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

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Running title: Estimating Age at a Specified Length

<A>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 using standard frequentist methods to compute confidence intervals and compare estimates of age at the specified length among populations. We provide a parameterization of the von Bertalanffy growth function that has age at a specified length as a parameter. With this parameterization, age at a specified length is directly estimated and standard methods can be used to construct confidence intervals and make among-group comparisons for this parameter. We demonstrate use of the new parameterization with two datasets.

# <A>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 in Beverton–Holt equilibrium yield models (was in 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 resulted in increased use of 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. 2013). 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 higher grows more slowly than a population with a lower . Thus, may be a useful parameter 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 (CIs) for derived in this manner. However, likelihood profiles (Hilborn and Mangel 1997; Ritz and Streibig 2008) cannot be used to construct CIs for the derived and usual methods [extra sum-of-squares tests (Ritz and Streibig 2008), likelihood ratio tests (Kimura 1980), or information criterion approaches (Burnham and Anderson 2002)] for comparing models cannot be used to determine if differs among populations. These statistical shortcomings could be overcome if was directly estimated as a parameter in the VBGF rather than being derived from other parameters in the VBGF.

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 brief 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.

# <A>Theoretical Development

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

or, equivalently,

, (2)

where is when *t* = 0 (i.e., y-intercept; Figure 1). With simple additions (or subtractions) of zeroes, equations (1) and (2) can be expressed, respectively, as

and

.

Comparison of these expressions reveals the algebraic similarity between the two parameterizations. This similarity suggests that the VBGF may be expressed as

, (3)

where when *t* = . Thus, when , is the theoretical age at a mean length of zero (i.e., the *x*-intercept) and equation (3) reduces to equation (1) with replaced by . Similarly, when , is the mean length at age zero (i.e., the *y*-intercept) and equation (3) reduces to equation (2) with replaced by . Thus, equations (1) and (2) are special cases of equation (3) and only differ in whether they are parameterized to estimate the *x*- or *y*-intercept (Figure 1). These intercepts may be of little biological interest (especially ) or poorly estimated because they are outside the domain or range of the data.

A specific value of or may be chosen so that equation (3) passes through any specific point on the VBGF curve (Figure 1), and a biologically interesting parameter is then estimated. 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 equation (3) to data. Conversely, and the focus of this brief, 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 equation (3) to data. Thus, because is a parameter directly estimated from fitting equation (3) to data, all methods for computing CIs for function parameters may be used and common statistical methods may be used to identify differences in among populations.

Note that equation (3) appears to have four parameters, but either is set to a constant value and is estimated or is set to a constant value and is estimated. Thus, equation (3) has three estimable parameters, as do equations (1) and (2).

# <A>Methods

We demonstrate the use of equation (3) to estimate with two examples. First, we use length-at-age data for Lake Whitefish *Coregonus clupeaformis* in Lake Michigan to demonstrate that the fit of equation (3) is equivalent to the fits of equations (1) and (2) and that direct estimates of from equation (3) equal the derived estimates of from equations (1) and (2). Second, we use length-at-age data for Walleyes *Sander vitreus* in Lake Winnibigoshish (Minnesota) 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 trapnetters 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. The TLs of Lake Whitefish were measured to the nearest millimeter, and integer ages were estimated from thin-sectioned otoliths. Full collection details for these data are provided by Belnap (2014). As in the Belnap (2014) study, we estimate the age at which a mean TL of 480 mm was reached (i.e., ); this is the TL at which Lake Whitefish are fully vulnerable to commercial and tribal harvest in Lake Michigan (Ebener et al. 2008). Equations (1)-(3) were fitted 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 equations (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 version 1.0-2 (Baty et al. 2015). A value of was derived from each bootstrap sample for equations (1) and (2). To further compare the equivalency of equations (1)-(3), the 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% CI was used instead of the 95% CI 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 during September 2012. The TLs were measured to the nearest millimeter, integer ages were estimated from cracked otoliths viewed with a fiber optic light, and sex was determined by visual examination of the 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 by Ogle 2016) to identify which of eight possible models best fit these data. The eight models were modifications of equation (3) where all parameters, two parameters, one parameter, or no parameters differed between the two sexes. All models were fit with the default Gauss-Newton algorithm in the nls() function of R. The confint() function from the MASS package (Venables and Ripley 2002) was used to construct 95% profile likelihood CIs for all function parameters in the final model. The profile likelihood method, rather than bootstrapping, was used for these CIs to illustrate that this method can be used to estimate the CI for from equation (3).

# <A>Results

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

The (*F* = 147.43; df = 1, 482; *P* < 0.001) and (*F* = 128.30; df = 1, 482; *P* < 0.001) parameters differed significantly between male and female Walleyes in Lake Winnibigoshish, whereas *K* did not (*F* = 3.21; df = 1, 481; *P* = 0.074; Figure 2). Best-fit model equations for both sexes were

for females

and

for males.

The was greater for female (95% CI = 641-707 mm) than male (95% CI = 560-616 mm) Walleyes, whereas was lower for females (95% CI = 3.78-3.95 years) than males (95% CI = 4.61-4.93 years). These results suggest that female Walleyes in Lake Winnibigoshish reached the minimum slot length limit (432 mm) before and achieved a longer asymptotic mean length than males.

# <A>Discussion

Equation (3) is a simple parameterization of the VBGF that includes the typical and original VBGF parameterizations as special cases. However, Equation (3) is flexible in that it may also be used to estimate mean length for any specific age or to estimate age for any specific mean length rather than only intercept values as with the typical and original VBGFs. We expect the primary use of equation (3) among fisheries scientists will be to estimate age at a specific length (i.e., ). Thus, we demonstrated that point- and bootstrapped-interval estimates for from equation (3) match those derived from parameters estimated with equations (1) and (2). We also showed how, in contrast to equations (1) and (2), standard frequentist methods can be used with equation (3) to estimate CIs for (e.g., profile likelihood) and to determine whether differs among populations (e.g., extra sums-of-squares tests).

A direct estimate of (though estimated as ) may also be made by replacing in equation (1) with (i.e., subtracting from each observed length). However, from fitting this modified equation is underestimated by a constant . If is also subtracted from in equation (1), then will be estimated on the original scale. These two ad hoc modifications simply convert equation (1) to equation (3). Additionally, the VBGF parameterizations of Schnute and Fournier (1980) and Francis (1988) have two or three parameters, respectively, that represent mean lengths at specific ages. Specific mean lengths could be chosen in these parameterizations such that ages at those mean lengths are estimated. However, is dropped from the Schnute and Fournier (1980) parameterization and both and are dropped from the Francis (1988) parameterization.

Equation (3) is an alternative parameterization of the VBGF that allows a direct and conceptually consistent -- rather than derived and ad hoc -- estimate of (or ). In addition, direct estimates of and are maintained with equation (3). It is important to note, however, that equation (3) is not a fundamentally new growth model. Thus, the usual cautions and caveats related to the applicability, fitting, and data requirements of a VBGF (Knight 1968; Roff 1980; Day and Taylor 1997; Lester et al. 2004; Katsanevakis and Maravelias 2008; Haddon 2011; van Poorten and Walters 2015) still apply to equation (3). Equation (3) can be used to directly estimate three growth-related parameters of interest, but those estimates are only useful if the VBGF is an adequate model of the data and the data are representative of the population of interest.

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<A>Supplementary Information

R code for all figures and analyses.

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TABLE 1. Estimated parameters [, *K*, , , and, for equation (3), ], derived variables ( for equations 1 and 2), and predicted mean lengths-at-ages 8 () and 20 (), with 90% confidence intervals in parentheses, and residual sum-of-squares (RSS) from fitting equations (1)-(3) to the Big Bay de Noc genetic stock of Lake Whitefish.

|  |  |  |  |
| --- | --- | --- | --- |
| Parameter/ Variable | Equation (1) | Equation (2) | Equation (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

FIGURE. 1. Examples of equations (1)-(3) with = 250, = 0.7, *t*0 = -0.7, and *L*0 = 74. Three points on the curve are shown with gray circles: () specifically defines equation (1), (0) specifically defines equation (2), and () generically defines equation (3).

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FIGURE. 2. Fits of equation (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.