Estimating Age at a Specified Length from the von Bertalanffy Growth Function

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Abstract

Estimating the time required (i.e., age) for fish in a population to reach a specific length (e.g., legal harvest length) is useful for understanding population dynamics and simulating the potential effects of length-based harvest regulations. The age at which a population reaches a specific mean length is typically estimated by fitting a von Bertalanffy growth function to length-at-age data and then rearranging the best-fit equation to solve for age at the specified length. This process precludes use of some statistical methods for computing confidence intervals and statistically comparing estimates of age at the specified length among populations. We provide a new parameterization of the von Bertalanffy growth function that allows the age at a specified length to be directly estimated so that standard methods to construct confidence intervals and make among-group comparisons for these values can be used. We demonstrate use of the new parameterization with two datasets.

Keywords: Nonlinear modeling, Lake Whitefish, Walleye, von Bertalanffy

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# Introduction

The length of time () required for fish in a population to reach a specified mean length () is useful for understanding the dynamics of fish populations. The value usually represents the age when fish become vulnerable to fishing mortality as (originally denoted as ) in Beverton-Holt equilibrium yield models (Beverton and Holt, 1957). These models have long been used to simulate fishery responses to changes in fishing mortality (Beverton and Holt, 1957; Ricker, 1975; Quinn and Deriso, 1999). Release of the Fisheries Analysis and Simulation Tools (FAST; Slipke and Maceina, 2001) and Fisheries Analysis and Modeling Simulator (FAMS, Slipke and Maceina, 2014) software packages facilitated using these Beverton-Holt models to simulate the effects of length-based harvest regulations on freshwater fisheries (e.g., Isermann et al., 2002; Brenden et al., 2007; Colvin et al., 2014). The value may also be valuable outside of this modeling framework because it provides a measure of cumulative growth up to age that likely responds (or is related) to abiotic and biotic factors that affect growth of fish (Brett, 1979; Lorenzen, 2016). For example, at a fixed , a population with a larger grows slower than a population with a lower . Thus, may be useful for comparing growth among populations.

Typically, has been estimated by fitting a von Bertalanffy growth function (VBGF) to length and age data and then algebraically rearranging the best-fit equation to solve for age given the specified length (Beverton and Holt, 1957; Gulland, 1973; Clark, 1983; Allen and Miranda, 1995; Slipke and Maceina, 2001). The delta method (Seber and Wild, 2003; Ritz and Streibig, 2008) or bootstrapping (Hilborn and Mangel, 1997; Ritz and Streibig, 2008) may be used to approximate standard errors and confidence intervals for derived in this manner. However, likelihood profiles (Hilborn and Mangel, 1997; Ritz and Streibig, 2008) cannot be used to construct confidence intervals for the derived and usual methods (extra sum-of-squares tests (Ritz and Streibig, 2008), likelihood ratio tests (Kimura, 19890), or information criterion (Burnham and Anderson, 2002) approaches) for comparing models cannot be used to determine if differs among populations. These statistical shortcomings could be overcome if was directly estimated as a function parameter rather than being derived from other function parameters.

Additionally, some parameters in the usual VBGF may be illogical and poorly estimated (i.e., imprecise) because they represent values outside the domain of observed ages. In some instances, these parameters have been fixed at constant values (Isermann et al., 2007; Weber et al., 2011), which may negatively affect estimates of other parameters and values derived from these parameters, such as . In contrast, is unlikely to be outside the domain of observed ages and, thus, is likely to be logically and precisely estimated if it is a parameter in a VBGF.

Therefore, the objectives of this note are to (1) describe a VBGF that has as a directly estimated parameter and (2) demonstrate how this VBGF can be used to directly estimate and identify differences in between populations.

# Theory

The most commonly used parameterization of the VBGF from Beverton and Holt (1957) is

(1)

where is the expected or mean length at time (hereafter, age) , is the asymptotic mean length, is a measure of the exponential rate at which approaches (Schnute and Fournier, 1980), and is the theoretical age at which would be zero (i.e., the x-intercept; Figure 1). For use further below, Eq. (1) can be expressed as

(1a)

The original parameterization of the VBGF from von Bertalanffy (1938) is

(2)

where is when *t* = 0 (i.e., y-intercept; Figure 1). Eq (2) can be algebraically shown to equal

which, for use further below, can also be expressed as

(2a)

The similarities of Eqs. (1a) and (2a) suggest that the VBGF may be expressed as

(3)

where when *t* = . Geometrically, setting to a constant vertically shifts the growth curve (i.e., subtract from all ) such that is estimated as an x-intercept. Similarly, setting to a constant horizontally shifts the growth curve (i.e., subtract from all ) such that is estimated as a y-intercept. Thus, when (i.e., no vertical shift), is the theoretical age at a mean length of zero (i.e., the x-intercept) and with replaced by . Similarly, when (no horizontal shift), is the mean length at age zero (i.e., the y-intercept) and with replaced by . Thus, Eqs. (1) and (2) are special cases of Eq. (3) and only differ in whether they are parameterized to estimate the original (i.e., not shifted) x- or y-intercept (Figure 1).

Of more interest is that Eq. (3) may be used to estimate or for any point on the VBGF curve (Figure 1). For example, may be set to a specific age of biological interest such that the mean length at that age () is a parameter estimated from fitting Eq. (3) to data. Conversely, and the focus of this note, may be set to a specific length of biological interest such that the age for fish of that mean length () is a parameter estimated from fitting Eq. (3) to data. Thus, because is a parameter directly estimated from fitting Eq. (3) to data, all methods for computing confidence intervals for function parameters may be used and common statistical methods may be used to identify differences in among populations.

, as do Eqs. (1) and (2)

# Methods

We demonstrate use of Eq. (3) for estimating with two examples. First, length-at-age data for Lake Michigan lake whitefish (*Coregonus clupeaformis*) are used to demonstrate that the fit of Eq. (3) is equivalent to the fits of Eqs. (1) and (2), and that direct estimates of from Eq. (3) equal derived estimates of from Eqs. (1) and (2). Second, length-at-age data for Lake Winnibigoshish (Minnesota) walleye (*Sander vitreus*) are used to show how model comparison methods can be used to assess differences in (and other function parameters) between groups (i.e., sexes).

Lake whitefish were captured by commercial trap-netters from locations in and around Green Bay, Lake Michigan in October 2012 and 2013 and were genetically assigned to the Big Bay de Noc stock. Total length (TL) was measured to the nearest mm and integer ages were estimated from thin-sectioned otoliths. Full collection details for these data are in Belnap (2014). As in Belnap (2014), we estimate the age required to reach a mean TL of 480 mm (i.e., *t*480), which is the TL at which lake whitefish are fully vulnerable to commercial and tribal harvest in Lake Michigan (Ebener et al., 2008). Eqs. (1)-(3) were fit to these data using the default Gauss-Newton algorithm of the nls() function in the R environment (R Development Core Team, 2017). Starting values were obtained by visually fitting each equation to the observed data (Ritz and Streibig, 2008; Ogle, 2016). Alternative starting values were used to confirm that a global rather than a local minimum was obtained (McCullough, 2008). Results from fitting Eqs. (1) and (2) were algebraically rearranged to estimate . For each equation, 999 non-parametric bootstrap samples of mean-centered residuals were computed with the nlsBoot() function from the nlstools package v1.0-2 (Baty et al., 2015). A was derived for each bootstrap sample for Eqs. (1) and (2). To further compare the equivalency of Eqs. (1)-(3), predicted mean lengths at ages 8 and 20 were computed from each bootstrap sample for all three equations. Approximate 90% confidence intervals (CI) for each function parameter, derived estimate, and predicted mean length-at-age were the 5th and 95th percentile values of the 999 bootstrap estimates. The 90% confidence intervals were used to eliminate the tail portion of the bootstrapped distributions to better compare the equivalency of estimated parameters and derived values across equations.

Gillnets were used to capture walleye from two locations in Lake Winnibigoshish in September 2012. Total length was measured to the nearest mm, integer ages were estimated from cracked otoliths viewed with a fiber optic light, and sex was determined by visually examining gonads. We estimated because 432 mm was the lower end of a protective slot limit for Lake Winnibigoshish walleye in 2012. We used extra sum-of-squares tests in a sequential step-down process (as described in Ogle, 2016) to identify which of eight possible models best fit these data. The eight models were modifications of Eq. (3) where all, two, one, or no parameters differed between the two sexes. All models were fit with the default Gauss-Newton algorithm in nls() of R. The confint() function from the MASS package (Venables and Ripley, 2002) was used to construct 95% profile likelihood CI for all function parameters in the final model. The profile likelihood method, rather than bootstrapping, was used for these CI to illustrate that the likelihood profile method can be used to estimate CI for from Eq. (3).

# Results

Point estimates for all parameters and derived values, including , shared between Eqs. (1)-(3) were equivalent (Table 1). Confidence intervals for all parameters and derived values shared between Eqs. (1)-(3) were similar, but not exactly equal due to the inherent stochasticity of the bootstrap method (Table 1). Lake whitefish from the Big Bay de Noc genetic stock reached a total length of 480 mm at approximately 8 years of age.

The (*F*1,482 = 147.43, *P* < 0.001) and (*F*1,482 = 128.30, *P* < 0.001) parameters, but not *K* (*F*1,481 = 3.21, *P* = 0.074), differed significantly between male and female Lake Winnibigoshish walleye (Figure 2). The was greater for female (95% CI: 641-707 mm) than male (95% CI: 560-616 mm) walleye, whereas was lower for female (95% CI: 3.78-3.95 years) than male (95% CI: 4.61-4.93 years) walleye. These results suggest that female walleye in Lake Winnibigoshish reached the minimum slot length limit (432 mm) before and achieved a longer maximum mean length than males.

# Conclusion

Eq. (3) is a simple parameterization of the VBGF that includes the typical and original VBGF parameterizations as special cases. However, Eq. (3) is flexible in that it may also be used to estimate mean length for any specific age or age for any specific mean length, rather than only intercept values as with the typical and original VBGFs. Point- and bootstrapped-interval estimates for age at a specific length (i.e., ) from Eq. (3) match those derived from parameters estimated with Eqs. (1) and (2). However, Eq. (3) allows for use of likelihood profile methods to estimate confidence intervals and model selection procedures to statistically determine if age at the specified mean length differs among populations. We suggest using Eq. (3) when interest lies in estimating or testing for differences among populations in , , and a point on the growth curve other than one of the intercepts.

# Acknowledgments

We thank Matthew Belnap for collection of lake whitefish data which were obtained during a project funded by the Great Lakes Fishery Commission. We thank the Minnesota Department of Natural Resources for use of the walleye data from Lake Winnibigoshish. This paper was improved by discussions with and reviews by Travis Brenden, XXX, and two anonymous reviewers. Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the U.S. Government.

# Supplementary Information

R code for all figures and analyses.

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Table 1. Estimated parameters (, *K*, , , and, for Eq. (3), ), derived variables ( for Eqs. (1) and (2) and predicted mean lengths-at-ages 8 () and 20 ()), with 90% confidence intervals in parentheses, and AICc from fitting Eqs. (1)-(3) to the Big Bay de Noc genetic stock of lake whitefish.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter/ Variable | Eq. (1) | Eq. (2) | Eq. (3) |
|  | 550.83 (540.45, 572.97) | 550.83 (540.99, 574.34) | 550.83 (541.33, 577.59) |
| *K* | 0.197 (0.108, 0.300) | 0.197 (0.097, 0.297) | 0.197 (0.093, 0.306) |
|  | -2.386 (-9.834, 1.027) | -- | -- |
|  | -- | 206.31 (-214.67, 380.72) | -- |
|  | 8.04 (7.09, 8.65)a | 8.04 (7.02, 8.67)a | 8.04 (7.03, 8.64) |
|  | 479.38 (469.10, 489.68) | 479.38 (468.89, 489.62) | 479.38 (469.42, 489.57) |
|  | 544.08 (537.65, 550.31) | 544.08 (538.22, 549.73) | 544.08 (538.65, 550.62) |
| RSS | 320685.4 | 320685.4 | 320685.4 |

aValue derived by rearranging the equation to solve for *t* with a length of 480 mm.

# Figure Labels

Fig. 1. Examples of Eqs. (1)-(3) with = 250, = 0.7, *t*0 = -0.7, and *L*0 = 73.8. Three points on the curve are shown with gray circles -- () specifically defines Eq. (1), (0) specifically defines Eq. (2), and () generically defines Eq. (3).

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Fig. 2. Fits of Eq. (3) to female (open squares, dotted line) and male (open circles, dashed line) total length-at-age data for walleye captured from Lake Winnibigoshish in September, 2012. Points are slightly offset from the integer ages to reduce overlap between sexes. Point estimates and 95% confidence intervals are shown for each sex along the y-axis for and along the x-axis for . The gray horizontal line is at *Lr* = 432 mm. One 581 mm age-16 male is not shown.



