10 Condition

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10.1 INTRODUCTION

The analysis of fish condition has become a standard practice in the management of fish populations as a measure of both individual and cohort (e.g., age- or size-group) wellness. Condition has been generically described as the well-being or robustness of an individual fish (Le Cren 1951; Bulow et al. 1981; Blackwell et al. 2000). It has typically been estimated by comparing an individual fish weight to a standard weight for a given length and assuming that larger ratios (condition index) reflect a healthier physiological state (Bolger and Connolly 1989; Murphy et al. 1991) or by directly measuring physiological parameters related to the energy stores, such as tissue lipid content (Craig 1977; Fechhelm et al. 1995). All methods of calculating condition share the common goal of controlling for or removing the confounding effects of absolute body size when comparing body mass or other measures of nutritional state (Jakob et al. 1996). This is particularly important for organisms with indeterminate growth, such as fishes (Reist 1985).

Measures of condition are generally intended to be an indicator of tissue energy reserves, with the expectation that a fish in good condition should demonstrate faster growth rates, greater reproductive potential, and higher survival than will a lesser-conditioned counterpart, given comparable environmental conditions. Subsequently, fish condition is of keen interest to fisheries scientists, and numerous studies have investigated the relationship between measures of fish condition and parameters such as growth, fecundity, population structure, life history adaptations, environmental conditions, or management actions such as stocking (Cone 1989; Brown and Murphy 1991; Gabelhouse 1991; Blackwell et al. 2000). Although measures of condition in fish can be sensitive or related to factors that might logically affect energy storage or fitness in an individual, there is commonly substantial interspecies, seasonal, environmental, and spatial variation that influences our ability to interpret changes in fish condition.

Fisheries scientists often must assess population status, effects of management actions, and anthropogenic influences on the resource they are managing (Brown and Austin 1996). Fish condition, if appropriately interpreted, may characterize components of the environment in which the fish exists (e.g., habitat,

prey availability, and competition) and provide insights into ecological and physiological processes (e.g., overwintering mortality, seasonal storage of lipids, and maturation). Thus, measures or indices of fish condition can be valuable components of a fisheries scientist's assessment over multiple ecological scales. A critical component for interpreting fish condition data in a useful and applicable manner is the correct application of statistical methodologies when collecting and analyzing data. The objective of this chapter is to provide a brief overview of fish condition measures, focusing on condition indices, and illustrate commonly used techniques to analyze, summarize, and interpret condition data.

10.2 WEIGHT–LENGTH RELATIONSHIPS

Anderson and Neumann (1996) noted that length and weight statistics are cornerstones in the foundation of fisheries management and research. Weight–length data have generally been used either to describe mathematically the relationship between weight and length (Keys 1928) for purposes of conversion from one to the other or to measure individual variation from an expected weight at a given length as an indicator of condition (Le Cren 1951; Bolger and Connolly 1989). It is often advantageous to describe the weight–length relationship of a population to discern changes in body form. The power function,

$$W = aL^b, \tag{10.1}$$

generally describes the weight–length relationship of most fishes, where W is weight, L is length, a is a constant, and b is an exponent usually between 2.5 and 4.0 (a fish growing isometrically or maintaining the same shape across length categories has an exponent of 3.0). The functional exponent b, which describes the curve of the relationship, is generally different among species and can be sensitive to biotic and abiotic influences, leading to different values of b between sexes or localities, even within the same species.

10.2.1 Regression of Weight –Length Data

Because body form typically changes with increasing length (i.e., allometric growth; $b \neq 3.0$), untransformed weight–length data are related in a curvilinear fashion (Figure 10.1A). Although a curve can be fitted to the weight–length relationship for estimation of the power function coefficients (nonlinear regression), these types of data are more easily analyzed by linear regression after logarithmically transforming the data (Figure 10.1B). Based on the ordinary least-squares regression model ($y_i = \beta_0 + \beta_1 x_i + \varepsilon$), equation (10.1) becomes

$$\log_{10}(W) = a + b(\log_{10}L), \tag{10.2}$$

where W (corresponding to the response or dependent y_i) and L (independent x_i) are weight and length, respectively, a (β_0) is the y-intercept ($\log_{10}$ scaling), and

b (β_1) the slope of the line. The error (ε) associated with estimating y_i (W) from a regression line is implicit in equation (10.2).

The regression assumptions of linearity, normality, homoscedasticity (equal variance of y at each level of x), and independence (no changes in y at a given x due to an influence such as sampling over time) must be met for meaningful interpretation of the regression coefficients (Neter et al. 1989). If a population (i.e., group or cohort of interest) is randomly sampled over a relatively short period, logarithmically transformed weight–length data generally conform to the basic assumptions and are related in a highly significant linear fashion. Biases can be introduced into weight–length data by, among other things, introducing measurement error, combining temporally or spatially separated samples for which physiological or environmental changes may have affected body form (e.g., pre- and postspawn or lotic and lentic individuals), or by incompletely and nonrandomly sampling the entire size structure of the population (e.g., presence or absence of a resource-limited size category). Suspected transgression of the linearity, variance, and independence assumptions can be initially assessed with residual analyses, where residuals (the difference between the observed weight and the corresponding weight predicted by the regression line) or the error associated with using the regression model are plotted against the independent variable (length) or the predicted value of y. Graphically, residuals should appear as a constant band around zero, with no obvious patterns (Figure 10.1C, D, E, and F). Most statistical packages will provide an option for these analyses. The transformed weight–length data generally approximate a normal distribution and small departures from normality do not create serious problems; however, data normality should not be assumed, especially when using the regression coefficients as indices of population condition or the residuals as an index to individual condition. A normal probability plot is a general test to ensure normality of the data (Figure 10.1G).

A linear relation can be a reasonably good approximation for nonlinear data provided the values of the independent variable do not cover a wide range (Steel and Torrie 1980), such as comparisons of individuals in a relatively narrow subset of all lengths sampled (e.g., a small section of the curve). Furthermore, simple linear regression often statistically provides an adequate fit to untransformed weight–length data when assessing statistics such as r^2; however, better results can be obtained with transformation or nonlinear analysis. Thus, it is unadvisable to fit a linear model to curvilinear data. The logarithmic transformation enhances the relationship by accounting for more of the variation in weight (demonstrated by an increased r^2) and minimizing overall model error, or the distance of individual points from the regression line. The logarithmic transformation enhances our ability to predict weight from length and to interpret the slope and intercept of the relationship. A power function (nonlinear regression or curve fitting) of the untransformed data provides the same explanatory power as linear regression of the transformed variables; however, the exponential nature of the relationship makes interpretation and comparison of weight–length relationships more difficult (Box 10.1).

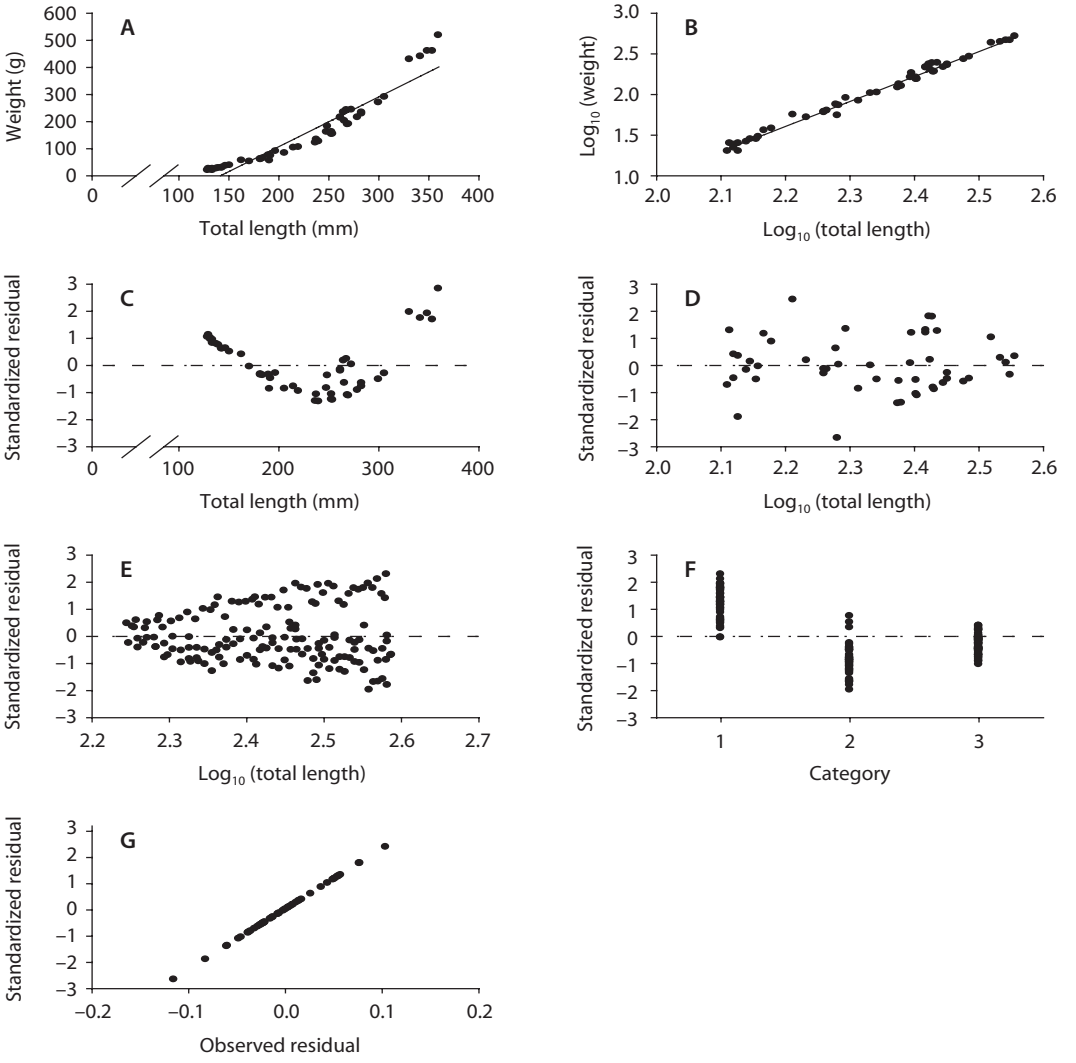

Figure 10.1 Graphical depiction of the curvilinear relationship of (A) untransformed length–weight data from the low-elevation stream Yellowstone cutthroat trout population described in Box 10.1 versus (B) the linear nature of the same data after $\log_{10}$ transformation. (C) A typical diagnostic residual plot clearly illustrates the nonlinearity of the untransformed data, whereas (D) more evenly distributed residuals exist for the transformed data, a pattern that is indicative of linear, homoscedastic, and independent data. (E) The funnel-shaped residual pattern from a separate data set demonstrates unequal variances in the dependent variable (weight), as might be typical when sexually mature fish are collected in pre- and postspawning condition. (F) The up and down pattern of residuals when graphed by sampling time indicate that the data may not be independent but rather influenced by season (1 = prespawn, 2 = postspawn, and 3 = late summer). Normal probability plots can be built or graphed in several ways; here, (G) a normal probability plot of the ranked observed residuals (*x*) versus their paired standardized residual (*y;* calculated assuming a normal distribution) demonstrates the linear relationship indicative of normal weight–length data. A nonlinear relationship would indicate nonnormality or skewness of the data. Other plots, such as a box-plot, can also be used to check data normality.

The least-squares regression coefficients estimated from the log-transformed data can be used to compare relative condition differences among populations or to assess temporal changes in condition within a population (Cone 1989). Bolger and Connolly (1989) indicated that the regression coefficients can suggest significant differences among populations but that estimates of intercept and slope should be considered together to provide a valid interpretation. If the regression slopes of two populations are similar, a larger intercept could indicate a population in better overall condition, or at least heavier fish at a given length. Likewise, a steeper slope would indicate increasingly (with length) better condition if population intercepts were similar. Intersecting regression lines (one population having a greater slope but lesser intercept than another) could indicate general differences in condition among small and large individuals. Carlander (1969) suggested that slopes less than 3.0 might indicate populations in crowded or stunted condition. However, Murphy et al. (1991) cautioned that coefficient analysis should be used to compare only the general form of specific populations because it tends to average out differences in condition between size-classes, an important component of condition analysis if, for example, a fisheries scientist were assessing the effect of prey abundance on different size-classes of fish (e.g., Marwitz and Hubert 1997).

10.2.2 Analysis of Covariance to Test Differences in Regression Lines

Comparisons of weight-at-length (condition) data across multiple populations are often an important consideration, but the length range of individuals sampled often varies in space and time, and different-sized groups of fish may be in better or worse condition. The ANCOVA can control for the effects of differing size ranges (length as the covariate) and is a more powerful test for homogeneity of regres-sion coefficients (i.e., test for differences in slopes between two or more lines with the null hypothesis that coefficients are equal; Zar 1984) where spatial (e.g., el-evation) or temporal (e.g., season) effects might influence inferences regarding population wellness, as modeled by weight. Simply because the length variable is

not statistically significantly different between or among the populations of interest using a means comparison test (*t*-test or analysis of variance [ANOVA]) does not mean length will not confound a comparison of population condition. Rather it is the strength of the covariates' association to both the treatment and response variables together that determines the covariates' influence on our inference regarding condition. On the other hand, ANCOVA should be used with caution when length distributions are completely disparate, as interpretation of the results may become more speculative than meaningful (Agresti and Finlay 1986).

The general assumptions of ANCOVA when applied to weight–length data are (1) that length measurements are fixed, measured without error, and independent of treatments; (2) the regression of weight on length disregarding the treatment is linear (linearity of within-group regressions); (3) there is homogeneity of within-group regressions, and (4) the residuals are normally and independently distributed with zero mean and common variance. The ANCOVA is an inappropriate tool when heterogeneity of regression coefficients and residual variances exists. Assumption two is regularly achieved by some sort of data transformation. Similarly, weight is typically normally distributed and, furthermore, data transformation has a normalizing effect. Assumption three requires that the regression lines associated with the treatment groups have a common slope or parallelism; slope discrepancies will result in a conservative ANCOVA *F*-test, for which the likelihood of type I error (rejecting a true null hypothesis) is actually lower than the nominal alpha. Heterogeneity of error variances is of most concern when sample sizes among groups differ and will result in a conservative *F*-test if the larger and smaller samples sizes are associated with the larger and smaller variances, respectively. If the opposite is true, then the test becomes liberal (i.e., the true alpha is greater than then the nominal alpha) (Vila-Gispert and Moreno-Amich 2001).

We initially want to determine slope similarity. Building on equation (10.2), the complete ANCOVA model contains the response variable (weight, W), an intercept (β_0), two independent variables, the covariate (length, L) and a dummy variable that represents potential effects on weight that are of interest (X; for example, habitat effects are coded 1 for low-elevation stream and 0 for low-elevation lake), and an interaction term (length × habitat code, L_iX_i) in the form

$$W_i = \beta_0 + \beta_1 L_i + \beta_2 X_i + \beta_3 L_i X_i + \varepsilon_i , \tag{10.5}$$

where weight and length are $\log_{10}$ transformed. The relationship can be modeled using a general linear model (GLM) approach or using regression. If the two slopes differ, the interaction term will be significant in the model, indicating that the regression lines intersect at some point (note that point may be outside the range of data collected) and the trend lines are different. This type of result suggests that individual fish in the two populations gain weight at different rates as they increase in length and may indicate, among other things, resource limitations (or availability) for different size categories within (temporal comparisons) or

between (spatial comparisons) populations. If the slopes are statistically different (i.e., we know the lines are different), further testing of intercept differences is difficult to interpret and often of little interest because magnitude of treatment effect varies depending on length and the intercept of a weight–length relationship (length = 0) is generally not relevant.

If fish from two populations maintain similar incremental weight gains with increasing length, then the slopes will not be significantly different; however, one population could be significantly heavier or better conditioned at a given length than another. Thus, we generally want to determine the magnitude of the elevational difference between the lines by assessing the *y*-intercepts. In other words, are the lines truly the same or are they separated in regression space with similar slopes? Here equation (10.5) is reduced to the form

$$W_i = \beta_0 + \beta_1 L_i + \beta_2 X_i + \varepsilon_i \tag{10.6}$$

by removing the interaction term from the analysis. Separate lines or intercept differences are noted by a significant test of the dummy variable (X) in the model.

In its simplest form, ANCOVA is used, as described above, to control for length differences between two populations or categories of treatment (e.g., a habitat treatment of lotic and lentic environments); however, it can be used to assess multiple populations and multiple treatments by simply adding additional dummy variables and the associated interaction terms to equation (10.4). In Box 10.2, we provide an example of ANCOVA based on the two populations of Yellowstone cutthroat trout analyzed in Box 10.1. Both the CI comparisons in Box 10.1 and ANCOVA in Box 10.2 provide results that indicate the slopes of the two lines are not significantly different. However, contrary to interval comparison, the ANCOVA analysis suggests that the intercepts are different. This discrepancy is likely due to two factors. First, the length distributions of the samples are not similar, an important consideration with interval comparison. Second, ANCOVA, which controls for length, and interval comparison ask slightly different questions—the latter asks whether the intercepts of two lines are different when the lines are allowed to float freely or have their own slopes, whereas the ANCOVA test asks whether the intercepts are different when lines are forced to have a common slope.