A METHOD FOR GROWTH CURVE COMPARISONS

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ABSTRACT

Suppose one has a sample of pairs of age and length measurements from each of two or more populations of fish. The mathematical forms of the growth curves associated with the populations are assumed to be specified but each form contains at least one unknown parameter. Presented in this paper is a data analytic approach to the problem of deciding which, if any, of the populations have essentially the same growth curve and which have different ones.

A common problem in fisheries research is that of comparing two or more growth curves. This problem arises whenever investigators gather data for the purpose of trying to determine whether or not different species or the sexes of a given species of fish grow at different rates, or for the purpose of assessing growth variation of a species from environment to environment, area to area, or stratum to stratum in which it is found.

Since the models generally used for the age-length relationships (e.g., von Bertalanffy, Laird-Gompertz, logistic, etc.) are most often nonlinear in the unknown parameters and cannot be linearized by transformations of the variates, the usual techniques for comparing regression equations are not applicable. Up to this point little has been done in the way of development of quantitative methods for determining whether or not unknown growth curves do in fact differ. Thus the investigator can often do little more than visually examine plots of age-length data for samples from the various populations being compared and arrive at some rather subjective conclusions.

An exception is a paper by Allen (1976) which treats the special case where each of the growth curves being compared belongs to the von Bertalanffy family. There are, of course, numerous instances where the von Bertalanffy model is not appropriate and the Allen procedure does not apply if it is not. Further, even if this model is appropriate, some severe assumptions need to be made in order to apply the analysis. These include: 1) the equality of the scale parameters for all curves being compared, 2) the true value of the common scale parameter being exactly equal to its estimated value, and 3) the usual normality, independence, and equality of variance assumptions for the error term. The first assumption quite clearly biases the procedure in favor of the null hypothesis of equality of the growth curves, while validity of the second seems to be too much to hope for.

Gallucci and Quinn (1979) also discuss the growth curve comparison problem for the von Bertalanffy case. They essentially reparameterize the model and test the hypothesis of equality of one of the new parameters for all curves being compared, assuming, apparently, that the other two have the same value for all of the curves. The comments in the preceding paragraph also apply to these authors' work.

The purpose of this paper is to point out how some predictive sample reuse techniques, described in a recent paper by Geisser and Eddy (1979), can be adapted and applied to a growth curve comparison problem where two or more populations are being studied, the growth curves associated with each of the populations are unknown and are to be compared, and a sample of age-length data is available from each population. The problem then is to use the data to decide which, if any, of the population growth curves are the same and which are different.

We will assume that the growth curves associated with each of the populations are specified except for the values of unknown parameters. These specifications often would be made by plotting the sets of age-length data, fitting various possible models suggested by the data plots, and selecting the models which best fit the data. The growth curves can, but need not, belong to the von Bertalanffy family. In fact, they can belong to any family. Thus, in essence, we are

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considering a much more general and widely applicable problem than that discussed by Allen (1976) and by Gallucci and Quinn (1979). For the technique presented here, the only assumption that is made is that the forms of the population growth curves can be specified. No parameters are assumed to be known or equal, and no distributional assumptions are made.

The solution, described in the following sections, of our growth curve comparison problem is not obtained via a classical statistical hypothesis testing approach. That is, we do not formulate an appropriate null hypothesis and derive a criterion which dictates when and only when it should be rejected. Instead, in the spirit of Geisser and Eddy (1979), we formulate various possible models and give a data analytic approach to selecting the one model preferred by the data.

A difficulty, which plagues classical hypothesis testing, does not exist for the approach described here. It is the necessity of specifying a significance level. Historically, significance levels such as 0.10, 0.05, and 0.01 have routinely been used for tests without objective justification. Yet the choice of a significance level affects the conclusions arrived at. For example, it is quite possible to find that a hypothesis can be rejected at the 0.05 level, but not at the 0.01 level. Further, the choice of a significance level affects the probability of rejecting a false hypothesis. Lowering the significance level usually lowers the probability of rejecting a false hypothesis. Requiring one to specify a significance level presumes that one has a sound basis for controlling the probability of rejecting one of two possible hypotheses when it is true, that one can objectively assign a significance level which controls this probability, and that controlling this probability is more crucial than controlling the probability of not rejecting the hypothesis when it is false. The contention here is that for many, if not most, scientific investigations, the consequences of rejecting one hypothesis when it is true are no more serious than rejecting the other when it is true. That is, often an investigator has no reason to favor either hypothesis, but merely wants to know which one is more reasonable, given the data that has been collected.

THE TWO POPULATIONS CASE

Suppose that two populations of fish are being studied. For example, the first population might consist of all fish of a given species inhabiting one area while the second might consist of all fish of this species inhabiting a different area. Suppose we are interested in comparing the growth curves associated with the two populations.

We consider two possible models, say M_1 and M_2. The model M_1 specifies that the growth curves are the same, while under M_2 the two growth curves differ.

Let x and y represent, respectively, the age and length of a fish. Then we rewrite M_1 and M_2 as

$$M_1: \quad y = f(x;\theta) + \epsilon \tag{1}$$
no matter which of the two populations fish belongs to.

$$M_2: \quad y = f_1(x;\theta_1) + \epsilon \tag{2}$$
if the fish belongs to the first population.

$$y = f_2(x;\theta_2) + \epsilon \tag{3}$$
if the fish belongs to the second population.

Here $f(x; \theta)$, $f_1(x; \theta_1)$, and $f_2(x; \theta_2)$ are each functions of x. θ, θ_1, and θ_2 are each vectors of unknown parameters and f, f_1, and f_2 are specified except for the values of elements of θ, θ_1, and θ_2. Essentially, f, f_1, and f_2 represent three different growth curves which are specified except for the values of unknown parameters present in each. The function f represents the expected length of a fish whose age is x, assuming equal growth curves for the two populations, while f_1 and f_2 are, respectively, the expected lengths for fish of age x from the first and second populations, assuming the growth curves differ. As usual, ϵ represents the unknown, random error term.

We now give a data analytic approach for selecting one of the two possible models M_1 or M_2. The data used to make the selection are pairs of age-length measurements for samples of fish from each of the two populations.

Let (x_{11}, y_{11}), $(x_{12}, y_{12}),\ldots,(x_{1n}, y_{1n})$ represent a sample of n pairs of observations of x and y from the first population and (x_{21}, y_{21}), $(x_{22}, y_{22}),\ldots,$ (x_{2m}, y_{2m}) represent a sample of m pairs of observations of x and y from the second population. These $n + m$ pairs of observations are the data gathered by the investigator and we want to use these data to select either M_1 or M_2.

Assume, for the moment, that M_2 is correct. For $j = 1, 2,\ldots,n$, let $\hat{\theta}_{1(j)}$ represent the vector of

(least squares, say) estimates of the elements of θ_1 found by taking the relationship between x and y to be given by Equation (2) and using the data (x_{11}, y_{11}), $(x_{12}, y_{12}),\ldots,(x_{1(j-1)}, y_{1(j-1)})$, $(x_{1(j+1)}, y_{1(j+1)}),\ldots,(x_{1n}, y_{1n})$, that is, all of the n pairs of observations of x and y from the first population except for the jth pair. Set

$$D_{21} = \sum_{j=1}^{n} [y_{1j} - f_1(x_{1j}; \hat{\theta}_{1(j)})]^2.$$

Note that the second term inside the brackets is the predicted length for the jth fish in the sample from the first population, assuming M_2 is correct. The observed length of this fish is the first term inside the brackets. Thus D_{21} is the sum of the squares of the differences between the observed and predicted fish lengths for the fish in the first population sample, for model M_2.

Similarly, for $j = 1, 2,\ldots,m$, let $\hat{\theta}_{2(j)}$ represent the vector of (least squares, say) estimates of the elements of θ_2 found by taking the relationship between x and y to be given by Equation (3) and using the data (x_{21}, y_{21}), $(x_{22}, y_{22}),\ldots,(x_{2(j-1)}, y_{2(j-1)})$, $(x_{2(j+1)}, y_{2(j+1)}),\ldots,(x_{2m}, y_{2m})$, i.e., all of the m pairs of observations of x and y from the second population except for the jth pair. Set

$$D_{22} = \sum_{j=1}^{n} [y_{2j} - f_2(x_{2j}; \hat{\theta}_{2(j)})]^2$$

and $D_2 = D_{21} + D_{22}$.

The quantity D_{22} has an interpretation similar to that given to D_{21}. Putting these two together, we see that D_2 represents the sum of the squares of the differences between the observed fish lengths and the predicted fish lengths for all $n + m$ fish in the samples, under model M_2.

Next, assume that M_1 is correct, pool the data, and consider the $n + m$ pairs (x_{11}, y_{11}), $(x_{12}, y_{12}),\ldots, (x_{1n}, y_{1n})$, (x_{21}, y_{21}), $(x_{22}, y_{22}),\ldots, (x_{2m}, y_{2m})$. Let (x_j,y_j) represent the jth of these $n + m$ pairs, for $j = 1,\ldots,n + m$. Further, for $j = 1, 2,\ldots, n + m$, let $\hat{\theta}_{(j)}$, represent the vector of (least squares, say) estimates of the elements of θ obtained by taking the relationship between x and y to be given by Equation (1) and using the data (x_1,y_1), $(x_2,y_2),\ldots,(x_{j-1},y_{j-1})$, $(x_{j+1},y_{j+1}),\ldots,$ (x_{n+m},y_{n+m}), that is, all $n + m$ pairs of observations of x and y from the first and second populations except for the jth pair. The sum of the squares of the differences between the observed

and predicted fish lengths for all $n + m$ fish in the samples, under M_1, is

$$D_1 = \sum_{j=1}^{n+m} [y_j - f(x_j; \hat{\theta}_{(j)})]^2.$$

Our rule for selecting either of M_1 or M_2 can be simply stated as follows. Select M_1 if $D_1 \leq D_2$, otherwise select M_2. This rule is a very natural and objective one. It is based on whether the data (i.e., the observed fish lengths) are better predicted by one growth curve or two. If the sum of squares of the differences between observed and predicted lengths under M_1 does not exceed the sum of squares of the differences between observed and predicted lengths under M_2 (i.e., $D_1 \leq D_2$), the data are better predicted by one growth curve than by two and M_1 should be selected. Otherwise, they are better predicted by two distinct growth curves and M_2 should be selected.

AN EXAMPLE

To illustrate the procedure described in the previous section, we consider an example. The numbers given in the first two columns of Table 1 are the ages and corresponding lengths of 15 fish taken from the first of two populations, while the numbers in the first two columns of Table 2 are the ages and corresponding lengths of 14 fish taken from the second population. These data are hypothetical. In fact they were generated by a computer.

We want to use these two sets of data to decide which of two models, M_1 or M_2, is preferred, where under M_1 the growth curves for the two populations are the same, and under M_2 the two populations have different growth curves.

Among several growth curves, including the von Bertalanffy, Laird-Gompertz, and logistic ones, the best fit, for both data sets as well as the combined data set, was provided by the logistic. The average length of a fish whose age is x, for a logistic growth curve, is

$$f(x;a,b,c) = \frac{a}{1 + e^{-(bx+c)}} \qquad (4)$$

where a, b, and c are unknown parameters.

Thus, we take M_1 to specify that the average length of a fish whose age is x is Equation (4) no

TABLE 1.—Ages, lengths, parameter estimates, and predicted lengths, under models M_1 and M_2, for 15 Population I fish.

Age	Length	Least squares estimates of a_1, b_1, c_1 under M_2	Predicted length under M_2	Least squares estimates of a, b, c under M_1	Predicted length under M_1
1	4.0	55.27, 0.36, −2.70	4.9	55.67, 0.36, −2.62	5.2
2	8.3	54.76, 0.38, −2.80	6.2	55.44, 0.36, −2.66	6.9
3	5.6	55.86, 0.34, −2.56	9.9	55.91, 0.34, −2.56	10.0
5	16.0	55.11, 0.37, −2.73	15.9	55.57, 0.35, −2.63	16.5
6	20.9	55.13, 0.37, −2.74	20.3	55.56, 0.35, −2.64	20.8
7	27.7	55.40, 0.36, −2.77	24.8	55.70, 0.35, −2.65	25.4
8	31.9	55.43, 0.36, −2.73	29.9	55.70, 0.35, −2.64	30.4
9	32.9	54.62, 0.38, −2.76	35.7	55.28, 0.36, −2.65	35.6
10	40.2	55.24, 0.36, −2.71	39.4	55.62, 0.35, −2.63	39.5
11	39.9	54.88, 0.38, −2.81	44.0	55.37, 0.36, −2.67	43.7
12	45.6	55.15, 0.37, −2.74	46.4	55.56, 0.36, −2.64	46.4
13	49.6	54.96, 0.36, −2.72	48.6	55.51, 0.35, −2.63	48.7
14	53.0	54.32, 0.37, −2.71	50.0	55.26, 0.35, −2.63	50.4
16	54.2	54.23, 0.37, −2.74	52.2	55.27, 0.36, −2.64	52.8
17	51.5	56.97, 0.35, −2.68	54.8	56.25, 0.35, −2.62	54.2

TABLE 2.—Ages, lengths, parameter estimates, and predicted lengths, under models M_1 and M_2, for 14 Population II fish.

Age	Length	Least squares estimates of a_2, b_2, c_2 under M_2	Predicted length under M_2	Least squares estimates of a, b, c under M_1	Predicted length under M_1
1	6.5	55.65, 0.35, −2.60	5.3	55.43, 0.36, −2.66	5.0
2	6.4	56.09, 0.34, −2.52	7.7	55.62, 0.35, −2.62	7.1
3	8.0	56.24, 0.33, −2.48	10.4	55.69, 0.35, −2.60	9.7
4	14.1	55.74, 0.35, −2.60	12.9	55.47, 0.36, −2.66	12.5
5	17.6	55.84, 0.35, −2.59	16.8	55.53, 0.36, −2.66	16.3
6	21.8	55.90, 0.35, −2.58	21.1	55.58, 0.36, −2.65	20.7
8	31.4	56.05, 0.34, −2.56	30.6	55.65, 0.36, −2.64	30.4
9	34.4	55.48, 0.35, −2.59	35.9	55.46, 0.36, −2.64	35.4
11	43.0	55.78, 0.35, −2.57	43.5	55.54, 0.36, −2.64	43.3
13	49.1	55.83, 0.34, −2.56	48.8	55.54, 0.35, −2.63	48.7
14	50.4	55.92, 0.35, −2.57	50.7	55.58, 0.35, −2.64	50.6
15	52.3	55.78, 0.35, −2.56	52.0	55.50, 0.35, −2.64	52.0
16	54.3	55.25, 0.35, −2.57	52.7	55.24, 0.36, −2.64	52.8
17	53.0	56.53, 0.34, −2.55	54.4	55.78, 0.35, −2.63	53.9

matter which population it belongs to. On the other hand, we take M_2 to specify that the average length of a fish whose age is x is Equation (4) with a, b, and c replaced, respectively, by a_i, b_i, and c_i, if the fish belongs to population i, for $i = 1, 2$. Note that in the notation of the previous section θ is the vector whose elements are a, b, and c, while θ_i is the vector whose elements are a_i, b_i, and c_i, for $i = 1, 2$. Also $n = 15$ and $m = 14$, for this example.

The ith row, or threesome, for $i = 1, \ldots, 15$, of the third column of Table 1 is the set of least squares estimates of a_1, b_1, and c_1 obtained by assuming M_2 to be correct and using all of the age-length data pairs in Table 1, except for the ith pair, to estimate a_1, b_1, and c_1. For example, when the data point (8, 31.9) is ignored, the least squares estimates of a_1, b_1, and c_1 are, respectively, 55.43, 0.36, and −2.73. The fourth column of Table 1 gives the predicted lengths for each of the first population fish, assuming M_2 is correct. That is, the ith element in this column is

$$\frac{\hat{a}_{1(i)}}{1 + e^{-(\hat{b}_{1(i)}x_i + \hat{c}_{1(i)})}} \tag{5}$$

where x_i is the ith element of the first column and $\hat{a}_{1(i)}$, $\hat{b}_{1(i)}$, and $\hat{c}_{1(i)}$ represent the ith threesome of the third column.

The ith row, or threesome, for $i = 1, \ldots, 15$, of the fifth column of Table 1 is the set of least squares estimates of a, b, and c obtained by assuming M_1 to be correct and using all of the age-length data pairs in Tables 1 and 2, except for the ith pair in Table 1, to estimate a, b, and c. The last column of Table 1 gives the predicted lengths for each of the first population fish, assuming M_1 is correct. The ith element of this column is (5) after $\hat{a}_{1(i)}$, $\hat{b}_{1(i)}$, and $\hat{c}_{1(i)}$ have been replaced by $\hat{a}_{(i)}$, $\hat{b}_{(i)}$, and $\hat{c}_{(i)}$, where the latter threesome is the ith row of column five.

The discussion of columns three, four, five, and six of Table 2 is completely analogous to that given in the preceding two paragraphs for these

columns of Table 1. Thus, essentially, the fourth and sixth columns of Table 2 give the predicted lengths of the second population sampled fish for models M_2 and M_1, respectively.

In the notation of the previous section, D_{21} is the sum of the squares of the differences between the corresponding elements of columns two and four of Table 1. We find that $D_{21} = 87.31$, for this example. Similarly, D_{22} is the sum of the squares of the differences between the corresponding elements of columns two and four of Table 2 and we find that $D_{22} = 19.39$. Further, $D_2 = D_{21} + D_{22} = 106.70$. Finally, D_1 is the sum of the squares of the differences between the corresponding elements of columns two and six of Tables 1 and 2. We find that $D_1 = 86.77$ and since $D_1 < D_2$, the model, M_1, of equal growth curves for the two populations is the one best supported by the data.

For this example, the length of the jth fish from population i was taken to be

$$Y_{ij} = \frac{a}{1 + e^{-(bx_{ij} + c)}} + \epsilon_{ij}$$

for $i = 1, 2$, where x_{ij} is the age of the jth fish from population i, $a = 55$, $b = 0.35$, $c = -2.55$ and the ϵ_{ij}'s were each normal random variates with mean zero and standard deviation equal to two. The normal variates were generated using the algorithm of Box and Muller (1958). Thus, in essence, we generated both data sets using the same growth curve and the procedure described in the previous section made the correct selection.

MORE THAN TWO POPULATIONS

The procedure used to compare the growth curves for two populations is easily extended to the case where the growth curves for three or more populations are to be compared. As before, we begin by formulating all possible or plausible models. The number of possible models increases considerably as the number of populations being studied increases. For example, if there are three populations, there are five possible models, say $M_1, \ldots, M_5$. Here M_1 specifies that all three growth curves are the same. M_2 specifies that the growth curves for the first two populations are the same but they differ from that for the third population. M_3 specifies that the first and third populations have the same growth curve but the second population's growth curve is different. M_4

specifies that the first population's growth curve differs from those for the second and third populations but the latter two are the same. Finally, M_5 specifies that all three growth curves differ. Once again we assume that the forms of the common and distinct growth curves are specified for each model, but each contains one or more unknown parameters.

Once the models have been formulated, the problem is to use data to select one of them as being most plausible. The data consist of samples of pairs of age-length measurements from the populations being studied. For each model, we compute the sum of the squares of the differences between observed and predicted lengths for all of the fish in the samples, where the predicted lengths are computed by assuming the model is correct. The model selected as most appropriate, by the data, is the one that corresponds to the smallest sum of squares.

In order to compute the sums of squares, we must calculate a predicted length for each fish in the samples, under each model. For a given fish and a given model, the fish's predicted length is calculated by noting the population from which it came and grouping together all data points from this population and the populations, if any, whose growth curves are asserted, by the given model, to be equal to the growth curve for the fish's population. The fish's age and length measurements are then eliminated from the group of data points and the remaining data points in the group are used to estimate the unknown parameters in the asserted common growth curve. Once these estimates are obtained, unknown parameters in the asserted common growth curve are replaced by their estimates, and the fish's age is substituted into the result to obtain the fish's predicted length.

As an example, consider the data given in Table 3. These data represent the ages and corresponding lengths of 20 fish taken from each of three populations. Once again, the data have been generated by a computer. Our goal is to use the data to select one of five possible models, $M_1, \ldots, M_5$, where the M_i's are delineated in the first paragraph of this section.

For this example, a growth curve of the form

$$y = a(1 - e^{-be^{cx}}) + \epsilon \qquad (6)$$

fits each data set better than the von Bertalanffy, Laird-Gompertz, and logistic growth curves. The first term on the right hand side of Equation (6) is

essentially a constant times an extreme value for minima distribution function. This growth curve does not appear to have been used in the literature as yet. But it probably should be considered as a possible model whenever the other three are tried, as I have found cases where it fits real data better than the others.

TABLE 3.—Ages and lengths of 20 fish from each of the three populations.

Age	Population I length	Population II length	Population III length
1	4.7	5.0	5.3
2	5.4	7.5	6.1
3	10.0	14.2	10.8
4	12.6	11.0	13.5
5	19.0	17.8	20.0
6	16.0	17.5	17.2
7	19.0	19.2	20.1
8	22.3	27.9	23.5
9	28.1	27.7	29.2
10	27.2	34.1	28.2
11	38.0	32.7	38.8
12	41.5	40.8	41.8
13	42.1	48.1	41.7
14	49.9	51.5	48.9
15	53.3	53.3	51.4
16	57.0	56.3	54.3
17	56.3	55.9	52.8
18	58.3	57.9	54.1
19	59.6	60.2	55.0
20	59.9	57.9	55.1

Because Equation (6) fits each data set so well, one takes each of the common and distinct growth curves for each model to be in the form of Equation (6). Then for each model one calculates a predicted length for each of the 60 fish in the samples and a sum of squares of the differences between observed and predicted lengths. For the models $M_1,\ldots,M_5$, these sums of squares, are respectively, 334.27, 298.58, 346.45, 331.58, and 312.94. Since the second of these is the smallest, the model, M_2, which asserts that the growth curves for the first two populations are the same but that for the third population is different is the selected one.

Each of the fish lengths for this example was calculated using Equation (6), where y represents length and x represents age. Once again, ϵ was taken to be a normal random variate with mean zero and a standard deviation of 2. For each of the fish in the first two of the three samples, $a = 60$, $b = 0.10$, and $c = 0.20$. For the 20 fish in the third sample, $a = 55$, $b = 0.12$, and $c = 0.20$. Thus the first two data sets were generated using the same growth curve, but the third data set was generated using a different growth curve. Our procedure made the correct selection.

SOME CONCLUDING REMARKS

It is, in general, not feasible to attempt to carry out the calculations required for our growth curve comparison procedure by hand or with a desk calculator. This is because nonlinear regression analyses are usually required and there are many of them. However, the computations are easily programmed for a computer.

For many growth studies, rather massive amounts of data are gathered. If the amount of data available is excessively large, computer time and costs may become prohibitive. It is natural to ask whether the number of computations required can be reduced by doing away with the process of eliminating a data point from a data set before estimating parameters. Indeed, if this could be done, the number of least squares analyses needed would be drastically reduced. Unfortunately, however, it cannot be done. For it can be shown that if it is done, the selected model will always be the one which asserts different growth curves for all populations.

Often though, when there is a large amount of data, each age in the samples is common to many fish. In this case, a possible procedure is to work with the data points consisting of ages and average lengths, thus reducing the number of data points considerably. However, if the numbers of lengths used to calculate the average lengths vary widely from age to age, then it seems sensible to use weighted sums of squares of differences between observed and predicted lengths, and weighted least squares estimates of parameters, with the weights, in each case, being the numbers of lengths used to calculate the average lengths. The idea is that the larger the number of observations used to calculate an average, the closer the average should be to the true growth curve ordinate and, thus, the more weight that should be assigned to it. This modification of the present procedure was used in Boehlert and Kappenman (1980).

The dangers of extrapolation, after regression analyses, are well known. Thus, the practice of obtaining a predicted value for the dependent variable for a subject whose independent variable value lies outside the range of independent variable values used to carry out the regression analysis, is generally discouraged. There may be instances where extrapolation will bias our comparison procedure away from one or more models. The easiest way of checking to see if it does, in

any given situation, is to examine the observed and predicted length differences for each model. Differences, corresponding to youngest or oldest fish, being excessively large for one or more models might be an indication that extrapolation is biasing the procedure. This difficulty did not appear in the examples used in this paper, but it is possible to imagine rare cases where it could be a problem. If this problem does arise, it is easily remedied. One can always eliminate from a sum of squares of differences between observed and predicted lengths those differences whose predicted lengths are obtained by extrapolation. If this is done, the sums of squares in the model selection criterion should be replaced by averages of squares of differences.

For each of the examples given in this paper, all of the specified growth curves were taken to be of the same form. This is not necessary. Any growth curve can be given any form. For example, in the two population case, the common growth curve, for the model of equality of growth curves, can have a mathematical form which is different from the forms of the growth curves specified under the model of different growth curves. And, in fact, the latter two forms can be different from each other. Thus it is possible to handle the case where M_1 specifies equal growth curves and the common growth curve belongs to, say, the logistic family, while M_2 specifies differ-

ent growth curves and the curves belong to, say, the Laird-Gompertz family or one belongs to the Laird-Gompertz family and the other belongs to the generalized extreme value for minima family.

Finally, it should be pointed out that although this paper has been concerned solely with growth curve comparisons, the procedure described here can be applied to the general problem of comparing regression equations. The regression equations of interest can be either linear or nonlinear functions of the unknown parameters. Where they are nonlinear is of particular interest since such comparisons have apparently not been discussed in the literature.

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