

Gompertz, logistic and brody functions to model the growth of fish species *Siganus rivulatus*

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Abstract: The purpose of this study is to apply the Gompertz, Logistic and Brody models, which are mostly used in literature because of having good capacities to describe growth, thanks to the nonlinear structures. Also compare the mentioned models in terms of the mean squared error and the coefficient of determination criterions. SPSS 20 statistical software package programme is used on the length-age data of the fish species *Siganus rivulatus* individuals (member of the Siganidae family) (Forsskål, 1775).

Keywords: Determination Coefficient, Growth Function, Mean Squared Error, Parameter Estimation.

Introduction

In Actuarial Science, the investigation of a newborn individual's lifetime until the age of X or dying at the age of X requires the analysis of distribution of the random variable $T(X)$, the length of life until death. The tables summarizing the distribution of the random variable $T(X)$ which shows the length of life until death are named "life-tables." These types of tables used not only in organizing life insurance or demographics in statistics, but also regarding the reliability of complex mechanical and electronic systems in engineering, in assessment of effectiveness of treatment methods for serious diseases in biostatistics, and in the analysis of the life-span of a plan in biology (Thorrold, 1987; Srivastava, 2003; Yıldızbakan, 2005).

Scientists, who work on life functions, tested the data of their research on different mathematical models and determined the most suitable models, or they interpreted the data sets they obtained using different models. Such models were also used in the assessment of the growth of living beings based on age in the field of aquaculture (Bayhan et al., 2008; Hossucu et al., 2003; Katsanevakis et al., 2006; Manasırılı et al., 2011). For example, these models were used to express the growth in fish by Throlled (1987) or different growth models were handled to determine the best fit models in fish data by researchers (e.g. Arslan et al., 2014; Bertalanffy, 1938; Ricker, 1958;

Rogers-Bennett et al., 2007) used Richards, Logistic, Gaussian, Tanaka, Ricker and von Bertalanffy functions to investigate the growth and fatality models of oysters and provided annual growth projections. Yeldan (1996) used the data of *Siganus rivulatus* individuals to calculate the growth parameters of von Bertalanffy growth model. Chen et al. (2011) used the von Bertalanffy growth function in modelling fish growth for 16 populations and did statistical comparison of growth between populations or sexes.

At this point, we have to answer an important question: Why it is important to give a growth model for the length-age relationship of the living? It is important because, size-age data can theoretically be used to estimate fish consumption rates (Essington, 2011) also having the growth model for a species population provides access to information of two important parameters, one is growth constant and the other is theoretical length (or maximum size) of this species. The growth constant of a species gives information about how much this species has grown up in a year. The theoretical length gives information about what age a fish can reach the maximum size. Also estimating these two parameters and having estimated growth model can give tips on answer for the questions "How many fish are in the sea?", "How much is suitable for hunting?", "How egg yield changes according to age, length and species?", "How to reduce fish production

cost?”, “How can fish mortality be reduced?”, “Which is the most suitable feeding strategy?” etc.

Because of the reasons given above, specific age structure and development rates should be revealed by the researchers. In this study, the real data, handled by Yeldan (1996), is taken into consideration to observe the performance of three different growth models (Gompertz, Logistic and Brody) used frequently in literature (Koya et al., 2013; Carey, 2009; Kiche et al., 2014). That is, Gompertz, Logistic and Brody models are used for the length-age data of the fish species *S. rivulatus* (Rabbit Fish) to constitute the growth models. In such models, model construction study can be done by calculation of model parameters. Thus, owing to this study one can see how Gompertz, Logistic and Brody models are formed for such data. Also their performances can be examined numerically to make an inference and compared to each other. In accordance with this purpose, Gompertz, Logistic and Brody models are established for the data of interest. Then the results gathered from these established models by using the SPSS Statistical Software Package Program are assessed using coefficients of determination (R^2) and mean squared error (MSE) criterions.

In the light of the above motivations, the contents of the article are arranged as follows: The general meaning of survival functions is given and the models of interest are introduced by using probability of sudden death. The data of *S. rivulatus* are taken from Yeldan (1996) who described the model by using Von-Bertalanfy growth model. The model parameters are calculated for each model and the best fit model to the concerned real data with respect to MSE and R^2 criterions is given. In addition, the interested growth models’ performances are discussed by using MSE and R^2 values, and finally recommended future study subjects are given.

Methods

Growth Models: The functions which define a living beings’ survival after a certain age are called survival functions. For a random variable $T(X)$ denoting the life-length of a new born until the age of x , the distribution function of $T(X)$ can be defined as $F(x) = P(T(x) \leq x), x \geq 0$, where $P(T(x) \leq x)$ shows the probability of the life-length of a new born ($T(X)$) until the age of x . That is, the starting point of survival functions is the basic knowledge of probability. In this case, living after the age of x , that is, “survival” is formulized as $s(x) = 1 -$

$F(x) = P(T(X) > x), x \geq 0$ (Bowers, 1997). Note that, $s(x)$ has values in $[0,1]$ interval and can be interpreted as the probability for a single individual to survive at least x time units. Probabilities of survival function can be given as the density function

$$f(x) = -\frac{dS(x)}{dx} = -s'(x) \quad (1)$$

Then, $p_x = \frac{s(x+1)}{s(x)}$ denotes the probability of each of the new born that will survive to age x and the death probability can be given as $q_x = 1 - p_x$. The statement $P(T(x) \leq t) = {}_tq_x, t \geq 0$ shows the probability of death of an individual of the age x in t years. The statement $P(T(x) > t) = {}_t p_x = 1 - {}_tq_x = \frac{s(x+t)}{s(x)}, t \geq 0$ shows the probability of an individual of the ages of x to see the age $(x + t)$, or ${}_tq_x$ is the probability of death between ages of x and age $(x + t)$ (Bowers et al., 1997, De Moivre, 1971). Considering t getting smaller, the probability of dying between ages x and $x + t$ or the limiting death rate per unit time, for very small t , is called the force of mortality and denoted by $\mu(x) = \frac{f(x)}{s(x)}$ (Benjamin et al., 1942). Using equation (1), $\mu(x) = \frac{f(x)}{s(x)} = \frac{-s'(x)}{s(x)} = \frac{-d}{d(x)} \ln(s(x))$. By definition of $s(x)$ it is known that $s(0) = 1$, then the survival function for a newborn who survives at least age of x or the probability for a newborn to survive to exact age x is given as,

$$s(x) = \exp\left\{-\int_0^x \mu(y) dy\right\}$$

And, the survival function for an individual at age x surviving at age $x + t$ is given as,

$$\frac{s(x+t)}{s(x)} = \exp\left\{-\int_x^{x+t} \mu(y) dy\right\}$$

Certain mathematical life-time structures are provided in the literature regarding as survival functions. For example, since the probability of sudden death for an individual is $\mu(x) = BC^x$, then the survival function suggested by Gompertz (1825), is shown as $s(x) = \exp\left\{-\frac{B}{\ln C}(C^x - 1)\right\}, B > 0, C > 1, x \geq 0$ (Bowers, 1997), where B and C are constants. The parametric form of the Gompertz model used in implementation is $Y_t = A \cdot e^{(-t_0 \cdot e^{(-k \cdot t)})}$. The parameters, characterizing the growth curve, can be defined as follows: A is the asymptotic size of individual, t_0 is the initial size of individual, k is the growth constant, and Y_t is the size of

Table 1. Length values for age groups.

Age	Mean	Minimum	Maximum
0	3.616	2.5	17.7
2	13.050	9.0	16.5
3	14.371	10.8	19.2
4	15.873	11.3	21.8
5	17.174	13.0	20.3
6	18.931	14.7	23.0
7	19.243	17.5	20.8
Total	16.020	1.8	23.0

individual at the age of t .

The Brody and Logistic growth curves are obtained by taking the point of inflection $m = 1$ and $m = -1$, respectively in Richards growth model (Richards, 1959). The Richards model is preferable for data based on a sigmoidal behavior, due to the fact that the placement of the inflection point (changing point) is flexible. The Richards growth model may be shown as the formula $Y_t = A \cdot (1 - B \cdot e^{(-k \cdot t)})^m$. Here, Y_t is the size of the individual at the age of t , A is the maximum size of the individual, B is the ratio of the size gained after the birth and the adult size, k is the growth constant, t_0 is initial size and m is the changing point which gives information about the shape of the curve that occurs where the estimated change shifts from an increase to decrease.

Since m determines the point of inflection on the y axis, taking the second derivative of Y_t with respect to t , and making it equal to 0, the values $m = 0$ or $m = 1$ are found. Note that $m = 0$ gives a constant function and has no shifting from an increase to decrease. Taking $m = 1$ Brody model is obtained as follows;

$$Y_t = A \cdot (1 - B \cdot e^{(-k \cdot t)})^1, B = \frac{t_0}{A} - 1$$

The Logistic growth model obtained by using $m = -1$ in the Richards model is as follows;

$$Y_t = A \cdot (1 - B \cdot e^{(-k \cdot t)})^{-1}, B = 1 - \frac{t_0}{A}$$

Table 2. The model summary.

Source	Sum of Squares	Degrees of freedom	Mean Squares
Regression	1662,495	3	554,165
Residual	2,983	4	0,746
Uncorrected Total	1665,478	7	
Corrected Total	171,664	6	

$$a. R^2 = 1 - \frac{\text{Residual Sum of Squares}}{\text{Corrected Sum of Squares}} = 0.983$$

$MS_{\text{res}} = 0,746$

Dependent variable: size^a

In the next section, real data set is applied to Gompertz, Logistic and Brody models to find the parameters for each of this model.

Model fitting for the growth of *Siganus rivulatus* according to numerical data: In this section, the constants characterizing the growth models are obtained by fitting experimental data. Table 1 shows the length distribution of the 418 investigated *S. rivulatus* (Rabbit Fish) based on their age groups. The iteration is used by manipulating the constants until the sum of the squared errors is as small as possible. There are several parameters that are useful in characterizing the growth curve. One is the asymptote A , the value for A found by iteration is taken as 21 since this value is higher than but close to the maximum size of 19.243 in the data set. Derivations of the other parameters for the models are given in the following subsections.

Implementation of the Gompertz model: The constants for the Gompertz model $Y_t = A \cdot e^{(-t_0 \cdot e^{(-k \cdot t)})}$ that best fit the interested real data should be given first. For $t = 0$, if the value $Y_0 = 3.616$ is placed in the given equation, the value $t_0 = 1.759$ is found. Repeating the same steps for the age t , the parameter of growth rate k which decays Y_t exponentially is found as $k = 0.995$. Then the estimated Gompertz model is $Y_t = 21 \cdot e^{(-1.759 \cdot e^{(-0.995 \cdot t)})}$. ANOVA results for the estimated Gompertz model are given in Table 2.

Implementation of the Brody Growth Model: To find the best fit to the Brody growth model $Y_t = A \cdot (1 - B \cdot e^{(-k \cdot t)})^1$ for the given data, the correct constants should be found. Applying our data to Brody's growth model, for $Y_0 = 3.616$ and $A = 21$, B can be obtained as 0.172. Then taking $Y_2 = 13.050$ for similar calculation in the next step the parameter k is found as 0.705 and then the estimated model is given as $Y_t = 21 \cdot (1 - 0.172 \cdot e^{(-0.705 \cdot t)})$. ANOVA results are given for the

Table 3. The model summary.

Source	Sum of Squares	Degrees of freedom	Mean Squares
Regression	1663,958	3	554,563
Residual	1,520	4	0,380
Uncorrected Total	1665,478	7	
Corrected Total	171,664	6	

a. $R^2 = 1 - \frac{\text{Residual Sum of Squares}}{\text{Corrected Sum of Squares}} = 0.991$
 $MS_{\text{res}} = 0,380$
 Dependent variable: size^a

Table 4. The model summary.

Source	Sum of Squares	Degrees of freedom	Mean Squares
Regression	1660,514	3	553,505
Residual	4,964	4	1,241
Uncorrected Total	1665,478	7	
Corrected Total	171,664	6	

a. $R^2 = 1 - \frac{\text{Residual Sum of Squares}}{\text{Corrected Sum of Squares}} = 0.971$
 $MS_{\text{res}} = 1,241$
 Dependent variable: size^a

Table 5. The SPSS results for Gompertz, Brody and Logistic growth models.

Models	Source of Variation	Sum of Squares	Degrees of freedom	Mean Squared Error (MSE)	R ²
Gompertz Growth Model	Regression	1662.495	3	554.165	0.983
	Residual	2.983	4	0.746	
	Uncorrected Total	1665.478	7		
	Corrected Total	171.664	6		
Brody Growth Model	Regression	1663.958	3	554.653	0.991
	Residual	1.520	4	0.380	
	Uncorrected Total	1665.478	7		
	Corrected Total	171.664	6		
Logistic Growth Model	Regression	1660.514	3	553.505	0.971
	Residual	4.694	4	1.241	
	Uncorrected Total	1665.478	7		
	Corrected Total	171.664	6		

estimated Brody model in Table 3.

Implementation of the Logistic Growth Model: By taking $A=21$, if $Y_0=3.616$ is placed in the Logistic growth model $Y_t = A \cdot (1 - B \cdot e^{(-k \cdot t)})^{-1}$, the parameter B is found as 4.8066. Again by using the real data, summarized in Table I, if $Y_2=13.050$, $B = 4.8066$ and $A=21$, the parameter $k = -1.03$ is obtained. Then the fitted Logistic model for the size of *S. rivulatus* at the age of t can be given as $Y_t = 21 \cdot (1 - 4.8066 \cdot e^{(1.03 \cdot t)})^{-1}$ and the ANOVA results are given in Table 4. With aid of the fitted models given in previous section, using length-age information of *S. rivulatus* species, comparisons and analysis will be done in the next section.

Results and Data Analysis

The most commonly used models in age-related growth problems are asymptotic models. In such models obtaining the initial values of parameters, in other words, the determination of the initial value of the asymptotic size is of great importance. In this study, higher but closest to the observed highest average length has been considered to determine the initial value. The most important values to be checked at ANOVA table, derived during modeling process of determining above mentioned values, are R² and MSE, as MSE is a good measure to compare the errors whereas R² value reflects the parameters' percentage to explain the model. Therefore, a model with the highest

coefficient of determination and the lowest MSE will be considered as the best model. The Table 5 shows the R^2 and MSE values of the concerned distributions in this study.

As seen on Table 5, R^2 values reveal significantly high values for all the models meaning that parameters have high explanatory percentages to explain the fitted models. Though Brody model seems to give the best results in terms of this value, it appears that this model is better than Gompertz model only with 0.8 % difference. So, when R^2 criterion considered, there exists no significant advantage between Brody and Gompertz models. Also Logistic growth model has also very high value to explain the model.

When the models compared in terms of smallness of the MSE criterion, Logistic model seems to have the highest error, whereas Brody and Gompertz models reveal quite better results. On the other hand, although the Gompertz model gives better results compared to Logistic model, it failed to lower the MSE value to 0.380 levels like Brody model succeeded. Considering the R^2 criterion, there observed no significant difference between Brody and Gompertz. However, Brody model has a 0.8 % better R^2 value compared to Gompertz model. Also, Brody model is considered to be the best model within all the models thanks to its highest R^2 and lowest MSE values.

While deciding which growth function to use, knowledge about the time to reach the mature, in other words, the growth constant of the live species of interest should not be overlooked. In fact, the parameter m is the unique parameter which has no direct biological meaning. However, it is the main responsible for the different shapes of the curves. The inflection point is of significance, because it is associated with a change in the acceleration of the growth. If the values of m are, in general, lower for the first species than for the second, it can be assumed that the second species reached the mature weight before the first. That is, the parameter m exerts great influence on the time to an individual to reach the mature weight on the point of inflection of the growth curve. Therefore, for the interested species, the value of m , if known, should also be considered when it is decided which growth function should be used (Kiche et al., 2014).

Taking into consideration the obtained results, which summarized in Table 5, all non-linear models demonstrated good capacities of fitting to describe the growth kinetics of data. Although the Brody model

exhibited the highest R^2 and lowest MSE than the other parameter models, the two criteria R^2 and MSE, indicated that Gompertz model should also be taken into consideration for the growth modeling.

Discussion and Conclusions

The theory of growth makes a magical journey for mathematics and science and an example of the close relationship between the two. Through this relationship, parameters were estimated by applying a real data set and the estimated growth models were constituted and discussed in this study. Comparisons were done in terms of R^2 and MSE criterions.

In this study, Gompertz, Brody and Logistic survival models were constructed for the real data of *S. rivulatus* and they compared by means of R^2 and MSE values. Brody model was considered to be the best model within all the models for the related data. In order to look for more in-depth answers to the subject and make more contribution to the literature, the growth models discussed here are planned to be reworked on new data sets.

Beside of all, these benefits obtained through the partnership of mathematics and aquaculture. The ability to model the growth of *S. rivulatus* using calculus provides a significant foundation for the development of the population for livings, which is the great success for the proper management of fish and fisheries also. Having such specific age structure or rate population for livings is important because these models can give detailed information about population of fish species or fishing stocks etc.

As a result, with the curiosity of scientists and the collaboration of growth models and actuarial mathematics make us go one step further in the way of conservation of natural resources and of realize animals in danger of extinction.

Recommended further area of research: These three survival models may be used for different fish species. Their parameters may be estimated and compared to each other in order to determine the model that best fits the population. Also growth model suggested by Schnute (2011) may also be used in further studies. This will assist the fish farming sector as to reduce production costs, to reduce fish mortality, to use quality feed and to prevent excessive feed consumption. Also, making use of the close relationship between math and science and having the survival model for the population, fishing stocks and

populations living in the hunting grounds; the abilities of any hunting instrument used in hunting can also be observed. Having knowledge about population may also give knowledge about fish species in danger of extinction or fishing stocks for this particular case.

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