Technical Note: Two Programs for Performing Multigroup Longitudinal Data Analyses

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Many studies in physical anthropology involve taking repeated measurements on each of the individuals (experimental units) comprising several samples. A wide variety of data-analytic strategies have been proposed for such data sets (e.g., Kowalski and Guire, 1974; Goldstein, 1979; Guire and Kowalski, 1979; Nesselroade and Baltes, 1979; Marubini and Milani, 1986), but application of these methods is constrained by the lack of software for performing them. The purpose of this note is to briefly describe, and make available, SAS (Statistical Analysis System, SAS Institute, Inc., Box 8000, Cary, NC 27511) programs implementing two techniques for performing longitudinal data analyses. In particular, we have implemented the methods due to Potthoff and Roy (1964) and Rao (1958), both of which compare the patterns of growth in several independent groups of individuals.

THE POTTHOFF-ROY (PR) ANALYSIS

PR approached the problem of growth curve analysis by generalizing the standard multivariate analysis of variance (MANOVA) model into a form that accommodates fitting polynomial growth curves, constructing confidence bands about these curves, and testing hypotheses in the context of more complex experimental designs than had been previously considered. The form of this generalized model is

$$E(X) = B_\tau W' \qquad (1)$$

where $E(\cdot)$ is the expectation operator and X is a $N \times T$ data matrix containing the values of the variable whose growth is being studied at T times of measurement for each of N individuals. B is a $N \times G$ matrix specifying group membership; τ a $G \times P$ matrix containing the P (unknown) parameters fitting a polynomial of degree $D = P - 1$ to the average growth curves (AGCs) in the G groups; and W is the $T \times P$ within-individual or time design matrix specifying the actual times at which the measurements were taken (W' is the transpose of W). These times of measurement $t_1, t_2, \ldots, t_T$ need not be equally spaced, but they are assumed to be the same for each of the N individuals. See Schneiderman and Kowalski (1985) for a more detailed description of these quantities.

The generalized model (1) is transformed into the MANOVA model $E(Y) = B_\tau$ using

$$Y = XA^{-1}W(W'A^{-1}W)^{-1} \qquad (2)$$

where A is an arbitrary $T \times T$ symmetric, positive-definite matrix. Standard MANOVA methods can now be used to analyze model 1. In particular, our program determines the smallest D adequate to fit the AGCs in each of the groups, fits polynomials of this degree to the AGCs in each of the G groups, tests the equality of the resulting regression coefficients, and performs pairwise comparisons among the groups both

with respect to all the coefficients considered simultaneously and one coefficient at a time. Two forms of the multivariate tests are included: The first is for parallelism of the growth curves (all coefficients except for the intercept equal), the second for coincidence (all coefficients, including the intercepts, equal). Several different forms of these tests are computed, viz., those based on the Hotelling-Lawley trace, Pillai's trace, Wilks' criterion, and Roy's maximum root criterion. See, for example, Kshirsagar (1972) for more details concerning these statistics. The degree of the polynomial is determined using step-up goodness-of-fit tests comparing the "reduced model" of degree RD to the "full model" of degree FD (Neter et al., 1985). RD and FD are both user-specified and the comparisons begin with DR (often DR = 1), stepping up, if necessary, until an acceptable fit (at the 5% level of significance) is achieved. If no degree less than FD is adequate, FD is used. To bypass the tests and choose your own degree, simply take RD = FD.

With regards to the arbitrary matrix $\mathbf{A}$ in equation 2, we allow $\mathbf{A}$ to equal the identity matrix, the sample covariance matrix, or a matrix input by the user. Timm (1975) discusses the first two of these possibilities. Potthoff and Roy (1964) illustrate how the third option might arise in practice. It should be noted the PR method remains valid regardless of the choice of $\mathbf{A}$. The computer program performing this method is a SAS macro, called %POTROY, which uses PROC IML to compute the transformation (2) and PROC GLM to perform the MANOVAs.

RAO'S TIME METAMETER

Rao's (1958) analysis is based on a transformation of the time axis, $t \rightarrow t^*$, with respect to which the growth curves in the G groups are approximately linear, regardless of the shapes of the growth curves on the t-axis. This new time scale, t^*, is referred to as a time metameter and its structure can be estimated from the data in hand. Letting Δt_j^* (j = 2, 3, . . ., T) denote the length of the interval between the $(j - 1)^{st}$ and j^{th} time points on the transformed time axis t^*, Rao (1958) suggested that these quantities (and hence t^* itself) could be estimated by

$$\hat{\Delta t}_j^* = \frac{1}{N} \sum_{i=1}^{N} \Delta \mathbf{x}_{ij} \qquad (3)$$

ie., the mean values of the gains in the jth interval (on the t-axis) over all the individuals included in the sample. Here $\Delta \mathbf{x}_{ij}$ represents the differences between the observed values of x at successive time points for the ith individual (see Schneiderman and Kowalski, 1989).

Since the growth curves are linear, the $N \times T$ data matrix $\mathbf{X}$ can be reduced to a $N \times 2$ matrix containing the initial values of the measurement for each of the N individuals and an estimate of their growth rates. The average growth rates in each of the groups can now be compared using a simple univariate analysis of variance or covariance, adjusting for differences in the initial mean values, if necessary. We provide three different estimates of these rates, viz., for each i = 1, 2, . . ., N

$$b_i^{(1)} = \frac{\displaystyle\sum_{j=2}^{T} (\Delta \mathbf{x}_{ij})(\hat{\Delta t}_j^*)}{\displaystyle\sum_{j=2}^{T} (\hat{\Delta t}_j^*)^2} \qquad (4)$$

and

$$b_i^{(2)} = \frac{\displaystyle\sum_{j=2}^{T} \Delta \mathbf{x}_{ij}}{\displaystyle\sum_{j=2}^{T} \hat{\Delta t}_j^*} \qquad (5)$$

$$b_i^{(3)} = \frac{1}{T-1} \sum_{j=2}^{T} \frac{\Delta \mathbf{x}_{ij}}{\hat{\Delta t}_j^*} \qquad (6)$$

The choice between these estimators depends on what sorts of assumptions one is prepared to make concerning the variances of the Δx's. If these are assumed to be equal at each Δt_j^*, equation 4 is the least squares estimator; if they are presumed to be proportional to the size of the corresponding Δt_j^*,

then equation 5 is the least squares estimator; the least squares estimator is equation 6 if the variances of the Δx's are proportional to the square of the corresponding $\Delta t_j{}^*$. See Draper and Smith (1981) for a detailed discussion. For convenience, our program automatically computes all three of these estimators and performs analyses of variance and covariance on all three. The user is left to choose the analysis most appropriate for his/her data.

The program is in a SAS macro, %META, which uses PROC IML to compute the successive differences between the x-measurements and three estimates of the growth rate defined above, and PROC GLM to perform the analyses of variance and covariance on these growth rates. For the analysis of covariance, the initial value of the measurement is taken as the covariate. Scheffé comparisons between each pair of groups are also output.

DISCUSSION

We have described, and made available, two SAS programs for comparing the growth profiles in G independent groups of individuals. The PR method is quite structured; multivariate normality is assumed, polynomials are fit to the AGCs, and users must specify the form of the arbitrary matrix, **A**. The method based on Rao's time metameter, on the other hand, is somewhat less restrictive. No specific functional form for the growth curves is postulated and the times of measurement t_1, t_2, . . ., t_T need not even be known to employ the method. The first point is particularly germane when one has samples so small as to preclude the selection of a more structured model (polynomial or otherwise) for the growth curves; the point concerning the times of measurement may prove useful in "non-standard" problems as, for instance, when small samples of fossils from different, ordered but unknown geological ages are to be contrasted. Thus, several phylogenetic series from separate sites but based on the same set of geological strata could be formally compared with this procedure.

The apparently great flexibility and power of Rao's approach may, however, be somewhat compromised by problems of in-terpretation. Goldstein (1979) stated, "It would appear difficult to interpret differences in average growth rates using this kind of time scale which is defined solely in terms of the growth measurements themselves, and there seem to have been few applications of this technique." He also questioned the existence of a common transformation that would lead to linear growth for each individual. While we agree that interpretation is difficult, we should note that Rao (1958) stressed that "the emphasis . . . is not on obtaining a model adequately describing the growth of an individual but on examining whether differences exist between groups of growth curves." In a subsequent paper, Rao (1961) suggested that his technique might be of particular value to physical anthropologists, concluding, "Thus the maximum reduction of data without sacrificing essential information, leading to a satisfactory test and providing a direct answer to a relevant question appears to be feasible." An intermediate assessment was given by Hoel (1964). While using the word "ingenious" to describe Rao's approach, Hoel noted that its sensitivity (power) depends on the type of alternative to the null hypothesis of equal growth curves envisaged. In the case of two groups, Hoel (1964) showed that one can expect Rao's method to be most effective if one growth curve is consistently above the other, or if the two curves have approximately the same initial values but one rises faster than the other. It would be less powerful with respect to alternatives where the two curves had differing slopes and crossed midway through the observed time period.

In any case, both the PR and Rao methods for comparing the growth patterns in G independent groups would appear to be of potential value to the biomedical research community and they are offered here in the spirit of encouraging their use so that we will be able to gain experience with respect to both interpretation (cf. Kowalski, 1972) and such matters as the choice of **A** in the PR analysis (Timm, 1975).

Copies of the programs described above and additional documentation may be obtained by writing to E.D.S. at the Baylor College of Dentistry. Copies will be fur-

nished on 5¼″ floppy disks and the code is annotated to aid the reader in following the steps in the programs. Details concerning the actual execution of SAS will depend on how it was implemented at the user's particular installation. Complete manuscripts concerning both the PR and Rao procedures will be included upon request.

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LITERATURE CITED

Draper NR, and Smith H (1981) Applied Regression Analysis, 2nd ed. New York: Wiley.

Goldstein H (1979) The Design and Analysis of Longitudinal Studies. New York: Academic Press.

Guire KE, and Kowalski CJ (1979) Mathematical description and representation of developmental change functions on the intra- and interindividual levels. In: JR Nesselroade and PB Baltes (eds.): Longitudinal Research in the Study of Behavior and Development. New York: Academic Press, pp. 89–110.

Hoel PG (1964) Methods for comparing growth type curves. Biometrics *20*:859–872.

Kowalski CJ (1972) A commentary on the use of multivariate statistical methods in anthropometric research. Am. J. Phys. Anthropol. *36*:119–131.

Kowalski CJ, and Guire KE (1974) Longitudinal data analysis. Growth *38*:131–169.

Kshirsagar AM (1972) Multivariate Analysis. New York: Marcel Dekker.

Marubini E, and Milani S (1986) Approaches to the analysis of longitudinal data. In: Human Growth, A Comprehensive Treatise, Vol. 3. FT Falkner and JM Tanner (eds.) New York: Plenum Press, pp. 79–94.

Nesselroade JR, and Baltes PB (eds.) (1979) Longitudinal Research in the Study of Behavior and Development. New York: Academic Press.

Neter J, Wasserman W, and Kutner MH (1985) Applied Linear Statistical Models, 2nd ed. Homewood, IL: Irwin.

Potthoff RF, and Roy SN (1964) A generalized multivariate analysis of variance model useful especially for growth curve problems. Biometrika *51*:313–326.

Rao CR (1958) Some statistical methods for the comparison of growth curves. Biometrics *14*:1–17.

Rao CR (1961) Some observations on multivariate statistical methods in anthropological research. Bull. Int. Stat. Inst. *38*:99–109.

Schneiderman ED, and Kowalski CJ (1985) Implementation of Rao's one-sample polynomial growth curve model using SAS. Am. J. Phys. Anthropol. 67:323–333.

Schneiderman ED, and Kowalski CJ (1989) Implementation of Hills' growth curve analysis for unequal-time intervals using GAUSS. Am. J. Hum. Biol. *1*:31–42.

Timm NH (1975) Multivariate Analysis with Applications in Education and Psychology. Monterey, CA: Brooks/Cole.