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Application of the S-procedure in multiple comparisons for nonlinear models

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Abstract: Zerbe (1979) characterized the growth curve model as one of the nonlinear models. For these models, we propose a comprehensive procedure to identify significant differences in multiple comparisons of fully randomized growth curve models. Research applying Scheffé's S-procedure to growth curve models as a subclass of nonlinear models has yet to be conducted. Our findings demonstrate that the S-procedure is an effective method for discerning important differences within a fully randomized growth curve model.
Keywords: *Growth curves, Hypothesis testing, Multiple comparison, Nonlinear models, S-procedure.*

1. Introduction

The growth curve model is a statistical technique that enables researchers to analyze changes in a dependent variable over time. The model's academic development has evolved significantly, particularly in the domains of psychology, education, and health sciences, allowing for the investigation of individual growth trajectories.

The origins of growth curve modeling can be traced back to early longitudinal studies, which emphasized the importance of repeated observations. Traditional statistical methods like ANOVA and regression were often inadequate for these types of data, as they treated repeated measures as independent, ignoring the intrinsic correlation among them. In the late 20th century, advancements in hierarchical linear and structural equation modeling provided a robust framework for addressing these limitations. These methodologies highlight the individual variability in growth patterns, while accounting for individual and group differences.

The growth curve model is particularly useful in various contexts. In education, it can track student performance over time and allow researchers to assess the effectiveness of different teaching methods or interventions. For instance, researchers may compare students' academic trajectories before and after implementing a new educational program. Similarly, in psychology, growth curve modeling can be used to study developmental changes, such as cognitive abilities or behavioral issues, across different age groups, facilitating a nuanced understanding of individual trajectories.

The growth curve model serves as a versatile tool for understanding complex growth processes in diverse fields, enabling researchers to gain insights into the average effects within populations, individual variations, and the factors influencing these changes over time.

In this study, we analyze growth curve models with correlated observations across time and between groups or treatments. We compare different treatments, assuming the data consist of measurements of a single growth variable collected from the same individuals at various time points. Building on the work of Foutz (1984) and Foutz, Jensen, and Anderson (1985), we present an effective multiple comparison procedure for randomization analyses of growth and response curves. Zerbe and Murphy (1986) explored two multiple comparison procedures for supplementary randomization analyses of growth curves—one procedure extending the Scheffé method manages the Type I error rate for all possible contrast curves, whereas the other approach uses a stepwise testing procedure to manage the Type I error rate. In this study, we extend the S-procedure, which incorporates the approximation

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test proposed by Zerbe (1979). These methods are particularly beneficial in clinical trials comparing different treatments within the same patient group.

2. Growth Curve Model and Hypothesis Testing for τ

Potthoff and Roy (1964) defined the growth curve model as:

$$Z_{pxn} = A_{pxm}\tau_{mxr}B_{rxn} + \varepsilon_{pxn} \quad (1)$$

where τ is unknown; A and B are known matrices of ranks $m < p$ and $r < n$, respectively. Additionally, the columns of ϵ\epsilonϵ are independent p-variate normal vectors with a mean vector of 0 and a common covariance matrix Σ. Therefore, the cumulative distribution function of Z is:

$$F(Z \mid \tau, \Sigma) \sim N(A\tau B, \Sigma \otimes I_N) \quad (2)$$

where τ denotes the vector of the regression or growth curve coefficients, ⊗ denotes the Kronecker product, and $F(.)$ denotes the cumulative distribution function B. Zerbe (1979) defined the growth curve model under the basic assumptions of a completely randomized design. Consider a completely randomized design where n subjects are assigned to τ treatment groups. In group i, let $z_{ij}(t)$ denote the growth curve observed over time t for the subject assigned to position j in group i.

Let $z_{ik}(t)$ represent the growth curve that the k^{th} subject would exhibit if assigned to group i. Thus, $z_{ik}(t)$ is equivalent to $z_{ij}(t)$ when subject k is assigned to position j in group i. We can then formulate the following mathematical model for the population of all nr possible growth curves:

$$\varphi_{ik}(t) = \mu(t) + \tau_i(t) + \epsilon_k(t) \quad (3)$$

$$\text{where } \mu(t) = \bar{\mu}_{..}(t), \tau_i(t) = \bar{\mu}_{i.}(t) - \bar{\mu}_{..}(t), \varepsilon_i(t) = \bar{\mu}_{k.}(t) - \bar{\mu}_{..}(t) \quad (4)$$

Model (3) incorporates the grand mean growth curve, the effect curve attributable to group i, and the error curve specific to subject k. This model is built upon the population of all potential time-response curves and the probability framework established by the completely randomized design. Kempthorne (1955) and Zerbe (1979) developed a statistical model for the sample of random response curves $Z_{ij}(t)$ ($z_{ij}(t)$ being realizations), which is represented as follows:

$$Z(t) = \mu(t) + \tau_i(t) + E_{ij}(t) \quad (5)$$

In Model (5), $E_{ij}(t)$ are random error curves satisfying

$$E[E_{ij}(t)] = 0, E[E_{ij}(t)E_{i'j'}(u)] = (\delta_{ii'}\delta_{jj'} - \frac{1}{n})\sigma(t,u) \quad (6)$$

where $\delta_{ii'} = 1$ if $i = i'$ and $\delta_{ii'} = 0$ if $i \neq i'$, and $\sigma(t,u)$ measures the covariability between subject errors at times t and u.

To test the equality of the vectors of the growth curve coefficients across the r groups, we set up the following null hypothesis:

$$H_0 : \tau_1(t) = \tau_2(t) = \cdots = \tau_r(t) \quad (7)$$

We define the sample mean for the i^{th} group as given in

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$$\bar{Z}i_{.}(t) = \sum_{j=1}^{n_i} Z\,(t)/n_i \quad (8)$$

Equation (8) represents the pointwise best minimum variance linear unbiased estimator of $\mu(t) + \tau_{.}(t)$. Additionally, we define the overall sample mean for all groups as indicated in

$$Z_{..}(t) = \sum_{i=1}^{r} \sum_{j=1}^{n_i} Z(t)/n \quad (9)$$

Equation (9) is equal to the constant $\mu(t) + \tau_{.}(t)$, where $\bar{\tau}_{.}(t) = \sum_{i=1}^{r} n_i\, \tau_i/n$.

The randomization test introduced by Kempthorne (1955) provided a method for testing group effects at specified times. Kempthorne's approach has since been generalized to accommodate cases with unequal group sizes. Let

$$\mathrm{B(t)} = \sum_{i=1}^{r} n_i\, \{Z_{i.}(t) - \bar{Z}_{..}(t)\}^2 \quad (10a)$$

$$\mathrm{W(t)} = \sum_{i=1}^{r} \sum_{j=1}^{n_i} \left\{Z_{ij}(t) - \bar{Z}_{i.}(t)\right\}^2 \quad (10b)$$

and

$$\mathrm{T(t)} = \sum_{i=1}^{r} \sum_{j=1}^{n_i} \left\{Z_{ij}(t) - \bar{Z}_{..}(t)\right\}^2 \quad (10c)$$

Then, (10a), (10b), and (10c) are between, within, and total sum of squares at time t, respectively. Therefore,

$$F_{01}(t) = \{B(t)/(r-1)\}/\{(r-1)\hat{\sigma}^2(t)\} \quad (11)$$

where, $\hat{\sigma}^2(\mathrm{t}) = \mathrm{W(t)/(n-r)}$ is an appropriate statistic for Null Hypothesis (7).

The degrees of freedom of the approximate F test are approximately (r–1) and (n–r). Let $f_\alpha(t)$ denote the $100(1-\alpha)\%$ point of the exact distribution of $F_{01}(t)$. Then,

$$1 - \alpha = \Pr\{F_\tau(t) < f_\alpha(t) \mid H_0\} \quad (12)$$

3. S-procedure in Multiple Comparisons

The following null hypothesis can be tested using the confidence region test method:

$$H_0 :\ c_l\tau_l(t) - c_m\tau_m(t) = 0 \quad (13)$$

Let

$$B_\tau(\mathrm{t}) = \sum_{i=1}^{r} n_i\{(\bar{Z}_{i.}(t) - \tau_i(t)) - (\bar{Z}_{..}(t) - \bar{\tau}_{.}(t))\}^2 \quad (14)$$

Equation (14) denotes the between-groups sum of squares at time t for the variables $Z_{ij}(t) - \tau_i(t)$. We translate Scheffé's notation from the randomization block design to ours for a completely randomized design at time t. Scheffé (1959) proposed that the distribution of $Z_{ij}(t) - \tau_i(t)$ is the same as the distribution of $Z_{ij}(t)$ under the null hypothesis. Therefore, irrespective of the actual values of the treatment effect curves $\tau_i(t)$, $F_\tau(t) = B_\tau(t)/[(r-1)\hat{\sigma}^2(t)]$ follows the same distribution as $F_{01}(t)$ under the null hypothesis. Consequently, the probability remains the same regardless of $\tau_i(t)$.

$$1 - \alpha = \Pr\{F_\tau(t) < f_\alpha(t) \mid H_0\} \quad (15)$$

An approximate method for multiple comparisons is applied in the standard manner when $f_\alpha(t)$ is replaced with its conventional normal theory counterpart, which is based on the degrees of freedom of (r–1) and (n–r).

Scheffé (1959) also noted that approximating $f_\alpha(t)$ using the 100(1–α)% point of a standard F distribution with synthesized degrees of freedom, as discussed by Zerbe (1979), is not feasible for constructing simultaneous confidence limits. This is because the calculation depends on unspecified $\tau_i(t)'s$ values.

Consequently, Scheffé (1959) pointed out that the S-procedure provides a reliable approximation within the randomization model, as long as the normal theory test for the global null hypothesis retains its intended significance level in this model.

The exact $(1-\alpha)$-level simultaneous confidence intervals for all contrasts $\sum_{i=1}^{r} c_i\theta_i$ using the S-procedure work out to be

$$\sum_{i=1}^{r} c_{i\theta_i} \in \left[c_i\bar{X}_i \pm \{(r-1)F_\alpha(r-1,\delta)\}^{\frac{1}{2}} S\,\langle\sum_{i=1}^{r}\frac{c_i}{n_i}\rangle^{\frac{1}{2}}\right] \tag{16}$$

where $\bar{X}_i$ is the sample mean for the i^{th} treatment (1 ≤ I ≤ r) and $S^2 = MS_{error}$, with $\delta = \sum_{i=1}^{r} n_i - r$ degrees of freedom. For pairwise comparisons, the intervals given in Equation (16) simplify to the following conservative $(1-\alpha)$-level simultaneous confidence intervals:

$$\theta_i - \theta_j \in \left[\bar{X}_i - \bar{X}_j \pm \{(r-1)F_\alpha(r-1,\delta)\}^{\frac{1}{2}} S\,\langle\frac{1}{n_l} + \frac{1}{n_m}\rangle^{\frac{1}{2}}\right], 1 \le i < j \le r \tag{17}$$

We now extend these results from a specific point in time to a time interval. We can use the confidence intervals for $c_l\tau_l(t) - c_m\tau_m(t)$, $1 \le i < j \le r$.

$$c_l\tau_l(t) - c_m\tau_m(t) \in \left[\left(c_l\bar{Z}_{l.}(t) - c_m\bar{Z}_{m.}(t)\right) \pm \left\{(r-1)F_\alpha(t;r-1,n-r)S(t)\left(\frac{c_l^2}{n_l} + \frac{c_m^2}{n_m}\right\}^{\frac{1}{2}}\right] \tag{18}$$

where $S(t) = W_\alpha(t)/(n-r)$.

For pairwise comparison, when we take $c_l = 1$ and $c_m = -1$, the intervals given by Equation (18) simplify to the following conservative $(1-\alpha)$-level simultaneous confidence intervals:

$$\tau_l(t) - \tau_m(t) \in \left[\left(\bar{Z}_{l.}(t) - \bar{Z}_{m.}(t)\right) \pm \left\{(r-1)F_\alpha(t;r-1,n-r)S(t)\left(\frac{1}{n_l} + \frac{1}{n_m}\right)\right\}^{\frac{1}{2}}\right] \tag{19}$$

For testing Null Hypothesis (13), the F-test rejects H_0 at level α when

$$F_{02} = \frac{\left(\bar{Y}_{l.}(t) - \bar{Y}_{m.}(t)\right)^2}{S(t)\left(\frac{1}{n_l} + \frac{1}{n_m}\right)} > F_\alpha(t;r-1,n-r) \tag{20}$$

The test procedure based on Equation (20) is commonly known as the fully significant difference in the literature.

4. Conclusion

Potthoff and Roy (1964) investigated homoscedasticity testing and the inference of growth curve coefficients. Subsequent research has expanded their findings to explore various aspects of growth curve inference. However, research on the randomized growth curve model introduced by Zerbe (1979) remains relatively sparse, primarily given its lower prominence compared with the model developed by Potthoff and Roy. In this study, we propose utilizing the S-procedure to identify significant differences in multiple comparisons within the context of completely randomized growth curve models. The standard test is demonstrated to be an effective tool for conducting multiple comparisons within this model. We also demonstrate that the proposed method can successfully compare growth curve coefficients between groups. Nonetheless, additional research is warranted to address scenarios involving a larger number of groups and coefficients within the growth curve model.

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