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Performance of the Weibull individual growth model for weight at age data

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ABSTRACT

Introduction: Knowledge of different functions associated with a probability distribution, as well as their properties, can be translated into functions that provide information about different characteristics of the growth process under study.

Objectives: To analyze the relationship between individual growth models and the cumulative distribution functions of continuous random variables.

Methods: We compare the flexibility and goodness of fit of the Weibull-type model against the von Bertalanffy weight growth model. We fit these two growth models to two very different sets of age-weight data taken from the literature; the first comprises 22 pairs of Pacific halibut mean weight at age, and the second 900 pairs of striped bass weight-age-data.

Results: The Weibull-type growth model had greater flexibility and neglected less information available in the data sets than the von Bertalanffy model.

Conclusions: The Weibull model, derived from cumulative probability distribution, is a good choice to fit weight-at-age data as it is more flexible than the commonly used von Bertalanffy model.

Keywords: cumulative distribution function; age-weight relationship; model comparison; Weibull growth model; von Bertalanffy growth model.

RESUMEN

Eficacia del modelo de crecimiento individual de Weibull para datos de peso por edad

Introducción: El conocimiento de diferentes funciones asociadas a una distribución de probabilidad, así como sus propiedades, se puede traducir en funciones que proporcionen información sobre diferentes características del proceso de crecimiento en estudio.

Objetivos: Analizar la relación entre los modelos de crecimiento individuales y las funciones de distribución acumulativa de variables aleatorias continuas.

Métodos: Comparamos la flexibilidad y bondad de ajuste del modelo tipo Weibull con el modelo de crecimiento de peso de von Bertalanffy. Ajustamos estos dos modelos de crecimiento a dos conjuntos muy diferentes de datos edad-peso tomados de la literatura; el primero comprende 22 pares de lenguado del Pacífico usando peso medio por edad, y el segundo, 900 pares de corvina rayada con parejas de peso-edad.
Resultados: El modelo de crecimiento tipo Weibull tuvo mayor flexibilidad y descartó menos información disponible en los conjuntos de datos que el modelo de von Bertalanffy.
Conclusiones: El modelo de Weibull, derivado de una distribución de probabilidad acumulada, es una buena opción para ajustar datos de peso por edad, ya que es más flexible que el comúnmente utilizado modelo de von Bertalanffy.

Palabras clave: función de distribución acumulada; relación edad-peso; comparación de modelos; modelo de crecimiento de Weibull; modelo de crecimiento de von Bertalanffy.

INTRODUCTION

Growth of fishery production or biological production in general, implies an increase or decrease in production in weight / biomass / yield. However, mathematical biological models for assessing growth are commonly length growth models (von Bertalanffy, Gompertz, Logistic, Richards) (Katsanevakis, & Maravelias, 2008). Length is one of the most commonly used indicators for assessing growth, since it is less expensive, faster, and simpler to obtain from a sampling perspective. However, it is necessary to translate this information into weight by evaluating the relationship between length and weight (L-W) to return to assess biological production. In several studies growth is expressed in weight (Botello-Ruvalcaba et al., 2010; Luquín-Covarrubias et al., 2022).

Individual growth in fish is based in physiological processes and is the net result of two opposing processes, catabolism, and anabolism (von Bertalanffy, 1938). Specifically (von Bertalanffy, 1957), the origin of the von Bertalanffy (vB) model can be expressed as

$$\frac{dm}{dt} = nm^{\propto} - km^{\beta}$$

where m represents body weight, t is time; n and κ are constants of anabolism and catabolism, respectively. Here, α and β indicate that the rates of anabolism or catabolism are proportional to body weight m to the power of α or β, usually with $\alpha \leq \beta$ and $\beta = 1$. The ability to model growth in fish has a wide range of applications in population dynamics. For example, growth models are a vital component of many stock assessments as they reflect potential production of the species (Juan-Jordá et al., 2015). The most common practice in fish growth modelling is to select a priori a single model, generally the vB growth model (e.g., Haddon, 2011). Inference and estimation of parameters and their precision are based solely on that fitted model (Katsanevakis & Maravelias, 2008). An important restriction of the vB model when age-length data are available is that individual growth rate is monotonically decreasing. The fit is poor in the case of having age-length or age-weight data that have more than one inflection point (Knight, 1968; Knight, 1969).

It has been established that, seen as an individual growth model, the Weibull function is a derivation of the cumulative distribution function of a random variable that follows a Weibull random distribution (Swintek et al., 2019). The Weibull function has been successfully applied to growth of trees (Seo et al., 2023; Souza et al., 2021; Yang et al., 1978); as discussed below, this has not been the case for fish growth. The nexus between individual growth models and cumulative distribution functions proves invaluable, enabling understanding of distribution functions effectively. Describing the distribution of a random variable offers different options, including alternative functions. Familiarity with diverse functions –density, cumulative distribution, survival, and more– linked with probability distribution and their inherent properties, facilitates to extrapolate functions shedding light on distinct facets of the growth process (Marshall & Olkin, 2007).

In the present work we develop a Weibull age-weight model and compare its performance with the vB, using two sets of age and weight data. We compare the fit of these models based on the Akaike information criterion (Burnham & Anderson, 2002). The Weibull growth model is flexible (Meeker et al., 2022) which facilitates goodness of fit. Here, we first analyze the origin of the vB model for age and weight data and then develop the alternative Weibull departing from a cumulative distribution function. Because the two data sets used were very different in structure, it is expected that results shown here are general and useful in other situations.

MATERIALS AND METHODS

Theory and calculations: We caution that data for the present work are scarce; therefore, we used only two data sets available, as explained below. The length growth model of vB is given by the expression (von Bertalanffy, 1938):

$$L(t) = L_\infty\left[1 - exp\left(-k(t - t_0)\right)\right] \quad (1)$$

where $L\infty$ is asymptotic length, t_0 is the age for a null length and k is the intrinsic growth rate.

From equation 1 one can derive another model for growth in weight, using the power function relating weight (W) at length (L). The resulting model is (Table 1):

$$W(t) = W_\infty[1 - exp(-k(t - t_0\ ))]^b \quad (2)$$

where $W\infty$ is the maximum possible individual weight corresponding to asymptotic length, and b is the same as b in the weight-length relationship.

From model 1, one has that:

$$F(t) = \frac{L(t)}{L_\infty} = 1 - exp\left(-k(t - t_0)\right)\ ,\ t_0 \leq t \leq \infty \quad (3)$$

which is the proportion of the maximum theoretical length that an average individual has grown at age t.

Table 1

Description of parameters used in this work for both models (vB andWeibull) and data sets.

Model	Parameters	Description	Units
Weibull			
	W	Body weight	kg or lb
	t	Age	Years
	to	Location parameter	Years
	W∞	Maximum theoretical weight	kg or lb
	η	Scale parameter	Years
	η - |*to*|	Age corresponding to 63.2 % *W*∞	Years
	β	Shape parameter	
	c	Shape parameter	
	σ	Random error term	kg or lb
von Bertalanffy			
	W	Body weight	kg or lb
	t	Age	Years
	W∞	Maximum theoretical weight	kg or lb
	k	Brody growth rate coefficient	1/year
	to	Theoretical age for t = 0	Years
	b	Weight-length exponent	
	σ	Random error term	kg or lb

Because data were derived from tables, weight for Pacific halibut (*Hippoglossus stenolepis*) is in kg, and for striped bass (*Morone saxatilis*) is in pounds. Data for halibut were obtained from Quinn II and Deriso (1999), and those of bass were derived from Baum (2002).

Equation 3 has the properties of a cumulative distribution (Seber & Wild, 1989) and coincides with the cumulative exponential distribution with location parameter t_0 and failure rate k (Marshall & Olkin, 2007). The vB length growth model is widely used in fisheries, while the exponential distribution is fundamental in life span studies with wide application in reliability and medicine (Collet, 2015; Marshall & Olkin, 2007).

For the vB growth model in weight,

$$F(t) = \frac{W(t)}{W_\infty} = \left[1 - exp\left(-k(t - t_0\,)\right)\right]^b,\ t_0 \le t \le \infty \quad (4)$$

where F(t) is the generalized exponential cumulative distribution (Gupta & Kundu, 1999; Marshal & Orkin, 2007).

To derive a weight model which is an extension of the vB length model one begins with understanding the process involved in the extension of model 1. It is easy to realize that transforming length L(t) with a power function,

$$\left[1 - exp\left(-k(t - t_0)\right)\right] \quad (5)$$

is transformed into:

$$\left[1 - exp\left(-k(t - t_0)\right)\right]^b \quad (6)$$

A similar extension consists in transforming age t with the power function $t^{1/b}$, which results in a shape function given by

$$F(t) = 1 - exp\left\{-\left(k(t - t_0)\right)^b\right\} \quad (7)$$

This shape function coincides with one of the formulations of the Weibull distribution (Hallinan, 1993). It has found wide use in areas of reliability and in the analysis of survival to model life spans or failure times (Meeker et al., 2022; Thach, 2022). A convenient reparameterization of the Weibull distribution consists in expressing its cumulative distribution as

$$F(t) = 1 - exp\{-((t - t_0)/\,\eta)^{\beta}\} \quad (8)$$

where *ß* is the shape parameter and its value determines the form of the distribution, while η is the scale parameter because its location modifies the value of *t*; both η and *t* have the same units (time).

To get a better grasp of the meaning of *ß*, cumulative relative weight was calculated using equation 8 with $t_0 = 0$ and $t = \eta = 2$ for five values of *ß*. As observed (Fig. 1), at age $t = \eta = 2$, the growth is equal to 0.632 W_∞, regardless of the value of *ß*. The five curves, seen as

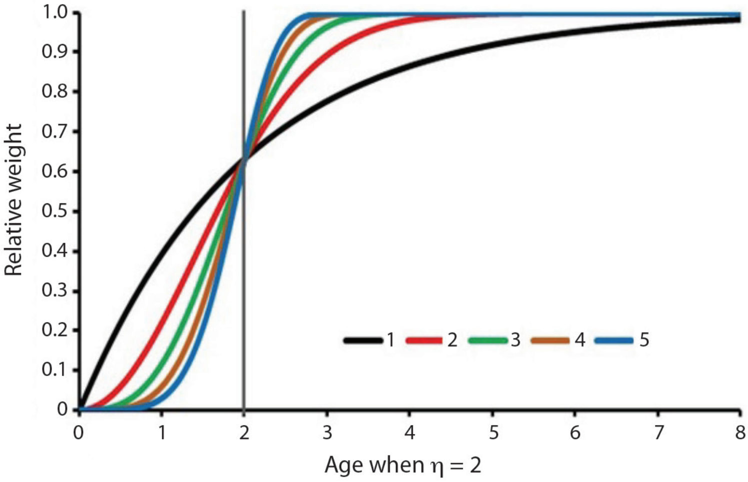

Fig. 1. Shape functions (generalized exponential cumulative distribution) of the Weibull growth model, for different values of the parameter (= 1, 2, 3, 4, 5).

cumulative distribution functions, coincide at $t = \eta = 2$; that is, in reliability research, when initial time = zero, for this model, the 0.632 quantile is equal $t = \eta = 2$.

As shown, parameter η is interpreted as the 0.632 quantile of asymptotic weight. A possible biological interpretation is discussed below. This behavior is easy to see expressed as follows:

$$F(k) = [1 - exp(-(\eta/\eta)^{\beta})] = 1 - exp\,(-1) = 0.632 \quad (9)$$

In contrast, when one repeats the exercise using the vB growth model, unlike the previous model, the curves remain in lower locations as the value of b is greater. This is because in the vB model, the shape function $F(t)$ takes values in the interval (0, 1) and consequently, when raised to an increasing exponent b it takes decreasing values (Fig. 2). The plots are ordered in reverse order to the values of b, and consequently, the graphs of the shape function do not intersect.

The density and survival functions of the Weibull distribution are given, respectively, by

$$f(t) = (\beta/\eta)((t - t_0)/\eta)^{(\beta-1)}[exp(-((t - t_0)/\eta)^{\beta})] \quad (10)$$

And

$$S(t) = 1 - F(t) = exp\{-((t - t_0)/\eta)^{\beta}\} \quad (11)$$

From the perspective of growth models, the Weibull type model is given in terms of the cumulative distribution function:

$$W(t) = W_{\infty}F(t) = W_{\infty}[1 - exp\{-((t - t_0)/\eta)^{\beta}\}] \quad (12)$$

Interestingly, in this distribution, the shape parameter *ß* relates to the form of the growth curve; when the average individual reaches age η - $|t_0|$ (Table 2), it will have grown 63.2 % of its asymptotic size plus an error term ε (e.g., Swintek et al., 2019).

Extensions of the vB length model: Thus far we have discussed the vB length growth model (1) and two extensions, growth in weight (2) and the Weibull model (12). As seen, expressions for the two extensions are, respectively (eq. 7) $F(t) = [1\text{-}exp(\text{-}k(t\text{-}t_0))]^b$ and (eq. 8) (t)= $[1\text{-}exp\{\text{-}((t\text{-}t_0)/\eta)^{\beta}\}]$.

In addition to being shape functions of individual growth models, they are also cumulative distribution functions. There is an additional distribution function which is a generalization of both; this is the generalized or exponential Weibull distribution.

The cumulative distribution of the latter is given by (Mudholkar & Hutson, 1996; Mudholkar & Srivastava, 1993; Mudholkar et al., 1995):

$$F(t) = [1 - exp\{-((t - t_0)/\eta)^{\beta}\}]^c \quad (13)$$

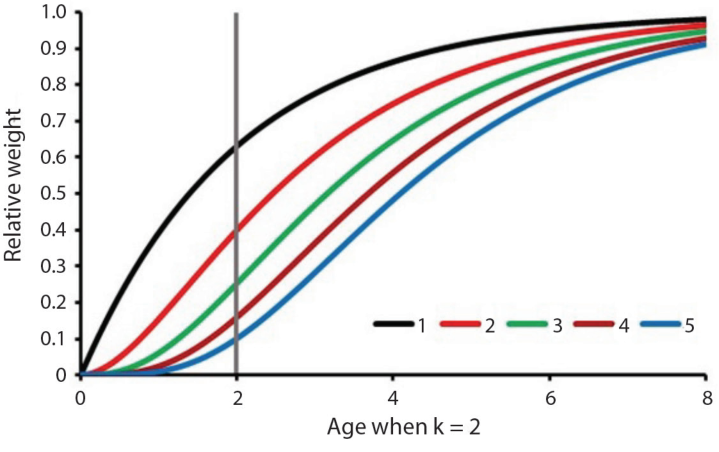

Fig. 2. Shape functions (generalized exponential cumulative distribution) of the von Bertalanffy growth model for different values of the parameter *ß* (= 1, 2, 3, 4, 5).

Table 2
Features of the von Bertalanffy, Weibull and Generalized Weibull weigth – age growth models applied to two data sets: Pacific halibut, *Hippoglossus stenolepis* and striped bass, *Morone saxatilis*.

Model	Equation	Parameters	Likelihood	Error structure and restrictions
Pacific halibut (*Hippoglossus stenolepis*)				
Von Bertalanffy	$W(t) = W_\infty[1 - exp(-k(t - t_0))]^b$	$W(t)$ is weight at time t; W_∞ is asymptotic weight; t_0 is the age for a null weight and k is the intrinsic growth rate; b is a parameter of the weight-length relationship ($W(t) = aL(t)^b$)		Additive (Normal) No restrictions
Weibull	$W(t) = W_\infty\left[1 - exp\{-((t - t_0)/\eta)^\beta\}\right]$	$W(t)$ is the weight at time t; ß is the shape parameter; η is the scale parameter because its location modifies the value of t.	$l(\theta) = \log[L(\theta)] = -{}^{n}/_{2}\, log(2\pi\sigma^2) - \sum_{i=1}^{n} \frac{(w_i - \mu_i)^2}{2\sigma^2}$	Parameterization of the 0.632 growth in time quantile $t_0 = 0$
Generalized Weibull	$W_i = W_\infty\left[1 - exp\{-((t_i - t_0)/\eta)^\beta\}\right]^c + \epsilon_i$	ß and c are both shape parameters; when c = 1 the function corresponds to the Weibull model, else is a generalized Weibull function		Parameterization of the 0.632 growth in time quantile $t_0 = 0$
Striped bass (*Morone saxatilis*)				
von Bertalanffy	$W(t) = W_\infty[1 - exp(-k(t - t_0))]^b$	$W(t)$ is weight at time t; W_∞ is asymptotic weight; t_0 is the age for null weight and k is the intrinsic growth rate; b is a parameter of the weight-length relationship ($W(t) = aL(t)^b$)		Multiplicative (Lognormal) No restrictions
Weibull	$W(t) = W_\infty\left[1 - exp\{-((t - t_0)/\eta)^\beta\}\right]$	$W(t)$ is the weight at time t; ß is the shape parameter; η is the scale parameter because its location modifies the value of t.	$l(\theta) = log[L(\theta)] = -{}^{n}/_{2}\, log(2\pi\sigma^2) - \sum_{i=1}^{n} \frac{(log\,(w_i) - log\,(\mu_i))^2}{2\sigma^2} - \sum_{i=1}^{n} log\,(w_i)$	Multiplicative (Lognormal) Error structure No restrictions
Generalized Weibull	$W_i = W_\infty\left[1 - exp\{-((t_i - t_0)/\eta)^\beta\}\right]^c + \epsilon_i$ $i = 1,2,\dots,n$ $\sim N(0,\sigma)$	ß and c are both shape parameters; when c = 1 the function corresponds to the Weibull model, else is a generalized Weibull function		Multiplicative (Lognormal) Error structure No restrictions $t_0 = 0$

where *ß* and *c* are both shape parameters; when $c = 1$ the function corresponds to the Weibull model, else is a generalized Weibull function. This is the shape function of the generalized Weibull model, which is expressed as follows when errors are additive:

$$W_i = W_\infty\left[1 - exp\left\{-((t_i - t_0)/\eta)^\beta\right\}\right]^c + \epsilon_i, i = 1,2,\dots,n.\ \epsilon_i \sim N(0,\sigma) \quad (14)$$

Derivation of confidence intervals for parameter values: We obtained confidence intervals for parameters using a method based on the likelihood function $L(\theta)$ or loglikelihood function $l(\theta) = ln[L(\theta)]$. We first obtained an information matrix I of parameters given by the negative values of the second derivatives of the loglikelihood $l(\theta)$ evaluated at the maximum likelihood estimates of the model parameters, $\hat{\theta} = (\hat{\theta}_1, \hat{\theta}_2, \dots, \hat{\theta}_k)$. For example, for the Weibull model we have the following parameter estimates $\hat{\theta}_1 = \hat{W}_\infty, \hat{\theta}_2 = \hat{k}, \hat{\theta}_3 = \hat{t}_0, \hat{\theta}_4 = \hat{b}, \hat{\theta}_5 = \hat{\sigma}$. The information matrix is given by:

$$I = -\left(\frac{\partial^2 l(\theta)}{\partial\theta_i\partial\theta_j}\right)\Big|_{\theta=\hat{\theta},1\le i,j,k} \quad (15)$$

The variance-covariance matrix $\Sigma = l^{-1}$ for parameters is obtained by inverting the information matrix, or:

$$\Sigma = I^{-1} \quad (16)$$

Estimates of the model parameter variances are the terms of the diagonal of the variance-covariance matrix. So, the variance of the *i*-th term of the parameter vector is:

$$\hat{V}(\hat{\theta}_i) = \Sigma_{(i,i)} \quad (17)$$

Similarly, the covariance between terms *i* and *j* of the parameter vector is term (*i*, *j*) of the variance-covariance matrix:

$$\widehat{Cov}(\hat{\theta}_i, \hat{\theta}_j) = \hat{\Sigma}_{(i,j)} \quad (18)$$

This is a squared, symmetric matrix, i.e.,

$$\widehat{Cov}(\hat{\theta}_i, \hat{\theta}_j) = \hat{\Sigma}_{(i,j)} = \hat{\Sigma}_{(j,i)} = \widehat{Cov}(\hat{\theta}_j, \hat{\theta}_i) \quad (19)$$

In the case of the Weibull model, the variances of the model parameter estimates are the terms of the diagonal of the variance-covariance matrix:

$$\left(\hat{V}(\hat{W}_\infty), \hat{V}(\hat{k}), \hat{V}(\hat{t}_0), \hat{V}(\hat{b}), \hat{V}(\hat{\sigma})\right) = diag(\hat{\Sigma}) \quad (20)$$

Once we have the variances of the parameter estimates, the process of calculating the confidence intervals (CI) has two stages. First, the parameters are estimated by maximum likelihood, and then the limits of the CI are obtained by the Normal approximation (Hoel et al., 1971; Meeker et al., 2022) as follows:

$$(\underline{\theta}_i, \overline{\theta}_i) = \left(\hat{\theta}_i - 1.96\widehat{se}(\hat{\theta}_i), \hat{\theta}_i + 1.96\widehat{se}(\hat{\theta}_i)\right) \quad (21)$$

All calculations were made using the statistical computing language R (R Core Team, 2023). Table 2 shows the features of the models contrasted and applied to the next two different data series, as well as the rationale of the analysis involved (parameters, likelihood function and type of error used).

First data set-small sample case: Firstly, using Pacific halibut (*Hippoglossus stenolepis*) 22-pair data set in Quinn II and Deriso (1999), a comparison was done of the vB and Weibull growth models for age-weight data (Table 2). Pacific halibut (*H. stenolepis*) are demersal species of flatfish that range throughout the North Pacific Ocean. They are among the largest of all flatfish: females may reach up to approximately 227 kg in weight and nearly three meters in length (International Pacific Halibut Commission [IPHC], 1998); they are relatively long-lived with the oldest individuals estimated to be 55 years of age (Forsberg, 2001). Maturity varies with sex, age, and size of the fish. Females grow faster but mature slower than males (IPHC, 1987). The average age at 50 percent maturity is eight years for males and 12 years for females (St-Pierre, 1984). The vB growth model parameter estimates for female ranged from: L_∞, 1.32 m to 2.39 m; *k*, 0.109 to 0.039 and t_0 0.418 to -1.538 (Perkins, 2015). According to the IPHC (1987), Pacific halibut can reach a maximum length of nine feet (~2.7 m) and maximum weight of 500 pounds (~227 kg).

It is important to note that parameter b was originally known ($b = 3.24$) from previously reported work (Quinn II et al., 1983). While adjusting the Weibull model, all parameters are estimated using equation 12, where, in terms of probability, $\eta - |t_0|$ corresponds to quantile 0.632 or 63.2 % of the asymptotic weight (Table 2).

To select the "best" of both models (i.e., vB and Weibull), we used the Akaike (1973) information criterion:

$$AIC = -2l(\hat{\theta}) + 2p \quad (22)$$

where $l(\hat{\theta})$ is the maximized log-likelihood and p is the number of model parameters. The value of AIC is interpreted as the loss of information available in the data set resulting in the model fit; lower values indicate better fits (Burnham & Anderson, 2002).

In the case of additive errors, we have the following expression for the log-likelihood:

$$l(\theta) = \log[L(\theta)] = -{}^{n}/_{2}\, log(2\pi\sigma^2) - \sum_{i=1}^{n} \frac{(w_i - \mu_i)^2}{2\sigma^2} \quad (23)$$

where weight μ_i at time t_i for the vB is given by equation (2), whereas for the Weibull model μ_i is given by equation (12). Log-likelihood values were obtained numerically using statistical software in R language (Ogle, 2016).

Parameters of vector θ estimated are vectors $\hat{\theta}$ which maximize the likelihood or log likelihood, that is:

$$\hat{\theta} = \underset{\Theta}{argmax} L(\theta) = \underset{\Theta}{argmax} l(\theta) \quad (24)$$

where Θ is the parametric space where search is done to find the maximum (log) likelihood. Although in some problems not too complicated one can obtain closed forms for the maximum likelihood estimator $\hat{\theta}$, commonly numerical procedures are used to maximize likelihood or log likelihood functions.

Second set-extensive data: For the second example, we used 900 pairs (age-weight) of striped bass *Morone saxatilis* from Arkansas, USA derived from an age (years)-weight (pounds) key (U.S. Fish & Wildlife Service [USFWS], 2010). Briefly, 900 individuals were distributed in a matrix, 100 per each of nine weight categories (4.5 to 39.5 kg) and from three to 15 years of age. The striped bass is a temperate anadromous fish species that is the basis of an important recreational and commercial fishery in the Eastern United States (Gervasi, 2015). Female striped bass mature between 5-6 years, and fecundity increases asymptotically with age (Brown et al., 2024). For several fish species such as red snapper, *Lutjanus campechanus* (Lowerre-Barbieri & Friess, 2022) and sablefish, *Anoplopoma fimbria* (Rodgveller et al., 2018) it has been determined that fecundity increases with fish age. Female striped bass mature between 5-6 years, and fecundity increases asymptotically with age (Brown et al., 2024). To add random variability in weight-at-age from the age-weight key, raw "observed" weights were multiplied by Normal random shocks (1, 1). How there are variability in weight grows as age increases; this pattern of increasing variation led us to consider growth models with an error term that acts multiplicatively.

For models with multiplicative error structure, the log likelihood function is given (Table 2) by (Quinn II & Deriso, 1999):

$$l(\theta) = log[L(\theta)] = -{}^{n}/_{2}\, log(2\pi\sigma^2) - \sum_{i=1}^{n} \frac{(log\,(w_i) - log\,(\mu_i))^2}{2\sigma^2} - \sum_{i=1}^{n} log\,(w_i) \quad (25)$$

weight μ_i at time t_i for the vB and Weibull models are given, respectively, by equations (2) and (12).

RESULTS

First data set-small sample case

vB growth model: For the vB model fit, Table 3 shows estimated parameter values and their uncertainties. Except for t_0, all estimates were significant (p-values < 0.001).

Weibull growth model: Table 4 shows that, for the Weibull model fit, parameter values for t_0 and β are non-significant judging by 1) the relatively large p values, and 2) the confidence intervals include zero. This provides an indication that the model might be over parameterized.

The parameterization was done in terms of the 0.632 quantile of growth in time.

To reduce over parameterization, we considered a restriction $t_0 = 0$, which yielded results shown in Table 5, where the rest of parameter values were significant. This is because by eliminating the need to obtain a fit of t_0, the relative standard error of parameter β decreased (from 55.6 to 7.2 %). The other estimated parameters (W_∞ and σ) both have small relative standard errors values; hence their confidence intervals are unchanged.

Table 6 shows results for the fit of the generalized Weibull growth model 16 to data shown in Table 2.

It should be noted that the lowest AIC value corresponds to the third model adjustment. In general, performance was better using the Weibull than the vB growth model.

Second data set-large sample size

vB growth model: Table 7 shows the estimates that result in the fit of the vB model to

Table 3

Estimated parameter values for the von Bertalanffy growth model using Pacific halibut, *Hippoglossus stenolepis*, data shown in Fig. 3A assuming additive errors.

Parameter	Estimate	Std error	Confidence interval	t-value	p-value
W_∞	68.60	4.92	(58.96, 78.25)	13.94	$< 10^{-20}$
k	0.122	0.02	(0.09, 0.15)	8.16	$< 10^{-8}$
t_0	3.037	0.91	(1.25, 4.83)	3.33	0.002
b	3.24				
σ	3.06	0.52	(2.06, 4.08)	5.96	$< 10^{-6}$
logLikMx	-54.80				
AIC	119.60				

Table 4

Maximum likelihood of parameter values for the Weibull growth model using 22 pairs of age-weight data for Pacific halibut, assuming additive errors.

Parameter	Estimate	Std error	Confidence interval	t-value	p-value
W_∞	56.79	1.80	(53.26, 60.33)	31.50	$< 10^{-50}$
η	24.22	10.19	(4.25, 44.19)	2.38	0.017
t_0	-7.32	10.22	(-27.32, 12.67)	-0.72	0.473
β	4.50	2.19	(0.21, 8.79)	2.05	0.040
σ	2.05	0.24	(1.60, 2.52)	8.59	$< 10^{-8}$
logLikMx	-53.55				
AIC	117.10				

Table 5
Maximum loglikelihood estimates of the Weibull parameter values using 22 pairs of age-weight data for Pacific halibut assuming additive errors.

Parameter	Estimate	Std error	Confidence interval	*t*-value	*p*-value
W_∞	59.78	2.84	(54.22, 65.35)	21.06	$< 10^{-50}$
η	17.62	0.66	(16.34, 18.90)	26.89	$< 10^{-50}$
t_0	0				
β	2.80	0.20	(2.42, 3.19)	14.16	$< 10^{-20}$
σ	2.54	0.38	(1.80, 3.28)	6.72	$< 10^{-8}$
logLikMx	-51.89				
AIC	113.77				

Two restrictions were used: 1) parameterization of the 0.632 growth in time quantile, and 2) $t_0 = 0$.

Table 6
Maximum loglikelihood parameter estimates for the generalized Weibull model using 22 pairs of age-weight data for Pacific halibut assuming additive errors.

Parameter	Estimate	Std error	Confidence interval	*t*-value	*p*-value
W_∞	57.37	1.98	(53.49, 61.25)	28.97	$< 10^{-50}$
η	21.04	0.86	(19.35, 22.73)	24.43	$< 10^{-50}$
t_0	0				
β	6.42	1.59	(3.28, 9.52)	4.02	$< 10^{-4}$
c	0.33	0.10	(0.14, 0.53)	3.39	$< 10^{-4}$
σ	2.53	0.42	(1.70, 3.36)	5.97	$< 10^{-6}$
logLikMx	-50.40				
AIC	112.80				

Two restrictions were used: 1) parameterization of the 0.632 growth in time quantile, and 2) $t_0 = 0$.

Table 7
Results of fitting the von Bertalanffy parameter to 900 pairs of age-weight data for striped bass.

Parameter	Estimate	Std error	Confidence interval	*t*-value	*p*-value
W_∞	51.56	2.26	(47.13, 55.99)	22.80	$< 10^{-50}$
k	0.17	0.02	(0.13, 0.21)	8.16	$< 10^{-8}$
t_0	-4.12	0.62	(-5.33, -2.91)	-6.66	$< 10^{-8}$
b	7.43	0.85	(5.77, 9.09)	8.79	$< 10^{-8}$
σ	0.28	0.01	(0.27, 0.30)	42.88	$< 10^{-50}$
$l(\hat{\theta})$	-168.27				
AIC	346.55				

the sample using 900 pairs of age-weight data for striped bass (*M. saxatilis*) shown in Fig. 3B, we observe in the age-weight data of this figure a reduced variation in the last two age classes (14 and 15 years); and a possible structure related to selectivity, i.e., larger weights seem to be capped between 40 and 50 pounds.

Estimates of all the parameters of this model are statistically different from zero, although the estimate of the parameter t_0 is very close to being non-significant because the standard error of this estimate has a high relative standard error or a small *t*-value (*t*-value = -6.66). This is because, can be seen in the scatterplot of the data (Fig. 3B), there is a reduced amount of information around zero, which is where we have the information about t_0. It is interesting to compare the estimate of this

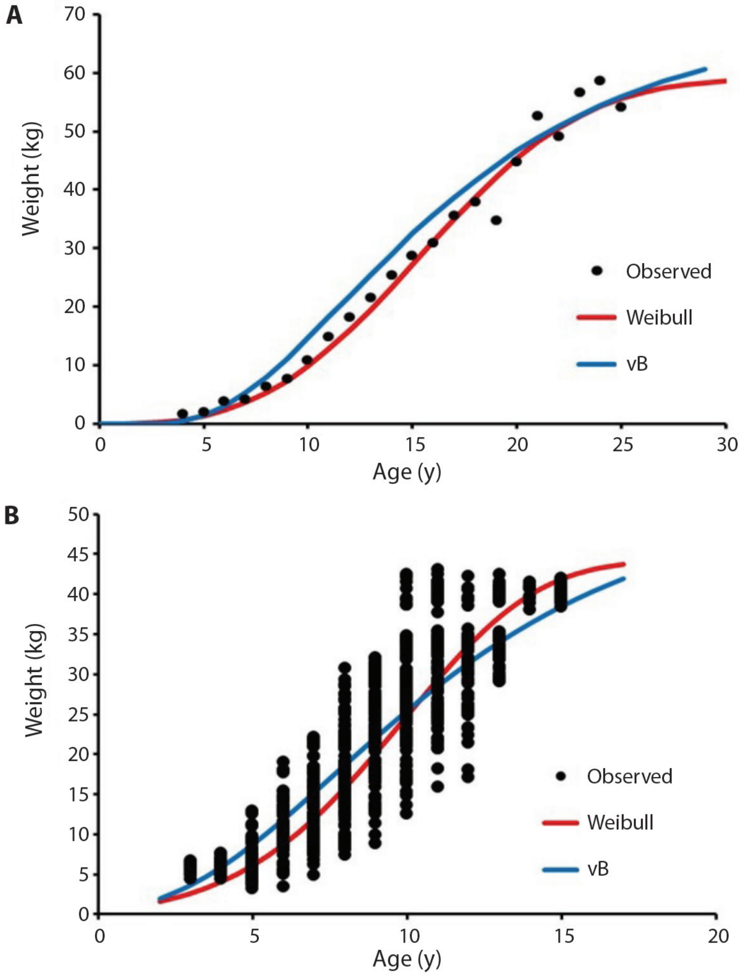

Fig. 3. Graphical comparison of fits of the von Bertalanffy and Weibull models to two data sets. **A.** Pacific halibut 22 pairs of mean weight-at-age. **B.** striped bass 900 data pairs of weight-at-age.

parameter in the case of a large data set and in the case of the small sample (Quinn II & Deriso, 1999). The *t*-value is of different orders (3.33 and -6.66). This is further discussed below.

Weibull growth model: Table 8 shows the estimates that result in the adjustment of the Weibull-type model to the sample of 900 age-weight pairs of data. In this fit, the estimates of all the parameters are significant and the estimate with the greatest uncertainty is t_0, in a similar way adjustment of the previous model, in both cases, the systematic part of the model is different, but the stochastic part (error term) is similar. Parameters W_∞ and *ß* have the lowest estimation uncertainties.

Generalized Weibull model: Table 9 shows the estimates that result in the adjustment of the generalized Weibull type model to the sample of 900 age and weight data pairs. The generalized Weibull type has one more parameter than the Weibull type model. This additional parameter causes this last model to be over parameterized, which is expressed in an estimate with a high uncertainty for parameter

Table 8
Results of fitting the Weibull model to 900 pairs of age-weight data for striped bass.

Parameter	Estimate	Std error	Conf interval	*t*-value	*p*-value
W_∞	44.23	2.58	(39.17, 49.29)	17.14	$< 10^{-50}$
η	17.89	1.63	(14.70, 21.08)	10.10	$< 10^{-30}$
t_0	-7.21	1.77	(-10.68, -3.75)	-4.08	$< 10^{-4}$
β	4.43	0.60	(3.26, 5.61)	7.37	$< 10^{-8}$
σ	0.28	0.01	(0.26, 0.29)	42.29	$< 10^{-50}$
$l(\hat{\theta})$	-123.23				
AIC	256.46				

Table 9
Results of fitting the generalized Weibull model to the data set of 900 pairs of age-weight data for striped bass.

Parameter	Estimate	Std error	Conf interval	*t*-value	*p*-value
W_∞	44.33	2.90	(38.64, 50.01)	15.29	$< 10^{-50}$
η	17.73	2.21	(13.41, 22.05)	8.04	$< 10^{-8}$
t_0	-6.99	2.28	(-11.45, -2.53)	-3.07	0.0027
β	4.51	0.49	(3.54, 5.47)	9.18	$< 10^{-8}$
c	0.96	0.11	(0.74, 1.18)	8.49	$< 10^{-8}$
σ	0.27	0.01	(0.26, 0.29)	42.76	$< 10^{-50}$
$l(\hat{\theta})$	-124.11				
AIC	260.22				

t_0. The latter results in a confidence interval for t_0, that contains zero (-6.1676, 1.1276), which indicates that the estimate of t_0 is not significant. Another parameter that has a low significance, although it is still significant, is parameter c, with a confidence interval (0.0731, 0.8465) very close to zero.

When comparing the values of the AIC, we observed a ranking of the goodness of fit of the three models, vB, Weibull type and generalized Weibull. Table 10 shows the values of the AIC index for the two example data sets considered herein. In the first example, it is assumed in the Weibull type model that parameter t_0 is zero, while in the second example this assumption is assumed for the generalized Weibull model.

Table 10
AIC values for three model fits to the data sets.

Model	Pacific halibut (22 obs.)	Striped bass (900 obs.)
von Bertalanffy	119.60	346.55
Weibull	117.10	256.46
Generalized Weibull	112.80	260.22

Comparison of fits: Relative performance of both models (vB and Weibull) fit to the two data sets can be graphically appreciated (Fig. 3). It can be observed how the "winner" Weibull model fits better the two data sets as compared to the "winner" vB model. Although we observe a reduced variation in the last two age classes (14 and 15 years); the figure also suggests a possible structure related to selectivity, i.e., larger weights seem to be capped between 40 and 50 pounds.

DISCUSSION

In the present work the case is made of using the Weibull growth function as an alternative to the vB model when pairs of age-weight data are available. It is striking to realize that often growth is analyzed in terms of length and as mentioned, this is the result of ease to obtaining length data. In fisheries studies it is less common to find weight at-age data to study growth, although there are good reasons to use weight. Allen and Hightower (2010) point out that weight can be used as a surrogate for fecundity or the contribution of females to the spawning population. Harvest regulations in some fisheries are set to allow the average weight of fish to increase, with the expectation that protecting large, highly fecund females will improve recruitment; or simply as targets of biological production expressed in biomass or number of individuals and its relative weight (catch quota). Information about growth also indicates the "health" of a population relative to its food resources and the quality of the aquatic environment. There are many fisheries that regulation is based on the weight of the individual such as abalone and some clams (Botello-Ruvalcaba et al., 2010; Luquín-Covarrubias et al., 2022). However, in aquaculture studies age-weight data are often obtained under the assumption of controlled conditions.

Since the Weibull distribution was conceived with the probability of failure in mind, it inherently tied to time. This intrinsic connection poses a significant challenge for its application in marine organisms. In fisheries management, age structure is a key predictor of population dynamics and is therefore crucial for sustainable management. Age information forms the basis for calculations of growth rate, mortality rate, and productivity (Campana, 2001).

Campana and Thorrold (2001) estimated that well over 1 million fish were aged worldwide in 1999, primarily using scales and otoliths. These efforts far exceed those routinely applied to non-fish species, underscoring the importance of age-structured information in fisheries science. Techniques for determining the age of organisms have not only improved in precision but have also streamlined the research and monitoring processes of marine populations. Among the most notable techniques are reading growth rings in otoliths (Fairfield et al., 2021), scales (Campana & Thorrold, 2001), and digital imaging, the latter offering greater precision and efficiency in reading (Villamor et al., 2016). Additionally, genetic DNA techniques are particularly valuable when other methods are not applicable, such as in the case of lobsters (Fairfield et al., 2021). The Weibull model could see more frequent use.

Comparison of t_0 values for both cases. vB model: we have two sets of data where the ages and weights are in similar ranges, and in both cases the data begins in age class 4. The level of information about t_0 is not similar, in the first model the error is additive and average age-weight data are used; while in the second model, the error is multiplicative, and 900 pairs of age-weight data are used. What is noticeable in the second example is the reduced uncertainty in the estimation of the error term, compared to the fit of the model to the data set of the first example (22 pairs of data).

We can see this in the magnitudes of the t-values of the fits to both models, t-value = 5.96 and t-value = 42.88, respectively. Weibull model: With both data sets, the systematic part of the model is different, but the stochastic part (error term) is similar. When fitting the vB model, the parameters W_∞ and k have the lowest estimation uncertainties. When comparing the quality of fit of the vB and Weibull type models, using the AIC we found that the second model has a better fit, since it has a lower AIC value (256.46) than the first model (346.55).

In the Weibull type model, we note that the age $t = \eta$ corresponds to the inflection point of the growth model, regardless of the value of the parameter β; whereas in the vB model the inflection point is not a parameter but is a function of the different model parameters. Accordingly, parameter β of the two models acts differently. In terms of metabolic processes, it can be thought that, for the Weibull model, catabolic processes dominate up to the value $\eta = t - |t_0|$; thereafter, anabolic processes dominate until asymptotic weight is reached. A similar interpretation is not straight forward in the vB growth model (Shi et al., 2014). In the vB model, catabolism is assumed proportional to body weight, and anabolism to surface area or body weight (Gamito, 1998). For individual growth, the Weibull model is a generalized version of the vB model and has also been related to the Schnute-Richards general growth model (Swintek et al., 2019). The Weibull function has also been proposed to model population growth because it has similar properties to the logistic, with an asymptotic size of *K*; in this case t_0 is not present; in other words, the model does not depend on t_0. In this case, parameter η expresses the value of time when the population is 0.63 *K* (Prager et al., 1989).

In growth studies, generally speaking, the Weibull model has been found to outperform other models including the Richards and Gompertz (Dagogo et al., 2023). A simplified, one-parameter version of the Weibull model was found to fit better pine tree growth as compared to other models, including that of Richards (Souza et al., 2021). The Weibull model best described live weight data of partridges compared to other eight other models commonly used, including logistic and Richards (Wen et al., 2019).

To our knowledge, for striped bass there had been no previous publications on individual growth using the Weibull model. In an earlier study, the vB model was used to fit individual growth data. The oldest fish were 12 years old and differences were found in parameters of males and females (Collins, 1982). For reared striped bass, the vB model was also fitted to growth data using tagging information. Maximum age estimated was 9 years and analyses were not conducted for separate sexes (Callihan et al., 2014).

As expected, the result obtained using the vB model with the Pacific halibut was similar to that of Quinn II and Deriso (1999). No studies using the Weibull model for this organism were found. For the Pacific halibut, in all cases, the Weibull model estimated lower asymptotic weights compared to the vB model. This is explained by the fact that the latter model assumes a rapid initial growth that decreases as it approaches the asymptote, whereas the Weibull model has a lower initial parameter (-7.32 and zero for two scenarios) compared to vB (3.037).

In all three cases of the Weibull model, using the AIC criterion, the best fit was achieved with growth parameterization and setting $t_0 = 0$.

The relationship between individual growth models and cumulative distribution functions is very useful because it allows us to use the knowledge we have about distribution functions (Marshall & Olkin, 2007), to obtain new growth models or extend existing models. Knowledge of different functions (such as density, cumulative distribution, and survival) associated with a probability distribution, as well as their properties, can be translated into functions that inform about characteristics of the growth process.

The recognition of the equivalence between individual growth models and the cumulative distribution functions $F(t)$ allows the use of knowledge about the distribution functions of continuous random variables. Various functions related to the cumulative distribution function can be used to express some type of information of the individual growth process. For example, the density function $f(t)$, which is the derivative of the cumulative distribution, can be associated with the growth rate $W_\infty f(t)$. The survival function $S(t)$, which is the complement of the cumulative distribution $S(t) = 1-F(t)$, gives us information about the proportion of an organism that remains to grow at time *t*, $W_\infty S(t)$.

In the study of lifetimes, the quantile function t_p is defined as the time at which a proportion *p* of failures will have occurred, it can be used to know the time at which an organism will have grown a proportion *p* of its maximum asymptotic size (Meeker et al., 2022). Knowledge of the density, survival, and quantile functions, among others, of a distribution associated with a given growth model allows us to have a better vision of the characteristics and properties of the individual growth model under study.

The vB length and weight growth models are two clear examples of the relationship between growth models and distributions. The length growth model is associated with the exponential distribution, and the vB weight growth model is associated with the generalized exponential distribution. That is, the vB weight growth model and the generalized exponential distribution are two simple extensions of the vB weight growth model and the exponential distribution, respectively.

It seems that the wide application of the vB weight growth model is not due to its quality of fit, since the fit of this model to growth data does not always outperform other models with which it competes, rather very often its use is chosen *a priori*. For this reason, it is worth asking if, in addition to the vB weight growth model, there is another model, which is an extension of the basic vB length growth model, and with a similar form, but with adequate flexibility in order to have a better quality of fit to age-weight growth data.

An extension of the exponential distribution that is well known and widely applied in the analysis of Survival and Reliability data is the Weibull distribution. The above suggests that a direct extension of the vB length growth model, additional to the vB weight growth model, is the Weibull growth model. An important advantage of the Weibull-type growth model is its flexibility, which yields better fits than other models, as shown in the comparative study shown herein.

Ethical statement: The authors declare that they all agree with this publication and made significant contributions; that there is no conflict of interest of any kind; and that we followed all pertinent ethical and legal procedures and requirements. All financial sources are fully and clearly stated in the acknowledgments section. A signed document has been filed in the journal archives.

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