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Identifying Latent Clinical Taxa, III: An Empirical Trial of the Normal Single-Indicator Method, Using MMPI Scale 5 to Identify the Sexes[1]

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ABSTRACT

A method of identifying latent taxa employing only a single indicator-variable but relying on the idealization of intra-taxon distribution normality was applied to real data, consisting of the Masculinity-femininity scores (MMPI Scale 5) of 665 females and 410 males. Making arbitrary cut-and-try assignments of the six latent distribution parameters N_m, $\bar{x}_m$, σ_m, N_f, $\bar{x}_f$, σ_f (the first 3 determining the last three via observational constraints), normal curve tables were entered to generate "theoretical" interval frequencies for the manifest (mixed-taxon) distribution, and chi-square tests for badness-of-fit were done on each of the 120 combinations of parameters-assignments. Choosing the best-fitting combination as estimators, these inferred values of the taxon base-rates and means were as close to the true values as scale coarseness permitted, but the estimated sigmas were in error by around one-fifth of their true values. Since both latent taxa violated the normality assumption (skew and leptokurtic), the successful outcome suggests satisfactory robustness. Results of this pilot study are considered sufficiently encouraging to justify (a) Monte Carlo and (b) further real-data tests of the method.

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[1] In a previous contribution to this Research Report series (Meehl, 1968, Section 3, pages 47-54) a method was proposed for identifying the presence of a latent taxonomic situation (dichotomous case) when only a single fallible indicator-variable is available, as contrasted with the (much preferable) situation in which a family of three or more construct-valid indicators are known to discriminate, which was the psychometric situation mainly emphasized in previous contributions (Meehl, 1965, 1968; but see also Dawes & Meehl, 1966). The mathematical rationale will not be repeated here, for which the reader is referred to the earlier report at the cited locus. Suffice it to say here that whereas the multiple-indicator methods make only weak assumptions about the distribution shapes for single indicators of the indicator-family, the present one-indicator technique relies upon an approximative assumption of intra-taxon normality, i.e., we assume that within each of the two latent taxa being sought for, the indicator in use is, while not precisely normal, sufficiently close to normal that the method can be used without gross distortion of the underlying reality.

[2] The reader is referred to equations [99]–[103] of PR-68-4 (page 51 of Meehl, 1968) which set up the simple algebra of the situation. One first assigns arbitrary base-frequency for one of the taxa. This determines the base-frequency for the other taxon. Holding these values fixed, one assigns an arbitrary mean to one of the taxa, which assignment, given the base-frequency values presupposed in the preceding step, determines the mean of the other taxon. Finally one assigns an arbitrary standard deviation to one of the taxa, which assignment, given the preceding assignments (and implied values) of the frequencies and means, determines the standard deviation of the other taxon. So that the arbitrary assignment of a base-frequency, a mean, and a sigma to one taxon determines the corresponding values for the other taxon. These consequences are algebraic identities and do not depend upon the normality assumptions. However, to generate an expected manifest-distribution frequency from any of the various combinations of latent assignments that thus arise, some assumption regarding distribution form must be made. If we make the normality assumption within taxa, each triad of arbitrary values (N_s, $\bar{x}_s$, σ_s) determines expected frequencies in class-intervals of the latent frequency function for the first postulated taxon; and in the same way the other

taxon's parameter values (N_n, $\bar{x}_n$, σ_n) that are determined algebraically by the first taxon's parameter values will generate as set of expected frequencies for each class interval of the latent frequency function for the second taxon. When these two latent frequency functions, flowing necessarily from the arbitrary parameter assignments (together with the normality postulate) are superimposed, we thereby generate an

[3] expected distribution of manifest frequencies (mixed taxa). That set of theoretically calculated frequencies is then compared with the observed, the discrepancy measured by chi-square as usual, and the chi-square value recorded as one point on a curve of theory-observation discrepancies. The entire process is then repeated, first for differing values of sigma (holding the frequencies and means fixed), then for the same range of values of sigma (holding fixed a different pair of means and taxon-rates); and, finally, running through the same set of sigmas and the same set of means but with another arbitrary set of frequencies. We thus generate a family of curve-families of chi-squares representing observation-theory discrepancies, and we assume that the minimum chi-square — hopefully a statistically nonsignificant one — corresponds to the underlying latent taxon situation.

Pending a large-scale Monte Carlo investigation of the sampling characteristics of the method, it was thought worthwhile to try it out on some real data in which we would pretend not to know which patients belonged to each latent taxon, what the latent means and sigmas were, or even what the relative proportions of the two latent taxa were, to see whether the method would give us anything like the right answers. It is not easy to locate a true taxonomy in the area of psychometrics, but one of the good ones, both because it does yield a genuine bimodality in personality scores and because it is completely objective on the criterion side, is biological sex. We therefore applied the method to the pseudo-problem of identifying the male-female taxonomy, using the MMPI masculinity-

[4] femininity scale as our single indicator-variable (Scale 5). The raw data were computer print-outs of the Mf scores of 410 males and 665 females which had previously been drawn randomly for another purpose from the University of Minnesota Hospital "General Psychiatric Population." The statistical characteristics of this pair of latent taxa on MMPI Scale 5 are shown in Table 1.

Table 1

The Values of the Sample Statistics for Each Taxon

	N	Base-Rates	$\bar{x}$	S.D.
Males	410	*P* = .38	24.73	5.75
Females	665	*Q* = .62	36.04	5.66
Total	1075	1.00	31.72	7.92

For this pilot study it was thought sufficient to try postulated frequencies for the male taxon ranging from 100 (base rate *P* = .09) to 500 (base rate *P* = .46) proceeding by 100-case increments; that is, the hypothesized male frequencies tried against observation were 100, 200, 300, 400, and 500, corresponding to hypothesized male base-rates of .09, .19, .28, .37, and .46 respectively.

Given the observed grand (mixed taxon) mean of $\bar{x}_t = 31.73$, and the observed grand (mixed taxon) standard deviation of 7.92, "safe" or "plausible" values of the hypothesized latent mean for the males were considered to run from around 15 (raw score) on MMPI Scale 5 to around double that value at $\bar{x}_m = 30$, and the variation in cut-

[5] and-try mean values for the males was run by five-unit steps; that is, we tried out latent taxon mean of the males at the four values $\bar{x}_m = 15$, $\bar{x}_m = 20$, $\bar{x}_m = 25$, and $\bar{x}_m = 30$.

Given the grand observed (mixed-taxon) sigma of 7.92, arbitrary cut-and-try values of the male taxon standard deviation were run from a low of 3 and proceeding by unit steps of 4, 5, 6, and 7 through 8.

From this logical tree of arbitrary values assigned to each of the three latent parameters, there follow, on the intra-taxon normality assumption, a set of 120 combinations (i.e., 5 arbitrary base rates x 4 arbitrary means x 6 arbitrary sigmas). This would mean a comparison of the observed (mixed-taxon) frequency distributions with each of the 120 cut-and-try distributions and the plotting of 120 chi-squares to identify the best fit. Actually not all of these chi-squares, and not even all of the curves within a curve-family, had to be computed and plotted, because some of the arbitrary parameter assignments generated negative variances for the second [actually female] taxon. The appearance of these negative variances caused us (foolishly) to double check for possible

computational error. There was no need to assume error on the usual grounds of the algebraic impossibility of a negative variance when a sum of squares of deviations from a mean is directly computed. When a variance is estimated by a combination of an observed dispersion and an arbitrary latent taxon value, as in the present procedure, a negative estimated variance can easily arise from sufficiently extreme [i.e., grossly erroneous] arbitrary assignments of the variance (together with the base-rate and mean of
[6] one taxon). The correct inference from the appearance of a negative variance is, of course, simply that these particular latent values are precluded by our empirical data, which is what we are investigating!

In calculating the observational distribution from the postulated latent values, from 35 to 52 intervals of unit width (integer increments) on the Mf (raw score) variable were employed, avoiding grouping coarseness problems. This amounts to intervals of width approximately .13 sigma on the manifest distribution, and approximately .18 sigma on each of the two latent taxon distributions. Calculated latent frequencies within a class interval were rounded off to the nearest integer, combining intervals at tails whenever the expected values were less than one (Cochran, 1954).

In Table 2 are shown the chi-square values and chi-square normal deviates indicating the discrepancy between the observed grand (mixed-taxon) distribution and the 120 theoretically calculated distributions generated by the various sets of arbitrary latent parameter values for the base-rates, means, and sigmas. Note that the lowest arbitrary mean value tried for males ($\bar{x}_m = 15$) gives rise to impossibly negative estimated variances for the other latent taxon at 4 of the 5 arbitrary base-rates.

The raw Mf scores on the manifest (mixed-taxon) frequency distribution ran from raw score = 9 through raw score = 49 inclusive (corresponding to T-scores from 106 to 28 for males, and from 24 to 95 for females, respectively), requiring a total of 41 ungrouped class-intervals to cover the empirically observed range.

[7]

Table 2

The Chi-square Values and Chi-square normal deviates

for Each of the 120 sets of Arbitrary Latent Values

$N_m = 100$

$\bar{x}_m$	σ_m	Intervals Range	Intervals Number	Degrees of Freedom (n)	χ^2	$\sqrt{2\chi^2} - \sqrt{2n-1}$	p
15	3	8 – 51	44	41	172	9.55	<.01
	4	6 – 51	45	42	157	8.61	<.01
	5	4 – 51	48	45	152	8.01	<.01
	6	2 – 51	50	47	155	7.97	<.01
	7	0 – 51	52	49	169	8.53	<.01
	8	0 – 50	51	48	224	11.42	<.01
20	3	11 – 54	44	41	80	3.32	<.01
	4	10 – 54	45	42	73	2.97	<.01
	5	8 – 54	47	44	72	2.67	<.01
	6	7 – 54	48	45	76	2.90	<.01
	7	5 – 54	50	47	85	3.40	<.01
	8	4 – 52	49	46	96	4.32	<.01
25	3	10 – 54	45	42	140	7.62	<.01
	4	10 – 54	45	42	130	7.01	<.01
	5	10 – 54	45	42	117	6.19	<.01
	6	10 – 54	45	42	105	5.38	<.01
	7	10 – 54	45	42	100	5.03	<.01
	8	9 – 54	46	43	96	4.64	<.01
30	3	8 – 56	49	46	138	7.07	<.01
	4	8 – 56	49	46	125	6.27	<.01
	5	8 – 56	49	46	113	5.49	<.01
	6	8 – 56	49	46	107	5.09	<.01
	7	10 – 54	45	42	107	5.52	<.01
	8	10 – 54	45	42	98	4.89	<.01

[8]

Table 2 (Cont.)

$N_m = 200$

$\bar{x}_m$	σ_m	Intervals Range	Intervals Number	Degrees of Freedom (n)	χ^2	$\sqrt{2\chi^2} - \sqrt{2n-1}$	p
15	3					Impossible as $\sigma_f^2 < 0$	
	4						
	5						
	6						
	7						
	8						
20	3	12 – 51	40	37	66	2.95	<.01
	4	10 – 51	42	39	45	0.71	.24*
	5	7 – 51	45	42	52	1.09	.14*
	6	5 – 51	47	44	77	3.08	<.01
	7	3 – 49	47	44	123	6.35	<.01
	8	1 – 48	48	45	272	13.89	<.01
25	3	11 – 55	45	42	192	10.49	<.01
	4	11 – 55	45	42	149	8.15	<.01
	5	11 – 55	45	42	124	6.64	<.01
	6	12 – 55	44	41	105	5.49	<.01
	7	7 – 54	48	45	90	3.99	<.01
	8	6 – 54	49	46	89	3.80	<.01
30	3	8 – 56	49	46	186	9.75	<.01
	4	8 – 56	49	46	163	8.52	<.01
	5	8 – 56	49	46	133	6.77	<.01
	6	8 – 56	49	46	116	5.69	<.01
	7	7 – 56	50	47	108	5.06	<.01
	8	10 – 54	45	42	101	5.10	<.01

[9]

Table 2 (Cont.)

$N_m = 300$

$\bar{x}_m$	σ_m	Intervals Range	Intervals Number	Degrees of Freedom (n)	χ^2	$\sqrt{2\chi^2} - \sqrt{2n-1}$	p
15	3					Impossible as $\sigma_f^2 < 0$	
	4						
	5						
	6						
	7						
	8						
20	3	11 – 45	35	32	1053	37.9	<.01
	4	9 – 43	35	32	1217	41.4	<.01
	5	7 – 42	36	33	2045	56.0	<.01
	6					Impossible as $\sigma_f^2 < 0$	
	7						
	8						
25	3	12 – 56	44	41	280	14.70	<.01
	4	12 – 56	44	41	188	10.40	<.01
	5	11 – 55	44	41	131	7.19	<.01
	6	9 – 55	46	43	104	5.20	<.01
	7	7 – 53	47	44	76	3.00	<.01
	8	5 – 52	48	45	70	2.40	<.01
30	3	6 – 58	53	50	267	13.20	<.01
	4	6 – 58	53	50	203	10.20	<.01
	5	8 – 56	49	46	163	8.52	<.01
	6	8 – 56	49	46	136	6.85	<.01
	7	8 – 56	49	46	108	5.16	<.01
	8	10 – 54	45	42	102	5.17	<.01

[10]

Table 2 (Cont.)

N_m = 400

$\bar{x}_m$	σ_m	Intervals Range	Intervals Number	Degrees of Freedom (n)	χ^2	$\sqrt{2\chi^2} - \sqrt{2n-1}$	p
15	3					Impossible as $\sigma_f^2 < 0$	
	4						
	5						
	6						
	7						
	8						
20	3						
	4						
	5						
	6						
	7						
	8						
25	3	16 – 56	41	38	318	16.60	<.01
	4	14 – 55	42	39	196	11.00	<.01
	5	11 – 55	45	42	118	6.25	<.01
Closest to True Value	6	9 – 53	45	42	72	2.89	<.01
	7	6 – 51	46	43	40	–.28	.61**
	8	4 – 48	45	42	70	2.72	<.01
30	3	5 – 61	57	54	380	17.42	<.01
	4	7 – 59	53	50	268	13.65	<.01
	5	7 – 59	53	50	198	9.95	<.01
	6	9 – 57	49	46	152	7.90	<.01
	7	8 – 57	50	47	112	5.34	<.01
	8	9 – 55	47	44	99	4.74	<.01

**Best fit in 120 trial values

[11]

Table 2 (Cont.)

$N_m = 500$

$\bar{x}_m$	σ_m	Intervals Range	Intervals Number	Degrees of Freedom (n)	χ^2	$\sqrt{2\chi^2} - \sqrt{2n-1}$	p
15	3						
	4						
	5						
	6						
	7						
	8						
20	3					Impossible as $\sigma_f^2 < 0$	
	4						
	5						
	6						
	7						
	8						
25	3	16 – 55	40	37	440	20.80	<.01
	4	14 – 54	41	38	203	11.40	<.01
	5	11 – 51	41	38	73	3.42	<.01
	6	8 – 48	41	38	68	3.00	<.01
	7	5 – 41	37	34	1269	42.30	<.01
	8					Impossible as $\sigma_f^2 < 0$	
30	3	6 – 60	55	52	508	21.70	<.01
	4	6 – 60	55	52	340	15.90	<.01
	5	5 – 55	51	48	292	14.40	<.01
	6	5 – 55	51	48	216	11.00	<.01
	7	8 – 57	50	47	113	5.49	<.01
	8	9 – 55	47	44	104	5.09	<.01

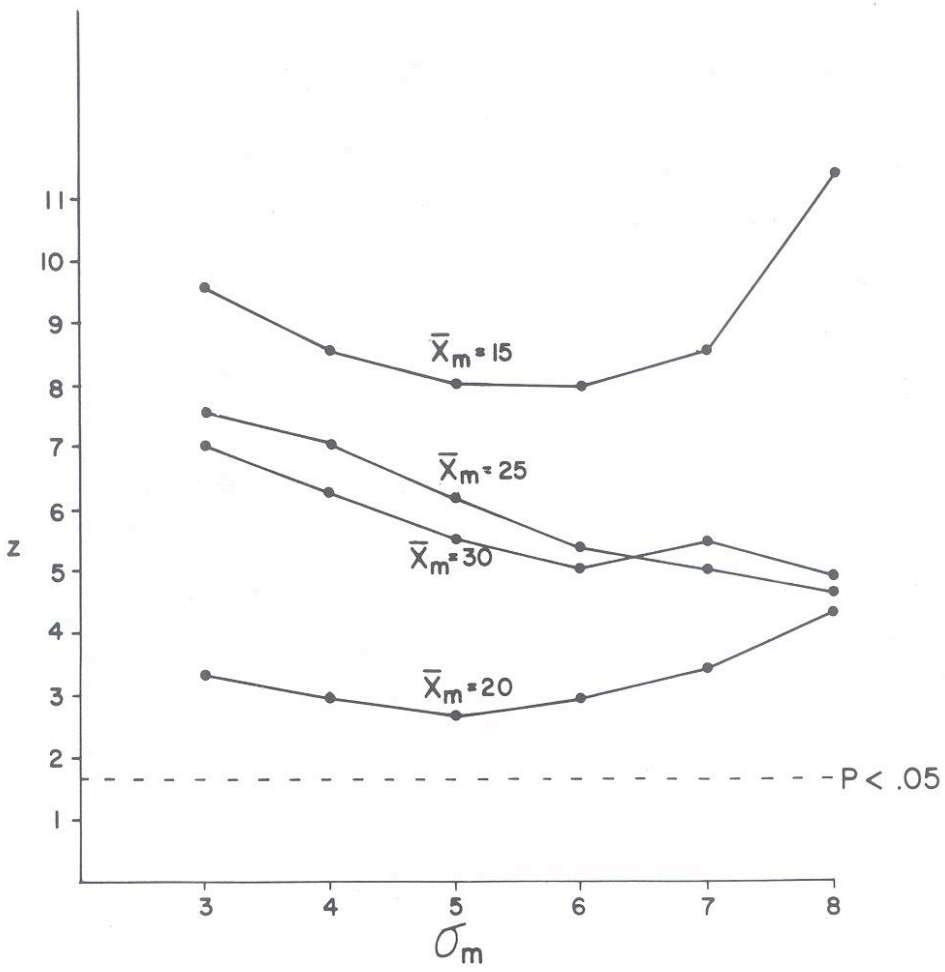
[12] The arbitrary parameter assignment method of course gives rise to non-zero "theoretical" values for class-intervals outside the empirical range of scores, and in other cases predicts near-zero frequencies for intervals that are actually occupied. Hence many of the chi-squares are based upon more than the 38 [= 41 – 3] degrees of freedom that would be involved in testing significance with 41 class intervals, and some are based on fewer d.f. than this. Consequently the degrees of freedom varied considerably from one goodness-of-fit test to another, rendering the obtained chi-square values not directly comparable without taking the varying degrees of freedom into account. Although we plotted and inspected the graphs of the raw chi-square values themselves, what is of proper interest for purposes of estimating the true values of the best-fitting hexad of arbitrary parameters is the function $\left(\sqrt{2\chi^2} - \sqrt{2n-1}\right)$ treatable as a normal deviate with unit variance for d.f. > 30. Table 2 shows the interval ranges, number of intervals, degrees of freedom, chi-square value, the associated value of the chi-square deviate $\sqrt{2\chi^2} - \sqrt{2n-1}$, and the *P*-value from normal curve tables. In the case of chi-square, of course, the proper *P*-value to use is the integral under the normal function from the given chi-square deviate upward, since probabilities associated with negative values of the normal chi-square deviate (as in the best-fitting combination $N_m = 400$, $\bar{x}_m = 25$, $\sigma_m = 7$, where the deviate is at $z = -.28$) are greater than ½, i.e., this assignment of parameters fits the empirical distribution better

[13] than one might expect on the average to fit it through random sampling fluctuations alone.

The chi-square deviate values in Table 2 are plotted as curve-families in Figures 1 through 5. Each figure represents a family of curves associated with one of the five arbitrary assignments of the base-rate N_m. Each curve within the family represented by a given figure shows the dependency of the chi-square deviate upon sigma assignment, given a fixed assignment of the latent mean $\bar{x}_m$. And each plotted point on a given curve within a family represents the chi-square deviate value obtained for an abscissa value of the indicated sigma, given the arbitrary mean generating the curve on which the point is found, and the arbitrary base-rate generating the family of curves represented in the figure. So each point on one of these graphs indicates a chi-square deviate, corrected for the variable degrees of freedom on which it was based, and reflecting the theoretical-

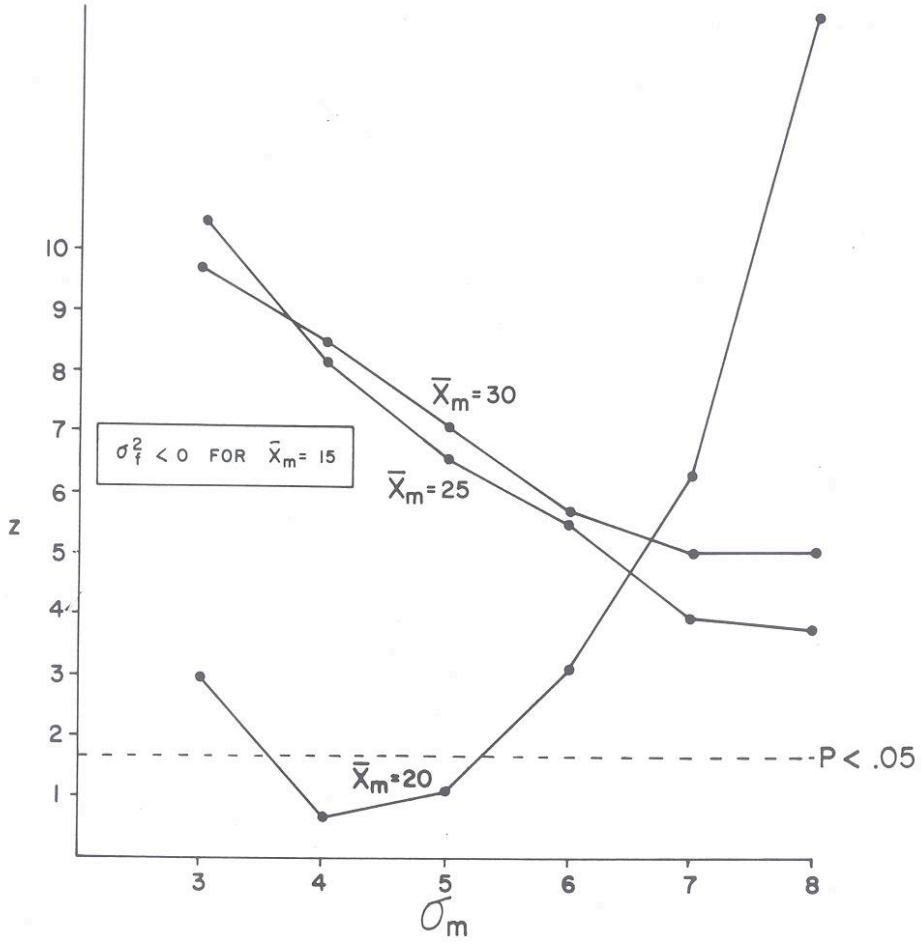
observed discrepancies yielded by the particular arbitrary parameter combination which gave rise to it. As the curves rise, they reflect increasingly unsatisfactory parametric assumptions about the latent situation. Thus, in Figure 1 the top curve shows the set of 6 chi-square deviates generated by arbitrary assignments of $\sigma = 3, 4, \ldots 8$ to the one latent taxon, when the arbitrary mean assigned to that taxon is 15, given the fixed arbitrary base-rate for that taxon arbitrarily assigned at $N_m = 100$. The four curves in Figure 1 show the dependence of the goodness-of-fit upon the six arbitrary standard deviation assignments, for each of the four

FIGURE 1



$z = \sqrt{2\chi^2} - \sqrt{2n-1}$ AS FUNCTION OF TRIAL VALUES OF σ_m AND $\bar{X}_m$ FOR $N_m = 100$

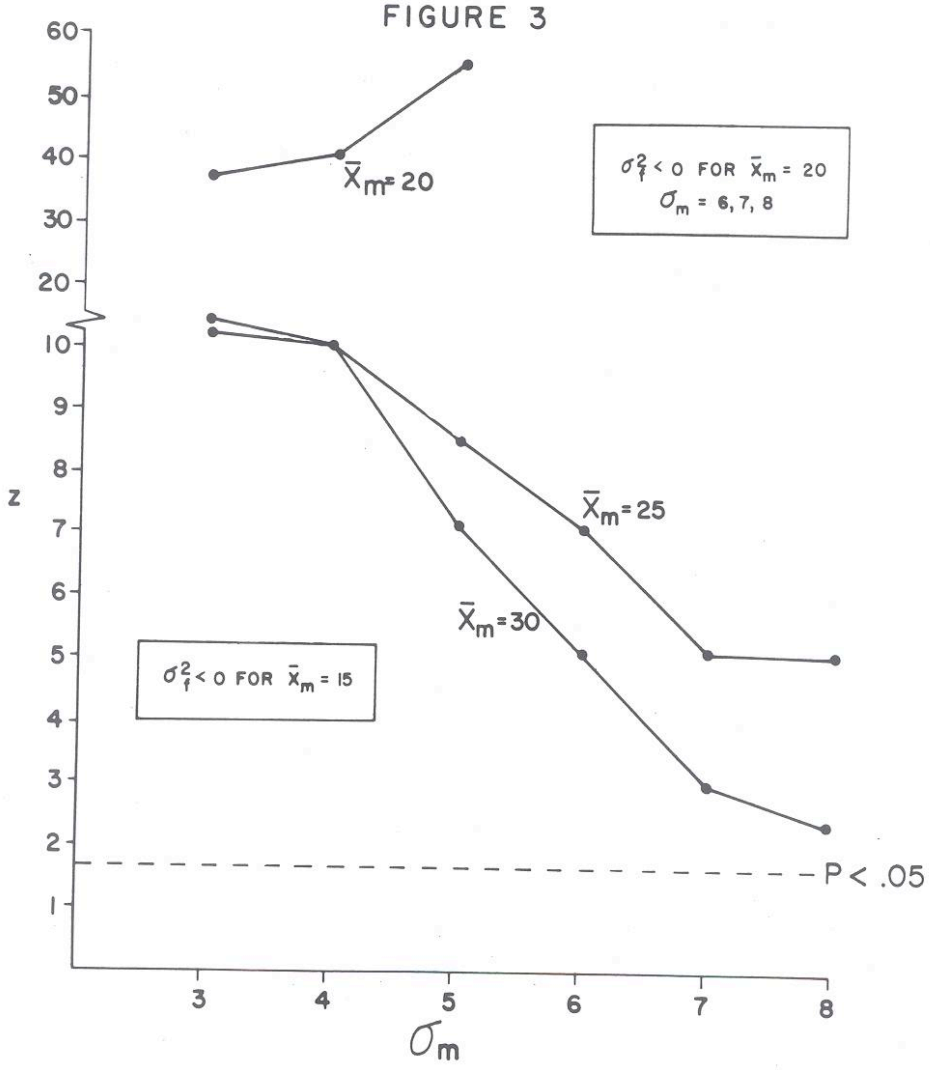
FIGURE 2



$z = \sqrt{2\chi^2} - \sqrt{2n-1}$ AS FUNCTION OF TRIAL VALUES OF σ_m AND $\bar{X}_m$ FOR $N_m = 200$

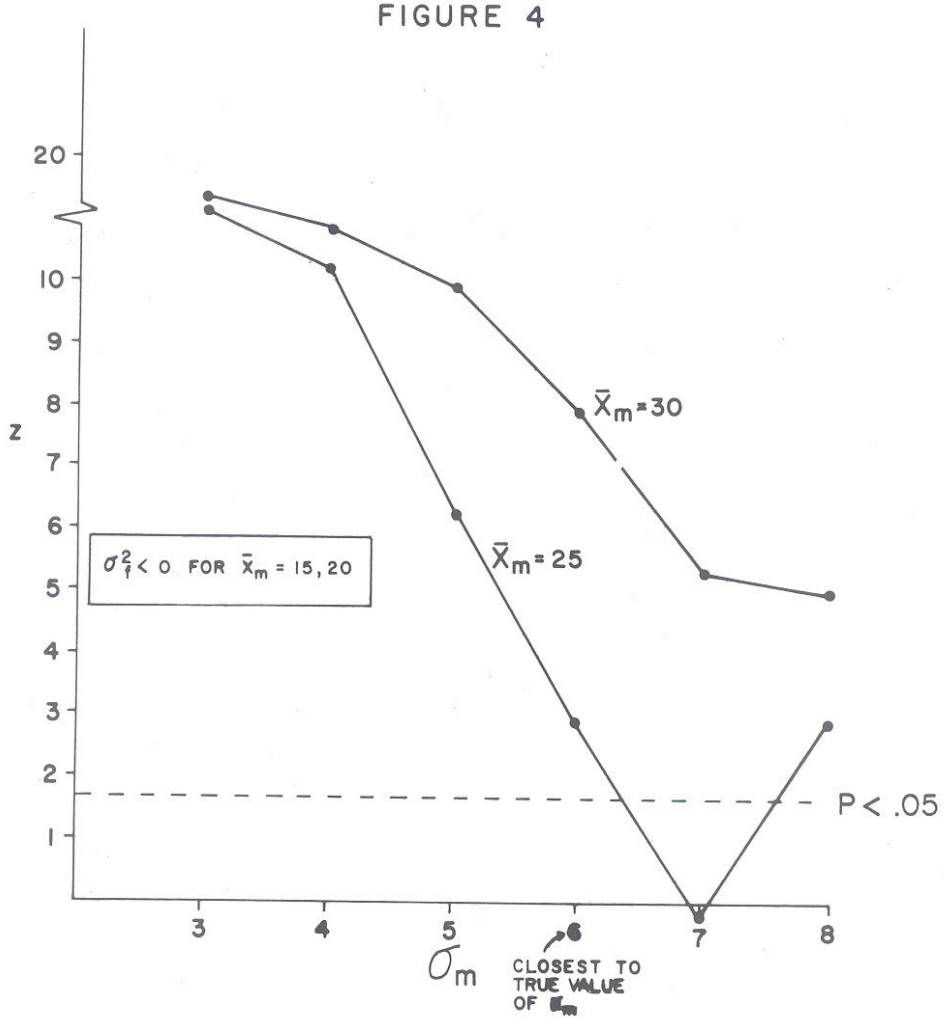
[16]

FIGURE 3



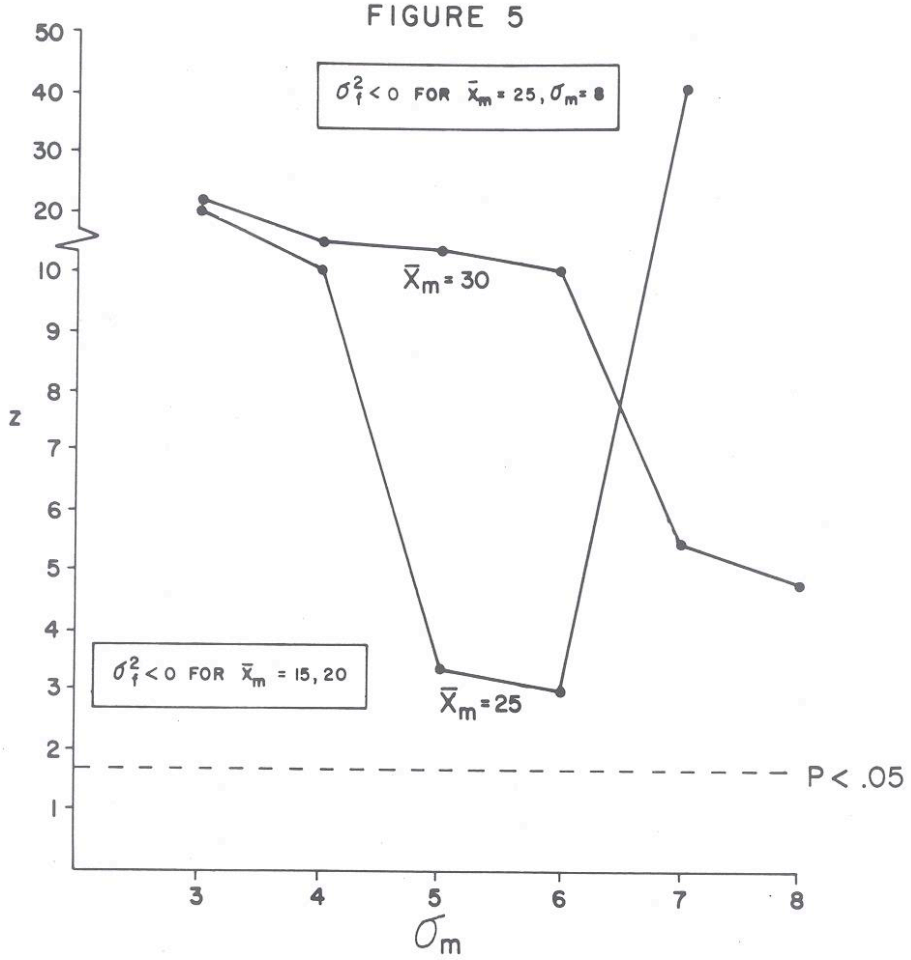
$z = \sqrt{2\chi^2} - \sqrt{2n-1}$ AS FUNCTION OF TRIAL VALUES OF σ_m AND $\bar{X}_m$ FOR $N_m = 300$

FIGURE 4



$z = \sqrt{2\chi^2} - \sqrt{2n-1}$ AS FUNCTION OF TRIAL VALUES OF σ_m AND $\bar{X}_m$ FOR $N_m = 400$

FIGURE 5



$z = \sqrt{2\chi^2} - \sqrt{2n-1}$ AS FUNCTION OF TRIAL VALUES OF σ_m AND $\bar{X}_m$ FOR $N_m = 500$

[19] arbitrary mean assignments, holding fixed an arbitrary base-rate assignment of 100. The other four figures are to be interpreted the same way.

Before considering the question of how well the minimum of minima of minima among all these curves succeeds in spotting the true latent values, certain general observations on the way the curve families behave are of some interest. The figure whose hypothetical base-rate is closest to the true one is of course Figure 4, with the first [= male] taxon being arbitrarily assigned a base rate of $N_m = 400$, which with 100-unit steps is as close as we can come to the true value of the number of males in this sample ($N_m = 410$). We note that this graph, and the graph based upon the next closest available base-rate assignment ($N_m = 500$, Figure 5) both exhibit a considerably greater "steepness" or "peakedness" than is true of the curves in Figures 1, 2, and 3. The "flattest" curves, in which the variation in arbitrary assignments of sigma values seems to make the least difference in the goodness-of-fit to the observed data, we see in the most far-out erroneous base rate value, at $N_m = 100$. Quaere, whether it is for some reason a general principle in this procedure, that a "good" estimate of base-rate is necessary in order for good-to-bad variations of the within-taxon parameter guesses to generate appreciable variation in goodness-of-fit to the observations.

In Figure 2, where the lowest arbitrary mean assignment ($\bar{x}_m = 15$) is not plottable because it results in an impossible negative variance for the female taxon, there seems to
[20] be something aberrated about the curve reflecting the first algebraically possible value of the arbitrary mean of $\bar{x}_m = 20$, in the sense that this curve cuts diametrically across the other two instead of running roughly parallel to them, as the curves in the other figures do.

The smallest chi-square deviate obtained (lowest empirical "badness-of-fit" point on any curve in any curve-family) is found in Figure 4, which corresponds to a postulated latent (male) taxon frequency of 400 (base-rate .37), the true value being 410 (base-rate .38); a postulated latent mean of $\bar{x}_m = 25$, the true value being 24.73; and an assigned latent sigma of 7 (the true value being $\sigma_m = 5.75$). So we do identify the correct curve-family, and the correct curve within the family, the estimated values being very close to the true ones; but we make an error of more than one raw-score unit in estimating the latent sigma, not attributable to scale coarseness, since the nearest rounded-off integral

value to the true male sigma should be at 6 on the abscissa, instead of at 7. It does not seem possible to say, upon contemplating this series of five figures, to what extent the error in sigma-assignment is attributable to the coarseness of the discontinuous intervals or to the fact that the intrataxon normality assumption is an idealization.

Fisher's *g*-statistics were calculated on the latent distributions of males and females, and (as was expected from previous work on the Mf scale) each of them differed significantly from normal curve form ($p < .001$, as to both skewness and kurtosis, and for both sexes). The male frequency function was considerably skewed to the right, the female to the left, and both curves were quite markedly leptokurtic. The accurate estimate

[21] of base-rates and latent means, in spite of these sizeable departures from the normal-curve idealization, speaks encouragingly for the method's robustness.

It would be gratifying to find that the true or truest parameter assignments yielded a nonsignificant *p*-value for chi-square and all others a significant one, but this is not the case. One-tailed probability $p < .05$ (obviously "super-fit" chi-squares are of no interest here) corresponds to a deviate $z = 1.65$, the dotted reference line shown in each figure, and parameter estimates providing a "satisfactory fit" ($p < .05$, $z < 1.65$) occur three times (in 120 trials) as seen in Figures 2 and 4. The arbitrary values yielding these good fits are indicated by an asterisk in Table 2. Note that the only assignment yielding a fit "better than chance expectation" — slightly <u>below</u> the expected chi-square deviate — is the $\sigma_m = 7$ value in Figure 4, i.e., the closest possible assignment of N_m and $\bar{x}_m$ to the true values. This is gratifying, but it must be admitted that the (<u>badly</u>-off) assignments in Figure 2 are uncomfortably "good"-looking and do not reach the 5% level either.

With steps of this coarseness, an investigator starting "blind" in search of the latent taxa, relying on a single indicator, and with <u>no</u> antecedent information as to the true base-rates, means, or sigmas, would in this study have concluded that the one taxon had a base-rate of approximately 400, a mean of approximately 25, and a standard deviation of approximately 7. But while this is the best value, he would perhaps feel somewhat nervous about the too-close competitors at $N_m = 200$. It remains true that a "blind, mechanical" choice based on the best-fitting values would have succeeded on these data.

[22] If a satisfactory general criterion can be set up for excluding graphically aberrant curves like the one found in Figure 2, the present results would indicate that the method has

considerable promise. It would seem that some kind of combined criterion of greater steepness or peakedness and reasonable parallelism within the curve-family should suffice to exclude the dangerously low chi-squares found in Figure 2, which assigns a seriously erroneous base-rate to the male taxon.

It turned out that the desk-calculator computations involved in this pilot study were far more onerous than had been initially anticipated. This fact, combined with the desirability of operating with finer steps plotting the curves (which with a logical tree of the present kind results in an inordinate increase in the necessary computations) led us to conclude that further work on the method with real data should await development of a computer program, as well as investigation of sampling stability problems by Monte Carlo methods. The present study is being reported as yielding moderate-to-strong suggestion that the proposed method has sufficient promise to justify a more thorough study.

[23]

REFERENCES

Cochran, W. G. (1954). Some methods for strengthening the common chi-square tests. *Biometrics, 10*, 417-451.

Dawes, R. M., & Meehl, P. E. (1966). Mixed group validation: a method for determining the validity of diagnostic signs without using criterion groups. *Psychological Bulletin, 66*, 63-67.

Meehl, P. E. (1965). *Detecting latent clinical taxa by fallible quantitative indicators lacking an accepted criterion* (Report No. PR-65-2). Minneapolis: University of Minnesota, Research Laboratories of the Department of Psychiatry.

Meehl, P. E. (1968). *Detecting latent clinical taxa, II: A simplified procedure, some additional hitmax cut locators, a single-indicator method, and miscellaneous theorems* (Report No. PR-68-4). Minneapolis: University of Minnesota, Research Laboratories of the Department of Psychiatry.