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# On a New Growth Model Namely Korkmaz Model Compared with Some Growth Models

Bazı Büyüme Modelleri ile Karşılaştırılan Korkmaz Modeli Olarak Adlandırılan Yeni Bir Büyüme Modeli Üzerine

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#### Abstract

For growth models, in addition to some classical growth models, I derived a new model. In this study, I derived a new model by using this expression: "Growth models has generally sigmoidal shape. In this shape there is one inflection point. Until this inflection point the graph is convex that's until this inflection point the growth rate is increasing. At this infection point the growth rate reaches maximum value. After this inflection point the graph is concave that's after this inflection point the growth rate is decreasing." Growth models were generally derived by using the last part of this situation. That's Growth models were generally derived by using this expression: "Growth rate goes to zero when the time is too large or approaches infinity". After introducing this new model, namely Korkmaz model, I applied two sets of data. In addition to Korkmaz model, I used growth models such as Logistic, Brody, Gompertz, and Von Bertalanffy. They are compared by using error sum of squares criteria. According to this criteria, it was seen that none of the models used has minimum error sum of squares for each data set. That's while one model is not the best model for one data set, that model could not be the best model for the other data set. Actually, Although Korkmaz model is not the best model for two sets of data by using error sum of squares criteria is not the best model for two sets of data by using error sum of squares criteria models in their studies on growth data was suggested to the researchers using growth models in their studies.

Keywords: Growth models, Korkmaz model

# Öz

Bazı klasik büyüme modellerine ek olarak büyüme modelleri için yeni bir model elde ettim. Bu çalışmada, yeni bir modeli bu ifadeyi kullanarak elde ettim :"Büyüme modelleri genellikle sigmoidal şekle sahiptir. Bu şekilde bir dönüm noktası vardır. Bu dönüm noktasına kadar grafik konveksdir yani bu dönüm noktasına kadar büyüme hızı artıyor. Bu dönüm noktasında büyüme hızı maksimum değere ulaşır. Bu dönüm noktasından sonra grafik konkavdır yani bu dönüm noktasından sonra büyüme hızı azalıyor." Büyüme modelleri genellikle bu durumun son kısmı kullanılarak elde edilir. Yani büyüme modelleri genellikle bu ifadeyi kullanarak elde edilir: "Zaman çok fazla olduğunda veya sonsuza yaklaştığında büyüme hızı sıfıra gider." Korkmaz modeli olarak adlandırılan bu yeni modelin tanıtımından sonra iki veri setine uygulama yaptım. Korkmaz modele ek olarak, Logistic, Brody, Gompertz, ve Von Bertalanffy gibi büyüme modelleri kullandım. Onlar hata kareler toplamı kriteri kullanılarak karşılaştırıldı. Bu kritere göre, modellerden hiçbirisinin her iki veri seti için en iyi model olmayabilir. Aslında, Korkmaz modeli her iki veri seti için hata kareler toplamı kalı korkmaz modeli her iki veri seti için en iyi model olmayabilir. Aslında, Korkmaz modeli her iki veri seti için hata kareler toplamı kriterini göre en iyi model olmamasına rağmen bu çalışmada Korkmaz modeli en iyi modellerden biridir. Bu sebeple, büyüme verileri üzerine çalışan araştırmacıların çalışmalarında kullandıkları klasik büyüme modellerine ek olarak Korkmaz modelinin kullanımı bu araştırmacılara önerilmektedir.

Anahtar Kelimeler: Büyüme modelleri, Korkmaz modeli

## 1. Introduction

Fitzhugh (1976) stated that a primary objective in fitting growth curves to data was to use their descriptive properties.

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Many mathematical equations representing growth have been developed (Brody 1945; Gompertz 1825; Von Bertalanffy 1957; Ricker 1979; Richards 1959). A growth curve is simply a mathematical relation between weight or length of an animal and time (Fabens 1965). Growth curves relate the interrelationships of the genetic ability of an animal to grow and mature and the environment in which the animal grows (Fitzhugh 1976). One of the main advantages in using a mathematical equation or model to describe growth is that it consolidates the information contained in the weight or length- age data into three or four biologically interpretable parameters. These parameters could then be compared between populations and the groups used (Goonewardene et al. 1981). The choice of a growth function to study this complex phenomenon of growth must depend on how accurately it fits the data at each specific age along the growth curve, as well as over all the data points. Once such a satisfactory growth function has been recognized it could be used for descriptive, predictive and comparative purposes in populations, on the assumption that it simulates the true biological model (Brown 1972).

While it is thought that many of the models generally empirical, static, and deterministic in form are based on a linear relationship between age and weight or length, similar to: weight or length = a + b(age); where a = intercept and b = slope (Russell, 1969), a classic growth curve has sigmoidal shape. This curve can be divided into two phases. While one of these phases is the self-accelerating phase, the other is self-inhibiting phase. The meeting point of these two phases is the infection point.

Some non-linear models such as the monomolecular or Brody function (Brody 1945) is of the decaying exponential type with no inflection point. For these models, the highest growth rate occurs at birth and decreases continually. The curve of logistic model (Ricker 1979) is symmetrical around its inflection point. Growth rate increases with age and weight or length until the inflection point, where it decreases until maximum age is reached. The curve of Gompertz model has an inflection point earlier than a curve of logistic models. In addition, the Gompertz curve is asymmetrical about its inflection point. The Richards function is essentially a modification of the monomolecular curve, with M added as an exponent to adjust the proportion of mature size at the inflection point. Richards (1959) adjusted the monomolecular curve with M to add flexibility, hence increasing its usefulness. Therefore, when M = 1, the monomolecular and Richards functions are identical (Bethard 1997).

The previously described functions (monomolecular, logistic, Gompertz, Bertalanffy, and Richards) all assume growth is a continuous process resulting in a smooth shaped growth curve (Bethard 1997).

## 1.1. Applications of Growth Curves

Fitting a growth curve to a group of animal weights assumes the actual growth curve is similar in shape to the curve being fit. With this assumption, parameters are estimated from field data. Fitting consists of estimating parameters such that the differences between observed and predicted values (residuals) are minimized. A "good fit" would be a situation where residuals are small. Graphical analysis is helpful in selecting a growth curve to fit (Bethard 1997).

## 1.2. Growth Rates

Size can be measured in weight, height, length, etc. Growth in weight (gain) can be classified into absolute, relative, and cumulative gain. Absolute gain is the change in weight per unit time, described by the equation

$$R = (y2 - y1) / (t2 - t1)$$

where  $(y_2 - y_1)$  is the observed weight difference,  $(t_2 - t_1)$  is the change in time, and R is growth rate.

This equation represents average growth rate over a period of time, a constant daily rate. For example, a 100 day old heifer that gained 100 kg would have an absolute growth rate of 1 kg per day. This heifer probably did not gain exactly 1 kg each day, rather she gained more or less than 1 kg per day for 100 days to average 1 kg absolute gain. Therefore, relative growth rates defined over a considerable length of time may not provide useful information pertaining to the profile of growth of the animal. The shorter the time period, the closer absolute growth rate is to true growth rate (Bethard 1997). Brody (1945) states that when absolute growth rate is reduced to an interval, dt, sufficiently short to eliminate changes in growth rate, the true growth rate, (dy/ dt ) is obtained. Brody (1945) therefore defined true growth rate as the instantaneous growth, (dy/dt).

Relative growth rate is simply growth rate on a percentage basis, or

R = (y2 - y1) / y1

where y1 is weight at the beginning of the time interval.

Similar to absolute growth rate, the relative growth rate does not represent true growth rate. True growth rate would be approached when (y2 - y1) is very small. Brody (1945) suggested using the average weight of the animal to calculate relative growth rates, or

(y2-y1)/[0.5(y2-y1)]

is a more accurate method of computing relative growth. However, both equations are not physiologically based, as time is not considered. Using the concept of instantaneous growth, Brody suggested using the formula

$$\frac{\frac{dy}{dt}}{\frac{y}{y}}$$

to compute instantaneous relative growth rate.

Although in theory instantaneous or true growth is desired in determining growth rates, calculation is impossible in a practical situation. However, Brody (1945) derived a method of determining absolute growth rate by using calculus. The derivation is as follows:

$$\begin{aligned} \frac{dy}{dt} &= ky\\ \frac{dy}{y} &= kdt\\ \int \frac{dy}{y} &= \int k \, dt\\ Iny &= InC + kt\\ y &= Ce^{kt} \end{aligned}$$

Instantaneous absolute growth rate is  $\frac{dy}{dt}$  and k represents instantaneous relative growth rate. The instantaneous relative growth rate k can be computed by:

k = (lny2 - lny1)/(t2-t1)

where (t2-t1) is the time interval.

Percentage growth rate would be k\*100. The constant C has the value of y when t = 0. Therefore, through mathematical manipulation, instantaneous growth for a given unit of time (k) rate can be determined. After that Brody found Brody model by using similar way. The derivation of Brody model (Brody 1945) is as follows: This model can be derived from the following differential equation 1

$$\frac{dy}{dt} = k(A-y)$$

$$\frac{dy}{(A-y)} = kdt$$

$$\int \frac{dy}{(A-y)} = \int kdt$$

$$-In(A-y) = kt = InC$$

$$InC - In(A-y) = kt$$

$$In\left(\frac{C}{A-y}\right) = kt$$

$$\frac{C}{A-y} = e^{kt}$$

$$y = A - Ce^{-kt}$$
(1)

$$y = A \left( 1 - \frac{C}{A} e^{-kt} \right)$$

$$y = A \left( 1 - b e^{-kt} \right)$$
(2)

where y is growth value, A is the maximum growth value, b and k are the growth parameters, t is time

Now the derivation of Logistic model (Ricker 1979) is as follows: This model can be derived from the following differential equation 3

$$\frac{dy}{dt} = ky\left(1 - \frac{y}{A}\right)$$

$$\frac{dy}{y\left(1 - \frac{y}{A}\right)} = kdt$$

$$\int \frac{A\,dy}{y(A - y)} = \int kdt$$
(3)

By using partial fractions on the left side of the equation, I will get:

$$\int \frac{dy}{y} + \int \frac{dy}{A-y} = kt$$

and then I will get Equation 4

$$Iny - In (A - y) = kt$$

$$In \left(\frac{y}{A - y}\right) = Ine^{kt}$$

$$\frac{y}{A - y} = ce^{kt}$$

$$y = \frac{A}{1 + be^{-kt}}$$
(4)

Now the derivation of Gompertz model (Gompertz 1825) is as follows: This model can be derived from the following differential equation 5

$$\frac{dy}{dt} = ky \ln\left(\frac{A}{y}\right)$$
$$\frac{dy}{y \ln\left(\frac{A}{y}\right)} = kdt$$
(5)

By using integration by substitution on the left side of the equation, I will get:

$$u = In\left(\frac{A}{y}\right) \quad du = \frac{\frac{-A}{y^2}}{\frac{A}{y}}dy = -\frac{dy}{y}$$
$$-\int \frac{du}{u} = \int kdt$$
$$-In|u| = kt - b$$
$$u = e^{-kt+b}$$

and then I will get Equation 6

$$In\left(\frac{A}{y}\right) = e^{-kt+b}$$

$$\frac{A}{y} = e^{-e^{-kt+b}}$$

$$y = Ae^{-e^{b-kt}}$$
(6)

The monomolecular or Brody model (Brody 1945) has no inflection point. For this model, the highest growth rate occurs at birth and decreases continually. As an animal gets older, growth value becomes closer to A, but never passes A. As age and growth value increase, growth rate declines linearly. The curve of logistic model is symmetrical around its inflection point. Growth rate increases with age and y until the inflection point, where it decreases until maximum age is reached. The Gompertz curve has an inflection point earlier than a logistic curve (Bethard 1997).

Now I want to represent a new model: the derivation of this new model (Korkmaz model) is as follows: Since the growth models are generally sigmoidal, the graph is convex until inflection point and then after this point the graph is concave (see Figure 1).

For that reason, this new model can be derived from the following differential equation 7 with initial conditions

$$\frac{d^2 y}{dt^2} = k(B - y)$$

$$y(t_i) = B$$

$$y^{11}(t_i) = 0$$
(7)

where y is the growth value with respect to time, t is time, B is the growth value at inflection point, k is a constant of convexity (k>0),  $t_i$  is the time of inflection point.

By solving this differential equation, firstly I will get:

$$(D^2 + k)y = kB \tag{8}$$



Figure 1. A sigmoidal Shape.

By solving the equation 8, I will solve  $y_1$  and  $y_2$  for homogenous and non-homogenous solutions, respectively. For that reason, secondly I will solve the equation 9 for homogenous part

$$(D^{2} + k)y_{1} = 0$$
  

$$y_{1} = c_{1}\cos\sqrt{k}t + c_{2}\sin\sqrt{k}t$$
(9)

thirdly I will solve the equation 10 for non-homogenous part

$$(D^{2} + k) y_{2} = kB$$
  

$$y_{2} = \frac{1}{(D^{2} + k)} kB = \frac{1}{k(\frac{D^{2}}{k} + 1)} kB$$
  

$$= \frac{1}{k} \left(1 - \frac{D^{2}}{k} + \left(\frac{D^{2}}{k}\right)^{2} - \left(\frac{D^{2}}{k}\right)^{3} + \dots\right) kB = B$$

Since the general solution is the following equation 10

$$y = y_1 + y_2 \tag{10}$$

I get the general solution of Korkmaz model in equation 11

$$y = c_1 \cos\sqrt{kt} + c_2 \sin\sqrt{kt} + B \tag{11}$$

By using the following initial conditions in equation 11

$$y(t_i) = B$$
$$y^{11}(t_i) = 0$$

I can get the equation 12

$$c_{1}\cos\sqrt{k}t_{i} + c_{2}\sin\sqrt{k}t_{i} = 0$$

$$c_{2} = \frac{-c_{1}\cos\sqrt{k}t_{i}}{\sin\sqrt{k}t_{i}} = -c_{1}\cot\sqrt{k}t_{i}$$

$$y^{1} = -c_{1}\sqrt{k}\sin\sqrt{k}t + c_{2}\sqrt{k}\cos\sqrt{k}t$$

$$y^{11} = -c_{1}k\cos\sqrt{k}t - c_{2}k\sin\sqrt{k}t$$
(12)

Since

$$y^{11}(t_i) = -c_1 k \cos \sqrt{k} t_i - c_2 k \sin \sqrt{k} t_i = 0$$

again I can get the equation 12

Now lets substitute equation 12 into the equation 11

So I can get the general solution of Korkmaz model in equation 13

$$y = c_1 \left[ \cos \sqrt{k} t - \cot \sqrt{k} t_i \sin \sqrt{k} t \right] + B \tag{13}$$

Lets say C for initial growth value when t=0,  $y(0) = c_1 + B = C$ 

$$c_1 = C - B$$

So I get Korkmaz model in meaningful parameters in equation 14

-0

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Age (year)	0	1	2	3	4	5	6	7	8	9
Mean Length (m)	0.41	3.23	7.45	11.41	14.83	18.11	18.95	19.69	21.50	23.40

**Table 1.** The Data from *Eucalyptus camaldulensis* Dehn

Table 2. The Mean Values of Fork Lengths (cm) of S. platycephalus from Zamanti Stream of the River Seyhan

Age (year)	1	2	3	4	5	6	7	8	9	10
Fork length (cm)	13.68	18.03	21.63	25.55	28.29	30.85	33.37	36.03	38.30	40.0

Table 3. The General Form of the Models Used in This Study

Models	y(t)
Korkmaz	$c_{1}\cos\sqrt{k}t + c_{2}\sin\sqrt{k}t + B \text{ or} \\c_{1}[\cos\sqrt{k}t - \cot\sqrt{k}t_{i}\sin\sqrt{k}t] + B \text{ or} \\(C-B)[\cos\sqrt{k}t - \cot\sqrt{k}t_{i}\sin\sqrt{k}t] + B$
Logistic	$rac{a}{1+e^{(b-cl)}}$
Brody	$a\left(1-be^{-ct} ight)$
Gompertz	$ae^{(-e^{(b-ct)})}$
Von Bertalanffy	$a(1-be^{-ct})^{\scriptscriptstyle 3}$

$$y = (C-B)\left[\cos\sqrt{k}t - \cot\sqrt{k}t_i\sin\sqrt{k}t\right] + B$$
(14)

## 2. Material and Methods

#### 2.1. Material

In this study one set of data taken from the tree, *Eucalyptus camaldulensis* Dehn. were used (Table 1). The set of data were taken from the study of Yıldızbakan (2005).

And the other set of data taken from the mean fork lengths of the growth features of the flathead trout found in Zamanti Stream of Seyhan River was used (Table 2). The set of data were taken from the study of Kara et al. (2011).

## 2.2. Methods

In this study firstly, general forms of Korkmaz model and the other models used in this study were given in Table 3.

# 3. Results

The results of Korkmaz model and the other models used in this study were given by using data of Table 1 and Table 2. While Table 3 shows the general form of the models used in this study, Table 4 and Table 5 shows the results of these models by using Table 1 and Table 2, respectively. According to errors sum of squares criteria, while in Table 4 Von Bertalanffy model is the best model with respect to the other models used in this study, in Table 5 Brody model is the best model with respect to the other models used in this study. The growth curves of Korkmaz model and classical models used in this study are seen in the same graphs (Figure 2 and Figure 3). As shown in Figure 2, all graphics are close to each other But as shown in Figure 3, all graphics are too close to each other.

As known that the parameters of Korkmaz model are meaningful that's C is initial growth value when  $t=0, t_i$  is the time of inflection point, B is the growth value at inflection point and k is a constant of convexity (k>0). For comparing these parameters for two sets of data, Table 6 and Table 7 were presented to the readers, respectively. In Table 6 the curve of Korkmaz model has an inflection point earlier than the curves of the other models used in this study. However, in Table 7 the curve of Von Bertalanffy has an inflection point earlier than the curves of the other models used in this study.

# 4. Conclusion

In this study, after introducing a new growth model namely Korkmaz model, I used this model in addition to classical growth models such as Logistic, Broody, Gompertz, Von Bertalanffy for two sets of data on growth. I used error sum of squares criteria for comparison the models used. According to this criteria, as seen in Table 4 and Table 5, while for the first set of data error sum of squares of Von Bertalanffy model has the most minimum value, for the second set of data error sum of squares of Brody model has the most minimum value. In addition, it was seen that none of the models used has minimum error sum of squares for each data set. That's while one model is the best model for one data set, that model could not be the best model for the other data set. Although in this study two sets of data taken from the tree, Eucalyptus camaldulensis Dehn. and the mean fork lengths of the growth features of the flathead trout found in Zamanti Stream of Seyhan River were used, Korkmaz model used in

this study could be used for any growth data. In other words, researchers using growth models in their studies could use Korkmaz model in addition to classical growth models in their studies on growth data. Actually, Although Korkmaz model is not the best model for two sets of data by using error sum of squares criteria, Korkmaz model is one of the best models in this study. For that reason, use of Korkmaz



Figure 2. The growth curves of all models used in this study according to the data of Table 1.

Color of Logistic, Broody, Korkmaz, Gompertz, Von Bertalanffy model: Yellow, Black, Red, Green and Blue, respectively. model in addition to classical growth models in their studies on growth data was suggested to the researchers.

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Figure 3. The growth curves of all models used in this study according to the data of Table 2.

Color of Logistic, Broody, Korkmaz, Gompertz, Von Bertalanffy, Model: Yellow, Black, Red, Green and Blue, respectively.

Models	y(t)	SSE
Logictic	$\frac{a}{1+e^{(b-ct)}}$	8.713
	a = 21.887, b = 2.369, c = 0.781	
Broody	$a(1 - be^{-ct})$	5 266
	a = 29.999, b = 1.014, c = 0.166	5.200
Korkmaz	$(C-B)\left[\cos\sqrt{k}t - \cot\sqrt{k}t_i\sin\sqrt{k}t\right] + B$	5 240
	$C = 0.174, B = 2.191, k = 0.035, t_i = 0.537$	3.240
Gompertz	$ae^{(-e^{(b-ct)})}$	2 017
	a = 23.071, b = 1.137, c = 0.488	3.917
V D (1 C	$y = a(1 - be^{-ct})^3$	2.975
von Dertaianffy	a = 23.897, b = 0.711, c = 0.392	2.875

Table 4. The Results of the Models Used in This Study According to the Data of Table 1

SSE: Error Sum of Squares.

Models	y(t)	SSE	
Logictic	$\frac{a}{1+e^{(b-ct)}}$	2.505	
	a = 43.250, b = 1.048, c = 0.333		
Korkmaz	$(C-B)[\cos\sqrt{kt} - \cot\sqrt{kt_i}\sin\sqrt{kt}] + B$	1 668	
	$C = 10.272, B = 15.137, k = 0.021, t_i = 1.325$	1.000	
Commente	$ae^{(-e^{(b-ct)})}$	1 0 4 1	
Gompertz	a = 46.730, b = 0.415, c = 0.219	1.241	
Ware Bartalar Ga	$y = a(1 - be^{-ct})^3$	0.027	
Von Bertalanny	a = 48.776, b = 0.413, c = 0.181	0.927	
Bue a las	$a(1 - be^{-ct})$	0 51(	
Bioody	a = 56.542, b = 0.845, c = 0.104	0.516	

Table 5. The Results of the Models Used in This Study according to the Data of Table 2

**SSE:** Error Sum of Squares.

Table 6.	The	Parameters	of	Korkmaz	Model	with	the	Other
Models U	Jsed a	according to	the	Data of T	able 1			

Models	C	B	t	k
Korkmaz	0.174	2.191	0.537	0.035
Logistic	1.873	10.943	3.032	0.781
Gompertz	1.021	8.487	2.328	0.488
Brody	-0.434	-	-	0.166
Von Bertalanffy	0.579	7.081	1.932	0.392

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**Table 7.** The Parameters of Korkmaz Model with the OtherModels Used according to the Data of Table 2

Models	С	В	t,	k
Korkmaz	10.272	15.137	1.325	0.021
Logistic	11.228	21.625	3.149	0.333
Gompertz	10.276	17.191	1.897	0.219
Brody	8.745	-	-	0.104
Von Bertalanffy	9.856	14.452	1.188	0.181

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