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On Hyperbolic Monomolecular Growth Model in Height/ Diameter Growth of PINES

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Original Research Article

Abstract

This paper proposed a hyperbolic monomolecular growth model (HMMGM). The stabilizing parameter θ was introduced into the existing growth equations using a hyperbolic sine function given by $\int \frac{1}{\sqrt{1+t^2}} dt$.

The reparametized equation namely, Hyperbolic Monomolecular Growth Equation, which was solved to obtain the proposed growth model. Residual errors were incorporated into the model additively and statistical tests of independence and normality of the error components was done. Pine data on height, Diameter and Age was used to test the comparative merits of the proposed model over its source model. The performance of the developed model based on data were tested in terms of general fitness and internal predictive status using model selection criteria like R-Square, Mean Square Error (MSE), and Akaike Information Criterion (AIC) among others.

1 Introduction

The processes of growth play an important role in various applied areas, such as biology, medicine, and forestry to mention but a few. Plant growth modeling has become a key research activity, particularly in the field of agriculture, forestry and environmental science [1-2]. Due to the growth of computer resources and sharing experience between biologist, mathematicians and computer scientists, the development of plants

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growth models has progressed enormously during the last two decades [3-4]. These models are vitally important for forest management planning. Forecasting the growth and yield of individual stand is a prerequisite for planning the management of forest at any level [5-8]. Therefore managers need to have an appreciation for the various modeling techniques [9-10] and their limitations. [11-12] gave an overview of models used in forest ecosystem management. These authors described the very first ecosystem models to be used, which were maps in displaying the location of hunting grounds, forest and pastures.

[13] employed a modification of the generalized Chapman - Richard growth function based on Von Bertalanffy's growth model to examine growth data from a permanent sample plot of Usonigbe forest Reserve in Nigeria. In addition [13] used the Markov model to assess tree population changes and future stand structures in the untreated natural forests and used the value of dominant latent root to examine the stable state of distribution of the population in the untreated forests of Usonigbe. He observed that most members of a given size remained in the respective size class at some future date because of the slow growth rate. [14] applied matrix models to study the population dynamics of trees in Idanre Forest Reserve. He used the population growth matrix model to predict long-term growth of the untreated natural forests, of particular interest was the stand density and basal area growth and developed a linear programming approach to determine the maximum sustainable yield in the forest of Idanre. He also developed a stochastic matrix model for simulating secondary succession in the untreated forest and was able to project the composition of the stand using the current species composition. [14] concluded that increased growth rate (30-40%) was required to reach a stable state in the forest. [15] used the matrix modeling procedure to project the compositions in Oban, Omo, Owan and Sapoba Forest Reserves. He investigated the stable structure and obtained the stand table projection using matrix multiplication sequence.

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;

$$\frac{dH}{dt} = r(K - H) \tag{1}$$

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 Methodology

According to [16-17], the hyperbolic functions can be defined in terms of the exponential function and the three main types of hyperbolic functions, and the sketch of their graphs are giving below.

Considering the Figs. 1, 2 and 3 in respect to biological studies, it is believed that a tree height/Dbh at time t can only be greater or equal to height/dbh at time (t + n). Hence, the hyperbolic sine function and its inverse provide an alternative method for evaluating;

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

and evaluating equation 2 gives the result below as obtained in [16,17].

$$sinh^{-1}(x) = log \left| x + \sqrt{1 + x^2} \right| \tag{3}$$

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 [18].
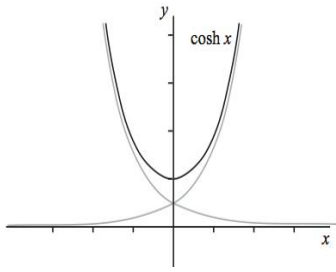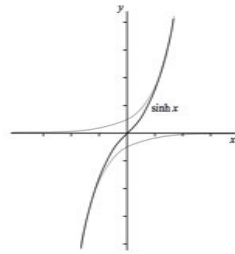
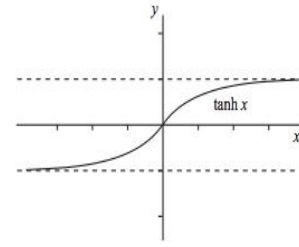**Fig. 1. Cosh Function**   **Fig. 2. Sinh Function**   **Fig. 3. Tanh Function**

3 Hyperbolic Monomolecular Growth Model (HMMGM)

Let the hyperbolic sine function be conditioned on the monomolecular growth equation in (1) then we have that;

$$\frac{dH}{dt} = (K - H)\left[r + \frac{\theta}{\sqrt{1 + t^2}}\right] \tag{4}$$

Separating variables we have that;

$$\frac{dH}{K - H} = \left[r + \frac{\theta}{\sqrt{1 + t^2}}\right] dt \tag{5}$$

Integrating both sides we have;

$$-\ln(K - H) = \mathrm{rt} + \theta \mathrm{arcsinh}(t) + C_1$$
$$\ln(K - H)^{-1} = \mathrm{rt} + \theta \mathrm{arcsinh}(t) + C_1 \tag{6}$$

Taking the exponential of both sides we have;

$$(K - H)^{-1} = Ae^{\mathrm{rt} + \theta \mathrm{arcsinh}(t)} \tag{7}$$
$$\frac{1}{K - H} = Ae^{\mathrm{rt} + \theta \mathrm{arcsinh}(t)}$$

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

$$1 = KAe^{\mathrm{rt} + \theta \mathrm{arcsinh}(t)} - HAe^{\mathrm{rt} + \theta \mathrm{arcsinh}(t)}$$
$$HAe^{\mathrm{rt} + \theta \mathrm{arcsinh}(t)} = KAe^{\mathrm{rt} + \theta \mathrm{arcsinh}(t)} - 1 \tag{8}$$

Making H the subject of the formula results into;

$$H = \frac{KAe^{\mathrm{rt} + \theta \mathrm{arcsinh}(t)} - 1}{Ae^{\mathrm{rt} + \theta \mathrm{arcsinh}(t)}} \tag{9}$$

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

$$H = K - Ae^{-\mathrm{rt} - \theta \mathrm{arcsinh}(t)} \tag{10}$$

where K is the maximum sustainable Pine height, A is the initial height as at when data collection started, r is the intrinsic rate of growth and θ is the stabilizing parameter (Allometric parameter).

Data on Height and diameter at breast height of Pines (*Pinus caribaea*) were obtained from the growth and yield section of Sustainable forest management Department, Forestry Research Institute of Nigeria, Ibadan with their respective ages. Hence, we applied the modeling two forms namely Age-height and Age-Diameter of pines (*Pinus caribaea*). This is stated below as;

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

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

where H is the Top height, D is the diameter at breast height, t is the Age of the tree, K is the asymptote, A is the initial height/diameter, r is the rate of growth and ε is the error term. Methods of estimating parameters of nonlinear models and model selection criteria as suggested by [19-23], were used in this study.

4 Results and Discussion

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	-21.1905067

Genereal fittness of the proposed over its source model were compared in term of R^2, Mean Square Error (MSE) and Akaike Information Criterion (AIC) as shown in Table 1. To further assess the fitness potential of the proposed model, the predicted and observed height and diameter were also plotted in Figs. 4 - 7. This is to show the relationship and how best the models predicted the observed data on height and diameter of pines.
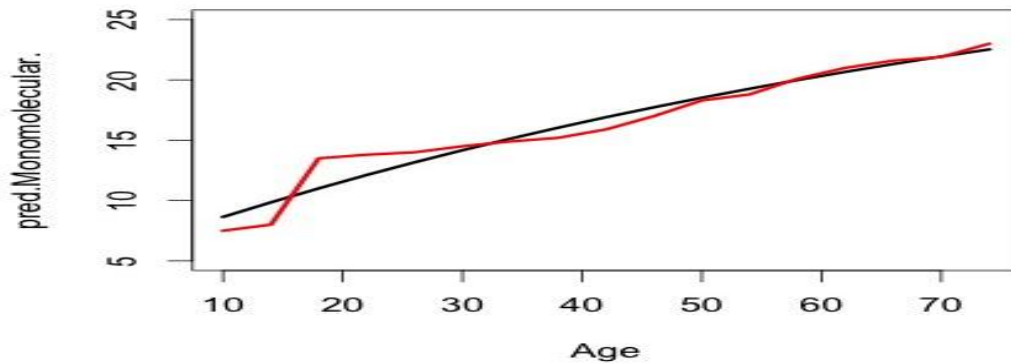
Fig. 4. Observed Height against Predicted height (Monomolecular growth model)

A residual analysis was carried out to test for possible violations of the assumptions of the models. This was studied in terms of normality and independence of the error term. The result of this is given below in Tables 2 and 3.
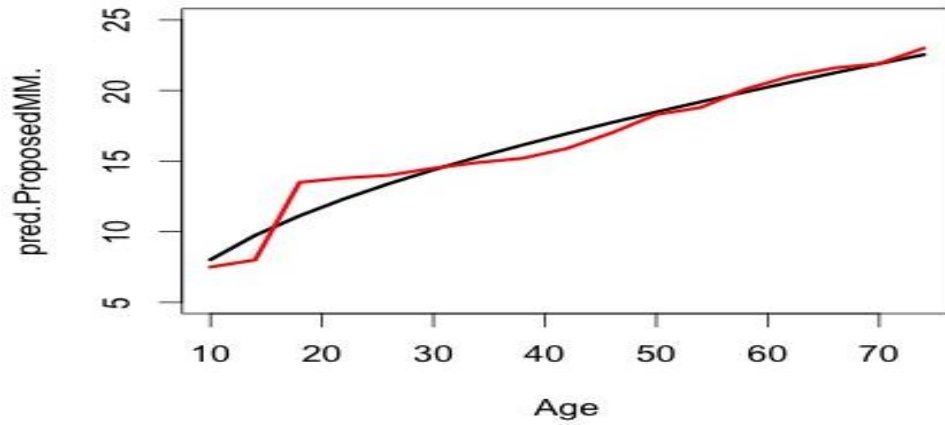
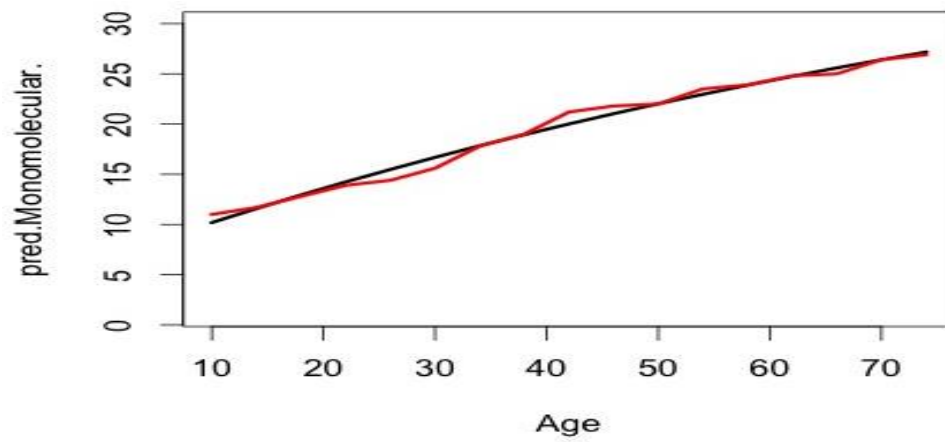**Fig. 5. Observed Height against Predicted height (Hyperbolic monomolecular growth model)**

Fig. 6. Observed Diameter against Predicted diameter (Monomolecular growth model)
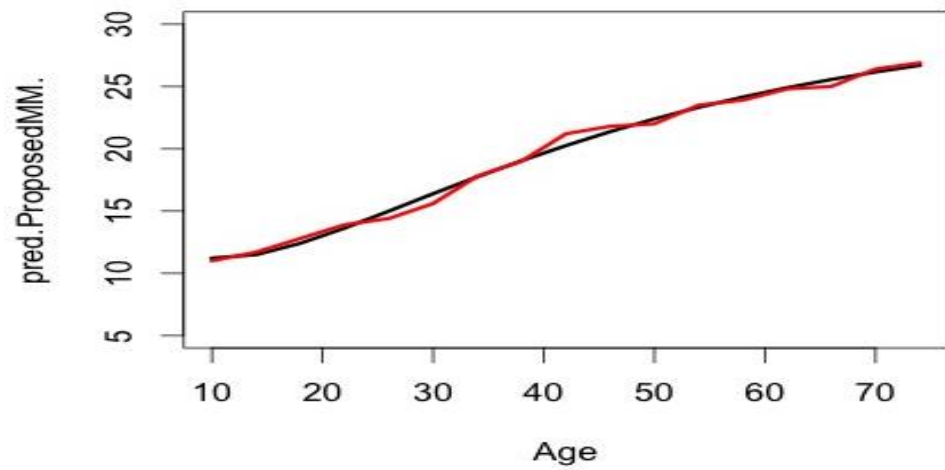

Fig. 7. Observed Diameter against Predicted diameter (Hyperbolic monomolecular growth model)

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 Tables 2 and 3 above showed that the assumption of the error term was not violated as the runs test, Kolmogorov Smirnov (K-S) test and Shapiro Wilk (S-W) test computed showed that the error term is independent and normal in its distribution.

5 Conclusion and Recommendation

Based on the results obtained in this study using the Pine data collected from the Department of Forest Management, Forestry Research Institute of Nigeria, It is our believe that we have showed the general fitness of the proposed model over its source model. This has suggested a new growth model called the Hyperbolic Monomolecular Growth model. 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 model to the scientific community and practitioners and urge comparison of them with classical models before decisions on model selection are made.

Competing Interests

Authors have declared that no competing interests exist.

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