Chapter 2: Parameter Estimation of Certain Three parameter Nonlinear Growth Models

2.1 Introduction

The three parameter non-linear models namely Monomolecular, Gompertz and Logistic are commonly used to determine the growth and development of various systems [[45], [46]]. These models are particular cases of the generalized Chapman-Richards model [52]. Many forestry researchers made extensive and profound studies on these models [[22], [52], [89], [91]]. In this Chapter, the growth models Monomolecular, Gompertz and Logistic, which are widely used by forestry scholars, are fitted by estimating the parameters using various methods of estimations.

Logistic Growth Model: 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:

$$\frac{dw/dt}{A-w} = b_0 + b_1 w, \tag{2.1}$$

where b_0, b_1 are constants and w and t are the dependent and independent respectively. The solution of the differential equation is-

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

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

$$w(t) = \frac{A}{(1 + \beta \exp(-kt))}. \tag{2.2}$$

where $k = b_1 A$ is related to the rate of increasing of w, A is the upper asymptote and β is a location parameter [57]. The curve of the model **(2.2**) is S-shaped and all the parameters are positive. Also the shape of the curve is symmetric about its point of inflection [18].

Monomolecular growth Model: 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 decreases linearly as size increases. Then,

$$\frac{dw}{dt} = k(A-w), \tag{2.3}$$

where w is the expected size of an organism at time t, A represents the limiting size of the organism and k is the growth rate parameter [18]. From this differential equation, the required model may be written as

$$w(t) = A(1 - \beta \exp(-kt)), \tag{2.4}$$

where β is the biological constant.

Gompertz Growth Model: 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 can be derived by solving the differential equation

$$\frac{dw}{dt} = kw \log\left(\frac{A}{w}\right). \tag{2.5}$$

By integrating **(2.5**), the Gompertz model is obtained as

$$w(t) = A \exp(-\beta \exp(-kt)), \tag{2.6}$$

where w is the number of tumor cells at time *t*, $A > 0$ 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 [[22], [42]].Although this curve is a S-shaped like the logistic, it is not symmetrical about its point of inflection [18].

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 [[55], [57], [76]]. The aim of the study is to estimate the parameters of the models by using various methods of estimation. By selecting an appropriate method of estimation, the best fit model is selected based on five sets of well-known forestry data sets. Also the proper initial (guess) value specification plays a very important role in parameter estimation of nonlinear models using iterative methods. The first four methods of this study provide the initial value specification for the parameters of Monomolecular, Gompertz and Logistic growth models.

2.2 Objective

The aim of this chapter is to develop a suitable method of estimation to estimate the parameters of Monomolecular, Gompertz and Logistic growth models. Five well-known forestry data are used for testing the validity of the proposed methods based on the certain statistical selection criteria.

2.3 Methods and materials

The maximum diameter data and top height growth of *babul (Acacia Nilotica) tree* are used for testing the validity of the methods. These two sets of data, presented in **Table 2.1**, were based on the analysis of sample plot data of Uttar Pradesh, Maharashtra and Madhya Pradesh [37]. The top height age, the cumulative basal area production and the mean diameter at breast height data, originated from the Bowmont Norway spruce thinning experiment, sample plot 3661 [[21], [22]] are also used. These data sets are repeatedly measured on a five-year cycle from age 20 to 64 and are presented in **Table 2.2**.

Table 2.1: Top height and Maximum diameter growth data of Babul tree in India.

Age (year)	5	10	15	20	25
Top height(m)	8.14	12.19	14.93	16.70	17.98
Maximum diameter (cm)	12.19	20.83	26.92	31.49	34.29

Table 2.2: Top height, cumulative basal area production and mean diameter at breast height growth data from Bowmont Norway spruce thinning experiment, sample plot 3661.

Age (year)	20	25	30	35	40	45	50	55	60	64
Top height ($\boldsymbol{m}$)	7.3	9.0	10.9	12.6	13.9	15.4	16.9	18.2	19.0	20
Cumulative basal area production ($\boldsymbol{m^2}$)	37.99	49	60.41	68.91	78.73	89.83	98.6	107	114.8	119.54
Mean diameter at breast height ($\boldsymbol{cm}$)	8.40	10.40	12.35	14.74	17.13	19.50	21.49	23.82	25.55	26.50

2.3.1 Stationarity of the data

A stochastic process is said to be stationary if its mean and variance are constant over time and the value of covariance between two time periods depends only on the distance between the two time periods and not on the actual time at which the covariance computed [33]. In this work, theoretical correlogram and Augmented Dickey-Fuller (ADF) unit root test have been used to check the stationarity of the data. The autocorrelation function (ACF) and partial autocorrelation function (PACF) of the data sets are plotted from Figure 2.1 to Figure 2.10.

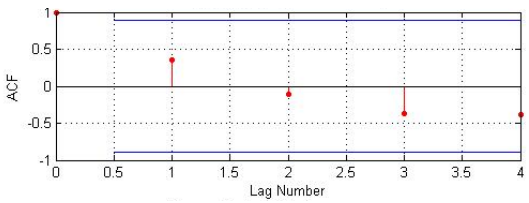

Figure 2.1: ACF of top height growth data of Babul tree in India

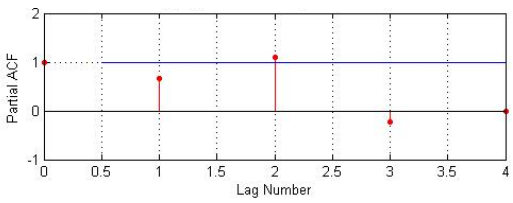

Figure 2.2: PACF of top height growth data of Babul tree in India

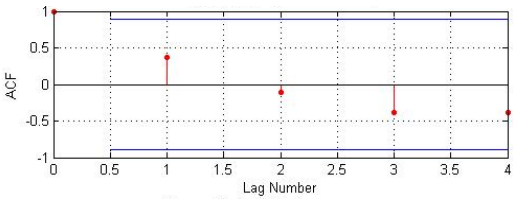

Figure 2.3: ACF of Maximum diameter growth data of Babul tree in India

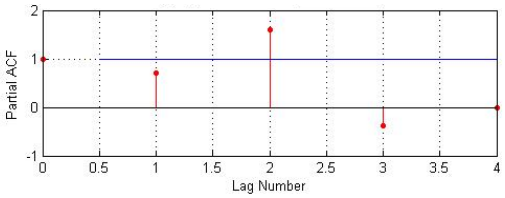

Figure 2.4: PACF of Maximum diameter growth data of Babul tree in India

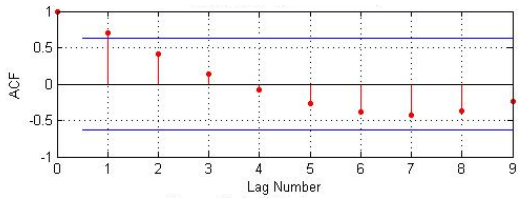

Figure 2.5: ACF of top height growth data from Bowmont Norway spruce thinning experiment.

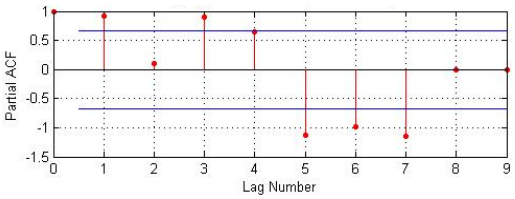

Figure 2.6: PACF of top height growth data from Bowmont Norway spruce thinning experiment.

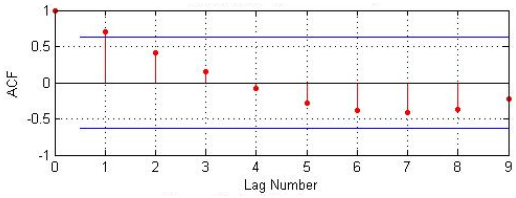

Figure 2.7: ACF cumulative basal area production data from Bowmont Norway spruce thinning experiment.

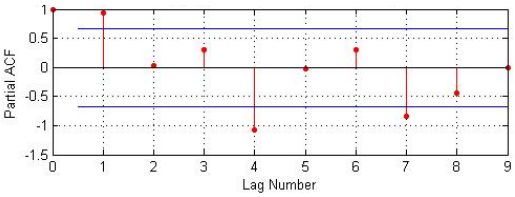

Figure 2.8: PACF of cumulative basal area production data from Bowmont Norway spruce thinning experiment.

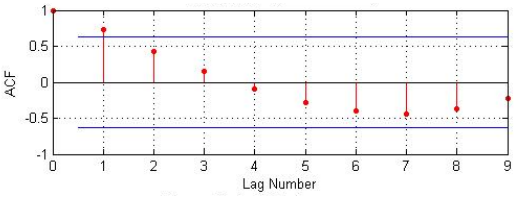

Figure 2.9: ACF of mean diameter at breast height growth data from Bowmont Norway spruce thinning experiment.

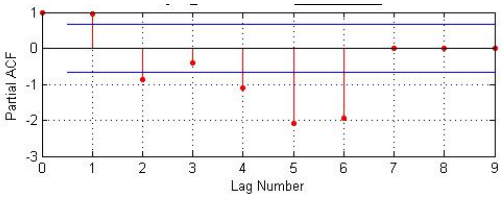

Figure 2.10: PACF of mean diameter at breast height growth data from Bowmont Norway spruce thinning experiment.

From the Figure 2.1 to Figure 2.10 it is clear that all the data sets presented in **Table 2.1** and **Table 2.2** have seasonal effect. Now the Augmented Dickey-Fuller (ADF) unit root test has been used to check the stationarity of the data sets, which are presented in Table **2.3**. From Table **2.3**, it is observed that, for all data sets, the $p-$values are less then 5%. It means that, the null hypothesis H_0, considering the process is a unit root, can be rejected. For top height and maximum diameter growth data of Babul tree, unit root test is not applicable due to less number of observations. Although, in case of small data set, variables are relatively stationary in short term. And hence, all the data sets presented in this work are stationary.

Table 2.3: $\boldsymbol{p-}$ values of ADF test for different data sets.

Data	$\boldsymbol{p-}$ **value**
Top height growth data from Bowmont Norway spruce thinning experiment.	0.008173
Cumulative basal area production data from Bowmont Norway spruce thinning experiment	0.000002
Mean diameter at breast height growth data from Bowmont Norway spruce thinning experiment	0.01491

2.3.2 Method of estimation

The Monomolecular, Gompertz and Logistic nonlinear growth can be expressed as:

$$w_i = f(t_i, \mathbf{B}) + \varepsilon_i, \tag{2.7}$$

$i = 1,2,\cdots,n,$ where n be the number of observations, w is the response variable, t is the independent variable, $\mathbf{B}$ is the vector of parameters A, β and k. ε_i is a random error in the model with mean zero and constant variance. The selection process described in the chapter 1 is used to select the best fit growth model with a suitable method of estimation for the parameters. A software package is developed in

FORTRAN 77 for each method of estimation. The following six methods of estimation have been developed to fit the growth models.

2.3.2.1 Method A: Estimation based on three equidistant points.

In this method, three equidistant points, t_1, t_2, t_3 have been considered 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.

a) Parameter estimates for the Monomolecular growth model are:

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

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

$$\hat{k} = \frac{1}{d}\ln\left(\frac{w_2 - w_1}{w_3 - w_2}\right), \tag{2.8}$$

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

b) Parameter estimations for the Gompertz growth model are:

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

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

$$\hat{k} = \frac{1}{d}\ln\left(\frac{y_2 - y_1}{y_3 - y_2}\right), \tag{2.9}$$

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

c) Parameter estimations for the Logistic growth model are:

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

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

$$\hat{k} = \frac{1}{d}\ln\left(\frac{z_2 - z_1}{z_3 - z_2}\right), \tag{2.10}$$

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

2.3.2.2 Method B: Estimation based on three partial sums.

In this method, the range of the total observations is divided into three equal parts. That is, if the number of observations is n then consider m such that $m = \frac{n}{3}$. Now let S_1be the sum of first m observations, S_2 be the sum of second m observations and S_3 be the last m observations.

a) Parameter estimations for Monomolecular growth model are:

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

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

$$\hat{k} = \frac{1}{m}\ln\frac{S_2 - S_1}{S_3 - S_2}\,. \tag{2.11}$$

b) Parameter estimations for Gompertz growth model:

In this method for Gompertz model, first taking the natural logarithm, ln, of both sides and then consider as $y_i = \ln w_i\,; i = 1, \cdots, n.$ let L_1be 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 m y_is. Then

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

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

$$\hat{k} = \frac{1}{m}\ln\left(\frac{L_2 - L_1}{L_3 - L_2}\right). \tag{2.12}$$

c) Parameter estimations for Logistic growth model:

Lor logistic model, 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

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

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

$$\hat{k} = \frac{1}{m} \ln\left(\frac{L_2 - L_1}{L_3 - L_2}\right). \tag{2.13}$$

2.3.2.3 Method C: Composite method assuming that the parameter k is known from three equidistant points.

In this method first the growth models are linearized as $Y = P + Q\,X$, assuming the parameter k is known. The estimated value of $\hat{k}$ is taken from the method of three equidistance points. Hence, the other parameters A and β are estimated using the method of least square [40].

$$\widehat{\boldsymbol{Q}} = \frac{\boldsymbol{n}\sum \boldsymbol{XY} - (\sum \boldsymbol{X})(\sum \boldsymbol{Y})}{\boldsymbol{n}\sum \boldsymbol{X^2} - (\sum \boldsymbol{X})^2},$$

$$\hat{P} = \bar{Y} - \hat{Q}\bar{X}. \tag{2.14}$$

Where for

a) Monomolecular model $Y = w, A = P, Q = -A\beta$ and $X = \exp(-kt)$,
b) Gompertz model $Y = \ln w\,, P = \ln A\,, Q = -\beta$ and $X = \exp(-kt)$ and
c) Logistic model $Y = \frac{1}{w},\ P = \frac{1}{A}, Q = \frac{\beta}{A}$ and $X = \exp(-kt)$.

2.3.2.4 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 $\hat{k}$ is taken from the method of three partial sums.

2.3.2.5 Method E: Newton-Raphson method under the assumption that the parameter A is known.

a) For Monomolecular and Gompertz growth model

In this method, assume that the parameter A is known. Then to estimate the other two unknown parameters, the sum of residuals square Φ is minimized, where

$$\Phi = \sum_{i=1}^{n} \big(w_i - f(t_i, \mathbf{B})\big)^2, \tag{2.15}$$

where w_i and t_i denote the dependent and independent variables respectively. The sum of squared residuals is a function of β and k. Now differentiating **(2.15)**, with respect to β and k, two normal equations are obtained as

$$f = \Phi_\beta = \sum_{i=1}^{n} \big\{\big(w_i - f(t_i, \mathbf{B})\big)\big\} \left[\frac{\partial f(t_i, \mathbf{B})}{\partial \beta}\right], \tag{2.16}$$

$$g = \Phi_k = \sum_{i=1}^{n} \big\{\big(w_i - f(t_i, \mathbf{B})\big)\big\} \left[\frac{\partial f(t_i, \mathbf{B})}{\partial k}\right]. \tag{2.17}$$

Then the Newton-Raphson method for two variables [62] is used to estimate the parameters β and k.

b) For Logistic Growth model

For Logistic model, after taking ln on both sides, the model can be written as

$$y = p + q \exp ct, \tag{2.18}$$

where $y = \frac{1}{w}, p = \frac{1}{A}, q = \frac{\beta}{A}$ and $c = -k$.

Now the model can be written as

$$y_i = f(t_i, \mathbf{B}), \;\; i = 1,2, \cdots, n, \tag{2.19}$$

where **B** is the vector of parameters p, q and c. For the Logistic model (**2.18**), the parameter p is assumed to be known. Hence, the parameter q and c are estimated in the same way that has been done for the Monomolecular and the Gompertz model.

After getting the value of β and k (q and c, in case of Logistic), the value of A (p, in case of Logistic) is estimated as:

a) Taking the natural logarithm, ln, on both side of monomolecular model (**2.4**)

$$\ln A = \ln \frac{w_i}{1 - \beta \exp(-ki)}, \text{for } i = 1, \cdots, n \tag{2.20}$$

Hence the parameter $\hat{A}$ is estimated as

$$\hat{A} = \left(\frac{\prod_{i=1}^{n} w_i}{\prod_{i=1}^{n} (1 - \beta \exp(-ki))} \right)^{\frac{1}{n}}. \tag{2.21}$$

b) Taking the natural logarithm, ln, on both side of Gompertz model **(2.6)**,

$$\ln \frac{A}{w} = \beta e^{-ki}, \;\; \text{for } i = 1, \cdots, n\,. \tag{2.22}$$

Hence the parameter $\hat{A}$ may be estimated as

$$\hat{A} = \left\{ \prod_{i=1}^{n} w_i \left(e^{\beta e^{-k}} \frac{e^{-nk} - 1}{e^{-k} - 1} \right) \right\}^{1/n}. \tag{2.23}$$

c) The Logistic model **(2.18**) can be written as,

$$p = y_i - be^{ci}, \text{for } i = 1, \cdots, n \tag{2.24}$$

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

$$\hat{p} = \frac{1}{n} \left(\sum_{i=1}^{n} y_i - b \sum_{i=1}^{n} e^{ci} \right). \tag{2.25}$$

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

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

a) Linear transformation of Monomolecular Growth Model

Here the linear transformation of the Monomolecular model **(2.4**) has been taken under the assumption that the parameter k is known

$$\begin{gathered} y_i = a + bz_i, \text{where } y_i = w_i, z_i = \exp(-ik), \\ \text{for } i = 1, \cdots, n\,. \end{gathered} \tag{2.26}$$

Here $\hat{A} = a$ and $\hat{\beta} = -\frac{b}{a}$.

b) Linear transformation of Logistic Growth Model

For Logistic model **(2.2**), the linear form is

$$y_i = a + bz_i, \text{where } y_i = \frac{1}{w_i}, z_i = \exp(-ik), \text{for } i = 1, \cdots, n\,. \tag{2.27}$$

Here $\hat{A} = \frac{1}{a}$ and $\hat{\beta} = \frac{b}{a}$.

Hence, the sum of the squared residuals Φ for **(2.26**) and **(2.27**) can be written as

$$\Phi = \sum_{i=1}^{n} (y_i - a - bz_i)^2\,, \text{for } i = 1, \cdots, n. \tag{2.28}$$

Now differentiating **(2.28**) with respect to a and b, two normal equations are obtained as

$$f = \Phi_a = \sum_{i=1}^{n} (y_i - a - bz_i), \tag{2.29}$$

$$g = \Phi_b = \sum_{i=1}^{n} \{(y_i z_i - az_i - bz_i{}^2\}. \tag{2.30}$$

Then, the Newton-Raphson method for two variables is used to estimate the parameters a and b. After estimating parameters a and b using **(2.29**) and **(2.30**), the unknown parameter k can also be estimated by using Newton-Raphson method

$$\Phi_k = \sum_{i=1}^{n} \{(y_i - a - bexp(-ki))(ib\exp(-ki)\}. \tag{2.31}$$

c) Parameter estimation of Gompertz model:

The sum of squared residuals is given as

$$\Phi = \sum_{i=1}^{n} \left(w_i - Ae^{-\beta z_i}\right)^2, \tag{2.32}$$

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

Now differentiating **(2.32)** and proceeding like Monomolecular and Gompertz models, the parameters β and A are obtained.

After estimating the parameters β and A, the unknown parameter k is estimated using Newton-Raphson method by minimizing

$$\Phi = \sum_{i=1}^{n} \left(w_i - Ae^{-\beta e^{-ki}}\right)^2. \tag{2.33}$$

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

2.4 Results and discussion

2.4.1 Properties of the growth models

There is a clear relationship between the properties of different mathematical models and the estimation of their respective parameters. If the properties of nonlinear mathematical models are to be known then it may helpful to estimate the parameters to be estimated. Indeed, even a few cases, because of the absence of knowledge of these properties, it might appear to face different problems to use in different natural growth. Some basic properties of the mentioned model are provided in **Table 2.4**. It is observed that the upper asymptote and the domain of the independent variable are same for each model with A and $[0, \infty)$ respectively.

Table 2.4: Summary of some basic properties of the growth models.

	Logistic	Gompertz	Monomolecular
Integral form of the growth function	$\frac{A}{1+\beta e^{-Kt}}$	$Ae^{-Be^{-Kt}}$	$A(1-Be^{-Kt})$
Starting point of the growth function	$\frac{A}{1+B}$	Ae^{-B}	$A(1-B)$
Growth rate	$\frac{ABKe^{-KT}}{(1+Be^{-Kt})^2}$	$ABKe^{-Be^{-kt}}e^{-kt}$	$ABKe^{-kt}$
Relative growth rate as function of time	$\frac{BK}{e^{Kt}+B}$	$\frac{BKe^{-Be^{-kt}}}{e^{kt}-B}$	$\frac{BK}{e^{kt}-1}$
Relative growth rate as function of response variable	$K\left(1-\frac{y}{A}\right)$	$\frac{Ky\ ln\frac{A}{y}}{A\left(1-\ln\frac{A}{y}\right)}$	$\frac{BK(A-y)}{A(B-1)+y}$
Second derivative of the growth function	$ABK^2e^{-Kt}(1+Be^{-Kt})^{-2}\{2Be^{-Kt}(1-Be^{-Kt})^{-1}-1\}$	$ABK^2e^{-Be^{-kt}}e^{-kt}(-1+e^{-kt})$	$-ABK^2e^{-Kt}$
Point of inflection $(y(t)=)$	$\frac{A}{2}$	$\frac{A}{e}$	Does not exist
Domain of the dependent variable	$\left[\frac{A}{1+B},A\right]$	$[Ae^{-B},A]$	$[A(1-B),A]$

2.4.2 Initial value specification

The Newton-Raphson method requires an initial value for each parameter is estimated. The method A to method D may be useful for estimating the starting values for the parameter estimates. In this study, the initial values are provided by any one of these four methods of estimation.

2.4.3 Parameter estimates and analysis

Gompertz, monomolecular and logistic growth models have been fitted to top height and maximum diameter growth data of babul trees compiled from Uttar Pradesh, Maharashtra and Madhya Pradesh of India. The parameters of these models have been estimated using six methods of estimation.

2.4.3.1 For top height growth of babul tree

The estimation of parameters for the growth models along with the summary of statistical analysis to top height growth data of babul tree are presented from **Table 2.5** to **Table 2.7**. Based on six model selection criteria as discussed in the first Chapter, the results are summarized as below.

Step I: The Logistic model estimated by method B and D are rejected due to the non-logical estimation of the parameters. All the methods have estimated the asymptotes smaller than the dominant height of babul tree (17.98m). The estimated parameters of the rest of the models are logically consistent and biologically significant.

Step II: Gompertz growth model (method B, D and E) and Logistic model (method A, C, E and F) are rejected due to having less than 95% level of significance.

Step III: Considering the relative value of RMSE, the five best results are selected in this step. Comparing the values of RMSE, Monomolecular growth models with all its methods of estimation are promoted to the next level.

Step IV: In the fourth step, no results are eliminated as all surviving results have R_a^2 value 0.99.

Step V: All surviving results along with the 95% confidence level are demonstrated in Table 2.16. It is observed no results are eliminated as all the parameters of the surviving results are significantly different from zero at 95% confidence level.

Step VI: From the final step, the best fit growth model is selected. In case of top height growth data of babul tree, the Monomolecular growth model (methods A, C, D, E and F) is found to be more suitable as the value of $R^2_{prediction}$ and R^2 (99.99 and 99.99 respectively) are better than the remaining surviving growth models.

Table 2.5: Fitting of the Logistic growth model for top height growth of babul trees.

Age	Observed Data	Method					
		A	B	C	D	E	F
5	8.14	8.14	8.14	8.19	8.11	8.15	8.17
10	12.19	11.86	12.19	11.91	12.33	12.07	12.04
15	14.93	14.93	14.93	14.98	15.27	15.10	15.08
20	16.70	16.91	16.28	16.95	16.73	16.88	16.90
25	17.98	17.98	16.84	18.01	17.35	17.75	17.81
Parameters	A	18.97	17.19	18.99	17.73	18.43	18.55
	β	2.950	3.013	2.926	3.219	3.019	2.991
	k	0.796	0.997	0.796	0.997	0.873	0.855
χ^2		0.012	0.088	0.011	0.032	0.008	0.007
RMSE		0.176	0.543	0.17	0.326	0.162	0.151
R^2(in %)		99.75	97.61	99.76	99.13	99.78	99.81
R_a^2		0.99	0.90	0.99	0.96	0.99	0.99
$R^2_{prediction}$ (in %)		99.65	92.35	99.64	97.53	99.50	99.62

Table 2.6: Fitting of the Gompertz growth model for top height growth of babul trees.

Age	Observed Data	Method					
		A	B	C	D	E	F
5	8.14	8.14	8.14	8.18	8.10	8.54	8.18
10	12.19	12.03	12.19	12.05	12.26	11.78	12.09
15	14.93	14.93	14.93	14.94	15.11	14.58	14.96
20	16.70	16.83	16.53	16.82	16.77	16.79	16.80
25	17.98	17.98	17.40	17.96	17.68	18.43	17.90
Parameters	A	19.52	18.32	19.49	18.64	22.13	19.32
	β	1.579	1.615	1.567	1.661	1.439	1.575
	k	0.591	0.689	0.591	0.689	0.413	0.606
χ^2		0.003	0.021	0.003	0.008	0.053	0.002
RMSE		0.092	0.272	0.084	0.164	0.363	0.077
R^2(in %)		99.93	99.40	99.94	99.78	98.92	99.95
R_a^2		0.99	0.97	0.99	0.99	0.95	0.99
$R^2_{prediction}$ (in %)		99.89	98.05	99.91	99.40	97.99	99.90

Table 2.7: Fitting of the Monomolecular growth model for top height growth of babul trees.

Age	Observed Data	Method					
		A	B	**C**	**D**	**E**	**F**
5	8.14	8.14	8.14	8.14	8.16	8.14	8.14
10	12.19	12.21	12.19	12.19	12.18	12.19	12.19
15	14.93	14.93	14.93	14.91	14.89	14.91	14.91
20	16.70	16.76	16.78	16.74	16.73	16.74	16.74
25	17.98	17.98	18.04	17.96	17.98	17.96	17.96
Parameters	A	20.46	20.66	20.44	20.58	20.47	20.47
	β	0.899	0.896	0.898	0.893	0.897	0.897
	k	0.400	0.391	0.400	0.391	0.398	0.398
χ^2		.0002	.0006	.0001	.0002	.0001	.0001
RMSE		0.026	0.046	0.021	0.024	0.020	0.020
R^2(in %)		99.99	99.98	99.99	99.99	99.99	99.99
R_a^2		0.99	0.99	0.99	0.99	0.99	0.99
$R^2_{prediction}$ (in %)		99.99	99.96	99.99	99.99	99.99	99.99

2.4.3.2 For maximum diameter growth of babul tree

The estimation of parameters for the growth models and the summary of statistical analysis to maximum diameter growth data of babul tree are presented from **Table 2.8** to **Table 2.10**. In this case, logistic growth model (method B and D) and Gompertz growth model (method B) are rejected due to the non-logical estimation of the

parameters. In all the cases, some of their parameters estimate of asymptotic parameters smaller than the dominant diameter of babul tree (34.29cm). The eliminated results in each step are also highlighted accordingly from **Table 2.8** to **Table 2.10**. Gompertz growth model (method A, C, D, E and F) and Logistic model (method A, C, E and F) are rejected due to having less than 95% level of significance. In the third step, comparing the values of RMSE, Monomolecular growth models with all its methods of estimation are promoted to the next level. No results are eliminated in step V as all the parameters of this model are significantly different from zero at 95% confidence level (**Table 2.16**). And finally, the best fit model has been selected and find that Monomolecular growth model with method C, D, E and F give the similar results with the $R^2_{prediction}$ and R^2 values 99.97 and 99.99 respectively.

Table 2.8: Fitting of the Logistic growth model for top height growth of babul trees.

Age	Observed Data	Method					
		A	B	C	D	E	F
5	12.19	12.19	12.19	12.30	12.12	12.21	12.23
10	20.83	19.82	20.83	20.01	21.28	20.52	20.45
15	26.92	26.92	26.92	27.20	28.03	27.61	27.56
20	31.49	31.71	29.69	32.06	31.19	31.74	31.80
25	34.29	34.29	30.70	34.67	32.36	33.63	33.79
Parameters	A	36.45	31.19	36.86	32.94	34.89	35.16
	β	4.719	4.885	4.737	5.378	4.933	4.888
	k	0.863	1.142	0.8634	1.142	0.976	0.958
χ^2		0.053	0.529	0.052	0.172	0.037	0.032
$RMSE$		0.464	1.796	0.497	1.026	0.461	0.423
R^2 $(in\ \%)$		99.66	94.85	99.60	98.32	99.66	99.71
R^2_a		0.98	0.79	0.98	0.93	0.98	0.98
$R^2_{prediction}$ $(in\ \%)$		99.58	84.12	99.35	95.31	99.24	99.43

Table 2.9: Fitting of the Gompertz growth model for top height growth of babul trees.

Age	Observed Data	Method					
		A	B	C	D	E	F
5	12.19	12.19	12.19	12.29	12.06	13.17	12.30
10	20.83	20.31	20.83	20.43	21.12	19.94	20.55
15	26.92	26.92	26.92	27.04	27.62	26.23	27.13
20	31.49	31.46	30.44	31.58	31.41	31.42	31.53
25	34.29	34.29	32.28	34.41	33.40	35.39	34.20

Parameters	A	38.14	34.07	38.25	35.34	44.57	37.65
	β	2.064	2.147	2.053	2.247	1.849	2.067
	k	0.593	0.737	0.593	0.737	0.416	0.614
χ^2		0.014	0.162	0.010	0.047	0.165	0.007
$RMSE$		0.235	1.015	0.205	0.528	0.829	0.170
$R^2\ (in\ \%)$		99.91	98.36	99.93	99.55	98.90	99.95
R_a^2		0.99	0.93	0.99	0.98	0.96	0.99
$R^2_{prediction}\ (in\ \%)$		99.89	94.96	99.91	98.89	97.87	99.93

Table 2.10: Fitting of the Monomolecular growth model for top height growth of babul trees.

Age	Observed Data	Method					
		A	B	**C**	**D**	**E**	**F**
5	12.19	12.19	12.19	12.18	12.17	12.18	12.17
10	20.83	20.82	20.83	20.85	20.87	20.85	20.86
15	26.92	26.92	26.92	26.98	27.00	26.98	26.99
20	31.49	31.24	31.21	31.32	31.32	31.32	31.32
25	34.29	34.29	34.24	34.39	34.37	34.39	34.38
Parameters	A	41.67	41.46	41.80	41.65	41.83	41.72
	β	1.000	1.002	1.002	1.004	1.002	1.003
	k	0.346	0.349	0.346	0.349	0.3458	0.348
χ^2		0.002	0.003	0.001	0.001	0.001	0.001
$RMSE$		0.113	0.126	0.093	0.092	0.093	0.092
$R^2\ (in\ \%)$		99.98	99.98	99.99	99.99	99.99	99.99
R_a^2		0.99	0.99	0.99	0.99	0.99	0.99
$R^2_{prediction}\ (in\ \%)$		99.96	99.95	99.97	99.97	99.97	99.97

2.4.3.3 For top height growth from the Bowmont Norway spruce Thinning Experiment

The Monomolecular, Gompertz and Logistic nonlinear models are also been fitted to top height age-growth data from the Bowmont Norway spruce Thinning Experiment. The Parameter estimates for these three models with the corresponding observed and predicted height values have been presented from **Table 2.11** to **Table 2.13**. The statistical analyses for each method of estimations are also presented.

For top height age-growth data, no result is rejected in the first step as all are logically consistent and biologically significant. The eliminated results in each step are highlighted accordingly in from **Table 2.11** to **Table 2.13**. It is also observed that no

results are eliminated in step II, IV and V, as all results have calculated χ^2 value less then tabulated value at 95% level of significance, all surviving results have 0.99 of R_a^2 value and all of their parameters are significantly different from zero (**Table 2.16**). From the step III, five least RMSE values are chosen and given by Gompertz growth model (method B, C, D and F) and Monomolecular growth model (method F). Finally, the best fit growth model is selected and find that Gompertz growth model (method F) with the $R^2_{prediction}$ and R^2 values 99.92 and 99.93 respectively.

Table 2.11: Fitting of the Logistic growth model for top height growth from the Bowmont Norway spruce Thinning Experiment.

Age	Observed Data	Logistic					
		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
Parameters	A	23.33	22.44	23.88	22.63	22.25	22.39
	β	2.80	2.75	2.93	2.80	2.78	2.78
	k	.28	.31	.28	.31	.31	.31
χ^2		0.03	0.02	0.04	0.02	0.02	0.02
RMSE		.174	.139	.232	.149	.154	.152
R^2(in %)		99.82	99.89	99.68	99.87	99.86	99.86
R_a^2		0.99	0.99	0.99	0.99	0.99	0.99
$R^2_{prediction}$ (in %)		99.80	99.86	99.56	99.84	99.83	99.83

Table 2.12: Fitting of the Gompertz growth model for top height growth from the Bowmont Norway spruce Thinning Experiment.

Age	Observed Data	Gompertz					
		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
Parameters	A	25.62	25.83	25.76	25.78	23.93	25.01
	β	1.49	1.50	1.49	1.50	1.47	1.48
	k	.18	.18	.18	.18	.21	.19
χ^2		0.014	0.01	0.009	0.009	0.011	0.007
RMSE		.137	.121	.117	.118	.132	.104
R^2(in %)		99.89	99.91	99.92	99.92	99.89	99.93
R_a^2		0.99	0.99	0.99	0.99	0.99	0.99
$R^2_{prediction}$ (in %)		99.87	99.88	99.89	99.89	99.86	99.92

Table 2.13: Fitting of the Monomolecular growth model for top height growth from the Bowmont Norway spruce Thinning Experiment.

Age	Observed Data	Monomolecular					
		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
Parameters	A	33.40	37.88	33.67	37.45	33.52	32.78
	β	.84	.86	.85	.86	.85	.84
	k	.07	.06	.07	.06	.08	.09
χ^2		0.012	0.016	0.01	0.014	0.01	0.01
RMSE		.137	.168	.123	.148	.123	.122
R^2(in %)		99.89	99.84	99.91	99.87	99.91	99.91
R_a^2		0.99	0.99	0.99	0.99	0.99	0.99
$R^2_{prediction}$ (in %)		99.85	99.73	99.88	99.81	99.88	99.88

2.4.3.4 For mean diameter at breast height growth from the Bowmont Norway spruce Thinning Experiment

The estimation of parameters for the growth models along with the summary of statistical analysis to mean diameter at breast height are presented in **Table 2.14**. The eliminated results in each step are also highlighted accordingly in **Table 2.14**.

Table 2.14: Fitting of the growth models for mean diameter at breast height from the Bowmont Norway spruce Thinning Experiment.

Model	Method	A	β	k	χ^2	RMSE	R^2(in %)	R_a^2	$R^2_{prediction}$ (in %)
Monomolecular	A	254.2485	0.9757	0.0090	0.07	0.415	99.56	0.99	99.29
	B	197.0727	0.9708	0.0123	0.10	0.480	99.37	0.99	98.92
	C	252.0445	0.9756	0.0090	0.07	0.393	99.58	0.99	99.36
	D	190.6542	0.9682	0.0123	0.07	0.380	99.61	0.99	99.38
	E	106.9216	0.9460	0.0238	0.06	0.346	99.68	0.99	99.52
	F	82.7384	0.9328	0.0327	0.06	0.337	99.69	0.99	99.53
Gompertz	A	42.5918	1.8758	0.1445	0.04	0.303	99.75	0.99	99.57
	B	42.4126	1.8908	0.1469	0.04	0.318	99.72	0.99	99.52
	C	42.3118	1.8732	0.1445	0.03	0.278	99.79	0.99	99.65
	D	41.6907	1.8628	0.1469	0.03	0.267	99.80	0.99	99.69
	E	33.2335	1.7768	0.2038	0.10	0.361	99.65	0.99	99.57
	F	38.0838	1.8153	0.1653	0.03	0.229	99.86	0.99	99.79
Logistic	A	33.1059	3.9194	0.2871	0.02	0.205	99.87	0.99	99.80
	B	32.7692	3.8763	0.2891	0.01	0.173	99.92	0.99	99.86
	C	32.7681	3.8575	0.2871	0.01	0.164	99.93	0.99	99.88
	D	32.5522	3.8346	0.2891	0.01	0.157	99.93	0.99	99.88
	E	32.8134	3.8648	0.2869	0.01	0.166	99.92	0.99	99.87
	F	32.7599	3.8566	0.2873	0.01	0.164	99.93	0.99	99.89

In case of mean diameter at breast growth, Monomolecular growth model (method A, B, C, D, E and F) is eliminated due to non-biologically realistic estimates of their asymptotic parameter(A). It is also observed that no results are eliminated in step II, IV and V, as all results have calculated χ^2 value less then tabulated value at 95% level of significance, all surviving results have 0.99 of R_a^2 value (**Table 2.14**) and all of their parameters are significantly different from zero (Table 2.16). The Logistic growth model with method B, C, D, E and F are promoted to the next step as they have less value of RMSE in step III. Finally, based on R^2 and $R^2_{prediction}$, the better

result is chosen and it is find Logistic growth model (method F) with the $R^2_{prediction}$ and R^2 values 99.89 and 99.93 respectively.

2.4.3.5 For cumulative basal area production from the Bowmont Norway spruce Thinning Experiment

The estimation of parameters for the growth models and the summary of statistical analysis to cumulative basal area production are presented in **Table 2.15**. The eliminated results in each step are highlighted accordingly in the **Table 2.15**. In this case, the Monomolecular growth model (method A, B, C, D, E and F) is eliminated in the step I due to non-biologically realistic estimates of their asymptotic parameter (A). Moreover, no results are eliminated in step II, IV and V. The results promoted in the step III are Gompertz growth model (method A, C and F) and Logistic growth model (method A and B). Finally, the best result is selected and found as Gompertz growth model for method F with the $R^2_{prediction}$ and R^2 values 99.90 and 99.92 respectively.

Table 2.15: Estimated parameters along with the statistical analysis for cumulative basal area production.

Model	Method	A	β	k	χ^2	RMSE	R^2(in %)	R^2_a	$R^2_{prediction}$ (in %)
Monomolecular	A	254.9126	0.8990	0.0547	0.16	1.198	99.79	0.99	99.69
	B	427.8732	0.9350	0.0275	0.22	1.577	99.66	0.99	99.42
	C	252.7398	0.8988	0.0547	0.10	0.961	99.87	0.99	99.81
	D	419.6737	0.9319	0.0275	0.20	1.381	99.73	0.99	99.59
	E	260.2751	0.9008	0.0524	0.10	0.970	99.87	0.99	99.81
	F	246.9026	0.8973	0.0566	0.10	0.958	99.87	0.99	99.81
Gompertz	A	154.2372	1.6701	0.1880	0.09	0.867	99.89	0.99	99.87
	B	175.1747	1.7565	0.1589	0.15	1.141	99.82	0.99	99.72
	C	155.2063	1.6914	0.1880	0.08	0.784	99.91	0.99	99.89

	D	174.9517	1.7589	0.1589	0.15	1.115	99.83	0.99	99.74
	E	147.5676	1.6857	0.2055	0.14	1.068	99.84	0.99	99.80
	F	158.9386	1.7017	0.1812	0.07	0.748	99.92	0.99	99.90
Logistic	A	139.8948	3.4201	0.3000	0.15	0.895	99.89	0.99	99.87
	B	141.2550	3.5000	0.2998	0.14	0.897	99.89	0.99	99.87
	C	143.9179	3.6409	0.3000	0.22	1.277	99.77	0.99	99.69
	D	144.0177	3.6430	0.2998	0.22	1.285	99.77	0.99	99.68
	E	130.6011	3.3809	0.3409	0.22	1.380	99.73	0.99	99.73
	F	130.7002	3.3812	0.3405	0.21	1.369	99.74	0.99	99.64

From the results, it is observed that for top height growth data of babul tree, Monomolecular growth model along with methods A, C, D, E and F is found to be more suitable than the remaining growth models whereas Monomolecular growth model with method C, D, E and F provides a better fit for maximum growth data. In case of for top height age data and for cumulative basal area production from the Bowmont Norway spruce thinning experiment, the Gompertz growth model (method F) and for the mean diameter at breast height data, originated from the Bowmont Norway spruce thinning experiment, the Logistic growth model (method F) produced a better fit than the others.

Table 2.16: 95% Confidence intervals of the parameters of the candidate models.

Data	Models	Method	A		β		k	
			Lower limit	Upper limit	Lower limit	Upper limit	Lower limit	Upper limit
Top height growth of babul trees.	Monomolecular	A	19.497	21.438	0.855	0.942	0.337	0.463
		B	18.895	22.427	0.823	0.969	0.282	0.499
		C	19.681	21.199	0.864	0.932	0.351	0.449
		D	19.656	21.511	0.854	0.931	0.333	0.448
		E	19.717	21.214	0.864	0.930	0.350	0.447
		F	19.719	21.216	0.864	0.930	0.350	0.446
Maximum diameter growth of babul trees	Monomolecular	A	36.172	47.168	0.907	1.093	0.227	0.465
		B	35.563	47.366	0.899	1.104	0.219	0.480
		C	37.346	46.261	0.927	1.077	0.250	0.442
		D	37.286	46.005	0.928	1.080	0.254	0.446
		E	37.351	46.307	0.926	1.077	0.250	0.442

		F	37.328	46.101	0.928	1.079	0.253	0.444
Top height growth data from the Bowmont	Gompertz	B	24.358	27.301	1.464	1.542	0.161	0.198
		C	24.347	27.174	1.462	1.538	0.162	0.198
		D	24.357	27.211	1.462	1.538	0.162	0.198
		F	23.890	26.124	1.451	1.516	0.173	0.206
	Monomolecular	F	28.680	36.889	0.831	0.857	0.061	0.095
mean diameter at breast height	Logistic	B	31.296	34.243	3.710	4.043	0.269	0.309
		C	31.346	34.190	3.699	4.016	0.268	0.306
		D	31.226	33.878	3.685	3.984	0.271	0.307
		E	31.368	34.258	3.704	4.025	0.268	0.306
		F	31.344	34.176	3.699	4.014	0.268	0.306
Cumulative basal area	Gompertz	A	144.385	164.089	1.623	1.717	0.167	0.209
		C	146.229	164.183	1.649	1.734	0.169	0.207
		F	149.522	168.356	1.660	1.743	0.163	0.199
	Logistic	A	133.630	146.159	3.253	3.588	0.276	0.324
		B	134.872	147.638	3.329	3.671	0.276	0.323

2.5 Conclusion

The main focus of this Chapter is to develop some new method of estimations required for estimating the parameters of three nonlinear models, namely, Gompertz, Monomolecular and Logistic. The validity of these methods is tested with five experimental data sets. All the results are demonstrated and analyzed in the last section. It is observed that the method F produces better results for all five sets of data considered in this study with all growth models. It is also observed that the method A requires only three equidistant points. So, if only a few observations are available then the method A may be more appropriate.

It is also noted that, in the estimation of parameters, all the nonlinear iterative methods require certain initial values. This study introduces four methods of estimation (method A, B, C and D) which may be helpful to provide the initial values of the parameters for use of any iteration method.

*****