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RAPID PARAMETER ESTIMATION OF THREE PARAMETER NONLINEAR GROWTH MODELS

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ABSTRACT

The aim of this study is to determine a suitable method to estimate the parameters of some non-linear growth models using various methods of estimation. Six different estimation methods are used for estimating the parameters of the Monomolecular, Gompertz and Logistic growth models. Three different forestry data sets are used for testing the validity of the methods. The best fit method is selected on the basis of root mean square error (RMSE). It is found that the first four methods of estimation used in this paper are very useful to specify the initial values in the estimation of the parameters using any iterative procedures. It is noted that the most suitable growth model for the top height growth data is the Gompertz model which may be obtained by estimating the parameters using the Newton-Raphson method under the assumption that the rate parameter (k) is known. For the same method, the Gompertz growth model also gives the proper explanation for cumulative basal area production. The Logistic growth model is found to be most suitable for the mean diameter at breast height with the Composite method assuming that the rate parameter $(k)$is known from method of three partial sums.

Keywords: *Gompertz model, Logistic model, Monomolecular model, Nonlinear growth model, parameter estimation.*

1. INTRODUCTION

Growth is defined as variation and development in tissues and organs of an organism over time. Growth model is one type of simplified representation of a real system, which represents the behaviour of the system. The three parameter non-linear models, Monomolecular, Gompertz and Logistic are commonly used to determine the growth and development of various systems [5, 6]. These models are particular cases of the generalized Chapman-Richards function [8]. Many forestry researchers made extensive and profound studies on these models [3, 8, 13, 14]. In this study, the growth models Monomolecular, Gompertz and Logistic, which are special cases of the generalized Chapman- Richards function for parameter $m = 0, m = 1$, and $m = 2$ respectively, which are widely used by forestry scholars, have been selected to fit by estimating the parameters using various method of estimations.

Logistic model was developed by Belgian mathematician Pierre Verhulst, who suggested that the rate of population increase may be limited, that is, it may depend on population density. At low densities, the population growth rate is high. Population growth rate declines with population numbers. The dynamics of the population is described by the differential equation:

$$\frac{dw/dt}{\alpha - w} = b_0 + b_1 w, \tag{1}$$

where b_0, b_1 are constant and w and t are the dependent and independent respectively. Which has the following solution

$$\exp\{(b_0 + b_1\alpha)t\} = \beta(w + b_0/b_1)(\alpha - w)^{-1}.$$

If $w(-\infty) = 0$, b_0 must be zero. Hence the logistic growth model is given by

$$w(t) = \frac{\alpha}{(1+\beta \exp(-kt))}. \tag{2}$$

where $k = b_1\alpha$ is related to the rate of increasing of w, α is the upper asymptote and β is a location parameter[10]. The curve has an S-shape and all the parameters are positive. Also the shape of the curve is symmetric about its point of inflection [1].

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The mathematical representation of monomolecular growth is borrowed from physical chemistry, where it describes a first order irreversible chemical reaction. In plant nutrition and soil fertility it is also known as the Mitscherlich growth. The monomolecular model has no inflection point and the growth rate decrease linearly as size increasing. Then,

$$\frac{dw}{dt} = k(\alpha - w), \tag{3}$$

where w is the expected size of an organism at time t, α represents the limiting size of the organism and k is the growth rate parameter [1]. From this differential equation, the required model may be written as

$$w(t) = \alpha(1 - \beta \exp(-kt)), \tag{4}$$

where β is the biological constant. This function rises steadily from a point $\alpha(1-\beta)$to the limiting value of α.

The Gompertz Model named after Benjamin Gompertz (1779 – 1865). Gompertz model is a sigmoid function. The Gompertz equation arises from models of self-limited growth where the rate decreases exponentially with time. The model was first introduced to describe the growth in the number of tumor cells which usually follows a sigmoidal growth pattern. The model is a solution of the differential equation

$$\frac{dw}{dt} = kw \log\left(\frac{\alpha}{w}\right). \tag{5}$$

By integrating (5), the Gompertz model may be obtained as

$$w(t) = \alpha \exp(-\beta \exp(-kt)), \tag{6}$$

where w is the number of tumor cells at time t, $\alpha > 0$ is the upper limit, $\beta > 0$ is the biological constant, $k > 0$ is the parameter governing the rate at which the response variable approaches its potential maximum [3,4]. Although this curve is an S-shaped one like the logistic. It is not symmetrical about its point of inflection [1].

Nonlinear models are more difficult to specify and estimate the parameters than linear models. But for prediction purpose it is very important to distinguish these parameters properly. Lots of methods of estimation were developed by various authors[3, 9, 10, 12]. The aim of the paper is to estimate the parameters of the models by using various methods of estimation. By selecting appropriate method of estimation, the best fit model may be obtained based on three sets of well-known forestry data sets. Also the initial (guess) value specification plays a very important role in parameter estimation of nonlinear models using certain iterative methods. The first four methods of this paper will provide the initial value specification for the parameters of Monomolecular, Gompertz and Logistic growth models.

2. MATERIAL AND METHODS

The top height age data originated from the Bowmont Norway spruce thinning experiment, sample plot 3661 [3] has been considered. Top height age data were repeatedly measured on a five year cycle from age 20 to 64 and are presented in Table i. The cumulative basal area production and mean diameter at breast height [2] are also used for testing the validity of the methods.

Table i. Top height growth data from Bowmont Norway spruce thinning experiment, sample plot 3661 [3].

Top height (m)	7.3	9.0	10.9	12.6	13.9	15.4	16.9	18.2	19.0	20
Age (year)	20	25	30	35	40	45	50	55	60	64

The Monomolecular, Gompertz and Logistic nonlinear growth models quantifying the top height age data can be expressed as:

$$w_i = f(t_i, \mathbf{B}) + \varepsilon_i, \tag{7}$$

$i = 1,2,\cdots,n$, where n be the number of observations, w is the response variable, t is the independent variable, **B** is the vector of parameters α, β and k. ε_i is a random error in the model with mean zero and constant variance. Root mean square error (RMSE) may be used to select the best fit growth model with a suitable method of estimation for the parameters. The best fitted growth model is generally selected based on lowest RMSE. A software package has been developed in FORTRAN 77 for the fitting of the models. The following six methods of estimation have been considered for selecting the best fit model based on RMSE.

2.1 METHOD OF ESTIMATION

2.1.1 Method A: Estimation based on three equidistant points.

In this method, we use three equidistant points, t_1, t_2, t_3, from the given data set. Let n be the number of observations, t_2 be the $\frac{t_1+n}{2}th$ observation and t_1 be the observation between the first observation and the $(n-2)th$ observation so that the RMSE is least corresponding to that observation.

Let $d = t_2 - t_1$, then t_3 be the $(t_2 + d)th$ observation. Then the required parameter estimates for the Monomolecular growth model are:

$$\hat{\alpha} = \frac{w_2^2 - w_1 w_3}{2w_2 - w_1 - w_3},$$

$$\hat{\beta} = \frac{(w_2 - w_1)^2}{w_2^2 - w_1 w_3}\left(\frac{w_2 - w_1}{w_3 - w_2}\right)^{t_1/d},$$

$$\hat{k} = \frac{1}{d}\ln\left(\frac{w_2 - w_1}{w_3 - w_2}\right), \tag{8}$$

where $y_i = w_{t_i}$ for $i = 1, 2$ and 3.

The required parameter estimations for the Gompertz growth model are:

$$\hat{\alpha} = \exp\left(\frac{y_2^2 - y_1 y_3}{2y_2 - y_1 - y_3}\right),$$

$$\hat{\beta} = -\left(\frac{(y_2 - y_1)^2}{y_3 - 2y_2 + y_1}\left(\frac{y_2 - y_1}{y_3 - y_2}\right)^{t_1/d}\right),$$

$$\hat{k} = \frac{1}{d}\ln\left(\frac{y_2 - y_1}{y_3 - y_2}\right), \tag{9}$$

where $y_i = \ln w_{t_i}$ for $i = 1, 2$ and 3.

The required parameter estimations for the Logistic growth model are:

$$\hat{\alpha} = \frac{2z_2 - z_1 - z_3}{z_2^2 - z_1 z_3},$$

$$\hat{\beta} = \frac{\left(\frac{(z_2 - z_1)^2}{(z_3 - 2z_2 + z_1)}\left(\frac{z_2 - z_1}{z_3 - z_2}\right)^{t_1/d}\right)}{\left(\frac{z_2^2 - z_1 z_3}{2z_2 - z_1 - z_3}\right)},$$

$$\hat{k} = \frac{1}{d}\ln\left(\frac{z_2 - z_1}{z_3 - z_2}\right), \tag{10}$$

where $z_i = \frac{1}{w_{t_i}}$ for $i = 1, 2$ and 3.

2.1.2 Method B: Estimation based on three partial sums.

For Monomolecular growth model, in this method, we divide the range of observations into three equal parts. That is if we consider the number of observations is n then we have to consider$m$ such that $m = \frac{n}{3}$. Now let S_1 be the sum of first m observations, S_2 be the sum of second m observations and S_3 be the last m observations. Then the nonlinear parameter estimations for Monomolecular growth model are:

$$\hat{\alpha} = \frac{1}{m}.\frac{S_2^2 - S_1 S_3}{2S_2 - S_1 - S_3},$$

$$\hat{\beta} = \frac{m(S_2 - S_1)^3\{(S_2 - S_1)^{\frac{1}{m}} - (S_3 - S_2)^{\frac{1}{m}}\}}{(S_3 - S_2)^{\frac{1}{m}}(S_2^2 - S_1S_3)(2S_2 - S_3 - S_1)},$$

$$\hat{k} = \frac{1}{m}\log\frac{S_2 - S_1}{S_3 - S_2}. \quad (11)$$

In this method for Gompertz we have to take the natural logarithm, ln, of both sides and then consider as $y_i = \ln w_i ; i = 1, \cdots, n.$ let L_1 be the sum of first m y_is, L_2 be the sum of second m y_is and L_3 be the sum of last my_is. Then the nonlinear parameter estimations for the Gompertz model are:

$$\hat{\alpha} = \exp\left(\frac{1}{m}.\frac{L_1L_3 - L_2^2}{L_3 - 2L_2 + L_1}\right),$$

$$\hat{\beta} = \frac{(L_2 - L_1)^3}{(L_3 - 2L_2 + L_1)^2}\left\{\left(\frac{L_2 - L_1}{L_3 - L_2}\right)^{\frac{1}{m}} - 1\right\},$$

$$\hat{k} = \frac{1}{m}\ln\left(\frac{L_2 - L_1}{L_3 - L_2}\right). \quad (12)$$

Similarly for logistic model, we have to consider y_i as the reciprocal of w_i; $i = 1, \cdots, n.$ let R_1be the sum of first m y_is, R_2 be the sum of second m y_is and R_3 be the sum of last m y_is. Then the nonlinear parameter estimates for the Logistic model are:

$$\hat{\alpha} = \mathrm{m}/\left(\frac{R_1R_3 - R_2^2}{R_3 - 2R_2 + R_1}\right),$$

$$\hat{\beta} = \frac{\frac{(R_2 - R_1)^3}{(R_3 - 2R_2 + R_1)^2}\left\{1 - \left(\frac{R_2 - R_1}{R_3 - R_2}\right)^{\frac{1}{m}}\right\}}{\left(\frac{1}{m}.\frac{R_1R_3 - R_2^2}{R_3 - 2R_2 + R_1}\right)},$$

$$\hat{k} = \frac{1}{m}\ln\left(\frac{L_2 - L_1}{L_3 - L_2}\right). \quad (13)$$

2.1.3 Method C: Composite method assuming that the parameter *k* is known from three equidistant points.
The growth models can be linearised as $Y = A + B\,X$, assuming the parameter *k* is known. The estimated value of $\hat{k}$ may be obtained from the method of three equidistance points. Hence, the other parametersα and β can be estimated using the method of least square [7].

$$\hat{B} = \frac{n\sum XY - (\sum X)(\sum Y)}{n\sum X^2 - (\sum X)^2},$$

$$\hat{A} = \bar{Y} - \hat{B}\bar{X}. \quad (14)$$

where for monomolecular model $Y = w, A = \alpha, B = -\alpha\beta$ and $X = \exp(-kt)$, for Gompertz model $Y = \ln w$, $A = \ln\alpha\,, B = -\beta$ and $X = \exp(-kt)$ and for Logistic model $Y = \frac{1}{w}$, $A = \frac{1}{\alpha}, B = \frac{\beta}{\alpha}$ and $X = \exp(-kt)$.

2.1.4 Method D: Composite method assuming that the parameter $\hat{k}$ is known from method of three partial sums.
The procedure for this method is similar to the earlier one. Here, the estimated value of $\hat{k}$ may be obtained from the method of three partial sums, instead using the method of three equidistance points.

2.1.5 Method E: Newton-Raphson method under the assumption that the parameter α is known.
For this method, we consider that the parameter α is known. Then to estimate the other two unknown parameters, the sum of residual square Φ has been minimized, where

$$\Phi = \sum_{i=1}^{n}\big(w_i - f(t_i, \mathbf{B})\big)^2, \quad (15)$$

where w_i and $t_i$denote the dependent and independent observations respectively. The sum of squared residuals is a function of β and k. Now differentiating (15), with respect to β and k, two normal equations may be obtained as

$$f = \Phi_\beta = \sum_{i=1}^{n}\{(w_i - f(t_i, \mathbf{B}))\}\left[\frac{\partial f(t_i,\mathbf{B})}{\partial \beta}\right], \quad (16)$$

$$g = \Phi_k = \sum_{i=1}^{n}\{(w_i - f(t_i, \mathbf{B}))\}\left[\frac{\partial f(t_i,\mathbf{B})}{\partial k}\right]. \quad (17)$$

Now the Newton-Raphson method for two variables [11] may be used to estimate the parameters β and k.

For Logistic model, we have to take ln on both sides. Then the model takes the form

$$y = a + b\exp ct, \quad (18)$$

where $y = \frac{1}{w}, a = \frac{1}{\alpha}, b = \frac{\beta}{\alpha}$ and $c = -k$. Now it can be written as

$$y_i = f(t_i, \mathbf{B}), \quad i = 1,2,\cdots,n \quad (19)$$

where y is the response variable, t is the independent variable, **B** is the vector of parameters a, b and c. For the Logistic model (18), the parameter a is assumed to be known. Hence the parameter b and c may be estimated in the same way that we have done for the Monomolecular and the Gompertz model.

After getting the value of β and k (b and c, in case of Logistic), the value of α (a, in case of Logistic) can be estimated as:

Taking the natural logarithm,ln, on both side of monomolecular model(4)

$$\ln \alpha = \ln \frac{w_i}{1-\beta \exp(-ki)}, \text{for } i = 1,\cdots,n \quad (20)$$

Hence $\hat{\alpha}$ may be estimated as

$$\hat{\alpha} = \left(\frac{\prod_{i=1}^{n} w_i}{\prod_{i=1}^{n}(1-\beta \exp(-ki))}\right)^{\frac{1}{n}}. \quad (21)$$

Taking the natural logarithm, ln, on both side of Gompertz model(6),

$$\ln \frac{\alpha}{w} = \beta e^{-ki}, \text{ for } i = 1,\cdots,n. \quad (22)$$

Hence $\hat{\alpha}$ may be estimated as

$$\hat{\alpha} = \left\{\prod_{i=1}^{n} w_i \left(e^{\beta e^{-k}\frac{e^{-nk}-1}{e^{-k}-1}}\right)\right\}^{1/n}. \quad (23)$$

The Logistic model (18) can be written as,

$$a = y_i - be^{ci}, \quad \text{for } i = 1,\cdots,n \quad (24)$$

Hence $\hat{a}$ may be estimated as

$$\hat{a} = \frac{1}{n}(\sum_{i=1}^{n} y_i - b\sum_{i=1}^{n} e^{ci}). \quad (25)$$

This process may be repeated using a pre defined stopping criteria.

2.1.6 Method F: Newton- Raphson method under the assumption that the parameter k is known.

Let us take the linear transformation of the Monomolecular model (4) under the assumption that the parameter k is known

$y_i = a + bz_i$, where $y_i = w_i,\ z_i = \exp(-ik),\ \text{for } i = 1,\cdots,n.$ (26)

Hence $\hat{\alpha} = a$ and $\hat{\beta} = -\frac{b}{a}$.

Similarly, for Logistic model (2), the linear form will be

$y_i = a + bz_i$, where $y_i = \frac{1}{w_i}, z_i = \exp(-ik)$, for $i = 1, \cdots, n$. (27)

Hence $\hat{\alpha} = \frac{1}{a}$ and $\hat{\beta} = \frac{b}{a}$.

Hence, the sum of the residual squares Φ for (26) and (27) may be written as

$\Phi = \sum_{i=1}^{n}(y_i - a - bz_i)^2$, for $i = 1, \cdots, n$ (28)

Now differentiating (28) with respect to a and b, two normal equations may be obtained as
$f = \Phi_a = \sum_{i=1}^{n}(y_i - a - bz_i)$, (29)

$g = \Phi_b = \sum_{i=1}^{n}\{(y_i z_i - az_i - bz_i{}^2\}$. (30)

Now Newton-Raphson method for two variables may be used to estimate the parameters a and b. After estimating parameters a and b using (29) and (30), the unknown parameter k can also be estimated using

$\Phi_k = \sum_{i=1}^{n}\{(y_i - a - bexp(-ki))(ib\exp(-ki)\}$, (31)

by Newton-Raphson method.

Gompertz model under the assumption that the parameter k is known initially.

The sum of squared residuals may be given as

$\Phi = \sum_{i=1}^{n}\left(w_i - \alpha e^{-\beta z_i}\right)^2$, (32)

where $z_i = \exp(-ik)$, for $i = 1, \cdots, n$.

Now differentiating (32) and proceeding in like manner to the Monomolecular and Gompertz models, the parameters β and α may be obtained.

After estimating the parameters $\beta$and α, the unknown parameter k has to be estimated by minimizing
$\Phi = \sum_{i=1}^{n}\left(w_i - \alpha e^{-\beta e^{-ki}}\right)^2$, (33)

Using Newton-Raphson method.

The process may be repeated using a pre-defined stopping criterion.

3. RESULTS

3.1 Initial value specification

The Newton-Raphson method requires an initial value for each parameter be estimated. Initial value specification is one of the most difficult problems encountered in estimating parameters of nonlinear model [1]. If the initial values are too far away from the actual value then the Newton-Raphson method may not converge or we need a large number of iterations [11]. The method A to method D may be useful for estimating the starting values for the parameter estimates. In this paper, the initial values are provided by any one of these four methods of estimation.

3.2 Parameter Estimates and Analysis

The Monomolecular, Gompertz and Logistic nonlinear models have been fitted to top height age growth data from the Bowmont Norway spruce Thinning Experiment; sample plot 3661. The parameters of these models have been estimated using six methods of estimation. Parameter estimates for the three fitted models with the corresponding observed and predicted to height values have been presented from Table ii to Table iv. Also presented the computed RMSE value for each nonlinear models. It is observed that the Monomolecular model has the smallest RMSE, 0.122m, with method F (Table ii), the Logistic model has the smallest RMSE, 0.139m, with method B (Table iii), the Gompertz model has the smallest RMSE, 0.104m, with method F (Table iv).

Table ii: Monomolecular top height age (my^{-1}) parameter estimates for a Norway spruce stand.

Age (year)	Height (m)	(A)	(B)	(C)	(D)	(E)	(F)
20	7.30	7.29	7.26	7.23	7.34	7.23	7.20
25	9.00	9.16	9.10	9.13	9.15	9.13	9.12
30	10.90	10.90	10.84	10.89	10.86	10.89	10.90
35	12.60	12.51	12.47	12.52	12.46	12.52	12.54
40	13.90	14.01	14.00	14.04	13.97	14.04	14.06
45	15.40	15.40	15.44	15.45	15.38	15.45	15.46
50	16.90	16.69	16.79	16.75	16.71	16.76	16.76
55	18.20	17.89	18.06	17.96	17.96	17.97	17.97
60	19.00	19.00	19.25	19.09	19.13	19.09	19.08
65	20.00	20.03	20.38	20.14	20.24	20.13	20.11
	α	33.4000	37.8786	33.6730	37.4481	33.5168	32.7841
	β	.8421	.8602	.8458	.8555	.8455	.8436
	k	.0744	.0621	.0744	.0621	.0750	.0780
RMSE		.137	.168	.123	.148	.123	**.122**

Table iii: Logistic top height age (my^{-1}) parameter estimates for a Norway spruce stand.

Age (year)	Height (m)	(A)	(B)	(C)	(D)	(E)	(F)
20	7.30	7.50	7.41	7.44	7.38	7.34	7.37
25	9.00	9.00	8.99	8.95	8.97	8.96	8.98
30	10.90	10.60	10.67	10.58	10.66	10.69	10.69
35	12.60	12.24	12.38	12.26	12.38	12.43	12.43
40	13.90	13.86	14.04	13.93	14.06	14.12	14.11
45	15.40	15.40	15.57	15.52	15.61	15.66	15.66
50	16.90	16.80	16.93	16.98	17.00	17.02	17.03
55	18.20	18.05	18.10	18.28	18.19	18.18	18.19
60	19.00	19.11	19.07	19.40	19.18	19.12	19.15
65	20.00	20.00	19.85	20.34	19.98	19.88	19.92
	α	23.3317	22.4399	23.8832	22.6302	22.2479	22.3873
	β	2.8000	2.7522	2.9319	2.8042	2.7819	2.7811
	k	.2822	.3051	.2822	.3051	.3149	.3112
RMSE		.174	**.139**	.232	.149	.154	.152

The cumulative basal area production and mean diameter at breast height are also used and the parameter estimates with RMSE value for the Monomolecular, Gompertz and Logistic models are presented in Table v, vi and vii respectively. It is observed that the least RMSE values for Monomolecular and Gompertz growth model for cumulative basal area production are given by method F and which are 0.958m and 0.748m respectively and for the Logistic model is given by method A and which is 0.895m. Again the least RMSE value of Monomolecular, Gompertz and Logistic growth model for mean diameter at breast height are found to be 0.337m, 0.229m and 0.157m with Method F, method F and method D respectively.

Table iv: Gompertz top height age (my^{-1}) parameter estimates for a Norway spruce stand.

Age (year)	Height (m)	(A)	(B)	(C)	(D)	(E)	(F)
20	7.30	7.32	7.36	7.36	7.36	7.22	7.33
25	9.00	9.00	9.05	9.05	9.05	9.02	9.05
30	10.90	10.69	10.75	10.75	10.75	10.82	10.79
35	12.60	12.35	12.42	12.42	12.42	12.54	12.47
40	13.90	13.93	14.01	14.00	14.00	14.15	14.06
45	15.40	15.40	15.50	15.48	15.48	15.60	15.53
50	16.90	16.75	16.86	16.84	16.84	16.90	16.86
55	18.20	17.96	18.08	18.06	18.06	18.03	18.04
60	19.00	19.05	19.17	19.15	19.15	19.00	19.09
65	20.00	20.00	20.14	20.11	20.11	19.84	20.00
	α	25.6216	25.8296	25.7603	25.7841	23.9316	25.0070
	β	1.4998	1.5028	1.4998	1.5003	1.4734	1.4833
	k	.1801	.1798	.1801	.1798	.2061	.1892
RMSE		.137	.121	.117	.118	.132	**.104**

Table v: Estimated parameters of Monomolecular model along with RMSE for mean diameter at breast height and cumulative basal area production.

Data	Method of estimation	α	β	k	RMSE
Mean diameter at breast height	A	254.2485	0.9757	0.0090	0.415
	B	197.0727	0.9708	0.0123	0.458
	C	252.0445	0.9756	0.0090	0.390
	D	190.6542	0.9682	0.0123	0.378
	E	106.9216	0.9460	0.0238	0.346
	F	82.7384	0.9328	0.0327	**0.337**
Cumulative basal area production	A	254.9126	0.8990	0.0547	1.198
	B	427.8732	0.9350	0.0275	1.577
	C	252.7398	0.8988	0.0547	0.961
	D	419.6737	0.9319	0.0275	1.381
	E	260.2751	0.9008	0.0524	0.970
	F	246.9026	0.8973	0.0566	**0.958**

Table vi. Estimated parameters of Gompertz model along with RMSE for mean diameter at breast height and cumulative basal area production.

Data	Method of estimation	α	β	k	RMSE
Mean diameter at breast height	A	42.5918	1.8758	0.1445	0.303
	B	42.4126	1.8908	0.1469	0.320
	C	42.3118	1.8732	0.1445	0.278
	D	41.6907	1.8628	0.1469	0.267
	E	33.2335	1.7768	0.2038	0.361
	F	38.0838	1.8153	0.1653	**0.229**
Cumulative basal area production	A	154.2372	1.6701	0.1880	0.867
	B	175.1747	1.7565	0.1589	1.141
	C	155.2063	1.6914	0.1880	**0.784**
	D	174.9517	1.7589	0.1589	1.115
	E	147.5676	1.6857	0.2055	1.068
	F	158.9386	1.7017	0.1812	**0.748**

Table vii. Estimated parameters of Logistic model along with RMSE for mean diameter at breast height and cumulative basal area production.

Data	Method of estimation	α	β	k	RMSE
Mean diameter at breast height	A	33.1059	3.9194	0.2871	0.206
	B	32.7692	3.8763	0.2891	0.173
	C	32.7681	3.8575	0.2871	0.164
	D	32.5522	3.8346	0.2891	**0.157**
	E	32.8134	3.8648	0.2869	0.166
	F	32.7599	3.8566	0.2873	0.164
Cumulative basal area production	A	139.8948	3.4201	0.3000	**0.895**
	B	141.2550	3.5000	0.2998	0.897
	C	143.9179	3.6409	0.3000	1.277
	D	144.0177	3.6430	0.2998	1.285
	E	130.6011	3.3809	0.3409	1.380
	F	130.7002	3.3812	0.3405	1.369

Table viii: RMSE computed using new methods and using SAS for the top height age data.

Models	Method of Estimation	RMSE	Method of Estimation	RMSE
Monomolecular Model	F	0.122	SAS	0.109
Gompertz model	F	0.104	SAS	0.109
Logistic model	B	0.139	SAS	0.152

4. DISCUSSION

The main focus of this paper is to provide some method of estimations required for estimating the parameters of some nonlinear models. The validity of these methods has been tested with some experimental data sets. In estimation of parameters, all the non-linear iterative methods require certain initial value which may be obtained from any one of the first four methods.

It is observed from the above results that the Gompertz model with method F produced the best fit for the top height age growth data. Method F is defined as the Newton-Raphson method under the assumption that the parameter k is known. Furthermore the methods presented in the paper produced similar RMSE to those computed using SAS [3], as illustrated in Table viii.

It is observed from the Table ii to Table iv, that the method A; which requires only three equidistant points, the composite method C and iterative method F provide almost same RMSE. If only a few observations are available then the method A and C may be more appropriate.

For cumulative basal area production, the Gompertz growth model with method F provided better RMSE (0.748m) than the other growth models. Again the Monomolecular growth model has the least RMSE for mean diameter at breast height with the method D and which is 0.157m.

Six methods of estimation have been investigated for rapid estimation of parameters of Monomolecular, Logistic and Gompertz models. A comparative study has also been made based on three sets of well-known forestry data. It is noted from our results that method F may be used for estimation of parameters of Monomolecular and Gompertz models, whereas for Logistic model the first four methods may be used.

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