a) Without Correction for Nuisance Covariance

	Cognitive Slippage	Magical Ideation	Perceptual Aberration
Schizotypes	16.38 (8.92)	12.53 (5.58)	7.43 (6.45)
Non-Schizotypes	8.15 (6.47)	8.08 (5.33)	4.26 (3.85)
Schizotype BR	10%	10%	8%

(b) With Correction for Nuisance Covariance

	Cognitive Slippage	Magical Ideation	Perceptual Aberration
Schizotypes	19.31 (8.01)	13.72 (5.10)	16.14 (4.87)
Non-Schizotypes	8.15 (6.44)	8.08 (5.32)	4.25 (3.82)
Schizotype BR	7%	8%	2%

Note: Means are shown with standard deviations in parentheses.

Figure 1 Illustration of the Maximum Covariance Taxonomic Search Procedure.

(a)

Frequency

f(n)

f(s)

Scores

(b)

Frequency

Hitmax

f(n)

f(s)

Scores

(c)

Frequency

f(n)

Hitmax

f(s)

Scores

(d)

Hitmax

Covariance

Scores

(Moderately Valid Indicator Variable)

Figure 2 Typical MAMBAC Curves for Taxonic and Non-Taxonic Situations (From Meehl & Yonce, 1994) and the Obtained MAMBAC Curves.
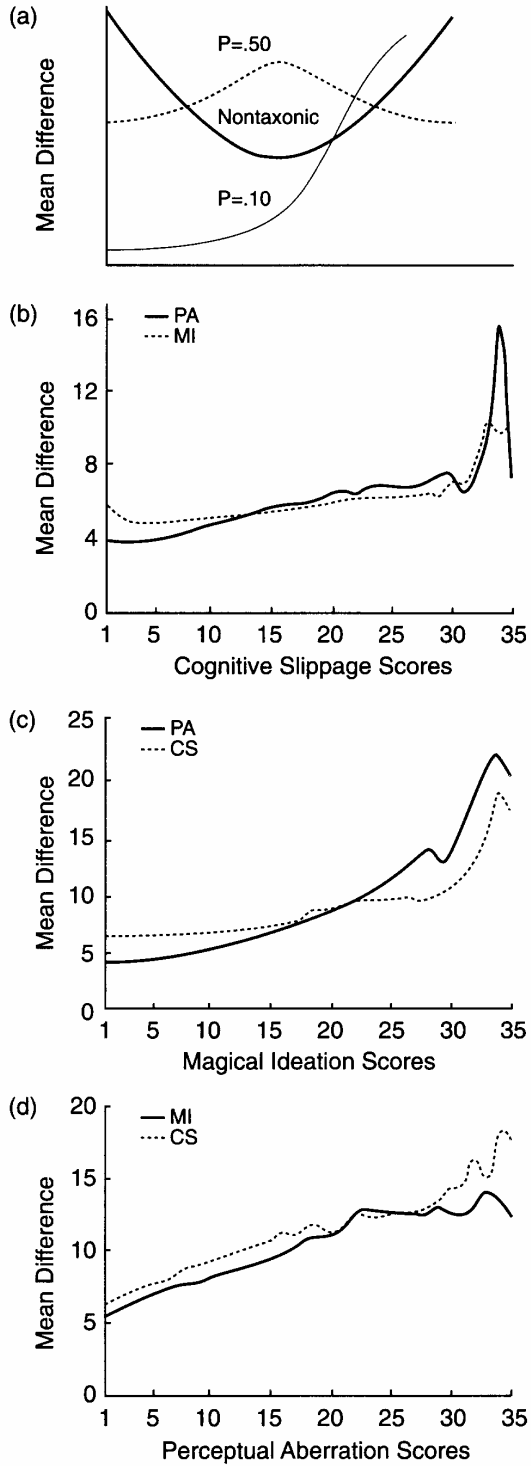
Figure 3 Covariance Curves using a sliding interval of three scores and employing a smoothing technique to the resulting curve
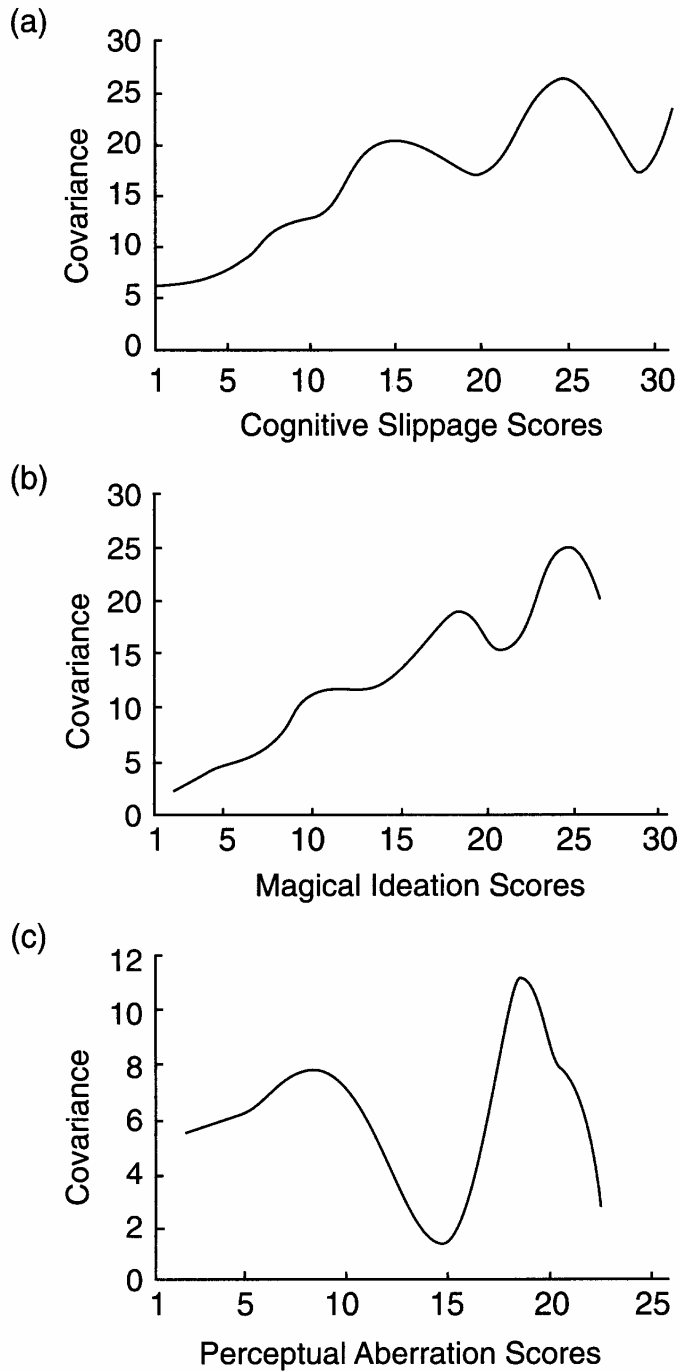
Figure 4 The Latent Distributions (both actual and relative) for Schizotypes and Non-Schizotypes on the Three Measures of Schizotypic Signs.
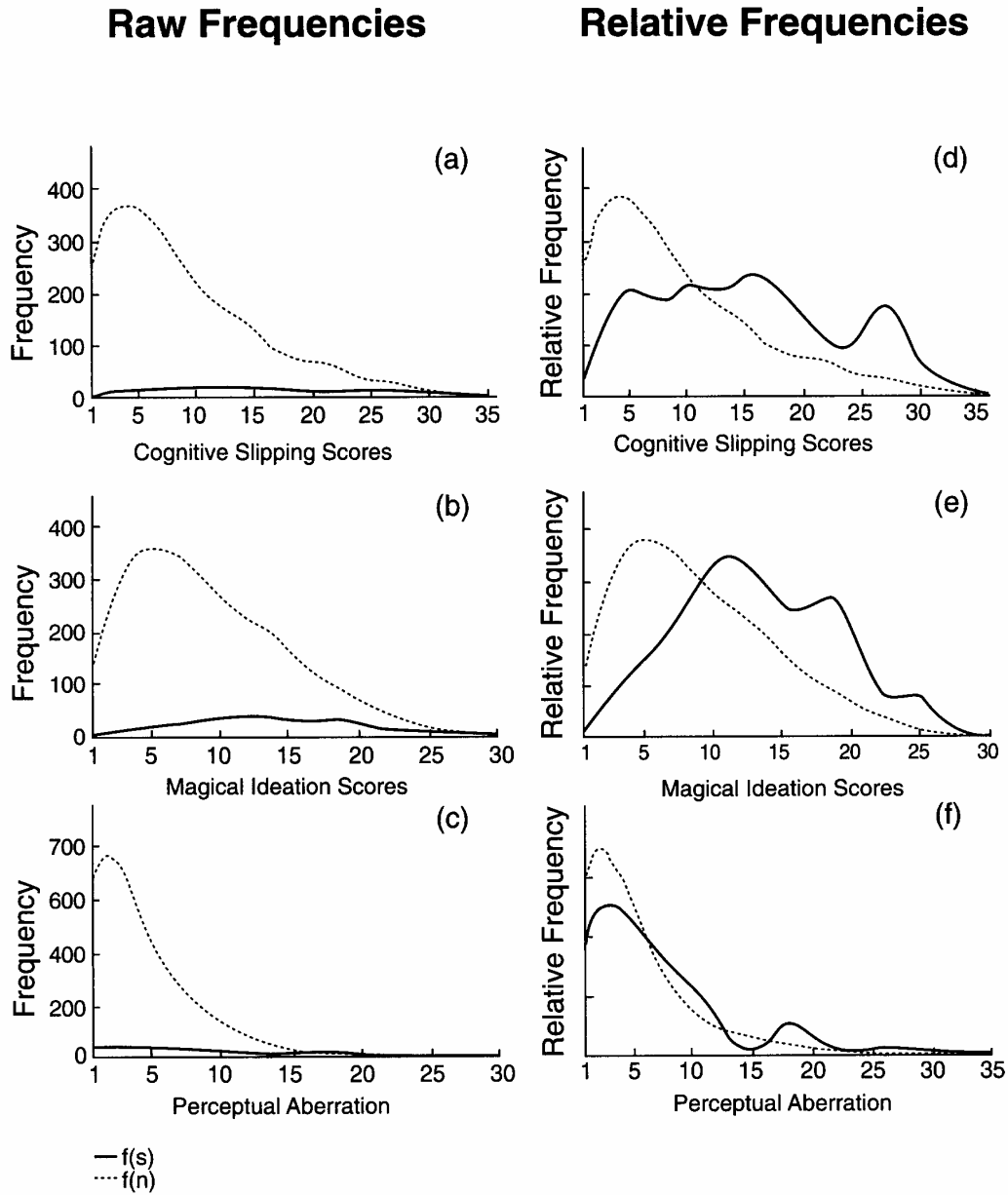
Figure 5 The Latent Distributions (both actual and relative), Corrected for Nuisance Covariance, for Schizotypes and Non-Schizotypes on the Three Measures of Schizotypic Signs
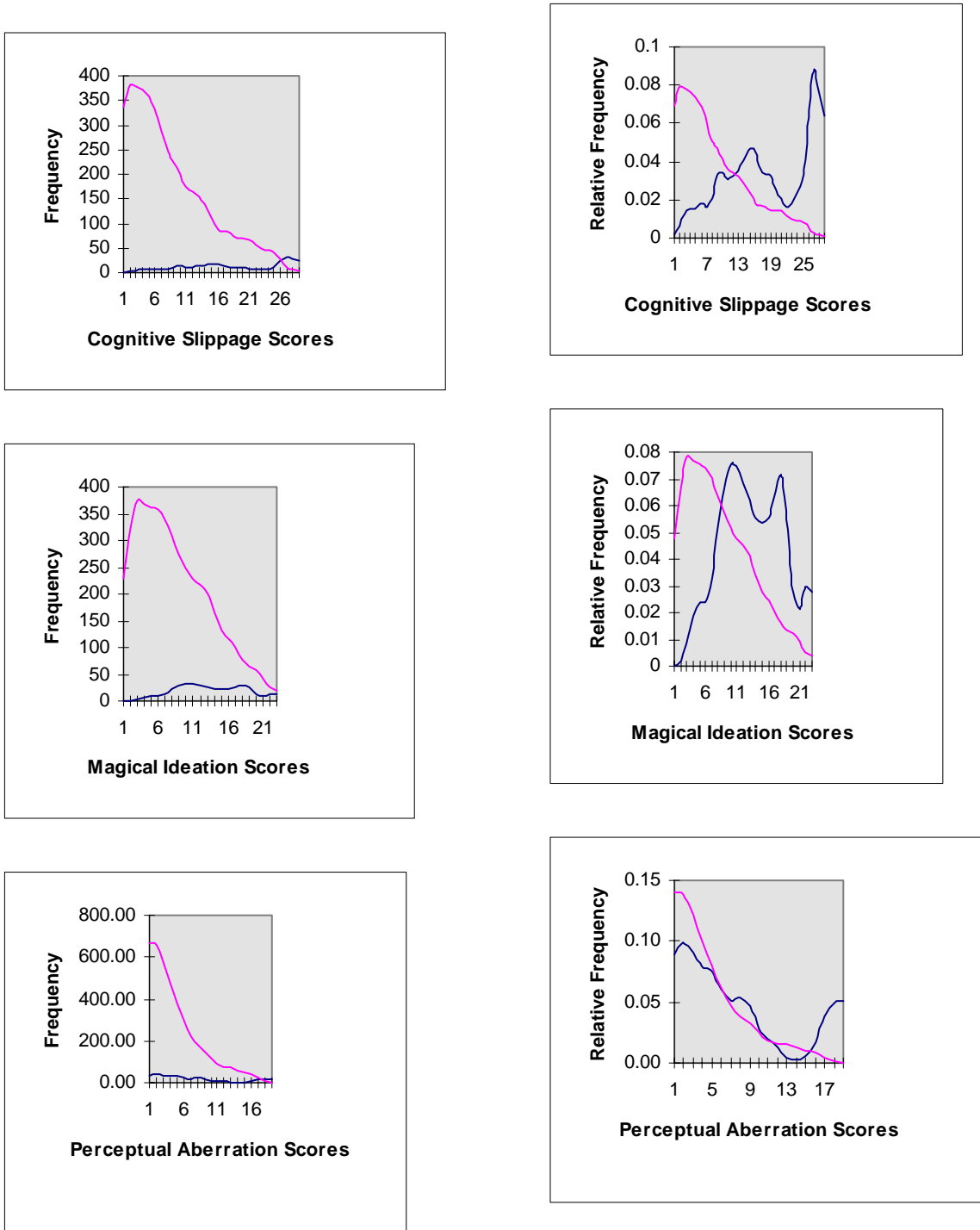
Figure 6 Illustrating the Effects of Too Small a Mean Separation Between Taxonomic Groups When Attempting to Identify a Low Base Rate Taxonomy