On Hyperbolic Monomolecular growth model in Height/Diameter growth of PINES

S. O. OYAMAKIN AND A. U. CHUKWU

Abstract

This paper proposed a hyperbolic monomolecular growth model (HMMGM). It came as a solution to the improved monomolecular growth equation which was developed by injecting an allometric parameter θ into the intrinsic rate of growth of the monomolecular growth equation using a hyperbolic sine function. Its ability in model prediction was compared with the classical monomolecular growth model an approach which mimicked the natural variability of height/diameter increment with respect to age and therefore provides a more realistic height/diameter predictions using goodness of fit tests and model selection criteria. The Kolmogorov Smirnov test and Shapiro-Wilk test was also used to test the compliance of the error term to normality assumptions while using testing the independence of the error term using the runs test. The mean function of top height/Dbh over age using the two models under study predicted closely the observed values of top height/Dbh in the hyperbolic monomolecular nonlinear growth models better than the source model (classical monomolecular growth model) while the results of R^2 , Adj. R^2 , MSE and AIC confirmed the predictive power of the Hyperbolic Monomolecular growth models over its source model.

Additional Key Words and Phrases: height, Dbh, forest, *Pinus caribaea*, hyperbolic, monomolecular

1. INTRODUCTION

Growth is one of the well-known features in biological creatures (Burkhart and Strub, 1974). Growth models describe the changing size of something over time. Forest growth models are very useful for forest managers and forestry researchers in many respects. A forest growth model aims to describe the dynamics of the forest closely and precisely enough to meet the needs of the forester or forestry researcher.

The monomolecular model assumes a carrying capacity of K , that is, the maximum sustainable growth is K . The originator of this model suggested that the growth of the species is directly proportional to the difference between the maximum sustainable constant K and the total height. The model has a differential form given as;

$$\frac{\partial H}{\partial t} = r(K - H)$$

The process of developing a mathematical model is termed mathematical modeling. A model may help to explain a system and to study the effects of different components, and also to make predictions about behavior. A model may be deterministic or stochastic. A deterministic growth model gives an estimate of the expected growth of a system. Given the same initial conditions, a deterministic model will always predict the same result. A stochastic model attempts to illustrate natural variation by providing different predictions, each with a specific probability of occurrence.

Deterministic and stochastic models serve complementary purposes. In forestry, deterministic models are effective for determining the expected yield, and may be used to indicate the optimum stand condition. Stochastic models may indicate the reliability of these predictions, and the risks associated with any particular regime. Both deterministic and stochastic predictions can be obtained from some models. Although stochastic models can provide some useful information not available from deterministic models, most of the information needed for forest planning and managements can be provided efficiently also with the use of deterministic models.

Forest managers rely on growth and yield models to assess whether their short-term plans will meet long-term sustainability goals. Growth models assist forest researchers and managers in many ways. Some important uses include the ability to predict future yields and to help consider alternative cultivation practices. Models provide an efficient way to prepare resource forecasts, but a more important role may be their ability to explore management options and silvicultural alternatives EK, A.R., E.T. Birdsall, and R.J.Spear (1984). Growth models provide a reliable way to examine silvicultural and harvesting options, to determine the sustainable timber yield, and examine the impacts of forest management and harvesting on other values of the forest. Forest managers may require information on the present status of the resource (e.g. numbers of trees by species and sizes for selected strata), forecasts of the nature and timing of future harvests, and estimates of the maximum sustainable harvest. Forest simulation models or forest growth models are very useful for forest managers and forestry researchers in many respects. A forest growth model aims to describe the

dynamics of the forest closely and precisely enough to meet the needs of the forester or forestry researcher.

A mathematical description of a real world system is often referred to as a mathematical model. A system can be formally defined as a set of elements also called components. A set of trees in a forest stand, producers and consumers in an economic system are examples of components. The elements (components) have certain characteristics or attributes and these attributes have numerical or logical values. Among the elements, relationships exist and consequently the elements are interacting. The state of a system is determined by the numerical or logical values of the attributes of the system elements. Experimenting on the state of a system with a model over time is termed simulation (Kansal et al. 2000). Sustainable forest management relies to a large extent, measure on the predictions of the future conditions of individual stands which is achieved by predicting the increment from the current stand structure and updating the current values at each cycle of iteration using a functional growth model. Trees structural changes over time can be monitored and modeled under different cutting cycles, cutting intensities and optimal management policies can be arrived at based on the results of such simulation runs.

The total height (Ht) of a tree is important for computing and estimating tree volume, stand characteristics and features through site index, but accurate measurement of this variable is time consuming. As a result, foresters often choose to measure only a few trees' heights and estimate the remaining heights with height-diameter equations. Foresters can also use height-diameter equations to indirectly estimate height growth by applying the equations to a sequence of diameters that were either measured directly in a continuous inventory or predicted indirectly by a diameter-growth equation (Zeide 1993). The diameter-growth prediction method is very useful in modeling growth and yield of trees due to lack of approximations in measuring the diameter of trees. Curtis (1967) investigated several equations for Douglas-fir that included tree diameter outside bark at breast height (DBH) as an explanatory variable.

In this paper, an alternative nonlinear growth model called the hyperbolic monomolecular growth model was introduced and compared with the existing classical monomolecular model, which is an improvement on the exponential growth model, by Malthus.

2. MATERIALS AND METHODS

Consider a nonlinear model

$$H_i = f(D_i, \mathbf{B}) + \mathcal{E}_i \quad (1)$$

$i = 1, 2, \dots, n$, Where H is the response variable, D is the independent variable, $\mathbf{B}$ is the vector of the parameters β_j to be estimated ($\beta_1, \beta_2 \dots \dots, \beta_p$), $\mathcal{E}_i$ is a random error term, p is the number of unknown parameters, n is the number of observation. The estimator of β_j 's are found by minimizing the sum of squares residual (SS_{RSS}) function

$$SS_{RSS} = \sum_{i=1}^n [H_i - f(D_i, B)]^2 \quad (2)$$

Under the assumption that the $\mathcal{E}_i$ are normal and independent with mean zero and common variable σ^2 . Since H_i and D_i are fixed observations, the sum of squares residual is a function of $\mathbf{B}$, these normal equations take the form of

$$\sum_{i=1}^n \{H_i - f(D_i, \mathbf{B})\} \left[\frac{\partial f(D_i, \mathbf{B})}{\partial \beta_j} \right] = 0 \quad (3)$$

For $j = 1, 2, \dots, p$. When the model is nonlinear in the parameters so are the normal equations consequently, for the nonlinear model consider the table 2, it is impossible to obtain the closed solution of the least squares estimate of the parameter by solving the p normal equations describe in Eq (3). Hence an iterative method must be employed to minimize the ss_{Res} (Draper and Smith 1981, Ratkowsky 1983, Marquardt 1963, Seber & Wild 1989, Fekedulegn 1996).

The hyperbolic functions have similar names to the trigonometric functions, but they are defined in terms of the exponential function. The three main types of hyperbolic functions, and the sketch of their graphs are giving below.

Fig 2 Cosh Function **Fig 3** Sinh Function **Fig 4** Tanh Function

Hence, the hyperbolic sine function and its inverse provide an alternative method for evaluating;

$$\int \frac{1}{\sqrt{1+x^2}} dx$$

If we make the substitution, then;

$$\sqrt{1+x^2} = \sqrt{1+\sinh^2(u)} = \sqrt{\cosh^2(u)} = \cosh(u)$$

Where the second equality follows from the identity $\cosh^2(u) - \sinh^2(u) = 1$ and the last equality from the fact that $\cosh(u) > 0$ for all u . Hence;

$$\int \frac{1}{\sqrt{1+x^2}} dx = \int \frac{\cosh(u)}{\cosh(u)} du = \int du = u + c = \sinh^{-1}(x) + c$$

The following proposition is a consequence of the integral above i.e.

$$\frac{d}{dx} \sinh^{-1}(x) = \frac{1}{\sqrt{1+x^2}}$$

Also, using the substitution $x = \tan(u)$, $-\frac{\pi}{2} < u < \frac{\pi}{2}$, that

$$\int \frac{1}{\sqrt{1+x^2}} dx = \log |x + \sqrt{1+x^2}| + c$$

Since two anti-derivatives of a function can differ at most by a constant, there must exist a constant k such that

$$\sinh^{-1}(x) = \log |x + \sqrt{1+x^2}| + k$$

for all x . Evaluating both sides of this equality at $x = 0$, we have

$$0 = \sinh^{-1}(0) = \log(1) + k = k$$

Thus $k = 0$ and

$$\sinh^{-1}(x) = \log \left| x + \sqrt{1 + x^2} \right|$$

for all x . Since the hyperbolic sine function is defined in terms of the exponential function, we should not find it surprising that the inverse hyperbolic sine function may be expressed in terms of the natural logarithm function.

3. HYPERBOLASTIC MONOMOLECULAR GROWTH MODEL (HMMGM)

$$\frac{\partial H}{\partial t} = (K - H) \left[r + \frac{\theta}{\sqrt{1 + t^2}} \right]$$

Separating variables we have that;

$$\frac{\partial H}{K - H} = \left[r + \frac{\theta}{\sqrt{1 + t^2}} \right] dt$$

Integrating both sides we have;

$$-\ln(K - H) = rt + \theta \operatorname{arcsinh}(t) + C_1$$

$$\ln(K - H)^{-1} = rt + \theta \operatorname{arcsinh}(t) + C_1$$

Taking the exponential of both sides we have;

$$(K - H)^{-1} = Ae^{rt + \theta \operatorname{arcsinh}(t)}$$

$$\frac{1}{K - H} = Ae^{rt + \theta \operatorname{arcsinh}(t)}$$

Multiply both sides by $(K - H)$ to have;

$$1 = KAe^{rt + \theta \operatorname{arcsinh}(t)} - HAe^{rt + \theta \operatorname{arcsinh}(t)}$$

$$HAe^{rt + \theta \operatorname{arcsinh}(t)} = KAe^{rt + \theta \operatorname{arcsinh}(t)} - 1$$

Making H the subject of the formula results into;

$$H = \frac{KAe^{rt+\theta\text{arcsinh}(t)} - 1}{Ae^{rt+\theta\text{arcsinh}(t)}}$$

Divide through by $Ae^{rt+\theta\text{arcsinh}(t)}$ to obtain;

$$H = K - Ae^{-rt-\theta\text{arcsinh}(t)}$$

Therefore, we shall apply the two models below on Age-height and Age-Diameter of pines (*pinus caribaea*) growth;

$$(1) H = K - Ae^{-rt-\theta\text{arcsinh}(t)} + \varepsilon, \text{ and } D = K - Ae^{-rt-\theta\text{arcsinh}(t)} + \varepsilon$$

$$(2) H = K - Ae^{-rt} + \varepsilon, \text{ and } D = K - Ae^{-rt} + \varepsilon$$

4. RESULTS AND DISCUSSION

Figures and Tables

Table 1 below shows the goodness of fit results of the monomolecular (source) and hyperbolic monomolecular growth model (Proposed) with their respective coefficient of determination (R^2), Mean Square error (MSE) and Akaike Information Criterion (AIC) for age-height/age-diameter models.

Table 1 Summary of model selection criteria computed for the Proposed and Source models

Models	SSE	N	K	R^2	MSE	AIC
SOURCE(Ht)	17.548	17	3	94.60%	1.253	6.539352867
PROPOSED(Ht)	14.862	17	4	95.40%	1.143	5.715102687
SOURCE(Dbh)	5.88	17	3	98.70%	0.42	-12.0481619
PROPOSED(Dbh)	3.053	17	4	99.30%	0.235	-21.19050672

Also, the predicted and observed height and diameter were plotted to show the relationship and how best the models predicted the observed data on height and diameter of pines. This is also shown in the figure below:

Fig 5 Observed Height against Predicted height (Monomolecular growth model)

Fig 6 Observed Height against Predicted height (Hyperbolic monomolecular growth model)

Fig 7 Observed Diameter against Predicted diameter (Monomolecular growth model)

Fig 8 Observed Diameter against Predicted diameter (Hyperbolic monomolecular growth model)

Testing for independence of errors (Run test) and Normality of Error (Shapiro-Wilk test)

Two assumptions made in the models are:

- Errors are independent
- Errors are normally distributed.

These assumptions were verified by examining the residuals. If the fitted models are correct, residuals should exhibit tendencies that tend to confirm or at least should not exhibit a denial of the assumptions.

Hence, we tested the following hypotheses stated below;

H_0 : Errors are independent (Using Runs Test)

H_1 : Errors are not independent

And

H_0 : Errors are normally distributed (Using Shapiro-Wilk test and K-S test)

H_1 : Errors are not normally distributed

Let m be the number of pluses and n be the number of minuses in the series of residuals. The test is based on the number of runs(r), where a run is defined as a sequence of symbols of one kind separated by symbols of another kind. A good large sample approximation to the sampling distribution of the number of runs is the normal distribution with mean;

$$Mean = \frac{2mn}{m+n} + 1$$

and,

$$Variance(\sigma^2) = \frac{2mn(2mn - m - n)}{(m+n)^2(m+n-1)}$$

Therefore, for large samples like ours the required test statistic is;

$$Z = \frac{(r + h - \mu)}{\sigma} \sim N(0,1)$$

where,

$$h = \begin{cases} 0.5, & \text{if } r < \mu \\ -0.5, & r > \mu \end{cases}$$

Also, the required test statistic for the test of normality (Shapiro-Wilk test) is given by;

$$W = \frac{S^2}{b}$$

Where;

$$S^2 = \sum a(k)\{x_{n+1-k} - x_{(k)}\}$$

and,

$$b = \sum (x_i - \bar{x})^2$$

In the above, the parameter k takes the values;

$x_{(k)}$ is the k^{th} order statistic of the set of residuals and the values of coefficient $a(k)$ for different values of n and k are given in the Shapiro-Wilk table. H_0 is rejected at level α i.e. W is less than the tabulated value.

Table 2 Result of the test of independence of Residuals using Run Test

Residual	Test Value	No of Runs	Z	Asymp. Sig.(2 tailed)
Mono. Height	-0.0006	6	-1.494	0.135 ^{ns}
Mono. Diameter	0.0000	8	-0.488	0.626 ^{ns}
HMGM. Height	0.0024	6	-1.494	0.135 ^{ns}
HMGM.Diameter	0.0035	10	0.015	0.988 ^{ns}

^{ns} not significant**Table 3** Result of the test of normality of Residuals using K-S & S-W Tests

Residual	Kolmogorov-Sminov		Shapiro-Wilk	
	Statistic	Asmp. Sig.	Statistic	Asmp. Sig.
Mono. Height	0.150	0.200^{ns}	0.961	0.649^{ns}
Mono. Diameter	0.193	0.094^{ns}	0.945	0.386^{ns}
HMGM. Height	0.150	0.200^{ns}	0.958	0.603^{ns}
HMGM.Diameter	0.131	0.200^{ns}	0.973	0.863^{ns}

^{ns} not significant

The results as given in table 2 and 3 above showed that the assumption of the error term was not violated as the runs test, K-S test and S-W test computed showed that the error term is independent and normal in its distribution.

5. CONCLUSION AND RECOMMENDATION

We have succeeded in introducing a new growth model using the hyperbolic function. The mean function of top height and Dbh over age using the Hyperbolic Monomolecular growth model predicted closely the observed values of top height and Diameter of Pines. Finally, our proposed models show very promising results and using the above discussed data sets, they fitted the data with smaller AIC, MSE, and higher prediction accuracy than its source model. We strongly believe that choosing a flexible and highly accurate predictive model such as ours can significantly improve

the outcome of a study because the accuracy of a model is what determines its utility. Hence, we recommend usage of our proposed models to the scientific community and practitioners and urge comparison of them with classical models before decisions on model selection are made.

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S. O. Oyamakin
Department of Statistics,
University of Ibadan, Nigeria

A. U. Chukwu
Department of Statistics,
University of Ibadan, Nigeria