ESTIMATING PARAMETERS OF NONLINEAR GROWTH MODELS:
A COMPARISON OF JACKKNIFE AND STANDARD LEAST SQUARES

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Abstract

ESTIMATING PARAMETERS OF NONLINEAR GROWTH MODELS: A COMPARISON OF JACKKNIFE AND STANDARD LEAST SQUARES

by Charles E. Peterson, Jr.

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This study investigates and assesses a statistical technique called the "jackknife," in estimating parameters of a nonlinear growth model, in particular the asymptote. The resultant parameter estimates and variances obtained with the jackknife were compared to the same obtained with a conventional nonlinear regression program. The growth data were generated from the Logistic function using the Monte Carlo method, for an array of biological errors, measurement errors, and maximum population ages. In addition to fitting the correct (Logistic) growth function, the Monomolecular and Chapman-Richards functions were also fitted to determine the extent to which both the jackknifed and conventional estimates were influenced by a model which was either mis-specified or over-complex.

Large error and limitations on maximum population age sampled were primary causes of severe bias in both estimation procedures. In general, however, jackknifing seldom demonstrated improvement over the conventional nonlinear regression procedure. Furthermore, when the conventional procedure resulted in large bias or variability in estimates of the asymptote, the jackknife worsened the situation as often as not.

In other words, the jackknife cannot be expected to overcome or rectify problems incurred with either the sampled data or choice of growth function. Moreover, the success and failure of jackknifing nonlinear parameter estimates is closely tied to the same considerations of conventional nonlinear estimation techniques, including initial guesses of the parameter value, maximum allowable iterations, and tolerance criteria for convergence. All of these considerations must be properly addressed in any future evaluations of the jackknife for estimating parameters of nonlinear growth functions.

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I thank my family, my friends, and the staff and faculty of the College of Forest Resources for their continuous encouragement and support. Finally, I dedicate this work to the memory of Professor Ken Turnbull, who taught and inspired by example, and was the standard for scientific integrity, rigor and excellence.

1.0 INTRODUCTION AND STATEMENT OF OBJECTIVES

The increased efficiency and availability of computers over the past two decades have paved the way for rapid developments in modeling plant growth, both as a crop and an individual plant, as well as components of the individual plant. Many of these models have been used in forestry to express forest growth. In simplest form, these models are single equations, often obtained from fitted regressions; a more complex model (e.g. a simulator) might be constructed from two or more equations linked together. The accuracy and precision of these models or estimators is often measured by a statistical property called mean squared error (M.S.E.). The two components of the M.S.E. are variance and bias, either of which may be difficult (or impossible) to measure. In fact, "realistic" variance estimates for estimators of forest growth have lagged far behind the vast array of forest growth models and simulators assembled in the past two decades.

The purpose of this study is to investigate and assess a statistical technique for estimating parameters of a nonlinear growth model, particularly the asymptote, with less bias and as "good or better" variance estimates than estimates produced by conventional estimation procedures. One such procedure with potential for industrial application is called the "jackknife," which is basically a sub-sampling technique, "re-using" the sample data. The jackknife also shows promise of producing reliable variance estimates in cases where derivations of estimators are either complex or wholly intractible. This procedure has only recently been considered for estimating biological growth parameters. If the jackknife technique demonstrates its usefulness in producing reliable variance estimates for single-equation predictive models, the potential for validation of linked forest growth models could be enhanced.

After selecting the jackknife as the statistical technique to test, it was necessary to select a growth function for application. As Causton and Venus (1981) point out, ". . . a danger inherent in the use of a quantitative approach is to lose sight of one's biological goal and to enter a labyrinth of mathematics without ever emerging into the biological world." In the present study, the jackknife method is applied to three classical nonlinear models which are often used to express biological growth:

(i) Logistic
(ii) Monomolecular
(iii) Chapman-Richards generalization of Bertalanffy's model.

Growth data for this study were generated from the Logistic function using the Monte Carlo method, with final data sets containing both biological error and sampling error. Each of the above models was then fitted to the generated growth data, using a conventional nonlinear regression program. Asymptotic levels of growth were estimated, both with and without jackknifing, for an array of biological errors, measurement errors, and maximum population ages. Although the correct model form for the data was the Logistic, both the Monomolecular and the

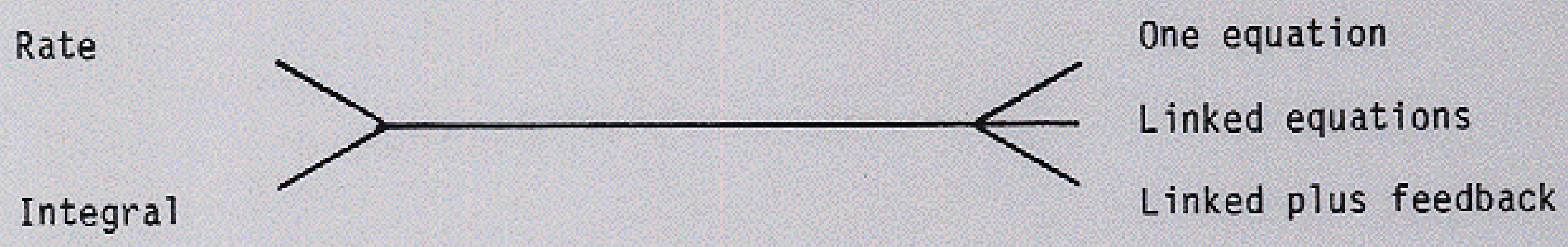
Chapman-Richards functions were fitted to determine the extent to which both jackknifed and conventional estimates were influenced by either mis-specifying the growth model (i.e. Monomolecular) or using a more complex model (i.e. Chapman-Richards). Estimates of the asymptote were tested for bias and normality of distribution.

2.0 LITERATURE REVIEW

2.1 Forest Growth Models

Numerous forest growth models have been employed in various structures and for various purposes. In complexity of structure, the simplest model is a single equation for either growth rate or total yield. If Y represents yield, and the growth rate dY/dt is expressed as a function of time (t) and other variables, then Y itself may be expressed alternatively as a function of t and other variables. This alternative expression of Y is the integral of the rate function. The importance of choosing the rate form over the integral form of a nonlinear model was identified by Gertner (1980). He concluded that when errors of successive tree measurements are correlated, the form of the model is more important than the method of estimation.

More complex systems consist of two or more equations linked together to produce the desired estimate. A feedback or governing mechanism may also be added to a system of linked equations to act on or limit the growth process. Thus, forms of the model may vary in degree of complexity:



Examples of these models are summarized in Table 1, and are identified as to whether the principle driving function is of the integral or rate form. Some of these models reflect classical growth forms which have been applied to a wide variety of plant and animal populations; others constitute an empirical regression approach which is specific to the species and/or forested region.

The models reviewed here are limited to three "classical" growth functions which have been widely studied and used over the past twenty years:

(i) Logistic
(ii) Monomolecular
(iii) Chapman-Richards generalization of Bertalanffy's model.

Each model is examined in this study as a single growth equation, without linkage to any other models. This contrast is interesting since all three nonlinear models can be used either singularly or in combination with other equations to model the desired outcome. All three functions are asymptotic. Hence the asymptote (Y_∞) is the common parameter of interest. The Monomolecular function has no inflection point and thus cannot make use of that trend in growth data. On the other hand, one might expect the Chapman-Richards function to perform as well as either of the other two functions in estimating Y_∞, since the other two functions are special cases of the more general Chapman-Richards function.

Table 1.

Examples of growth modeling in forestry

Single Equation	Linked Equation	Linked plus Feedback
I - Schumacher & Hall (1933)	R - Warrack (1959)	I,R - Lee (1967)
I - MacKinney, et. al. (1937)	R - Buckman (1962)	R - Mitchell (1969)
I - Meyer (1940)	R - Clutter (1963)	I - Hatch (1971)
R - Buckman (1962)	R - Curtis (1967)	I - Arney (1972)
R - Lemon & Schumacher (1962)	R - Moser & Hall (1969)	R - Stage (1973)
I - Turnbull (1963)	I - Sullivan (1969)	I,R - Hegyi (1974)
I,R - Pienaar (1965)	R - Moser (1972)	R - Ek (1974)
I - Brickell (1968)	I - Sullivan & Clutter (1973)	I,R - Daniels & Burkhart (1975)
R - King (1970)	I - Burkhart & Stub (1974)	I - Bruce, et. al. (1977)
I - Pienaar & Turnbull (1973)	I - Smalley & Bailey (1974)	R - U.S.D.A. Forest Service (1979)
R - Dahms (1975)	I - Wiley & Murray (1974)	I - Curtis, et. al. (1981)
I - Wiley, et. al. (1978)	R - Wiley (1978)	
I,R - Machado (1978)	I - Campos (1979)	
	I - Farrar (1979)	

Each model is identified as to the form of principle growth function(s):

I = integral
R = rate
I,R = both integral and rate

Growth data used in this study (discussed in Chapter 3.0) were generated from the Logistic function. Therefore, the Logistic model represents the most appropriate of the three models for estimating maximum attainable growth in the data set. In absence of this knowledge, however, the other two models represent alternative choices of simplicity (Monomolecular) or complexity (Chapman-Richards). They also provide a situation for assessing the jackknife technique when the correct form of model is mis-specified.

2.1.1 Logistic Function

P.F. Verhulst (1838) first proposed the Logistic equation to model human populations:

$$Y_t = Y_\infty \left[1 + be^{-kt}\right]^{-1} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \quad (1)$$

where Y_t is population size at time t, Y_∞ is the upper asymptote (maximum value of Y_t), b and k are constants. Pearl and Reed (1920) subsequently "rediscovered" this function in describing population growth in the United States. It can be shown that $dY/dt = kY(Y_\infty - Y)$; that is, growth rate is proportional to the product of Y and its deficiency from the maximum value. This expression provides a more realistic model for growth in a limited environment than does a non-asymptotic function. The sigmoid or S-shaped curve represented by the Logistic function is depicted in Figure 1a.

The Logistic function was used by MacKinney, et. al. (1937) to construct yield tables for second-growth stands of loblolly pine (Pinus taeda L.) and provide an estimate of maximum yield. However, they noted that the Logistic function is symmetrical about the inflection point and decided that this model was too restrictive in its standard form. They expanded the exponent of e in (1) to a polynomial form to gain flexibility:

$$Y_t = Y_\infty \left[1 + be^{(a_0 + a_1 x_1 + \ldots + a_n x_n)}\right]^{-1} \quad \ldots\ldots\ldots \tag{2}$$

Variations from the standard Logistic function have been more recently used for modelling tree mortality (Hamilton and Edwards, 1976; Monserud, 1976; Buckman, 1979).

2.1.2 Monomolecular Function

The Monomolecular or Mitscherlich (1930) function, also used by von Bertalanffy (1934, 1938), was first used to model response of crop yield to additions of fertilizer.

$$Y_t = Y_\infty \left[1 + be^{-kt}\right] \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \tag{3}$$

As illustrated in Figure 1b, the curve is asymptotic but not S-shaped.

Since growth of most populations is believed to follow a sigmoid curve, the Monomolecular curve is not frequently used to model population growth. Monomolecular equations were introduced in forestry literature by H.A. Meyer (1940) for estimating site index (i.e., potential for productivity) by using height curves. He acknowledged that this expression did not allow for inflection of the height curve in very young trees or trees of small diameter.

2.1.3 Chapman-Richards Growth Function

Bertalanffy (1951) modified the Monomolecular function (equation 3) to express an isometric (Ricker, 1975) growth relationship:

$$Y_t = Y_\infty \left[1 + be^{-kt}\right]^3$$

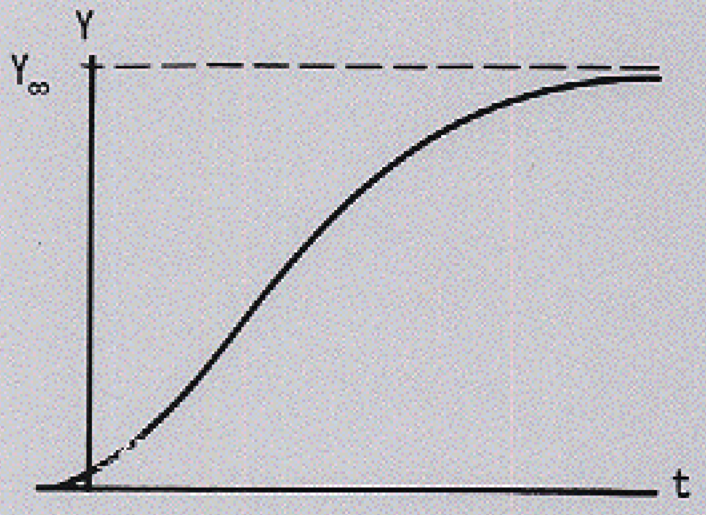


Figure 1a. Example of a sigmoid or S-shaped curve (e.g. Logistic).

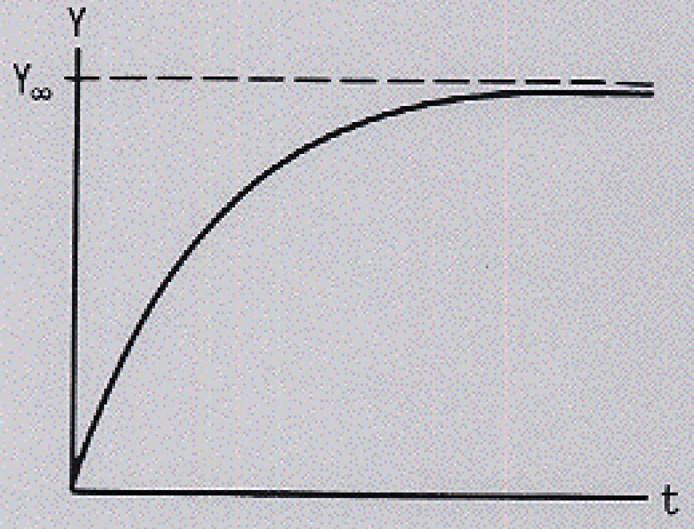


Figure 1b. Example of a Monomolecular curve.

which can be rewritten as

$$Y_t = Y_\infty \left[1 + be^{-kt}\right]^{1/(1-\frac{2}{3})} \quad \ldots\ldots\ldots\ldots\ldots\ldots (4)$$

Richards (1959) and Chapman (1961), analysing plant growth and fish growth respectively, thought a constant of 2/3 was too inflexible. Independently they both generalized Bertalanffy's model by adding a fourth parameter (m). Turnbull (1963) introduced this function to the forestry literature as the Chapman-Richards model:

$$Y_t = Y_\infty \left[1 + be^{-kt}\right]^{1/(1-m)} \quad \ldots\ldots\ldots\ldots\ldots\ldots (5)$$

Turnbull's application of equation 5 to forest stand growth was in estimating net volume yield. Pienaar (1965) used the Chapman-Richards model principally to test basal area growth hypotheses using both thinned and unthinned plantation data. The same expression has since been widely used to estimate height growth in constructing site index curves (Brickell, 1968; Lundgren and Dolid, 1970; Trousdell, et. al., 1970; Machado, 1978) in addition to diameter growth (Hahn and Leary, 1979) and basal area (Machado, 1978).

Both the Logistic (equation 1) and the Monomolecular (equation 3) models are special cases of the Chapman-Richards function (equation 5). Setting $m = 2$ and $m = 0$ results in the Logistic and Monomolecular expressions, respectively. These values of m specified for derivatives of the Chapman-Richards function will also yield the correct derivatives for the Logistic and Monomolecular models. That is, for the generalized model, differentiated with respect to time:

$$\frac{dY}{dt} = \left(\frac{k}{1-m}\right) Y \left[\left(\frac{Y_\infty}{Y}\right)^{1-m} - 1\right] \quad \ldots\ldots\ldots\ldots\ldots\ldots \tag{6}$$

$$\frac{d^2Y}{dt^2} = \left(\frac{k}{1-m}\right) \frac{dY}{dt} \left[m\left(\frac{Y_\infty}{Y}\right)^{1-m} - 1\right] \quad \ldots\ldots\ldots\ldots\ldots\ldots \tag{7}$$

Equation 6 expresses the instantaneous growth rate whereas equation 7 depicts acceleration. Setting the equation 6 equal to zero and solving for Y identifies the point at which dy/dt is maximal, that is the point of inflection on the Chapman-Richards sigmoid growth curve:

$$\max \frac{dY}{dt} \text{ is at } Y = Y_\infty\,(m)^{1/(1-m)} \quad \ldots\ldots\ldots\ldots\ldots\ldots \tag{8}$$

These relationships are depicted graphically in Figure 2. The inflection point for the Logistic curve (m=2) occurs at $Y = Y_\infty/2$ and for the Bertalanffy function (m=2/3) at $Y = (8/27)Y_\infty$. The parameter (m) allows some flexibility as to where the inflection point occurs, which is precisely what both Chapman and Richards sought and attained. The flexibility of the Chapman-Richards model is illustrated in Figure 3. Subsequently, this generalized function has become very popular as a growth model.

2.2 Properties of Estimators

Each of the growth models reviewed in the previous section is used in this study to estimate the maximum (i.e. asymptote) of the simulated data set. The reliability or confidence we place in an estimator is

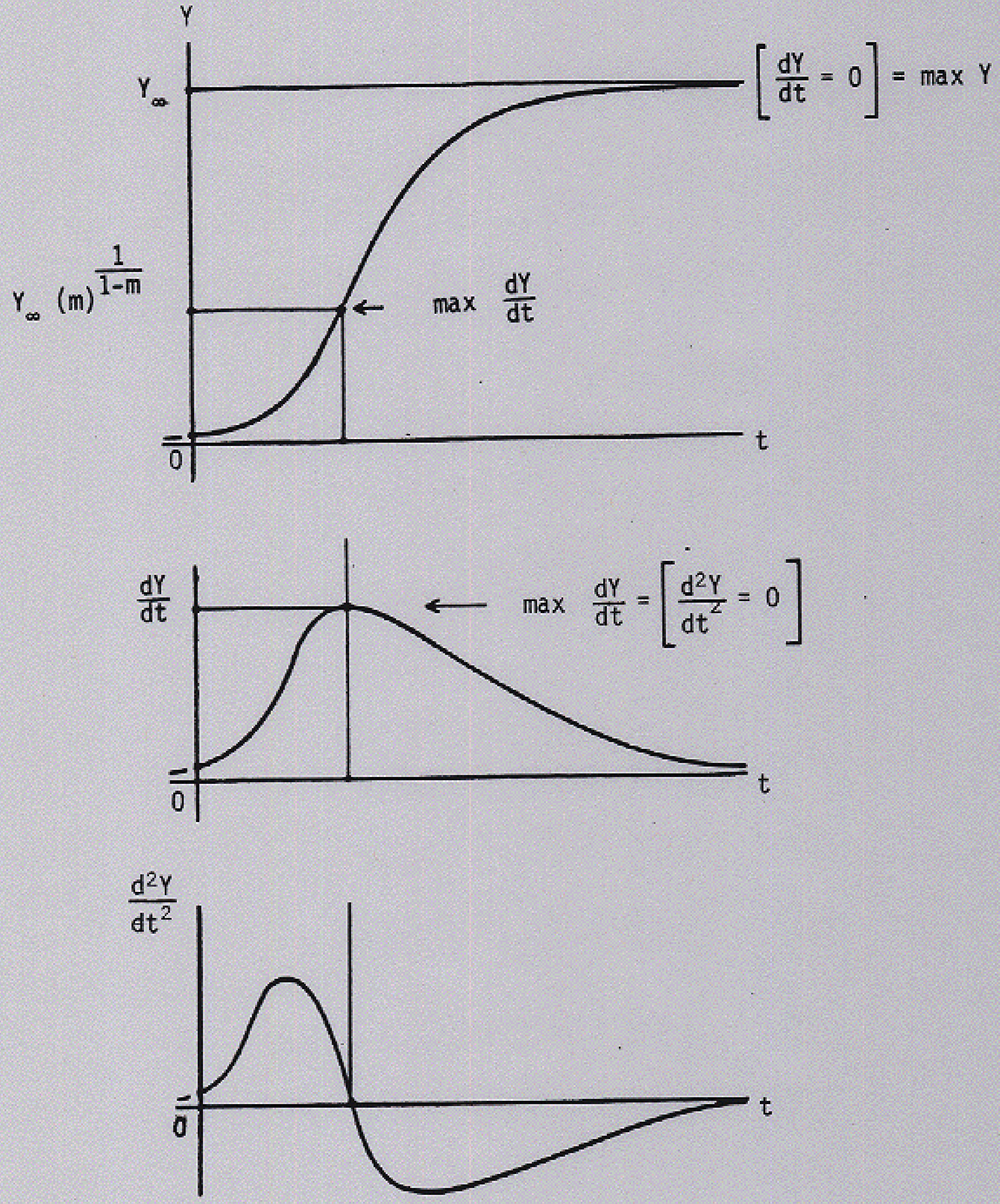


Figure 2. Generalized representation of the first- and second-derivative forms of sigmoid growth (after Fletcher, 1974).

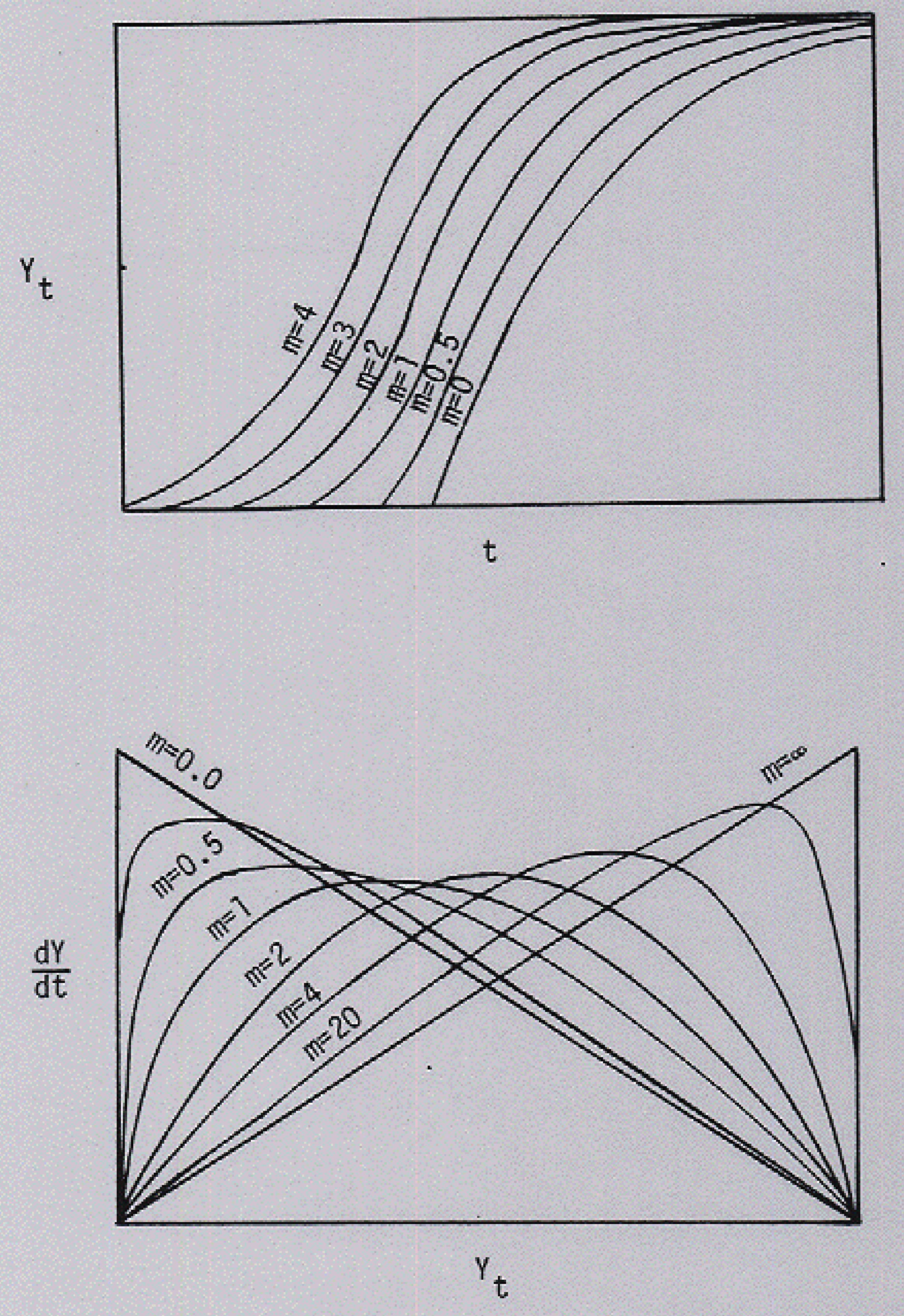


Figure 3. Family of growth curves generated from the Chapman-Richards model by varying parameter m (after Richards, 1959).

usually judged according to its statistical characteristics. The most commonly recognized statistical characteristics of a parameter estimate are sufficiency, consistency, and mean squared error. Sufficiency involves the reduction of sample data to a statistic (e.g. the average), involving no loss of information. Consistency reflects the large sample behavior of an estimate. A consistent estimate approaches the true value as sample size n is increased (i.e. $n \quad \infty$). That is, if Y_n is a consistent estimate of Y, and n is large, then Y_n is, with high probability, close to Y.

Finally, mean squared error (M.S.E.) is a measure of both precision and accuracy (Cochran, 1963) of an estimate -- if the estimate has zero bias, then M.S.E. is the variance of the estimate:

$$\begin{aligned} \text{M.S.E.} &= E(\hat{Y}_n - Y_n)^2 \\ &= \text{Var}\,(\hat{Y}_n) + b^2\,(Y_n,\hat{Y}_n) \quad \cdots\cdots\cdots\cdots\cdots\cdots \quad (9) \end{aligned}$$

where $b(Y_n,\hat{Y}_n) = E(\hat{Y}_n) - Y_n$, and is called the bias of $\hat{Y}_n$

$\hat{Y}_n$ is the estimate of a parameter Y_n

$\text{Var}\,(\hat{Y}_n)$ is the variance of $\hat{Y}_n$

$E(\hat{Y}_n)$ is the mean of $\hat{Y}_n$

Although each of these characteristics is important in an estimator, the mean squared error is of major interest in this study since the statistical quality of a growth estimate depends largely on the error structure of the model (more detailed theoretical information may be found in

Bickel and Doksum, 1977). Additionally, this study concerns the error of estimate from a single model only. (error structure of linked models, dealt with in part by the classical theory of error propagation, is reviewed in Appendix E). Distribution of the errors is usually assumed to follow the normal or Gaussian[†] law of errors. As Aitken (1952) notes, "the role of the normal distribution in statistics is not unlike that of the straight line in geometry."

Errors usually reflect uncertainties (i.e. natural variation) in data gathered, how it is measured or collected, and statistical methods used to extract information from sampled data. In a conventional laboratory situation, error of a measured variable or function of measured variables is generally a composite of several errors (i.e. method, laboratory, observer, etc.), notwithstanding error between laboratories or methods. According to Tippett (1950), much laboratory work is done with the assumption that such errors (some positive and some negative) cancel each other out in the long run, with final confidence resting on numerous replications and averaging of results.

Errors, or uncertainties, have always been a concern in forest mensuration. In forestry, the reliability of stand volume or yield is dependent upon how accurately single tree volume is determined. There are numerous measurement errors that can be made in determining tree volume, such as errors in cross-sectional area and/or height.

[†] Karl Pearson (1924) argues that DeMoivre should be credited with discovery of the normal curve.

Chaturvedi (1926) provides an excellent discussion of these potential errors and the place of accuracy in the work of the practical forester. As an example, he demonstrates that in assuming an elliptical cross-section to be circular (i.e. using a diameter tape), error is always in a positive direction, whereas the use of callipers to determine diameter results in error in a negative direction. Propagation of error causes these uncertainties to be transmitted from data to parameter estimates, and to the function of the estimated parameter that is required in the final result. Tippett (1950) suggests that experiments are sometimes more influenced by experimental error than by natural variation of the observation itself. Field experimentors (e.g. foresters) cannot, however, generally exercise the control of greenhouse or laboratory situations. Under "field" conditions, it is often impossible or difficult at best, to partition variation into components of inherent biological error and error added from measurement and estimation. Therefore, since the data of the present study is generated to reflect variability which might be found in nature, natural variation (i.e. biological error) is assumed to have a major influence on the outcome.

2.3 Monte Carlo Methods

A Monte Carlo procedure was used in this study to create a data set and to compare the two estimation procedures. In the Monte Carlo method, simulated observations are created using random numbers (usually generated by a computer). It is then possible to study the behavior (e.g. statistical properties) of the observations. If the sample of simulated observations is large, this, in effect, represents the population. Of course it is essential that the artificially created observations reflect those observations that would be taken in a real situation. A good general discussion and bibliography of Monte Carlo methods is provided by Hammersley and Hanscomb (1975).

The Monte Carlo approach is used in this study to assess methods of estimating the asymptote and its variance from data generated for a logistic function. Each generated data set has independent measurement errors normally distributed, with mean zero, and with variance additive in some test cases and multiplicative in others.

2.4 Jackknife Procedure

The jackknife technique is based on an idea originally proposed by Quenouille (1949, 1956) for reduction of bias in estimation. This concept was later extended by Tukey (1958, 1962), who also used the technique to construct approximate confidence intervals for the parameter of interest. The jackknife technique basically consists of splitting the data sample (n) into m subgroups of size h (i.e. $n = mh$). If $h = 1$, then the maximum number of subgroups is $m = n$. If $h > 1$, and thus $m < n$, the m subgroups should be chosen at random.

In his excellent review of the jackknife, Miller (1974) asserts that its main application is with regard to inference on variances. In earlier work, Miller (1968) compared the jackknife to alternative techniques for testing variances and concluded that "...the jackknife seems to work well, if it works at all." The best use of the jackknife is generally made in conjunction with a transformation in order to stabilize variance (Miller, 1968; Arvesen and Schmitz, 1970). Bissell and Ferguson point out that in addition to the "normalizing" effect on variances, the logarithmic transformation usually helps avoid problems such as negative jackknifed estimates of variance or absolute values of correlation coefficients greater than one. These problems would be situations where the jackknife has not worked at all.

Bissell and Ferguson (1975) note that the jackknife's reduction of bias should improve the mean squared error even if the variance itself is not reduced. More importantly they demonstrate the potential of jackknifing to overcome "previously intractable problems of variance estimation and significance testing."

Consider Y_1, Y_2, ..., Y_n as a sample of independent and identically distributed random variables, with an unknown parameter θ, which we want to estimate from the sample. Assume $\hat{\theta}$ estimates θ from sample size n, and let $\hat{\theta}_{-j}$ be a "partial estimate" based on sample size h(m-1), where the j^{th} subgroup of size h has been deleted from m subgroups. Subsampling m times with replacement will eventually give m partial estimates $\hat{\theta}_{-1}, \hat{\theta}_{-2}, \ldots, \hat{\theta}_{-m}$

Let $\theta_{*j} = m\hat{\theta} - (m-1)\theta_{-j} \qquad j = 1, 2, \ldots, m$

The partial estimates are combined with the whole-sample estimate to give values which Tukey calls "pseudo-values."

The jackknifed estimate of θ is then the average of the pseudo-values:

$$\hat{\theta}_{*} = \frac{1}{m}\sum_{j=1}^{m} \hat{\theta}_{*j} = \left[m\hat{\theta} - \left(\frac{m-1}{m}\right) \sum_{j=1}^{m} \hat{\theta}_{-j} \right] = \left[m\hat{\theta} - (m-1)\bar{\hat{\theta}} \right] \quad . \; . \; . \; (10)$$

$$\text{where} \qquad \bar{\hat{\theta}} = \frac{1}{m}\sum_{j=1}^{m} \hat{\theta}_{-j}$$

Quenouille originally conceived the jackknife to eliminate bias of order 1/n from a serial correlation estimator. That is, if bias can be expressed in reciprocal powers of n, or

$$B(\theta) = E\,(\hat{\theta} - \theta) = \frac{a_1}{n} + \frac{a_2}{n^2} + \frac{a_3}{n^3} + \quad . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; . \; (11)$$

then it can be shown that for any permissible value of h

$$B(\hat{\theta}_{*}) = E\,(\hat{\theta}_{*} - \theta\,) = -\left(\frac{m}{m-1}\right)\frac{a_2}{n^2} + \quad . \; . \; . \; . \; . \; . \; . \; . \; (12)$$

Clearly, the magnitude of bias eliminated is greatly affected by sample size n. The bias reduction through jackknifing was subsequently examined and characterized by a number of authors (Schucany, et. al., 1971; Gray and Schucany, 1972). They extended the technique to eliminate higher orders of bias.

Tukey reasoned further that the pseudo-values could be treated as approximate independently and identically distributed random variables such that the statistic

$$\frac{\theta_* - \theta}{S_T} \;\dot{\sim}\; t_{T',m-1} \quad \cdots\cdots\cdots\cdots \quad (13)$$

where $t_{T',m-1}$ has an approximate t distribution with m-1 degrees of freedom. The variance S_T^2 is determined from the pseudo-values in the usual way:

$$S_T^2 = \frac{1}{m(m-1)} \sum_{j=1}^{m} (\hat{\theta}_{*j} - \hat{\theta}_*)^2 \quad \cdots\cdots\cdots\cdots \quad (14)$$

These relationships are easily generalized for situations with two or more parameters, with vectors replacing above quantities such that:

$$T_*^2 = (\underset{\sim}{\hat{\theta}}_* - \underset{\sim}{\theta})' \, (S_T^2)^{-1} \, (\underset{\sim}{\hat{\theta}}_* - \underset{\sim}{\theta}) \quad \cdots\cdots\cdots\cdots \quad (15)$$

follows approximately a Hotellings T^2 distribution. Examples may be found in Gray and Schucany (1972), Miller (1974), and Bissell and Ferguson (1975).

There has been very little in the way of industrial or forestry applications of the jackknife technique. Arvesen and Schmitz (1970) applied it to variance component problems in genetics. Yang and Kung (1983) used jackknifing and order statistics with double sampling to estimate the bole volume. The estimation involved a simple linear relationship (Y = a+bx) and a small sub-sample (n=4). However, Bissell and

Ferguson (1975) have pointed out that as sample size is increased, the jackknife procedure for order statistics completely degenerates. Schreuder and Brink (1983) examine the feasibility of jackknife procedures for multi-phase sampling in forest inventories and offer some guidance in avoiding erratic results and/or excessive computing costs. More recently, Gregoire (1984) has used jackknifing with ratio estimators in Monte Carlo simulation of forest populations of timber volume, leaf area, and branch biomass. All of these examples appear to have been successful, and have potential for further application, with the exception of Yang and Kung, whose use of order statistics and small sample is limiting (Bissell and Ferguson, 1975).

The jackknife procedure has only recently been applied to estimation problems involving nonlinear regression. Duncan (1978) used the jackknife to construct confidence regions in nonlinear regression. He introduced both additive (mean = 0) and multiplicative (mean = 1) errors in his Monte Carlo simulation of models with the following functional forms:

$$\text{(I)} \quad f(x;\theta) = \frac{\theta_1}{\theta_1 - \theta_2}\left[e^{-\theta_2 x} - e^{-\theta_1 x}\right] \ldots\ldots\ldots\ldots \tag{16}$$

$$\text{(II)} \quad f(x;\theta) = 1 - \frac{1}{\theta_1 - \theta_2}\left[\theta_1 e^{-\theta_2 x} - \theta_2 e^{-\theta_1 x}\right] \ldots\ldots\ldots \tag{17}$$

$$\text{(III)} \quad f(x;\theta) = 1000 \quad \theta_1^{\theta_2 x} \ldots\ldots\ldots\ldots\ldots\ldots\ldots \tag{18}$$

Error distributions considered by Duncan were normal, contaminated normal, and double exponential. Data consisted of four replications of a six-point design (i.e., $m = 4$ groups of size $h = 6$), a very small sample for nonlinear regression. Thus, for regression estimates, a jackknifed estimate for sample size n would require n regressions if $h=1$ (i.e. each regression fitted to $n-1$ data points), whereas the conventional method would be to fit one regression to all n data points. Duncan simulated four jackknife procedures, with $h=1$, 2, 3, and 6 ($h=6$ involves removing an entire replicate). This simulation was repeated 500 times. Although the "empirical percentage coverage of nominal 95 percent confidence regions" was satisfactory for a univariate confidence region, the success of varying jackknife procedures diminished as compared to the univariate case when a joint bivariate confidence region was desired. In this case only the standard jackknife ($h = 1$) was recommended.

Fox, et. al. (1980) applied the standard jackknife and two (weighted and unweighted) linear jackknife methods which require only a single fit, to nonlinear functions of linear regression parameters. They chose Duncan's (1978) models to compare jackknifing methods. Linear approximations for confidence regions were obtained from the linear term of a Taylor expansion on θ_{-j}, where θ_{-j} is the least squares partial estimate of θ when the j^{th} data point is deleted. Hinkley's (1977) weighted jackknife approach was also used in hopes of improving variance estimates.

Huber (1977) discusses the jackknife in relation to "robust" estimators and Efron (1982) discusses its role in "bootstrap" statistical methods. A good bibliography of jackknife research for further reading has been compiled by Parr and Schucany (1980).

Theoretically then, it has been established that the jackknife procedure can eliminate bias of order 1/n and thus improve variance about a parameter estimate for linear regression models, whether the same could hold true for eliminating bias and improving variance of a parameter estimate in nonlinear regression was an open question. However, it seemed reasonable to explore this potential, and so the jackknife procedure was chosen in this study to see how well it performed in estimating both the asymptote of a nonlinear model and the variance about that asymptote, in comparison to a conventional method of estimation.

3.0 APPLICATION OF JACKKNIFE TECHNIQUE

3.1 Generating Growth Data

In order to obtain simulated observations, it was necessary to choose specific values for the Y_∞, b, and k parameters of the Logistic model. A least squares regression was fitted to initial stand volume growth data from the Regional Forest Nutrition Research Project (Hazard and Peterson, 1984) at the University of Washington. The data used were initial stand conditions of unthinned well-stocked second-growth Douglas-fir [Pseudotsuga menziesii (Mirb.) Franco] from plots established in 1969-1970. The oldest of these stands was about 65 years total age. Using this data, it was estimated that maximum volume (Y_∞) would be obtained at about 150 years total stand age. Values obtained -- $Y_\infty = 24090$ (cubic feet per acre), $b = 16.07$, and $k = 0.05523$ -- were used to develop all simulated observations studied. Age 120 years was arbitrarily chosen as the maximum age for which samples would be generated in this study. Also, since Y_∞ might be estimated quite closely if data existed all the way out to 120 years, it was of interest to see how well Y_∞ could be estimated if data extended to ages less than 120 years.

Next, it was necessary to develop a method of generating growth data, in order to use the Monte Carlo method to compare the jackknife technique with the usual nonlinear least squares in fitting the growth model. Once the Logistic function was selected as the model from which to generate growth data, two error processes were considered -- biological error (e_b) and measurement error (e_m). Biological error is the variation in growth due to random effects in nature, particularly climatic factors. Since growth is a cumulative process, such variations at any time need to be built into the growth process. In the Monte Carlo process this was carried out as follows:

The integral form of the Logistic (equation 1) was solved for t to yield

$$t = -\log_e \left[\left(\frac{Y_\infty}{Y} - 1\right)/b\right] \div k \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (19)$$

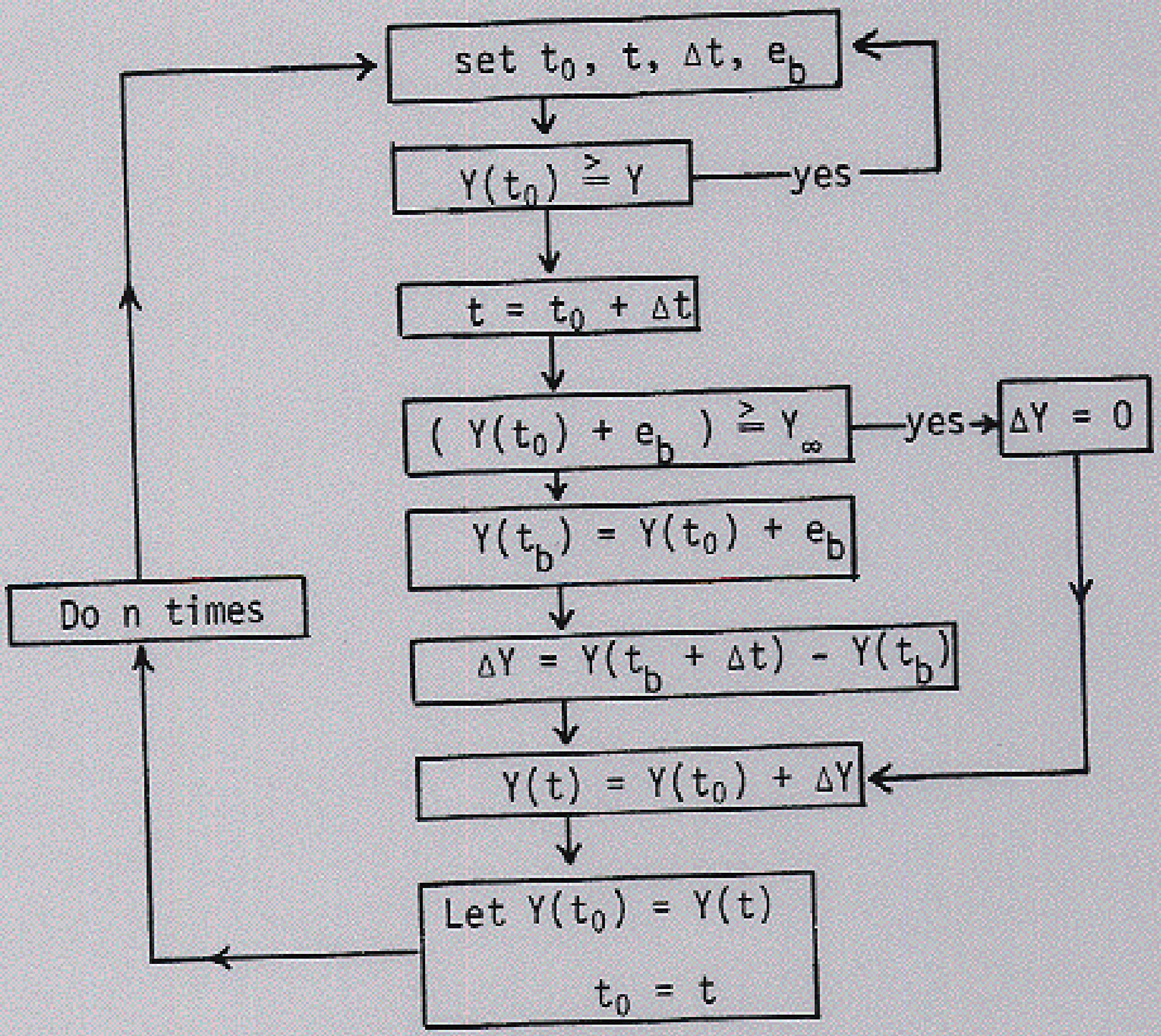
For each point in time at which an "observation" is made, a random biological error (e_b) was added algebraically to Y and

$$t_b = -\log_e \left\{\left(\frac{Y_\infty}{Y + e_b} - 1\right)/b\right\} \div k \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (20)$$

The growth increment ΔY in time increment Δt was then computed as

$$\Delta Y = Y(t_b + \Delta t) - Y(t_b) \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots (21)$$

where $Y(t_b + \Delta t)$ became the basic "observation" for the next time period, before addition of biological error. This process is flow charted in Figure 4. For this simulation it was assumed that biological errors and measurement errors were normally distributed with zero means and respective variances σ_b^2 and σ_m^2.



where $\Delta t = t - t_0$ is the projection time interval

$Y(t_0)$ = starting yield in absence of e_b

e_b = biological error randomly generated

and $Y(t_0)$, t_0, t, Δt, e_b, and e_b-seed are specified initially

Figure 4. Propagation of biological noise in growth data generated from the Logistic function.

As shown in Figure 5, the end result of a positive deviation (+ e_b) is Y(t) lying above the expected point on the curve corresponding to time t. If deviation is negative, Y(t) falls below the curve, and for $e_b = 0$, Y(t) lies exactly on the curve. This deviated Y(t) then becomes the starting point to which another e_b is added, thereby propagating growth with error until maximum (asymptotic) yield Y_∞ is attained. In this way, biological variation is propagated with stand growth so that the final set of generated data points contains inherent "noise" that might be found in nature. Variation about the asymptote is less than what might be expected due to the constraint of zero volume increment for volume data, which in the presence of variation, exceeds the true asymptote. That is, generating data as such may lead to possible bias in maximum yield (Y_∞) for large ages. One could also argue that biological variation among stands should be less when they are nearing the age of maximum yield, and that final yield should not exceed that which is a biological maximum. However, this does not present any major problems since the primary interest in $\hat{Y}_\infty$ is when the sampled data range is less than the range which includes the asymptotic data (i.e. less than 120 years).

Finally, in this study, additional random deviates were added to the generated data points, to represent measurement error (e_m). Since there were no iterative constraints for measurement noise added to the data from simulated biological growth, the final data set includes points which exceed the true asymptote. Independent replicates of data were

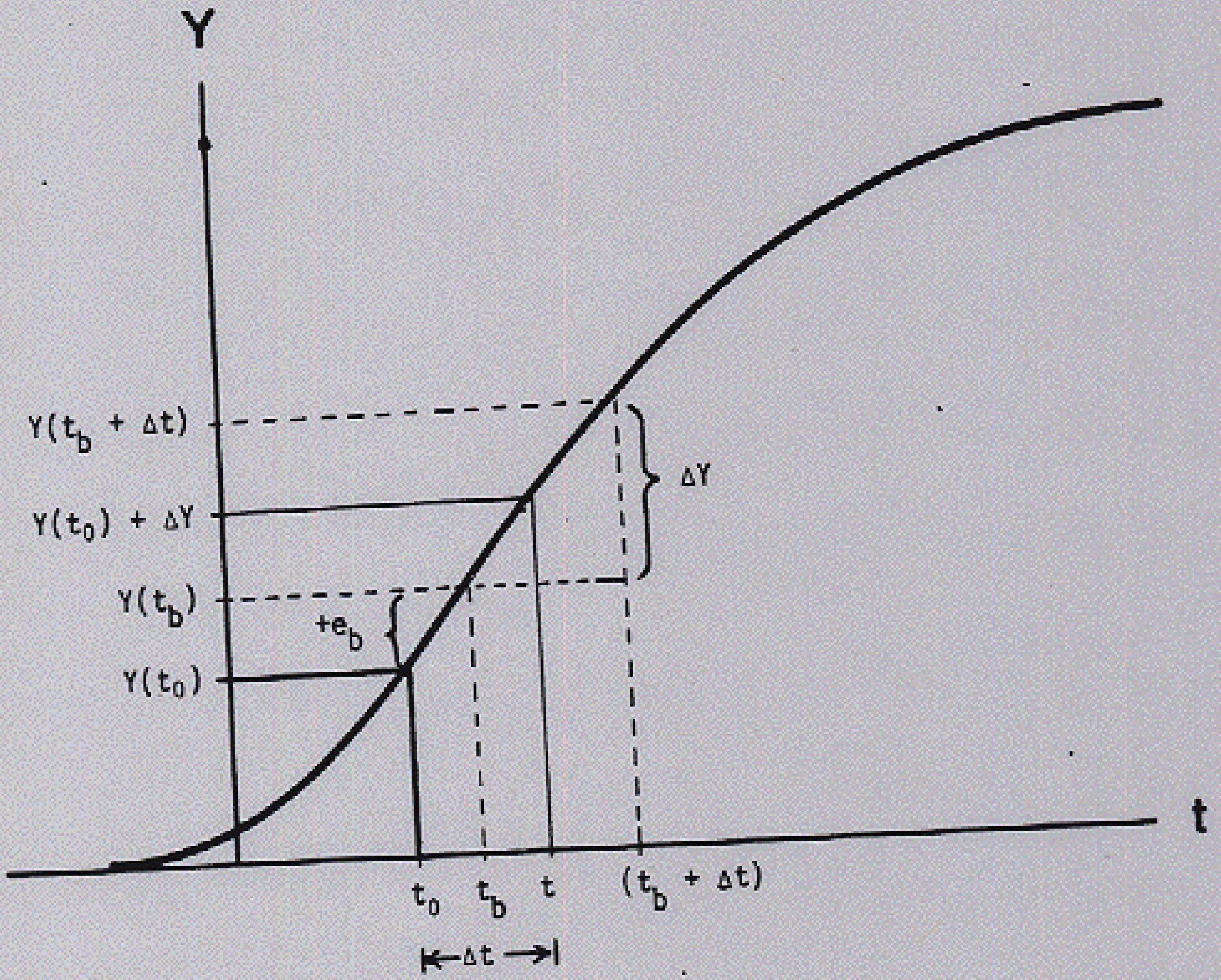


Figure 5. Propagating a positive error deviation over one time increment to generate volume with biological variation in growth.

created in this manner, using increments of five years to finally obtain volume up to 120 years from a starting volume at age forty years. The different combinations of biological and measurement error for various (maximum age) sample sizes are diagrammed in Figures 6 and 7.

Having generated the simulated growth data in this way, the study explores results of estimating parameters of the Logistic function, and particularly the asymptote. A standard nonlinear least squares estimation procedure is explored, both with and without the jackknife method. When the study was initiated, it was hoped that the jackknife technique would reduce bias and/or variance of the nonlinear least squares procedure. Thus, the study compares bias and variance of estimates obtained by two methods (conventional and jackknife). The study also evaluates effects of mis-specifying the model (e.g. fitting the simpler Monomolecular or the more complex Chapman-Richards to Logistic-generated data), or the final estimate.

Examples of generated growth data are portrayed on scattergrams in Appendix D for combinations of both multiplicative and additive forms of biological error, both with and without measurement error.

3.1.1 Choice of Errors

The multiplicative errors (e.g., 15*AGE) were chosen to allow variability or "noise" to increase with time (i.e., age of the stand), whereas additive errors (e.g. 1000 cubic feet per acre) represent a constant variation in growth across time. A wider range of errors was used for e_m (measurement error), assuming that sampling error can be

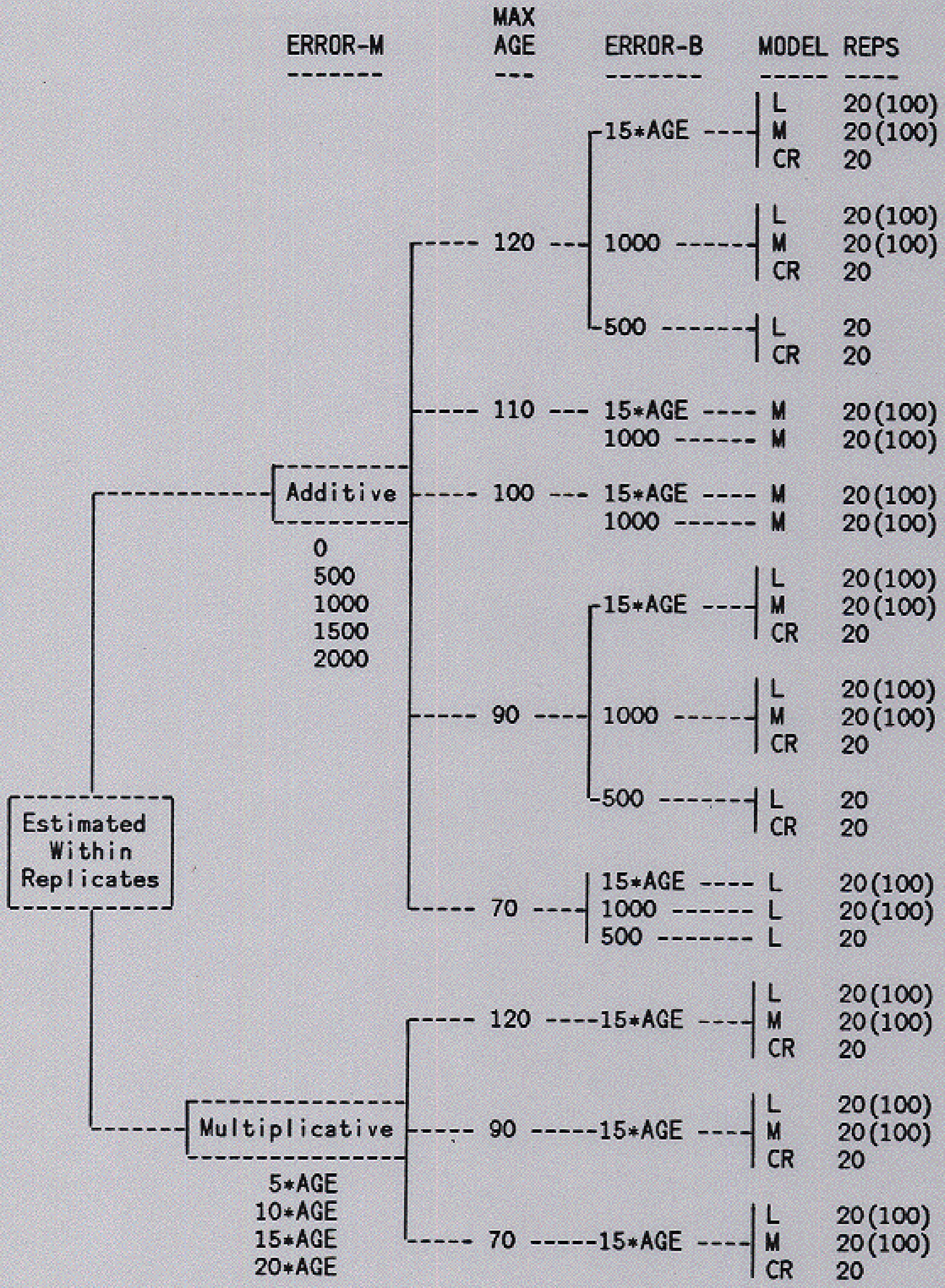


Figure 6. Combinations of measurement error, maximum age, biological error, and replications for estimating Y_∞ using the Logistic (L), Monomolecular (M), and Chapman-Richards (CR) models; estimated with replications.

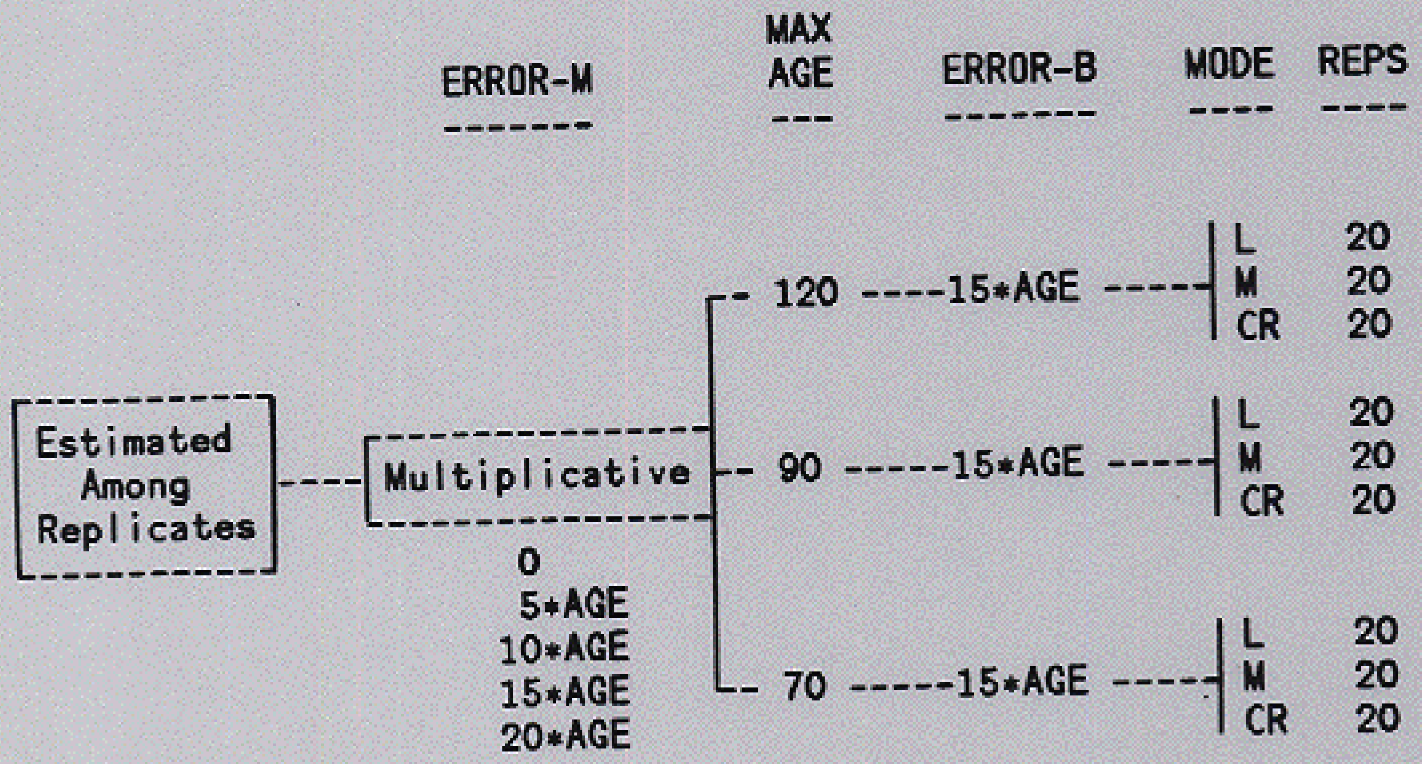


Figure 7. Combinations of measurement error, maximum age, biological error, and replications for estimating Y_∞, using the Logistic (L), Monomolecular (M), and Chapman-Richards (CR) models; estimated among replications.

controlled more easily than the natural variation (e_b) in a population. In other words, the effects of varying e_m might be of greater interest than would a wide range of e_b. It would be desirable to test the jackknife procedure over a wide range of both biological and measurement errors, and perhaps a wider range of ages. However, due to the large number of regressions needed for jackknifing, it was necessary to choose combinations of age and error that would allow favorable comparison of estimates within a manageable frame of time and computing costs.

Because of this consideration, comparisons of the three growth functions were made on ages and specified errors which represent a subset of those used in estimating parameters of the Logistic model alone. The Chapman-Richards function, which contains four parameters, was limited to a maximum of twenty replicates since it required many more iterations and more computing time than either of the other two models. Additional samples for the Monomolecular model (ages 100 and 110 years) were used after it was observed that the reduction in sample range, from 120 years to 90 years, had a much more pronounced effect on estimating Y_∞ than it did on either the Logistic or Chapman-Richards functions. Additional samples were used to check for a more systematic departure of $\hat{Y}_\infty$ from the true Y_∞.

3.1.2 Design Matrix

The reasons for purposely selecting maximum ages, e_b, e_m, and replications, are perhaps made clearer through examining the design matrix. A schematic example of a regression is shown in Figure 8. Note the age

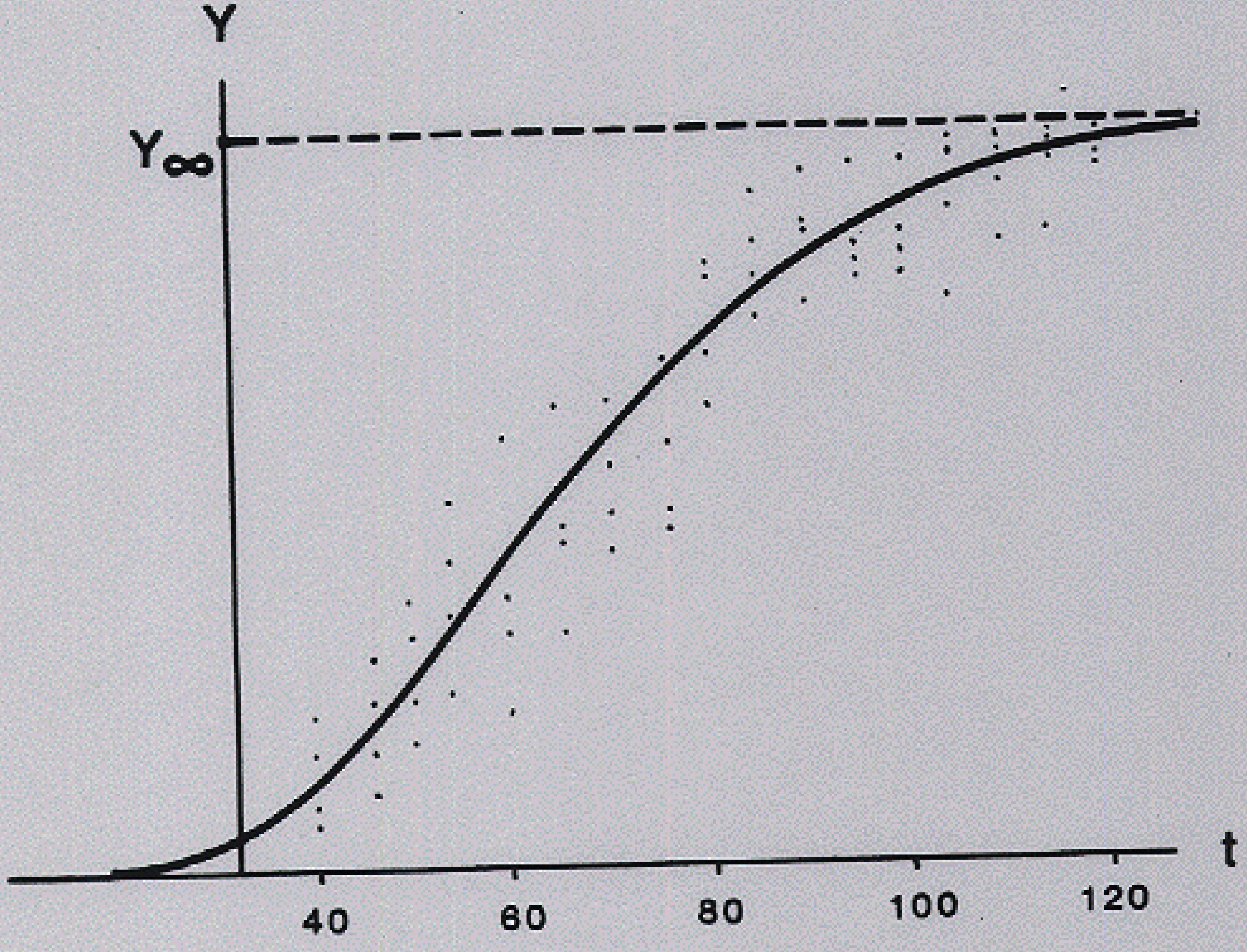


Figure 8. Design Matrix: example of a four-fold replication on a 17-point regression design.

range along the horizontal axis is from 40 to 120 years, with uniform 5-year intervals. This allows for 17 points, with each point replicated four times, representing a 17-point design matrix which is replicated four times. The asymptote (Y_∞) of the Logistic growth function might be estimated from this body of data using any of the following methods:

(1) Usual (nonlinear least squares) estimate from all (n = 68) data points, requiring one regression.

(2) Usual estimate for each replicate followed by averaging the four estimates of Y_∞, requiring four regressions.

(3) Jackknifed estimate, removing observations one at a time (i.e. h=1) from the entire data set, requiring n + 1 = 69 regressions.

(4) Jackknifed estimate for each replicate, removing observations one at a time from each replicate, followed by averging the four jackknife estimates. This would require 17 + 1 = 18 regressions per replicate or a total of 72 regressions. This procedure is referred to as jackknifing within replicates.

(5) Jackknifed estimate, removing each replicate, requiring 4 + 1 = 5 regressions. This is actually jackknifing h = 17 observations at a time albeit constrained to a replication, in order to preserve integrity of the design matrix. In other words, this form of estimation is jackknifing among rather than within replicates.

The above examples illustrate jackknifing, when choosing either $h = 1$ observation or $h = 1$ replicate (17 observations). Although jackknifing $1 < h < 17$ is also possible, this was not considered here since selecting the group size (h) entails some arbitrariness. In the present study, jackknifing was predominantly by method #4 (previous page), although method #5 is briefly examined.

3.2 Tests of Hypotheses

The parameter of interest for all three models fitted was the asymptote $\hat{Y}_\infty$. It is generally assumed, under the central limit theorem (Bickel and Doksum, 1977), that the distribution of random variables is approximately normal. This assumption was also made in this study. The normality of $\hat{Y}_\infty$ was examined with the Kolmogorov-Smirnov (KS) test and bias was tested using Student's t-test. The KS test is a nonparametric test based on the absolute difference between cumulative observed and cumulative expected frequency distributions -- i.e. the difference between the empirical distribution function $\hat{F}_n(Y_\infty)$ and a hypothesized distribution function $F_n\left(\frac{Y_\infty - \mu}{\sigma}\right)$ for some μ and σ^2 (Bickel and Doksum, 1977), where μ and σ^2 are the population mean and variance, respectively, and F_n is a distribution function. The sample statistic (D_n) for testing normality is based on the absolute maximum distance (D_{max}) between the two distributions:

$$D_n = \frac{D_{max}}{n} = \left| \hat{F}_n\ (Y_\infty) - F_n\left(\frac{Y_\infty - \mu}{\sigma}\right) \right|$$

3.2.1 Normality

Typical KS testing may vary according to the hypothesis stated; three are possible in this situation:

A. $\hat{Y}_\infty \simeq N(\text{true } Y_\infty, \sigma^2 \text{ known})$

B. $\hat{Y}_\infty \simeq N(\text{true } Y_\infty, \sigma^2 \text{ unknown})$

C. $\hat{Y}_\infty \simeq N(Y_\infty \text{ unknown}, \sigma^2 \text{ unknown})$

For the present study, hypothesis C is of interest since the mean and variance are both estimated from the sample. Although the KS program which was used (Sokal and Rolf, 1969) tests hypothesis C, standard tables of critical D_{max} values are designed for hypothesis A. When it becomes necessary to use the sample mean ($\bar{\hat{Y}}_\infty$) and variance (s^2) to estimate μ and σ^2, then

$$D_n^* = \max \left| \hat{F}_n (Y_\infty) - F_n^* \left(\frac{\hat{Y}_\infty - \bar{\hat{Y}}_\infty}{s} \right) \right|$$

D_n^* and D_n do not have the same distribution. Lilliefors (1967) has, however, provided a table for distribution of D_{max} values to test normality of estimated Y_∞ under hypothesis C. If departure of $\hat{Y}_\infty$ from normality is significant, this might in turn affect subsequent tests employing Student's t statistic, since the t-test assumes normal populations. However, even though departure from normality results in an approximate t, the t-test is still considered robust (Wonnacott and Wonnacott, 1977).

Two additional test statistics, representing measures of skewness and kurtosis, were also computed to examine departures from normality. Skewness is a tendency for the distribution to be heavier in one tail than the other (see Figure 9). Kurtosis is a measure of the tendency for a distribution to have heavy tails ("high peak") or light tails ("low peak"). These two characteristics are measured by two statistics known as G1 and G2. The values and significance of these statistics are tabulated in Appendices A, B, and C, for the Logistic, Monomolecular, and Chapman-Richards models, respectively. The G1 statistic indicates how asymmetric the distribution is -- G1 < 0 indictes a left tail to the distribution (skewed to the left) whereas G1 > 0 indicates the distribution is skewed to the right. The G2 statistic is a measure of how "peaked" the distribution is -- G2 < 0 indicates a platykurtic distribution and G2 > 0 indictes a leptykurtic distribution.

3.2.2 Bias

The combinations of models, errors (e_b and e_m), maximum ages sampled, and estimation procedures (jackknifed nonlinear regression and standard nonlinear regression) provided an opportunity to address numerous questions with formal tests of hypotheses regarding bias:

(1) Do either or both estimation procedures yield an estimate which is significantly different (i.e. biased estimation procedure) than the <u>true</u> asymptote?

$H_1 : E(\hat{Y}_\infty) = \text{true } Y_\infty$

(2) Is the jackknifed estimate significantly different from a standard nonlinear regression estimate of Y_∞?

$$H_2 : E(\hat{Y}_{\infty J}) = E(\hat{Y}_{\infty N})$$

(3) Does the bias of the estimate, if any, depend on the magnitude or the type (additive or multiplicative) of measurement error:

$$H_3 : E(\hat{Y}_{\infty J}) \quad \text{is independent of } e_m$$

$$E(\hat{Y}_{\infty N}) \quad \text{is independent of } e_m$$

(4) Do the results of testing H_1 through H_3 above, depend on the number of replications (i.e. increased from 20 to 100)?

(5) Since data sets were generated to follow a Logistic growth curve, what are the effects of mis-specifying the model and does jackknifing overcome this problem?

In addition to testing hypotheses H_1 through H_3 for each of the alternative (Monomolecular and Chapman-Richards) models, the estimates could also be compared between models for comparable ages, and comparable error levels of both e_b, and e_m. For example,

$$H_4 : E(\hat{Y}_{\infty JL}) = E(\hat{Y}_{\infty JCR})$$

$$\text{or} \quad E(\hat{Y}_{\infty NL}) = E(\hat{Y}_{\infty NCR})$$

where subscripts J = Jackknifed nonlinear least sqares
N = Nonjackknifed nonlinear least squares
L = Logistic model
CR = Chapman-Richards model

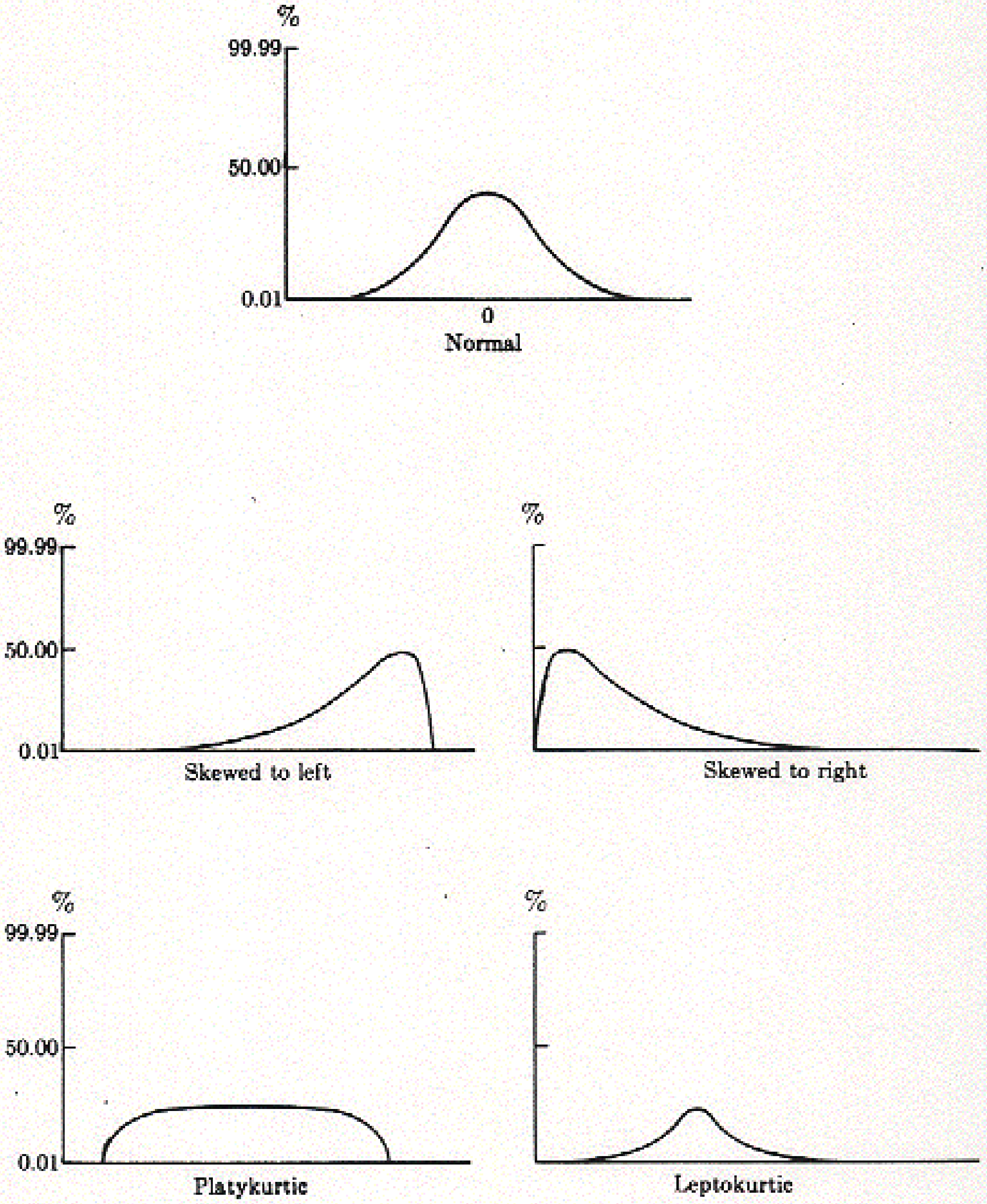


Figure 9. Examples of skewness and kurtosis in frequency distributions (after Sokal and Rohlf, 1969).

For a selected subset of age and error combinations common to all three models, the above hypotheses were re-evaluated as to the effect of jackknifing among replicates, versus within replicates. The above hypotheses regarding bias were tested using an appropriate t statistic.

3.3 Levels of Significance

All hypotheses were tested at 0.001, 0.01, 0.05, 0.10, and 0.20 α levels of significance. At the outset of the research, it was thought that increasing amounts of measurement error in combination with other factors (e.g. maximum age sampled) might result in some corresponding pattern of increasing or decreasing levels of significance. Upon completion of the tests or hypotheses, there was no discernable pattern in levels of significance. Therefore, the levels of significance for all tests of hypotheses are summarized according to 0.05, 0.01, and 0.001 α levels -- these levels are denoted in the tables by *, **, and *** respectively, with NS denoting nonsignificance ($\alpha > 0.05$).

4.0 COMPARISON OF JACKKNIFE WITH STANDARD LEAST SQUARES

Statistics pertaining to distribution tests including Kolmogorov-Smirnov (KS), skewness (G1) and kurtosis (G2) are tabulated in Appendices A, B, and C for the respective Logistic, Monomolecular, and Chapman-Richards models. Tables showing the departure of $\hat{Y}_\infty$ from true Y_∞ (24090 cubic feet per acre) are given in the main text. The terms "NONJ" and "JACK" are used throughout the remaining sections and tables of results for the sake of abbreviation. "JACK" results are based on _jackknifing_ in conjunction with standard nonlinear least squares regression, whereas "NONJ" results are derived from _nonjackknifed_ or the usual standard nonlinear least squares regression.

Examples of the bias due to error and maximum age on the estimates of Y_∞ are also illustrated graphically for each model fitted to the data. These figures generally depict bias of estimates from the usual or standard (i.e. nonjackknifed) fitting techniques, since in most cases the jackknifing resulted in either the same amount or more bias.

4.1 Fitting the Logistic Model

Results begin with the Logistic growth model since data to which each model was fitted were generated from the Logistic function.

4.1.1 Normality of Estimates within Replicates

For both JACK (jackknifed) and NONJ (nonjackknifed) estimates, departures from normality occur more consistently when maximum age is lowered (Tables A1 and A2). The NONJ procedure appears to give rise to more departures from normality than does the JACK procedure. Skewness (Tables A3 and A4) and kurtosis (Tables A5 and A6) became significant when e_m was increased, and when maximum age was lowered. There were also instances where both G_1 and G_2 statistics differed in the opposite directions for comparable NONJ and JACK estimates. That is, for a given e_b, e_m, and maximum age, the JACK Y_∞'s may be skewed left while the NONJ estimates of Y_∞ are skewed right. Also, the frequency of NONJ Y_∞'s appear to be platykurtic, compared to a leptykurtic frequency of jackknifed Y_∞'s. There does not appear to be any advantage of jackknife over standard (nonjackknifed) regression using these criteria. Expanding to 100 replicates (Tables A7 through A12), it appears that maximum age had more influence on the significance of distribution tests than e_b, e_m, or the estimation procedure.

4.1.2 Bias of estimates within replicates

Tables 2 through 5 show jackknife and standard regression estimates to be not significantly different from true Y_∞ (24090) for most age and error combinations.

The effect of error and the maximum age on bias of the estimated asymptote can be more clearly seen in Figures 10 to 16. Although the figure shows estimates from the nonjackknife method only, the same pattern was present in jackknifed estimates. That is, bias increased with shortened age range and, as larger measurement error was introduced, the standard error of the average jackknifed estimate increased. Figures 10 to 13, based on 20 replicates, exhibit trends of means which are biased

Table 2. Average estimated Y_∞ minus true Y_∞ (24090), using the Logistic model (std dev in parentheses); jackknifed within 20 replicates.

							ERROR-M				
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	290	1448	2396	5033	7809	1582	5420	11900	11471
			(752)	(4166)	(6615)	(11084)	(15989)	(4879)	(15750)	(22300)	(24542)
		JACK	284	905	-980	823	8210	696	4998	15244	10810
			(992)	(8757)	(16706)	(19971)	(27010)	(10977)	(26422)	(44905)	(46766)
	90	NONJ	-46	-138	475	1698	591	-199	964	475	1244
			(669)	(1050)	(1439)	(5039)	(3181)	(1190)	(4440)	(2907)	(6096)
		JACK	-61	-267	-75	1242	-3511	-338	-684	-2179	-5606
			(696)	(937)	(1424)	(6785)	(4342)	(1204)	(4455)	(2651)	(12775)
	120	NONJ	-12	89	658	598	1083	-42	-3	-402	1520
			(627)	(863)	(1259)	(1609)	(2357)	(722)	(940)	(881)	(6125)
		JACK	-12	64	438	355	56	-70	-109	-631	-796
			(622)	(842)	(1076)	(1452)	(1262)	(718)	(969)	(734)	(1416)
500	70	NONJ	127	--	--	--	--	1447	5301	11854	11896
			(437)	--	--	--	--	(5005)	(15548)	(22235)	(25450)
		JACK	98	--	--	--	--	-103	5331	15824	15343
			(455)	--	--	--	--	(11542)	(25988)	(44487)	(57048)
	90	NONJ	-62	--	--	--	--	-212	1050	617	1719
			(224)	--	--	--	--	(1105)	(5097))	(3222	(7356)
		JACK	-76	--	--	--	--	-330	-492	-1811	-2974
			(233)	--	--	--	--	(1110)	(6354)	(2537)	(21684)
	120	NONJ	-79	--	--	--	--	-114	-81	-423	878
			(168)	--	--	--	--	(359)	(688))	(777)	(3660)
		JACK	-79	--	--	--	--	-144	-184	-663	-395
			(168)	--	--	--	--	(361)	(705)	(634)	(1054)
1000	70	NONJ	309	--	--	--	--	1378	5440	11940	11031
			(980)	--	--	--	--	(4246)	(15206)	(22579)	(23979)
		JACK	262	--	--	--	--	-1032	5980	14970	8347
			(1107)	--	--	--	--	(7044)	(26114)	(42538)	(42575)
	90	NONJ	31	--	--	--	--	-116	1066	568	1695
			(378)	--	--	--	--	(1152)	(4846)	(3007)	(6743)
		JACK	8	--	--	--	--	-255	-540	-1957	-4685
			(368)	--	--	--	--	(1200)	(4564)	(2408)	(14907)
	120	NONJ	-49	--	--	--	--	-87	-36	-439	978
			(304)	--	--	--	--	(382)	(788)	(666)	(3844)
		JACK	-50	--	--	--	--	-120	-141	-657	-259
			(299)	--	--	--	--	(375)	(791)	(581)	(1543)

Table 3. Average estimated Y_∞ minus true Y_∞ (24090), using the Logistic model (std dev in parentheses); jackknifed within 100 replicates.

							ERROR-M				
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	24 (911)	458 (2940)	1099 (6079)	3776 (9744)	5927 (13806)	2956 (6616)	2622 (8342)	9583 (19152)	9930 (21989)
		JACK	-6 (1105)	-1840 (5593)	-1797 (13354)	1434 (18880)	2767 (25627)	859 (13420)	-1989 (17027)	9632 (63090)	5995 (48788)
	90	NONJ	-30 (757)	168 (1224)	403 (2395)	982 (4760)	1783 (6534)	191 (1699)	756 (3234)	1914 (6992)	2786 (8124)
		JACK	-33 (785)	26 (1244)	-221 (2338)	-834 (6198)	-1929 (12188)	-82 (1618)	-1222 (2781)	740 (17779)	-4395 (14986)
	120	NONJ	37 (559)	62 (673)	145 (931)	292 (1279)	670 (2647)	84 (721)	62 (825)	142 (1454)	652 (2082)
		JACK	35 (556)	39 (672)	32 (876)	3 (1241)	-527 (3593)	59 (721)	4 (780)	-246 (1113)	-462 (2084)
1000	70	NONJ	229 (788)	-- --	-- --	-- --	-- --	3362 (6833)	2152 (8492)	12518 (43552)	-24090 0
		JACK	210 (971)	-- --	-- --	-- --	-- --	2469 (15595)	-1034 (16164)	29694 (256543)	-24090 0
	90	NONJ	-26 (591)	-- --	-- --	-- --	-- --	163 (1535)	-231 (2465)	1696 (6101)	2765 (8021)
		JACK	-44 (586)	-- --	-- --	-- --	-- --	-129 (1485)	-1364 (2602)	-646 (11970)	-5228 (15849)
	120	NONJ	14 (348)	-- --	-- --	-- --	-- --	68 (568)	-48 (750)	129 (1484)	627 (2061)
		JACK	13 (345)	-- --	-- --	-- --	-- --	44 (571)	-170 (711)	-202 (1037)	-440 (1934)

Table 4. Significance level for test of significance between estimated Y_∞ and true Y_∞ (24090), using the Logistic model; jackknifed within 20 replicates.

							ERROR-M				
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	NS	NS	NS	NS	*	NS	NS	*	NS
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	NS
	90	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	NS
		JACK	NS	NS	NS	NS	**	NS	NS	**	NS
	120	NONJ	NS	NS	*	NS	NS	NS	NS	NS	NS
		JACK	NS	NS	NS	NS	NS	NS	NS	**	*
500	70	NONJ	NS	--	--	--	--	NS	NS	*	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS
	90	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	**	NS
	120	NONJ	*	--	--	--	--	NS	NS	*	NS
		JACK	*	--	--	--	--	NS	NS	***	NS
1000	70	NONJ	NS	--	--	--	--	NS	NS	*	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS
	90	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	**	NS
	120	NONJ	NS	--	--	--	--	NS	NS	**	NS
		JACK	NS	--	--	--	--	NS	NS	***	NS

Table 5. Significance level for test of significance between estimated Y_∞ and true Y_∞ (24090), using the Logistic model; jackknifed within 100 replicates.

ERROR-B	MAX AGE		ERROR-M								
			0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	NS	NS	NS	NS	NS	*	NS	*	*
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	NS
	90	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	NS
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	NS
	120	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	NS
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	NS
1000	70	NONJ	NS	--	--	--	--	*	NS	NS	--
		JACK	NS	--	--	--	--	NS	NS	NS	--
	90	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	*	NS	NS
	120	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS

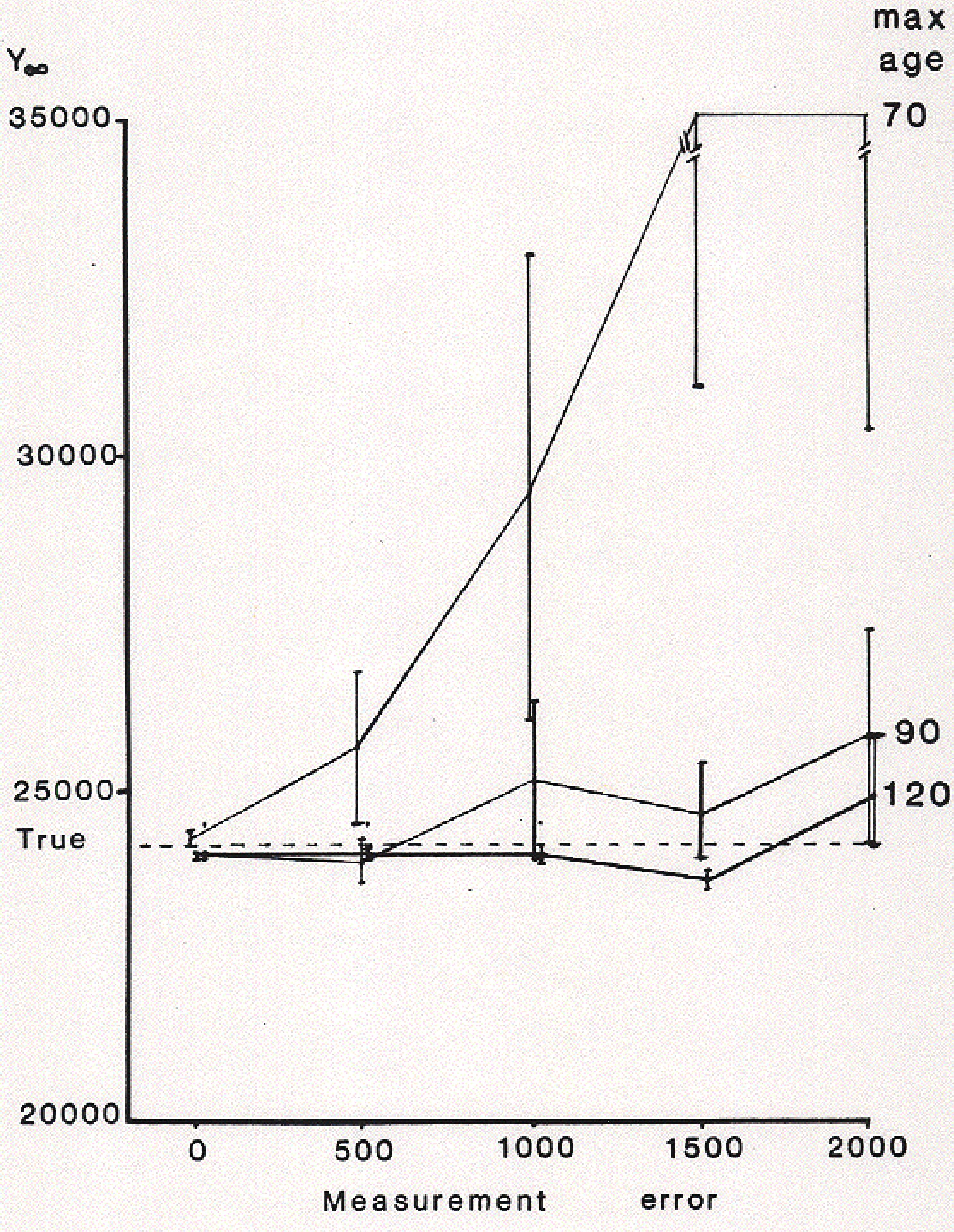


Figure 10. Estimates of Y_∞ as a function of e_m with 1 s.e. ($\not\!/$ indicates value greater than limits on the graph), from standard regression within replicates, averaged across 20 replicates; Logistic model; e_b = 500.

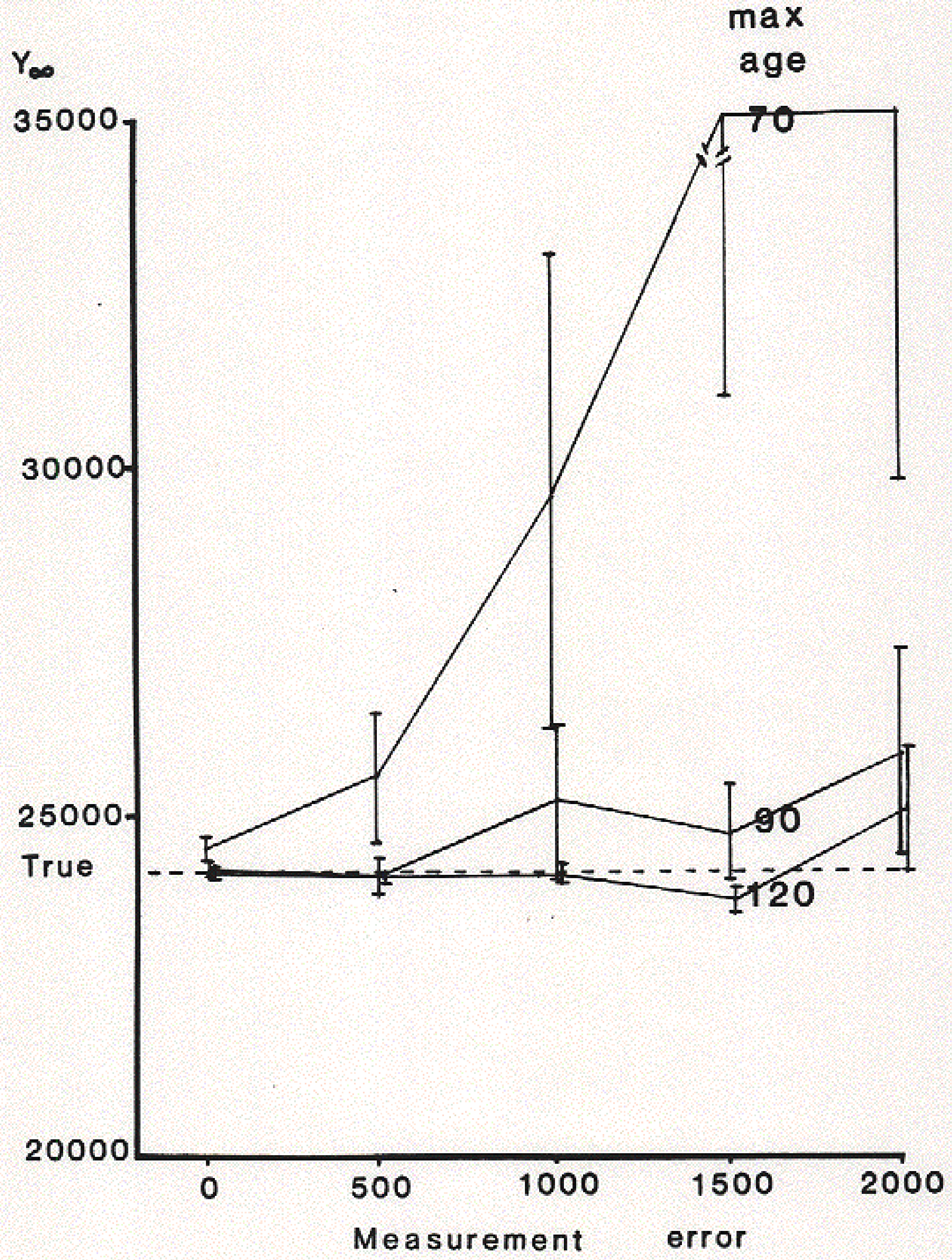


Figure 11. Estimates of Y_∞ as a function of e_m with 1 s.e. (⫽ indicates value greater than limits on the graph) from standard regression within replicates, averaged across 20 replicates; Logistic model; e_b = 1000.

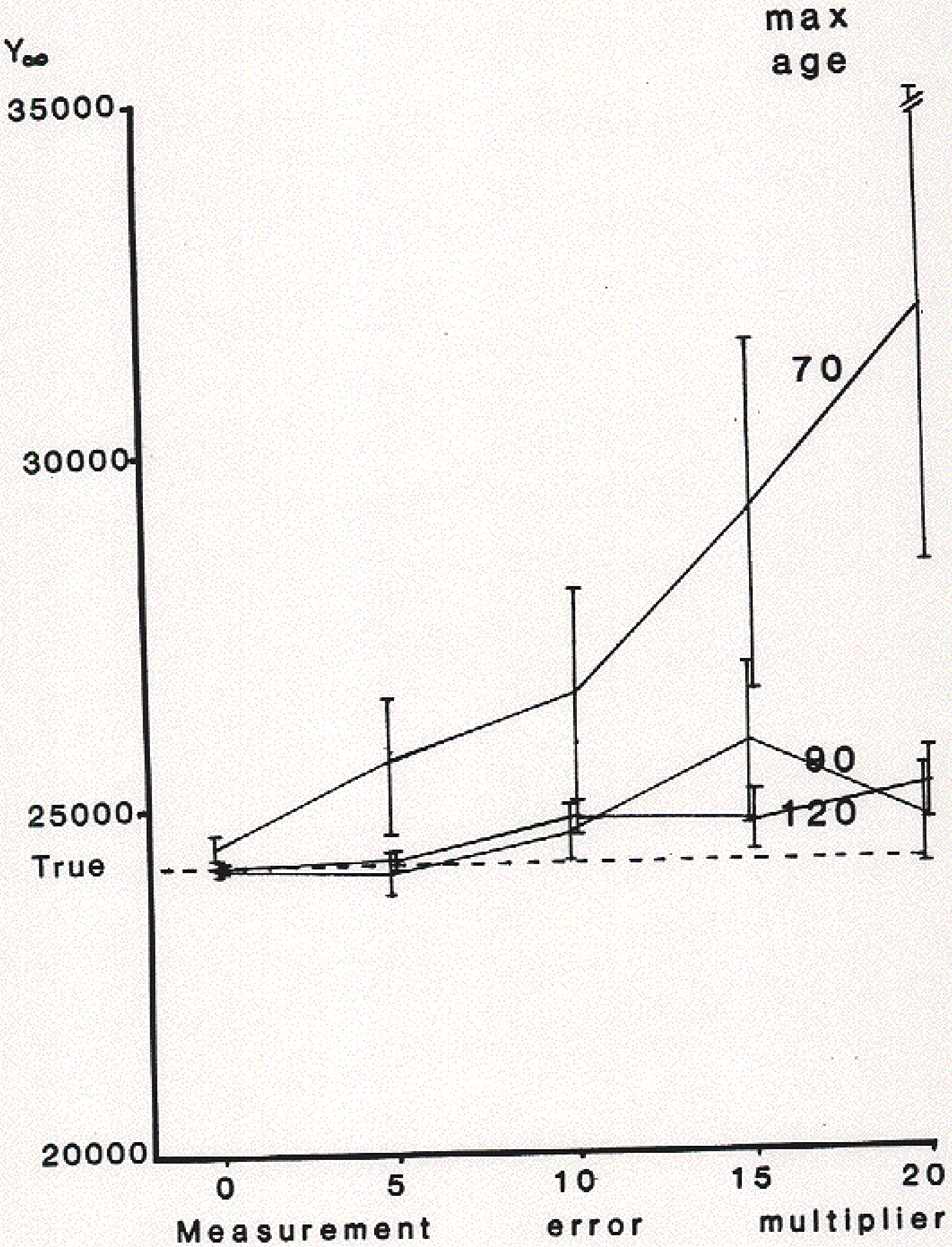


Figure 12. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e., from standard regression within replicates, averaged across 20 replicates; Logistic model; e_b = 15*AGE.

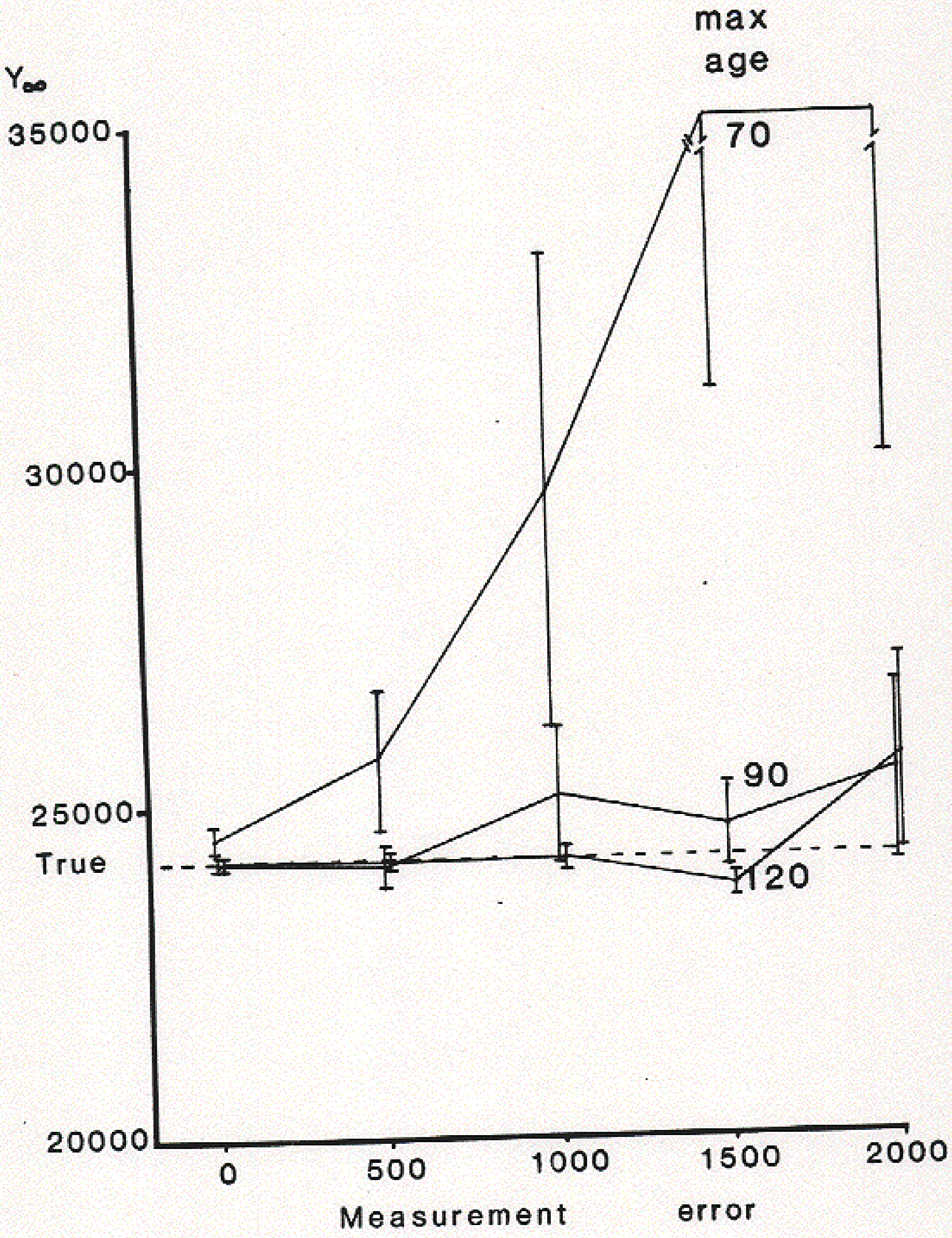


Figure 13. Estimates of Y_∞ as a function of e_m with 1 s.e. (≁ indicates value greater than limits on the graph), from standard regression within replicates, averaged across 20 replicates; Logistic model; e_b = 15*AGE.

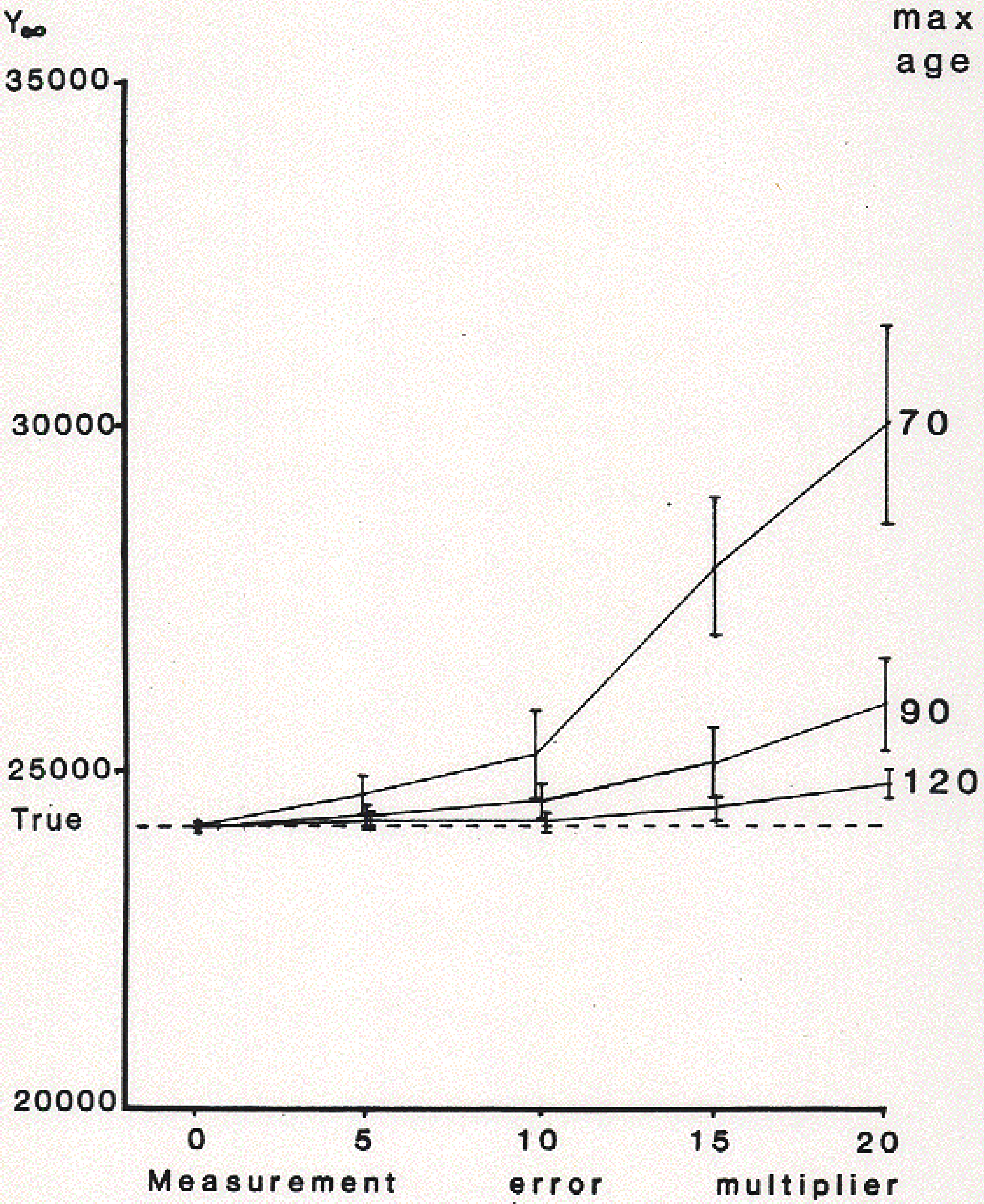


Figure 14. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e., from standard regression within replicates, averaged across 100 replicates; Logistic model; e_b = 15*AGE.

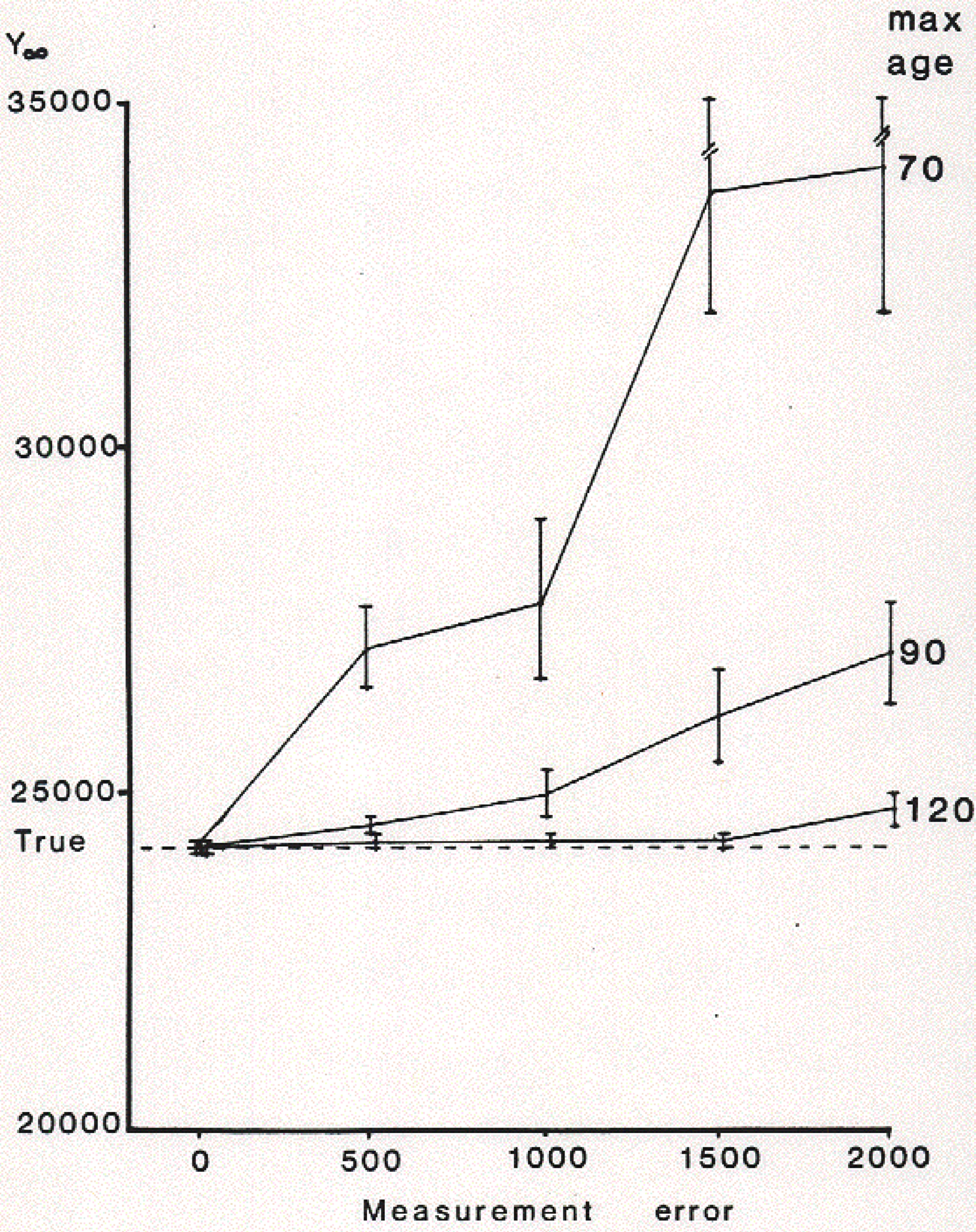


Figure 15. Estimates of Y_∞ as a function of e_m with 1 s.e. (⫲ indicates value greater than limits on the graph), from standard regression within replicates, averaged across 100 replicates; Logistic model; e_b = 15*AGE.

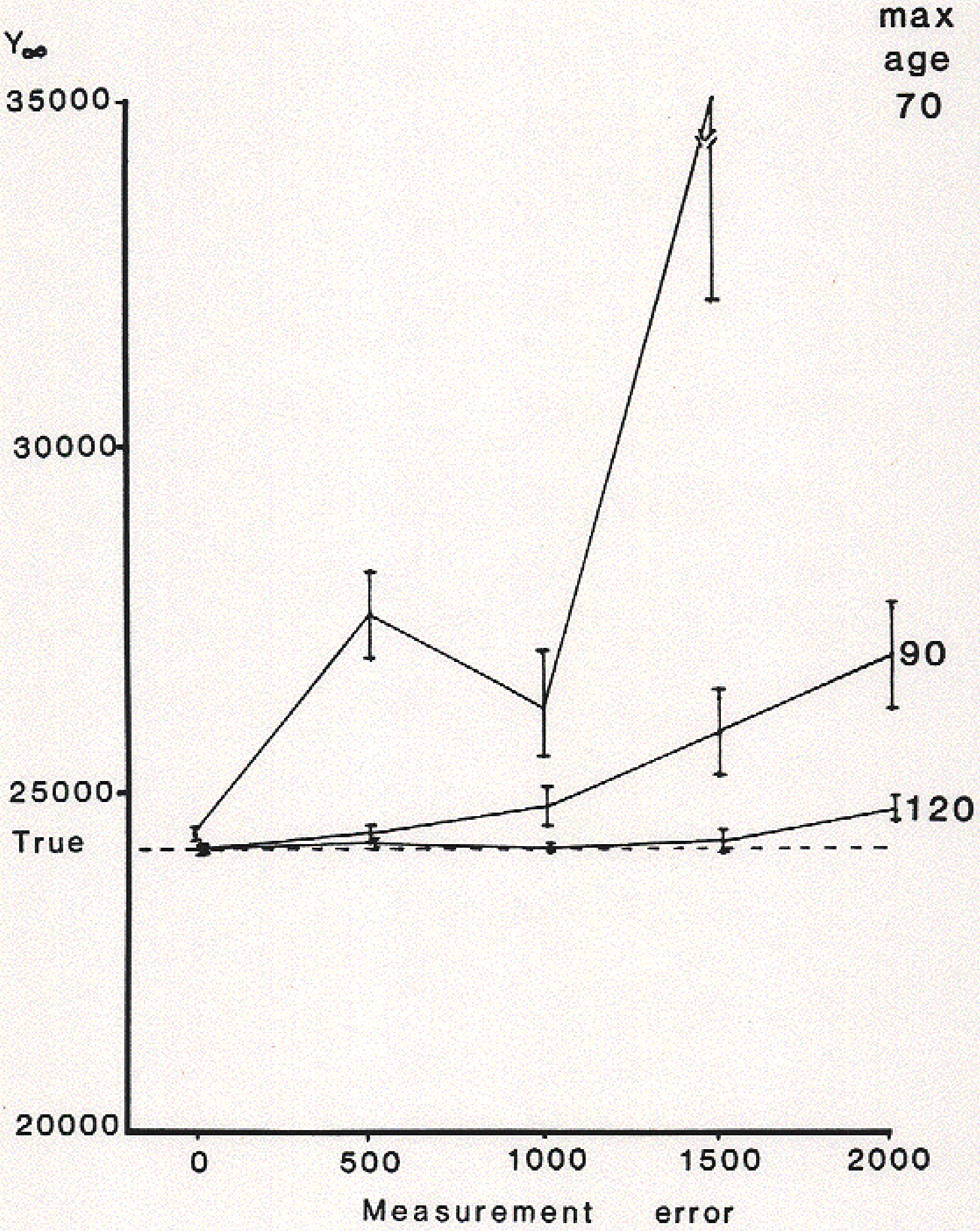


Figure 16. Estimates of Y_∞ as a function of e_m with 1 s.e. ($\nparallel$ indicates value greater than limits on the graph), from standard regression within replicates, averaged across 100 replicates; Logistic model; e_b = 1000.

slightly upwards as e_m is increased -- this is more pronounced as maximum age is decreased. Figures 14 to 16, based on means of 100 replicates, show the same trends in bias, with the bias increasing in a way which is less erratic than those averages of 20 replicates.

4.1.3 Bias of estimates among replicates

The values of $\hat{Y}_\infty$ minus true Y_∞ are given in Table 6, with the levels of significance for those differences given in Table 7. With the exception of one entry, none of the estimates differed significantly from the true value. Figures 17 and 18 graphically depict the bias of the respective NONJ estimates and JACK estimates, when jackknifing is among replicates. It can be seen that the resultant pattern is very much the same for both estimation techniques. The lack of a significant departure from true Y_∞ appears to be due mainly to the large variation or standard error of the estimates for maximum age 70.

A comparison of Tables 2 and 6 indicates less bias and variability associated with estimates for Y_∞ among replicates compared to respective estimates of Y_∞ within replicates. The bias for age 70 appears to be less from estimation among replicates (Figure 17) than when estimating within replicates (Figure 12).

4.2 Fitting the Monomolecular Model

Although data were generated from the Logistic function, the Monomolecular model (equation 3) is of interest since it represents a simpler description of growth without inflection, which may be adequate

Table 6. Average estimated Y_∞ minus true Y_∞ (24090), using the Logistic model(1 s.e. in parentheses); jackknifed among 20 replicates.

MAX		ERROR-M				
AGE		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	249	447	326	3197	1990
		(148)	(631)	(1390)	(2849)	(3230)
	JACK	247	405	182	3664	1053
		(174)	(663)	(1340)	(2701)	(3441)
90	NONJ	-77	-220	164	324	-188
		(86)	(178)	(372)	(523)	(624)
	JACK	-79	-225	147	268	-223
		(147)	(221)	(356)	(657)	(585)
120	NONJ	-51	6	480	259	531
		(49)	(85)	(169)	(207)	(296)
	JACK	-53	2	470	243	514
		(136)	(175)	(276)	(331)	(329)

Table 7. Significance level for test of significance between estimated Y_∞ and true Y_∞ (24090), using the Logistic model; jackknifed among 20 replicates.

MAX AGE		ERROR-M				
		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	NS	NS	NS	NS	NS
	JACK	NS	NS	NS	NS	NS
90	NONJ	NS	NS	NS	NS	NS
	JACK	NS	NS	NS	NS	NS
120	NONJ	NS	NS	*	NS	NS
	JACK	NS	NS	NS	NS	NS

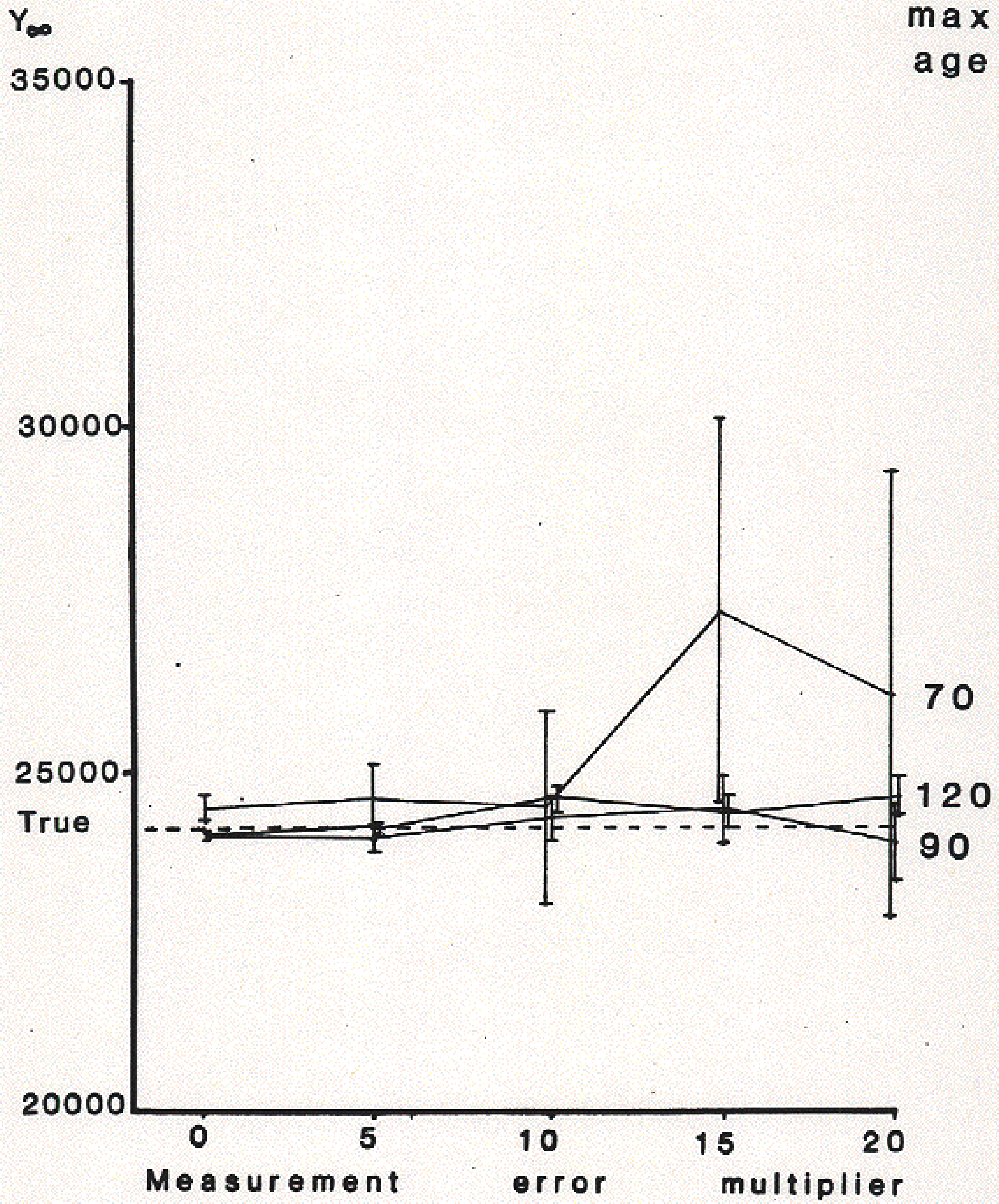


Figure 17. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e., from standard regression among 20 replicates; Logistic model; e_b = 15*AGE.

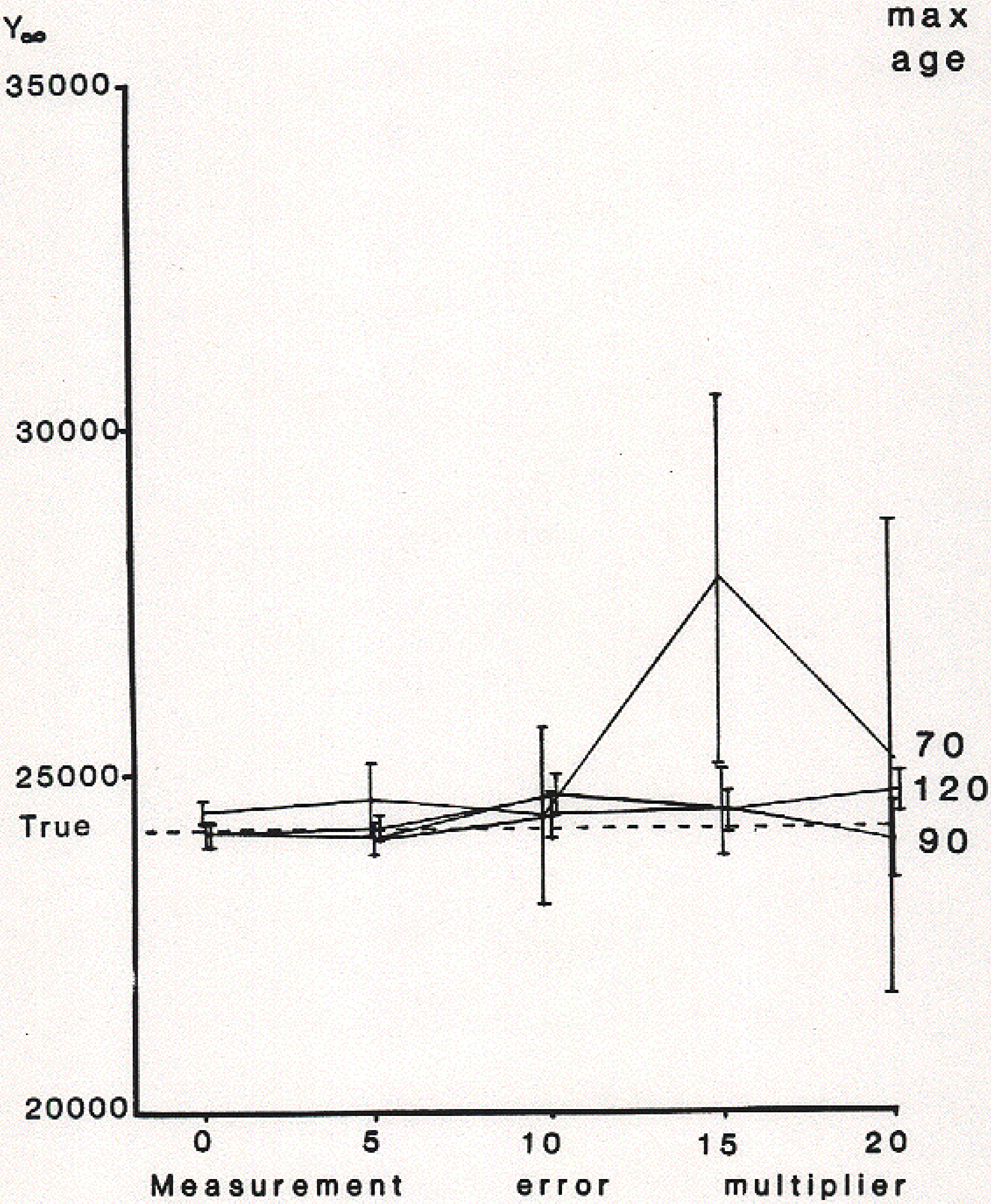


Figure 18. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e., from regressions jackknifed among 20 replicates; Logistic model; e_b = 15*AGE.

if Y_∞ is the primary concern and if the sample is sufficient. On the other hand, this model is mis-specified since it cannot make use of inflection in the data.

4.2.1 Normality of estimates within replicates

The KS statistics and corresponding significance levels in tables B1 and B2 suggest that with lower maximum age, the JACK procedure results in more significant departures of $\hat{Y}_\infty$ from normality than does the NONJ method. The skewness (Tables B3 and B4) and kurtosis (Tables B5 and B6) of Y_∞ estimated from the monomolecular model are largely nonsignificant except for the greater measurement errors. Tables B7 through B12, based on 100 replications, show that statistical significance was detected for nearly all age and error combinations, but particularly when maximum age was less than 110 years.

4.2.2 Bias of estimates within replicates

The differences for average estimated Y_∞ minus true Y_∞ are given in Tables 8 and 9, respectively, for 20 and 100 replications. The differences increase with larger e_m and lower maximum age. The levels of significance for these departures are given in Tables 10 and 11. Clearly, the bias of Y_∞ estimates is highly significant for both estimation procedures, even with zero measurement error.

The overall effect of maximum age and measurement error on bias and variability is depicted in Figures 19 to 24. Maximum age appears to have a greater impact than e_m on bias of the estimates. Figures 22 to 24 (100 replications) indicate that within the maximum age sampled, the increased e_m can also contribute to bias. However, it is also clear

Table 8. Average estimated Y_∞ minus true Y_∞ (24090), using the Monomolecular model (std dev in parentheses) ; jackknifed within 20 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	7630	7590	10205	10968	8696	7349	7881	8912	8390
			(2314)	(4199)	(5326)	(7851)	(8887)	(5033)	(6810)	(7929)	(10403)
		JACK	7323	7584	9690	13252	11407	7676	8080	7453	4600
			(2604)	(6683)	(9212)	(18860)	(25043)	(10750)	(15151)	(16114)	(22029)
	100	NONJ	4314	4077	6743	7677	5277	4432	6816	4649	8641
			(1610)	(1971)	(4626)	(6583)	(6644)	(2294)	(6282)	(6433)	(12165)
		JACK	4412	3736	5781	8783	3356	4330	6030	1970	13579
			(1659)	(1880)	(4240)	(13386)	(9671)	(2269)	(10812)	(9211)	(65396)
	110	NONJ	2973	3008	5056	3981	5423	2953	3637	2878	6642
			(1159)	(1435)	(4622)	(3379)	(6131)	(1424)	(4235)	(3065)	(9633)
		JACK	3145	3143	3507	2722	3456	2926	2838	1109	7620
			(1155)	(1452)	(2307)	(2793)	(9312)	(1426)	(4774)	(1769)	(23422)
	120	NONJ	2163	2409	3498	3533	4349	2131	2272	1570	4831
			(1122)	(1667)	(2511)	(3399)	(4880)	(1391)	(2154)	(1712)	(8234)
		JACK	2315	2494	2733	2912	3918	2209	2055	1044	3577
			(1121)	(1625)	(2190)	(2696)	(9154)	(1400)	(2139)	(1265)	(9857)
1000	90	NONJ	7793	--	--	--	--	7528	7889	8857	8338
			(1262)	--	--	--	--	(4562)	(6644)	(8124)	(10259)
		JACK	7409	--	--	--	--	7216	8695	5406	527
			(1375)	--	--	--	--	(7623)	(17838)	(16137)	(18023)
	100	NONJ	4565	--	--	--	--	4779	7244	4759	8013
			(931)	--	--	--	--	(2211)	(6310)	(6312)	(9876)
		JACK	4640	--	--	--	--	4672	6016	1789	3407
			(884)	--	--	--	--	(2282)	(9205)	(7176)	(18848)
	110	NONJ	2989	--	--	--	--	2981	3408	2788	6329
			(639)					(1187)	(3043)	(2680)	(8204)
		JACK	3146	--	--	--	--	2897	2373	1189	1440
			(636)					(1206)	(2716)	(1565)	(17368)
	120	NONJ	2054	--	--	--	--	1993	2119	1430	4151
			(503)	--	--	--	--	(727)	(1618)	(1230)	(5933)
		JACK	2198	--	--	--	--	2051	1918	986	1994
			(493)	--	--	--	--	(729)	(1617)	(951)	(4666)

Table 9. Average estimated Y_∞ minus true Y_∞ (24090), using the Monomolecular model (std dev in parentheses) ; jackknifed within 100 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	7824	8729	9248	9376	9412	8722	9664	8500	9556
			(2777)	(4409)	(6722)	(8173)	(8511)	(5585)	(7295)	(8458)	(10343)
		JACK	7648	7594	9330	11253	8987	8719	9524	4446	8112
			(2968)	(6431)	(13654)	(18790)	(17931)	(10380)	(18550)	(16132)	(22744)
	100	NONJ	4595	4868	5524	5816	6053	5202	5552	6282	7287
			(1600)	(2127)	(4401)	(5401)	(6674)	(3213)	(4605)	(6871)	(9302)
		JACK	4663	4544	4321	3961	4277	4872	3593	3088	5657
			(1590)	(2221)	(5094)	(8854)	(10838)	(3946)	(6483)	(9880)	(21717)
	110	NONJ	3039	3087	3890	4283	3996	3213	3492	3750	5746
			(1167)	(1479)	(3177)	(5019)	(6254)	(1755)	(3302)	(4635)	(7464)
		JACK	3187	3117	3502	3011	1969	3210	2304	2246	1067
			(1166)	(1504)	(3644)	(5316)	(15130)	(1766)	(5108)	(6844)	(28857)
	120	NONJ	2261	2326	2526	2874	4359	2387	2475	2551	3938
			(964)	(1219)	(1817)	(2467)	(7064)	(1334)	(1780)	(2910)	(4618)
		JACK	2416	2422	2341	2164	4547	2478	2258	1996	1042
			(965)	(1220)	(1592)	(2385)	(17883)	(1348)	(1564)	(3305)	(5067)
1000	90	NONJ	7762	--	--	--	--	8770	6666	8529	9613
			(2134)	--	--	--	--	(5517)	(5993)	(8476)	(10662)
		JACK	7408	--	--	--	--	8926	6122	3992	8168
			(2059)	--	--	--	--	(10945)	(13137)	(17727)	(24945)
	100	NONJ	4647	--	--	--	--	5235	5009	6613	7403
			(1203)	--	--	--	--	(2800)	(4102)	(7174)	(9428)
		JACK	4749	--	--	--	--	4782	3464	4490	6264
			(1164)	--	--	--	--	(2824)	(5182)	(18134)	(25599)
	110	NONJ	3080	--	--	--	--	3274	3127	3731	6130
			(776)	--	--	--	--	(1520)	(2700)	(4267)	(9333)
		JACK	3241	--	--	--	--	3276	2418	1967	7895
			(759)	--	--	--	--	(1532)	(2534)	(3858)	(59001)
	120	NONJ	2192	--	--	--	--	2328	2097	2496	3919
			(580)	--	--	--	--	(1056)	(1327)	(2926)	(4754)
		JACK	2343	--	--	--	--	2418	1901	2067	899
			(578)	--	--	--	--	(1084)	(1240)	(4004)	(4929)

Table 10. Significance level for test of significance between estimated Y_∞ and true Y_∞ (24090), using the Monomolecular model; jackknifed within 20 replicates.

ERROR-B	MAX AGE		ERROR-M								
			0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	***	***	***	***	***	***	***	***	**
		JACK	***	***	***	**	NS	**	*	NS	NS
	100	NONJ	***	***	***	***	**	***	***	**	**
		JACK	***	***	***	**	NS	***	*	NS	NS
	110	NONJ	***	***	***	***	***	***	**	***	**
		JACK	***	***	***	***	NS	***	*	*	NS
	120	NONJ	***	***	***	***	***	***	***	***	*
		JACK	***	***	***	***	NS	***	***	**	NS
1000	90	NONJ	***	--	--	--	--	***	***	***	**
		JACK	***	--	--	--	--	***	*	NS	NS
	100	NONJ	***	--	--	--	--	***	***	**	**
		JACK	***	--	--	--	--	***	**	NS	NS
	110	NONJ	***	--	--	--	--	***	***	***	**
		JACK	***	--	--	--	--	***	***	**	NS
	120	NONJ	***	--	--	--	--	***	***	***	**
		JACK	***	--	--	--	--	***	***	***	NS

Table 11. Significance level for test of significance between estimated Y_∞ and true Y_∞ (24090), using the Monomolecular model; jackknifed within 100 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	***	***	***	***	***	***	***	***	***
		JACK	***	***	***	***	***	***	***	**	***
	100	NONJ	***	***	***	***	***	***	***	***	***
		JACK	***	***	***	***	***	***	***	**	**
	110	NONJ	***	***	***	***	***	***	***	***	***
		JACK	***	***	***	***	NS	***	***	**	NS
	120	NONJ	***	***	***	***	***	***	***	***	***
		JACK	***	***	***	***	*	***	***	***	*
1000	90	NONJ	***	--	--	--	--	***	***	***	***
		JACK	***	--	--	--	--	***	***	*	**
	100	NONJ	***	--	--	--	--	***	***	***	***
		JACK	***	--	--	--	--	***	***	*	*
	110	NONJ	***	--	--	--	--	***	***	***	***
		JACK	***	--	--	--	--	***	***	***	NS
	120	NONJ	***	--	--	--	--	***	***	***	***
		JACK	***	--	--	--	--	***	***	***	NS

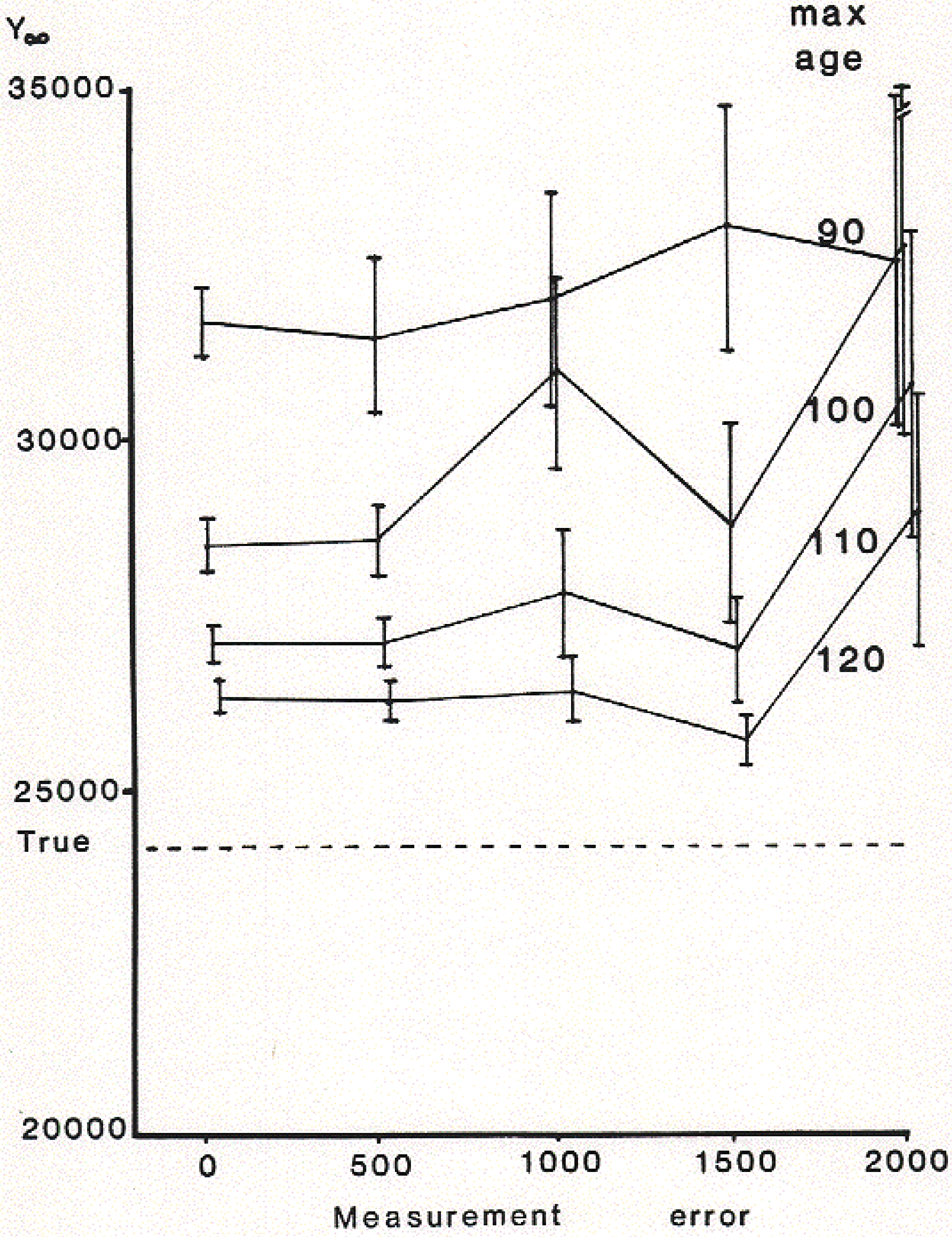


Figure 19. Estimates of Y_∞ as a function of e_m with 1 s.e. (⫽ indicates value greater than limits on the graph), from standard regression within replicates, averaged across 20 replicates; Monomolecular model; e_b = 15*AGE.

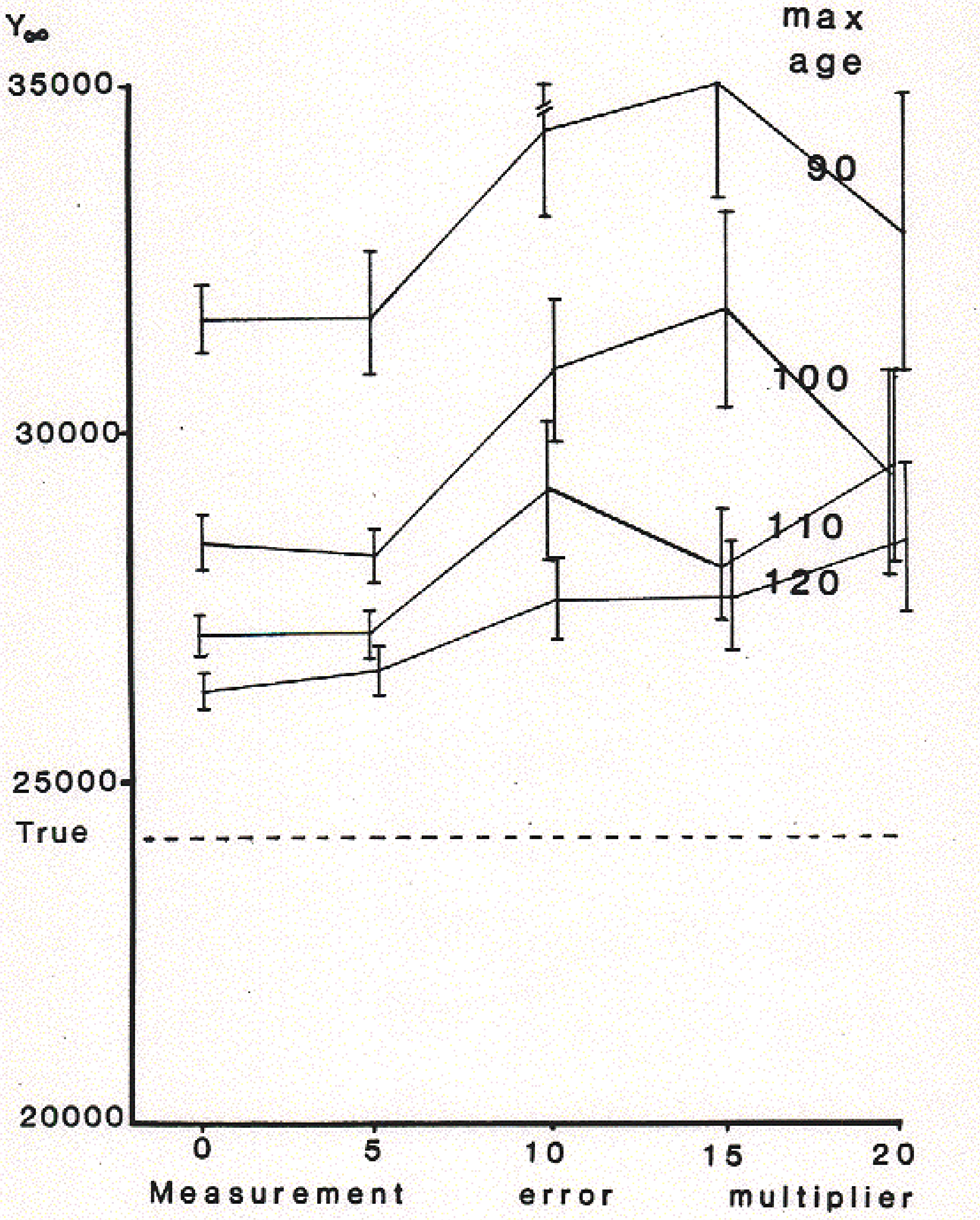


Figure 20. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e. (≠ indicates value greater than limits on the graph), from standard regression within replicates, averaged across 20 replicates; Monomolecular model; e_b = 15*AGE.

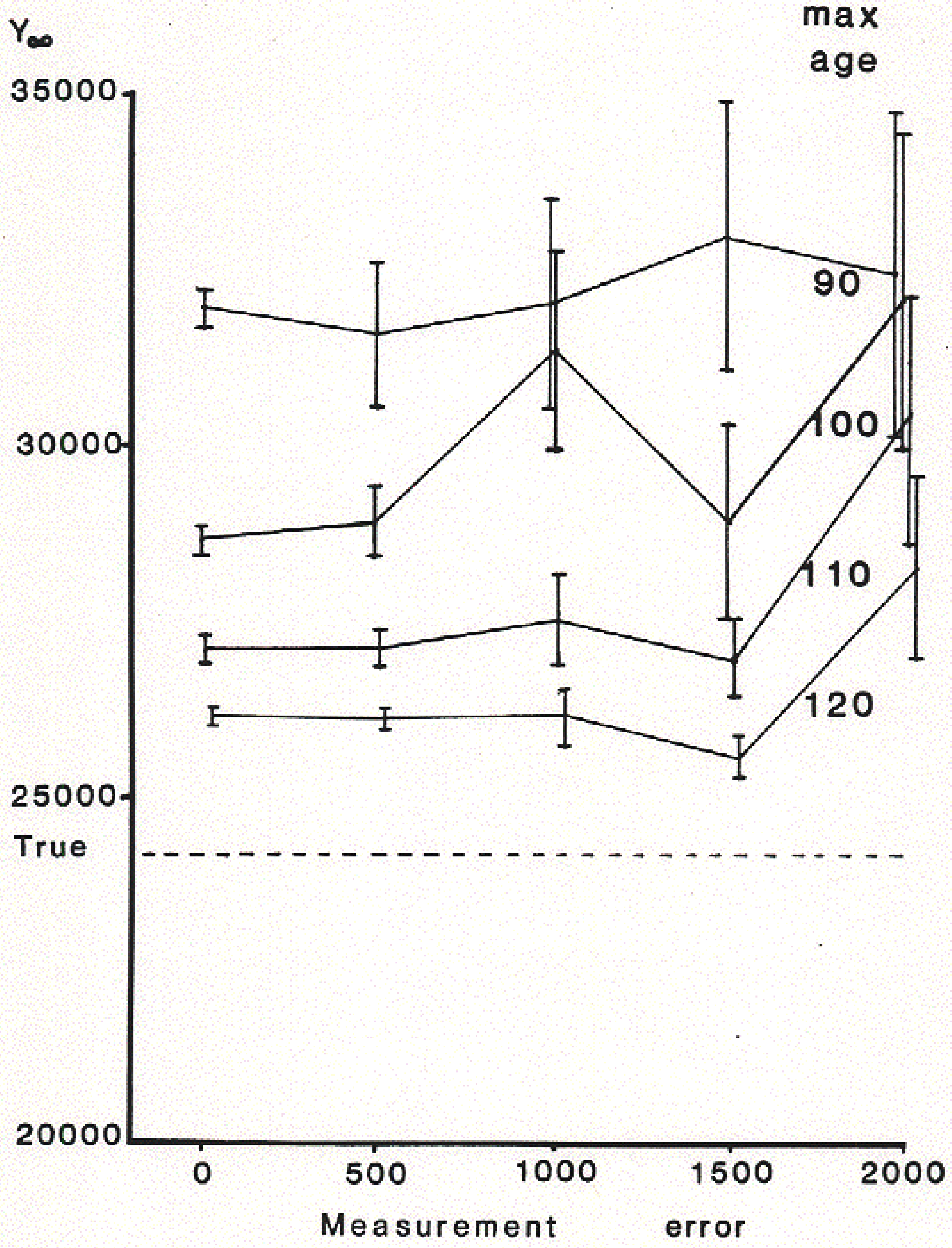


Figure 21. Estimates of Y_∞ as a function of e_m with 1 s.e., from standard regression within replicates, averaged across 20 replicates; Monomolecular model; e_b = 1000.

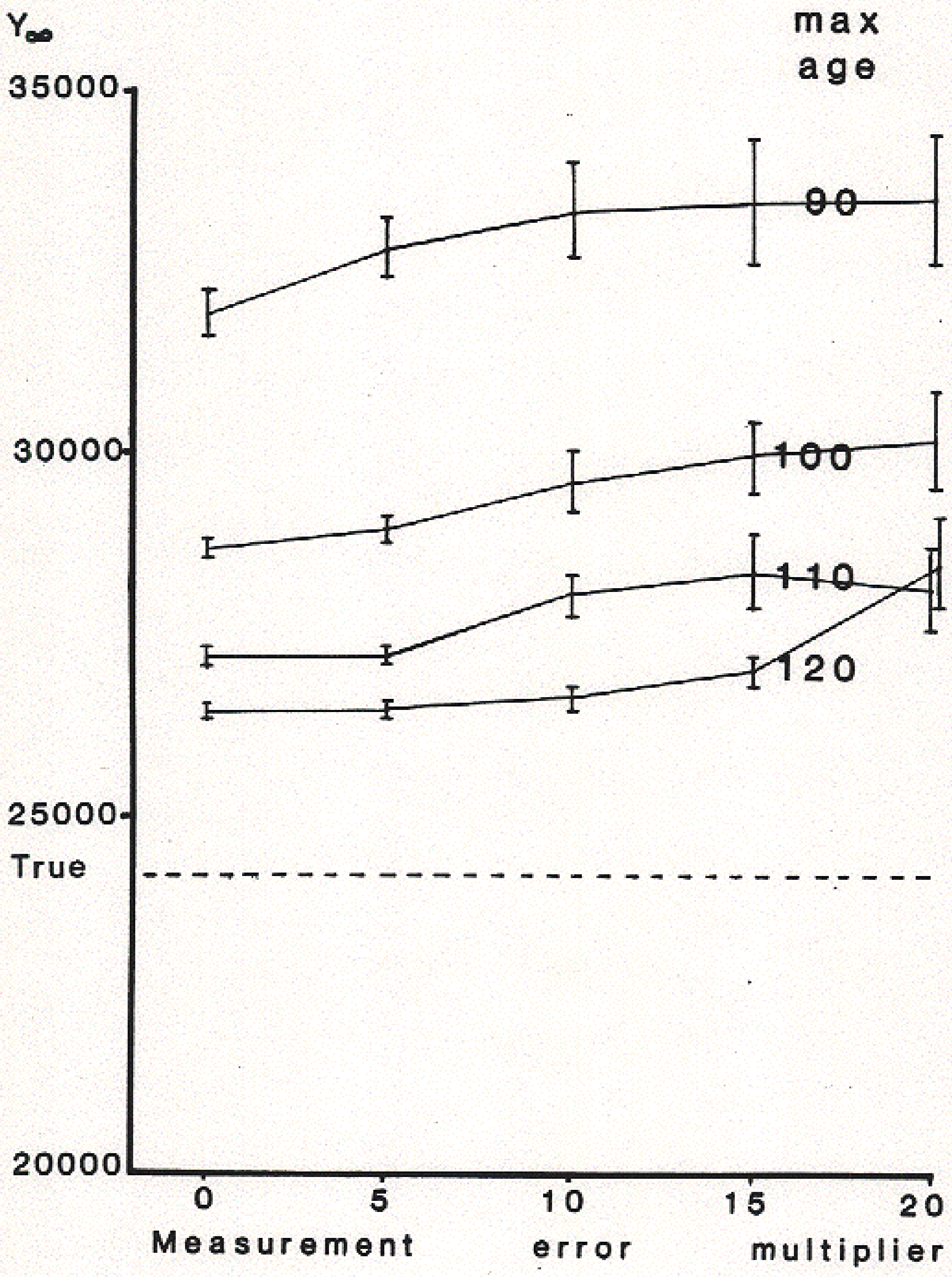


Figure 22. Estimates of Y∞ as a function of e_m multiplier *AGE with 1 s.e., from standard regression within replicates, averaged across 100 replicates; Monomolecular model; e_b = 15*AGE.

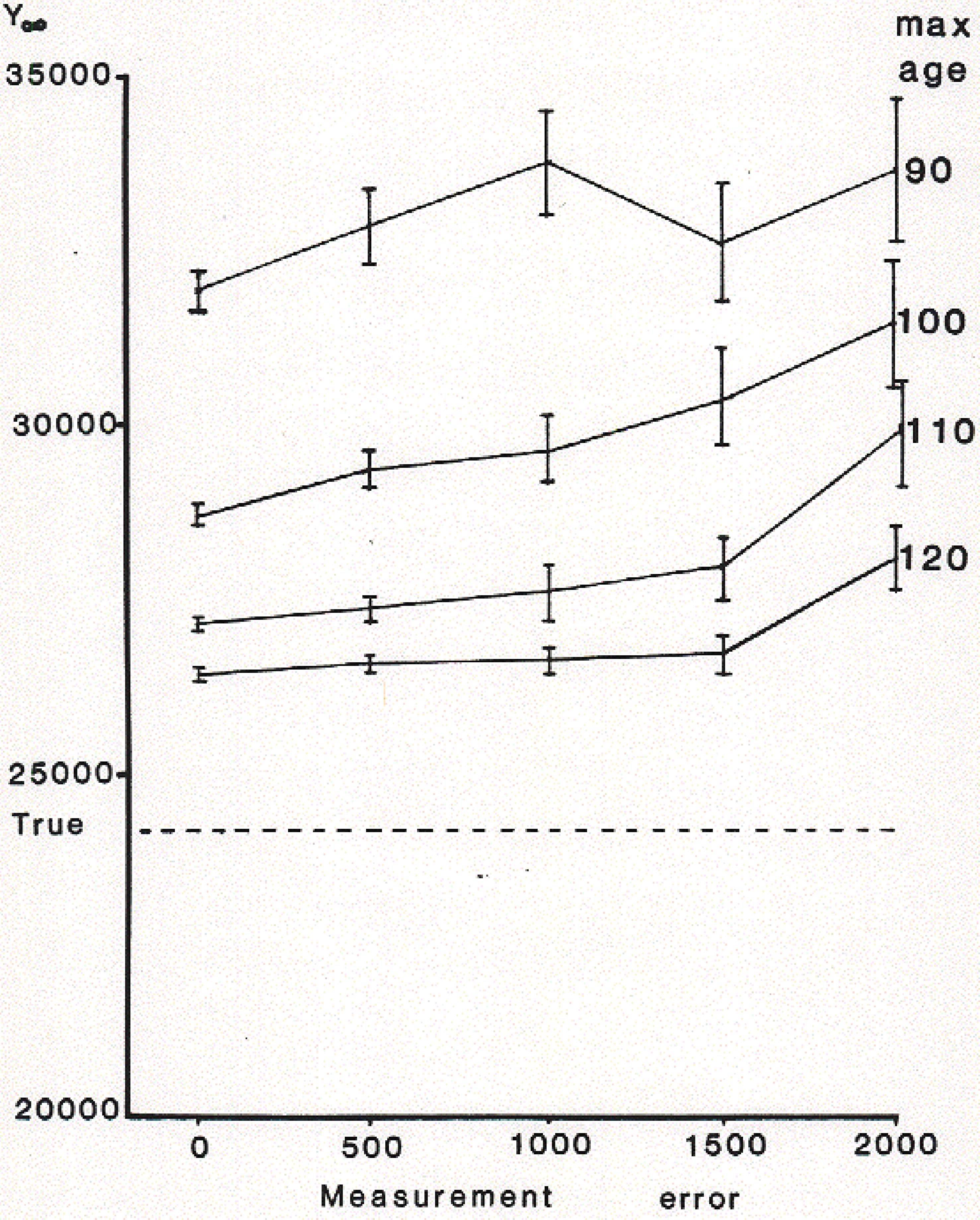


Figure 23. Estimates of Y_∞ as a function of e_m with 1 s.e., from standard regression within replicates, averaged across 100 replicates; Monomolecular model; e_b = 15*AGE.

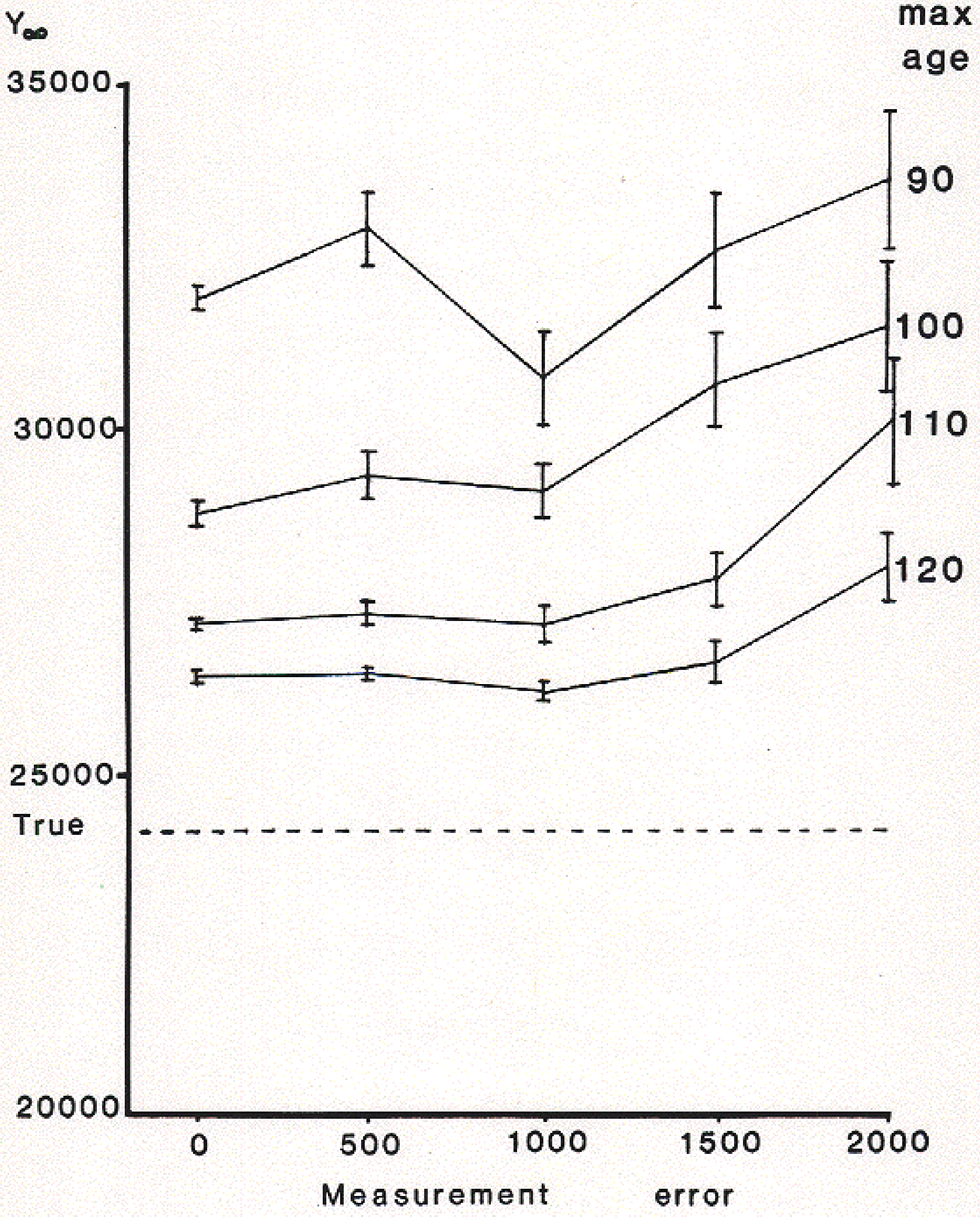


Figure 24. Estimates of Y_∞ as a function of e_m with 1 s.e., from standard regression within replicates, averaged across 100 replicates; Monomolecular model; e_b = 1000.

that with zero measurement error, estimation over the full (age) range of data is significantly biased from using the Monomolecular model.

4.2.3 Bias of estimates among replicates

Tables 12 and 13 give the values and significance levels, respectively, for differences between true Y_∞ and $\hat{Y}_\infty$. Nearly all estimates of Y_∞ depart from the true asymptote, with a high level of significance. Figures 25 (standard estimates) and 26 (jackknifed estimates) show that, although bias increases slightly with increasing e_m, most bias is due to a lower maximum age. In fact, when the two estimation procedures differed, the jackknife generally produced an estimate with more variability and greater bias.

4.3 Fitting the Chapman-Richards Model

The Chapman-Richards function (equation 5) represents a model with more flexibility (albeit more complexity) than the Logistic function. However, the Logistic model is a special case of the Chapman-Richards model with the parameter m set equal to two. Therefore, this is not so much mis-specifying the model, as it is using a model of unnecessary complexity.

4.3.1 Normality of estimates within replicates

The KS test results are located in Tables C1 to C6 of Appendix C. Departures from normality are generally significant with large additive e_m and lower maximum age. Results regarding skewness (Table C3) show that the G1 statistic was often negative for the JACK estimate while

Table 12. Average estimated Y_∞ minus true Y_∞ (24090), using the Monomolecular model (1 s.e. in parentheses); jackknifed among 20 replicates.

MAX AGE		ERROR-M				
		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	20273	20956	20603	26953	18880
		(1897)	(5481)	(11819)	(21460)	(18019)
	JACK	20268	20394	56367	22463	90314
		(688)	(2490)	(25103)	(7766)	(30171)
90	NONJ	7377	6912	8453	8866	6350
		(498)	(798)	(1698)	(2422)	(2408)
	JACK	7891	6879	8336	12813	23134
		(806)	(772)	(1389)	(4583)	(5577)
120	NONJ	2064	2186	3005	2586	2986
		(138)	(199)	(389)	(456)	(644)
	JACK	2059	2176	2979	2543	2947
		(238)	(316)	(512)	(630)	(596)

Table 13. Significance level for test of significance between estimated Y_∞ and true Y_∞ (24090), using the Monomolecular model; jackknifed among 20 replicates.

MAX AGE		ERROR-M				
		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	***	**	NS	NS	NS
	JACK	***	***	*	**	**
90	NONJ	***	***	***	**	*
	JACK	***	***	***	*	***
120	NONJ	***	***	***	***	***
	JACK	***	***	***	***	***

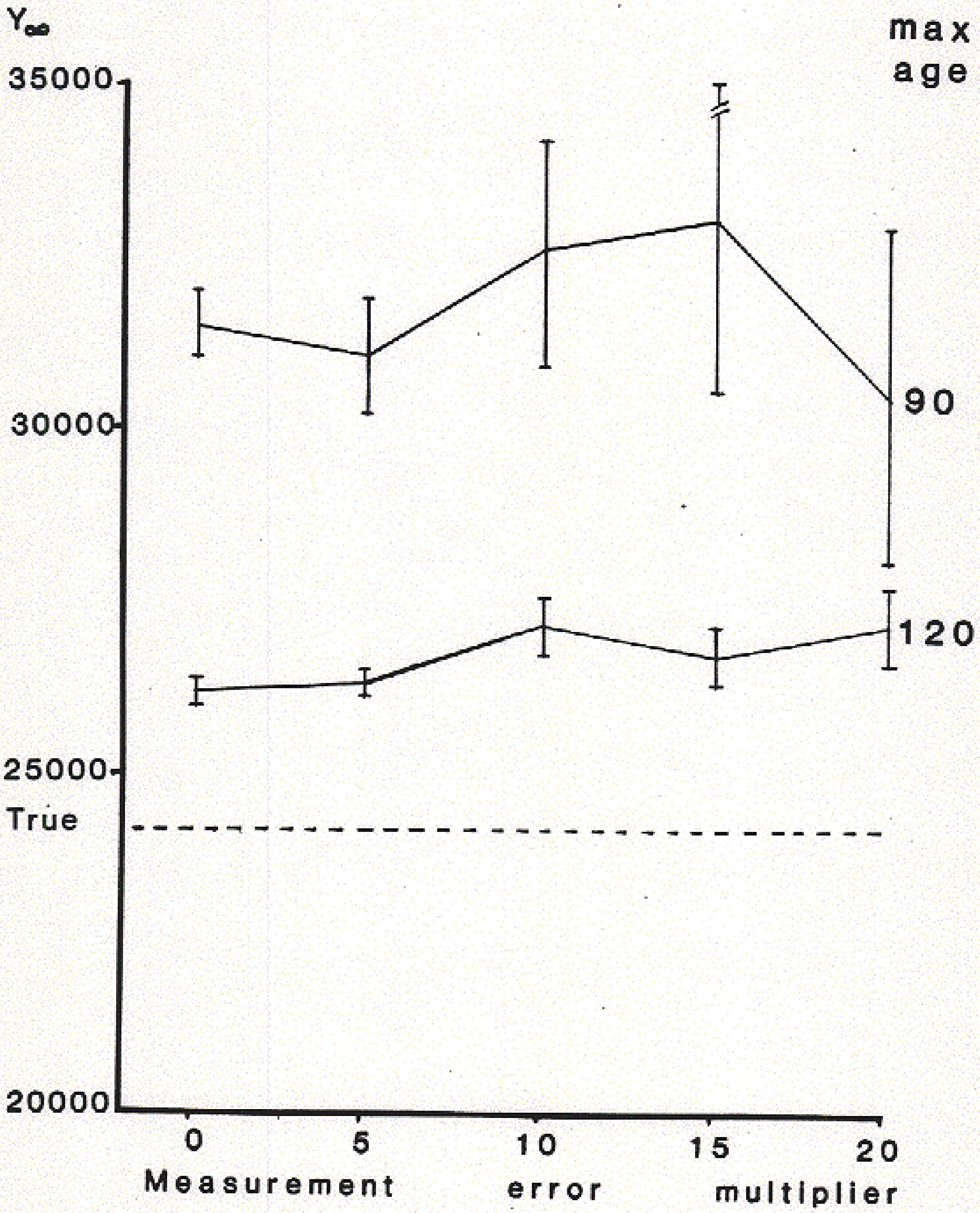


Figure 25. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e. (≠ indicates value greater than limits on the graph), from standard regression among 20 replicates; Monomolecular model; e_b = 15*AGE.

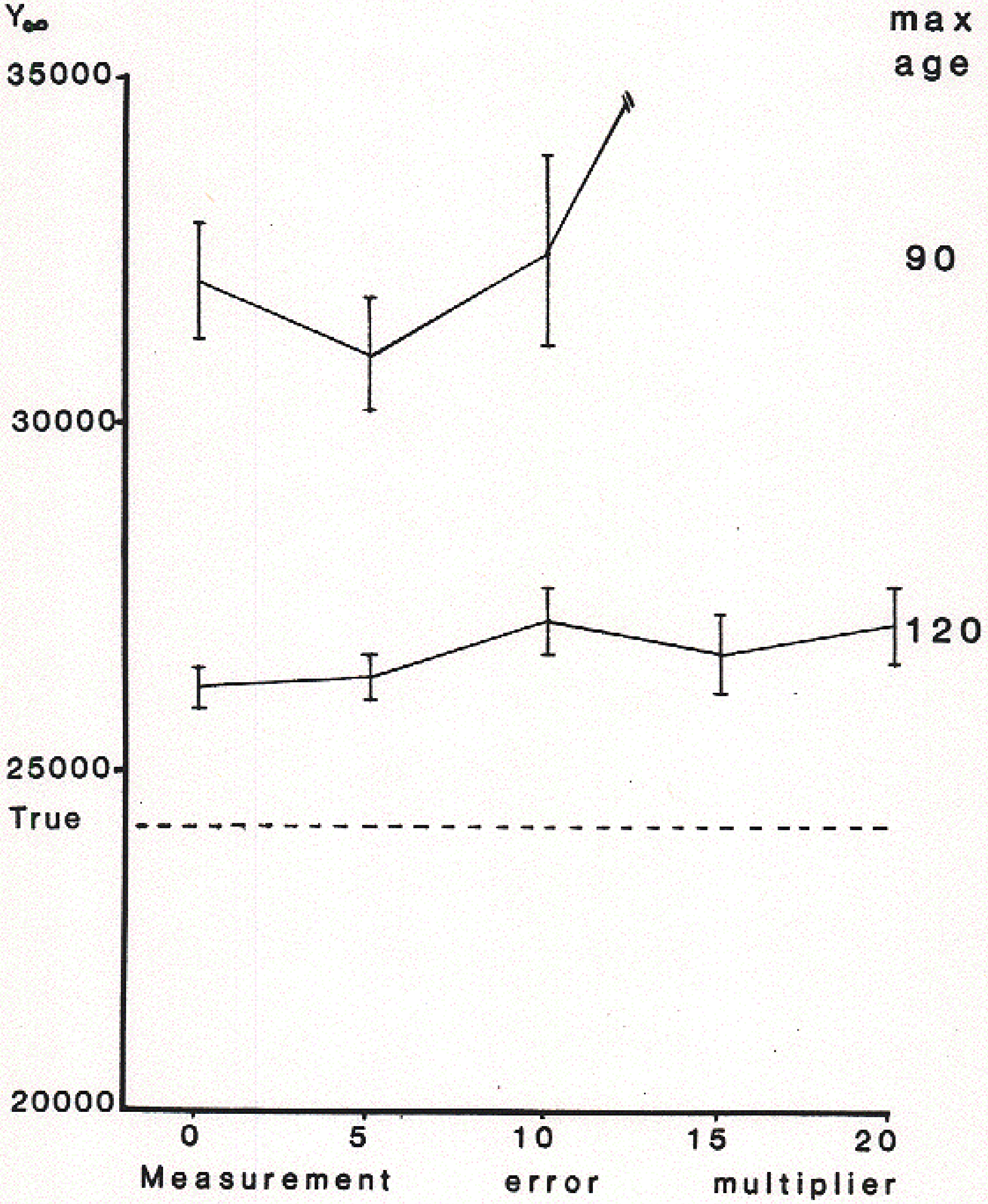


Figure 26. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e. (⫽ indicates value greater than limits on the graph), from regressions jackknifed among 20 replicates; Monomolecular model; e_b = 15*AGE.

positive for the NONJ estimate. When e_m = 2000, kurtosis (Tables C5 and C6) was often greater for $\hat{Y}_\infty$ from the NONJ procedure although both procedures resulted in estimates of Y_∞ exhibiting significant kurtosis.

4.3.2 Bias of estimates within replicates

The differences from average $\hat{Y}_\infty$ minus true Y_∞ are given in Table 14. The tests for bias (Table 15) were generally nonsignificant across the combinations of error and maximum age for the two estimation procedures. Graphic examples of how $\hat{Y}_\infty$ varies by error and maximum age are given in Figures 27 to 29 for the NONJ procedure.

Recall that when the parameter m of the Chapman-Richards function equals two, the function reduces to the Logistic function. The average estimated m minus true m (which equals two) is given in Table 16. Some of these differences, while smaller for the jackknife procedure, are also accompanied by large standard deviations, and thus often appear as nonsignificant differences in Table 17. In fact, standard deviations tend to increase as e_m increases, though not necessarily when maximum age is lowered from 120 to 90 years. The effects of e_m and selected maximum age on m are shown in Figures 30 through 32 for the NONJ method. Note that bias upwards is affected more by e_m than maximum age.

4.3.3 Bias of estimates among replicates

The average estimates of Y_∞ minus true Y_∞ are given in Table 18; most of these differences are not significant (Table 19). This may be due to large variation accompanying a difference, rather than the difference itself. Also when maximum ages sampled are 90 years and 70 years (Table 18), the average jackknifed $\hat{Y}_\infty$ appears to have less variation and smaller bias than the accompanying average $\hat{Y}_\infty$ from the NONJ method, albeit the differences are nonsignificant (Table C9). This difference in variation between the JACK and NONJ estimation procedures is also evident in Figures 33 and 34, for the respective techniques.

The differences between estimated m and true m, and respective significance levels, are given in Tables 20 and 21. In most cases, the standard error was greater for the NONJ estimate of m than when m was estimated using the JACK procedure. And, in Table 21, bias was significant only for jackknifed estimates. Figures 35 and 36 portray the estimates of m from the NONJ and JACK procedures, respectively.

4.4 All Models Compared

Three growth functions have been identified for use in this study:

Logistic . . . . $Y_t = Y_\infty \; [1 + be^{-kt}]^{-1}$
Monomolecular . . . $Y_t = Y_\infty \; [1 + be^{-kt}]$
Chapman-Richards . . $Y_t = Y_\infty \; [1 + be^{-kt}]^{1/(1-m)}$

The Logistic and Monomolecular models can be derived from the Chapman-Richards generalized growth function when m equals two and m equals zero, respectively. All three models have the asymptote Y_∞ as a common parameter and thus Y_∞ has provided a basis for examining model mis-specification, in addition to estimation procedures. Since the growth data was generated from the Logistic function, it is reasonable to expect a "best" estimate of Y_∞ will be obtained when that model is fitted. The major difference among the models is in structure -- the Monomolecular function lacks the flexibility of an inflection point.

Table 14. Average estimated Y_∞ minus true Y_∞ (24090), using the Chapman-Richards model (std dev in parentheses) ; jackknifed within 20 replicates.

	MAX		ERROR-M								
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	-330	-492	280	1112	112	-201	480	-288	-568
			(840)	(1151)	(1927)	(3897)	(3344)	(1519)	(4090)	(2349)	(3544)
		JACK	-361	-483	76	895	-3707	273	-1391	-4785	-13968
			(1120)	(1806)	(3342)	(5066)	(5159)	(2370)	(4851)	(4466)	(18697)
	120	NONJ	29	107	585	480	927	-31	-135	-394	1475
			(783)	(965)	(1284)	(1744)	(2265)	(777)	(855)	(923)	(7444)
		JACK	29	-40	305	993	-200	-251	-106	-192	318
			(783)	(1374)	(2003)	(3314)	(3159)	(633)	(2016)	(1303)	(7657)
500	90	NONJ	-281	--	--	--	--	-323	494	-107	-327
			(359)	--	--	--	--	(1435)	(4432)	(2841)	(4031)
		JACK	-357	--	--	--	--	-364	-5280	-5015	-14181
			(538)	--	--	--	--	(2553)	(17205)	(7396)	(20894)
	120	NONJ	-90	--	--	--	--	-112	-169	-400	533
			(261)	--	--	--	--	(409)	(696)	(880)	(3691)
		JACK	-86	--	--	--	--	-151	243	140	-2854
			(263)	--	--	--	--	(587)	(1507)	(1860)	(6961)
1000	90	NONJ	-218	--	--	--	--	-245	538	-4	-248
			(535)	--	--	--	--	(1487)	(4237)	(2659)	(3944)
		JACK	-129	--	--	--	--	-48	-3754	-2531	-14167
			(794)	--	--	--	--	(2961)	(12480)	(6635)	(20113)
	120	NONJ	-79	--	--	--	--	-108	-144	-449	564
			(385)	--	--	--	--	(500)	(833)	(744)	(3763)
		JACK	-58	--	--	--	--	-198	111	-199	-3320
			(432)	--	--	--	--	(778)	(2673)	(1583)	(7276)

Table 15. Significance level for test of significance between estimated Y_∞ and true Y_∞ (24090), using the Chapman-Richards model; jackknifed within 20 replicates.

ERROR-B	MAX AGE						ERROR-M				
			0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	NS
		JACK	NS	NS	NS	NS	**	NS	NS	***	**
	120	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	NS
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	NS
500	90	NONJ	**	--	--	--	--	NS	NS	NS	NS
		JACK	**	--	--	--	--	NS	NS	**	**
	120	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS
1000	90	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	NS	**
	120	NONJ	NS	--	--	--	--	NS	NS	*	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS

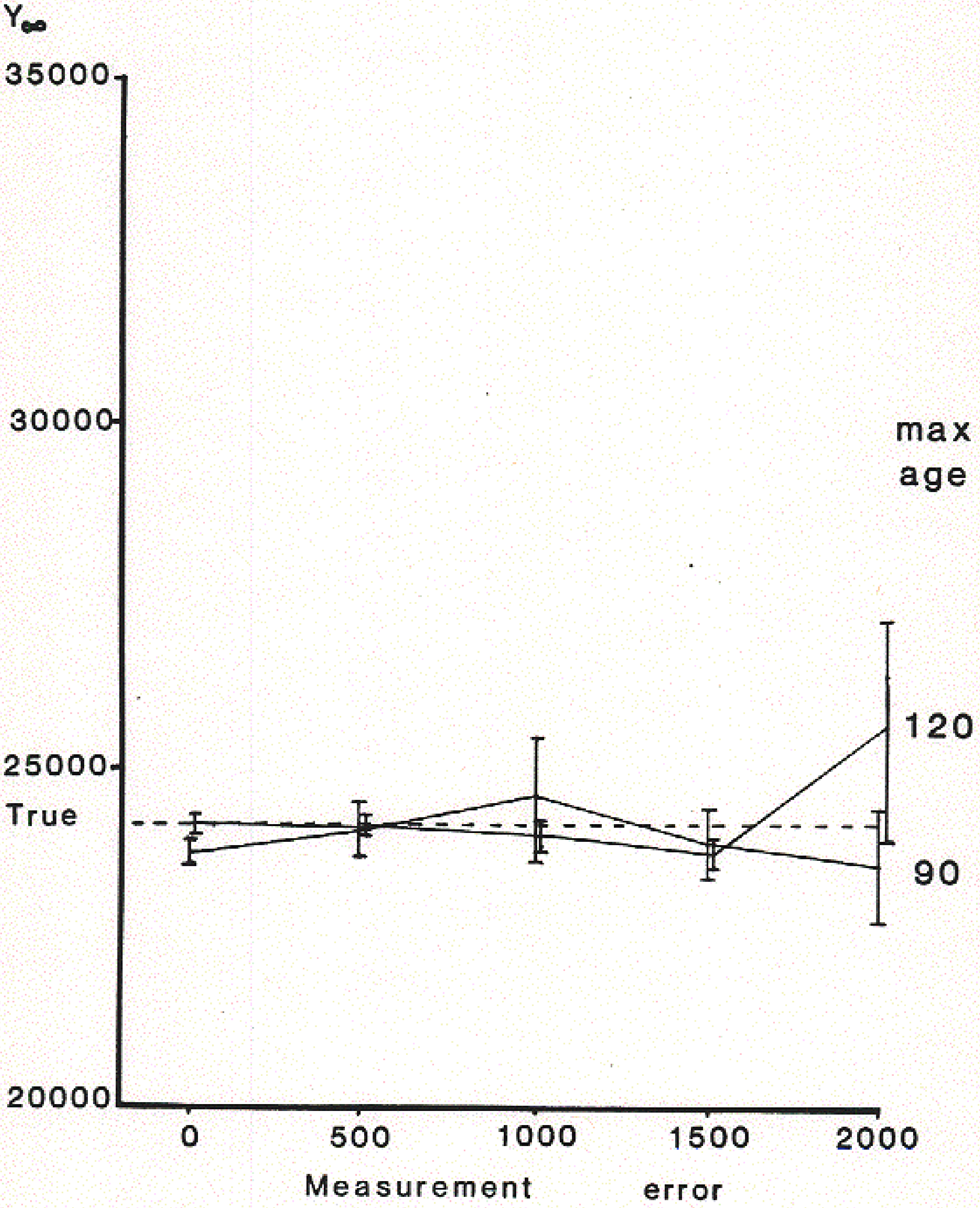


Figure 27. Estimates of Y_∞ as a function of e_m with 1 s.e., from standard regression within replicates, averaged across 20 replicates; Chapman-Richards model; e_b = 15*AGE.

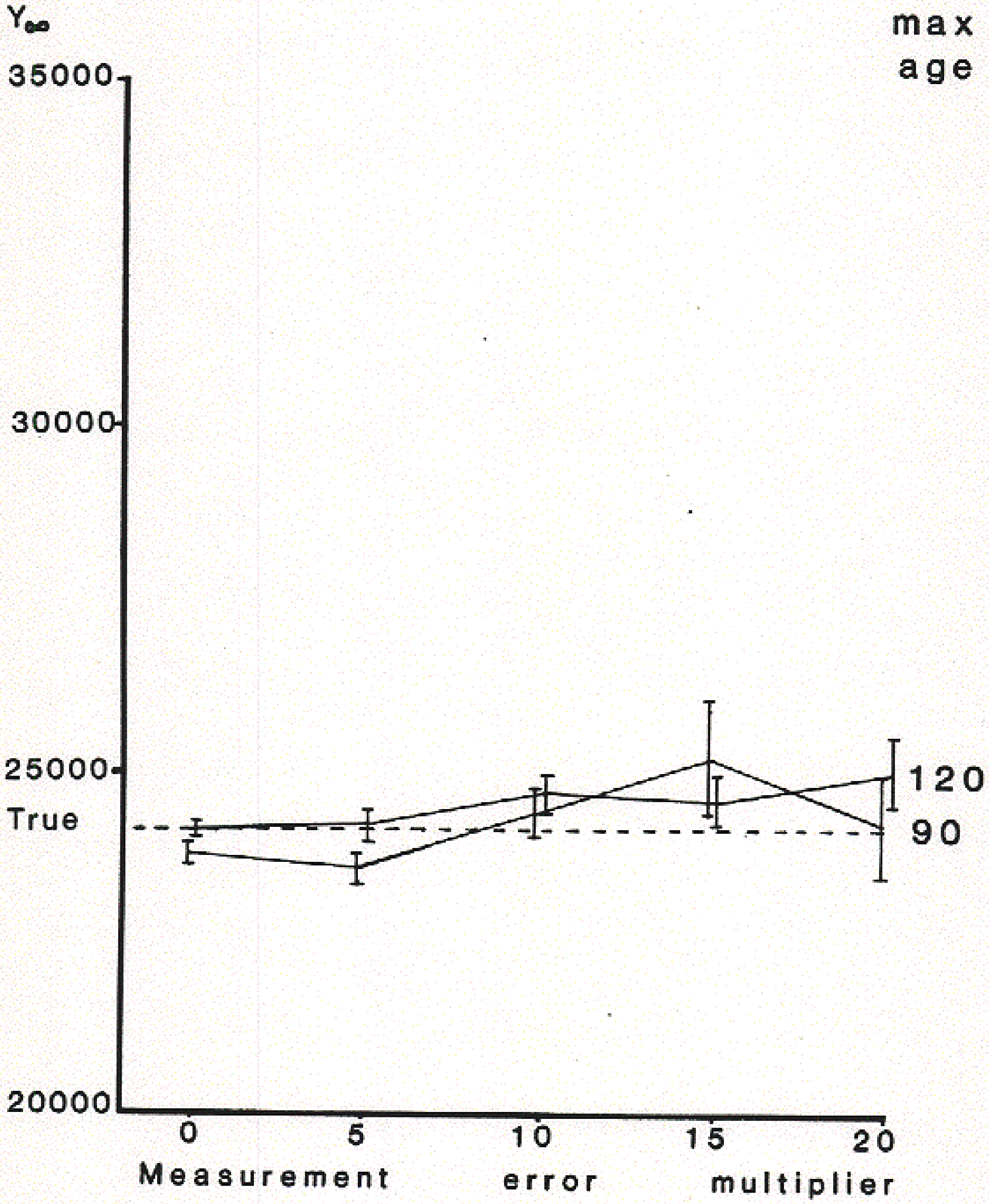


Figure 28. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e. from standard regression within replicates, averaged across 20 replicates; Chapman-Richards model; e_b = 15*AGE.

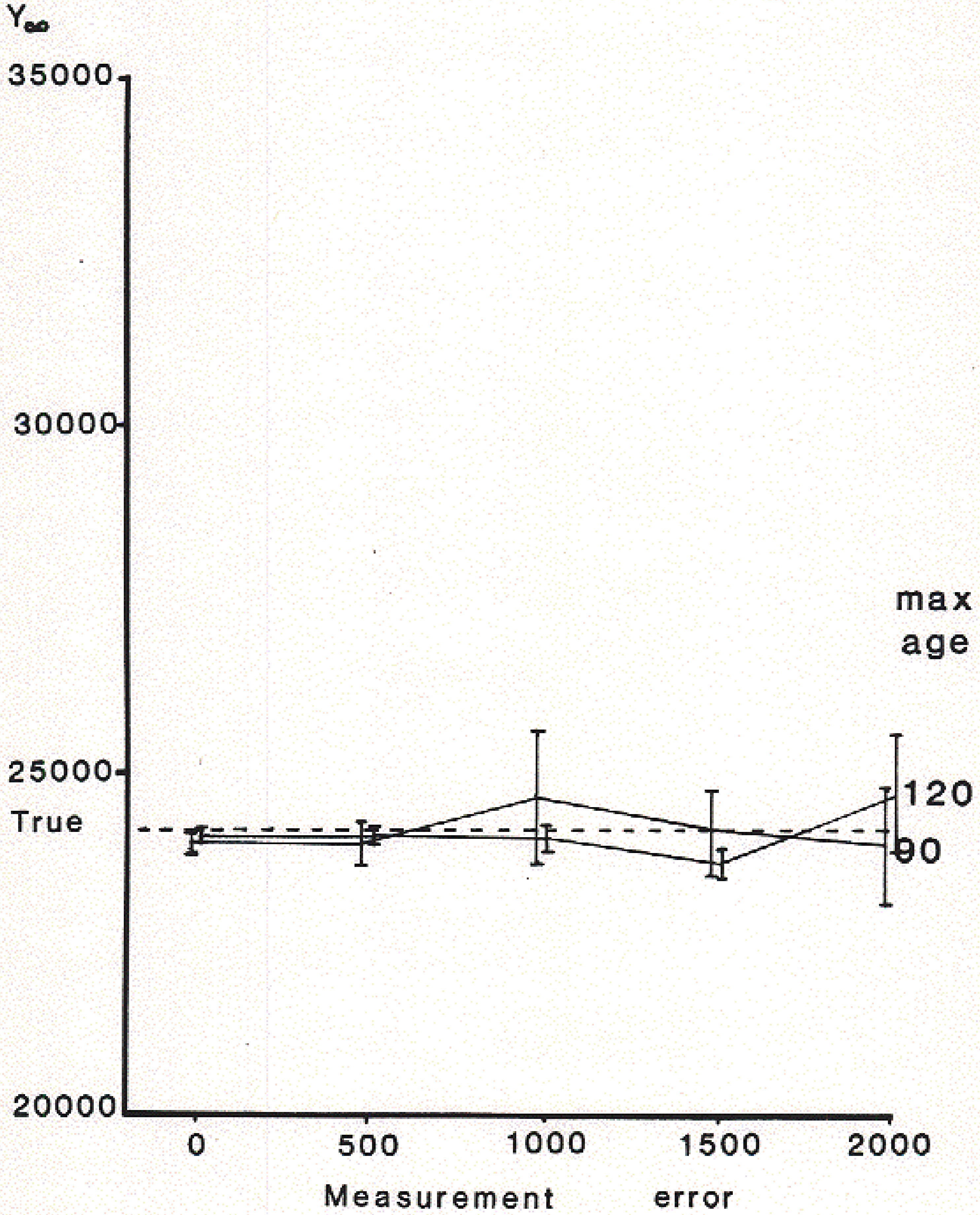


Figure 29. Estimates of Y_∞ as a function of e_m with 1 s.e., from standard regression within replicates, averaged across 20 replicates; Chapman-Richards model; e_b = 1000.

Table 16. Average estimated m minus true m(2), using the Chapman-Richards model (std dev in parentheses) ; jackknifed within 20 replicates.

ERROR-B	MAX AGE		ERROR-M 0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	0.27	0.39	0.41	0.41	0.7	0.14	0.34	0.59	1.11
			(0.327)	(0.595)	(1.007)	(0.984)	(1.039)	(0.72)	(0.836)	(0.986)	(1.436)
		JACK	0.27	0.01	0.16	0.45	1.37	-0.25	-0.24	1.96	2.59
			(0.548)	(1.698)	(3.276)	(5.655)	(6.425)	(2.012)	(2.814)	(3.615)	(5.85)
	120	NONJ	0.05	0.11	0.31	0.55	0.44	0.05	0.32	0.27	0.88
			(0.568)	(0.696)	(0.817)	(1.02)	(1.084)	(0.549)	(0.955)	(1.205)	(1.22)
		JACK	-0.23	0.15	-0.09	- 0.01	1.31	- 0.05	-0.16	-0.82	0.96
			(1.461)	(1.659)	(2.81)	(3.748)	(8.763)	(1.37)	(4.082)	(2.135)	(6.022)
500	90	NONJ	0.18	--	--	--	--	0.25	0.31	0.61	1.02
			(0.183)	--	--	--	--	(0.836)	(0.806)	(1.093)	(1.272)
		JACK	0.2	--	--	--	--	0.41	-0.3	2.24	1.74
			(3.07)	--	--	--	--	(2.824)	(2.476)	(4.486)	(4.309)
	120	NONJ	0.04	--	--	--	--	0.06	0.3	0.29	0.92
			(0.244)	--	--	--	--	(0.600)	(1.021)	(1.234)	(1.269)
		JACK	0.03	--	--	--	--	- 0.02	-0.93	-1.34	2.28
			(0.232)	--	--	--	--	(1.346)	(3.289)	(2.395)	(9.243)
1000	90	NONJ	0.22	--	--	--	--	0.27	0.28	0.43	1.04
			(0.311)	--	--	--	--	(0.973)	(0.797)	(0.946)	(1.303)
		JACK	0.11	--	--	--	--	0.3	-0.12	0.31	1.48
			(0.568)	--	--	--	--	(3.845)	(3.362)	(2.9)	(4.134)
	120	NONJ	0.11	--	--	--	--	0.16	0.41	0.32	0.92
			(0.337)	--	--	--	--	(0.693)	(1.169)	(1.207)	(1.228)
		JACK	0.05	--	--	--	--	0.12	0.08	-1.04	2.51
			(0.385)	--	--	--	--	(1.375)	(6.067)	(2.362)	(9.305)

Table 17. Significance level for test of significance between estimated m and true m(2), using the Chapman-Richards model; jackknifed within 20 replicates.

	MAX		ERROR-M								
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	**	**	NS	NS	**	NS	NS	*	**
		JACK	*	NS	NS	NS	NS	NS	NS	*	NS
	120	NONJ	NS	NS	NS	*	NS	NS	NS	NS	**
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	NS
500	90	NONJ	***	--	--	--	--	NS	NS	*	**
		JACK	NS	--	--	--	--	NS	NS	*	NS
	120	NONJ	NS	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	NS	*	NS
1000	90	NONJ	**	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	NS	NS	NS
	120	NONJ	NS	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	NS	NS	NS

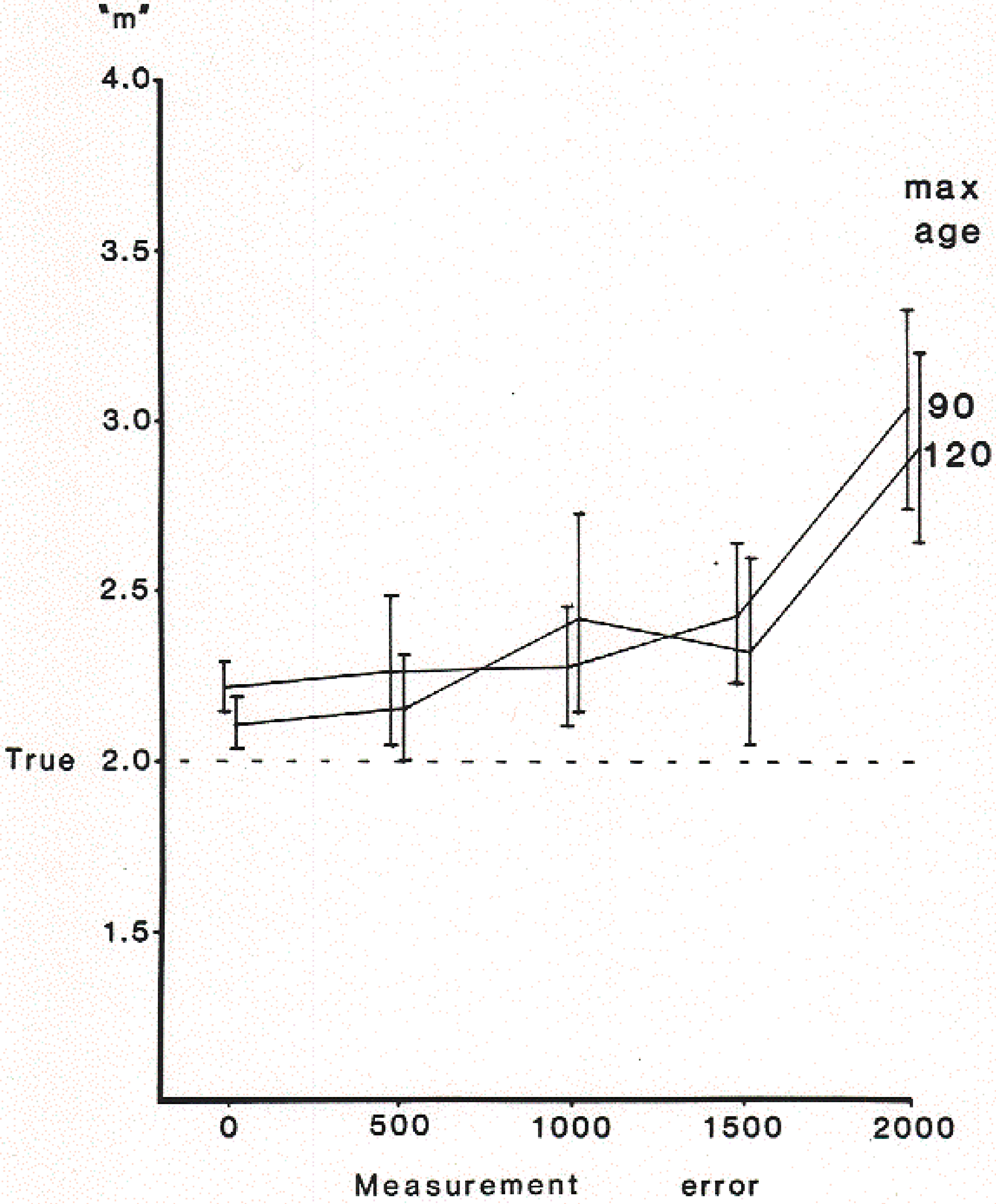


Figure 30. Estimates of m as a function of e_m with 1 s.e., from standard regression within replicates, averaged across 20 replicates; Chapman-Richards model; e_b = 1000.

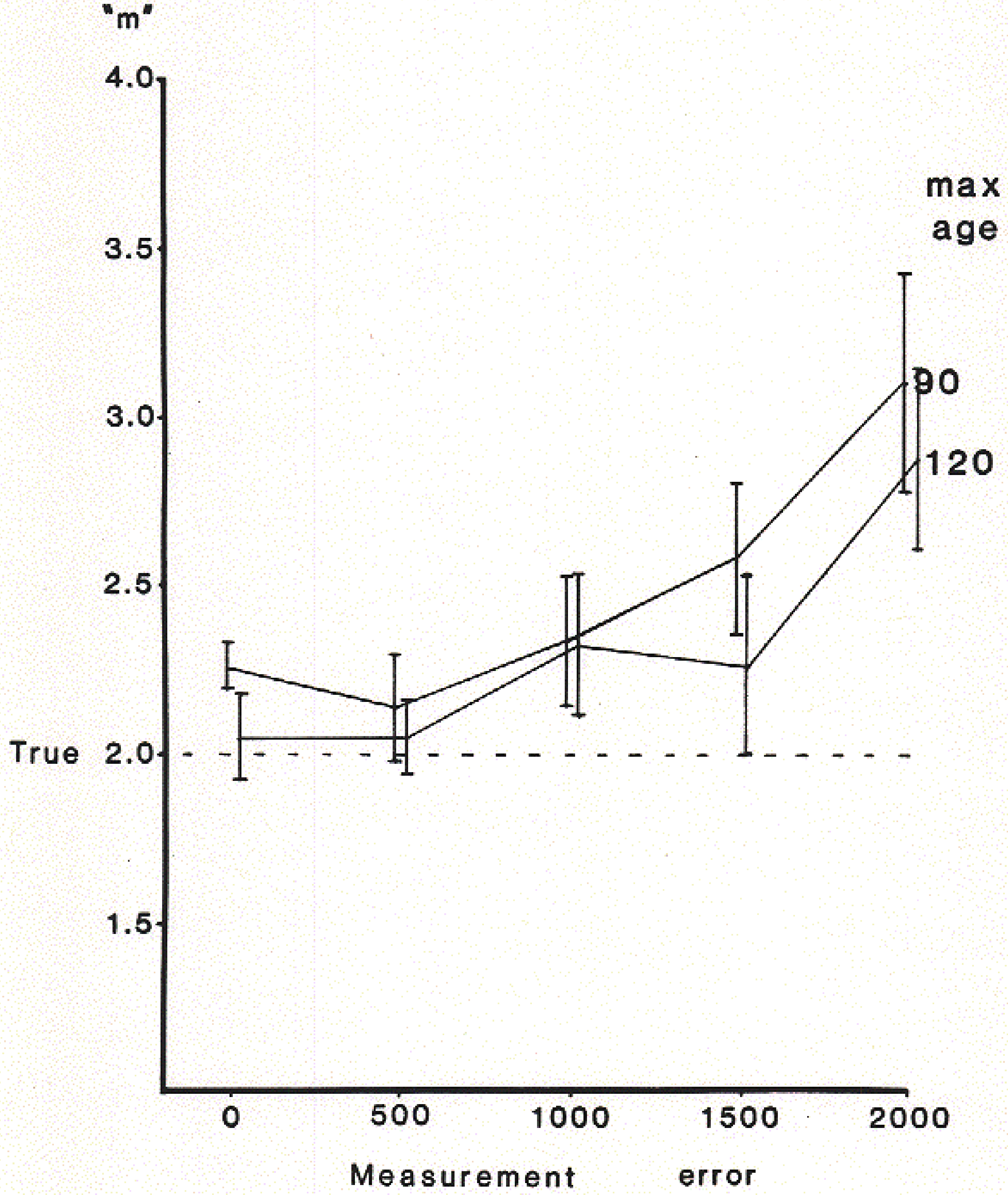


Figure 31. Estimates of m as a function of e_m with 1 s.e., from standard regression within replicates, averaged across 20 replicates; Chapman-Richards model; e_b = 15*AGE.

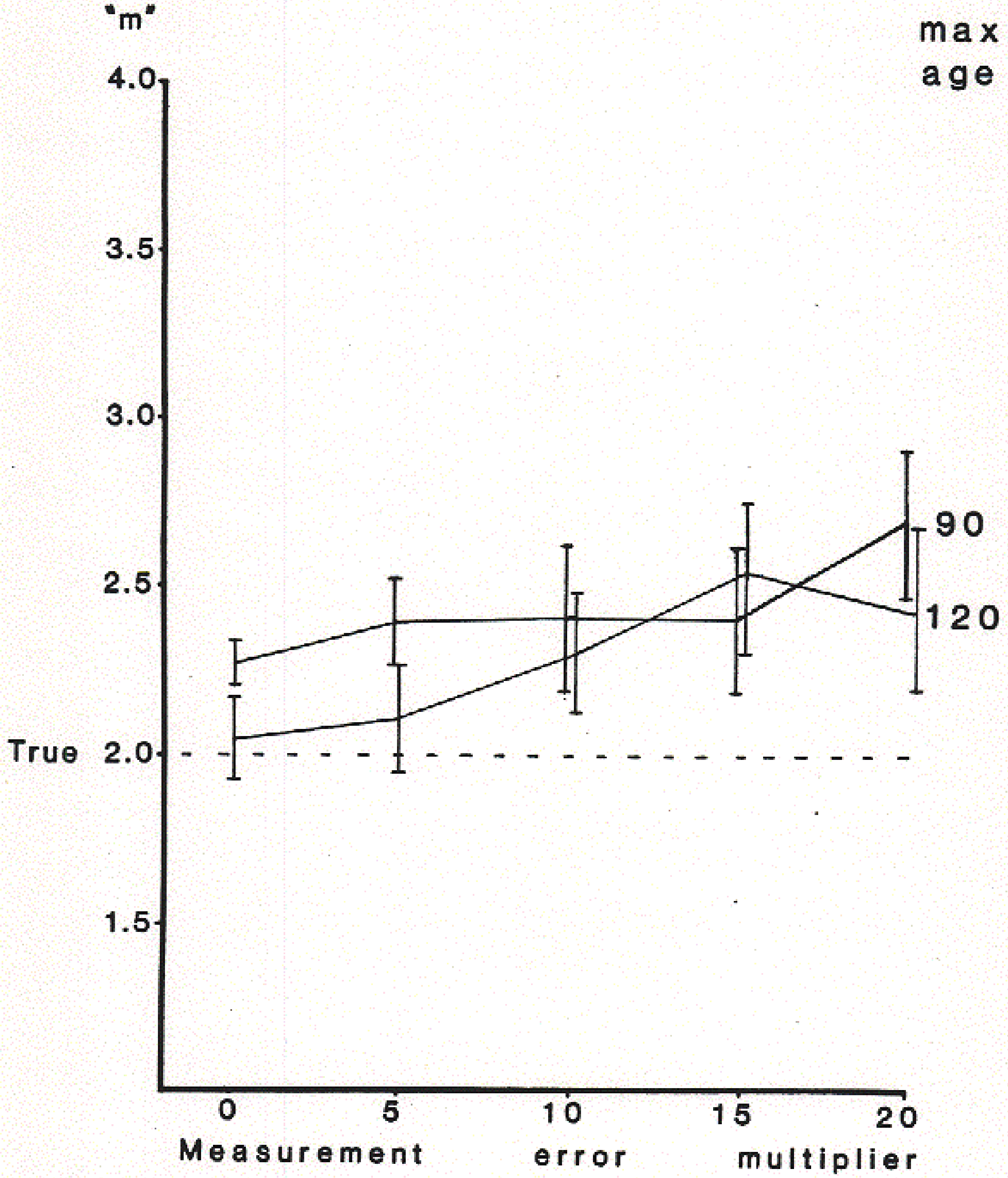


Figure 32. Estimates of m as a function of e_m multiplier *AGE with 1 s.e., from standard regression within replicates, averaged across 20 replicates; Chapman-Richards model; e_b = 15*AGE.

Table 18. Average estimated Y_∞ minus true Y_∞ (24090), using the Chapman-Richards model (1 s.e. in parentheses); jackknifed among 20 replicates.

MAX		ERROR-M				
AGE		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	-432	-242	-727	1917	1268
		(637)	(2719)	(5686)	(13516)	(14686)
	JACK	-433	-272	-561	2326	64
		(169)	(545)	(1182)	(2189)	(3021)
90	NONJ	-331	-566	-133	-205	-533
		(215)	(429)	(952)	(1261)	(1513)
	JACK	-227	49	-154	-82	-154
		(201)	(400)	(575)	(844)	(468)
120	NONJ	-9	148	586	280	719
		(86)	(160)	(326)	(366)	(582)
	JACK	-33	378	1095	225	180
		(213)	(271)	(350)	(587)	(480)

Table 19. Significance level for test of significance between estimated Y_∞ and true Y_∞ (24090), using the Chapman-Richards model; jackknifed among 20 replicates.

MAX AGE		ERROR-M 0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	NS	NS	NS	NS	NS
	JACK	*	NS	NS	NS	NS
90	NONJ	NS	NS	NS	NS	NS
	JACK	NS	NS	NS	NS	NS
120	NONJ	NS	NS	NS	NS	NS
	JACK	NS	NS	**	NS	NS

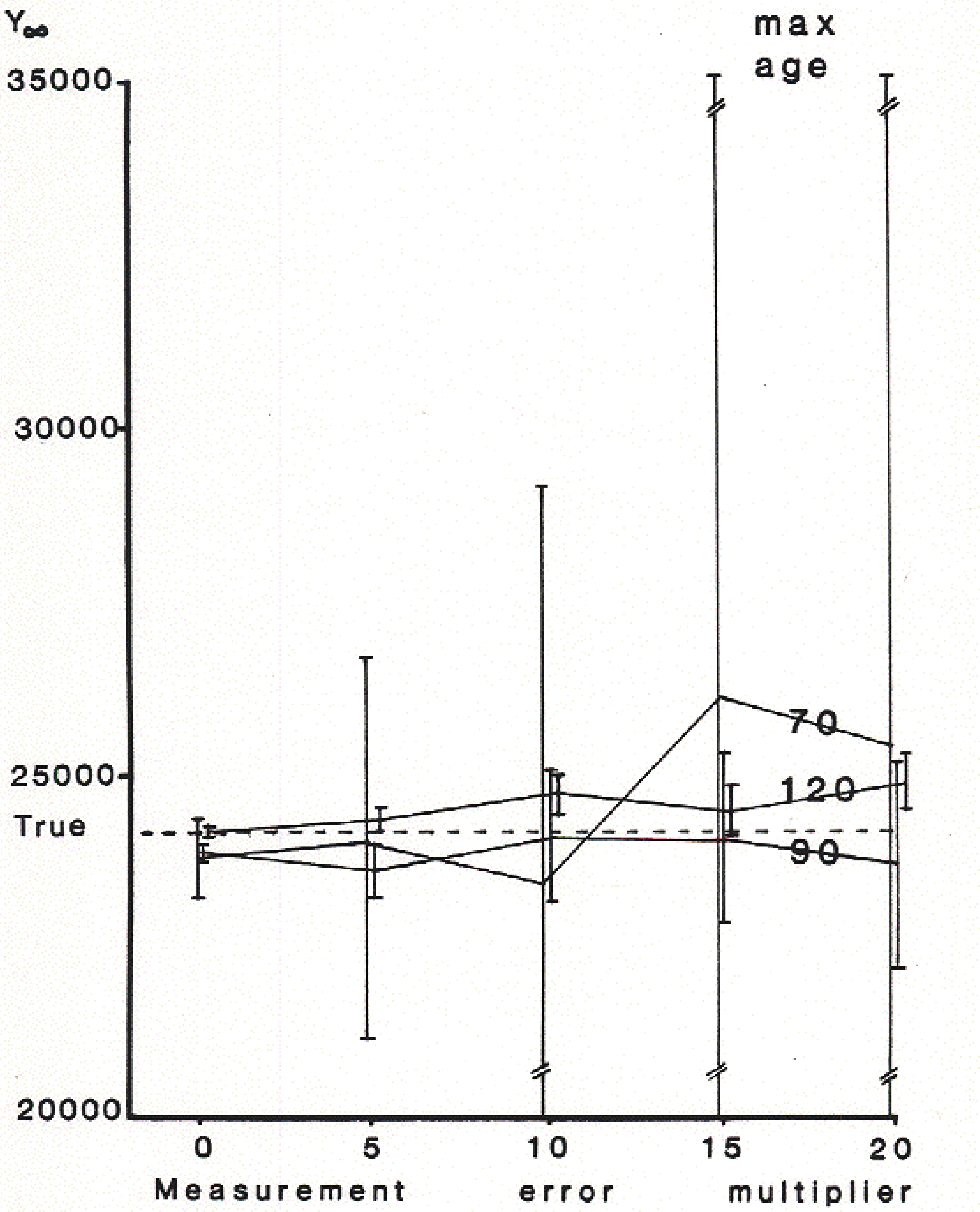


Figure 33. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e. (⫽ indicates value greater than limits on the graph), from standard regression among 20 replicates; Chapman-Richards model; e_b = 15*AGE.

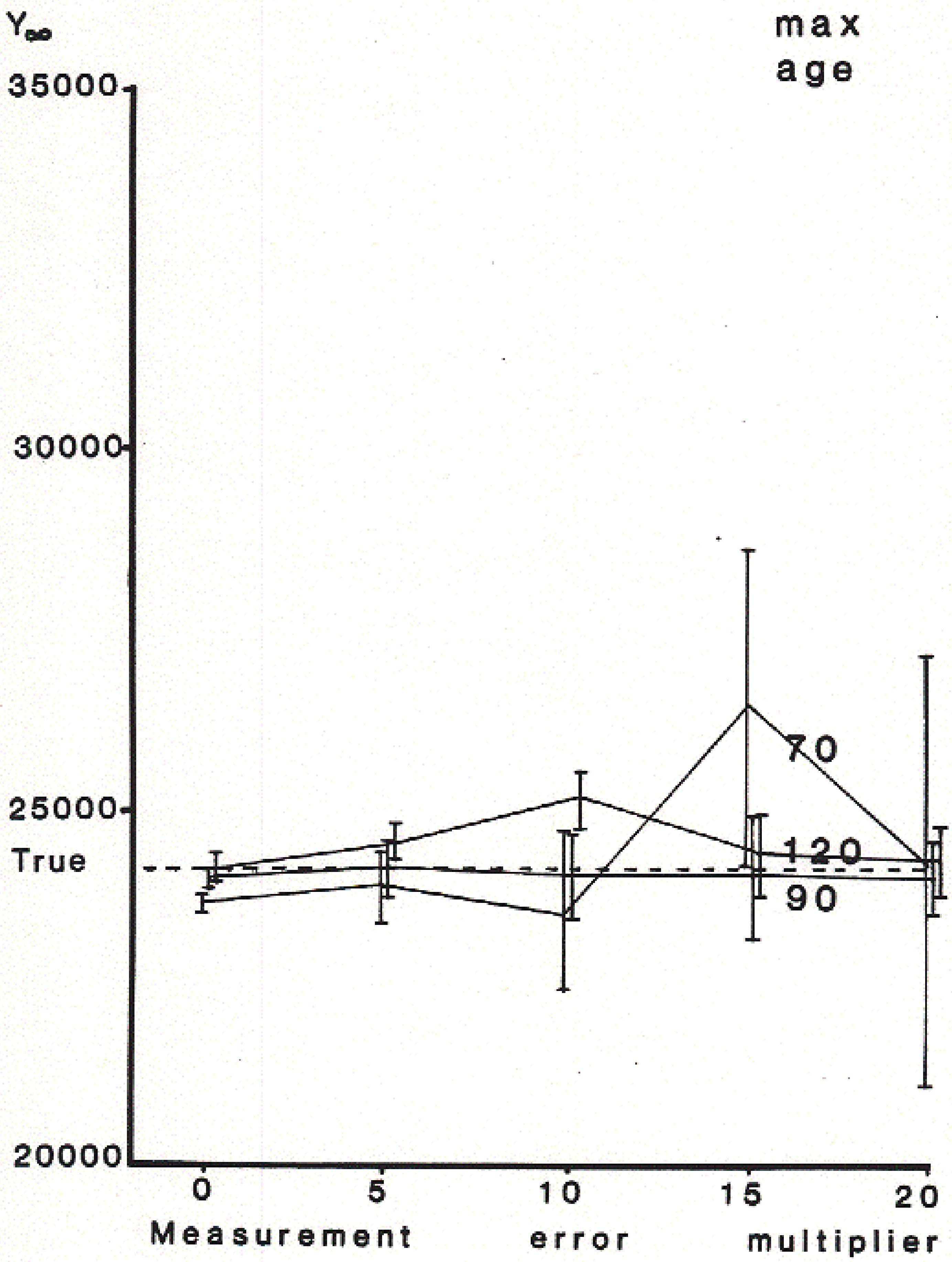


Figure 34. Estimates of Y_∞ as a function of e_m multiplier *AGE with 1 s.e., from regressions jackknifed among 20 replicates; Chapman-Richards model; e_b = 15*AGE.

Table 20. Average estimated m minus true m(2), using the Chapman-Richards model (1 s.e. in parentheses); jackknifed among 20 replicates.

MAX AGE		ERROR-M				
		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	0.23	0.22	0.38	0.29	0.17
		(0.253)	(1.054)	(2.426)	(3.830)	(4.842)
	JACK	0.23	0.22	0.26	0.10	0.27
		(0.012)	(0.048)	(0.173)	(0.132)	(0.288)
90	NONJ	0.20	0.29	0.21	0.41	0.30
		(0.176)	(0.375)	(0.751)	(1.062)	(1.387)
	JACK	0.10	-0.29	0.18	0.21	-0.07
		(0.096)	(0.282)	(0.306)	(0.522)	(0.121)
120	NONJ	-0.08	-0.25	-0.17	-0.04	-0.32
		(0.138)	(0.222)	(0.425)	(0.565)	(0.739)
	JACK	-0.07	-0.6	-0.97	-0.11	-0.59
		(0.179)	(0.224)	(0.301)	(0.609)	(0.292)

Table 21. Significance level for test of significance between estimated m and true m (2), using the Chapman-Richards model; jackknifed among 20 replicates.

MAX AGE				ERROR-M		
		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	NS	NS	NS	NS	NS
	JACK	***	***	NS	NS	NS
90	NONJ	NS	NS	NS	NS	NS
	JACK	NS	NS	NS	NS	NS
120	NONJ	NS	NS	NS	NS	NS
	JACK	NS	*	**	NS	NS

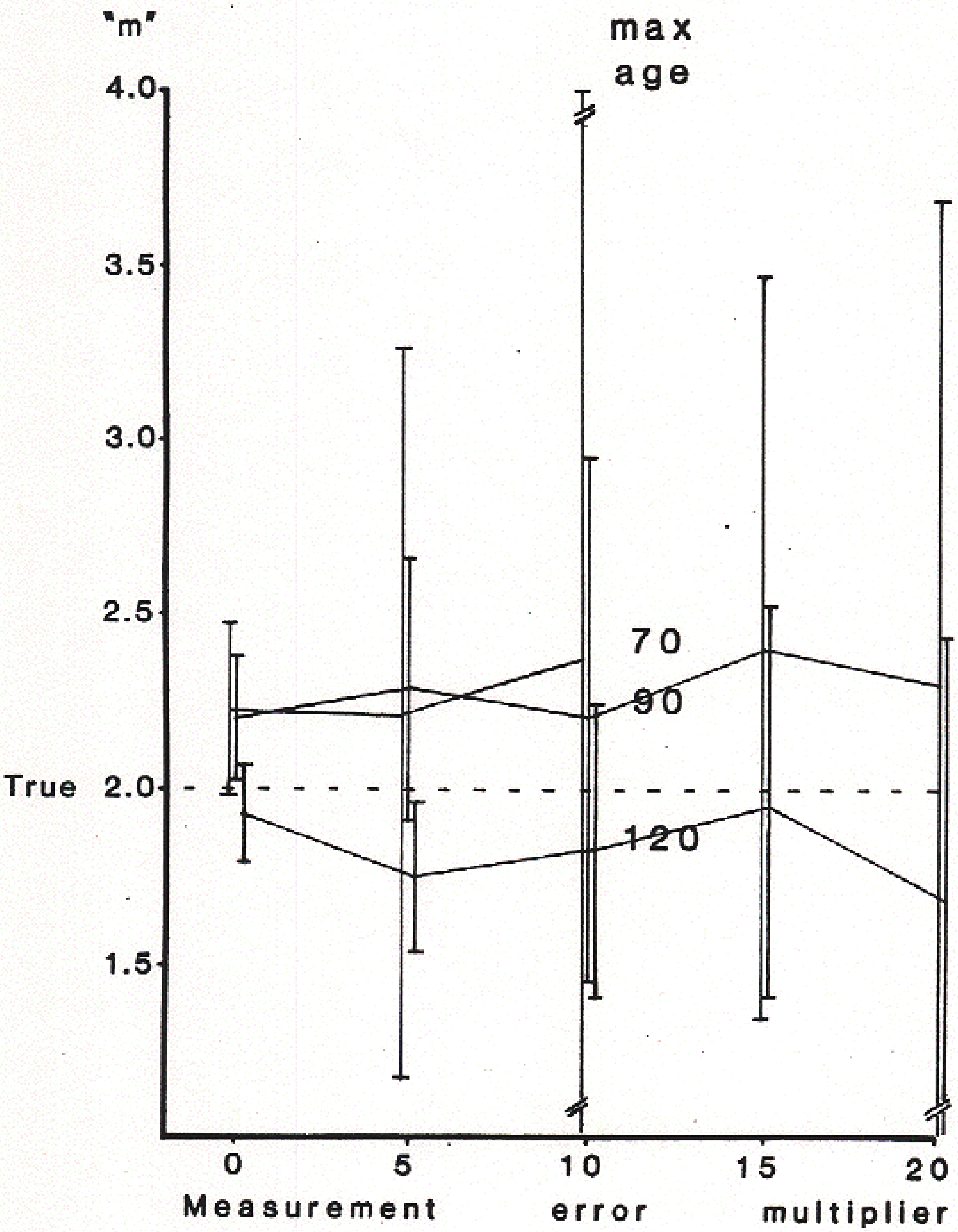


Figure 35. Estimates of m as a function of e_m multiplier *AGE with 1 s.e. (⫽ indicates value greater than limits on the graph), from standard regression among 20 replicates; Chapman-Richards model; e_b = 15*AGE.

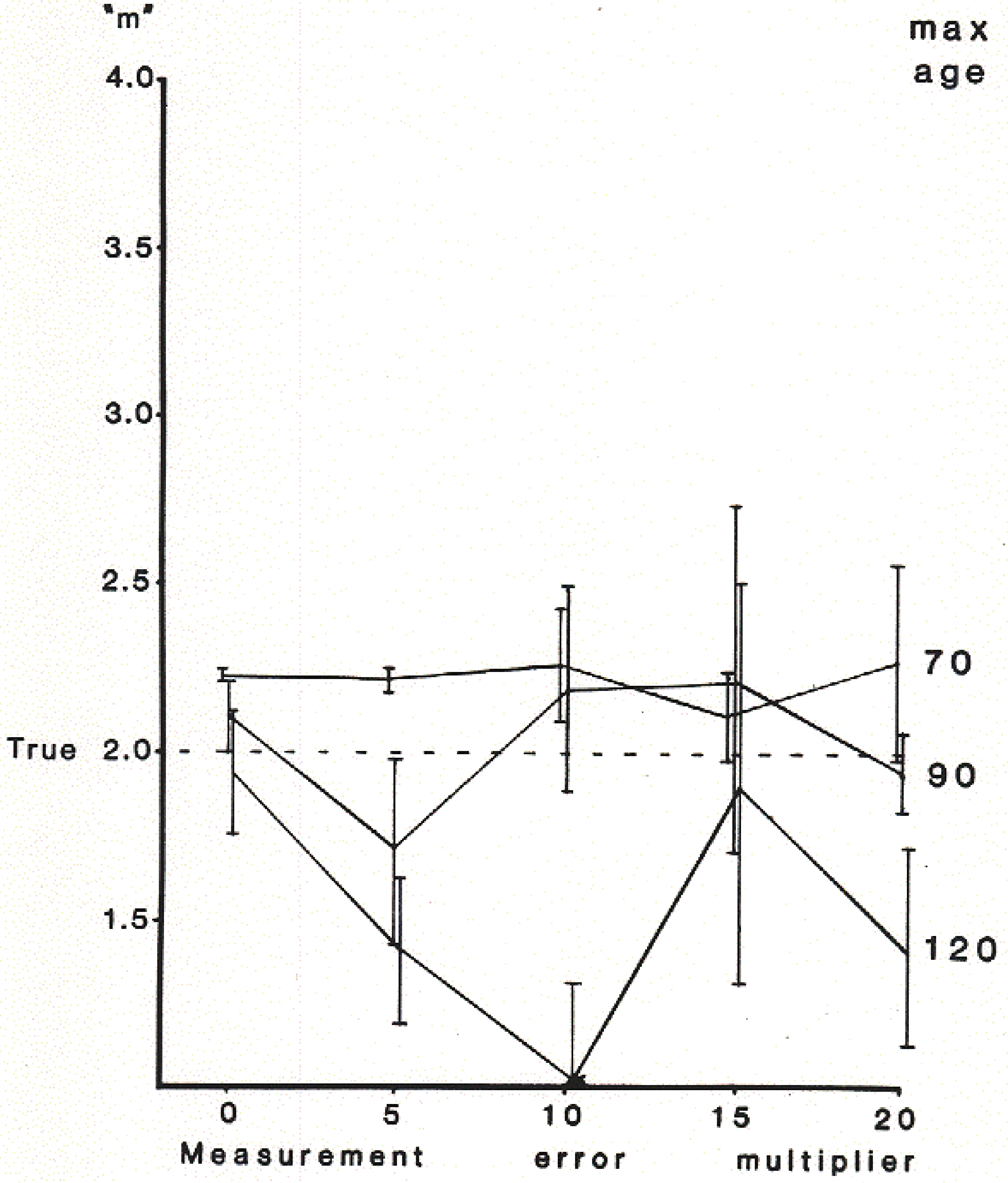


Figure 36. Estimates of m as a function of e_m multiplier *AGE with 1 s.e. (⫽ indicates value greater than limits on the graph), from regressions jackknifed among 20 replicates; Chapman-Richards model; e_b = 15*AGE.

With zero e_m, the Monomolecular estimate of Y_∞ differed significantly from both true Y_∞ (Tables 10 and 11), and the Logistic estimate of Y_∞, (Tables 22 to 24). It appears that e_b, e_m, maximum age, and estimation technique, as factors in bias, are all secondary to the inability of the Monomolecular function to make use of inflection in the growth data.

On the other hand, the Chapman-Richards $\hat{Y}_\infty$ and the Logistic $\hat{Y}_\infty$ are generally not significantly different for jackknifing within replicates (Table 25). Estimates of Y_∞ differ between the Chapman-Richards and Logistic models more frequently when estimation is among replicates (Table 26), rather than within replicates. In addition, the estimate of m changes as e_m increases, appearing to compensate for the added noise in the data. This compensation suggests possible interdependencies or correlations among growth parameters, which in turn may obscure biological inference about a population from changes in these growth parameters. This issue was raised earlier by Gallucci and Quinn (1979) while fitting the von Bertalanffy growth model to data from two spatial regions.

Table 22. Significance level for test of significance between Logistic Y_∞ and Monomolecular Y_∞ ; jackknifed within 20 replicates.

ERROR-B	MAX AGE		ERROR-M								
			0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	***	***	***	***	**	***	**	***	*
		JACK	***	***	***	*	*	**	*	*	NS
	120	NONJ	***	***	***	**	*	***	***	***	NS
		JACK	***	***	***	**	NS	***	***	***	NS
1000	90	NONJ	***	--	--	--	--	***	**	***	*
		JACK	***	--	--	--	--	***	*	NS	NS
	120	NONJ	***	--	--	--	--	***	***	***	NS
		JACK	***	--	--	--	--	***	***	***	NS

Table 23. Significance level for test of significance between Logistic Y_∞ and Monomolecular Y_∞ ; jackknifed within 100 replicates.

ERROR-B	MAX AGE		ERROR-M								
			0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	***	***	***	***	***	***	***	***	***
		JACK	***	***	***	***	***	***	***	NS	***
	120	NONJ	***	***	***	***	***	***	***	***	***
		JACK	***	***	***	***	**	***	***	***	**
1000	90	NONJ	***	--	--	--	--	***	***	***	***
		JACK	***	--	--	--	--	***	***	*	***
	120	NONJ	***	--	--	--	--	***	***	***	***
		JACK	***	--	--	--	--	***	***	***	*

Table 24. Significance level for test of significance between Logistic Y_{∞} and Autocatalytic Y_{∞} ; jackknifed among 20 replicates.

MAX AGE		ERROR-M				
		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	***	***	***	***	***
	JACK	***	***	***	***	***
90	NONJ	***	***	***	***	***
	JACK	***	***	***	***	***
120	NONJ	***	***	***	***	***
	JACK	***	***	***	***	***

Table 25. Significance level for test of significance between Logistic Y_∞ and Chapman-Richards Y_∞ ; jackknifed within 20 replicates.

ERROR-B	MAX AGE		ERROR-M								
			0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	NS
		JACK	NS	NS	NS	NS	NS	NS	NS	*	NS
	120	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	NS
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	NS
500	90	NONJ	*	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS
	120	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS
1000	90	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS
	120	NONJ	NS	--	--	--	--	NS	NS	NS	NS
		JACK	NS	--	--	--	--	NS	NS	NS	NS

Table 26. Significance level for test of significance between Logistic Y_∞ and Chapman-Richards Y_∞ ; jackknifed among 20 replicates.

MAX AGE		ERROR-M				
		0	5*AGE	10*AGE	15*AGE	20*AGE
70	NONJ	***	NS	NS	NS	NS
	JACK	***	**	NS	NS	NS
90	NONJ	***	**	NS	NS	NS
	JACK	*	*	NS	NS	NS
120	NONJ	NS	**	NS	NS	NS
	JACK	NS	***	***	NS	*

5.0 SUMMARY

The jackknife estimation procedure and a standard nonlinear estimation procedure have both been applied to simulated forest growth data (Y_t) in order to obtain an estimate of the asymptotic growth ($\hat{Y}_\infty$) or final yield. Since the growth data were generated from a Logistic model, the estimates of Y_∞ from the fitted Logistic model are of primary importance for assessing the jackknife technique. The Y_∞ estimates from the Monomolecular and Chapman-Richards functions are of importance inasmuch as they respectively represent model mis-specification and increased model complexity. The effects of biological error (e_b), measurement error (e_m), and maximum sample age (70, 90, and 120 years) on the distribution and bias of the Y_∞ estimates are summarized. The main objective was whether or not a jackknife procedure could offer any improvement or, in fact, even perform as well as conventional technique such as standard nonlinear least squares regression.

5.1 Distribution of Logistic $\hat{Y}_\infty$

In the construction of the simulated observations, both biological and measurement error were normally distributed with mean zero and variance additive in some instances and multiplicative in others. The estimates of Y_∞ for error and age combination studies were tested for departures from a normal distribution -- using a Kolmogorov-Smirnov (KS) test, along with separate tests for skewness and kurtosis. The KS statistic and kurtosis were generally significant ($\alpha > 0.05$ level) when maximum age excluded ages above 90 years. On the other hand, the distributions of $\hat{Y}_\infty$ were significantly skewed for all age and error combinations, with the exception of small additive e_m at maximum age of 120 years. This outcome was the same for both estimation procedures. That is, the jackknife afforded no improvement. Although Miller (1968) forwarned that the jackknife could not overcome non-normality in the data, the lack of normality in this case is not in the data, but rather the resultant estimates. It is not clear at this time why the estimates of Y_∞ are not distributed normally.

In magnitude, skewness and kurtosis both increased as e_m increased -- generally more with the jackknifed estimates of Y_∞, and sometimes in the opposite direction. That is, for a given combination of error and maximum age, the distribution of Y_∞ estimates from the jackknife procedure were significantly skewed left, whereas Y_∞ estimates from the standard method were skewed significantly to the right. Likewise, the distribution of jackknifed estimates was sometimes leptokurtic whereas the comparable distribution of standard nonlinear regression estimates was significantly platykurtic.

5.2 Bias of $\hat{Y}_\infty$

For most error and age combinations, neither the standard nor the jackknifed estimates of Y_∞ differed significantly from each other. The upward bias is obvious for both estimation procedures, as maximum age moves down from 120 years. However, the variability about these estimates increases to the point where the difference between true Y_∞ and the average of 20 or 100 estimates of Y_∞ is often not significant.

The biasedness of $\hat{Y}_\infty$ was less significant with estimation among replicates -- variation among the estimates was also reduced. Although this was true for both estimation procedures, jackknifing appeared to be particularly enhanced when applied among replicates. For this reason, maintaining integrity of the design matrix is important for jackknifing with nonlinear models. In other words, it would seem that jackknifing among replicates is more reliable than jackknifing within replicates. As an example, data sampled to a maximum age of 70 years, might already be too close to growth inflection age, so as to render estimates of Y_∞ useless. However, if data points are incremented every five years, as in this study, jackknifing within replicates means that at least one pseudo-estimate of Y_∞ will be based on data ranging from 40 to 65 years. That resulting pseudo-estimate may be so anomalous as to significantly affect the final jackknifed estimate, even if the other pseudo-estimates (based on maximum age of 70 years) were reasonable.

5.3 Effect on Y_∞ from Mis-specifying the Model

Problems of biasedness and large variability encountered with $\hat{Y}_\infty$ from the correct (i.e. Logistic) model were only exaggerated when the model specified was Monomolecular. This was especially evident with significant bias and departures from normality at maximum age of 120 years and zero e_m since the Monomolecular function assumes no inflection in the data and, therefore, cannot make use of that information. Merely having asymptotic data does not assure a reasonable estimate of the asymptote with the Monomolecular model.

As one might expect, results from the Chapman-Richards growth function are very similar to those obtained from specifying the correct Logistic model, since the Chapman-Richards model is not a misspecification, but rather represents a higher degree of model complexity. Within replications, skewness and kurtosis were somewhat greater (using both estimation techniques) than when the Logistic model was used. Jackknifing among replicates improved the estimates of Y_∞ such that most estimates were not significantly different from true Y_∞. The estimate of parameter m was generally near two but became quite variable as e_m increased; perhaps this contributed to the "appearance" of a relatively stable $\hat{Y}_\infty$ as e_m increased. The standard estimate of m was more variable when estimating among replicates, whereas the jackknifed estimate of m was more variable when estimating within replicates.

5.4 Conclusions

The jackknife procedure for estimating the asymptote Y_∞ was tested on a data set in such a way as to avoid over-complication. The data set itself was generated from a nonlinear asymptotic Logistic growth function, a model commonly used in biological growth studies; no transformations were made on the data. The error propagated into the growth data was drawn from a normal distribution of random deviates -- a common assumption in statistical analyses. Finally, since nonlinear regression is so widely used in data analyses, it was used as the basis against which to evaluate jackknifed estimates.

Generally, whether e_m was additive or multiplicative did not appear to affect the final estimate of Y_∞. Both estimation procedures produced $\hat{Y}_\infty$ with variability increasing as e_m was enlarged. With very large errors (e_m greater than 1000 or 10*AGE) the jackknifed estimates would sometimes differ from true Y_∞ by a ten-fold difference -- occasionally this large difference was negative.

Maximum age limitations caused severe bias to both estimation procedures. In fact, exclusion of older ages appeared to affect bias and departures from normality moreso than kind or magnitude of error.

When the data is known to be asymptotic but with uncertain inflection, it appears safe to use the Chapman-Richards generalization of Von Bertalanffy's model. However, this choice can present some problems. It is more complex (four parameters), usually requires more computing time, and may also necessitate increasing the allowed number of iterations for convergence.

Tolerance criteria for the fitting procedure may have to be changed, depending upon the scale of the data. In fact, the extra computing time required (and therefore costs) for using the Chapman-Richards model in this study precluded jackknifing within 100 replicates, and thus if the correct model was in doubt, jackknifing may not be realistic unless estimating among replicates.

An additional consideration may be estimation of parameters other than Y_∞. In this study it appeared that when e_m was increased, the estimate of m changed in a compensating way. Thus, if one was also interested in a biological significance of m, the interpretation may be spurious.

Finally, the t statistic was used to test for bias when in fact distribution tests indicated that the estimates of Y_∞ were not normally distributed. Although the t-test is fairly robust in the presence of a non-normal distribution, the assumption that the resulting levels of significance are exactly accurate may not be a good assumption. An alternative test for bias might be a nonparametric (distribution free) test. The outcome of a nonparametric test might be to reject hypotheses that are otherwise not rejected using the t-test.

5.5 Suggestions for Further Research

One must look closely at variability surrounding parameter estimates. In some cases, both the nonjackknifed and the jackknifed estimates of Y_∞ were not far from true Y_∞. However, sometimes the variability of these estimates increased (with increasing e_m) to the point of no significant difference between either estimation procedures, or estimates from true parameter values. As the standard nonlinear regression estimate degenerates, the jackknife procedure can do likewise, yielding equally bad and sometimes useless estimates of Y_∞. This is not so much a criticism of the jackknife, as it is perhaps a reflection of a test situation used here for which it may have been unrealistic to expect the jackknife procedure to perform well. In light of this, the following suggestions are offered for future research of the jackknife technique with nonlinear regression models.

(1) Initially, determine to what degree the final estimate is influenced by:

    i) starting guess of Y_∞
    ii) maximum allowable number of iterations
    iii) convergence criteria of the available least squares fitting program

(2) Jackknife <u>among</u> replicates instead of <u>within</u> replicates to avoid design matrix problems, as mentioned above. This should require several data sets, each of which would represent one Monte Carlo simulation. This would allow for some distribution tests and perhaps better estimates of bias.

(3) It might be better to hold down the number of replicates to 10 or 20, but run 100 to 500 Monte Carlo simulations.

(4) Avoid sampling data ranges down to excessively low ages (e.g., 70 years in this study) so that effects of e_b and e_m, both additive and multiplicative, are not masked. Avoid fitting the Monomolecular model for the same reasons.

(5) Examine the departures from normality of the estimates of the parameters -- if significant, test for bias using nonparametric methods.

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APPENDIX A

Logistic Model: Statistics for normality, skewness, and kurtosis of $\hat{Y}_\infty$, plus significance between jackknifed $\hat{Y}_\infty$ and standard $\hat{Y}_\infty$.

This appendix contains tables of statistics pertaining to $\hat{Y}_\infty$, using the Logistic growth model, where:

KS = Kolmogorov-Smirnov
ERROR-B = biological error propagated in the data
ERROR-M = measurement error added to the data set
MAX AGE = maximum age of sampled data
NONJ = nonjackknifed estimate from standard nonlinear regression
JACK = jackknifed estimate
std dev = standard deviation of the mean
std err = standard error of the estimate
NS = not significant at the 0.05 level
-- = no data for this combination

Table A1. The KS statistic (Dmax) for normality of $\hat{Y}_\infty$; Logistic model; jackknifed within 20 replicates.

ERROR-B	MAX AGE		ERROR-M 0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	0.12995	0.19432	0.14189	0.29079	0.21467	0.16617	0.27549	0.21557	0.27052
		JACK	0.08575	0.27076	0.20534	0.25626	0.25550	0.27536	0.32179	0.26467	0.26604
	90	NONJ	0.08869	0.15337	0.10503	0.28388	0.18616	0.19503	0.20960	0.12648	0.26998
		JACK	0.08014	0.14026	0.11738	0.36784	0.12984	0.17388	0.19915	0.14080	0.23913
	120	NONJ	0.20354	0.16199	0.13624	0.10520	0.20345	0.17471	0.17020	0.21856	0.33207
		JACK	0.21487	0.15838	0.13528	0.11459	0.20184	0.16002	0.13909	0.14629	0.16281
500	70	NONJ	0.13088	--	--	--	--	0.19819	0.26291	0.21917	0.26963
		JACK	0.09260	--	--	--	--	0.30683	0.32571	0.24048	0.28066
	90	NONJ	0.08604	--	--	--	--	0.16877	0.28290	0.14057	0.28359
		JACK	0.07810	--	--	--	--	0.15899	0.27844	0.13425	0.33553
	120	NONJ	0.11792	--	--	--	--	0.13625	0.09030	0.17432	0.30784
		JACK	0.11061	--	--	--	--	0.14319	0.10971	0.17517	0.16625
1000	70	NONJ	0.100[illegible]	--	--	--	--	0.13609	0.26624	0.23290	0.26703
		JACK	0.08476	--	--	--	--	0.27918	0.28197	0.27375	0.26067
	90	NONJ	0.08943	--	--	--	--	0.22183	0.25917	0.13296	0.26351
		JACK	0.11040	--	--	--	--	0.15384	0.23632	0.14345	0.27780
	120	NONJ	0.09944	--	--	--	--	0.18666	0.12021	0.09474	0.31067
		JACK	0.09323	--	--	--	--	0.18725	0.12375	0.08060	0.29186

Table A2. Significance level for test of significance of the KS statistic (Dmax); Logistic model; jackknifed within 20 replicates.

			ERROR-M								
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	NS	*	NS	**	*	NS	**	*	**
		JACK	NS	**	*	**	**	**	**	**	**
	90	NONJ	NS	NS	NS	**	NS	*	*	NS	**
		JACK	NS	NS	NS	NS	NS	NS	*	NS	**
	120	NONJ	*	NS	NS	NS	*	NS	NS	*	**
		JACK	*	NS	NS	NS	*	NS	NS	NS	NS
500	70	NONJ	NS	--	--	--	--	*	**	*	**
		JACK	NS	--	--	--	--	**	**	**	**
	90	NONJ	NS	--	--	--	--	NS	**	NS	**
		JACK	NS	--	--	--	--	NS	**	NS	**
	120	NONJ	NS	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	NS	NS	NS
1000	70	NONJ	NS	--	--	--	--	NS	**	**	**
		JACK	NS	--	--	--	--	**	**	**	**
	90	NONJ	NS	--	--	--	--	*	**	NS	**
		JACK	NS	--	--	--	--	NS	**	NS	**
	120	NONJ	NS	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	NS	NS	**

Table A3. The G1 statistic for skewness of $\hat{Y}_\infty$ from the KS test; Logistic model; jackknifed within 20 replicates.

							ERROR-M				
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	-0.2058	2.1670	0.9114	2.2230	1.4430	1.1200	2.3110	1.2610	1.3260
		JACK	-0.5095	2.5730	0.5503	1.9480	1.3580	2.9980	2.5800	1.1060	0.9253
	90	NONJ	-0.2224	1.2905	-0.4010	3.1024	0.9855	1.5941	2.9991	0.4542	2.7196
		JACK	0.0884	0.4220	-0.0604	3.8746	-1.3199	1.2661	2.5117	-0.3933	0.3920
	120	NONJ	0.6147	0.7365	0.3920	0.2768	1.6340	0.5833	0.5686	0.5364	3.9561
		JACK	0.6194	0.7252	0.1271	0.1254	1.2887	0.5533	0.5310	0.1311	-0.6846
500	70	NONJ	0.9249	--	--	--	--	1.3170	2.3960	1.2490	1.2850
		JACK	0.1835	--	--	--	--	2.9310	2.6300	1.1350	1.3820
	90	NONJ	-0.5259	--	--	--	--	1.2580	3.4780	0.6217	2.9860
		JACK	-0.5776	--	--	--	--	1.0232	3.3638	-0.1265	3.3500
	120	NONJ	0.3390	--	--	--	--	-0.3551	-0.0286	0.1565	3.6803
		JACK	0.3536	--	--	--	--	-0.3872	0.0651	-0.2112	0.9904
1000	70	NONJ	0.3678	--	--	--	--	0.6424	2.2100	1.2950	1.3340
		JACK	0.2677	--	--	--	--	1.4480	2.2440	1.1510	0.7901
	90	NONJ	-0.7253	--	--	--	--	1.6320	3.3850	0.3527	2.5240
		JACK	-0.6379	--	--	--	--	1.4436	2.8267	0.6603	2.3620
	120	NONJ	-0.3934	--	--	--	--	0.2353	0.1649	-0.0450	3.6692
		JACK	-0.3774	--	--	--	--	0.1634	-0.0010	-0.4972	2.3565

Table A4. Significance level of test for significant skewness; Logistic model; jackknifed within 20 replicates.

			ERROR-M								
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	NS	***	NS	***	*	*	***	*	*
		JACK	NS	***	NS	**	*	***	***	*	NS
	90	NONJ	NS	*	NS	***	NS	**	***	NS	***
		JACK	NS	NS	NS	***	*	*	***	NS	NS
	120	NONJ	NS	NS	NS	NS	**	NS	NS	NS	***
		JACK	NS	NS	NS	NS	*	NS	NS	NS	NS
500	70	NONJ	NS	--	--	--	--	*	***	*	*
		JACK	NS	--	--	--	--	***	***	*	*
	90	NONJ	NS	--	--	--	--	*	***	NS	***
		JACK	NS	--	--	--	--	NS	***	NS	***
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	NS	NS	NS
1000	70	NONJ	NS	--	--	--	--	NS	***	*	*
		JACK	NS	--	--	--	--	*	***	*	NS
	90	NONJ	NS	--	--	--	--	**	***	NS	***
		JACK	NS	--	--	--	--	*	***	NS	***
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	NS	NS	***

Table A5. The G2 statistic for kurtosis of $\hat{Y}_\infty$ from the KS test; Logistic model; jackknifed within 20 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	1.2850	6.2600	-0.1558	5.6230	1.4540	0.6327	6.0190	0.5765	1.2660
		JACK	0.9825	9.0380	2.1200	4.0590	1.2680	10.4300	7.1200	0.1602	-0.0955
	90	NONJ	-0.8058	2.4618	-0.5853	11.6700	-0.1351	2.8712	11.2600	-0.6624	8.8775
		JACK	-0.5406	-1.0031	0.0502	16.2700	3.1451	1.8096	8.9733	1.6203	6.0339
	120	NONJ	-0.0955	-0.1945	-0.7775	-0.0495	2.1852	-0.7866	-0.4245	-0.4244	16.6400
		JACK	-0.0143	-0.2292	-1.2122	0.0928	1.7483	-0.8255	-0.3981	-0.6250	3.5591
500	70	NONJ	1.8530	--	--	--	--	1.3740	6.5630	0.5516	0.8336
		JACK	0.0371	--	--	--	--	10.0900	7.5080	0.1797	1.5600
	90	NONJ	-0.0119	--	--	--	--	2.0750	13.8900	-0.8625	10.4000
		JACK	0.0213	--	--	--	--	1.1446	13.6000	3.2205	13.9000
	120	NONJ	-0.6967	--	--	--	--	-1.0425	-0.5801	-1.5527	15.0000
		JACK	-0.5865	--	--	--	--	-1.0458	-0.8213	-1.4184	0.8476
1000	70	NONJ	0.4964	--	--	--	--	-0.2463	5.6300	0.7042	1.2830
		JACK	0.9280	--	--	--	--	1.8970	5.4940	0.3621	-0.4607
	90	NONJ	0.1216	--	--	--	--	3.2240	13.3000	-1.1190	7.5090
		JACK	-0.0106	--	--	--	--	2.8951	10.4700	1.7498	9.5690
	120	NONJ	-0.9061	--	--	--	--	-1.2407	-1.0410	-1.0714	14.8300
		JACK	-0.9104	--	--	--	--	-1.3529	-1.0732	-0.4237	6.5552

Table A6. Significance level of test for significant kurtosis; Logistic model; jackknifed within 20 replicates.

							ERROR-M				
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	NS	***	NS	***	NS	NS	***	NS	NS
		JACK	NS	***	*	***	NS	***	***	NS	NS
	90	NONJ	NS	*	NS	***	NS	**	***	NS	***
		JACK	NS	NS	NS	***	**	NS	***	NS	***
	120	NONJ	NS	NS	NS	NS	*	NS	NS	NS	***
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	**
500	70	NONJ	NS	--	--	--	--	NS	***	NS	NS
		JACK	NS	--	--	--	--	***	***	NS	NS
	90	NONJ	NS	--	--	--	--	NS	***	NS	***
		JACK	NS	--	--	--	--	NS	***	**	***
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	NS	NS	NS
1000	70	NONJ	NS	--	--	--	--	NS	***	NS	NS
		JACK	NS	--	--	--	--	NS	***	NS	NS
	90	NONJ	NS	--	--	--	--	**	***	NS	***
		JACK	NS	--	--	--	--	**	***	NS	***
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	NS	NS	***

Table A7. The KS statistic (Dmax) for normality of $\hat{Y}_{\infty}$; Logistic model; jackknifed within 100 replicates.

ERROR-B	MAX AGE		ERROR-M 0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	0.04469	0.10093	0.17058	0.19853	0.20233	0.17673	0.17759	0.19184	0.18888
		JACK	0.05210	0.14019	0.23748	0.23893	0.24227	0.21229	0.21217	0.21765	1.00000
	90	NONJ	0.05814	0.07364	0.12977	0.18736	0.25086	0.10507	0.11659	0.22987	0.18634
		JACK	0.07100	0.08197	0.10951	0.23141	0.27870	0.10009	0.09878	0.37953	0.26600
	120	NONJ	0.05586	0.06168	0.06108	0.08002	0.17565	0.05546	0.06510	0.14462	0.09888
		JACK	0.05497	0.06859	0.06670	0.09845	0.22056	0.06566	0.05665	0.08459	0.12530
1000	70	NONJ	0.05605	--	--	--	--	0.14454	0.15645	0.30439	zzzzz
		JACK	0.07197	--	--	--	--	2.00000	0.22168	3.00000	zzzzz
	90	NONJ	0.08371	--	--	--	--	0.13318	0.15580	0.23781	0.19917
		JACK	0.07514	--	--	--	--	0.09055	0.14166	0.31854	0.26229
	120	NONJ	0.05089	--	--	--	--	0.05143	0.05957	0.14312	0.11455
		JACK	0.05182	--	--	--	--	0.06284	0.06082	0.06857	0.10867

zzzzz indicates that large outliers precluded tests

Table A8. Significance level for test of significance of the KS statistic (Dmax); Logistic model; jackknifed within 100 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	NS	*	**	**	**	**	**	**	**
		JACK	NS	**	**	**	**	**	**	**	**
	90	NONJ	NS	NS	**	**	**	**	**	**	**
		JACK	NS	NS	**	**	**	*	*	**	**
	120	NONJ	NS	NS	NS	NS	**	NS	NS	**	*
		JACK	NS	NS	NS	*	**	NS	NS	NS	**
1000	70	NONJ	NS	--	--	--	--	**	**	**	zzzzz
		JACK	NS	--	--	--	--	**	**	**	zzzzz
	90	NONJ	NS	--	--	--	--	**	**	**	**
		JACK	NS	--	--	--	--	*	**	**	**
	120	NONJ	NS	--	--	--	--	NS	NS	**	**
		JACK	NS	--	--	--	--	NS	NS	NS	**

zzzzz indicates that large outliers precluded tests

Table A9. The G1 statistic for skewness of $\hat{Y}_\infty$ from the KS test; Logistic model; jackknifed within 100 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	0.2728	2.0534	1.3145	1.1890	1.3209	1.0012	1.1227	1.9994	1.9463
		JACK	0.1763	2.0583	2.7524	3.0500	1.3225	2.2195	2.0704	4.5268	2.4970
	90	NONJ	0.2971	0.6396	1.6090	3.6080	2.6642	1.2597	3.1531	3.3351	2.2058
		JACK	0.2699	0.7011	1.5923	5.1040	0.6265	0.8869	-0.5947	4.4478	2.6684
	120	NONJ	0.1888	0.5202	0.7129	0.5705	1.6981	0.4213	0.6614	2.5330	0.8523
		JACK	0.1960	0.5151	0.5279	0.7464	-5.4600	0.4608	0.4245	0.5893	-1.8816
1000	70	NONJ	0.0008	--	--	--	--	0.9391	0.9937	8.0884	zzzzz
		JACK	-0.1219	--	--	--	--	2.2854	1.2420	9.7128	zzzzz
	90	NONJ	0.1884	--	--	--	--	1.1370	2.6220	2.9264	1.9657
		JACK	0.2260	--	--	--	--	1.0702	2.5310	3.8302	1.4089
	120	NONJ	0.2775	--	--	--	--	0.2631	0.1986	3.6984	1.1031
		JACK	0.2769	--	--	--	--	0.3255	0.2672	0.5822	-1.3374

zzzzz indicates that large outliers precluded tests

Table A10. Significance level of test for significant skewness; Logistic model; jackknifed within 100 replicates.

			ERROR-M								
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	NS	***	***	***	***	***	***	***	***
		JACK	NS	***	***	***	***	***	***	***	***
	90	NONJ	NS	**	***	***	***	***	***	***	***
		JACK	NS	**	***	***	*	***	*	***	***
	120	NONJ	NS	*	**	*	***	NS	**	***	***
		JACK	NS	*	*	**	***	NS	NS	*	***
1000	70	NONJ	NS	--	--	--	--	***	***	***	zzzzz
		JACK	***	--	--	--	--	***	***	***	zzzzz
	90	NONJ	NS	--	--	--	--	***	***	***	***
		JACK	NS	--	--	--	--	***	***	***	***
	120	NONJ	NS	--	--	--	--	NS	NS	***	***
		JACK	NS	--	--	--	--	NS	NS	*	***

zzzzz indicates that large outliers precluded tests

Table A11. The G2 statistic for kurtosis of $\hat{Y}_\infty$ from the KS test; Logistic model; jackknifed within 100 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	0.174	7.998	1.207	0.632	0.939	0.007	0.393	5.858	5.345
		JACK	-0.050	12.080	11.850	14.720	1.239	6.850	6.406	27.268	10.117
	90	NONJ	-0.525	1.440	3.882	17.800	7.261	2.271	17.891	13.974	5.775
		JACK	-0.592	1.663	5.130	38.820	19.007	1.029	3.487	22.066	15.605
	120	NONJ	-0.223	0.262	0.694	0.443	3.329	0.312	9.245	11.924	1.261
		JACK	-0.222	0.282	0.091	0.994	45.790	0.411	0.280	0.539	8.687
1000	70	NONJ	0.076	--	--	--	--	-0.090	-0.234	74.470	zzzzz
		JACK	-0.232	--	--	--	--	6.368	1.618	96.094	zzzzz
	90	NONJ	0.961	--	--	--	--	1.639	12.370	10.738	3.937
		JACK	0.883	--	--	--	--	2.043	16.560	17.841	9.181
	120	NONJ	-0.327	--	--	--	--	-0.133	0.697	24.343	1.699
		JACK	-0.363	--	--	--	--	-0.103	0.888	1.150	6.674

zzzzz indicates that large outliers precluded tests

Table A12. Significance level of test for significant kurtosis; Logistic model; jackknifed within 100 replicates.

	MAX		ERROR-M								
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	70	NONJ	NS	***	*	NS	NS	NS	NS	***	***
		JACK	NS	***	***	***	*	***	***	***	***
	90	NONJ	NS	**	***	***	***	***	***	***	***
		JACK	NS	***	***	***	***	*	***	***	***
	120	NONJ	NS	NS	NS	NS	***	NS	NS	***	**
		JACK	NS	NS	NS	*	***	NS	NS	NS	***
1000	70	NONJ	NS	--	--	--	--	NS	NS	***	zzzzz
		JACK	NS	--	--	--	--	***	**	***	zzzzz
	90	NONJ	*	--	--	--	--	***	***	***	***
		JACK	NS	--	--	--	--	***	***	***	***
	120	NONJ	NS	--	--	--	--	NS	NS	***	***
		JACK	NS	--	--	--	--	NS	NS	*	***

zzzzz indicates that large outliers precluded tests

APPENDIX B

Autocatalytic Model: Statistics for normality, skewness, and kurtosis of $\hat{Y}_\infty$, plus significance between jackknifed $\hat{Y}_\infty$ and standard $\hat{Y}_\infty$.

This appendix contains tables of statistics pertaining to $\hat{Y}_\infty$, using the Monomolecular growth model, where:

KS = Kolmogorov-Smirnov

ERROR-B = biological error propagated in the data

ERROR-M = measurement error added to the data set

MAX AGE = maximum age of sampled data

NONJ = nonjackknifed estimate from standard nonlinear regression

JACK = jackknifed estimate

std dev = standard deviation of the mean

std err = standard error of the estimate

NS = not significant at the 0.05 level

-- = no data for this combination

Table B1. The KS statistic (Dmax) for normality of $\hat{Y}_\infty$; Monomolecular model; jackknifed within 20 replicates.

ERROR-B	MAX AGE		ERROR-M								
			0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	0.09740	0.15943	0.09894	0.11346	0.19913	0.29727	0.12005	0.13048	0.22905
		JACK	0.13156	0.19897	0.21756	0.27048	0.28967	0.33813	0.25978	0.33467	0.22905
	100	NONJ	0.22215	0.14743	0.10751	0.17838	0.20097	0.12671	0.16509	0.27840	0.30095
		JACK	0.20968	0.15087	0.16671	0.23178	0.29538	0.11747	0.27808	0.31536	0.38650
	110	NONJ	0.15011	0.13138	0.23244	0.09793	0.21869	0.14009	0.25573	0.16920	0.27495
		JACK	0.15669	0.14244	0.08329	0.12090	0.33969	0.17486	0.28233	0.08873	0.40100
	120	NONJ	0.20918	0.17987	0.12749	0.17118	0.23355	0.19166	0.14808	0.17319	0.31991
		JACK	0.19996	0.17635	0.17032	0.14088	0.33368	0.17024	0.10891	0.14428	0.37412
1000	90	NONJ	0.08759	--	--	--	--	0.24003	0.17515	0.16873	0.24195
		JACK	0.09029	--	--	--	--	0.27632	0.21554	0.29377	0.17169
	100	NONJ	0.12233	--	--	--	--	0.11990	0.22909	0.23831	0.28485
		JACK	0.11067	--	--	--	--	0.09838	0.26187	0.23983	0.23928
	110	NONJ	0.13527	--	--	--	--	0.18471	0.17164	0.09411	0.25513
		JACK	0.11767	--	--	--	--	0.12207	0.22462	0.08645	0.30364
	120	NONJ	0.08403	--	--	--	--	0.14288	0.15944	0.11470	0.28706
		JACK	0.09575	--	--	--	--	0.10891	0.12924	0.14121	0.32601

Table B2. Significance level for test of significance of the KS statistic (Dmax); Monomolecular model; jackknifed within 20 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	NS	NS	NS	*	**	NS	NS	*
		JACK	NS	*	*	**	**	**	**	**	NS
	100	NONJ	*	NS	NS	NS	*	NS	NS	**	**
		JACK	*	NS	NS	**	**	NS	**	**	**
	110	NONJ	NS	NS	**	NS	*	NS	**	NS	**
		JACK	NS	NS	NS	NS	**	NS	**	NS	**
	120	NONJ	*	NS	NS	NS	**	*	NS	NS	**
		JACK	*	NS	NS	NS	**	NS	NS	NS	**
1000	90	NONJ	NS	--	--	--	--	**	NS	NS	**
		JACK	NS	--	--	--	--	**	*	**	NS
	100	NONJ	NS	--	--	--	--	NS	*	**	**
		JACK	NS	--	--	--	--	NS	**	**	**
	110	NONJ	NS	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	*	NS	**
	120	NONJ	NS	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	NS	NS	**

Table B3. The G1 statistic for skewness of $\hat{Y}_\infty$ from the KS test; Monomolecular model; jackknifed within 20 replicates.

ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	ERROR-M 20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	0.1922	1.8643	-0.2190	0.0847	0.7457	2.2836	0.5714	0.3121	0.9209
		JACK	0.8576	3.0050	1.0506	1.2312	1.6560	3.3920	1.9400	2.0650	1.3066
	100	NONJ	1.2203	0.4434	1.1119	0.4071	1.7882	1.0732	0.7096	1.5590	1.9108
		JACK	1.6018	0.7540	1.0348	1.0398	2.1921	0.6104	2.3067	2.2186	4.0850
	110	NONJ	0.6979	0.4312	2.5432	0.5280	1.5108	0.4997	2.8340	0.6515	1.7650
		JACK	0.6876	0.6284	0.4256	0.2077	3.7015	0.5203	3.2893	0.0751	3.7960
	120	NONJ	0.7913	1.0866	0.7334	0.9273	1.9297	0.7902	1.2516	0.7442	2.9780
		JACK	0.7812	1.0452	0.1241	0.6964	4.0700	0.7417	1.0510	0.8209	3.7490
1000	90	NONJ	-0.6840	--	--	--	--	1.7753	0.6010	0.5033	0.8947
		JACK	-0.1655	--	--	--	--	2.4016	1.4586	2.7889	0.9686
	100	NONJ	0.1415	--	--	--	--	0.2300	0.6140	1.6485	1.1946
		JACK	0.1626	--	--	--	--	0.2284	1.8569	2.0254	3.1276
	110	NONJ	-0.2312	--	--	--	--	0.7547	1.8269	0.3080	1.5255
		JACK	-0.2328	--	--	--	--	0.6265	1.8125	-0.3394	1.1638
	120	NONJ	-0.2032	--	--	--	--	0.2145	0.4500	0.0917	2.7172
		JACK	-0.1442	--	--	--	--	0.2754	0.3200	0.0196	3.0619

Table B4. Significance level of test for significant skewness; Monomolecular model; jackknifed within 20 replicates.

							ERROR-M				
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	**	NS	NS	NS	***	NS	NS	NS
		JACK	NS	***	NS	*	**	***	**	***	*
	100	NONJ	*	NS	*	NS	**	*	NS	**	**
		JACK	**	NS	NS	NS	***	NS	***	***	***
	110	NONJ	NS	NS	***	NS	**	NS	***	NS	**
		JACK	NS	NS	NS	NS	***	NS	***	NS	***
	120	NONJ	NS	*	NS	NS	**	NS	*	NS	***
		JACK	NS	NS	NS	NS	***	**	NS	NS	***
1000	90	NONJ	NS	--	--	--	--	**	NS	NS	NS
		JACK	NS	--	--	--	--	***	*	***	NS
	100	NONJ	NS	--	--	--	--	NS	NS	**	*
		JACK	NS	--	--	--	--	NS	**	***	***
	110	NONJ	NS	--	--	--	--	NS	**	NS	**
		JACK	NS	--	--	--	--	NS	**	NS	*
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	NS	NS	***

Table B5. The G2 statistic for kurtosis of $\hat{Y}_\infty$ from the KS test; Monomolecular model; jackknifed within 20 replicates.

							ERROR-M				
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	-0.4282	4.9580	-0.7918	-1.0578	-1.0497	4.9580	-0.1562	-1.2774	-0.4550
		JACK	0.6460	10.9700	0.5915	0.3078	1.6420	13.0000	4.3900	3.5900	1.4585
	100	NONJ	1.4659	-0.7865	2.6553	-1.2792	3.2757	2.7466	-0.9284	2.1296	3.9533
		JACK	3.5140	-0.3406	1.7886	0.7338	4.8399	0.8292	5.1068	8.6070	17.5460
	110	NONJ	-0.2601	-0.9276	8.3054	0.4262	2.2242	-0.4074	10.0340	-0.1822	2.3000
		JACK	-0.2682	-0.7878	0.2882	-0.7271	15.2940	-0.3919	12.4930	-0.3625	15.1040
	120	NONJ	0.3707	0.4047	-0.2280	0.6689	3.5388	-0.4886	1.4829	-0.0345	10.0800
		JACK	0.4869	0.2481	-0.8672	0.8311	17.4000	-0.5506	1.0840	0.8052	15.0000
1000	90	NONJ	0.0915	--	--	--	--	2.9780	-0.7795	-0.9519	-0.4119
		JACK	-1.0762	--	--	--	--	6.9600	1.9746	8.6700	0.6197
	100	NONJ	-0.9607	--	--	--	--	-0.3594	-1.2504	2.8528	0.0571
		JACK	-0.9743	--	--	--	--	-0.2028	3.6904	7.4481	12.0460
	110	NONJ	-1.0665	--	--	--	--	1.9694	4.8547	-0.6460	1.6818
		JACK	-0.8933	--	--	--	--	1.2867	4.3860	-0.3227	7.6490
	120	NONJ	-0.5941	--	--	--	--	-1.3600	-0.9050	-0.8428	8.7300
		JACK	-0.6053	--	--	--	--	-1.2416	-0.7964	0.9354	11.1300

Table B6. Significance level of test for significant kurtosis; Monomolecular model; jackknifed within 20 replicates.

			ERROR-M								
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	***	NS	NS	NS	***	NS	NS	NS
		JACK	NS	***	NS	NS	NS	***	***	**	NS
	100	NONJ	NS	NS	*	NS	**	*	NS	*	***
		JACK	**	NS	NS	NS	***	NS	***	***	***
	110	NONJ	NS	NS	***	NS	*	NS	***	NS	*
		JACK	NS	NS	NS	NS	***	NS	***	NS	***
	120	NONJ	NS	NS	NS	NS	**	NS	NS	NS	***
		JACK	NS	NS	NS	NS	***	NS	NS	NS	***
1000	90	NONJ	NS	--	--	--	--	**	NS	NS	NS
		JACK	NS	--	--	--	--	***	NS	***	NS
	100	NONJ	NS	--	--	--	--	NS	NS	**	NS
		JACK	NS	--	--	--	--	NS	**	***	***
	110	NONJ	NS	--	--	--	--	NS	***	NS	NS
		JACK	NS	--	--	--	--	NS	***	NS	***
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	NS	NS	***

Table B7. The KS statistic (Dmax) for normality of $\hat{Y}_\infty$; Monomolecular model; jackknifed within 100 replicates.

ERROR-B	MAX AGE		ERROR-M 0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	0.07243	0.11883	0.10221	0.13089	0.11072	0.12179	0.12633	0.12935	0.11620
		JACK	0.07137	0.15295	0.20843	0.24817	0.22590	0.20992	0.22568	0.22107	0.19933
	100	NONJ	0.11632	0.05618	0.15440	0.13568	0.14237	0.10996	0.12387	0.16987	0.19513
		JACK	0.09149	0.09207	0.18840	0.23991	0.24651	0.16380	0.19780	0.25812	0.32525
	110	NONJ	0.08249	0.08381	0.14546	0.17278	0.16481	0.05947	0.14932	0.16035	0.17465
		JACK	0.07663	0.07297	0.13850	0.17822	0.33230	0.06343	0.27227	0.28783	0.36657
	120	NONJ	0.06335	0.07256	0.09782	0.08381	0.24045	0.08568	0.10472	0.15199	0.15201
		JACK	0.05945	0.08890	0.06533	0.12789	0.34444	0.07345	0.07611	0.17204	0.16211
1000	90	NONJ	0.10013	--	--	--	--	0.12945	0.11361	0.15692	0.13718
		JACK	0.06443	--	--	--	--	0.22952	0.23428	0.22066	0.19906
	100	NONJ	0.09638	--	--	--	--	0.14467	0.10609	0.18379	0.20508
		JACK	0.08927	--	--	--	--	0.14465	0.18510	0.28066	0.33663
	110	NONJ	0.06830	--	--	--	--	0.04769	0.14528	0.14880	0.17728
		JACK	0.05241	--	--	--	--	0.04761	0.14509	0.16449	0.40710
	120	NONJ	0.06987	--	--	--	--	0.08727	0.08131	0.15212	0.16378
		JACK	0.07366	--	--	--	--	0.08974	0.07954	0.21226	0.16833

Table B8. Significance level for test of significance of the KS statistic (Dmax); Monomolecular model; jackknifed within 100 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	**	*	**	**	**	**	**	**
		JACK	NS	**	**	**	**	**	**	**	**
	100	NONJ	**	NS	**	**	**	**	**	**	**
		JACK	*	*	**	**	**	**	**	**	**
	110	NONJ	NS	NS	**	**	**	NS	**	**	**
		JACK	NS	NS	**	**	**	NS	**	**	**
	120	NONJ	NS	NS	*	NS	**	NS	**	**	**
		JACK	NS	*	NS	**	**	NS	NS	**	**
1000	90	NONJ	*	--	--	--	--	**	**	**	**
		JACK	NS	--	--	--	--	**	**	**	**
	100	NONJ	*	--	--	--	--	**	**	**	**
		JACK	*	--	--	--	--	**	**	**	**
	110	NONJ	NS	--	--	--	--	NS	**	**	**
		JACK	NS	--	--	--	--	NS	**	**	**
	120	NONJ	NS	--	--	--	--	NS	NS	**	**
		JACK	NS	--	--	--	--	*	NS	**	**

Table B9. The G1 statistic for skewness of $\hat{Y}_{\infty}$ from the KS test; Monomolecular model; jackknifed within 100 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	0.7117	0.6802	0.6554	0.4758	0.4303	0.6817	0.3005	1.0079	0.6135
		JACK	0.6859	1.2909	1.5948	1.3965	1.4306	2.1181	1.1380	1.9656	0.9321
	100	NONJ	0.6926	0.5460	1.4395	0.9813	1.4427	1.5604	1.1049	1.1643	1.1860
		JACK	0.7693	0.8460	2.1788	2.4613	2.7020	3.3070	1.8858	1.9132	2.8410
	110	NONJ	0.4639	0.7299	1.7048	1.9393	2.3968	0.5794	2.4880	2.0012	2.1464
		JACK	0.4603	0.8768	4.4976	3.0746	1.9853	0.6430	-5.9660	5.3181	0.7013
	120	NONJ	0.3285	0.8021	1.2309	1.1277	2.8264	0.7797	0.6247	2.6870	1.6400
		JACK	0.3176	0.7730	0.7634	1.3386	6.8906	0.8249	0.4176	4.6940	0.7157
1000	90	NONJ	0.7452	--	--	--	--	0.9123	0.6714	1.0106	0.7407
		JACK	0.7168	--	--	--	--	2.1854	2.3976	1.6216	1.2896
	100	NONJ	0.8263	--	--	--	--	1.4173	1.1158	1.1426	1.2049
		JACK	0.7866	--	--	--	--	0.8325	3.2653	2.7868	3.5630
	110	NONJ	0.4685	--	--	--	--	0.5289	1.8242	1.8618	4.1860
		JACK	0.3628	--	--	--	--	0.4993	1.9416	2.6248	9.4140
	120	NONJ	0.4084	--	--	--	--	0.5035	0.5277	3.5100	1.8689
		JACK	0.4205	--	--	--	--	0.5667	0.6111	6.3600	-0.1298

Table B10. Significance level of test for significant skewness; Monomolecular model; jackknifed within 100 replicates.

ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	ERROR-M 20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	**	**	**	NS	NS	**	NS	***	*
		JACK	**	***	***	***	***	***	***	***	***
	100	NONJ	**	*	***	***	***	***	***	***	***
		JACK	**	***	***	***	***	***	***	***	***
	110	NONJ	NS	**	***	***	***	*	***	***	***
		JACK	NS	***	***	***	***	**	***	***	**
	120	NONJ	NS	**	***	***	***	**	*	***	***
		JACK	NS	**	**	***	***	***	NS	***	**
1000	90	NONJ	**	--	--	--	--	***	**	***	**
		JACK	**	--	--	--	--	***	***	***	***
	100	NONJ	***	--	--	--	--	***	***	***	***
		JACK	**	--	--	--	--	***	***	***	***
	110	NONJ	NS	--	--	--	--	*	***	***	***
		JACK	NS	--	--	--	--	*	***	***	***
	120	NONJ	NS	--	--	--	--	*	*	***	***
		JACK	NS	--	--	--	--	*	*	***	***

Table B11. The G2 statistic for kurtosis of $\hat{Y}_\infty$ from the KS test; Monomolecular model; jackknifed within 100 replicates.

	MAX		ERROR-M								
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	0.213	-0.043	-0.486	-0.952	-0.856	-0.537	-1.191	0.932	-0.535
		JACK	0.223	9.540	1.988	0.891	1.674	4.985	0.843	4.956	0.833
	100	NONJ	0.179	0.579	1.885	0.479	3.221	3.607	0.830	0.487	0.443
		JACK	0.494	1.119	6.505	7.659	8.512	16.595	8.814	5.865	10.575
	110	NONJ	*	1.067	4.270	4.324	7.424	0.538	9.412	5.156	5.631
		JACK	0.104	1.759	31.780	12.945	37.360	0.738	52.900	32.730	37.530
	120	NONJ	-0.061	1.118	2.248	2.134	9.770	0.934	0.081	11.300	3.238
		JACK	0.079	1.110	0.466	3.631	53.000	1.044	-0.508	33.700	19.000
1000	90	NONJ	1.934	--	--	--	--	0.121	-0.444	0.764	-0.282
		JACK	1.231	--	--	--	--	4.675	6.017	3.566	1.800
	100	NONJ	1.747	--	--	--	--	2.734	1.407	0.357	0.581
		JACK	1.387	--	--	--	--	3.485	17.220	18.700	18.437
	110	NONJ	0.599	--	--	--	--	0.418	4.577	5.232	25.399
		JACK	0.346	--	--	--	--	0.363	5.775	10.264	91.890
	120	NONJ	-0.124	--	--	--	--	-0.029	1.011	18.600	3.835
		JACK	-0.127	--	--	--	--	-0.082	0.968	51.900	8.139

Table B12. Significance level of test for significant kurtosis; Monomolecular model; jackknifed within 100 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	NS	NS	*	NS	NS	*	NS	NS
		JACK	NS	***	***	NS	***	***	NS	***	NS
	100	NONJ	NS	NS	***	NS	***	***	NS	NS	NS
		JACK	NS	*	***	***	***	***	***	***	***
	110	NONJ	NS	*	***	***	***	NS	***	***	***
		JACK	NS	***	***	***	***	NS	***	***	***
	120	NONJ	NS	*	***	***	***	NS	NS	***	***
		JACK	NS	*	NS	***	***	*	NS	***	***
1000	90	NONJ	***	--	--	--	--	NS	NS	NS	NS
		JACK	*	--	--	--	--	***	***	***	***
	100	NONJ	***	--	--	--	--	***	**	NS	NS
		JACK	**	--	--	--	--	***	***	***	***
	110	NONJ	NS	--	--	--	--	NS	***	***	***
		JACK	NS	--	--	--	--	NS	*	***	***

APPENDIX C

Chapman-Richards Model: Statistics for normality, skewness, and kurtosis of $\hat{Y}_\infty$, plus significance between jackknifed $\hat{Y}_\infty$ and standard $\hat{Y}_\infty$.

This appendix contains tables of statistics pertaining to $\hat{Y}_\infty$, using the Chapman-Richards growth model, where:

KS = Kolmogorov-Smirnov
ERROR-B = biological error propagated in the data
ERROR-M = measurement error added to the data set
MAX AGE = maximum age of sampled data
NONJ = nonjackknifed estimate from standard nonlinear regression
JACK = jackknifed estimate
std dev = standard deviation of the mean
std err = standard error of the estimate
NS = not significant at the 0.05 level
-- = no data for this combination

Table C1. The KS statistic (Dmax) for normality of $\hat{Y}_{\infty}$; Chapman-Richards model; jackknifed within 20 replicates.

	MAX						ERROR-M				
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	0.11030	0.11514	0.13064	0.18383	0.20854	0.16167	0.28327	0.09468	0.27056
		JACK	0.12732	0.11686	0.09584	0.14391	0.10497	0.06832	0.12031	0.16483	0.22615
	120	NONJ	0.17334	0.14042	0.13369	0.15346	0.16941	0.13634	0.17951	0.14376	0.41391
		JACK	0.17334	0.16542	0.09140	0.19190	0.10688	0.11007	0.13105	0.10906	0.25889
500	90	NONJ	0.16246	--	--	--	--	0.14192	0.32219	0.17134	0.28428
		JACK	0.09214	--	--	--	--	0.13974	0.32920	0.15899	0.26780
	120	NONJ	0.10677	--	--	--	--	0.09373	0.11173	0.13487	0.30051
		JACK	0.12655	--	--	--	--	0.09103	0.12457	0.11275	0.29074
1000	90	NONJ	0.07069	--	--	--	--	0.12681	0.26586	0.18042	0.26133
		JACK	0.12463	--	--	--	--	0.12598	0.29269	0.17363	0.26340
	120	NONJ	0.06524	--	--	--	--	0.13521	0.18101	0.09611	0.33745
		JACK	0.09752	--	--	--	--	0.12351	0.22334	0.18712	0.29169

Table C2. Significance level for test of significance of the KS statistic (Dmax); Chapman-Richards model; jackknifed within 20 replicates.

	MAX		ERROR-M								
ERROR-B	AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	NS	NS	NS	*	NS	**	NS	**
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	*
	120	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	**
		JACK	NS	NS	NS	*	NS	NS	NS	NS	**
500	90	NONJ	NS	--	--	--	--	NS	**	NS	**
		JACK	NS	--	--	--	--	NS	**	NS	**
	120	NONJ	NS	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	NS	NS	**
1000	90	NONJ	NS	--	--	--	--	NS	**	NS	**
		JACK	NS	--	--	--	--	NS	**	NS	**
	120	NONJ	NS	--	--	--	--	NS	NS	NS	**
		JACK	NS	--	--	--	--	NS	*	NS	**

Table C3. The G1 statistic for skewness of $\hat{Y}_\infty$ from the KS test; Chapman-Richards model; jackknifed within 20 replicates.

ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	ERROR-M 20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	0.3083	0.3979	0.2106	2.2180	1.2614	0.6046	3.1306	0.4263	2.0042
		JACK	0.1445	0.5658	-0.8344	0.0706	-0.5971	-0.6463	-1.0635	-0.2286	-1.7081
	120	NONJ	0.5426	0.3038	0.0238	0.3538	1.4542	0.4688	0.9214	0.4327	4.2070
		JACK	0.5426	0.9819	-0.7068	2.1125	-0.4780	0.0886	0.4326	0.4740	3.0139
500	90	NONJ	-0.7000	--	--	--	--	0.5190	3.6610	1.2550	2.6066
		JACK	-0.4030	--	--	--	--	-1.1197	-3.8961	-1.6614	-2.3618
	120	NONJ	0.1258	--	--	--	--	-0.1883	0.2479	0.2934	3.7584
		JACK	0.1432	--	--	--	--	-0.4017	0.6542	1.7244	-2.8993
1000	90	NONJ	-0.3554	--	--	--	--	0.8591	3.5697	0.5658	1.9583
		JACK	-0.4139	--	--	--	--	-1.5047	-3.8205	-0.8476	-1.7921
	120	NONJ	-0.2157	--	--	--	--	0.1221	0.9330	0.0132	3.9190
		JACK	0.2867	--	--	--	--	0.6953	1.7391	1.4128	-2.5846

Table C4. Significance level of test for significant skewness; Chapman-Richards model; jackknifed within 20 replicates.

ERROR-B	MAX AGE		ERROR-M								
			0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	NS	NS	***	*	NS	***	NS	***
		JACK	NS	NS	NS	NS	NS	NS	NS	NS	**
	120	NONJ	NS	NS	NS	NS	*	NS	NS	NS	***
		JACK	NS	NS	NS	***	NS	NS	NS	NS	***
500	90	NONJ	NS	--	--	--	--	NS	***	*	***
		JACK	NS	--	--	--	--	*	***	**	***
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	NS	**	***
1000	90	NONJ	NS	--	--	--	--	NS	***	NS	**
		JACK	NS	--	--	--	--	**	***	NS	**
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	**	*	***

Table C5. The G2 statistic for kurtosis of $\hat{Y}_\infty$ from the KS test; Chapman-Richards model; jackknifed within 20 replicates.

			ERROR-M								
ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	-0.0819	-1.1478	-1.0095	6.6250	1.3194	-0.0942	11.9100	-0.6052	4.3119
		JACK	0.1753	-0.8609	0.7553	0.3601	0.0490	0.5395	4.1463	0.7382	2.1055
	120	NONJ	-0.0263	-0.9797	-1.4015	-0.6488	1.7029	-0.5872	1.0893	-0.9667	18.3300
		JACK	-0.0263	0.6858	1.1082	6.3016	0.2318	-0.3881	2.8866	-0.2647	11.7047
500	90	NONJ	1.4805	--	--	--	--	0.1364	15.0900	2.0419	7.9012
		JACK	0.9398	--	--	--	--	0.5748	16.3000	5.7479	5.6644
	120	NONJ	-0.8982	--	--	--	--	0.1482	-0.6184	-1.2134	15.6300
		JACK	-0.8047	--	--	--	--	0.2561	-0.4408	4.4981	9.6360
1000	90	NONJ	-0.3095	--	--	--	--	0.5599	14.4520	-0.3841	3.6500
		JACK	-0.5359	--	--	--	--	5.1805	16.0910	4.1163	2.5246
	120	NONJ	-0.2591	--	--	--	--	-0.9218	0.5057	-0.8764	16.6000
		JACK	0.4529	--	--	--	--	-0.1651	6.8123	2.4920	7.5153

Table C6. Significance level of test for significant kurtosis; Chapman-Richards model; jackknifed within 20 replicates.

ERROR-B	MAX AGE		0	5*AGE	10*AGE	15*AGE	ERROR-M 20*AGE	500	1000	1500	2000
15*AGE	90	NONJ	NS	NS	NS	***	NS	NS	***	NS	***
		JACK	NS	NS	NS	NS	NS	NS	***	NS	*
	120	NONJ	NS	NS	NS	NS	NS	NS	NS	NS	***
		JACK	NS	NS	NS	***	NS	NS	**	NS	***
500	90	NONJ	NS	--	--	--	--	NS	***	NS	***
		JACK	NS	--	--	--	--	NS	***	***	***
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	NS	***	***
1000	90	NONJ	NS	--	--	--	--	NS	***	NS	**
		JACK	NS	--	--	--	--	***	***	***	*
	120	NONJ	NS	--	--	--	--	NS	NS	NS	***
		JACK	NS	--	--	--	--	NS	***	*	***

APPENDIX D

Examples of growth data generated from the Logistic growth function, containing propagated biological errors and added measurement errors, of either additive or multiplicative type. Data were generated at each 5-year interval, with biological error also introduced at each 5-year interval. Measurement error was added to the completed data set.

Figure D1. Scattergram of growth data generated from the Logistic growth function; biological error = 15*AGE, and measurement error = 0.

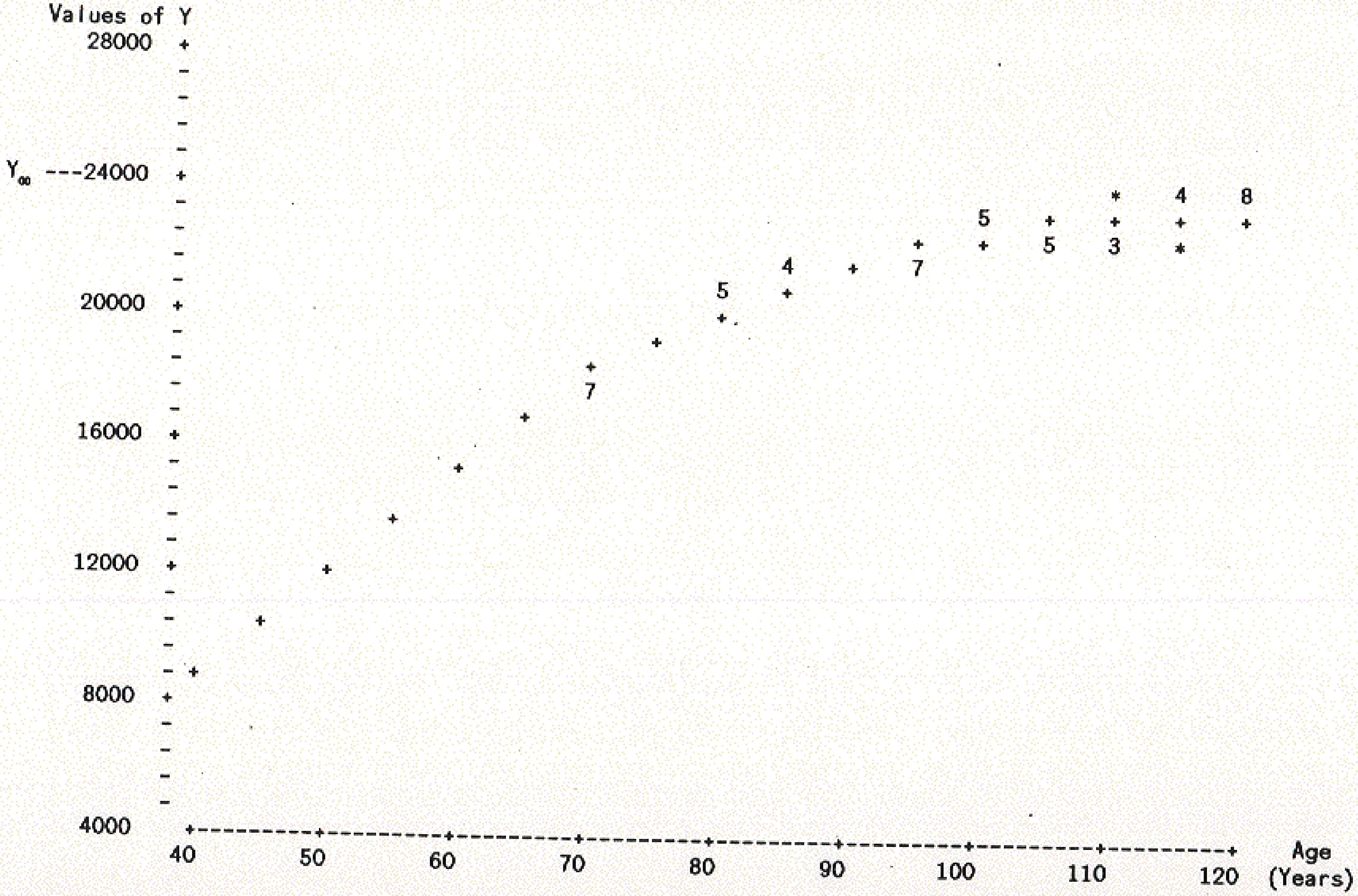

Values of Y
28000
Y_∞ ---24000
20000
16000
12000
8000
4000
40
50
60
70
80
90
100
110
120
Age
(Years)
7
5
4
7
5
5
3
4
8

Figure D2. Scattergram of growth data generated from the Logistic growth function; biological error = 1000, and measurement error = 0.

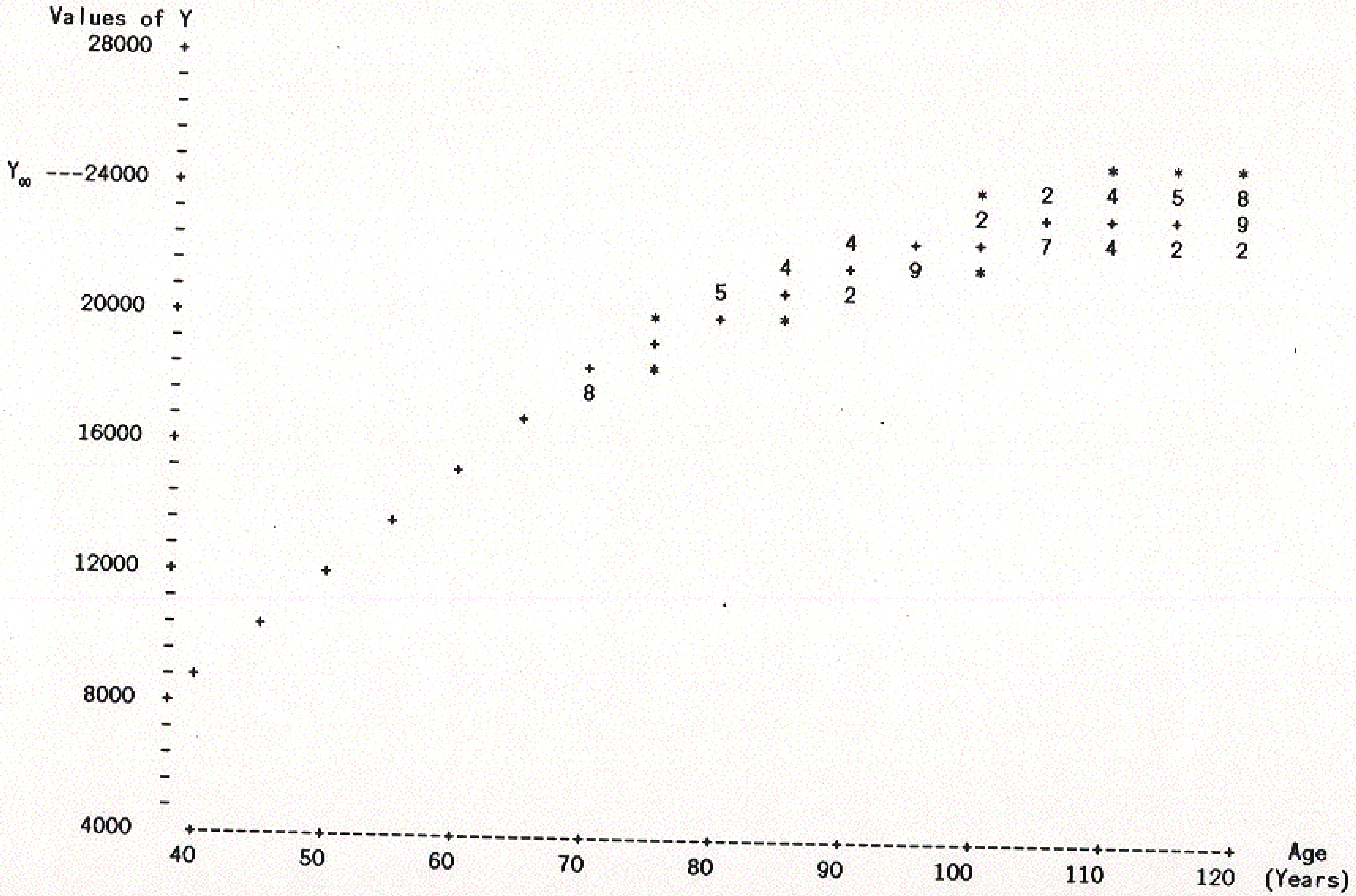

Values of Y
28000
Y∞ ---24000
20000
16000
12000
8000
4000
40
50
60
70
80
90
100
110
120
Age
(Years)
8
5
4
4
2
9
2
2
7
4
4
5
2
8
9
2

Figure D3. Scattergram of growth data generated from the Logistic growth function; biological error = 15*AGE, and measurement error = 15*AGE.

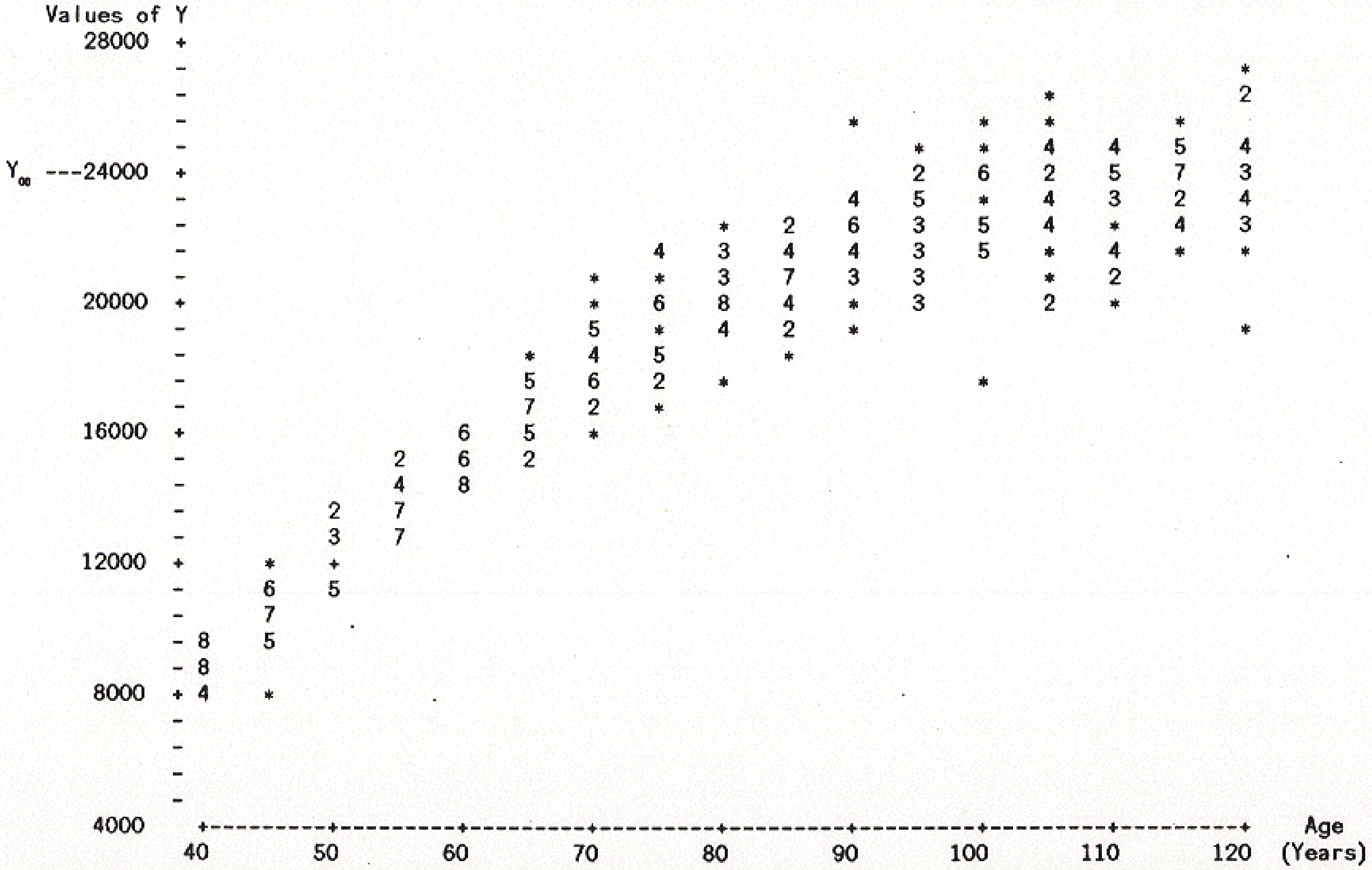

Values of Y
28000
Y_∞ ---24000
20000
16000
12000
8000
4000
40
50
60
70
80
90
100
110
120
Age (Years)

Figure D4. Scattergram of growth data generated from the Logistic growth function; biological error = 15*AGE, and measurement error = 1000.

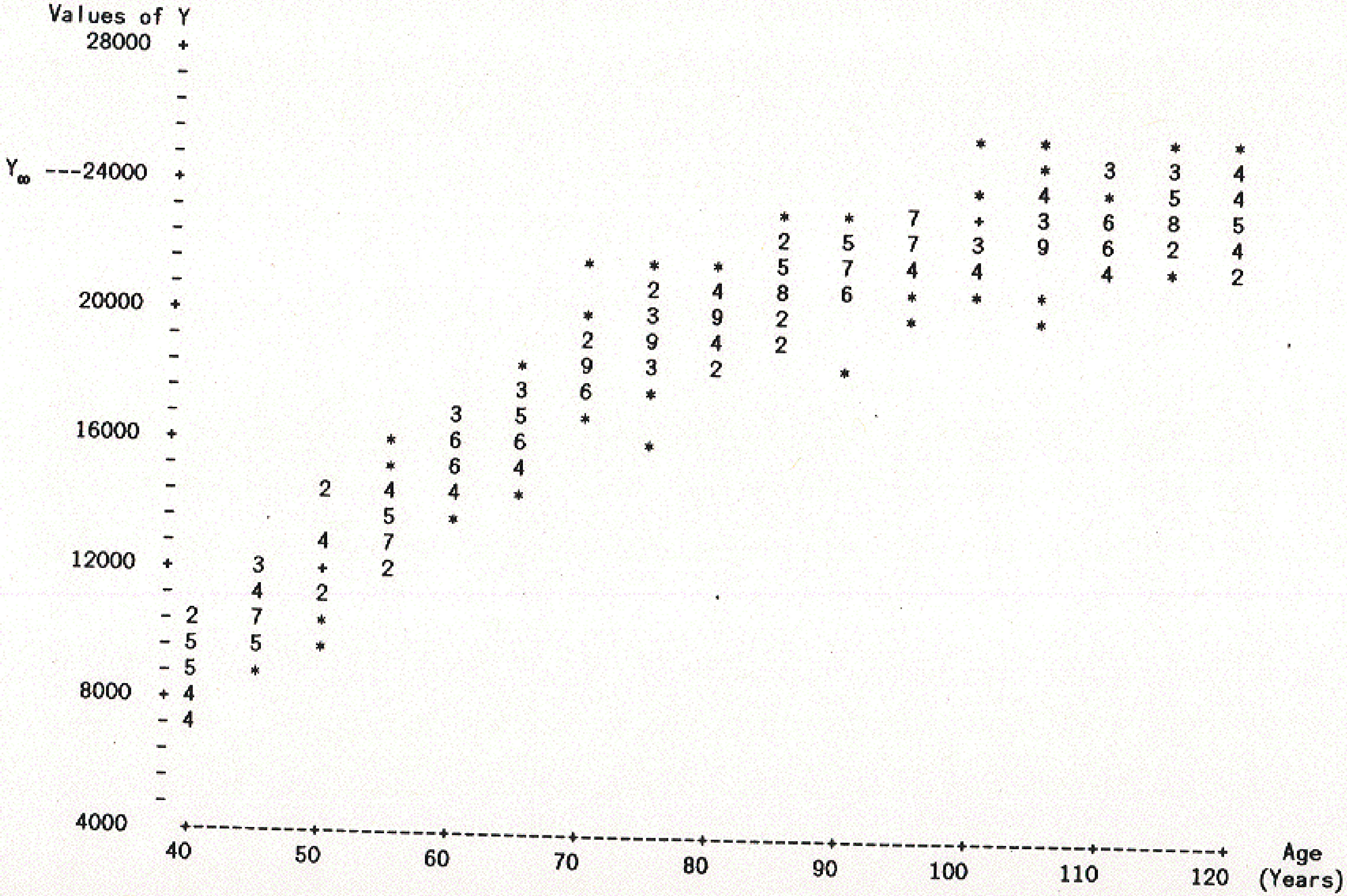
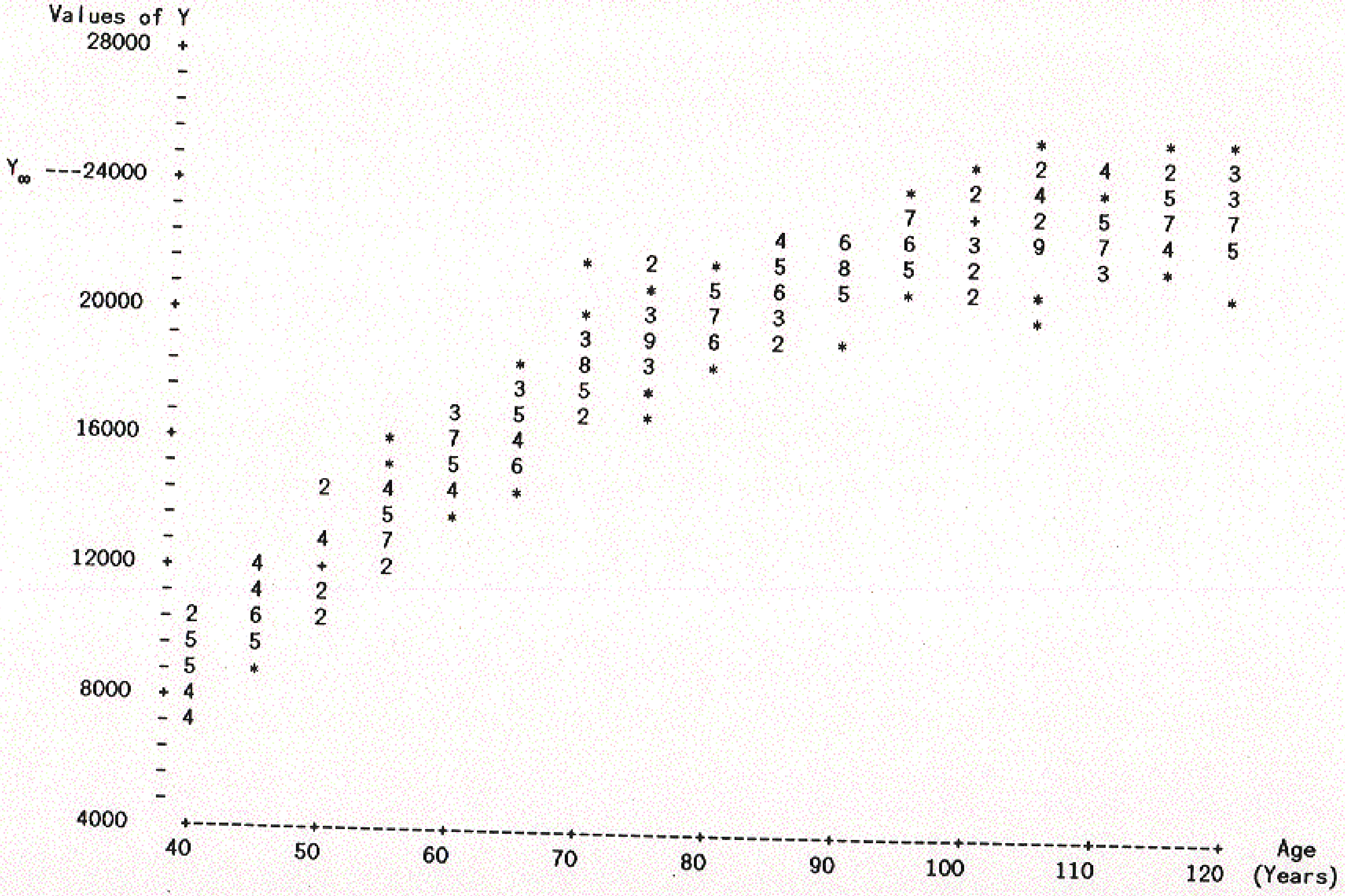

Values of Y
28000
Y∞ ---24000
20000
16000
12000
8000
4000
40
50
60
70
80
90
100
110
120
Age (Years)

Figure D5. Scattergram of growth data generated from the Logistic growth function; biological error = 1000, and measurement error = 1000.


Values of Y
28000
Y∞ ---24000
20000
16000
12000
8000
4000
40
50
60
70
80
90
100
110
120
Age
(Years)

APPENDIX E

Classical error propagation formulae for single estimates, and situations when two or more estimates are linked together to form a final estimate.

Simple approximations of error can usually be obtained with a little algebra, whereas more complicated error propagation is derived through the calculus using the principle of least squares or some other suitable method.

The propagation of error has been discussed by numerous authors such as Deming (1964), Tippett (1950, 1952), Bevington (1969), Tukey (1958a, 1958b, 1958c), Topping (1972), and Clifford (1973). The classical propagation formulae, using the linear term in Taylor's series, assume the errors to be small. Thus, if $y = f(x)$ and if Δx is the error in x, and Δy is likewise the error in y, then the error (Δy) in y is approximated by $\Delta x \frac{dy}{dx}$ or $\Delta x \cdot f'(x)$.

This error propagation is exact in the linear case and approximate for a nonlinear model. As an example, consider tree height as a function of tree diameter -- H(D). Then the above approximate formula in this case becomes:

$$\Delta H = \Delta D \cdot H'(D) \quad \ldots\ldots\ldots\ldots (1)$$

Suppose we have two alternative equations expressing H as a function of D:

(a) $H = 10.0 + 5.0\,(D)$ . . . . (2)

(b) $H = 10.0 + 0.5\,(D)^2$ . . . . (3)

Then the respective error propagations or approximate error formulations are:

(c) $\Delta H = \Delta D(5)$ . . . . (4)

(d) $\Delta H = \Delta D(1.0)(D)$ . . . . (5)

For these H-D relationships, each of which may be appropriate equations for their respective forest stands, Table E1 shows possible values of error in diameter with corresponding approximate errors and true errors in height.

Suppose that D = 10 is correct for either stand. Clearly, if D is taken to be 11 inches (i.e. $\Delta D = 1$), then the error in height (ΔH) should be 5 feet for equation (2) and 10.5 feet for equation (3). From our error propagation formulae we would compute

$$\hat{\Delta H} = \Delta D(5) = 1 \times 5 = 5 \text{ for the linear model}$$

and

$$\hat{\Delta H} = \Delta D(1.0)(D) = 1 \times 1 \times 10 = 10 \text{ for the nonlinear model.}$$

Thus the propagation formula (equation 1) is exact in the linear case and approximate (off by 0.5 feet) in the nonlinear case. For a larger error of 2 inches, the propagation formula is still exact for the linear model but more inexact for the nonlinear model.

Table E1. Example of propagating error from diameter to height for both the linear case and the nonlinear case.

D	ΔD	Linear H(D) Formula (2)	True Error	$\hat{\Delta H}$	Nonlinear H(D)* Formula (3)	True Error	$\hat{\Delta H}$*
10	0	60	0	0	60.0	--	
11	1	65	5	5	70.5	10.5	10
12	2	70	10	10	82.0	22	24

Extending Taylor's series for approximating small errors in a function of several measured variables, consider F = f(x,y,z) where x, y, and z have small errors Δx, Δy, and Δz. The error ΔF can be approximated as

$$\Delta F \simeq \frac{\partial F}{\partial x}\Delta x + \frac{\partial F}{\partial y}\Delta y + \frac{\partial F}{\partial z}\Delta z = F_x\,\Delta x + F_y\,\Delta y + F_z\,\Delta z \quad \ldots\ldots \text{(6)}$$

Topping (1972) refers to this result as the "principle of superposition of errors." If we square both sides of the equation, we get

$$\begin{aligned}(\Delta F)^2 &= (F_x\,\Delta x)^2 + (F_y\,\Delta y)^2 + (F_z\,\Delta z)^2\\ &\quad + 2F_x F_y\,\Delta x\,\Delta y + 2F_x F_z\,\Delta x\,\Delta z + 2F_y F_z\,\Delta y\,\Delta z \quad \ldots\ldots \text{(7)}\end{aligned}$$

Replacing each term by its average value and letting Δx, Δy, and Δz have variances $\pm\sigma_x^2$, $\pm\sigma_y^2$, and $\pm\sigma_z^2$, respectively, then

$$\begin{aligned}\sigma_F^2 &\simeq (F_x\,\sigma_x)^2 + (F_y\,\sigma_y)^2 + (F_z\,\sigma_z)^2\\ &\quad + 2(F_x F_y\,\sigma_x\,\sigma_y\,r_{xy} + F_x F_z\,\sigma_x\,\sigma_z\,r_{xz} + F_y F_z\,\sigma_y\,\sigma_z\,r_{yz}) \quad \ldots \text{(8)}\end{aligned}$$

where r_{xy}, r_{xz}, r_{yz} = respective correlations between Δx and Δy, Δx and Δz, Δy and Δz.

This reduces to

$$\sigma_F^2 = (F_x\,\sigma_x)^2 + (F_y\,\sigma_y)^2 + (F_z\,\sigma_z)^2 \quad \ldots\ldots\ldots\ldots\ldots \text{(9)}$$

for Δx, Δy, Δz uncorrelated.

Deming (1964) calls this expression the propagation of mean square error or propagation of variance.

In general, if errors $e_1, e_2, \ldots e_n$ are uncorrelated, the standard error of any function of means $x_1, x_2, \ldots, x_n$, can be denoted by σ and given by

$$\sigma^2 = (F_{x_1} \sigma_1)^2 + (F_{x_2} \sigma_2)^2 + \ . \ . \ . + (F_{x_n} \sigma_n)^2 \quad \ldots\ldots\ldots (10)$$

of which the standard errors of compound quantities such as the sum, product, multiple, and power are special cases (Topping, 1972). Thus, the standard error of

$$x_1 + x_2 \text{ is } \sqrt{(\sigma_1^2 + \sigma_2^2)} \quad \ldots\ldots\ldots\ldots\ldots\ldots (11)$$

$$x_1 - x_2 \text{ is } \sqrt{(\sigma_1^2 + \sigma_2^2)} \quad \ldots\ldots\ldots\ldots\ldots\ldots (12)$$

$$kx_1 \text{ is } k\sigma_1 \quad \ldots\ldots\ldots\ldots\ldots\ldots (13)$$

$$x_1 \ x_2 \text{ is } \sqrt{(x_1^2 \ \sigma_2^2 + x_2^2 \ \sigma_1^2)} \quad \ldots\ldots\ldots\ldots\ldots\ldots (14)$$

$$x_1 \ x_2 \ x_3 \text{ is } \sigma \text{ where } \left[\sigma/(x_1 \ x_2 \ x_3)\right]^2 = \left(\frac{\sigma_1}{x_1}\right)^2 + \left(\frac{\sigma_2}{x_2}\right)^2 + \left(\frac{\sigma_3}{x_3}\right)^2 \quad \ldots (15)$$

$$x_1^k \text{ is } \sigma \text{ where } \frac{\sigma}{x_1^k} = \frac{k\sigma_1}{x_1} \text{ or } \sigma = k \ \sigma_1 \ x_1^{k-1} \quad \ldots\ldots\ldots\ldots (16)$$

Consider the cross-sectional area of a tree stem as a power function (#6 above) where

$$A = \pi r^2 = \pi d^2/4 \quad \ldots\ldots\ldots\ldots\ldots\ldots (17)$$

For an error in radius r, the resulting error in area A is

$$\Delta A = \frac{\partial A}{\partial r} \Delta r = 2\pi r \ \Delta r = \frac{2A}{r} \Delta r \quad \ldots\ldots\ldots\ldots\ldots\ldots (18)$$

and thus the fractional error in area is

$$\frac{\Delta A}{A} = \frac{2\ \Delta r}{r} = \frac{2\ \Delta d}{d} \qquad \ldots\ldots\ldots\ldots\ldots\ldots\ldots (19)$$

(i.e., 5% error in r or d results in a 10% error in A).

Tukey (1958a) notes that "...the classical propagation formula is much better than seems to be usually recognized." Keyfitz (1966), through linkage of successive differentials, utilized these classical propagation formulae to derive variances of complex demographic functions.

The propagation of error, as already reviewed, assumes that $F = f(x_1, x_2, \ldots x_n)$ is differentiable ($\frac{\partial F}{\partial x_n}$ exists). However, if the function has no continuous derivative or, in fact, is intractable, methods other than classical propagation formulae may have to be utilized. An example of this need can be found in the concept of statistical tolerancing for assembly line quality control (Ku, 1966) in which the component parts of a mechanism are considered to be as important as the final product. Evans (1974, 1975) provides a good review of statistical tolerancing, in which an iterative process (trial and error) involves working back and forth between tolerances of mechanism and individual components, until tolerances (probability distribution) of the latter are deemed satisfactory.

Evans (1975) outlines methods for estimating moments of a response distribution of error:

i) linear propagation of error

ii) nonlinear propagation of error

iii) quadrature techniques

iv) Monte Carlo approach

He suggests computing numerical estimates of the derivatives, using nonlinear error propagation derived from expansion (Taylor's) about means up to the 6th order. One could thus make use of co-moments of higher orders as expounded upon by Tukey (1958a, b, c), who points out that "...the methods of using higher cumulants are often of most value when they demonstrate the unimportance of the correction." Again, if the derivative is unavailable, Evans suggests using a numerical approach to integration (quadrature technique) and, finally, the Monte Carlo method, which does not limit precision.

VITA

Charles Edward Peterson, Jr. was born May 11, 1947 in Volga, South Dakota, and raised on a farm near Arlington, South Dakota. He attended Laketon District #37 for eight years of elementary education, followed by four years of secondary education at Arlington High School. The period of January, 1967 to November, 1969 was spent in the U. S. Army, after which he enrolled at the University of South Dakota. He graduated in 1973 with a Bachelor of Science degree in mathematics, and added a Master of Science degree in forest management from the University of Washington in 1975. From 1975 to 1980 he was employed as biometrician for the Regional Forest Nutrition Research Project at the University of Washington. From 1980 until present he has served as Mensuration Director on the same project.